

Altered genes in CCM models with 2 validations enrichment data.

# enriched genes	category	description	enriched genes	FDR value	term name
28	GO Component	actin cytoskeleton	ARHGEF5 MYH9 CNN2 ADD1 FERMT3 TJP1 FLT1 CAPN2 SDPR ZYX SNCA TPM4 FYN MYO1C MYH10 TPM3 FLNA CNN3 SPTAN1 CLIC4 TPM2 FSCN1 MYO1B SEPT7 FLNB SPTBN2 CFL1 TLN2	6.94E-14	GO.0015629
130	GO Component	cytoplasmic part	RCN1 ARHGEF5 MAP2K5 PLOD1 MYH9 CYP24A1 MMP2 EHD4 APLP1 GAPDH RBP1 GNB4 PPP3R1 PLEK ENO1 MT2A CDC25B HSPB1 BCL2L2 PXDN ARF3 PDGFRA THBS1 COL8A1 VWF DNAJB6 CNN2 PRKCG NGEF TUBB4A ARHGAP31 CAD ADD1 EXOC68 FERMT3 TJP1 FLT1 PLOD2 APP KIT NPC1L1 CCRS5 CAPN2 ANXA5 ITGA2 NOS3 MELK CKB CCT2 PLK1 TUBA1A GLOD4 BCL2L1 CDC25A SDPR ARF4 MMP14 BRSK1 DAB2 NQO1 CALR CDC25C STXB6 ZYX FLNC PRKCH RARB CYP2R1 LCK SNCA CAV1 RG512 TUBB4B PTGES DOK4 PTMA TPM4 ANXA2 ANXA6 FYN FN1 FAS ARHGEF26 PTRF MYO1C MYH10 DPP4 TGM2 DLL1 ARHGAP30 COPA TPM3 GSTO1 SLK FLNA CNN3 PTPN1 SDC4 SPTAN1 DNM1 TLR4 CLIC4 ANXA1 TBC1D4 TPM2 PIR PSIP1 SDC1 FSCN1 XRCC5 MYO1B G6PD PPP3CA CAMK2B LDHB BCL2 CAMK2A SEPT7 PAICS CDC42 SUN1 PDIA6 TOP2B FLNB SPTBN2 CFL1 ARF1 VIM NUMB APBA2 PRKCSH MCM3	6.94E-14	GO.0044444
142	GO Component	cytoplasm	RCN1 ARHGEF5 MAP2K5 PLOD1 MYH9 CYP24A1 MMP2 EHD4 APLP1 GAPDH RBP1 GNB4 PPP3R1 PLEK ENO1 MT2A CDC25B HSPB1 BCL2L2 PXDN ARF3 PDGFRA THBS1 COL8A1 VWF DNAJB6 CNN2 PRKCG AKT3 NGEF TUBB4A ARHGAP31 CAD ADD1 EXOC68 FERMT3 TJP1 FLT1 PLOD2 APP KIT NPC1L1 CCRS5 CAPN2 ANXA5 ITGA2 NOS3 MELK CKB CCT2 PLK1 TUBA1A TUBA1C GLOD4 DDB1 BCL2L1 CDC25A SDPR ARF4 MMP14 BRSK1 DAB2 NQO1 CALR CDC25C STXB6 ZYX FLNC PRKCH RARB CYP2R1 LCK SNCA CAV1 RG512 TUBB4B PTGES MAP4K4 DOK4 PTMA TPM4 ANXA2 ANXA6 FYN FN1 FAS ARHGEF26 PTRF SFPQ MYO1C MYH10 DPP4 ARHGEF15 TGM2 DLL1 ARHGAP30 COPA TPM3 GSTO1 SLK FLNA CNN3 PTPN1 SDC4 SPTAN1 DNM1 TLR4 CLIC4 ANXA1 TBC1D4 TPM2 PIR PSIP1 SDC1 FSCN1 XRCC5 MYO1B G6PD PPP3CA CAMK2B LDHB BCL2 CAMK2A DYRK1A SEPT7 PAICS CDC42 SUN1 PDIA6 TOP2B WEE1 FLNB SPTBN2 CFL1 ARF1 VIM NUMB APBA2 TLN2 PRKCSH CAMK1D MCM3	1.28E-13	GO.0005737
88	GO Component	cytosol	ARHGEF5 MAP2K5 MYH9 GAPDH RBP1 GNB4 PPP3R1 PLEK ENO1 MT2A CDC25B HSPB1 BCL2L2 DNAJB6 PRKCG NGEF TUBB4A ARHGAP31 CAD ADD1 TJP1 APP CAPN2 ANXA5 NOS3 CKB CCT2 PLK1 TUBA1A BCL2L1 CDC25A SDPR ARF4 MMP14 DAB2 NQO1 CALR CDC25C ZYX FLNC PRKCH LCK SNCA RG512 TUBB4B DOK4 PTMA TPM4 ANXA2 FYN FAS ARHGEF26 PTRF MYO1C MYH10 TGM2 ARHGAP30 COPA TPM3 GSTO1 FLNA CNN3 PTPN1 SPTAN1 CLIC4 ANXA1 TBC1D4 TPM2 PIR PSIP1 FSCN1 XRCC5 G6PD PPP3CA CAMK2B LDHB BCL2 CAMK2A SEPT7 PAICS CDC42 PDIA6 TOP2B FLNB SPTBN2 CFL1 ARF1 VIM	1.72E-12	GO.0005829
52	GO Component	cytoskeleton	ARHGEF5 MAP2K5 MYH9 GAPDH CDC25B HSPB1 CNN2 TUBB4A ADD1 FERMT3 TJP1 FLT1 APP CAPN2 NOS3 CCT2 PLK1 TUBA1A TUBA1C BCL2L1 SDPR MMP14 BRSK1 ZYX FLNC NR112 LCK SNCA TUBB4B TPM4 FYN MYO1C MYH10 TPM3 FLNA CNN3 SPTAN1 DNM1 CLIC4 TPM2 FSCN1 MYO1B CAMK2B DYRK1A SEPT7 CDC42 FLNB SPTBN2 CFL1 VIM TLN2 MCM3	2.51E-11	GO.0005856
155	GO Component	intracellular	RCN1 ARHGEF5 MAP2K5 PLOD1 MYH9 CYP24A1 MMP2 EHD4 APLP1 CCL2 GAPDH RBP1 GNB4 PPP3R1 PLEK ENO1 MT2A CDC25B HSPB1 BCL2L2 PXDN ARF3 PDGFRA THBS1 COL8A1 VWF RORA DNAJB6 CNN2 PRKCG AKT3 NGEF TUBB4A ARHGAP31 CAD ADD1 EXOC68 FERMT3 TJP1 FLT1 PLOD2 APP CSF1R KIT NPC1L1 CCRS5 CAPN2 ANXA5 ITGA2 NOS3 MELK CKB CCT2 PLK1 TUBA1A TUBA1C GLOD4 DDB1 BCL2L1 CDC25A SDPR ARF4 MMP14 BRSK1 DAB2 TENC1 NQO1 CALR CDC25C STXB6 ZYX RORC FLNC PRKCH RARB CYP2R1 NR112 LCK SNCA CAV1 RG512 TUBB4B PTGES USP1 MAP4K4 DOK4 PTMA TPM4 ANXA2 ANXA6 FYN FN1 FAS ARHGEF26 PTRF SFPQ EPAH2 MYO1C RXRG MYH10 DPP4 ARHGEF15 TGM2 DLL1 ARHGAP30 COPA TPM3 GSTO1 SLK FLNA CNN3 PTPN1 SDC4 SPTAN1 DNM1 TLR4 CLIC4 RXRB ANXA1 TBC1D4 TPM2 PIR PSIP1 SDC1 FSCN1 XRCC5 MYO1B G6PD PPP3CA CAMK2B LDHB BCL2 CAMK2A DYRK1A SEPT7 PAICS CDC42 SUN1 PDIA6 RARG TOP2B WEE1 FLNB PBK SPTBN2 CFL1 ARF1 VIM NR1H4 NUMB APBA2 TLN2 PRKCSH CAMK1D MCM3	1.12E-10	GO.0005622
48	GO Component	cell projection	ARHGEF5 MYH9 PLEK HSPB1 PDGFRA PRKCG NGEF TUBB4A ARHGAP31 CAD FERMT3 TJP1 APP NPC1L1 CAPN2 ITGA2 CKB ARF4 BRSK1 NQO1 SNCA CAV1 RG512 ANXA2 FYN ARHGEF26 EPAH2 MYO1C MYH10 DPP4 ARHGEF15 FLNA CNN3 DNM1 CLIC4 ANXA1 FSCN1 MYO1B PPP3CA CAMK2B CAMK2A DYRK1A SEPT7 CDC42 CFL1 ARF1 VIM TLN2	6.20E-10	GO.0042995
152	GO Component	intracellular part	RCN1 ARHGEF5 MAP2K5 PLOD1 MYH9 CYP24A1 MMP2 EHD4 APLP1 GAPDH RBP1 GNB4 PPP3R1 PLEK ENO1 MT2A CDC25B HSPB1 BCL2L2 PXDN ARF3 PDGFRA THBS1 COL8A1 VWF RORA DNAJB6 CNN2 PRKCG AKT3 NGEF TUBB4A ARHGAP31 CAD ADD1 EXOC68 FERMT3 TJP1 FLT1 PLOD2 APP CSF1R KIT NPC1L1 CCRS5 CAPN2 ANXA5 ITGA2 NOS3 MELK CKB CCT2 PLK1 TUBA1A TUBA1C GLOD4 DDB1 BCL2L1 CDC25A SDPR ARF4 MMP14 BRSK1 DAB2 NQO1 CALR CDC25C STXB6 ZYX RORC FLNC PRKCH RARB CYP2R1 NR112 LCK SNCA CAV1 RG512 TUBB4B PTGES USP1 MAP4K4 DOK4 PTMA TPM4 ANXA2 ANXA6 FYN FN1 FAS ARHGEF26 PTRF SFPQ MYO1C RXRG MYH10 DPP4 ARHGEF15 TGM2 DLL1 ARHGAP30 COPA TPM3 GSTO1 SLK FLNA CNN3 PTPN1 SDC4 SPTAN1 DNM1 TLR4 CLIC4 RXRB ANXA1 TBC1D4 TPM2 PIR PSIP1 SDC1 FSCN1 XRCC5 MYO1B G6PD PPP3CA CAMK2B LDHB BCL2 CAMK2A DYRK1A SEPT7 PAICS CDC42 SUN1 PDIA6 RARG TOP2B WEE1 FLNB PBK SPTBN2 CFL1 ARF1 VIM NR1H4 NUMB APBA2 TLN2 PRKCSH CAMK1D MCM3	1.03E-09	GO.0044424
33	GO Component	cell junction	ARHGEF5 ITGB4 MYH9 PDGFRA CNN2 PRKCG ARHGAP31 ADD1 FERMT3 TJP1 APP KIT ITGA2 BCL2L1 BRSK1 TENC1 ZYX PRKCH SNCA RG512 CDH5 EPAH2 DPP4 DLL1 FLNA SDC4 CLIC4 FSCN1 PPP3CA CAMK2B CAMK2A SPTBN2 CFL1	1.26E-09	GO.0030054
41	GO Component	cytoskeletal part	ARHGEF5 MAP2K5 MYH9 CDC25B HSPB1 CNN2 TUBB4A ADD1 FERMT3 TJP1 APP CAPN2 CCT2 PLK1 TUBA1A TUBA1C BCL2L1 BRSK1 ZYX LCK TUBB4B TPM4 FYN MYO1C MYH10 TPM3 FLNA SPTAN1 DNM1 CLIC4 TPM2 FSCN1 MYO1B CAMK2B SEPT7 CDC42 FLNB SPTBN2 CFL1 VIM MCM3	1.88E-09	GO.0044430
84	GO Component	cell periphery	ARHGEF5 ITGB4 MYH9 CYP24A1 MMP2 EHD4 APLP1 GAPDH PPP3R1 PLEK ENO1 HSPB1 PDGFRA THBS1 PRKCG ADD1 ICAM1 EXOC68 TJP1 FLT1 APP CSF1R KIT NPC1L1 CCRS5 CAPN2 ANXA5 ITGA2 NOS3 MELK SDPR ARF4 MMP14 DAB2 TENC1 CALR STXB6 FLNC JAG2 PRKCH LCK SNCA CAV1 RG512 CDH5 ANXA2 FYN FN1 FAS PTRF EPAH2 MYO1C MYH10 DPP4 TGM2 DLL1 FLNA SDC4 SPTAN1 DNM1 TLR4 CLIC4 ANXA1 SDC1 FSCN1 XRCC5 MYO1B G6PD PPP3CA CAMK2B LTBR CAMK2A SEPT7 CDC42 PDIA6 FLNB SPTBN2 CFL1 ARF1 VIM NUMB APBA2 TLN2 ABC81	1.88E-09	GO.0071944

82	GO Component	plasma membrane	ARHGEF5 ITGB4 MYH9 CYP24A1 MMP2 EHD4 APLP1 GAPDH PPP3R1 PLEK ENO1 HSPB1 PDGFRA THBS1 PRKCG ADD1 ICAM1 TJP1 FLT1 APP CSF1R KIT NPC1L1 CCR5 CAPN2 ANXA5 ITGA2 NOS3 MELK SDPR ARF4 MMP14 DAB2 TENC1 CALR STXB6P FLNC JAG2 PRKCH LCK SNCA CAV1 RG512 CDH5 ANXA2 FYN FN1 FAS PTRF EPAH2 MYO1C MYH10 DPP4 TGM2 DLL1 FLNA SDC4 DNM1 TLR4 CLIC4 ANXA1 SDC1 FSCN1 XRCC5 MYO1B G6PD PPP3CA CAMK2B LTB4R CAMK2A SEPT7 CDC42 PDIA6 FLNB SPTBN2 CFL1 ARF1 VIM NUMB APBA2 TLN2 ABCB1	4.84E-09	GO.0005886
45	GO Component	plasma membrane bounded cell projection	MYH9 PLEK HSPB1 PDGFRA PRKCG NGEF TUBB4A ARHGAP31 CAD APP NPC1L1 CAPN2 ITGA2 CKB ARF4 BRSK1 NQO1 SNCA CAV1 RG512 ANXA2 FYN ARHGEF26 EPAH2 MYO1C MYH10 DPP4 ARHGEF15 FLNA CNN3 DNM1 CLIC4 ANXA1 FSCN1 MYO1B PPP3CA CAMK2B CAMK2A DYRK1A SEPT7 CDC42 CFL1 ARF1 VIM TLN2	4.84E-09	GO.0120025
18	GO Component	membrane raft	ICAM1 APP CAPN2 NOS3 TUBA1A SDPR LCK CAV1 ANXA2 FYN FAS PTRF MYO1C DPP4 DLL1 SDC4 LDHB LTB4R	6.24E-09	GO.0045121
16	GO Component	cell cortex	MYH9 ENO1 EXOC6B CAPN2 MELK STXB6P SNCA CAV1 ANXA2 MYH10 FLNA SPTAN1 SEPT7 FLNB SPTBN2 CFL1	7.82E-09	GO.0005938
69	GO Component	intracellular non-membrane-bounded organelle	ARHGEF5 MAP2K5 MYH9 MMP2 GAPDH RBP1 ENO1 CDC25B HSPB1 DNAJB6 CNN2 TUBB4A ADD1 FERMT3 TJP1 FLT1 APP CAPN2 NOS3 CCT2 PLK1 TUBA1A TUBA1C BCL2L1 SDPR MMP14 BRSK1 DAB2 ZYX FLNC NR12 LCK SNCA CAV1 RG512 TUBB4B TPM4 ANXA2 FYN SFPQ MYO1C MYH10 TPM3 FLNA CNN3 SDC4 SPTAN1 DNM1 CLIC4 TPM2 PSIP1 FSCN1 XRCC5 MYO1B PPP3CA CAMK2B DYRK1A SEPT7 CDC42 RARG TOP2B WEE1 FLNB SPTBN2 CFL1 VIM NR1H4 TLN2 MCM3	1.01E-08	GO.0043232
161	GO Component	cell part	RCN1 ARHGEF5 MAP2K5 PLOC1 ITGB4 MYH9 CYP24A1 MMP2 EHD4 APLP1 CCL2 GAPDH RBP1 GNB4 PPP3R1 PLEK ENO1 MT2A CDC25B HSPB1 BCL2L2 PXD1 ARF3 PDGFRA THBS1 COL8A1 VWF RORA DNAJB6 CNN2 PRKCG AKT3 NGEF TUBB4A ARHGAP31 CAD ADD1 ICAM1 EXOC6B FERMT3 TJP1 FLT1 PLOC2 APP CSF1R KIT NPC1L1 CCR5 CAPN2 ANXA5 ITGA2 NOS3 MELK CKB CCT2 PLK1 TUBA1A TUBA1C GLOD4 DDB1 BCL2L1 CDC25A SDPR ARF4 MMP14 BRSK1 DAB2 TENC1 NQO1 CALR CDC25C STXB6P ZYX RORC FLNC JAG2 PRKCH RARB CYP2R1 NR12 LCK SNCA CAV1 RG512 TUBB4B PTGES USP1 MAP4K4 CDH5 DOK4 PTMA TPM4 ANXA2 ANXA6 FYN FN1 FAS ARHGEF26 PTRF SFPQ EPAH2 MYO1C RXRG MYH10 DPP4 ARHGEF15 TGM2 DLL1 ARHGAP30 COPA TPM3 GSTO1 SLK FLNA CNN3 PTPN1 SDC4 SPTAN1 DNM1 TLR4 CLIC4 RXRB ANXA1 TBC1D4 TPM2 PIR PSIP1 SDC1 FSCN1 XRCC5 MYO1B G6PD PPP3CA CAMK2B LDHB LTB4R BCL2 CAMK2A DYRK1A SEPT7 PAI1 CDC42 SUN1 PDIA6 RARG TOP2B WEE1 FLNB PBK SPTBN2 CFL1 ARF1 VIM NR1H4 NUMB APBA2 TLN2 PRKCSH ABCB1 CAMK1D MCM3	1.06E-08	GO.0044464
49	GO Component	vesicle	EHD4 THBS1 VWF CNN2 ICAM1 FERMT3 FLT1 APP KIT NPC1L1 CCR5 NOS3 CCT2 TUBA1A BCL2L1 MMP14 BRSK1 DAB2 CALR ZYX SNCA CAV1 TUBB4B ANXA2 ANXA6 FYN FN1 MYO1C DPP4 DLL1 ARHGAP30 COPA PTPN1 SPTAN1 DNM1 TLR4 CLIC4 ANXA1 TBC1D4 XRCC5 MYO1B CAMK2B CAMK2A SUN1 PDIA6 FLNB VIM NUMB APBA2	1.53E-08	GO.0031982
25	GO Component	perinuclear region of cytoplasm	EHD4 APLP1 GAPDH MT2A ARF3 DNAJB6 PRKCG APP CAPN2 ITGA2 CALR CDC25C SNCA CAV1 PTGES ANXA2 ANXA6 FYN SLK FLNA TLR4 CLIC4 MYO1B ARF1 MCM3	1.53E-08	GO.0048471
9	GO Component	stress fiber	MYH9 CNN2 ZYX TPM4 MYH10 TPM3 FSCN1 SEPT7 FLNB	2.79E-08	GO.0001725
47	GO Component	cytoplasmic vesicle	EHD4 THBS1 VWF CNN2 FERMT3 FLT1 APP KIT NPC1L1 CCR5 NOS3 CCT2 TUBA1A BCL2L1 MMP14 BRSK1 DAB2 CALR ZYX SNCA CAV1 TUBB4B ANXA2 ANXA6 FYN FN1 MYO1C DPP4 DLL1 ARHGAP30 COPA PTPN1 SPTAN1 DNM1 TLR4 CLIC4 ANXA1 XRCC5 MYO1B CAMK2B CAMK2A SUN1 PDIA6 FLNB VIM NUMB APBA2	3.45E-08	GO.0031410
18	GO Component	cell leading edge	ITGB4 MYH9 PLEK ARHGAP31 APP ARF4 ANXA2 ARHGEF26 EPAH2 MYO1C MYH10 DPP4 SLK FSCN1 CFL1 ARF1 VIM TLN2	7.49E-08	GO.0031252
18	GO Component	cytoplasmic region	MYH9 ENO1 HSPB1 TUBB4A EXOC6B CAPN2 MELK STXB6P SNCA CAV1 ANXA2 MYH10 FLNA SPTAN1 SEPT7 FLNB SPTBN2 CFL1	2.30E-07	GO.0099568
50	GO Component	plasma membrane part	ITGB4 MYH9 PLEK PDGFRA THBS1 PRKCG ICAM1 TJP1 FLT1 APP CSF1R KIT NPC1L1 CCR5 ANXA5 ITGA2 NOS3 SDPR ARF4 MMP14 CALR JAG2 LCK CAV1 CDH5 ANXA2 FYN FN1 FAS PTRF EPAH2 MYO1C MYH10 DPP4 TGM2 DLL1 SDC4 TLR4 ANXA1 SDC1 FSCN1 G6PD LTB4R CAMK2A SEPT7 SPTBN2 CFL1 ARF1 NUMB ABCB1	2.95E-07	GO.0044459
23	GO Component	cell surface	ITGB4 ENO1 PDGFRA THBS1 ICAM1 APP CSF1R KIT CCR5 ANXA5 ITGA2 CALR CDH5 ANXA2 FAS EPAH2 DPP4 SDC4 TLR4 CLIC4 ANXA1 SDC1 ABCB1	4.01E-07	GO.0009986
29	GO Component	neuron projection	HSPB1 PRKCG NGEF TUBB4A CAD APP CAPN2 ITGA2 CKB ARF4 BRSK1 NQO1 SNCA RG512 FYN MYO1C MYH10 ARHGEF15 FLNA CNN3 DNM1 FSCN1 PPP3CA CAMK2B CAMK2A DYRK1A CDC42 ARF1 VIM	1.67E-06	GO.0043005
135	GO Component	organelle	RCN1 ARHGEF5 MAP2K5 PLOC1 MYH9 CYP24A1 MMP2 EHD4 GAPDH RBP1 PPP3R1 ENO1 MT2A CDC25B HSPB1 BCL2L2 PXD1 ARF3 PDGFRA THBS1 COL8A1 VWF RORA DNAJB6 CNN2 PRKCG AKT3 TUBB4A CAD ADD1 ICAM1 FERMT3 TJP1 FLT1 PLOC2 APP CSF1R KIT NPC1L1 CCR5 CAPN2 ITGA2 NOS3 MELK CKB CCT2 PLK1 TUBA1A TUBA1C GLOD4 DDB1 BCL2L1 CDC25A SDPR ARF4 MMP14 BRSK1 DAB2 CALR CDC25C ZYX RORC FLNC RARB CYP2R1 NR12 LCK SNCA CAV1 RG512 TUBB4B PTGES USP1 PTMA TPM4 ANXA2 ANXA6 FYN FN1 FAS PTRF SFPQ MYO1C RXRG MYH10 DPP4 TGM2 DLL1 ARHGAP30 COPA TPM3 FLNA CNN3 PTPN1 SDC4 SPTAN1 DNM1 TLR4 CLIC4 RXRB ANXA1 TBC1D4 TPM2 PIR PSIP1 SDC1 FSCN1 XRCC5 MYO1B G6PD PPP3CA CAMK2B BCL2 CAMK2A DYRK1A SEPT7 CDC42 SUN1 PDIA6 RARG TOP2B WEE1 FLNB PBK SPTBN2 CFL1 ARF1 VIM NR1H4 NUMB APBA2 TLN2 PRKCSH CAMK1D MCM3	1.75E-06	GO.0043226
25	GO Component	supramolecular polymer	MMP2 ENO1 HSPB1 COL8A1 DNAJB6 TUBB4A CCT2 TUBA1A TUBA1C FLNC SNCA TUBB4B TPM4 FYN MYO1C TPM3 FLNA SDC4 DNM1 TPM2 FSCN1 MYO1B PPP3CA FLNB VIM	1.75E-06	GO.0099081
10	GO Component	cell cortex part	MYH9 ENO1 EXOC6B CAPN2 STXB6P FLNA SPTAN1 SEPT7 SPTBN2 CFL1	1.78E-06	GO.0044448
11	GO Component	myelin sheath	GNB4 TUBB4A CKB CCT2 TUBA1A TUBB4B ANXA2 DNM1 FSCN1 LDHB BCL2	2.11E-06	GO.0043209
133	GO Component	intracellular organelle	RCN1 ARHGEF5 MAP2K5 PLOC1 MYH9 CYP24A1 MMP2 EHD4 GAPDH RBP1 PPP3R1 ENO1 MT2A CDC25B HSPB1 BCL2L2 PXD1 ARF3 PDGFRA THBS1 COL8A1 VWF RORA DNAJB6 CNN2 PRKCG AKT3 TUBB4A CAD ADD1 FERMT3 TJP1 FLT1 PLOC2 APP CSF1R KIT NPC1L1 CCR5 CAPN2 ITGA2 NOS3 MELK CKB CCT2 PLK1 TUBA1A TUBA1C GLOD4 DDB1 BCL2L1 CDC25A SDPR ARF4 MMP14 BRSK1 DAB2 CALR CDC25C ZYX RORC FLNC RARB CYP2R1 NR12 LCK SNCA CAV1 RG512 TUBB4B PTGES USP1 PTMA TPM4 ANXA2 ANXA6 FYN FN1 FAS PTRF SFPQ MYO1C RXRG MYH10 DPP4 TGM2 DLL1 ARHGAP30 COPA TPM3 FLNA CNN3 PTPN1 SDC4 SPTAN1 DNM1 TLR4 CLIC4 RXRB ANXA1 TBC1D4 TPM2 PIR PSIP1 SDC1 FSCN1 XRCC5 MYO1B G6PD PPP3CA CAMK2B BCL2 CAMK2A DYRK1A SEPT7 CDC42 SUN1 PDIA6 RARG TOP2B WEE1 FLNB PBK SPTBN2 CFL1 ARF1 VIM NR1H4 NUMB APBA2 TLN2 PRKCSH CAMK1D MCM3	2.11E-06	GO.0043229
8	GO Component	actin filament	TPM4 FYN MYO1C TPM3 FLNA TPM2 FSCN1 MYO1B	2.41E-06	GO.0005884
31	GO Component	plasma membrane bounded cell projection part	PLEK HSPB1 PRKCG NGEF TUBB4A CAD APP NPC1L1 CAPN2 ITGA2 CKB ARF4 BRSK1 NQO1 SNCA RG512 FYN EPAH2 MYO1C MYH10 DPP4 ARHGEF15 FLNA CNN3 DNM1 FSCN1 PPP3CA DYRK1A SEPT7 CDC42 CFL1	2.41E-06	GO.0120038

109	GO Component	organelle part	RCN1 ARHGEF5 MAP2K5 PLOC1 MYH9 CYP24A1 MMP2 EHD4 GAPDH RBP1 PPP3R1 ENO1 CDC25B HSPB1 BCL2L2 ARF3 THBS1 COL8A1 VWF RORA DNAJB6 CNN2 TUBB4A CAD ADD1 FERMT3 TJP1 PLOC2 APP CSF1R NPC1L1 CAPN2 NOS3 CCT2 PLK1 TUBA1A TUBA1C DD1 BCL2L1 CDC25A SDPR MMP14 BRSK1 DAB2 CALR CDC25C ZYX RORC RARB CYP2R1 NR1I2 LCK SNCA CAV1 RG512 TUBB4B PTGES USP1 PTMA TPM4 ANXA2 ANXA6 FYN FN1 FAS PTRF SFPQ MYO1C RXRG MYH10 COPA TPM3 FLNA PTPN1 SDC4 SPTAN1 DNM1 TLR4 CLIC4 RXRB ANXA1 TPM2 PIR PSIP1 SDC1 FSCN1 XRC5 MYO1B PPP3CA CAMK2B BCL2 CAMK2A DYRK1A SEPT7 CDC42 SUN1 PDIA6 RARG TOP2B WEE1 FLNB SPTBN2 CFL1 ARF1 VIM NR1H4 PRKCSH MCM3	2.82E-06	GO.0044422
34	GO Component	whole membrane	CYP24A1 EHD4 BCL2L2 ICAM1 APP CAPN2 NOS3 TUBA1A BCL2L1 SDPR DAB2 CALR LCK SNCA CAV1 ANXA2 ANXA6 FYN FAS PTRF MYO1C DPP4 DLL1 COPA SDC4 TLR4 ANXA1 MYO1B CAMK2B LDHB LTB4R BCL2 CAMK2A SUN1	2.82E-06	GO.0098805
12	GO Component	contractile fiber part	MMP2 ENO1 HSPB1 DNAJB6 FLNC TPM4 TPM3 FLNA SDC4 TPM2 PPP3CA FLNB	4.28E-06	GO.0044449
24	GO Component	supramolecular fiber	MMP2 ENO1 HSPB1 DNAJB6 TUBB4A CCT2 TUBA1A TUBA1C FLNC SNCA TUBB4B TPM4 FYN MYO1C TPM3 FLNA SDC4 DNM1 TPM2 FSCN1 MYO1B PPP3CA FLNB VIM	4.39E-06	GO.0099512
16	GO Component	cell-cell junction	MYH9 CNN2 PRKCG ADD1 TJP1 APP KIT ZYX PRKCH CDH5 DPP4 FLNA CLIC4 FSCN1 PPP3CA CFL1	4.54E-06	GO.0005911
12	GO Component	myofibril	MMP2 ENO1 HSPB1 DNAJB6 FLNC TPM4 TPM3 FLNA SDC4 TPM2 PPP3CA FLNB	4.85E-06	GO.0030016
32	GO Component	neuron part	HSPB1 PRKCG NGEF TUBB4A CAD APP CAPN2 ITGA2 CKB BCL2L1 ARF4 BRSK1 NQO1 SNCA RG512 FYN MYO1C MYH10 ARHGEF15 FLNA CNN3 DNM1 FSCN1 PPP3CA CAMK2B CAMK2A DYRK1A SEPT7 CDC42 SUN1 PDIA6 RARG TOP2B WEE1 FLNB SPTBN2 CFL1 ARF1 VIM APBA2	4.96E-06	GO.0097458
106	GO Component	intracellular organelle part	RCN1 ARHGEF5 MAP2K5 PLOC1 MYH9 CYP24A1 EHD4 GAPDH RBP1 PPP3R1 CDC25B HSPB1 BCL2L2 ARF3 THBS1 COL8A1 VWF RORA DNAJB6 CNN2 TUBB4A CAD ADD1 FERMT3 TJP1 PLOC2 APP CSF1R NPC1L1 CAPN2 NOS3 CCT2 PLK1 TUBA1A TUBA1C DD1 BCL2L1 CDC25A SDPR MMP14 BRSK1 DAB2 CALR CDC25C ZYX RORC RARB CYP2R1 NR1I2 LCK SNCA CAV1 RG512 TUBB4B PTGES USP1 PTMA TPM4 ANXA2 ANXA6 FYN FN1 FAS PTRF SFPQ MYO1C RXRG MYH10 COPA TPM3 FLNA PTPN1 SDC4 SPTAN1 DNM1 TLR4 CLIC4 RXRB ANXA1 TPM2 PIR PSIP1 SDC1 FSCN1 XRC5 MYO1B PPP3CA CAMK2B BCL2 CAMK2A DYRK1A SEPT7 CDC42 SUN1 PDIA6 RARG TOP2B WEE1 FLNB SPTBN2 CFL1 ARF1 VIM NR1H4 PRKCSH MCM3	6.03E-06	GO.0044446
12	GO Component	external side of plasma membrane	PDGFRA THBS1 ICAM1 KIT CCR5 ANXA5 ITGA2 CALR CDH5 TLR4 ANXA1 SDC1	6.30E-06	GO.0009897
26	GO Component	plasma membrane region	MYH9 PLEK PRKCG TJP1 NPC1L1 NOS3 SDPR ARF4 CAV1 ANXA2 FN1 PTRF EPHA2 MYO1C MYH10 DPP4 DLL1 ANXA1 FSCN1 CAMK2A SEPT7 SPTBN2 CFL1 ARF1 NUMB ABCB1	1.00E-05	GO.0098590
16	GO Component	side of membrane	PDGFRA THBS1 ICAM1 KIT CCR5 ANXA5 ITGA2 CALR LCK CDH5 FYN PTPN1 TLR4 ANXA1 SDC1 G6PD	1.11E-05	GO.0098552
11	GO Component	sarcomere	MMP2 ENO1 HSPB1 DNAJB6 FLNC TPM4 TPM3 FLNA TPM2 PPP3CA FLNB	1.12E-05	GO.0030017
10	GO Component	ruffle	MYH9 PLEK ARF4 ANXA2 ARHGEF26 EPHA2 MYO1C FSCN1 CFL1 TLN2	1.76E-05	GO.0001726
123	GO Component	membrane-bounded organelle	RCN1 ARHGEF5 MAP2K5 PLOC1 MYH9 CYP24A1 MMP2 EHD4 GAPDH RBP1 PPP3R1 ENO1 MT2A CDC25B HSPB1 BCL2L2 PXD1 ARF3 PDGFRA THBS1 COL8A1 VWF RORA DNAJB6 CNN2 PRKCG AKT3 CAD ADD1 ICAM1 FERMT3 FLT1 PLOC2 APP CSF1R KIT NPC1L1 CCR5 CAPN2 ITGA2 NOS3 MELK CKB CCT2 PLK1 TUBA1A TUBA1C GLOD4 DD1 BCL2L1 CDC25A SDPR ARF4 MMP14 BRSK1 DAB2 CALR CDC25C ZYX RORC RARB CYP2R1 NR1I2 SNCA CAV1 RG512 TUBB4B PTGES USP1 PTMA ANXA2 ANXA6 FYN FN1 FAS PTRF SFPQ MYO1C RXRG DPP4 TGM2 DLL1 ARHGAP30 COPA FLNA PTPN1 SDC4 SPTAN1 DNM1 TLR4 CLIC4 RXRB ANXA1 TBC1D4 PIR PSIP1 SDC1 XRC5 MYO1B G6PD PPP3CA CAMK2B BCL2 CAMK2A DYRK1A SEPT7 CDC42 SUN1 PDIA6 RARG TOP2B WEE1 FLNB PBK CFL1 ARF1 VIM NR1H4 NUMB APBA2 PRKCSH CAMK1D MCM3	2.08E-05	GO.0043227
100	GO Component	membrane	ARHGEF5 PLOC1 ITGB4 MYH9 CYP24A1 MMP2 EHD4 APLP1 GAPDH PPP3R1 PLEK ENO1 HSPB1 BCL2L2 ARF3 PDGFRA THBS1 PRKCG AKT3 NGEF ADD1 ICAM1 TJP1 FLT1 PLOC2 APP CSF1R KIT NPC1L1 CCR5 CAPN2 ANXA5 ITGA2 NOS3 MELK TUBA1A BCL2L1 SDPR ARF4 MMP14 DAB2 TENC1 CALR STXB6 FLNC JAG2 PRKCH CYP2R1 LCK SNCA CAV1 RG512 PTGES CDH5 ANXA2 ANXA6 FYN FN1 FAS PTRF EPHA2 MYO1C MYH10 DPP4 TGM2 DLL1 COPA FLNA PTPN1 SDC4 SPTAN1 DNM1 TLR4 CLIC4 ANXA1 SDC1 FSCN1 XRC5 MYO1B G6PD PPP3CA CAMK2B LDHB LTB4R BCL2 CAMK2A SEPT7 CDC42 SUN1 PDIA6 RARG FLNB SPTBN2 CFL1 ARF1 VIM NUMB APBA2 TLN2 ABCB1	2.68E-05	GO.0016020
22	GO Component	synapse	MYH9 LAMA5 PRKCG CAD APP ITGA2 BCL2L1 ARF4 BRSK1 SNCA RG512 FYN MYH10 CNN3 DNM1 PPP3CA CAMK2B CAMK2A CDC42 ARF1 APBA2 TLN2	2.80E-05	GO.0045202
12	GO Component	extracellular matrix	APLP1 LAMA4 PXD1 LAMA5 THBS1 COL8A1 VWF MMP14 CALR ANXA2 FN1 MMRN2	5.69E-05	GO.0031012
69	GO Component	intracellular organelle lumen	RCN1 ARHGEF5 CYP24A1 RBP1 PPP3R1 CDC25B THBS1 COL8A1 VWF RORA DNAJB6 CNN2 CAD ADD1 FERMT3 APP CSF1R CCT2 PLK1 DD1 BCL2L1 CDC25A SDPR MMP14 BRSK1 DAB2 CALR CDC25C RORC RARB NR1I2 SNCA RG512 TUBB4B PTGES USP1 PTMA ANXA2 FN1 FAS PTRF SFPQ MYO1C RXRG FLNA SDC4 SPTAN1 DNM1 CLIC4 RXRB ANXA1 PIR PSIP1 SDC1 XRC5 PPP3CA CAMK2B BCL2 CAMK2A DYRK1A PDIA6 RARG TOP2B WEE1 CFL1 VIM NR1H4 PRKCSH MCM3	8.54E-05	GO.0070013
29	GO Component	cytoplasmic vesicle part	EHD4 THBS1 VWF CNN2 FERMT3 APP NPC1L1 NOS3 CCT2 BCL2L1 DAB2 CALR SNCA CAV1 TUBB4B ANXA2 ANXA6 FN1 MYO1C COPA SPTAN1 TLR4 CLIC4 ANXA1 XRC5 MYO1B CAMK2B CAMK2A SUN1	9.14E-05	GO.0044433
11	GO Component	adherens junction	MYH9 ARHGAP31 ADD1 TJP1 ITGA2 TENC1 ZYX CDH5 EPHA2 DLL1 SDC4	9.90E-05	GO.0005912
19	GO Component	somatodendritic compartment	PRKCG TUBB4A CAD APP CAPN2 CKB ARF4 NQO1 SNCA RG512 FYN MYH10 ARHGEF15 FLNA CNN3 PPP3CA DYRK1A CDC42 SPTBN2	1.20E-04	GO.0036477
7	GO Component	basement membrane	APLP1 LAMA4 LAMA5 COL8A1 ANXA2 FN1 MMRN2	1.30E-04	GO.0005604
3	GO Component	muscle thin filament tropomyosin	TPM4 TPM3 TPM2	1.40E-04	GO.0005862
13	GO Component	apical part of cell	TJP1 APP NPC1L1 CAV1 FN1 DPP4 DLL1 CLIC4 ANXA1 MYO1B SPTBN2 NUMB ABCB1	1.40E-04	GO.0045177
18	GO Component	synapse part	LAMA5 PRKCG CAD APP ITGA2 BCL2L1 ARF4 BRSK1 SNCA FYN MYH10 CNN3 DNM1 PPP3CA CAMK2A CDC42 ARF1 APBA2	2.40E-04	GO.0044456
12	GO Component	cytoplasmic vesicle lumen	THBS1 VWF CNN2 FERMT3 APP CCT2 CALR TUBB4B ANXA2 FN1 SPTAN1 XRC5	2.70E-04	GO.0060205
8	GO Component	cell-substrate junction	ITGB4 MYH9 ARHGAP31 ITGA2 TENC1 ZYX EPHA2 SDC4	2.80E-04	GO.0030055
15	GO Component	dendrite	PRKCG APP CAPN2 CKB ARF4 NQO1 RG512 FYN MYH10 ARHGEF15 FLNA CNN3 PPP3CA DYRK1A CDC42	3.50E-04	GO.0030425
6	GO Component	cortical cytoskeleton	MYH9 CAPN2 FLNA SPTAN1 SPTBN2 CFL1	4.30E-04	GO.0030863
23	GO Component	microtubule cytoskeleton	MAP2K5 MYH9 GAPDH CDC25B HSPB1 TUBB4A APP CCT2 PLK1 TUBA1A TUBA1C BCL2L1 BRSK1 LCK TUBB4B MYH10 SPTAN1 DNM1 CLIC4 CAMK2B SEPT7 CDC42 MCM3	4.60E-04	GO.0015630
58	GO Component	endomembrane system	RCN1 PLOC1 EHD4 GAPDH PXD1 ARF3 THBS1 COL8A1 VWF CNN2 FERMT3 FLT1 PLOC2 APP KIT CCR5 CAPN2 NOS3 CCT2 TUBA1A BCL2L1 ARF4 MMP14 BRSK1 DAB2 CALR CYP2R1 SNCA CAV1 TUBB4B PTGES ANXA2 ANXA6 FYN FN1 PTRF MYO1C TGM2 COPA PTPN1 SDC4 SPTAN1 DNM1 TLR4 ANXA1 TBC1D4 SDC1 XRC5 MYO1B CAMK2B BCL2 CDC42 SUN1 PDIA6 ARF1 NUMB APBA2 PRKCSH	5.70E-04	GO.0012505
11	GO Component	secretory granule lumen	THBS1 VWF CNN2 FERMT3 APP CCT2 TUBB4B ANXA2 FN1 SPTAN1 XRC5	7.10E-04	GO.0034774

5	GO Component	cortical actin cytoskeleton	MYH9 CAPN2 SPTAN1 SPTBN2 CFL1	7.30E-04	GO.0030864
10	GO Component	endocytic vesicle	NOS3 CALR ZYX CAV1 MYO1C DPP4 CAMK2B CAMK2A FLNB VIM	8.50E-04	GO.0030139
20	GO Component	secretory vesicle	THBS1 VWF CNN2 FERMT3 APP KIT CCT2 BCL2L1 BRSK1 CALR SNCA CAV1 TUBB4B ANXA2 FN1 SPTAN1 DNM1 XRCC5 SUN1 APBA2	9.60E-04	GO.0099503
4	GO Component	podosome	ARHGEF5 FERMT3 TJP1 FSCN1	0.001	GO.0002102
7	GO Component	focal adhesion	MYH9 ARHGAP31 ITGA2 TENC1 ZYX EPHA2 SDC4	0.001	GO.0005925
11	GO Component	axon part	HSPB1 NGEF TUBB4A CAD APP ITGA2 BRSK1 SNCA MYH10 DNM1 FSCN1	0.001	GO.0033267
7	GO Component	nuclear periphery	CAD RG512 SFPQ CLIC4 PSIP1 CFL1 VIM	0.001	GO.0034399
6	GO Component	brush border	MYH9 NPC1L1 MYO1C MYH10 MYO1B FLNB	0.0012	GO.0005903
61	GO Component	protein-containing complex	ARHGEF5 PLOD1 ITGB4 MYH9 GAPDH PPP3R1 ENO1 HSPB1 BCL2L2 LAMA5 PDGFRA THBS1 COL8A1 CAD ADD1 EXOC68 FERMT3 TJP1 FLT1 APP CSF1R ITGA2 CCT2 PLK1 TUBA1A DDB1 BCL2L1 CALR STXB6 SNCA CAV1 ANXA2 FN1 FAS PTRF SFPQ MYO1C MYH10 COPA FLNA DNM1 TLR4 CLIC4 ANXA1 SDC1 FSCN1 XRCC5 MYO1B PPP3CA BCL2 DYRK1A SEPT7 CDC42 SUN1 PDIA6 RARG TOP2B ARF1 VIM PRKCSH MCM3	0.0012	GO.0032991
109	GO Component	intracellular membrane-bounded organelle	RCN1 ARHGEF5 MAP2K5 PLOD1 MYH9 CYP24A1 MMP2 EHD4 GAPDH RBP1 PPP3R1 ENO1 MT2A CDC25B HSPB1 BCL2L2 PXDN ARF3 PDGFRA THBS1 COL8A1 VWF RORA DNAJB6 PRKCG AKT3 CAD ADD1 PLOD2 APP CSF1R KIT CAPN2 ITGA2 NOS3 MELK CKB CCT2 PLK1 TUBA1C GLOD4 DDB1 BCL2L1 CDC25A SDPR ARF4 MMP14 BRSK1 DAB2 CALR CDC25C ZYX RORC RARB CYP2R1 NR1I2 SNCA CAV1 RG512 TUBB4B PTGES USP1 PTMA ANXA2 ANXA6 FYN PTN1 FAS PTRF SFPQ MYO1C RXRG TGM2 ARHGAP30 COPA FLNA PTPN1 SDC4 SPTAN1 DNM1 CLIC4 RXRB ANXA1 PIR PSIP1 SDC1 XRCC5 G6PD PPP3CA CAMK2B BCL2 CAMK2A DYRK1A SEPT7 CDC42 SUN1 PDIA6 RARG TOP2B WEE1 PBK CFL1 ARF1 VIM NR1H4 NUMB PRKCSH CAMK1D MCM3	0.0018	GO.0043231
6	GO Component	nuclear matrix	CAD RG512 SFPQ CLIC4 CFL1 VIM	0.0019	GO.0016363
5	GO Component	platelet alpha granule lumen	THBS1 VWF FERMT3 APP FN1	0.0019	GO.0031093
15	GO Component	polymeric cytoskeletal fiber	TUBB4A CCT2 TUBA1A TUBA1C TUBB4B TPM4 FYN MYO1C TPM3 FLNA DNM1 TPM2 FSCN1 MYO1B VIM	0.0022	GO.0099513
79	GO Component	nucleus	ARHGEF5 MAP2K5 MYH9 CYP24A1 MMP2 EHD4 GAPDH RBP1 PPP3R1 ENO1 MT2A CDC25B HSPB1 PDGFRA RORA DNAJB6 PRKCG AKT3 CAD ADD1 APP CSF1R CAPN2 ITGA2 NOS3 MELK CKB PLK1 TUBA1C DDB1 BCL2L1 CDC25A SDPR MMP14 BRSK1 DAB2 CALR CDC25C ZYX RORC RARB NR1I2 SNCA RG512 PTGES USP1 PTMA FYN FAS PTRF SFPQ MYO1C RXRG FLNA DNM1 CLIC4 RXRB ANXA1 PIR PSIP1 XRCC5 G6PD PPP3CA CAMK2B BCL2 CAMK2A DYRK1A SEPT7 SUN1 RARG TOP2B WEE1 PBK CFL1 VIM NR1H4 NUMB CAMK1D MCM3	0.0024	GO.0005634
5	GO Component	cell-cell adherens junction	MYH9 ADD1 TJP1 ZYX CDH5	0.0024	GO.0005913
24	GO Component	extracellular region part	MMP2 APLP1 CCL2 LAMA4 PXDN LAMA5 THBS1 COL8A1 VWF ICAM1 FLT1 APP KIT ANXA5 CKB MMP14 CALR SNCA ANXA2 FN1 COPA MMRN2 ANXA1 PDIA6	0.0028	GO.0044421
55	GO Component	nuclear part	ARHGEF5 CYP24A1 GAPDH RBP1 PPP3R1 CDC25B RORA DNAJB6 CAD ADD1 APP CSF1R PLK1 DDB1 BCL2L1 CDC25A SDPR BRSK1 DAB2 CALR CDC25C RORC RARB NR1I2 SNCA RG512 PTGES USP1 PTMA FAS PTRF SFPQ MYO1C RXRG FLNA DNM1 CLIC4 RXRB ANXA1 PIR PSIP1 XRCC5 G6PD PPP3CA CAMK2B BCL2 CAMK2A DYRK1A SUN1 RARG TOP2B WEE1 CFL1 VIM NR1H4 MCM3	0.0033	GO.0044428
2	GO Component	myosin II filament	MYH9 MYH10	0.0034	GO.0097513
6	GO Component	Z disc	HSPB1 DNAJB6 FLNC FLNA PPP3CA FLNB	0.0035	GO.0030018
36	GO Component	extracellular region	MMP2 APLP1 CCL2 LAMA4 PLEK PXDN LAMA5 THBS1 COL8A1 VWF CNN2 ICAM1 FERMT3 FLT1 APP KIT ANXA5 CKB CCT2 MMP14 CALR SNCA TUBB4B ANXA2 FN1 FAS DPP4 DL1 COPA FLNA MMRN2 SDC4 SPTAN1 ANXA1 XRCC5 PDIA6	0.0041	GO.0005576
2	GO Component	calcineurin complex	PPP3R1 PPP3CA	0.0049	GO.0005955
5	GO Component	ruffle membrane	PLEK ARF4 EPHA2 MYO1C CFL1	0.0049	GO.0032587
7	GO Component	lamellipodium	ARHGAP31 APP EPHA2 MYH10 DPP4 FSCN1 CFL1	0.0054	GO.0030027
3	GO Component	lamellipodium membrane	EPHA2 DPP4 CFL1	0.0054	GO.0031258
11	GO Component	postsynapse	PRKCG APP ARF4 SNCA FYN MYH10 CNN3 PPP3CA CAMK2A CDC42 ARF1	0.0058	GO.0098794
2	GO Component	macropinosome	MMP14 ANXA2	0.0063	GO.0044354
7	GO Component	actin-based cell projection	PDGFRA APP MYO1C CLIC4 FSCN1 MYO1B CDC42	0.0063	GO.0098858
8	GO Component	distal axon	NGEF CAD APP ITGA2 BRSK1 SNCA MYH10 FSCN1	0.0063	GO.0150034
20	GO Component	extracellular space	MMP2 CCL2 PXDN LAMA5 THBS1 ICAM1 FLT1 APP KIT ANXA5 CKB MMP14 CALR SNCA ANXA2 FN1 COPA MMRN2 ANXA1 PDIA6	0.0064	GO.0005615
6	GO Component	dendritic spine	APP ARF4 MYH10 CNN3 PPP3CA CDC42	0.0067	GO.0043197
9	GO Component	spindle	MAP2K5 MYH9 CDC25B HSPB1 APP PLK1 MYH10 SEPT7 CDC42	0.0076	GO.0005819
12	GO Component	cell body	TUBB4A CAD CKB CCT2 NQO1 SNCA FYN MYH10 FLNA CNN3 CDC42 SPTBN2	0.0076	GO.0044297
4	GO Component	extracellular matrix component	LAMA4 LAMA5 COL8A1 FN1	0.0076	GO.0044420
73	GO Component	membrane part	PLOD1 ITGB4 MYH9 APLP1 PLEK PDGFRA THBS1 PRKCG ICAM1 TJP1 FLT1 PLOD2 APP CSF1R KIT NPC1L1 CCR5 CAPN2 ANXA5 ITGA2 NOS3 TUBA1A BCL2L1 SDPR ARF4 MMP14 DAB2 CALR STXB6 JAG2 CYP2R1 LCK SNCA CAV1 PTGES CDH5 ANXA2 FYN FN1 FAS PTRF EPHA2 MYO1C MYH10 DPP4 TGM2 DLL1 COPA PTPN1 SDC4 DNM1 TLR4 CLIC4 ANXA1 SDC1 FSCN1 G6PD CAMK2B LDHB LTB4R BCL2 CAMK2A SEPT7 CDC42 SUN1 PDIA6 RARG FLNB SPTBN2 CFL1 ARF1 NUMB ABCB1	0.0077	GO.0044425
12	GO Component	axon	HSPB1 NGEF TUBB4A CAD APP ITGA2 BRSK1 SNCA MYH10 DNM1 FSCN1 DYRK1A	0.0078	GO.0030424
6	GO Component	leading edge membrane	PLEK ARF4 EPHA2 MYO1C DPP4 CFL1	0.0078	GO.0031256
27	GO Component	endoplasmic reticulum	RCN1 PLOD1 EHD4 PXDN THBS1 COL8A1 VWF PLOD2 APP CAPN2 BCL2L1 CALR CYP2R1 SNCA CAV1 PTGES FYN FN1 PTRF TGM2 COPA PTPN1 CAMK2B BCL2 CDC42 PDIA6 PRKCSH	0.0088	GO.0005783
2	GO Component	Bcl-2 family protein complex	BCL2L2 BCL2L1	0.0093	GO.0097136
9	GO Component	early endosome	EHD4 APP CAV1 ANXA2 PTPN1 TLR4 ANXA1 MYO1B NUMB	0.0104	GO.0005769
3	GO Component	immunological synapse	MYH9 ICAM1 LCK	0.0108	GO.0001772
3	GO Component	spindle midzone	APP PLK1 CDC42	0.0108	GO.0051233
2	GO Component	fibrinogen complex	THBS1 FN1	0.0112	GO.0005577
2	GO Component	nuclear envelope lumen	APP PTGES	0.0112	GO.0005641
2	GO Component	spectrin	SPTAN1 SPTBN2	0.0112	GO.0008091
6	GO Component	midbody	PLK1 ANXA2 MYH10 CLIC4 SEPT7 CDC42	0.0115	GO.0030496
4	GO Component	myosin complex	MYH9 MYO1C MYH10 MYO1B	0.0118	GO.0016459
4	GO Component	sarcoplasm	THBS1 CALR FLNC CAMK2B	0.0123	GO.0016528
14	GO Component	cytoplasmic vesicle membrane	NPC1L1 NOS3 BCL2L1 DAB2 CALR SNCA CAV1 MYO1C COPA CLIC4 ANXA1 CAMK2B CAMK2A SUN1	0.0127	GO.0030659
6	GO Component	exocytic vesicle	APP BCL2L1 BRSK1 SNCA DNM1 APBA2	0.0136	GO.0070382
4	GO Component	rough endoplasmic reticulum	PLOD1 PLOD2 APP SNCA	0.0146	GO.0005791
4	GO Component	lipid droplet	GAPDH RBP1 CAV1 ANXA2	0.0146	GO.0005811
4	GO Component	caveola	NOS3 SDPR CAV1 PTRF	0.0146	GO.0005901
8	GO Component	endoplasmic reticulum lumen	RCN1 THBS1 COL8A1 APP CALR FN1 PDIA6 PRKCSH	0.0147	GO.0005788
5	GO Component	sarcolemma	PPP3R1 FLNC ANXA2 ANXA1 PPP3CA	0.0147	GO.0042383
5	GO Component	phagocytic vesicle	CALR ZYX MYO1C FLNB VIM	0.0147	GO.0045335
15	GO Component	secretory granule	THBS1 VWF CNN2 FERMT3 APP KIT CCT2 CALR CAV1 TUBB4B ANXA2 FN1 SPTAN1 XRCC5 SUN1	0.0156	GO.0030141
8	GO Component	apical plasma membrane	NPC1L1 CAV1 FN1 DPP4 DLL1 ANXA1 SPTBN2 ABCB1	0.0167	GO.0016324

4	GO Component	extracellular exosome	ICAM1 ANXA2 FN1 ANXA1	0.0178	GO.0070062
48	GO Component	nuclear lumen	ARHGEF5 CYP24A1 RBP1 PPP3R1 CDC25B RORA DNAJB6 CAD ADD1 CSF1R PLK1 DDB1 CDC25A SDPR BRSK1 DAB2 CDC25C RORC RARB NR1I2 RGS12 USP1 PTMA FAS PTRF SFPQ MYO1C RXRG FLNA DNM1 COPA TPM3 SLK FLNA ANXA1 PIR PSIP1 XRCC5 PPP3CA CAMK2B BCL2 CAMK2A DYRK1A RARG TOP2B WEE1 CFL1 VIM NR1H4 MCM3	0.0184	GO.0031981
4	GO Component	microvillus	PDGFRA MYO1C CLIC4 FSCN1	0.0191	GO.0005902
8	GO Component	cell projection membrane	PLEK NPC1L1 ARF4 EPAH2 MYO1C DPP4 FSCN1 CFL1	0.0195	GO.0031253
10	GO Component	neuronal cell body	TUBB4A CAD CKB NQO1 SNCA MYH10 FLNA CNN3 CDC42 SPTBN2	0.0198	GO.0043025
20	GO Component	endoplasmic reticulum part	RCN1 PLOD1 THBS1 COL8A1 PLOD2 APP CAPN2 CALR CYP2R1 CAV1 PTGES FYN FN1 COPA PTPN1 CAMK2B BCL2 CDC42 PDIA6 PRKCSH	0.0208	GO.0044432
42	GO Component	nucleoplasm	ARHGEF5 CYP24A1 RBP1 PPP3R1 CDC25B RORA DNAJB6 CAD ADD1 CSF1R PLK1 DDB1 CDC25A SDPR BRSK1 CDC25C RORC RARB NR1I2 USP1 PTMA FAS PTRF SFPQ MYO1C RXRG DNM1 RXRB ANXA1 PIR PSIP1 XRCC5 PPP3CA CAMK2B BCL2 CAMK2A DYRK1A RARG TOP2B WEE1 NR1H4 MCM3	0.0218	GO.0005654
15	GO Component	endosome	EHD4 FLT1 APP CCR5 TUBA1A MMP14 CAV1 ANXA2 ANXA6 FYN PTPN1 TLR4 ANXA1 MYO1B NUMB	0.024	GO.0005768
5	GO Component	extrinsic component of plasma membrane	LCK ANXA2 FYN ANXA1 NUMB	0.0267	GO.0019897
2	GO Component	perinuclear endoplasmic reticulum	CAPN2 FYN	0.0271	GO.0097038
2	GO Component	exocyst	EXOC6B STXB6	0.0298	GO.0000145
4	GO Component	filopodium	APP FSCN1 MYO1B CDC42	0.0298	GO.0030175
2	GO Component	filamentous actin	MYO1C FSCN1	0.0298	GO.0031941
2	GO Component	invadopodium	DPP4 FSCN1	0.0298	GO.0071437
6	GO Component	basolateral plasma membrane	TJP1 CAV1 ANXA2 MYO1C ANXA1 NUMB	0.0305	GO.0016323
5	GO Component	endocytic vesicle membrane	NOS3 CALR CAV1 CAMK2B CAMK2A	0.0305	GO.0030666
11	GO Component	lysosome	KIT CAPN2 CCT2 DAB2 SNCA TUBB4B ANXA2 ANXA6 SDC4 ANXA1 SDC1	0.0322	GO.0005764
5	GO Component	synaptic vesicle	BCL2L1 BRSK1 SNCA DNM1 APBA2	0.0322	GO.0008021
3	GO Component	cleavage furrow	MYH9 MYH10 SEPT7	0.0322	GO.0032154
8	GO Component	presynapse	CAD ITGA2 BCL2L1 BRSK1 SNCA DNM1 CAMK2A APBA2	0.0322	GO.0098793
4	GO Component	Golgi lumen	APP MMP14 SDC4 SDC1	0.0333	GO.0005796
2	GO Component	glial cell projection	APP FYN	0.0341	GO.0097386
5	GO Component	growth cone	NGEF APP SNCA MYH10 FSCN1	0.0345	GO.0030426
4	GO Component	melanosome	MMP14 ANXA2 ANXA6 PDIA6	0.037	GO.0042470
2	GO Component	costamere	FLNC SDC4	0.037	GO.0043034
3	GO Component	neuromuscular junction	MYH9 APP MYH10	0.038	GO.0031594
9	GO Component	nuclear envelope	GAPDH APP BCL2L1 CALR SNCA PTGES MYO1C BCL2 SUN1	0.0388	GO.0005635
3	GO Component	tethering complex	EXOC6B STXB6 CDC42	0.0393	GO.0099023
5	GO Component	vacuolar lumen	CCT2 TUBB4B ANXA2 SDC4 SDC1	0.0444	GO.0005775
3	GO Component	sarcoplasmic reticulum	THBS1 CALR CAMK2B	0.0444	GO.0016529
2	GO Component	mast cell granule	KIT ANXA1	0.045	GO.0042629
4	GO Component	acrosomal vesicle	KIT CALR CAV1 SUN1	0.0463	GO.0001669
2	GO Component	acrosomal membrane	CAV1 SUN1	0.0479	GO.0002080
2	GO Component	rough endoplasmic reticulum membrane	PLOD1 PLOD2	0.0479	GO.0030867
121	GO Function	protein binding	ARHGEF5 PLOD1 ITGB4 MYH9 APLP1 CCL2 GAPDH LAMA4 PPP3R1 PLEK ENO1 CDC25B HSPB1 BCL2L2 PXD1 LAMA5 PDGFRA THBS1 VWF RORA DNAJB6 CNN2 NGEF ARHGAP31 CAD ADD1 ICAM1 FERMT3 TJP1 FLT1 APP CSF1R KIT NPC1L1 CCR5 CAPN2 ITGA2 NOS3 CKB CCT2 PLK1 TUBA1A DDB1 BCL2L1 CDC25A SDPR ARF4 MMP14 BRSK1 DAB2 TENC1 NQO1 CALR CDC25C STXB6 FLNC JAG2 PRKCH RARB LCK SNCA CAV1 TUBB4B CDH5 PTMA TPM4 ANXA2 ANXA6 FYN FN1 FAS ARHGEF26 PTRF SFPQ MYO1C MYH10 DPP4 ARHGEF15 TGM2 DLL1 COPA TPM3 SLK FLNA CNN3 PTPN1 SDC4 SPTAN1 DNM1 TLR4 ANXA1 TBC1D4 TPM2 PSIP1 SDC1 FSCN1 XRCC5 MYO1B G6PD PPP3CA CAMK2B LDHB BCL2 CAMK2A DYRK1A SEPT7 PAICS CDC42 SUN1 RARG TOP2B FLNB SPTBN2 CFL1 ARF1 VIM NR1H4 NUMB TLN2 PRKCSH CAMK1D	1.38E-22	GO.0005515
153	GO Function	binding	RCN1 ARHGEF5 MAP2K5 PLOD1 ITGB4 MYH9 CYP24A1 MMP2 EHD4 APLP1 CCL2 GAPDH LAMA4 RBP1 GNB4 PPP3R1 PLEK ENO1 MT2A CDC25B HSPB1 BCL2L2 PXD1 LAMA5 ARF3 PDGFRA THBS1 VWF RORA DNAJB6 CNN2 PRKCG AKT3 NGEF TUBB4A ARHGAP31 CAD ADD1 ICAM1 FERMT3 TJP1 FLT1 PLOD2 APP CSF1R KIT NPC1L1 CCR5 CAPN2 ANXA5 ITGA2 NOS3 MELK CKB CCT2 PLK1 TUBA1A TUBA1C DDB1 BCL2L1 CDC25A SDPR ARF4 MMP14 BRSK1 DAB2 TENC1 NQO1 CALR CDC25C STXB6 ZFY RORC FLNC JAG2 PRKCH RA RB CYP2R1 NR1I2 LCK SNCA CAV1 TUBB4B PTGES MAP4K4 CDH5 PTMA TPM4 ANXA2 ANXA6 FYN FN1 FAS ARHGEF26 PTRF SFPQ EPAH2 MYO1C RXRG MYH10 DPP4 ARHGEF15 TGM2 DLL1 COPA TPM3 SLK FLNA CNN3 PTPN1 SDC4 SPTAN1 DNM1 TLR4 RXRB ANXA1 TBC1D4 TPM2 PIR PSIP1 SDC1 FSCN1 XRCC5 MYO1B G6PD PPP3CA CAMK2B LDHB BCL2 CAMK2A DYRK1A SEPT7 PAICS CDC42 SUN1 RARG TOP2B WEE1 FLNB BCL2 SPTBN2 CFL1 ARF1 VIM NR1H4 NUMB APBA2 TLN2 PRKCSH ABC1 CAMK1D MCM3	4.35E-19	GO.0005488
66	GO Function	anion binding	ARHGEF5 MAP2K5 PLOD1 MYH9 EHD4 APLP1 PLEK ARF3 PDGFRA THBS1 PRKCG AKT3 TUBB4A CAD FLT1 PLOD2 APP CSF1R KIT ANXA5 ITGA2 NOS3 MELK CKB CCT2 PLK1 TUBA1A TUBA1C SDPR ARF4 BRSK1 STXB6 PRKCH LCK SNCA TUBB4B PTGES MAP4K4 ANXA2 ANXA6 FYN FN1 EPAH2 MYO1C MYH10 TGM2 SLK DNM1 ANXA1 XRCC5 MYO1B CAMK2B CAMK2A DYRK1A SEPT7 PAICS CDC42 TOP2B WEE1 PBK SPTBN2 ARF1 NR1H4 ABC1 CAMK1D MCM3	1.86E-14	GO.0043168
52	GO Function	identical protein binding	PLOD1 MYH9 APLP1 GAPDH PLEK ENO1 HSPB1 BCL2L2 PDGFRA THBS1 VWF DNAJB6 CAD ADD1 APP CSF1R KIT PLK1 BCL2L1 NQO1 FLNC LCK SNCA CAV1 TPM4 ANXA2 ANXA6 FYN FN1 FAS PTRF SFPQ DPP4 SLK FLNA SDC4 DNM1 TLR4 ANXA1 TPM2 SDC1 G6PD CAMK2B LDHB BCL2 CAMK2A DYRK1A SEPT7 PAICS CDC42 FLNB VIM	5.47E-14	GO.0042802
56	GO Function	enzyme binding	ARHGEF5 PPP3R1 PLEK ENO1 CDC25B HSPB1 PDGFRA VWF NGEF CAD APP CSF1R KIT NPC1L1 CKB CCT2 PLK1 BCL2L1 CDC25A SDPR ARF4 BRSK1 TENC1 CALR CDC25C STXB6 PRKCH LCK SNCA CAV1 CDH5 ANXA2 FYN FN1 FAS ARHGEF26 SFPQ MYO1C DPP4 ARHGEF15 FLNA PTPN1 SDC4 SPTAN1 DNM1 TBC1D4 XRCC5 PPP3CA CAMK2B LDHB BCL2 CAMK2A CDC42 TOP2B SPTBN2 PRKCSH	1.13E-12	GO.0019899
55	GO Function	carbohydrate derivative binding	ARHGEF5 MAP2K5 MYH9 EHD4 APLP1 ARF3 PDGFRA THBS1 PRKCG AKT3 TUBB4A CAD FLT1 APP CSF1R KIT ITGA2 NOS3 MELK CKB CCT2 PLK1 TUBA1A TUBA1C ARF4 BRSK1 PRKCH LCK TUBB4B MAP4K4 ANXA6 FYN FN1 EPAH2 MYO1C MYH10 TGM2 SLK DNM1 TLR4 XRCC5 MYO1B CAMK2B CAMK2A DYRK1A SEPT7 PAICS CDC42 TOP2B WEE1 PBK ARF1 ABC1 CAMK1D MCM3	2.35E-12	GO.0097367
58	GO Function	small molecule binding	ARHGEF5 MAP2K5 PLOD1 MYH9 EHD4 GAPDH RBP1 ARF3 PDGFRA PRKCG AKT3 TUBB4A CAD FLT1 PLOD2 CSF1R KIT NOS3 MELK CKB CCT2 PLK1 TUBA1A TUBA1C ARF4 BRSK1 PRKCH LCK CAV1 TUBB4B MAP4K4 ANXA6 FYN EPAH2 MYO1C MYH10 TGM2 SLK DNM1 XRCC5 MYO1B G6PD CAMK2B LDHB LTB4 CAMK2A DYRK1A SEPT7 PAICS CDC42 TOP2B WEE1 PBK ARF1 NR1H4 ABC1 CAMK1D MCM3	7.32E-12	GO.0036094

53	GO Function	nucleotide binding	ARHGEF5 MAP2K5 MYH9 EHD4 GAPDH ARF3 PDGFRA PRKCG AKT3 TUBB4A CAD FLT1 CSF1R KIT NOS3 MELK CKB CCT2 PLK1 TUBA1A TUBA1C ARF4 BRSK1 PRKCH LCK TUBB4B MAP4K4 ANXA6 FYN EPHA2 MYO1C MYH10 TGM2 SLK DNM1 XRCC5 MYO1B G6PD CAMK2B LDHB LTB4R CAMK2A DYRK1A SEPT7 PAICS CDC42 TOP2B WEE1 PBK ARF1 ABCB1 CAMK1D MCM3	8.06E-12	GO.0000166
49	GO Function	ribonucleotide binding	ARHGEF5 MAP2K5 MYH9 EHD4 ARF3 PDGFRA PRKCG AKT3 TUBB4A CAD FLT1 CSF1R KIT NOS3 MELK CKB CCT2 PLK1 TUBA1A TUBA1C ARF4 BRSK1 PRKCH LCK TUBB4B MAP4K4 ANXA6 FYN EPHA2 MYO1C MYH10 TGM2 SLK DNM1 XRCC5 MYO1B CAMK2B CAMK2A DYRK1A SEPT7 PAICS CDC42 TOP2B WEE1 PBK ARF1 ABCB1 CAMK1D MCM3	1.88E-11	GO.0032553
48	GO Function	purine ribonucleoside triphosphate binding	ARHGEF5 MAP2K5 MYH9 EHD4 ARF3 PDGFRA PRKCG AKT3 TUBB4A CAD FLT1 CSF1R KIT MELK CKB CCT2 PLK1 TUBA1A TUBA1C ARF4 BRSK1 PRKCH LCK TUBB4B MAP4K4 ANXA6 FYN EPHA2 MYO1C MYH10 TGM2 SLK DNM1 XRCC5 MYO1B CAMK2B CAMK2A DYRK1A SEPT7 PAICS CDC42 TOP2B WEE1 PBK ARF1 ABCB1 CAMK1D MCM3	1.88E-11	GO.0035639
35	GO Function	protein-containing complex binding	MYH9 GNB4 LAMA5 PDGFRA THBS1 VWF ADD1 ICAM1 FERMT3 APP ITGA2 PLK1 DDB1 MMP14 CALR FLNC RARB LCK SNCA TPM4 FYN FN1 MYO1C MYH10 TPM3 FLNA PTPN1 DNM1 TPM2 FSCN1 XRCC5 MYO1B CFL1 VIM TLN2	1.88E-11	GO.0044877
48	GO Function	purine ribonucleotide binding	ARHGEF5 MAP2K5 MYH9 EHD4 ARF3 PDGFRA PRKCG AKT3 TUBB4A CAD FLT1 CSF1R KIT MELK CKB CCT2 PLK1 TUBA1A TUBA1C ARF4 BRSK1 PRKCH LCK TUBB4B MAP4K4 ANXA6 FYN EPHA2 MYO1C MYH10 TGM2 SLK DNM1 XRCC5 MYO1B CAMK2B CAMK2A DYRK1A SEPT7 PAICS CDC42 TOP2B WEE1 PBK ARF1 ABCB1 CAMK1D MCM3	4.61E-11	GO.0032555
95	GO Function	ion binding	RCN1 ARHGEF5 MAP2K5 PLOC1 MYH9 CYP24A1 MMP2 EHD4 APLP1 PPP3R1 PLEK ENO1 MT2A PXDNI ARF3 PDGFRA THBS1 RORA PRKCG AKT3 TUBB4A CAD FLT1 PLOC2 APP CSF1R KIT CAPN2 ANXA5 ITGA2 NOS3 MELK CKB CCT2 PLK1 TUBA1A TUBA1C SDPR ARF4 MMP14 BRSK1 TENC1 CALR STXB6 ZYX RORC JAG2 PRKCH RARB CYP2R1 NR1I2 LCK SNCA TUBB4B PTGES MAP4K4 CDH5 TPM4 ANXA2 ANXA6 FYN FN1 EPHA2 MYO1C XRGR MYH10 TGM2 DLL1 SLK PTPN1 SPTAN1 DNM1 RXRB ANXA1 PIR XRCC5 MYO1B PPP3CA CAMK2B CAMK2A DYRK1A SEPT7 PAICS CDC42 RARG TOP2B WEE1 PBK SPTBN2 ARF1 NR1H4 PRKCSH ABCB1 CAMK1D MCM3	5.31E-11	GO.0043167
23	GO Function	actin binding	MYH9 CNN2 ADD1 CCR5 NOS3 FLNC SNCA TPM4 MYO1C MYH10 TPM3 FLNA CNN3 SPTAN1 TPM2 FSCN1 MYO1B CAMK2B DYRK1A FLNB SPTBN2 CFL1 TLN2	6.57E-11	GO.0003779
31	GO Function	cytoskeletal protein binding	MYH9 GAPDH CNN2 ADD1 NPC1L1 CCR5 CAPN2 NOS3 PLK1 BRSK1 FLNC SNCA TPM4 ANXA2 FYN MYO1C MYH10 TPM3 FLNA CNN3 SPTAN1 DNM1 TPM2 FSCN1 MYO1B CAMK2B DYRK1A FLNB SPTBN2 CFL1 TLN2	6.60E-10	GO.0008092
16	GO Function	calmodulin binding	MYH9 PPP3R1 CNN2 ADD1 TP1 NOS3 FAS MYO1C MYH10 CNN3 SPTAN1 MYO1B PPP3CA CAMK2B CAMK2A CAMK1D	7.68E-10	GO.0005516
43	GO Function	drug binding	MAP2K5 MYH9 EHD4 PPP3R1 MT2A PDGFRA PRKCG AKT3 CAD FLT1 CSF1R KIT NPC1L1 NOS3 MELK CKB CCT2 PLK1 BRSK1 PRKCH RARB NR1I2 LCK MAP4K4 FYN EPHA2 MYO1C MYH10 SLK FSCN1 XRCC5 MYO1B PPP3CA CAMK2B CAMK2A DYRK1A PAICS TOP2B WEE1 PBK ABCB1 CAMK1D MCM3	1.76E-09	GO.0008144
25	GO Function	protein kinase activity	MAP2K5 CCL2 PDGFRA PRKCG AKT3 CAD FLT1 CSF1R KIT MELK PLK1 BRSK1 PRKCH LCK MAP4K4 FYN EPHA2 SLK CAMK2B CAMK2A DYRK1A CDC42 WEE1 PBK CAMK1D	6.75E-09	GO.0004672
38	GO Function	signaling receptor binding	ITGB4 APLP1 CCL2 LAMA4 PXDNI LAMA5 PDGFRA THBS1 VWF ICAM1 FERMT3 APP ITGA2 ARF4 MMP14 CALR JAG2 RARB LCK CAV1 TUBB4B CDH5 FYN FN1 MYO1C DPP4 DLL1 COPA FLNA PTPN1 DNM1 TLR4 ANXA1 CAMK2A CDC42 RARG CFL1 NR1H4	2.90E-08	GO.0005102
13	GO Function	actin filament binding	MYH9 ADD1 FLNC TPM4 MYO1C MYH10 TPM3 FLNA TPM2 FSCN1 MYO1B CFL1 TLN2	5.18E-08	GO.0051015
26	GO Function	kinase activity	MAP2K5 CCL2 PDGFRA PRKCG AKT3 CAD FLT1 CSF1R KIT MELK CKB PLK1 BRSK1 PRKCH LCK MAP4K4 FYN EPHA2 SLK CAMK2B CAMK2A DYRK1A CDC42 WEE1 PBK CAMK1D	2.79E-07	GO.0016301
33	GO Function	protein dimerization activity	PLOC1 MYH9 PLEK ENO1 HSPB1 BCL2L2 PDGFRA VWF ADD1 APP CSF1R KIT CAPN2 ITGA2 BCL2L1 CAV1 TPM4 ANXA6 SFPQ DPP4 SLK FLNA DNM1 TLR4 ANXA1 TPM2 G6PD PPP3CA CAMK2B BCL2 CAMK2A TOP2B ARF1	3.07E-07	GO.0046983
35	GO Function	ATP binding	MAP2K5 MYH9 EHD4 PDGFRA PRKCG AKT3 CAD FLT1 CSF1R KIT MELK CKB CCT2 PLK1 BRSK1 PRKCH LCK MAP4K4 FYN EPHA2 MYO1C MYH10 SLK XRCC5 MYO1B CAMK2B CAMK2A DYRK1A PAICS TOP2B WEE1 PBK ABCB1 CAMK1D MCM3	4.10E-07	GO.0005524
8	GO Function	nuclear receptor activity	RORA RORC RARB NR1I2 RXRG RXRB RARG NR1H4	5.63E-07	GO.0004879
25	GO Function	protein homodimerization activity	PLOC1 MYH9 PLEK ENO1 HSPB1 BCL2L2 PDGFRA VWF ADD1 APP CSF1R KIT BCL2L1 TPM4 ANXA6 SFPQ DPP4 SLK FLNA ANXA1 TPM2 G6PD CAMK2B BCL2 CAMK2A	8.56E-07	GO.0042803
21	GO Function	GTPase binding	ARHGEF5 ENO1 PDGFRA NGEF KIT NPC1L1 ARF4 STXB6 PRKCH CAV1 ANXA2 FYN ARHGEF26 MYO1C ARHGEF15 FLNA SPTAN1 TBC1D4 CAMK2B CAMK2A SPTBN2	1.37E-06	GO.0051020
8	GO Function	steroid hormone receptor activity	RORA RORC RARB NR1I2 RXRG RXRB RARG NR1H4	1.47E-06	GO.0003707
19	GO Function	Ras GTPase binding	ARHGEF5 PDGFRA NGEF KIT NPC1L1 STXB6 PRKCH CAV1 ANXA2 FYN ARHGEF26 MYO1C ARHGEF15 FLNA SPTAN1 TBC1D4 CAMK2B CAMK2A SPTBN2	1.58E-06	GO.0017016
10	GO Function	integrin binding	LAMA5 THBS1 VWF ICAM1 FERMT3 APP ITGA2 MMP14 CALR FN1	2.55E-06	GO.0005178
42	GO Function	catalytic activity, acting on a protein	MAP2K5 PLOC1 MMP2 CCL2 GAPDH PPP3R1 CDC25B PDGFRA PRKCG AKT3 CAD FLT1 PLOC2 CSF1R KIT CAPN2 MELK PLK1 CDC25A MMP14 BRSK1 TENC1 CDC25C PRKCH LCK USP1 MAP4K4 FYN EPHA2 DPP4 TGM2 SLK PTPN1 PPP3CA CAMK2B CAMK2A DYRK1A CDC42 PDIA6 WEE1 PBK CAMK1D	3.32E-06	GO.0140096
76	GO Function	organic cyclic compound binding	ARHGEF5 MAP2K5 MYH9 CYP24A1 EHD4 GAPDH ENO1 PXDNI ARF3 PDGFRA RORA PRKCG AKT3 TUBB4A CAD FLT1 APP CSF1R KIT NOS3 MELK CKB CCT2 PLK1 TUBA1A TUBA1C DDB1 ARF4 BRSK1 CALR RORC PRKCH RARB CYP2R1 NR1I2 LCK SNCA CAV1 TUBB4B MAP4K4 ANXA6 FYN PTRF SFPQ EPHA2 MYO1C XRGR MYH10 TGM2 SLK DNM1 RXRB ANXA1 PSIP1 XRCC5 MYO1B G6PD CAMK2B LDHB LTB4R BCL2 CAMK2A DYRK1A SEPT7 PAICS CDC42 RARG TOP2B WEE1 PBK ARF1 VIM NR1H4 ABCB1 CAMK1D MCM3	3.65E-06	GO.0097159
75	GO Function	heterocyclic compound binding	ARHGEF5 MAP2K5 MYH9 CYP24A1 EHD4 GAPDH ENO1 PXDNI ARF3 PDGFRA RORA PRKCG AKT3 TUBB4A CAD FLT1 APP CSF1R KIT NOS3 MELK CKB CCT2 PLK1 TUBA1A TUBA1C DDB1 ARF4 BRSK1 CALR RORC PRKCH RARB CYP2R1 NR1I2 LCK SNCA TUBB4B MAP4K4 ANXA6 FYN PTRF SFPQ EPHA2 MYO1C XRGR MYH10 TGM2 SLK DNM1 RXRB ANXA1 PSIP1 XRCC5 MYO1B G6PD CAMK2B LDHB LTB4R BCL2 CAMK2A DYRK1A SEPT7 PAICS CDC42 RARG TOP2B WEE1 PBK ARF1 VIM NR1H4 ABCB1 CAMK1D MCM3	4.30E-06	GO.1901363
21	GO Function	kinase binding	PLEK CDC25B HSPB1 PLK1 BCL2L1 CDC25A SDPR BRSK1 TENC1 CDC25C LCK CAV1 FAS FLNA PTPN1 SDC4 DNM1 LDHB CDC42 TOP2B PRKCSH	5.24E-06	GO.0019900
11	GO Function	protein tyrosine kinase activity	MAP2K5 PDGFRA FLT1 CSF1R KIT MELK LCK FYN EPHA2 DYRK1A WEE1	8.33E-06	GO.0004713
20	GO Function	calcium ion binding	RCN1 EHD4 PPP3R1 THBS1 TUBB4A CAPN2 ANXA5 MELK CALR JAG2 SNCA CDH5 TPM4 ANXA2 ANXA6 DLL1 SPTAN1 ANXA1 PPP3CA PRKCSH	3.24E-05	GO.0005509
20	GO Function	protein domain specific binding	MYH9 GAPDH PPP3R1 BCL2L2 ARHGAP31 APP TUBA1A DDB1 BCL2L1 CDC25C LCK SNCA FYN FN1 TGM2 DNM1 BCL2 CDC42 ARF1 VIM	3.59E-05	GO.0019904

14	GO Function	GTP binding	ARHGEF5 EHD4 ARF3 TUBB4A TUBA1A TUBA1C ARF4 TUBB4B ANXA6 TGM2 DNM1 SEPT7 CDC42 ARF1	4.81E-05	GO.0005525
8	GO Function	structural constituent of cytoskeleton	TUBB4A TUBA1A TUBA1C TUBB4B SPTAN1 SPTBN2 VIM TLN2	6.01E-05	GO.0005200
19	GO Function	lipid binding	ARHGEF5 RBPI1 PLEK THBS1 RORA ANXA5 MELK SDPR STXB6P RORC SNCA CAV1 ANXA2 ANXA6 TLR4 ANXA1 MYO1B SPTBN2 NR1H4	6.01E-05	GO.0008289
74	GO Function	catalytic activity	MAP2K5 PLOD1 MYH9 CYP24A1 MMP2 CCL2 GAPDH PPP3R1 ENO1 CDC25B PXDN ARF3 PDGFRA PRKCG AKT3 TUBB4A CAD FLT1 PLOD2 CSF1R KIT CCR5 CAPN2 NOS3 MELK CKB PLK1 TUBA1A TUBA1C CDC25A ARF4 MMP14 BRSK1 TENC1 NQO1 CDC25C PRKCH CYP2R1 LCK SNCA TUBB4B PTGES USP1 MAP4K4 FYN EPHA2 MYO1C MYH10 DPP4 TGM2 GSTO1 SLK PTPN1 DNM1 ANXA1 PIR XRCC5 MYO1B G6PD PPP3CA CAMK2B LDHB CAMK2A DYRK1A PAICS CDC42 PDIA6 TOP2B WEE1 PBK ARF1 ABC1 CAMK1D MCM3	6.28E-05	GO.0003824
4	GO Function	actin-dependent ATPase activity	MYH9 MYO1C MYH10 MYO1B	6.49E-05	GO.0030898
6	GO Function	protein kinase C binding	PLEK HSPB1 SDPR SDC4 TOP2B PRKCSH	6.78E-05	GO.0005080
15	GO Function	protein serine/threonine kinase activity	MAP2K5 PRKCG AKT3 MELK PLK1 BRSK1 PRKCH MAP4K4 SLK CAMK2B CAMK2A DYRK1A CDC42 PBK CAMK1D	7.23E-05	GO.0004674
11	GO Function	Ras guanyl-nucleotide exchange factor activity	ARHGEF5 PDGFRA NGEF KIT FYN ARHGEF26 ARHGEF15 SPTAN1 CAMK2B CAMK2A SPTBN2	9.53E-05	GO.0005088
17	GO Function	protein kinase binding	PLEK CDC25B HSPB1 PLK1 BCL2L1 CDC25A SDPR BRSK1 CDC25C LCK CAV1 PTPN1 SDC4 DNM1 CDC42 TOP2B PRKCSH	1.50E-04	GO.0019901
33	GO Function	molecular function regulator	ARHGEF5 CCL2 GAPDH HSPB1 PXDN PDGFRA DNAJB6 NGEF ARHGAP31 APP KIT ANXA5 ARF4 JAG2 SNCA CAV1 RG512 ANXA2 FYN FN1 ARHGEF26 ARHGEF15 ARHGAP30 COPA FLNA SPTAN1 ANXA1 TBC1D4 XRCC5 CAMK2B BCL2 CAMK2A SPTBN2	1.50E-04	GO.0098772
12	GO Function	guanyl-nucleotide exchange factor activity	ARHGEF5 PDGFRA NGEF KIT ARF4 FYN ARHGEF26 ARHGEF15 SPTAN1 CAMK2B CAMK2A SPTBN2	1.60E-04	GO.0005085
18	GO Function	structural molecule activity	LAMA4 PXDN TUBB4A ADD1 TUBA1A TUBA1C CAV1 TUBB4B TPM4 COPA TPM3 SPTAN1 ANXA1 TPM2 SEPT7 SPTBN2 VIM TLN2	1.90E-04	GO.0005198
23	GO Function	transition metal ion binding	PLOD1 CYP24A1 MMP2 APLP1 MT2A RORA PRKCG CAD PLOD2 APP NOS3 MMP14 CALR RORC RARB CYP2R1 NR112 SNCA RXRG PTPN1 RARB RARG NR1H4	2.60E-04	GO.0046914
57	GO Function	metal ion binding	RCN1 MAP2K5 PLOD1 CYP24A1 MMP2 EHD4 APLP1 PPP3R1 ENO1 MT2A PXDN THBS1 RORA PRKCG TUBB4A CAD PLOD2 APP KIT CAPN2 ANXA5 ITGA2 NOS3 MELK PLK1 MMP14 BRSK1 TENC1 CALR ZYG1 RORC JAG2 PRKCH RARB CYP2R1 NR112 SNCA CDH5 TPM4 ANXA2 ANXA6 FYN RXRG TGM2 DLL1 PTPN1 SPTAN1 RARB ANXA1 PIR PPP3CA CAMK2A RARG TOP2B WEE1 NR1H4 PRKCSH	2.80E-04	GO.0046872
12	GO Function	tubulin binding	MYH9 GAPDH PLK1 BRSK1 SNCA FYN MYO1C MYH10 CNN3 DNM1 MYO1B DYRK1A	4.00E-04	GO.0015631
4	GO Function	microfilament motor activity	MYH9 MYO1C MYH10 MYO1B	4.50E-04	GO.0000146
9	GO Function	protein C-terminus binding	DAB2 LCK FN1 MYO1C DNM1 SDC1 XRCC5 TOP2B VIM	4.50E-04	GO.0008022
5	GO Function	non-membrane spanning protein tyrosine kinase activity	MELK LCK FYN DYRK1A WEE1	8.50E-04	GO.0004715
18	GO Function	nucleoside-triphosphatase activity	MYH9 ARF3 TUBB4A TUBA1A ARF4 TUBB4B MYO1C MYH10 DNM1 ANXA1 XRCC5 MYO1B CDC42 TOP2B ARF1 ABC1 MCM3	9.60E-04	GO.0017111
8	GO Function	phosphoprotein phosphatase activity	PPP3R1 CDC25B CDC25A TENC1 CDC25C LCK PTPN1 PPP3CA	0.0012	GO.0004721
14	GO Function	protein heterodimerization activity	BCL2L2 ADD1 APP CAPN2 ITGA2 BCL2L1 CAV1 TPM4 TLR4 TPM2 PPP3CA BCL2 TOP2B ARF1	0.0012	GO.0046982
3	GO Function	BH domain binding	BCL2L2 BCL2L1 BCL2	0.0012	GO.0051400
3	GO Function	phospholipase inhibitor activity	ANXA5 ANXA2 ANXA1	0.0015	GO.0004859
5	GO Function	transmembrane receptor protein tyrosine kinase activity	PDGFRA FLT1 CSF1R KIT EPHA2	0.0017	GO.0004714
6	GO Function	cytokine binding	PXDN THBS1 CSF1R KIT CCR5 FAS	0.0018	GO.0019955
4	GO Function	disordered domain specific binding	GAPDH BCL2L2 FYN FN1	0.0018	GO.0097718
6	GO Function	chaperone binding	VWF DNAJB6 APP CDC25A CALR FN1	0.0019	GO.0051087
9	GO Function	microtubule binding	MYH9 GAPDH PLK1 SNCA MYO1C MYH10 CNN3 DNM1 MYO1B	0.0025	GO.0008017
2	GO Function	CD8 receptor binding	LCK FYN	0.0029	GO.0042610
3	GO Function	retinoid X receptor binding	RARB RARG NR1H4	0.0029	GO.0046965
11	GO Function	phospholipid binding	PLEK THBS1 ANXA5 SDPR STXB6P SNCA ANXA2 ANXA6 ANXA1 MYO1B SPTBN2	0.0032	GO.0005543
3	GO Function	Ral GTPase binding	PRKCH MYO1C FLNA	0.0033	GO.0017160
5	GO Function	virus receptor activity	ICAM1 CCR5 ITGA2 EPHA2 DPP4	0.0036	GO.0001618
7	GO Function	Rho GTPase binding	ARHGEF5 NGEF STXB6P CAV1 ARHGEF26 ARHGEF15 FLNA	0.0036	GO.0017048
2	GO Function	procollagen-lysine 5-dioxygenase activity	PLOD1 PLOD2	0.0042	GO.0008475
3	GO Function	tau protein binding	SNCA FYN DYRK1A	0.0042	GO.0048156
9	GO Function	GTPase activity	ARF3 TUBB4A TUBA1A TUBA1C ARF4 TUBB4B DNM1 CDC42 ARF1	0.0048	GO.0003924
4	GO Function	calcium-dependent phospholipid binding	ANXA5 ANXA2 ANXA6 ANXA1	0.0052	GO.0005544
2	GO Function	phospholipase A2 inhibitor activity	ANXA2 ANXA1	0.0061	GO.0019834
7	GO Function	protein binding, bridging	MYH9 DDB1 DAB2 CAV1 ANXA1 FSCN1 SUN1	0.0062	GO.0030674
4	GO Function	sterol binding	RORA RORC CAV1 ANXA6	0.0062	GO.0032934
5	GO Function	steroid binding	RORA RORC CAV1 ANXA6 NR1H4	0.0063	GO.0005496
6	GO Function	protease binding	VWF KIT ANXA2 FN1 DPP4 BCL2	0.0068	GO.0002020
16	GO Function	zinc ion binding	MMP2 MT2A RORA PRKCG CAD MMP14 CALR RORC RARB NR112 SNCA RXRG PTPN1 RARB RARG NR1H4	0.0073	GO.0008270
2	GO Function	oxysterol binding	RORA RORC	0.0079	GO.0008142
2	GO Function	BH3 domain binding	BCL2L1 BCL2	0.0079	GO.0051434
3	GO Function	protein folding chaperone	HSPB1 CCT2 CALR	0.0087	GO.0044183
6	GO Function	iron ion binding	PLOD1 CYP24A1 PLOD2 CALR CYP2R1 SNCA	0.0097	GO.0005506
2	GO Function	creatine kinase activity	CKB MAP4K4	0.01	GO.0004111
4	GO Function	collagen binding	THBS1 VWF ITGA2 FN1	0.011	GO.0005518
3	GO Function	calmodulin-dependent protein kinase activity	CAMK2B CAMK2A CAMK1D	0.0111	GO.0004683
3	GO Function	ephrin receptor binding	APP FYN PTPN1	0.0111	GO.0046875
2	GO Function	calcium-dependent protein serine/threonine phosphatase activity	PPP3R1 PPP3CA	0.0122	GO.0004723
2	GO Function	vascular endothelial growth factor-activated receptor activity	PDGFRA FLT1	0.0122	GO.0005021
2	GO Function	T cell receptor binding	LCK FYN	0.0149	GO.0042608
2	GO Function	CD4 receptor binding	LCK FYN	0.0149	GO.0042609
3	GO Function	proteoglycan binding	THBS1 APP ITGA2	0.015	GO.0043394
4	GO Function	phosphatidylinositol-4,5-bisphosphate 3-kinase activity	PDGFRA KIT LCK FYN	0.015	GO.0046934
14	GO Function	oxidoreductase activity	PLOD1 CYP24A1 GAPDH PXDN PLOD2 NOS3 NQO1 CYP2R1 SNCA GSTO1 PIR G6PD LDHB PDIA6	0.0154	GO.0016491
6	GO Function	phosphatase binding	PPP3R1 CSF1R LCK CDH5 PTPN1 BCL2	0.0163	GO.0019902
9	GO Function	phosphoric ester hydrolase activity	PPP3R1 CDC25B CCR5 CDC25A TENC1 CDC25C LCK PTPN1 PPP3CA	0.0163	GO.0042578
5	GO Function	ion channel binding	CAV1 CDH5 FYN FLNA PRKCSH	0.0185	GO.0044325
33	GO Function	hydrolase activity	MYH9 MMP2 PPP3R1 CDC25B ARF3 TUBB4A CAD CCR5 CAPN2 TUBA1A TUBA1C CDC25A ARF4 MMP14 TENC1 CDC25C LCK TUBB4B USP1 MYO1C MYH10 DPP4 PTPN1 DNM1 ANXA1 XRCC5 MYO1B PPP3CA CDC42 TOP2B ARF1 ABC1 MCM3	0.0187	GO.0016787
5	GO Function	protein phosphatase binding	CSF1R LCK CDH5 PTPN1 BCL2	0.02	GO.0019903

4	GO Function	Rho guanyl-nucleotide exchange factor activity	ARHGEF5 NGEF ARHGEF26 ARHGEF15	0.0203	GO.0005089
3	GO Function	peptidase activator activity	APP CAV1 FN1	0.0203	GO.0016504
2	GO Function	calcium-dependent protein serine/threonine kinase activity	PRKCG CAMK2A	0.0225	GO.0009931
2	GO Function	oxidoreductase activity, acting on NAD(P)H, heme protein as acceptor	NOS3 NQO1	0.0259	GO.0016653
2	GO Function	protein membrane anchor	MYH9 SUN1	0.0259	GO.0043495
8	GO Function	ATPase activity, coupled	MYH9 MYO1C MYH10 ANXA1 XRCC5 MYO1B TOP2B ABCB1	0.027	GO.0042623
2	GO Function	peptide disulfide oxidoreductase activity	GSTO1 PDIA6	0.0288	GO.0015037
2	GO Function	cyclosporin A binding	PPP3R1 PPP3CA	0.0288	GO.0016018
2	GO Function	nitric-oxide synthase binding	CAV1 DNM1	0.0288	GO.0050998
3	GO Function	structural constituent of muscle	TPM4 TPM3 TPM2	0.0311	GO.0008307
2	GO Function	heparan sulfate proteoglycan binding	APP ITGA2	0.0318	GO.0043395
3	GO Function	NADP binding	GAPDH NOS3 G6PD	0.0323	GO.0050661
10	GO Function	cofactor binding	PLOD1 CYP24A1 GAPDH PXDN PLOC2 NOS3 CYP2R1 PTGES G6PD LDHB	0.0331	GO.0048037
7	GO Function	peptide binding	PPP3R1 APP ITGA2 CALR PTGES PPP3CA APBA2	0.0348	GO.0042277
7	GO Function	G protein-coupled receptor binding	ITGB4 APLP1 CC2 APP FYN FLNA DNM1	0.0359	GO.0001664
4	GO Function	phosphatidylinositol bisphosphate binding	PLEK STXB6 ANXA2 MYO1B	0.0363	GO.1902936
2	GO Function	protein kinase C activity	PRKCG PRKCH	0.0382	GO.0004697
5	GO Function	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	PLOD1 CYP24A1 PLOC2 NOS3 CYP2R1	0.0382	GO.0016705
3	GO Function	extracellular matrix binding	THBS1 ITGA2 ANXA2	0.0402	GO.0050840
4	GO Function	protein tyrosine phosphatase activity	CDC25B CDC25A CDC25C PTPN1	0.0433	GO.0004725
10	GO Function	enzyme activator activity	DNAJB6 ARHGAP31 APP CAV1 RGS12 FN1 ARHGEF15 ARHGAP30 TBC1D4 XRCC5	0.0457	GO.0008047
16	GO Function	enzyme regulator activity	GAPDH HSPB1 DNAJB6 ARHGAP31 APP ANXA5 SNCA CAV1 RGS12 ANXA2 FN1 ARHGEF15 ARHGAP30 ANXA1 TBC1D4 XRCC5	0.0469	GO.0030234
29	GO Function	transferase activity	MAP2K5 CCL2 GAPDH PDGFRA PRKCG AKT3 CAD FLT1 CSF1R KIT MEK1 CKB PLK1 BRSK1 PRKCH LCK MAP4K4 FYN EPHA2 TGM2 GSTO1 SLK CAMK2B CAMK2A DYRK1A CDC42 WEE1 PBK CAMK1D	0.0489	GO.0016740
70	GO Process	regulation of cellular component organization	ARHGEF5 MAP2K5 MYH9 EHD4 CCL2 PLEK ENO1 PDGFRA THBS1 DNAJB6 PRKCG NGEF ITGB4 ADD1 ICAM1 TJP1 APP CSF1R KIT CAPN2 ITGA2 CCT2 PLK1 DDB1 BCL2L1 MMP14 BRSK1 DAB2 CALR CDC25C STXB6 PRKCH SNCA CAV1 MAP4K4 ANXA2 FYN FN1 SFPQ EPHA2 MYO1C MYH10 DPP4 ARHGEF15 DLL1 SLK FLNA PTPN1 SDC4 SPTAN1 DNM1 TLR4 CLIC4 ANXA1 TBC1D4 SDC1 FSCN1 XRCC5 G6PD PPP3CA CAMK2B BCL2 DYRK1A SEPT7 CDC42 SPTBN2 CFL1 ARF1 VIM CAMK1D	1.88E-19	GO.0051128
127	GO Process	response to stimulus	ARHGEF5 MAP2K5 PLOD1 ITGB4 MYH9 CYP24A1 MMP2 EHD4 APLP1 CCL2 GAPDH GNB4 PPP3R1 PLEK ENO1 MT2A HSPB1 BCL2L2 PXDN LAMA5 PDGFRA THBS1 VWF RORA CNN2 PRKCG AKT3 NGEF ARHGAP31 CAD ADD1 ICAM1 FERMT3 TJP1 FLT1 PLOC2 APP CSF1R KIT NPC1L1 CCR5 CAPN2 ANXA5 ITGA2 NOS3 MEK1 CCT2 PLK1 DDB1 BCL2L1 CDC25A ARF4 MMP14 BRSK1 DAB2 TENC1 NQO1 CALR CDC25C ZFYX RORC JAG2 PRKCH RARB CYP2R1 NR1I2 LCK SNCA CAV1 RGS12 TUBB4B PTGES USP1 MAP4K4 CDH5 DOK4 ANXA2 ANXA6 FYN FN1 FAS ARHGEF26 SFPQ EPHA2 MYO1C RXRG MYH10 DPP4 TGM2 DLL1 ARHGAP30 GSTO1 SLK FLNA PTPN1 SDC4 SPTAN1 DNM1 TLR4 CLIC4 RXRB ANXA1 TBC1D4 PSIP1 SDC1 FSCN1 XRCC5 G6PD PPP3CA CAMK2B LTBR4 BCL2 CAMK2A CDC42 SUN1 PDIA6 RARG FLNB PBK SPTBN2 CFL1 ARF1 VIM NR1H4 PRKCSH ABCB1 CAMK1D	5.52E-19	GO.0050896
113	GO Process	cellular response to stimulus	ARHGEF5 MAP2K5 ITGB4 MYH9 CYP24A1 MMP2 EHD4 APLP1 CCL2 GAPDH GNB4 PPP3R1 PLEK MT2A HSPB1 BCL2L2 PXDN LAMA5 PDGFRA THBS1 RORA CNN2 PRKCG AKT3 NGEF ARHGAP31 CAD ADD1 ICAM1 FERMT3 TJP1 FLT1 APP CSF1R KIT NPC1L1 CCR5 CAPN2 ANXA5 ITGA2 NOS3 MEK1 PLK1 DDB1 BCL2L1 CDC25A ARF4 BRSK1 DAB2 TENC1 NQO1 CALR CDC25C ZFYX RORC JAG2 PRKCH RARB NR1I2 LCK SNCA CAV1 RGS12 PTGES USP1 MAP4K4 CDH5 ANXA2 ANXA6 FYN FN1 FAS ARHGEF26 SFPQ EPHA2 MYO1C RXRG TGM2 DLL1 ARHGAP30 GSTO1 SLK FLNA PTPN1 SDC4 SPTAN1 DNM1 TLR4 CLIC4 RXRB ANXA1 TBC1D4 SDC1 FSCN1 XRCC5 G6PD PPP3CA CAMK2B LTBR4 BCL2 CAMK2A CDC42 PDIA6 RARG FLNB PBK SPTBN2 CFL1 ARF1 VIM NR1H4 PRKCSH CAMK1D	5.52E-19	GO.0051716
96	GO Process	signal transduction	ARHGEF5 MAP2K5 ITGB4 MYH9 CYP24A1 MMP2 CCL2 GNB4 PPP3R1 PLEK MT2A HSPB1 BCL2L2 LAMA5 PDGFRA RORA CNN2 PRKCG AKT3 NGEF ARHGAP31 ADD1 ICAM1 FERMT3 TJP1 FLT1 APP CSF1R KIT CCR5 ANXA5 ITGA2 NOS3 MEK1 PLK1 DDB1 BCL2L1 ARF4 BRSK1 DAB2 TENC1 CALR CDC25C ZFYX RORC JAG2 PRKCH RARB NR1I2 LCK SNCA CAV1 RGS12 PTGES MAP4K4 CDH5 ANXA2 ANXA6 FYN FN1 FAS ARHGEF26 EPHA2 MYO1C RXRG TGM2 DLL1 ARHGAP30 GSTO1 SLK FLNA PTPN1 SDC4 SPTAN1 DNM1 TLR4 RXRB ANXA1 SDC1 FSCN1 PPP3CA CAMK2B LTBR4 BCL2 CAMK2A CDC42 PDIA6 RARG FLNB SPTBN2 CFL1 ARF1 VIM NR1H4 PRKCSH CAMK1D	1.40E-17	GO.0007165
98	GO Process	signaling	ARHGEF5 MAP2K5 ITGB4 MYH9 CYP24A1 MMP2 CCL2 GNB4 PPP3R1 PLEK MT2A HSPB1 BCL2L2 LAMA5 PDGFRA RORA CNN2 PRKCG AKT3 NGEF ARHGAP31 ADD1 ICAM1 FERMT3 TJP1 FLT1 APP CSF1R KIT CCR5 ANXA5 ITGA2 NOS3 MEK1 PLK1 DDB1 BCL2L1 ARF4 BRSK1 DAB2 TENC1 NQO1 CALR CDC25C ZFYX RORC JAG2 PRKCH RARB NR1I2 LCK SNCA CAV1 RGS12 PTGES MAP4K4 CDH5 ANXA2 ANXA6 FYN FN1 FAS ARHGEF26 EPHA2 MYO1C RXRG TGM2 DLL1 ARHGAP30 GSTO1 SLK FLNA PTPN1 SDC4 SPTAN1 DNM1 TLR4 RXRB ANXA1 SDC1 FSCN1 PPP3CA CAMK2B LTBR4 BCL2 CAMK2A CDC42 PDIA6 RARG FLNB SPTBN2 CFL1 ARF1 VIM NR1H4 APBA2 PRKCSH CAMK1D	1.61E-16	GO.0023052
98	GO Process	cell communication	ARHGEF5 MAP2K5 ITGB4 MYH9 CYP24A1 MMP2 CCL2 GNB4 PPP3R1 PLEK MT2A HSPB1 BCL2L2 LAMA5 PDGFRA RORA CNN2 PRKCG AKT3 NGEF ARHGAP31 ADD1 ICAM1 FERMT3 TJP1 FLT1 APP CSF1R KIT CCR5 ANXA5 ITGA2 NOS3 MEK1 PLK1 DDB1 BCL2L1 ARF4 BRSK1 DAB2 TENC1 NQO1 CALR CDC25C ZFYX RORC JAG2 PRKCH RARB NR1I2 LCK SNCA CAV1 RGS12 PTGES MAP4K4 CDH5 ANXA2 ANXA6 FYN FN1 FAS ARHGEF26 EPHA2 MYO1C RXRG TGM2 DLL1 ARHGAP30 GSTO1 SLK FLNA PTPN1 SDC4 SPTAN1 DNM1 TLR4 RXRB ANXA1 SDC1 FSCN1 PPP3CA CAMK2B LTBR4 BCL2 CAMK2A CDC42 PDIA6 RARG FLNB SPTBN2 CFL1 ARF1 VIM NR1H4 APBA2 PRKCSH CAMK1D	6.56E-16	GO.0007154
66	GO Process	regulation of localization	ARHGEF5 MAP2K5 EHD4 CCL2 GAPDH LAMA4 HSPB1 LAMA5 PDGFRA THBS1 DNAJB6 PRKCG AKT3 ICAM1 FERMT3 FLT1 APP CSF1R KIT CCR5 ITGA2 NOS3 CCT2 PLK1 BCL2L1 MMP14 BRSK1 DAB2 CALR STXB6 PRKCH LCK SNCA CAV1 MAP4K4 ANXA2 FYN FN1 PTRF EPHA2 MYO1C MYH10 DPP4 DLL1 GSTO1 SLK FLNA PTPN1 MMRN2 SDC4 DNM1 TLR4 CLIC4 ANXA1 TBC1D4 SDC1 G6PD PPP3CA CAMK2B BCL2 CAMK2A ARF1 NR1H4 NUMB ABCB1 CAMK1D	2.01E-15	GO.0032879
68	GO Process	cellular response to chemical stimulus	ARHGEF5 MAP2K5 CYP24A1 MMP2 EHD4 APLP1 CCL2 GAPDH MT2A HSPB1 PXDN LAMA5 PDGFRA THBS1 RORA CNN2 CAD ADD1 ICAM1 FLT1 APP CSF1R KIT CCR5 CAPN2 ITGA2 NOS3 MEK1 BCL2L1 NQO1 CALR ZFYX RORC RARB NR1I2 SNCA CAV1 CDH5 ANXA2 FYN FN1 FAS EPHA2 MYO1C RXRG GSTO1 PTPN1 TLR4 CLIC4 RXRB ANXA1 TBC1D4 SDC1 XRCC5 G6PD PPP3CA CAMK2B BCL2 CAMK2A CDC42 PDIA6 RARG FLNB CFL1 ARF1 VIM NR1H4	2.01E-15	GO.0070887

75	GO Process	response to stress	MAP2K5 PLOD1 ITGB4 MMP2 CCL2 GAPDH MT2A HSPB1 BCL2L2 PXD PDGFRA THBS1 VWF ROA PRKCG CAD ADD1 ICAM1 PLOD2 APP CSF1R KIT NPC1L1 CCR5 CAPN2 ANXA5 ITGA2 NOS3 MELK PLK1 DDB1 BCL2L1 ARF4 MMP14 BRSK1 NQO1 CALR CDC25C ZYX PRKCH LCK SNCA CAV1 TUBB4B PTGES USP1 FYN FN1 FAS SFPQ EPHA2 MYO1C MYH10 DPP4 SLK FLNA PTPN1 SDC4 TLR4 ANXA1 PSIP1 SDC1 XRCC5 G6PD PPP3CA CAMK2B LTBR4 BCL2 CAMK2A CDC42 PDIA6 FLNB VIM NR1H4 CAMK1D	3.17E-15	GO.0006950
96	GO Process	cellular component organization	ARHGEF5 ITGB4 MYH9 MMP2 EHD4 CCL2 GAPDH LAMA4 PLEK CDC25B PXD LAMA5 PDGFRA THBS1 COL8A1 VWF DNAJB6 CNN2 AKT3 TUBB4A ADD1 ICAM1 FERMT3 TJP1 APP CSF1R KIT CCR5 ITGA2 NOS3 CCT2 PLK1 TUBA1A TUBA1C DDB1 BCL2L1 SDPR ARF4 MMP14 BRSK1 DAB2 CALR ZYX FLNC SNCA CAV1 TUBB4B MAP4K4 CDH5 DOK4 PTMA TPM4 ANXA2 ANXA6 FYN FN1 FAS ARHGEF26 SFPQ EPHA2 MYO1C RXRG MYH10 TGM2 TPM3 SLK FLNA CNN3 PTPN1 SDC4 SPTAN1 DNM1 CLIC4 ANXA1 TPM2 PSIP1 FSCN1 XRCC5 MYO1B BCL2 CAMK2A SEPT7 CDC42 SUN1 RARG TOP2B WEE1 FLNB SPTBN2 CFL1 ARF1 VIM NR1H4 NUMB TLN2 ABCB1	3.17E-15	GO.0016043
69	GO Process	response to organic substance	MAP2K5 CYP24A1 MMP2 EHD4 APLP1 CCL2 GAPDH MT2A HSPB1 LAMA5 PDGFRA THBS1 ROA CNN2 PRKCG CAD ADD1 ICAM1 FLT1 APP CSF1R KIT CCR5 CAPN2 ANXA5 ITGA2 NOS3 BCL2L1 MMP14 NQO1 CALR ZYX RORC RARB NR1I2 SNCA CAV1 PTGES CDH5 ANXA2 FYN FN1 FAS EPHA2 MYO1C RXRG GSTO1 PTPN1 TLR4 RXRB ANXA1 TBC1D4 SDC1 FSCN1 XRCC5 G6PD PPP3CA CAMK2B BCL2 CAMK2A CDC42 PDIA6 RARG FLNB CFL1 ARF1 VIM NR1H4	4.53E-15	GO.0010033
61	GO Process	cellular response to organic substance	MAP2K5 CYP24A1 MMP2 EHD4 APLP1 CCL2 GAPDH MT2A HSPB1 LAMA5 PDGFRA THBS1 ROA CNN2 CAD ADD1 ICAM1 FLT1 APP CSF1R KIT CCR5 CAPN2 ITGA2 NOS3 BCL2L1 CALR ZYX RORC RARB NR1I2 SNCA CAV1 CDH5 ANXA2 FYN FN1 FAS MYO1C RXRG GSTO1 PTPN1 TLR4 RXRB ANXA1 TBC1D4 SDC1 FSCN1 XRCC5 PPP3CA CAMK2B BCL2 CAMK2A CDC42 PDIA6 RARG FLNB CFL1 ARF1 VIM NR1H4	4.53E-15	GO.0071310
50	GO Process	regulation of programmed cell death	ARHGEF5 MAP2K5 CCL2 GAPDH ENO1 HSPB1 BCL2L2 THBS1 DNAJB6 PRKCG NGEF ICAM1 APP CSF1R KIT CCR5 ANXA5 NOS3 MELK PLK1 DDB1 BCL2L1 ARF4 DAB2 NQO1 CALR RORC PRKCH RARB LCK SNCA CAV1 MAP4K4 FYN FAS ARHGEF26 SFPQ TGM2 DLL1 SLK FLNA PTPN1 ANXA1 G6PD BCL2 CAMK2A RARG CFL1 NR1H4 CAMK1D	8.45E-15	GO.0043067
40	GO Process	cytoskeleton organization	ARHGEF5 MYH9 CCL2 GAPDH PLEK LAMA5 PDGFRA DNAJB6 CNN2 TUBB4A ADD1 KIT PTK1 TUBA1A TUBA1C BRSK1 CALR ZYX TUBB4B TPM4 MYH10 TPM3 SLK FLNA CNN3 PTPN1 SPTAN1 ANXA1 TPM2 FSCN1 MYO1B BCL2 CDC42 SUN1 WEE1 FLNB SPTBN2 CFL1 VIM TLN2	1.13E-14	GO.0007010
49	GO Process	regulation of apoptotic process	ARHGEF5 MAP2K5 CCL2 GAPDH ENO1 HSPB1 BCL2L2 THBS1 DNAJB6 PRKCG NGEF ICAM1 APP CSF1R CCR5 ANXA5 NOS3 MELK PLK1 DDB1 BCL2L1 ARF4 DAB2 NQO1 CALR RORC PRKCH RARB LCK SNCA CAV1 MAP4K4 FYN FAS ARHGEF26 SFPQ TGM2 DLL1 SLK FLNA PTPN1 ANXA1 G6PD BCL2 CAMK2A RARG CFL1 NR1H4 CAMK1D	2.37E-14	GO.0042981
51	GO Process	regulation of cell death	ARHGEF5 MAP2K5 CCL2 GAPDH ENO1 HSPB1 BCL2L2 THBS1 DNAJB6 PRKCG NGEF ICAM1 APP CSF1R KIT CCR5 ANXA5 NOS3 MELK PLK1 DDB1 BCL2L1 ARF4 DAB2 NQO1 CALR RORC PRKCH RARB LCK SNCA CAV1 MAP4K4 FYN FAS ARHGEF26 SFPQ TGM2 DLL1 SLK FLNA PTPN1 TLR4 ANXA1 G6PD BCL2 CAMK2A RARG CFL1 NR1H4 CAMK1D	2.86E-14	GO.0010941
59	GO Process	cell surface receptor signaling pathway	ITGB4 MYH9 MMP2 CCL2 PPP3R1 PLEK MT2A HSPB1 BCL2L2 LAMA5 PDGFRA ROA CNN2 NGEF ICAM1 FERMT3 FLT1 APP CSF1R KIT CCR5 ITGA2 NOS3 DDB1 BCL2L1 ARF4 DAB2 ZYX RORC JAG2 LCK SNCA CAV1 CDH5 ANXA2 FYN FN1 FAS EPHA2 MYO1C DLL1 GSTO1 FLNA PTPN1 DNM1 TLR4 ANXA1 SDC1 FSCN1 PPP3CA CAMK2B BCL2 CAMK2A CDC42 RARG CFL1 ARF1 VIM NR1H4	3.66E-14	GO.0007166
37	GO Process	negative regulation of programmed cell death	MAP2K5 CCL2 ENO1 HSPB1 BCL2L2 THBS1 DNAJB6 PRKCG ICAM1 CSF1R KIT CCR5 ANXA5 NOS3 PLK1 DDB1 BCL2L1 ARF4 DAB2 NQO1 RORC PRKCH RARB SNCA CAV1 MAP4K4 FYN FAS DLL1 FLNA PTPN1 ANXA1 BCL2 RARG CFL1 NR1H4 CAMK1D	1.20E-13	GO.0043069
85	GO Process	negative regulation of cellular process	MAP2K5 MYH9 APLP1 CCL2 GAPDH PLEK ENO1 HSPB1 BCL2L2 PXD PDGFRA THBS1 ROA DNAJB6 PRKCG AKT3 NGEF TUBB4A ADD1 ICAM1 FLT1 APP CSF1R KIT CCR5 ANXA5 NOS3 PLK1 DDB1 BCL2L1 ARF4 MMP14 BRSK1 DAB2 TENC1 NQO1 CALR CDC25C STXB6P6 RORC PRKCH RARB NR1I2 LCK SNCA CAV1 RG512 PTGES MAP4K4 CDH5 ANXA2 FYN FN1 FAS SFPQ EPHA2 DPP4 ARHGEF15 DLL1 GSTO1 FLNA PTPN1 MNRN2 SDC4 SPTAN1 DNM1 TLR4 CLIC4 ANXA1 TBC1D4 XRCC5 G6PD PPP3CA BCL2 DYRK1A CDC42 RARG TOP2B PBK SPTBN2 CFL1 ARF1 VIM NR1H4 CAMK1D	1.72E-13	GO.0048523
75	GO Process	regulation of biological quality	MYH9 CCL2 GAPDH RBP1 PLEK MT2A HSPB1 PDGFRA THBS1 VWF ROA PRKCG AKT3 NGEF CAD ADD1 ICAM1 APP CSF1R KIT CCR5 ANXA5 ITGA2 NOS3 CKB CCT2 PLK1 DDB1 BCL2L1 BRSK1 TENC1 NQO1 CALR PRKCH CYP2R1 LCK SNCA CAV1 MAP4K4 ANXA2 ANXA6 FYN FN1 MYO1C MYH10 DPP4 ARHGEF15 TGM2 DLL1 COPA GSTO1 FLNA SPTAN1 TLR4 CLIC4 ANXA1 XRCC5 G6PD PPP3CA CAMK2B BCL2 CAMK2A SEPT7 CDC42 SUN1 PDIA6 RARG FLNB SPTBN2 CFL1 ARF1 VIM NR1H4 TLN2 ABCB1	1.72E-13	GO.0065008
145	GO Process	biological regulation	ARHGEF5 MAP2K5 ITGB4 MYH9 CYP24A1 MMP2 EHD4 APLP1 CCL2 GAPDH LAMA4 RBP1 GNB4 PPP3R1 PLEK ENO1 MT2A CDC25B HSPB1 BCL2L2 PXD LAMA5 PDGFRA THBS1 COL8A1 VWF ROA DNAJB6 CNN2 PRKCG AKT3 NGEF TUBB4A ARHGAP31 CAD ADD1 ICAM1 FERMT3 TJP1 FLT1 APP CSF1R KIT CCR5 CAPN2 ANXA5 ITGA2 NOS3 MELK CKB CCT2 PLK1 TUBA1A DDB1 BCL2L1 CDC25A ARF4 MMP14 BRSK1 DAB2 TENC1 NQO1 CALR CDC25C STXB6P6 ZYX RORC JAG2 PRKCH RARB CYP2R1 NR1I2 LCK SNCA CAV1 RG512 TUBB4B PTGES USP1 MAP4K4 CDH5 ANXA2 ANXA6 FYN FN1 FAS ARHGEF26 PTRF SFPQ EPHA2 MYO1C RXRG MYH10 DPP4 ARHGEF15 TGM2 DLL1 ARHGAP30 COPA GSTO1 SLK FLNA CNN3 PTPN1 MNRN2 SDC4 SPTAN1 DNM1 TLR4 CLIC4 RXRB ANXA1 TBC1D4 TPM2 PIR PSIP1 SDC1 FSCN1 XRCC5 G6PD PPP3CA CAMK2B LTBR4 BCL2 CAMK2A DYRK1A SEPT7 CDC42 SUN1 PDIA6 RARG TOP2B FLNB PBK SPTBN2 CFL1 ARF1 VIM NR1H4 NUMB APBA2 TLN2 PRKCSH ABCB1 CAMK1D	1.94E-13	GO.0065007

160	GO Process	cellular process	RCN1 ARHGEF5 MAP2K5 PLOC1 ITGB4 MYH9 CYP24A1 MMP2 EHD4 APLP1 CCL2 GAPDH LAMA4 BRP1 GNB4 PPP3R1 PLEK ENO1 MT2A CDC25B HSPB1 BCL2L2 PXDN LAMA5 ARF3 PDGFRA THBS1 COL8A1 VWF RORA DNAJB6 CNN2 PRKCG AKT3 NGEF TUBB4A ARHGAP31 CAD ADD1 ICAM1 EXOC68 FERMT3 TJP1 FLT1 PLOC2 APP CSF1R KIT NPCL1 CCR5 CAPN2 ANXA5 ITGA2 NOS3 MELK CKB CCT2 PLK1 TUBA1A TUBA1C DDB1 BCL2L1 CDC25A SDPR ARF4 MMP14 BRSK1 DAB2 TENC1 NQO1 CALR CDC25C ZYX RORC FLNC JAG2 PRKCH RARB CYP2R1 NR12 LCK SNCA CAV1 RG512 TUBB4B PTGES USP1 MAP4K4 CDH5 DOK4 PTMA TPM4 ANXA2 ANXA6 FYN FN1 FAS ARHGEF26 PTRF SFPQ EPHA2 MYO1C RXRG MYH10 DPP4 TGM2 DLL1 ARHGAP30 TPM3 GSTO1 SLK FLNA CNN3 PTPN1 MMRN2 SDC4 SPTAN1 DNM1 TLR4 CLIC4 RXRB ANXA1 TBC1D4 TPM2 PIR PSIP1 SDC1 FSCN1 XRCC5 MYO1B G6PD PPP3CA CAMK2B LDHB LTB4R BCL2 CAMK2A DYRK1A SEPT7 PAICS CDC42 SUN1 PDIA6 RARG TOP2B WEE1 FLNB PBK SPTBN2 CFL1 ARF1 VIM NR1H4 NUMB APBA2 TLN2 PRKCSH ABCB1 CAMK1D MCM3	2.27E-13	GO.0009987
38	GO Process	negative regulation of cell death	MAP2K5 CCL2 ENO1 HSPB1 BCL2L2 THBS1 DNAJB6 PRKCG ICAM1 APP CSF1R KIT CCR5 ANXA5 NOS3 PLK1 DDB1 BCL2L1 ARF4 DAB2 NQO1 RORC PRKCH RARB SNCA CAV1 MAP4K4 FYN FAS DLL1 FLNA PTPN1 ANXA1 BCL2 RARG CFL1 NR1H4 CAMK1D	2.37E-13	GO.0060548
89	GO Process	positive regulation of cellular process	ARHGEF5 MAP2K5 MYH9 MMP2 EHD4 CCL2 GAPDH PPP3R1 PLEK ENO1 CDC25B HSPB1 PDGFRA THBS1 RORA PRKCG AKT3 NGEF ADD1 ICAM1 FERMT3 FLT1 APP CSF1R KIT ITGA2 NOS3 MELK CCT2 PLK1 DDB1 BCL2L1 CDC25A ARF4 MMP14 DAB2 NQO1 CALR CDC25C RORC JAG2 PRKCH RARB NR12 LCK SNCA CAV1 MAP4K4 CDH5 ANXA2 FYN FN1 FAS ARHGEF26 PTRF SFPQ MYO1C RXRG MYH10 DPP4 ARHGEF15 TGM2 DLL1 GSTO1 SLK FLNA PTPN1 SDC4 DNM1 TLR4 RXRB ANXA1 PSIP1 SDC1 FSCN1 XRCC5 PPP3CA CAMK2B BCL2 CAMK2A DYRK1A SEPT7 CDC42 RARG CFL1 VIM NR1H4 NUMB CAMK1D	3.19E-13	GO.0048522
94	GO Process	developmental process	MAP2K5 PLOC1 ITGB4 MYH9 CYP24A1 MMP2 APLP1 CCL2 PPP3R1 PLEK CDC25B BCL2L2 LAMA5 PDGFRA THBS1 COL8A1 RORA PRKCG AKT3 NGEF CAD ADD1 ICAM1 FERMT3 TJP1 FLT1 APP CSF1R KIT CAPN2 ITGA2 NOS3 MELK CKB BCL2L1 ARF4 MMP14 BRSK1 DAB2 TENC1 NQO1 CALR RORC FLNC JAG2 PRKCH RARB LCK SNCA CAV1 USP1 MAP4K4 CDH5 DOK4 ANXA2 FYN FN1 FAS ARHGEF26 EPHA2 MYH10 ARHGEF15 TGM2 DLL1 FLNA CNN3 MMRN2 SDC4 SPTAN1 CLIC4 ANXA1 PIR SDC1 FSCN1 XRCC5 G6PD PPP3CA CAMK2B BCL2 CAMK2A DYRK1A SEPT7 CDC42 SUN1 RARG TOP2B WEE1 FLNB SPTBN2 CFL1 VIM NUMB APBA2 CAMK1D	3.27E-13	GO.0032502
81	GO Process	response to chemical	ARHGEF5 MAP2K5 CYP24A1 MMP2 EHD4 APLP1 CCL2 GAPDH MT2A HSPB1 PXDN LAMA5 PDGFRA THBS1 RORA CNN2 PRKCG CAD ADD1 ICAM1 FLT1 APP CSF1R KIT NPCL1 CCR5 CAPN2 ANXA5 ITGA2 NOS3 MELK BCL2L1 MMP14 NQO1 CALR ZYX RORC RARB CYP2R1 NR12 LCK SNCA CAV1 PTGES CDH5 DOK4 ANXA2 FYN FN1 FAS EPHA2 MYO1C RXRG MYH10 GSTO1 PTPN1 SPTAN1 DNM1 TLR4 CLIC4 RXRB ANXA1 TBC1D4 SDC1 FSCN1 XRCC5 G6PD PPP3CA CAMK2B BCL2 CAMK2A CDC42 PDIA6 RARG FLNB SPTBN2 CFL1 ARF1 VIM NR1H4 ABCB1	3.27E-13	GO.0042221
36	GO Process	negative regulation of apoptotic process	MAP2K5 CCL2 ENO1 HSPB1 BCL2L2 THBS1 DNAJB6 PRKCG ICAM1 CSF1R CCR5 ANXA5 NOS3 PLK1 DDB1 BCL2L1 ARF4 DAB2 NQO1 RORC PRKCH RARB SNCA CAV1 MAP4K4 FYN FAS DLL1 FLNA PTPN1 ANXA1 BCL2 RARG CFL1 NR1H4 CAMK1D	3.27E-13	GO.0043066
54	GO Process	anatomical structure morphogenesis	ITGB4 MYH9 MMP2 APLP1 CCL2 PPP3R1 LAMA5 PDGFRA THBS1 COL8A1 RORA AKT3 ADP1 FERMT3 FLT1 APP CSF1R CAPN2 ITGA2 NOS3 BCL2L1 MMP14 BRSK1 JAG2 RARB CAV1 MAP4K4 DOK4 ANXA2 FYN FN1 ARHGEF26 EPHA2 MYH10 ARHGEF15 TGM2 DLL1 FLNA MMRN2 SDC4 SPTAN1 CLIC4 SDC1 FSCN1 BCL2 CAMK2A CDC42 RARG TOP2B WEE1 FLNB SPTBN2 CFL1 NUMB	5.02E-13	GO.0009653
90	GO Process	anatomical structure development	MAP2K5 PLOC1 ITGB4 MYH9 MMP2 APLP1 CCL2 PPP3R1 PLEK CDC25B BCL2L2 LAMA5 PDGFRA THBS1 COL8A1 RORA PRKCG AKT3 NGEF CAD ADD1 ICAM1 FERMT3 TJP1 FLT1 APP CSF1R KIT CAPN2 ITGA2 NOS3 MELK CKB BCL2L1 ARF4 MMP14 BRSK1 DAB2 TENC1 CALR RORC FLNC JAG2 PRKCH RARB LCK CAV1 USP1 MAP4K4 CDH5 DOK4 ANXA2 FYN FN1 FAS ARHGEF26 EPHA2 MYH10 ARHGEF15 TGM2 DLL1 FLNA CNN3 MMRN2 SDC4 SPTAN1 CLIC4 ANXA1 PIR SDC1 FSCN1 XRCC5 G6PD PPP3CA CAMK2B BCL2 CAMK2A DYRK1A CDC42 SUN1 RARG TOP2B WEE1 FLNB SPTBN2 CFL1 VIM NUMB APBA2 CAMK1D	8.31E-13	GO.0048856
44	GO Process	movement of cell or subcellular component	ARHGEF5 ITGB4 MYH9 CCL2 HSPB1 LAMA5 PDGFRA THBS1 ICAM1 FLT1 APP CSF1R KIT CCR5 ITGA2 NOS3 ARF4 MMP14 LCK CAV1 DOK4 TPM4 FYN FN1 EPHA2 MYO1C MYH10 DPP4 TPM3 FLNA MMRN2 SDC4 SPTAN1 ANXA1 TPM2 SDC1 FSCN1 MYO1B CDC42 SUN1 TOP2B SPTBN2 CFL1 VIM	8.59E-13	GO.0006928
93	GO Process	positive regulation of biological process	ARHGEF5 MAP2K5 MYH9 MMP2 EHD4 CCL2 GAPDH PPP3R1 PLEK ENO1 CDC25B HSPB1 PDGFRA THBS1 COL8A1 RORA PRKCG AKT3 NGEF ADD1 ICAM1 FERMT3 FLT1 APP CSF1R KIT ITGA2 NOS3 MELK CCT2 PLK1 DDB1 BCL2L1 CDC25A ARF4 MMP14 DAB2 TENC1 CALR CDC25C RORC JAG2 PRKCH RARB NR12 LCK SNCA CAV1 MAP4K4 CDH5 ANXA2 FYN FN1 FAS ARHGEF26 PTRF SFPQ EPHA2 MYO1C RXRG MYH10 DPP4 ARHGEF15 TGM2 DLL1 GSTO1 SLK FLNA PTPN1 SDC4 DNM1 TLR4 RXRB ANXA1 PSIP1 SDC1 FSCN1 XRCC5 G6PD PPP3CA CAMK2B BCL2 CAMK2A DYRK1A SEPT7 CDC42 RARG CFL1 VIM NR1H4 NUMB ABCB1 CAMK1D	1.92E-12	GO.0048518
79	GO Process	system development	MAP2K5 ITGB4 MYH9 MMP2 APLP1 CCL2 PPP3R1 PLEK BCL2L2 LAMA5 PDGFRA THBS1 COL8A1 RORA PRKCG AKT3 NGEF CAD ADD1 ICAM1 FLT1 APP CSF1R KIT ITGA2 NOS3 MELK CKB BCL2L1 ARF4 MMP14 BRSK1 TENC1 CALR RORC JAG2 PRKCH RARB LCK CAV1 USP1 MAP4K4 CDH5 DOK4 ANXA2 FYN FN1 EPHA2 MYH10 ARHGEF15 TGM2 DLL1 FLNA MMRN2 SDC4 SPTAN1 CLIC4 ANXA1 PIR SDC1 XRCC5 G6PD PPP3CA CAMK2B BCL2 CAMK2A DYRK1A CDC42 SUN1 RARG TOP2B WEE1 FLNB SPTBN2 CFL1 VIM NUMB APBA2 CAMK1D	2.97E-12	GO.0048731
71	GO Process	cell differentiation	ITGB4 MYH9 CYP24A1 MMP2 CCL2 PPP3R1 PLEK CDC25B LAMA5 PDGFRA COL8A1 RORA NGEF ADD1 ICAM1 FERMT3 TJP1 FLT1 APP CSF1R KIT CAPN2 ITGA2 BCL2L1 ARF4 MMP14 BRSK1 DAB2 CALR RORC FLNC JAG2 PRKCH RARB LCK CAV1 MAP4K4 DOK4 ANXA2 FYN FN1 ARHGEF26 EPHA2 MYH10 DLL1 FLNA CNN3 SDC4 SPTAN1 CLIC4 ANXA1 PIR SDC1 XRCC5 G6PD PPP3CA CAMK2B BCL2 CAMK2A SEPT7 CDC42 SUN1 RARG TOP2B WEE1 FLNB SPTBN2 CFL1 VIM NUMB CAMK1D	4.02E-12	GO.0030154
87	GO Process	negative regulation of biological process	MAP2K5 MYH9 APLP1 CCL2 GAPDH PLEK ENO1 MT2A HSPB1 BCL2L2 PXDN PDGFRA THBS1 RORA DNAJB6 PRKCG AKT3 NGEF TUBB4A ADD1 ICAM1 FLT1 APP CSF1R KIT CCR5 ANXA5 NOS3 PLK1 DDB1 BCL2L1 ARF4 MMP14 BRSK1 DAB2 TENC1 NQO1 CALR CDC25C TXBP6 RORC PRKCH RARB NR12 LCK SNCA CAV1 RG512 PTGES MAP4K4 CDH5 ANXA2 FYN FN1 FAS SFPQ EPHA2 DPP4 ARHGEF15 DLL1 GSTO1 FLNA PTPN1 MMRN2 SDC4 SPTAN1 DNM1 TLR4 CLIC4 ANXA1 TBC1D4 XRCC5 G6PD PPP3CA BCL2 DYRK1A CDC42 RARG TOP2B PBK SPTBN2 CFL1 ARF1 VIM NR1H4 NUMB CAMK1D	5.37E-12	GO.0048519
37	GO Process	response to cytokine	MMP2 CCL2 GAPDH MT2A LAMA5 THBS1 RORA CNN2 ICAM1 CSF1R KIT CCR5 BCL2L1 ZYX RORC SNCA PTGES ANXA2 FYN FN1 FAS MYO1C GSTO1 TLR4 ANXA1 SDC1 FSCN1 XRCC5 CAMK2B BCL2 CAMK2A CDC42 RARG FLNB CFL1 ARF1 VIM	1.05E-11	GO.0034097
34	GO Process	regulation of locomotion	MAP2K5 CCL2 LAMA4 HSPB1 LAMA5 PDGFRA THBS1 AKT3 ICAM1 FERMT3 FLT1 APP CSF1R KIT ITGA2 NOS3 DDB1 MMP14 DAB2 CALR SNCA FN1 PTRF EPHA2 MYO1C SLK FLNA MMRN2 SDC4 CLIC4 ANXA1 BCL2 NUMB CAMK1D	1.52E-11	GO.0040012

133	GO Process	regulation of cellular process	ARHGEF5 MAP2K5 ITGB4 MYH9 CYP24A1 MMP2 EHD4 APLP1 CCL2 GAPDH LAMA4 GNB4 PPP3R1 PLEK ENO1 MT2A CDC25B HSPB1 BCL2L2 PXDN LAMA5 PDGFRA THBS1 RORA DNAJB6 CNN2 PRKCG AKT3 NGEF TUBB4A ARHGAP31 ADD1 ICAM1 FERMT3 TJP1 FLT1 APP CSF1R KIT CCR5 CAPN2 ANXA5 ITGA2 NOS3 MELK CCT2 PLK1 TUBA1A DDB1 BCL2L1 CDC25A ARF4 MMP14 BRSK1 DAB2 TENC1 NQO1 CALR CDC25C STXB6 ZFYX RORC JAG2 PRKCH RARB NR1I2 LCK SNCA CAV1 RG512 TUBB4B PTGES USP1 MAP4K4 CDH5 ANXA2 ANXA6 FYN FN1 FAS ARHGEF26 PTRF SFPQ EPHA2 MYO1C RXRG MYH10 DPP4 ARHGEF15 TGM2 DLL1 ARHGAP30 COPA GSTO1 SLK FLNA PTPN1 MMRN2 SDC4 SPTAN1 DNM1 TLR4 CLIC4 RXRB ANXA1 TBC1D4 PIR PSIP1 SDC1 FSCN1 XRC5 G6PD PPP3CA CAMK2B LTB4R BCL2 CAMK2A DYRK1A SEPT7 CDC42 PDIA6 RARG TOP2B FLNB PBK SPTBN2 CFL1 ARF1 VIM NR1H4 NUMB PRKCSH CAMK1D	2.12E-11	GO.0050794
35	GO Process	cellular response to cytokine stimulus	MMP2 CCL2 GAPDH MT2A LAMA5 THBS1 RORA CNN2 ICAM1 CSF1R KIT CCR5 BCL2L1 ZYX RORC ANXA2 FYN FN1 FAS MYO1C GSTO1 TLR4 ANXA1 SDC1 FSCN1 XRC5 CAMK2B BCL2 CAMK2A CDC42 RARG FLNB CFL1 ARF1 VIM	2.37E-11	GO.0071345
56	GO Process	immune system process	ARHGEF5 MYH9 CCL2 GAPDH PLEK MT2A PXDN PDGFRA THBS1 RORA CNN2 ADD1 ICAM1 FLT1 APP CSF1R KIT CCR5 MELK CCT2 CALR ZYX RORC JAG2 LCK SNCA CAV1 TUBB4B ANXA2 FYN FN1 FAS SFPQ EPHA2 MYO1C DPP4 DLL1 SDC4 SPTAN1 TLR4 ANXA1 PIR SDC1 XRC5 G6PD PPP3CA CAMK2B LTB4R BCL2 CAMK2A CDC42 FLNB SPTBN2 ARF1 VIM NR1H4	2.77E-11	GO.0002376
31	GO Process	regulation of cell migration	MAP2K5 CCL2 LAMA4 HSPB1 LAMA5 PDGFRA THBS1 AKT3 ICAM1 FERMT3 FLT1 APP CSF1R KIT ITGA2 NOS3 MMP14 DAB2 CALR FN1 EPHA2 MYO1C SLK FLNA MMRN2 SDC4 CLIC4 ANXA1 BCL2 NUMB CAMK1D	3.86E-11	GO.0030334
32	GO Process	regulation of cell motility	MAP2K5 CCL2 LAMA4 HSPB1 LAMA5 PDGFRA THBS1 AKT3 ICAM1 FERMT3 FLT1 APP CSF1R KIT ITGA2 NOS3 MMP14 DAB2 CALR FN1 PTRF EPHA2 MYO1C SLK FLNA MMRN2 SDC4 CLIC4 ANXA1 BCL2 NUMB CAMK1D	3.92E-11	GO.2000145
100	GO Process	multicellular organismal process	MAP2K5 ITGB4 MYH9 CYP24A1 MMP2 APLP1 CCL2 PPP3R1 PLEK CDC25B BCL2L2 LAMA5 PDGFRA THBS1 COL8A1 VWF RORA PRKCG AKT3 NGEF CAD ADD1 ICAM1 FLT1 APP CSF1R KIT NPC1L1 CAPN2 ANXA5 ITGA2 NOS3 MELK CKB PLK1 BCL2L1 ARF4 MMP14 BRSK1 DAB2 TENC1 CALR CDC25C RORC JAG2 PRKCH RARB LCK SNCA CAV1 USP1 MAP4K4 CDH5 DOK4 TPM4 ANXA2 FYN FN1 FAS EPHA2 MYH10 DPP4 ARHGEF15 TGM2 DLL1 COPA TPM3 FLNA MMRN2 SDC4 SPTAN1 DNM1 TLR4 CLIC4 ANXA1 TPM2 PIR SDC1 XRC5 G6PD PPP3CA CAMK2B LTB4R BCL2 CAMK2A DYRK1A SEPT7 CDC42 SUN1 RARG TOP2B WEE1 FLNB SPTBN2 CFL1 VIM NR1H4 NUMB APBA2 CAMK1D	4.51E-11	GO.0032501
34	GO Process	protein phosphorylation	MAP2K5 CCL2 CDC25B PDGFRA PRKCG AKT3 CAD FLT1 APP CSF1R KIT CCR5 MELK PLK1 BRSK1 PRKCH LCK MAP4K4 FYN EPHA2 SLK PTPN1 SPTAN1 TLR4 CAMK2B BCL2 CAMK2A DYRK1A CDC42 WEE1 PBK SPTBN2 CFL1 CAMK1D	4.57E-11	GO.0006468
43	GO Process	cell development	MYH9 PPP3R1 CDC25B LAMA5 PDGFRA ICAM1 FERMT3 TJP1 APP CSF1R KIT BCL2L1 ARF4 BRSK1 FLNC RARB MAP4K4 DOK4 ANXA2 FYN FN1 ARHGEF26 EPHA2 MYH10 DLL1 FLNA SDC4 SPTAN1 CLIC4 SDC1 G6PD PPP3CA BCL2 CAMK2A CDC42 RARG TOP2B WEE1 FLNB SPTBN2 CFL1 VIM NUMB	6.94E-11	GO.0048468
33	GO Process	regulation of cellular component movement	MAP2K5 CCL2 LAMA4 HSPB1 LAMA5 PDGFRA THBS1 AKT3 ICAM1 FERMT3 FLT1 APP CSF1R KIT ITGA2 NOS3 MMP14 DAB2 CALR CAV1 FN1 PTRF EPHA2 MYO1C SLK FLNA MMRN2 SDC4 CLIC4 ANXA1 BCL2 NUMB CAMK1D	7.65E-11	GO.0051270
82	GO Process	multicellular organism development	MAP2K5 ITGB4 MYH9 MMP2 APLP1 CCL2 PPP3R1 PLEK BCL2L2 LAMA5 PDGFRA THBS1 COL8A1 RORA PRKCG AKT3 NGEF CAD ADD1 ICAM1 FLT1 APP CSF1R KIT CAPN2 ITGA2 NOS3 MELK CKB BCL2L1 ARF4 MMP14 BRSK1 DAB2 TENC1 CALR RORC JAG2 PRKCH RARB LCK CAV1 USP1 MAP4K4 CDH5 DOK4 ANXA2 FYN FN1 FAS EPHA2 MYH10 ARHGEF15 TGM2 DLL1 FLNA MMRN2 SDC4 SPTAN1 CLIC4 ANXA1 PIR SDC1 XRC5 G6PD PPP3CA CAMK2B BCL2 CAMK2A DYRK1A CDC42 SUN1 RARG TOP2B WEE1 FLNB SPTBN2 CFL1 VIM NUMB APBA2 CAMK1D	8.93E-11	GO.0007275
136	GO Process	regulation of biological process	ARHGEF5 MAP2K5 ITGB4 MYH9 CYP24A1 MMP2 EHD4 APLP1 CCL2 GAPDH LAMA4 GNB4 PPP3R1 PLEK ENO1 MT2A CDC25B HSPB1 BCL2L2 PXDN LAMA5 PDGFRA THBS1 COL8A1 RORA DNAJB6 CNN2 PRKCG AKT3 NGEF TUBB4A ARHGAP31 ADD1 ICAM1 FERMT3 TJP1 FLT1 APP CSF1R KIT CCR5 CAPN2 ANXA5 ITGA2 NOS3 MELK CCT2 PLK1 TUBA1A DDB1 BCL2L1 CDC25A ARF4 MMP14 BRSK1 DAB2 TENC1 NQO1 CALR CDC25C STXB6 ZFYX RORC JAG2 PRKCH RARB NR1I2 LCK SNCA CAV1 RG512 TUBB4B PTGES USP1 MAP4K4 CDH5 ANXA2 ANXA6 FYN FN1 FAS ARHGEF26 PTRF SFPQ EPHA2 MYO1C RXRG MYH10 DPP4 ARHGEF15 TGM2 DLL1 ARHGAP30 COPA GSTO1 SLK FLNA PTPN1 MMRN2 SDC4 SPTAN1 DNM1 TLR4 CLIC4 RXRB ANXA1 TBC1D4 PIR PSIP1 SDC1 FSCN1 XRC5 G6PD PPP3CA CAMK2B BCL2 CAMK2A DYRK1A SEPT7 CDC42 PDIA6 RARG TOP2B FLNB PBK SPTBN2 CFL1 ARF1 VIM NR1H4 NUMB APBA2 PRKCSH ABC1 CAMK1D	1.07E-10	GO.0050789
25	GO Process	actin filament-based process	ARHGEF5 MYH9 PLEK PDGFRA CNN2 ADD1 KIT CALR ZYX TPM4 MYO1C MYH10 TPM3 FLNA CNN3 PTPN1 ANXA1 TPM2 FSCN1 MYO1B BCL2 CDC42 FLNB CFL1 VIM	1.10E-10	GO.0030029
23	GO Process	actin cytoskeleton organization	ARHGEF5 MYH9 PLEK PDGFRA CNN2 ADD1 KIT CALR ZYX TPM4 MYH10 TPM3 FLNA CNN3 PTPN1 ANXA1 TPM2 FSCN1 MYO1B BCL2 CDC42 FLNB CFL1	1.92E-10	GO.0030036
32	GO Process	regulation of cellular component biogenesis	ARHGEF5 PLEK THBS1 DNAJB6 TUBB4A ADD1 ICAM1 TJP1 KIT PLK1 DDB1 MMP14 STXB6 PRKCH SNCA CAV1 EPHA2 MYO1C ARHGEF15 SLK FLNA SDC4 SPTAN1 TLR4 SDC1 FSCN1 XRC5 DYRK1A SEPT7 CDC42 SPTBN2 ARF1	2.05E-10	GO.0044087
61	GO Process	animal organ development	MAP2K5 ITGB4 MYH9 MMP2 APLP1 CCL2 PPP3R1 PLEK BCL2L2 LAMA5 PDGFRA COL8A1 RORA AKT3 CAD ADD1 ICAM1 APP CSF1R KIT ITGA2 NOS3 MELK CKB BCL2L1 ARF4 MMP14 TENC1 CALR RORC JAG2 RARB LCK CAV1 ANXA2 FYN FN1 EPHA2 MYH10 ARHGEF15 TGM2 DLL1 FLNA SDC4 CLIC4 ANXA1 PIR SDC1 XRC5 G6PD PPP3CA BCL2 CDC42 SUN1 RARG TOP2B FLNB SPTBN2 CFL1 VIM NUMB	2.57E-10	GO.0048513
38	GO Process	phosphorylation	MAP2K5 CCL2 GAPDH ENO1 CDC25B PDGFRA PRKCG AKT3 CAD FLT1 APP CSF1R KIT CCR5 MELK CKB PLK1 BRSK1 PRKCH LCK SNCA MAP4K4 FYN EPHA2 SLK PTPN1 SPTAN1 TLR4 CAMK2B BCL2 CAMK2A DYRK1A CDC42 WEE1 PBK SPTBN2 CFL1 CAMK1D	2.69E-10	GO.0016310
50	GO Process	phosphate-containing compound metabolic process	MAP2K5 CCL2 GAPDH PPP3R1 PLEK ENO1 CDC25B ARF3 PDGFRA RORA PRKCG AKT3 CAD FLT1 APP CSF1R KIT CCR5 MELK CKB PLK1 CDC25A BRSK1 TENC1 CDC25C PRKCH LCK SNCA MAP4K4 FYN EPHA2 SLK PTPN1 SPTAN1 TLR4 G6PD PPP3CA CAMK2B LDHB BCL2 CAMK2A DYRK1A PAICS CDC42 WEE1 PBK SPTBN2 CFL1 ARF1 CAMK1D	2.72E-10	GO.0006796
45	GO Process	positive regulation of molecular function	ARHGEF5 MAP2K5 CCL2 PLEK CDC25B PDGFRA THBS1 DNAJB6 ARHGAP31 ADD1 ICAM1 FLT1 APP CSF1R KIT ITGA2 NOS3 CCT2 PLK1 ARF4 PRKCH LCK SNCA CAV1 RG512 MAP4K4 ANXA2 FYN FN1 FAS EPHA2 ARHGEF15 ARHGAP30 GSTO1 SLK PTPN1 SDC4 TLR4 TBC1D4 XRC5 PPP3CA BCL2 CAMK2A ABC1 CAMK1D	3.19E-10	GO.0044093
36	GO Process	positive regulation of cellular component organization	ARHGEF5 CCL2 PLEK ADD1 ICAM1 APP KIT ITGA2 CCT2 DDB1 DAB2 CALR SNCA CAV1 ANXA2 FYN FN1 SFPQ MYO1C ARHGEF15 DLL1 FLNA SDC4 DNM1 TLR4 ANXA1 SDC1 FSCN1 XRC5 PPP3CA CAMK2B BCL2 SEPT7 CDC42 CFL1 CAMK1D	3.78E-10	GO.0051130
42	GO Process	intracellular signal transduction	ARHGEF5 MAP2K5 CCL2 PPP3R1 PLEK HSPB1 BCL2L2 PDGFRA PRKCG AKT3 ARHGAP31 TJP1 APP CSF1R KIT CCR5 NOS3 MELK PLK1 BCL2L1 BRSK1 TENC1 CDC25C PRKCH MAP4K4 FYN EPHA2 ARHGAP30 GSTO1 SLK PTPN1 SPTAN1 TLR4 PPP3CA CAMK2B BCL2 CAMK2A CDC42 SPTBN2 CFL1 PRKCSH CAMK1D	4.74E-10	GO.0035556

65	GO Process	regulation of molecular function	ARHGEF5 MAP2K5 CCL2 GAPDH PLEK CDC25B HSPB1 PXDN PDGFRA THBS1 DNAJB6 NGEF ARHGAP31 ADD1 ICAM1 FLT1 APP CSF1R KIT ANXA5 ITGA2 NOS3 CCT2 PLK1 CDC25A ARF4 DAB2 NQO1 CDC25C JAG2 PRKCH LCK SNCA CAV1 RGS12 MAP4K4 ANXA2 FYN FN1 FAS ARHGEF26 EPHA2 ARHGEF15 ARHGAP30 COPA GSTO1 SLK FLNA CNN3 PTPN1 SDC4 SPTAN1 TLR4 ANXA1 TBC1D4 TPM2 XRCC5 PPP3CA CAMK2B BCL2 CAMK2A SPTBN2 NR1H4 ABCB1 CAMK1D	5.02E-10	GO.0065009
36	GO Process	locomotion	ARHGEF5 ITGB4 MYH9 CCL2 LAMA5 PDGFRA THBS1 ICAM1 FLT1 APP CSF1R KIT CCR5 ITGA2 NOS3 ARF4 MMP14 LCK CAV1 DOK4 FYN FN1 EPHA2 MYH10 DPP4 FLNA MMRN2 SDC4 SPTAN1 ANXA1 SDC1 FSCN1 SUN1 TOP2B SPTBN2 CFL1	5.26E-10	GO.0040011
36	GO Process	regulation of organelle organization	ARHGEF5 PLEK PDGFRA TUBB4A ADD1 ICAM1 APP CSF1R CAPN2 CCT2 PLK1 BCL2L1 CALR CDC25C STXBP6 SNCA ANXA2 SFPQ MYO1C ARHGEF15 FLNA SDC4 SPTAN1 CLIC4 ANXA1 TBC1D4 SDC1 FSCN1 XRCC5 BCL2 DYRK1A SEPT7 CDC42 SPTBN2 CFL1 ARF1	6.74E-10	GO.0033043
71	GO Process	regulation of response to stimulus	ARHGEF5 MAP2K5 MMP2 APLP1 CCL2 PPP3R1 PLEK ENO1 HSPB1 BCL2L2 PXDN PDGFRA THBS1 RORA DNAJB6 PRKCG AKT3 NGEF ARHGAP31 ICAM1 FLT1 APP CSF1R KIT ITGA2 NOS3 BCL2L1 MMP14 DAB2 CALR ZYX JAG2 PRKCH LCK SNCA CAV1 RGS12 USP1 MAP4K4 CDH5 ANXA2 FYN FN1 FAS ARHGEF26 SFPQ EPHA2 MYO1C ARHGEF15 TGM2 DLL1 ARHGAP30 COPA GSTO1 FLNA PTPN1 MMRN2 DNM1 TLR4 ANXA1 XRCC5 G6PD PPP3CA CAMK2B BCL2 DYRK1A CDC42 PBK NR1H4 ABCB1 CAMK1D	6.74E-10	GO.0048583
85	GO Process	localization	ARHGEF5 ITGB4 MYH9 EHD4 APLP1 CCL2 PPP3R1 PLEK HSPB1 LAMA5 ARF3 PDGFRA THBS1 VWF CNN2 TUBB4A CAD ADD1 ICAM1 EXOC6B FERMT3 FLT1 APP KIT NPCL1 CCR5 ANXA5 ITGA2 NOS3 CCT2 PLK1 TUBA1A TUBA1C BCL2L1 ARF4 MMP14 BRSK1 DAB2 CALR STXBP6 NR12 LCK SNCA CAV1 TUBB4B ANXA2 ANXA6 FYN FN1 EPHA2 MYO1C MYH10 DPP4 TGM2 DLL1 COPA FLNA MMRN2 SDC4 SPTAN1 DNM1 TLR4 CLIC4 ANXA1 TBC1D4 PSIP1 SDC1 FSCN1 XRCC5 MYO1B PPP3CA BCL2 CAMK2A CDC42 SUN1 PDIA6 TOP2B FLNB SPTBN2 CFL1 ARF1 NR1H4 APBA2 TLN2 ABCB1	7.19E-10	GO.0051179
24	GO Process	positive regulation of locomotion	HSPB1 PDGFRA THBS1 AKT3 ICAM1 FERMT3 FLT1 APP CSF1R KIT ITGA2 NOS3 DDB1 MMP14 DAB2 CALR FN1 PTRF MYO1C FLNA ANXA1 BCL2 NUMB CAMK1D	8.43E-10	GO.0040017
30	GO Process	cell migration	ARHGEF5 MYH9 CCL2 LAMA5 PDGFRA THBS1 ICAM1 FLT1 KIT CCR5 ITGA2 NOS3 ARF4 MMP14 LCK CAV1 FYN FN1 EPHA2 MYH10 DPP4 FLNA MMRN2 SDC4 ANXA1 SDC1 FSCN1 SUN1 TOP2B CFL1	8.51E-10	GO.0016477
27	GO Process	cytokine-mediated signaling pathway	MMP2 CCL2 MT2A LAMA5 RORA CNN2 ICAM1 CSF1R KIT CCR5 BCL2L1 RORC ANXA2 FYN FN1 FAS GSTO1 ANXA1 SDC1 FSCN1 CAMK2B BCL2 CAMK2A CDC42 CFL1 ARF1 VIM	9.48E-10	GO.0019221
19	GO Process	angiogenesis	MYH9 MMP2 CCL2 PPP3R1 LAMA5 PDGFRA THBS1 COL8A1 RORA FLT1 NOS3 MMP14 CAV1 ANXA2 FN1 EPHA2 DLL1 MMRN2 CLIC4	1.18E-09	GO.0001525
23	GO Process	positive regulation of cell motility	HSPB1 PDGFRA THBS1 AKT3 ICAM1 FERMT3 FLT1 APP CSF1R KIT ITGA2 NOS3 MMP14 DAB2 CALR FN1 PTRF MYO1C FLNA ANXA1 BCL2 NUMB CAMK1D	1.31E-09	GO.2000147
44	GO Process	regulation of transport	ARHGEF5 EHD4 CCL2 GAPDH THBS1 PRKCG ICAM1 APP CSF1R ITGA2 NOS3 BRSK1 DAB2 CALR STXBP6 SNCA CAV1 MAP4K4 ANXA2 FYN FN1 MYO1C MYH10 DPP4 DLL1 GSTO1 FLNA PTPN1 SDC4 DNM1 TLR4 CLIC4 ANXA1 TBC1D4 SDC1 G6PD PPP3CA CAMK2B BCL2 CAMK2A ARF3 NR1H4 ABCB1 CAMK1D	1.41E-09	GO.0051049
53	GO Process	regulation of developmental process	MAP2K5 MYH9 CCL2 LAMA4 HSPB1 LAMA5 PDGFRA THBS1 RORA AKT3 NGEF ADD1 ICAM1 FLT1 APP CSF1R KIT NOS3 MMP14 BRSK1 DAB2 CALR RORC PRKCH RARB SNCA CAV1 MAP4K4 CDH5 ANXA2 FYN FN1 EPHA2 MYH10 ARHGEF15 DLL1 FLNA MMRN2 TLR4 ANXA1 XRCC5 G6PD PPP3CA CAMK2B BCL2 SEPT7 CDC42 RARG CFL1 VIM NR1H4 NUMB CAMK1D	1.53E-09	GO.0050793
26	GO Process	regulation of cell adhesion	MAP2K5 CCL2 LAMA4 LAMA5 THBS1 COL8A1 ICAM1 FERMT3 ITGA2 MMP14 CALR JAG2 LCK CAV1 FYN FN1 EPHA2 DPP4 TGM2 DLL1 SLK FLNA SDC4 ANXA1 BCL2 CDC42	1.70E-09	GO.0030155
64	GO Process	regulation of signaling	ARHGEF5 MAP2K5 APLP1 CCL2 PLEK ENO1 HSPB1 BCL2L2 PXDN PDGFRA THBS1 RORA AKT3 NGEF ARHGAP31 ICAM1 FLT1 APP CSF1R KIT ITGA2 NOS3 BCL2L1 MMP14 BRSK1 DAB2 CALR JAG2 PRKCH LCK SNCA CAV1 RGS12 MAP4K4 ANXA2 FYN FN1 FAS ARHGEF26 SFPQ EPHA2 MYO1C DPP4 ARHGEF15 TGM2 DLL1 ARHGAP30 COPA GSTO1 FLNA PTPN1 MMRN2 DNM1 TLR4 ANXA1 PPP3CA CAMK2B BCL2 CAMK2A DYRK1A CDC42 PBK ARF1 NR1H4	2.11E-09	GO.0023051
29	GO Process	tube development	ITGB4 MYH9 MMP2 CCL2 PPP3R1 LAMA5 PDGFRA THBS1 COL8A1 RORA FLT1 CSF1R KIT NOS3 MMP14 RARB CAV1 ANXA2 FN1 EPHA2 TGM2 DLL1 MMRN2 SDC4 CLIC4 SDC1 BCL2 RARG CFL1	2.19E-09	GO.0035295
40	GO Process	negative regulation of response to stimulus	MAP2K5 APLP1 CCL2 PLEK ENO1 HSPB1 BCL2L2 PXDN PDGFRA THBS1 RORA AKT3 ICAM1 APP NOS3 BCL2L1 MMP14 DAB2 CALR SNCA CAV1 RGS12 MAP4K4 CDH5 ANXA2 FYN FAS EPHA2 GSTO1 PTPN1 MMRN2 DNM1 TLR4 ANXA1 PPP3CA BCL2 DYRK1A CDC42 PBK NR1H4	2.35E-09	GO.0048585
31	GO Process	cell motility	ARHGEF5 ITGB4 MYH9 CCL2 LAMA5 PDGFRA THBS1 ICAM1 FLT1 KIT CCR5 ITGA2 NOS3 ARF4 MMP14 LCK CAV1 FYN FN1 EPHA2 MYH10 DPP4 FLNA MMRN2 SDC4 ANXA1 SDC1 FSCN1 SUN1 TOP2B CFL1	2.56E-09	GO.0048870
22	GO Process	positive regulation of cell migration	HSPB1 PDGFRA THBS1 AKT3 ICAM1 FERMT3 FLT1 APP CSF1R KIT ITGA2 NOS3 MMP14 DAB2 CALR FN1 MYO1C FLNA ANXA1 BCL2 NUMB CAMK1D	3.72E-09	GO.0030335
63	GO Process	regulation of cell communication	ARHGEF5 MAP2K5 APLP1 CCL2 PLEK ENO1 HSPB1 BCL2L2 PXDN PDGFRA THBS1 RORA AKT3 NGEF ARHGAP31 ICAM1 FLT1 APP CSF1R KIT ITGA2 NOS3 BCL2L1 MMP14 BRSK1 DAB2 CALR JAG2 PRKCH LCK SNCA CAV1 RGS12 MAP4K4 FYN FN1 FAS ARHGEF26 SFPQ EPHA2 MYO1C DPP4 ARHGEF15 TGM2 DLL1 ARHGAP30 COPA GSTO1 FLNA PTPN1 MMRN2 DNM1 TLR4 ANXA1 PPP3CA CAMK2B BCL2 CAMK2A DYRK1A CDC42 PBK ARF1 NR1H4	3.94E-09	GO.0010646
27	GO Process	cellular component morphogenesis	MYH9 LAMA5 PDGFRA ADD1 FERMT3 APP CSF1R BCL2L1 BRSK1 MAP4K4 DOK4 FYN FN1 ARHGEF26 EPHA2 MYH10 FLNA SPTAN1 CLIC4 BCL2 CAMK2A CDC42 TOP2B WEE1 FLNB SPTBN2 NUMB	6.12E-09	GO.0032989
25	GO Process	tube morphogenesis	MYH9 MMP2 CCL2 PPP3R1 LAMA5 PDGFRA THBS1 COL8A1 RORA FLT1 CSF1R NOS3 MMP14 CAV1 ANXA2 FN1 EPHA2 TGM2 DLL1 MMRN2 SDC4 CLIC4 BCL2 RARG CFL1	6.37E-09	GO.0035239
19	GO Process	regulation of actin filament-based process	ARHGEF5 MYH9 PLEK PDGFRA CNN2 ADD1 ICAM1 CSF1R CAV1 MYO1C ARHGEF15 FLNA SDC4 SPTAN1 FSCN1 CDC42 SPTBN2 CFL1 ARF1	7.85E-09	GO.0032970
56	GO Process	regulation of multicellular organismal process	MAP2K5 GAPDH LAMA4 PLEK ENO1 HSPB1 LAMA5 PDGFRA THBS1 RORA AKT3 NGEF ADD1 ICAM1 FLT1 APP CSF1R KIT ANXA5 ITGA2 NOS3 MMP14 BRSK1 DAB2 CALR PRKCH RARB SNCA CAV1 MAP4K4 CDH5 ANXA2 ANXA6 FYN FN1 EPHA2 ARHGEF15 DLL1 GSTO1 FLNA MMRN2 TLR4 ANXA1 XRCC5 G6PD PPP3CA CAMK2B BCL2 SEPT7 CDC42 RARG CFL1 VIM NR1H4 NUMB CAMK1D	8.30E-09	GO.0051239
25	GO Process	cell morphogenesis	MYH9 LAMA5 ADD1 FERMT3 APP CSF1R BRSK1 MAP4K4 DOK4 FYN FN1 ARHGEF26 EPHA2 MYH10 FLNA SPTAN1 CLIC4 BCL2 CAMK2A CDC42 TOP2B WEE1 FLNB SPTBN2 NUMB	8.78E-09	GO.0000902
22	GO Process	regulation of cytoskeleton organization	ARHGEF5 PLEK PDGFRA TUBB4A ADD1 ICAM1 CSF1R CAPN2 PLK1 SNCA MYO1C ARHGEF15 FLNA SDC4 SPTAN1 CLIC4 FSCN1 DYRK1A CDC42 SPTBN2 CFL1 ARF1	9.12E-09	GO.0051493
16	GO Process	regulation of endocytosis	EHD4 CCL2 PRKCG APP ITGA2 DAB2 CALR SNCA CAV1 ANXA2 DLL1 PTPN1 DNM1 PPP3CA ARF1 CAMK1D	1.17E-08	GO.0030100

22	GO Process	vasculature development	MYH9 MMP2 CCL2 PPP3R1 LAMAS PDGFRA THBS1 COL8A1 RORA FLT1 NOS3 MMP14 CAV1 CDH5 ANXA2 FN1 EPHA2 MYH10 ARHGEF15 DLL1 MMRN2 CLIC4	1.30E-08	GO.0001944
15	GO Process	cell junction organization	ITGB4 LAMAS TJP1 CSF1R ITGA2 FLNC CDH5 FN1 FLNA FSCN1 BCL2 CDC42 NR1H4 NUMB TLN2	1.40E-08	GO.0034330
44	GO Process	regulation of multicellular organismal development	MAP2K5 LAMA4 HSPB1 LAMAS THBS1 AKT3 NGEF ADD1 FLT1 APP KIT NOS3 MMP14 BRSK1 DAB2 CALR PRKCH RARB SNCA CAV1 MAP4K4 CDH5 FYN FN1 EPHA2 ARHGEF15 DLL1 FLNA MMRN2 TLR4 ANXA1 XRCC5 G6PD PPP3CA CAMK2B BCL2 SEPT7 CDC42 RARG CFL1 VIM NR1H4 NUMB CAMK1D	1.40E-08	GO.2000026
37	GO Process	positive regulation of catalytic activity	ARHGEF5 MAP2K5 CCL2 PLEK CDC25B PDGFRA THBS1 DNAJB6 ARHGAP31 ICAM1 FLT1 APP CSF1R KIT ITGA2 NOS3 CCT2 PLK1 ARF4 LCK SNCA CAV1 RGS12 MAP4K4 FYN FN1 FAS EPHA2 ARHGEF15 ARHGAP30 SLK PTPN1 SDC4 TLR4 TBC1D4 XRCC5 BCL2	1.51E-08	GO.0043085
13	GO Process	cell junction assembly	ITGB4 LAMAS TJP1 ITGA2 FLNC CDH5 FN1 FLNA FSCN1 BCL2 CDC42 NR1H4 TLN2	1.53E-08	GO.0034329
29	GO Process	response to organic cyclic compound	CYP24A1 APLP1 CCL2 THBS1 RORA PRKCG CAD ICAM1 APP CCRS5 ITGA2 BCL2L1 MMP14 NQO1 CALR RORC RARB NR1I2 SNCA CAV1 PTGES RXRG RXRB ANXA1 SDC1 G6PD BCL2 RARG NR1H4	1.57E-08	GO.0014070
35	GO Process	negative regulation of cell communication	MAP2K5 APLP1 PLEK ENO1 HSPB1 BCL2L2 PXD1 THBS1 RORA ICAM1 APP NOS3 BCL2L1 MMP14 DAB2 CALR SNCA CAV1 RGS12 MAP4K4 FYN FAS EPHA2 GSTO1 PTPN1 MMRN2 DNM1 TLR4 PPP3CA BCL2 DYRK1A CDC42 PBK ARF1 NR1H4	1.73E-08	GO.0010648
22	GO Process	cell morphogenesis involved in differentiation	MYH9 LAMAS FERMT3 APP CSF1R BRSK1 DOK4 FYN FN1 ARHGEF26 EPHA2 MYH10 FLNA SPTAN1 CLIC4 BCL2 CAMK2A CDC42 TOP2B FLNB SPTBN2 NUMB	1.78E-08	GO.0000904
35	GO Process	negative regulation of signaling	MAP2K5 APLP1 PLEK ENO1 HSPB1 BCL2L2 PXD1 THBS1 RORA ICAM1 APP NOS3 BCL2L1 MMP14 DAB2 CALR SNCA CAV1 RGS12 MAP4K4 FYN FAS EPHA2 GSTO1 PTPN1 MMRN2 DNM1 TLR4 PPP3CA BCL2 DYRK1A CDC42 PBK ARF1 NR1H4	1.80E-08	GO.0023057
42	GO Process	regulation of intracellular signal transduction	ARHGEF5 MAP2K5 APLP1 CCL2 PLEK ENO1 HSPB1 BCL2L2 PDGFRA THBS1 RORA AKT3 NGEF ARHGAP31 ICAM1 FLT1 APP CSF1R KIT BCL2L1 CALR LCK CAV1 MAP4K4 FYN FN1 FAS ARHGEF26 SFPQ EPHA2 ARHGEF15 TGM2 ARHGAP30 GSTO1 PTPN1 TLR4 PPP3CA BCL2 DYRK1A CDC42 PBK NR1H4	2.34E-08	GO.1902531
29	GO Process	positive regulation of transport	ARHGEF5 CCL2 GAPDH APP CSF1R ITGA2 DAB2 CALR SNCA CAV1 ANXA2 FYN MYO1C MYH10 DLL1 GSTO1 FLNA SDC4 DNM1 TLR4 ANXA1 SDC1 G6PD PPP3CA BCL2 CAMK2A NR1H4 ABCB1 CAMK1D	2.40E-08	GO.0051050
41	GO Process	vesicle-mediated transport	MYH9 EHD4 APLP1 PLEK ARF3 THBS1 VWF CNN2 EXOC6B FERMT3 APP KIT ANXA5 CCT2 BCL2L1 ARF4 DAB2 CALR STXB6P SNCA CAV1 TUBB4B ANXA2 FYN FN1 MYO1C MYH10 TGM2 DLL1 COPA FLNA SPTAN1 DNM1 ANXA1 TBC1D4 XRCC5 MYO1B CDC42 PDIA6 SPTBN2 ARF1	2.64E-08	GO.0016192
21	GO Process	blood vessel development	MYH9 MMP2 CCL2 PPP3R1 LAMAS PDGFRA THBS1 COL8A1 RORA FLT1 NOS3 MMP14 CAV1 CDH5 ANXA2 FN1 EPHA2 MYH10 DLL1 MMRN2 CLIC4	2.88E-08	GO.0001568
30	GO Process	regulation of anatomical structure morphogenesis	MAP2K5 MYH9 CCL2 HSPB1 THBS1 AKT3 NGEF ICAM1 FLT1 CSF1R KIT NOS3 BRSK1 DAB2 CALR CDH5 FYN FN1 EPHA2 MYH10 DLL1 FLNA MMRN2 ANXA1 PPP3CA CAMK2B BCL2 SEPT7 CDC42 CFL1	2.88E-08	GO.0022603
36	GO Process	response to endogenous stimulus	MMP2 APLP1 CCL2 PDGFRA THBS1 RORA CAD ICAM1 APP KIT CAPN2 ITGA2 BCL2L1 MMP14 NQO1 CALR ZYX RORC RARB NR1I2 SNCA CAV1 CDH5 ANXA2 FYN RXRG PTPN1 TLR4 RXRB ANXA1 TBC1D4 SDC1 BCL2 CAMK2A RARG NR1H4	2.95E-08	GO.0009719
37	GO Process	response to oxygen-containing compound	CYP24A1 MMP2 APLP1 CCL2 PDGFRA THBS1 RORA CAD ICAM1 APP CCRS5 CAPN2 ITGA2 NOS3 BCL2L1 NQO1 CALR RORC SNCA CAV1 PTGES FYN FAS PTPN1 DNM1 TLR4 ANXA1 TBC1D4 SDC1 XRCC5 G6PD PPP3CA BCL2 CAMK2A RARG CFL1 NR1H4	3.22E-08	GO.1901700
48	GO Process	regulation of catalytic activity	ARHGEF5 MAP2K5 CCL2 GAPDH PLEK CDC25B HSPB1 PDGFRA THBS1 DNAJB6 NGEF ARHGAP31 ICAM1 FLT1 APP CSF1R KIT ANXA5 ITGA2 NOS3 CCT2 PLK1 CDC25A NQO1 CDC25C LCK SNCA CAV1 RGS12 MAP4K4 ANXA2 FYN FN1 FAS EPHA2 ARHGEF15 ARHGAP30 SLK CNN3 PTPN1 SDC4 TLR4 ANXA1 TBC1D4 TPM2 XRCC5 BCL2	3.26E-08	GO.0050790
35	GO Process	regulation of response to stress	ARHGEF5 MMP2 PLEK ENO1 HSPB1 PDGFRA THBS1 RORA DNAJB6 PRKCG AKT3 APP ITGA2 NOS3 BCL2L1 ZYX SNCA CAV1 USP1 MAP4K4 CDH5 ANXA2 FYN FAS SFPQ TGM2 PTPN1 TLR4 ANXA1 XRCC5 PPP3CA DYRK1A PBK NR1H4 ABCB1	3.77E-08	GO.0080134
19	GO Process	supramolecular fiber organization	PDGFRA DNAJB6 ADD1 APP ZYX SNCA TPM4 ANXA2 MYH10 TPM3 SLK FLNA TPM2 FSCN1 MYO1B BCL2 CDC42 CFL1 VIM	4.42E-08	GO.0097435
38	GO Process	neurogenesis	CCL2 PPP3R1 RORA NGEF APP CSF1R KIT ARF4 MMP14 BRSK1 CALR JAG2 PRKCH RARB MAP4K4 DOK4 FYN FN1 MYH10 DLL1 FLNA SDC4 SPTAN1 ANXA1 XRCC5 PPP3CA CAMK2B BCL2 CAMK2A CDC42 SUN1 TOP2B WEE1 SPTBN2 CFL1 VIM NUMB CAMK1D	4.58E-08	GO.0022008
21	GO Process	regulation of vesicle-mediated transport	EHD4 CCL2 PRKCG APP ITGA2 DAB2 CALR STXB6P SNCA CAV1 ANXA2 DLL1 PTPN1 SDC4 DNM1 ANXA1 TBC1D4 SDC1 PPP3CA ARF1 CAMK1D	4.75E-08	GO.0060627
31	GO Process	response to abiotic stimulus	PLOD1 MMP2 THBS1 RORA CNN2 ICAM1 PLOD2 APP KIT CAPN2 ITGA2 NOS3 DDB1 BCL2L1 CDC25A MMP14 BRSK1 NQO1 CYP2R1 CAV1 USP1 FYN FAS DPP4 TLR4 ANXA1 PSIP1 XRCC5 BCL2 SUN1 PBK	5.03E-08	GO.0009628
31	GO Process	positive regulation of phosphate metabolic process	ARHGEF5 MAP2K5 EHD4 CCL2 PLEK ENO1 CDC25B PDGFRA THBS1 ICAM1 FLT1 APP CSF1R KIT ITGA2 NOS3 PLK1 DAB2 SNCA CAV1 MAP4K4 ANXA2 FYN FAS SLK PTPN1 SDC4 TLR4 XRCC5 BCL2 NR1H4	5.03E-08	GO.0045937
24	GO Process	symbiont process	CCL2 GAPDH PDGFRA ICAM1 CCRS5 ITGA2 DDB1 BCL2L1 CDC25C ZYX LCK CAV1 ANXA2 FYN FN1 EPHA2 DPP4 PSIP1 XRCC5 DYRK1A CDC42 CFL1 ARF1 VIM	7.09E-08	GO.0044403
27	GO Process	response to lipid	CYP24A1 CCL2 THBS1 RORA CAD ICAM1 CCRS5 ITGA2 NOS3 NQO1 CALR RORC RARB NR1I2 SNCA CAV1 PTGES FAS RXRG TLR4 RXRB ANXA1 SDC1 XRCC5 BCL2 RARG NR1H4	7.70E-08	GO.0033993
39	GO Process	tissue development	PLOD1 ITGB4 MMP2 PPP3R1 LAMAS PDGFRA COL8A1 ICAM1 TJP1 CSF1R ITGA2 NOS3 MMP14 BRSK1 DAB2 CALR RORC JAG2 RARB CAV1 FN1 ARHGEF26 EPHA2 MYH10 TGM2 DLL1 FLNA CNN3 SDC4 CLIC4 ANXA1 SDC1 PPP3CA BCL2 CDC42 RARG FLNB CFL1 VIM	7.94E-08	GO.0009888
27	GO Process	anatomical structure formation involved in morphogenesis	ITGB4 MYH9 MMP2 CCL2 PPP3R1 LAMAS PDGFRA THBS1 COL8A1 RORA FLT1 CAPN2 ITGA2 NOS3 MMP14 CAV1 ANXA2 FN1 EPHA2 MYH10 TGM2 DLL1 MMRN2 SDC4 CLIC4 RARG CFL1	8.80E-08	GO.0048646
24	GO Process	positive regulation of cell death	ARHGEF5 CCL2 GAPDH THBS1 NGEF APP MEK1 BCL2L1 NQO1 RARB LCK SNCA CAV1 FYN FAS ARHGEF26 SFPQ TGM2 TLR4 ANXA1 BCL2 CAMK2A RARG CAMK1D	9.98E-08	GO.0010942
17	GO Process	regulation of supramolecular fiber organization	ARHGEF5 PLEK TUBB4A ADD1 ICAM1 APP SNCA MYO1C ARHGEF15 FLNA SDC4 SPTAN1 DYRK1A CDC42 SPTBN2 CFL1 ARF1	1.01E-07	GO.1902903
32	GO Process	negative regulation of signal transduction	MAP2K5 APLP1 PLEK ENO1 HSPB1 BCL2L2 PXD1 THBS1 RORA ICAM1 APP NOS3 BCL2L1 MMP14 DAB2 CALR SNCA CAV1 RGS12 FYN FAS EPHA2 GSTO1 PTPN1 MMRN2 DNM1 TLR4 BCL2 DYRK1A CDC42 PBK NR1H4	1.16E-07	GO.0009968
30	GO Process	plasma membrane bounded cell projection organization	MYH9 PLEK LAMAS TUBB4A APP CSF1R KIT PLK1 TUBA1A ARF4 BRSK1 TUBB4B MAP4K4 DOK4 FYN ARHGEF26 MYH10 FLNA SDC4 SPTAN1 FSCN1 BCL2 CAMK2A SEPT7 CDC42 TOP2B WEE1 SPTBN2 ARF1 NUMB	1.27E-07	GO.0120036
56	GO Process	regulation of signal transduction	ARHGEF5 MAP2K5 APLP1 CCL2 PLEK ENO1 HSPB1 BCL2L2 PXD1 PDGFRA THBS1 RORA AKT3 NGEF ARHGAP31 ICAM1 FLT1 APP CSF1R KIT NOS3 BCL2L1 MMP14 DAB2 CALR JAG2 PRKCH LCK SNCA CAV1 RGS12 MAP4K4 FYN FN1 FAS ARHGEF26 SFPQ EPHA2 MYO1C ARHGEF15 TGM2 DLL1 ARHGAP30 COPA GSTO1 FLNA PTPN1 MMRN2 DNM1 TLR4 PPP3CA BCL2 DYRK1A CDC42 PBK NR1H4	1.31E-07	GO.0009966

46	GO Process	multi-organism process	MMP2 CCL2 GAPDH ENO1 CDC25B HSPB1 BCL2L2 PDGFRA CAD ICAM1 APP KIT CCR5 ITGA2 NOS3 CCT2 PLK1 DDB1 BCL2L1 CALR CDC25C ZXY JAG2 LCK SNCA CAV1 PTGES ANXA2 FYN FN1 FAS EPHA2 DPP4 TLR4 CLIC4 PSIP1 XRCC5 BCL2 DYRK1A SEPT7 CDC42 SUN1 CFL1 ARF1 VIM NR1H4	1.85E-07	GO.0051704
23	GO Process	negative regulation of cellular component organization	THBS1 DNAJB6 NGEF TUBB4A ADD1 APP PLK1 BCL2L1 MMP14 SNCA CAV1 MAP4K4 FYN DPP4 ARHGEF15 SPTAN1 TBC1D4 XRCC5 PPP3CA DYRK1A CDC42 SPTBN2 VIM	1.91E-07	GO.0051129
21	GO Process	hemopoiesis	MYH9 PLEK PDGFRA RORA ADD1 APP CSF1R KIT REL BCL2L1 JAG2 LCK ANXA2 EPHA2 DLL1 ANXA1 PIR XRCC5 G6PD BCL2 CDC42	1.98E-07	GO.0030097
26	GO Process	circulatory system development	MAP2K5 MYH9 MMP2 CCL2 PPP3R1 LAMA5 PDGFRA THBS1 COL8A1 RORA CAD FLT1 NOS3 MMP14 CALR RARB CAV1 CDH5 ANXA2 FN1 EPHA2 MYH10 ARHGEF15 DLL1 MMRN2 CLIC4	1.99E-07	GO.0072359
17	GO Process	response to metal ion	MT2A THBS1 ADD1 ICAM1 APP KIT NQO1 CALR CYP2R1 SNCA CAV1 PTGES CLIC4 SDC1 G6PD PPP3CA BCL2	2.54E-07	GO.0010038
16	GO Process	regulation of actin cytoskeleton organization	ARHGEF5 PLEK PDGFRA ADD1 ICAM1 CSF1R MYO1C ARHGEF15 FLNA SDC4 SPTAN1 FSCN1 CDC42 SPTBN2 CFL1 ARF1	2.74E-07	GO.0032956
58	GO Process	positive regulation of metabolic process	ARHGEF5 MAP2K5 MYH9 EHD4 CCL2 PPP3R1 PLEK ENO1 CDC25B HSPB1 PDGFRA THBS1 RORA PRKCG ICAM1 FLT1 APP CSF1R KIT ITGA2 NOS3 CCT2 PLK1 DDB1 ARF4 MMP14 DAB2 CALR RORC RARB NR1I2 LCK SNCA CAV1 MAP4K4 ANXA2 FYN FN1 FAS SFPQ MYO1C RXRG DLL1 SLK PTPN1 SDC4 TLR4 RXRB ANXA1 PSIP1 XRCC5 PPP3CA BCL2 DYRK1A RARG VIM NR1H4 CAMK1D	2.78E-07	GO.0009893
20	GO Process	response to inorganic substance	MT2A THBS1 ADD1 ICAM1 APP KIT NOS3 NQO1 CALR CYP2R1 SNCA CAV1 PTGES FYN CLIC4 ANXA1 SDC1 G6PD PPP3CA BCL2	3.25E-07	GO.0010035
27	GO Process	cellular response to oxygen-containing compound	CYP24A1 MMP2 APLP1 CCL2 PDGFRA RORA ICAM1 APP CCR5 CAPN2 ITGA2 NOS3 BCL2L1 NQO1 RORC SNCA CAV1 FYN PTPN1 TLR4 ANXA1 TBC1D4 XRCC5 PPP3CA CAMK2A RARG NR1H4	3.67E-07	GO.1901701
56	GO Process	organelle organization	ARHGEF5 MYH9 CCL2 GAPDH PLEK CDC25B LAMA5 PDGFRA DNAJB6 CNN2 AKT3 TUBB4A ADD1 KIT NOS3 PLK1 TUBA1A TUBA1C DDB1 BCL2L1 BRSK1 CALR ZXY SNCA CAV1 TUBB4B PTMA TPM4 ANXA2 SFPQ MYH10 TPM3 SLK FLNA CNN3 PTPN1 SPTAN1 DNM1 ANXA1 TPM2 FSCN1 XRCC5 MYO1B BCL2 CAMK2A SEPT7 CDC42 SUN1 TOP2B WEE1 FLNB SPTBN2 CFL1 VIM NR1H4 TLN2	3.78E-07	GO.0006996
22	GO Process	positive regulation of apoptotic process	ARHGEF5 CCL2 GAPDH THBS1 NGEF APP REL BCL2L1 NQO1 RARB LCK SNCA CAV1 FAS ARHGEF26 SFPQ TGM2 ANXA1 BCL2 CAMK2A RARG CAMK1D	3.87E-07	GO.0043065
45	GO Process	nervous system development	APLP1 CCL2 PPP3R1 RORA PRKCG AKT3 NGEF APP CSF1R KIT CKB ARF4 MMP14 BRSK1 CALR JAG2 PRKCH RARB MAP4K4 DOK4 FYN FN1 MYH10 DLL1 FLNA SDC4 SPTAN1 ANXA1 XRCC5 PPP3CA CAMK2B BCL2 CAMK2A DYRK1A CDC42 SUN1 RARG TOP2B WEE1 SPTBN2 CFL1 VIM NUMB APBA2 CAMK1D	4.10E-07	GO.0007399
32	GO Process	defense response	CCL2 GAPDH MT2A THBS1 ICAM1 APP CSF1R KIT CCR5 ZXY LCK SNCA TUBB4B PTGES FYN FN1 FAS SFPQ MYO1C DPP4 TLR4 ANXA1 SDC1 XRCC5 CAMK2B LTB4R BCL2 CAMK2A FLNB VIM NR1H4 CAMK1D	4.34E-07	GO.0006952
37	GO Process	regulation of cell population proliferation	MAP2K5 MMP2 CCL2 CDC25B LAMA5 PDGFRA THBS1 AKT3 FLT1 APP CSF1R KIT ITGA2 NOS3 BCL2L1 TENC1 CALR JAG2 PRKCH RARB LCK CAV1 PTGES CDH5 ANXA2 FYN FN1 FAS DPP4 TGM2 DLL1 FLNA SDC4 ANXA1 XRCC5 BCL2 RARG	4.46E-07	GO.0042127
30	GO Process	cellular response to endogenous stimulus	MMP2 APLP1 CCL2 PDGFRA RORA CAD ICAM1 APP KIT CAPN2 ITGA2 BCL2L1 CALR ZXY RORC RARB NR1I2 SNCA CAV1 CDH5 FYN RXRG PTPN1 TLR4 RXRB ANXA1 TBC1D4 CAMK2A RARG NR1H4	4.87E-07	GO.0071495
55	GO Process	positive regulation of macromolecule metabolic process	ARHGEF5 MAP2K5 MYH9 EHD4 CCL2 PPP3R1 ENO1 CDC25B HSPB1 PDGFRA THBS1 RORA PRKCG ICAM1 FLT1 APP CSF1R KIT ITGA2 NOS3 CCT2 PLK1 DDB1 ARF4 MMP14 DAB2 CALR RORC RARB NR1I2 LCK SNCA CAV1 MAP4K4 ANXA2 FYN FN1 FAS SFPQ MYO1C RXRG DLL1 SLK PTPN1 SDC4 TLR4 RXRB PSIP1 XRCC5 PPP3CA BCL2 DYRK1A RARG VIM NR1H4	5.53E-07	GO.0010604
54	GO Process	cellular protein modification process	RCN1 MAP2K5 PLOC1 CCL2 GAPDH PPP3R1 CDC25B PDGFRA THBS1 PRKCG AKT3 CAD FLT1 PLOC2 APP CSF1R KIT CCR5 MELK PLK1 DDB1 CDC25A ARF4 BRSK1 TENC1 CDC25C PRKCH LCK USP1 MAP4K4 FYN FN1 SFPQ EPHA2 TGM2 SLK PTPN1 SPTAN1 TLR4 ANXA1 PPP3CA CAMK2B BCL2 CAMK2A DYRK1A CDC42 PDIA6 WEE1 PBK SPTBN2 CFL1 NR1H4 PRKCH CAMK1D	5.89E-07	GO.0006464
36	GO Process	positive regulation of multicellular organismal process	GAPDH PLEK ENO1 HSPB1 THBS1 RORA AKT3 ICAM1 FLT1 APP CSF1R KIT ITGA2 NOS3 MMP14 DAB2 CALR PRKCH RARB CAV1 CDH5 ANXA2 FYN FN1 DLL1 GSTO1 FLNA TLR4 ANXA1 XRCC5 PPP3CA CAMK2B BCL2 NR1H4 NUMB CAMK1D	7.09E-07	GO.0051240
13	GO Process	protein autophosphorylation	PDGFRA PRKCG CAD FLT1 CSF1R KIT MELK LCK FYN SLK CAMK2B CAMK2A DYRK1A	7.28E-07	GO.0046777
11	GO Process	positive regulation of endocytosis	CCL2 APP ITGA2 DAB2 CALR SNCA ANXA2 DLL1 DNM1 PPP3CA CAMK1D	7.42E-07	GO.0045807
16	GO Process	response to steroid hormone	THBS1 RORA CAD ICAM1 CALR RORC RARB NR1I2 CAV1 RXRG RXRB ANXA1 SDC1 BCL2 RARG NR1H4	7.63E-07	GO.0048545
53	GO Process	positive regulation of nitrogen compound metabolic process	ARHGEF5 MAP2K5 MYH9 EHD4 CCL2 PPP3R1 ENO1 CDC25B HSPB1 PDGFRA THBS1 RORA PRKCG ICAM1 FLT1 APP CSF1R KIT ITGA2 NOS3 CCT2 PLK1 DDB1 ARF4 MMP14 DAB2 RORC RARB NR1I2 LCK SNCA CAV1 MAP4K4 ANXA2 FYN FN1 FAS SFPQ RXRG DLL1 SLK PTPN1 SDC4 TLR4 RXRB PSIP1 XRCC5 PPP3CA BCL2 DYRK1A RARG VIM NR1H4	8.35E-07	GO.0051173
37	GO Process	regulation of phosphate metabolic process	ARHGEF5 MAP2K5 EHD4 CCL2 PLEK ENO1 CDC25B HSPB1 PDGFRA THBS1 ICAM1 FLT1 APP CSF1R KIT ITGA2 NOS3 PLK1 CDC25A DAB2 CDC25C SNCA CAV1 MAP4K4 ANXA2 FYN FN1 FAS EPHA2 SLK PTPN1 SDC4 TLR4 XRCC5 BCL2 PBK NR1H4	1.11E-06	GO.0019220
54	GO Process	positive regulation of cellular metabolic process	ARHGEF5 MAP2K5 MYH9 EHD4 CCL2 PPP3R1 PLEK ENO1 CDC25B HSPB1 PDGFRA THBS1 RORA PRKCG ICAM1 FLT1 APP CSF1R KIT ITGA2 NOS3 CCT2 PLK1 ARF4 MMP14 DAB2 RORC RARB NR1I2 LCK SNCA CAV1 MAP4K4 ANXA2 FYN FN1 FAS SFPQ RXRG DLL1 SLK PTPN1 SDC4 TLR4 RXRB ANXA1 PSIP1 XRCC5 PPP3CA BCL2 DYRK1A RARG VIM NR1H4	1.11E-06	GO.0031325
36	GO Process	positive regulation of protein metabolic process	ARHGEF5 MAP2K5 MYH9 EHD4 CCL2 ENO1 CDC25B HSPB1 PDGFRA THBS1 ICAM1 FLT1 APP CSF1R KIT ITGA2 PLK1 DDB1 MMP14 DAB2 LCK SNCA CAV1 MAP4K4 ANXA2 FYN FN1 FAS SLK PTPN1 SDC4 TLR4 XRCC5 BCL2 DYRK1A VIM	1.18E-06	GO.0051247
42	GO Process	positive regulation of response to stimulus	ARHGEF5 MAP2K5 MMP2 CCL2 PLEK HSPB1 PDGFRA THBS1 PRKCG AKT3 ICAM1 FLT1 APP CSF1R KIT ITGA2 BCL2L1 DAB2 CALR JAG2 PRKCH LCK SNCA CAV1 MAP4K4 FYN FAS SFPQ MYO1C TGM2 DLL1 GSTO1 FLNA PTPN1 TLR4 ANXA1 XRCC5 PPP3CA BCL2 CDC42 NR1H4 CAMK1D	1.21E-06	GO.0048584
31	GO Process	regulation of hydrolase activity	ARHGEF5 MAP2K5 CCL2 GAPDH PLEK PDGFRA THBS1 DNAJB6 NGEF ARHGAP31 ICAM1 FLT1 APP KIT ITGA2 NOS3 ARF4 LCK SNCA CAV1 RG512 FYN FN1 FAS EPHA2 ARHGEF15 ARHGAP30 CNN3 ANXA1 TBC1D4 TPM2	1.45E-06	GO.0051336
15	GO Process	extracellular matrix organization	ITGB4 MMP2 LAMA4 PXDN LAMA5 PDGFRA THBS1 COL8A1 VWF ICAM1 APP ITGA2 MM	1.46E-06	GO.0030198
25	GO Process	peptidyl-amino acid modification	MAP2K5 PLOC1 GAPDH PDGFRA PRKCG AKT3 CAD FLT1 PLOC2 CSF1R KIT MELK PLK1 PRKCH LCK FYN EPHA2 TGM2 CAMK2B BCL2 CAMK2A DYRK1A WEE1 NR1H4 CAMK1D	1.52E-06	GO.0018193
18	GO Process	regulation of cell morphogenesis	MYH9 CCL2 NGEF ICAM1 CSF1R KIT BRSK1 CALR FYN FN1 MYH10 FLNA ANXA1 PPP3CA CAMK2B SEPT7 CDC42 CFL1	1.55E-06	GO.0022604
12	GO Process	response to interferon-gamma	CCL2 GAPDH MT2A ICAM1 ZXY SNCA MYO1C TLR4 CAMK2B CAMK2A FLNB VIM	1.58E-06	GO.0034341
12	GO Process	epithelial cell development	ICAM1 TJP1 RARB ARHGEF26 EPHA2 DLL1 FLNA CLIC4 SDC1 RARG FLNB VIM	1.87E-06	GO.0002064

25	GO Process	response to hormone	THBS1 RORA CAD ICAM1 KIT ITGA2 MMP14 NQO1 CALR RORC RARB NR112 CAV1 ANXA2 FYN RXRG PTPN1 RXRB ANXA1 TBC1D4 SDC1 BCL2 CAMK2A RARG NR1H4	1.92E-06	GO.0009725
39	GO Process	response to external stimulus	ARHGEF5 CYP24A1 CCL2 GAPDH ENO1 HSPB1 PDGFRA THBS1 CNN2 CAD ICAM1 FLT1 AP P CSF1R KIT CCR5 ITGA2 NOS3 BCL2L1 MMP14 NQO1 SNCA CAV1 PTGES DOK4 FYN FAS EPHA2 MYH10 SPTAN1 TLR4 ANXA1 G6PD BCL2 SUN1 SPTBN2 CFL1 ARF1 NR1H4	2.01E-06	GO.0009605
22	GO Process	cell population proliferation	BCL2L2 LAMAS COL8A1 RORA CSF1R KIT ITGA2 MELK PLK1 BCL2L1 CDC25A MMP14 DAB2 CDC25C FYN EPHA2 MYH10 FSCN1 XRCC5 BCL2 NUMB ABCB1	2.17E-06	GO.0008283
35	GO Process	immune response	CCL2 GAPDH MT2A PXDN THBS1 RORA CNN2 ICAM1 APP CSF1R KIT CCR5 CCT2 ZYX RO RC LCK SNCA TUBB4B ANXA2 FYN FAS SFPQ MYO1C DLL1 SPTAN1 TLR4 ANXA1 XRCC5 CAMK2B LTB4R BCL2 CAMK2A FLNB VIM NR1H4	2.30E-06	GO.0006955
23	GO Process	positive regulation of hydrolase activity	ARHGEF5 CCL2 PLEK PDGFRA DNAJB6 ARHGAP31 ICAM1 FLT1 APP KIT ITGA2 ARF4 LCK SNCA CAV1 RGS12 FYN FN1 FAS EPHA2 ARHGEF15 ARHGAP30 TBC1D4	2.47E-06	GO.0051345
34	GO Process	positive regulation of cellular protein metabolic process	ARHGEF5 MAP2K5 MYH9 EHD4 CCL2 ENO1 CDC25B PDGFRA THBS1 ICAM1 FLT1 APP CSF1R KIT ITGA2 PLK1 MMP14 DAB2 LCK SNCA CAV1 MAP4K4 ANXA2 FYN FN1 FAS SLK PTPN1 SDC4 TLR4 XRCC5 BCL2 DYRK1A VIM	2.68E-06	GO.0032270
33	GO Process	generation of neurons	RORA NGEF APP CSF1R KIT ARF4 BRSK1 CALR JAG2 PRKCH RARB MAP4K4 DOK4 FYN FN1 MYH10 DLL1 FLNA SDC4 SPTAN1 XRCC5 PPP3CA CAMK2B BCL2 CAMK2A CDC42 TOP2B WEE1 SPTBN2 CFL1 VIM NUMB CAMK1D	2.68E-06	GO.0048699
15	GO Process	leukocyte differentiation	MYH9 RORA APP CSF1R KIT RORC JAG2 LCK ANXA2 EPHA2 DLL1 ANXA1 PIR BCL2 CDC42	2.70E-06	GO.0002521
20	GO Process	viral process	CCL2 PDGFRA ICAM1 CCR5 ITGA2 DDB1 BCL2L1 CDC25C ZYX LCK CAV1 FYN EPHA2 DPP4 PSIP1 XRCC5 DYRK1A CDC42 ARF1 VIM	2.74E-06	GO.0016032
26	GO Process	positive regulation of protein phosphorylation	ARHGEF5 MAP2K5 EHD4 CCL2 CDC25B PDGFRA THBS1 ICAM1 FLT1 APP CSF1R KIT PLK1 DAB2 SNCA CAV1 MAP4K4 ANXA2 FYN FAS SLK PTPN1 SDC4 TLR4 XRCC5 BCL2	2.93E-06	GO.0001934
65	GO Process	protein metabolic process	RCN1 MAP2K5 PLOC1 MYH9 MMP2 CCL2 GAPDH PPP3R1 CDC25B PDGFRA THBS1 VWF PRKCG AKT3 CAD ADD1 FLT1 PLOC2 APP CSF1R KIT NPC1L1 CCR5 CAPN2 MELK PLK1 DDB1 CDC25A ARF4 MMP14 BRSK1 TENC1 CALR CDC25C PRKCH LCK SNCA USP1 MAP4K4 ANXA2 FYN FN1 SFPQ EPHA2 DPP4 TGM2 SLK PTPN1 SPTAN1 TLR4 ANXA1 PPP3CA CAMK2B BCL2 CAMK2A DYRK1A CDC42 PDIA6 WEE1 PBK SPTBN2 CFL1 NR1H4 PRKCSH CAMK1D	2.93E-06	GO.0019538
22	GO Process	head development	MMP2 PDGFRA RORA AKT3 APP CSF1R CKB ARF4 MMP14 RARB FYN MYH10 DLL1 FLNA XRCC5 PPP3CA BCL2 SUN1 RARG TOP2B SPTBN2 NUMB	3.04E-06	GO.0060322
19	GO Process	tissue morphogenesis	ITGB4 PPP3R1 LAMAS CSF1R ITGA2 NOS3 MMP14 BRSK1 JAG2 EPHA2 TGM2 DLL1 FLNA SDC4 CLIC4 BCL2 CDC42 RARG CFL1	3.23E-06	GO.0048729
32	GO Process	regulation of protein phosphorylation	ARHGEF5 MAP2K5 EHD4 CCL2 CDC25B HSPB1 PDGFRA THBS1 ICAM1 FLT1 APP CSF1R KIT PLK1 CDC25A DAB2 CDC25C SNCA CAV1 MAP4K4 ANXA2 FYN FN1 FAS EPHA2 SLK PTPN1 SDC4 TLR4 XRCC5 BCL2 PBK	3.60E-06	GO.0001932
11	GO Process	cellular response to interferon-gamma	CCL2 GAPDH MT2A ICAM1 ZYX MYO1C TLR4 CAMK2B CAMK2A FLNB VIM	3.60E-06	GO.0071346
27	GO Process	cell activation	MYH9 PDGFRA VWF RORA CNN2 PRKCG ICAM1 APP KIT CCT2 RORC JAG2 PRKCH LCK SNCA TUBB4B ANXA2 FYN DPP4 DLL1 FLNA SPTAN1 TLR4 ANXA1 XRCC5 PPP3CA BCL2	3.91E-06	GO.0001775
13	GO Process	regulation of actin filament organization	ARHGEF5 PLEK ADD1 ICAM1 MYO1C ARHGEF15 FLNA SDC4 SPTAN1 CDC42 SPTBN2 CFL1 ARF1	3.96E-06	GO.0110053
10	GO Process	G2/M transition of mitotic cell cycle	CDC25B TUBB4A MELK PLK1 TUBA1A CDC25A CDC25C TUBB4B WEE1 ABCB1	4.04E-06	GO.0000086
65	GO Process	establishment of localization	MYH9 EHD4 APLP1 PPP3R1 PLEK HSPB1 ARF3 THBS1 VWF CNN2 CAD ADD1 EXOC6B FERMT3 APP KIT NPC1L1 CCR5 ANXA5 ITGA2 CCT2 PLK1 TUBA1A TUBA1C BCL2L1 ARF4 BRSK1 DAB2 CALR STXBPG NR112 LCK SNCA CAV1 TUBB4B ANXA2 ANXA6 FYN FN1 MYO1C MYH10 TGM2 DLL1 COPA FLNA SPTAN1 DNM1 TLR4 CLIC4 ANXA1 TBC1D4 PSIP1 XRCC5 MYO1B PPP3CA BCL2 CAMK2A CDC42 SUN1 PDIA6 SPTBN2 ARF1 NR1H4 APBA2 ABCB1	4.55E-06	GO.0051234
18	GO Process	regulation of body fluid levels	PLEK PDGFRA THBS1 VWF PRKCG CAD ANXA5 ITGA2 NOS3 PRKCH LCK CAV1 ANXA2 FYN COPA FLNA TLR4 CDC42	4.81E-06	GO.0050878
18	GO Process	cellular response to lipid	CYP24A1 CCL2 RORA ICAM1 CCR5 ITGA2 NOS3 CALR RORC RARB NR112 RXRG TLR4 RXRB ANXA1 XRCC5 RARG NR1H4	5.23E-06	GO.0071396
24	GO Process	regulation of cell development	NGEF ADD1 APP KIT BRSK1 CALR PRKCH RARB MAP4K4 CDH5 FYN FN1 DLL1 FLNA XRCC5 G6PD PPP3CA CAMK2B BCL2 CDC42 CFL1 VIM NUMB CAMK1D	5.55E-06	GO.0060284
75	GO Process	organonitrogen compound metabolic process	RCN1 MAP2K5 PLOC1 MYH9 MMP2 CCL2 GAPDH PPP3R1 ENO1 CDC25B PDGFRA THBS1 VWF RORA PRKCG AKT3 CAD ADD1 FLT1 PLOC2 APP CSF1R KIT NPC1L1 CCR5 CAPN2 NOS3 MELK CKB PLK1 DDB1 CDC25A ARF4 MMP14 BRSK1 TENC1 CALR CDC25C PRKCH LCK SNCA USP1 MAP4K4 ANXA2 FYN FN1 SFPQ EPHA2 DPP4 TGM2 GSTO1 SLK PTPN1 SDC4 SPTAN1 TLR4 ANXA1 SDC1 G6PD PPP3CA CAMK2B LDHB BCL2 CAMK2A DYRK1A PAICS CDC42 PDIA6 WEE1 PBK SPTBN2 CFL1 NR1H4 PRKCSH CAMK1D	5.62E-06	GO.1901564
35	GO Process	positive regulation of signaling	ARHGEF5 MAP2K5 CCL2 PDGFRA THBS1 AKT3 ICAM1 FLT1 APP CSF1R KIT ITGA2 BCL2L1 DAB2 CALR JAG2 PRKCH LCK SNCA CAV1 MAP4K4 ANXA2 FYN FAS SFPQ MYO1C TGM2 DLL1 GSTO1 FLNA PTPN1 TLR4 PPP3CA BCL2 NR1H4	6.41E-06	GO.0023056
27	GO Process	epithelium development	PPP3R1 LAMAS ICAM1 TPJ1 CSF1R ITGA2 MMP14 BRSK1 DAB2 JAG2 RARB ARHGEF2 EPHA2 TGM2 DLL1 FLNA CNN3 SDC4 CLIC4 ANXA1 SDC1 BCL2 CDC42 RARG FLNB CFL1 VIM	6.50E-06	GO.0060429
33	GO Process	homeostatic process	CCL2 RBPI MT2A PDGFRA RORA AKT3 ADD1 ICAM1 APP KIT CCR5 NOS3 CKB DDB1 TENC1 CALR LCK SNCA CAV1 ANXA6 TGM2 DLL1 GSTO1 TLR4 CLIC4 ANXA1 XRCC5 G6PD PPP3CA BCL2 PDIA6 ARF1 NR1H4	6.83E-06	GO.0042592
22	GO Process	regulation of response to external stimulus	CCL2 PLEK HSPB1 PDGFRA THBS1 RORA PRKCG APP ITGA2 NOS3 CALR ZYX SNCA CAV1 CDH5 ANXA2 TGM2 TLR4 ANXA1 PBK NR1H4 CAMK1D	6.98E-06	GO.0032101
14	GO Process	leukocyte migration	ARHGEF5 MYH9 CCL2 ICAM1 FLT1 KIT CCR5 LCK CAV1 FYN FN1 SDC4 ANXA1 SDC1	7.46E-06	GO.0050900
21	GO Process	innate immune response	CCL2 GAPDH MT2A ICAM1 APP CSF1R ZYX LCK SNCA TUBB4B FYN SFPQ MYO1C TLR4 ANXA1 XRCC5 CAMK2B CAMK2A FLNB VIM NR1H4	7.80E-06	GO.0045087
63	GO Process	transport	MYH9 EHD4 APLP1 PPP3R1 PLEK HSPB1 ARF3 THBS1 VWF CNN2 CAD ADD1 EXOC6B FERMT3 APP KIT NPC1L1 CCR5 ANXA5 CCT2 TUBA1A TUBA1C BCL2L1 ARF4 BRSK1 DAB2 CALR STXBPG NR112 LCK SNCA CAV1 TUBB4B ANXA2 ANXA6 FYN FN1 MYO1C MYH10 TGM2 DLL1 COPA FLNA SPTAN1 DNM1 TLR4 CLIC4 ANXA1 TBC1D4 PSIP1 XRCC5 MYO1B PPP3CA BCL2 CAMK2A CDC42 SUN1 PDIA6 SPTBN2 ARF1 NR1H4 APBA2 ABCB1	8.35E-06	GO.0006810
13	GO Process	mitotic cell cycle phase transition	CDC25B TUBB4A MELK PLK1 TUBA1A CDC25A CDC25C TUBB4B PPP3CA CAMK2A WEE1 ABCB1 MCM3	8.40E-06	GO.0044772
18	GO Process	cellular response to organic cyclic compound	CYP24A1 APLP1 CCL2 RORA ICAM1 APP ITGA2 CALR RORC RARB NR112 SNCA CAV1 RXRG RXRB ANXA1 RARG NR1H4	8.40E-06	GO.0071407
23	GO Process	cellular homeostasis	CCL2 MT2A PDGFRA ADD1 ICAM1 APP CCR5 NOS3 CKB TENC1 CALR LCK SNCA CAV1 ANXA6 TGM2 GSTO1 CLIC4 PPP3CA BCL2 PDIA6 ARF1 NR1H4	8.59E-06	GO.0019725
18	GO Process	regulation of cell activation	CCL2 PLEK PDGFRA THBS1 RORA APP NOS3 MMP14 LCK SNCA CAV1 FYN DPP4 SDC4 TLR4 ANXA1 BCL2 CDC42	8.59E-06	GO.0050865
19	GO Process	mitotic cell cycle process	CDC25B TUBB4A MELK PLK1 TUBA1A BCL2L1 CDC25A BRSK1 CDC25C TUBB4B MYH10 FLNA PPP3CA CAMK2A TOP2B WEE1 CFL1 ABCB1 MCM3	8.83E-06	GO.1903047

18	GO Process	endocytosis	MYH9 EHD4 APLP1 THBS1 APP BCL2L1 DAB2 CALR SNCA CAV1 FYN MYO1C TGM2 DLL1 DNM1 ANXA1 CDC42 PDIA6	9.45E-06	GO.0006897
20	GO Process	mitotic cell cycle	CDC25B TUBB4A MEK1 PLK1 TUBA1A BCL2L1 CDC25A BRSK1 CDC25C TUBB4B MYH10 FLNA PPP3CA CAMK2A TOP2B WEE1 PBK CFL1 ABCB1 MCN3	1.00E-05	GO.0000278
23	GO Process	regulation of nervous system development	NGEF APP KIT BRSK1 CALR PRKCH RAR SNCA MAP4K4 FYN FN1 ARHGEF15 DLL1 FLNA XRCC5 PPP3CA CAMK2B BCL2 RARG CFL1 VIM NUMB CAMK1D	1.06E-05	GO.0051960
12	GO Process	negative regulation of apoptotic signaling pathway	MAP2K5 ENO1 HSPB1 BCL2L2 THBS1 ICAM1 NOS3 BCL2L1 FYN FAS PTPN1 BCL2	1.11E-05	GO.2001234
57	GO Process	cellular protein metabolic process	RCN1 MAP2K5 PLOD1 MMP2 CCL2 GAPDH PPP3R1 CDC25B PDGFRA THBS1 PRKCG AKT3 CAD FLT1 PLOD2 APP CSF1R KIT CCR5 CAPN2 MEK1 PLK1 DDB1 CDC25A ARF4 BRSK1 TENC1 CDC25C PRKCH LCK SNCA USP1 MAP4K4 FYN FN1 SFPQ EPHA2 TGM2 SLK PTPN1 SPTAN1 TLR4 ANXA1 PPP3CA CAMK2B BCL2 CAMK2A DYRK1A CDC42 PDIA6 WEE1 PBK SPTBN2 CFL1 NR1H4 PRKCSH CAMK1D	1.21E-05	GO.0044267
10	GO Process	regulation of cell shape	MYH9 CCL2 ICAM1 CSF1R KIT FYN FN1 MYH10 ANXA1 SEPT7	1.30E-05	GO.0008360
16	GO Process	morphogenesis of an epithelium	PPP3R1 LAMA5 CSF1R MMP14 BRSK1 JAG2 EPHA2 TGM2 DLL1 FLNA SDC4 CLIC4 BCL2 CDC42 RARG CFL1	1.31E-05	GO.0002009
31	GO Process	regulation of immune system process	MMP2 CCL2 PPP3R1 THBS1 RORA ICAM1 APP KIT ITGA2 MMP14 CALR PRKCH LCK SNCA CAV1 FYN SFPQ MYO1C DPP4 DLL1 PTPN1 SDC4 TLR4 ANXA1 XRCC5 PPP3CA BCL2 CDC42 RARG NR1H4 CAMK1D	1.32E-05	GO.0002682
24	GO Process	regulation of protein localization	ARHGEF5 GAPDH DNAJB6 APP CSF1R CCT2 PLK1 BCL2L1 DAB2 PRKCH MAP4K4 FYN FN1 EPHA2 MYO1C MYH10 DPP4 PTPN1 TLR4 ANXA1 PPP3CA BCL2 NR1H4 NUMB	1.46E-05	GO.0032880
12	GO Process	T cell activation	MYH9 RORA ICAM1 KIT RORC JAG2 LCK FYN DPP4 ANXA1 PPP3CA BCL2	1.46E-05	GO.0042110
34	GO Process	positive regulation of cell communication	ARHGEF5 MAP2K5 CCL2 PDGFRA THBS1 AKT3 ICAM1 FLT1 APP CSF1R KIT ITGA2 BCL2L1 DAB2 CALR JAG2 PRKCH LCK SNCA CAV1 MAP4K4 FYN FAS SFPQ MYO1C TGM2 DLL1 GSTO1 FLNA PTPN1 TLR4 PPP3CA BCL2 NR1H4	1.52E-05	GO.0010647
20	GO Process	epithelial cell differentiation	PPP3R1 LAMA5 ICAM1 TJP1 ITGA2 DAB2 JAG2 RARB ARHGEF26 EPHA2 DLL1 FLNA CNN3 CLIC4 ANXA1 SDC1 CDC42 RARG FLNB VIM	1.55E-05	GO.0030855
8	GO Process	regulation of coagulation	PLEK PDGFRA THBS1 ANXA5 NOS3 CAV1 ANXA2 TLR4	1.55E-05	GO.0050818
16	GO Process	regulation of protein complex assembly	ARHGEF5 PLEK TUBB4A ADD1 ICAM1 DDB1 STXBP6 SNCA MYO1C SPTAN1 TLR4 FSCN1 DYRK1A CDC42 SPTBN2 ARF1	1.77E-05	GO.0043254
8	GO Process	regulation of cell junction assembly	THBS1 TJP1 MMP14 PRKCH CAV1 MYO1C SLK SDC4	1.82E-05	GO.1901888
17	GO Process	inflammatory response	CCL2 THBS1 ICAM1 APP CSF1R KIT CCR5 SNCA PTGES FN1 FAS TLR4 ANXA1 SDC1 LTBR NR1H4 CAMK1D	1.87E-05	GO.0006954
32	GO Process	positive regulation of signal transduction	ARHGEF5 MAP2K5 CCL2 PDGFRA THBS1 AKT3 ICAM1 FLT1 APP CSF1R KIT BCL2L1 DAB2 CALR JAG2 PRKCH LCK CAV1 MAP4K4 FYN FAS SFPQ MYO1C TGM2 DLL1 GSTO1 FLNA PTPN1 TLR4 PPP3CA BCL2 NR1H4	1.87E-05	GO.0009967
15	GO Process	positive regulation of cell adhesion	CCL2 COL8A1 ICAM1 ITGA2 CALR LCK CAV1 FYN FN1 DPP4 TGM2 FLNA SDC4 ANXA1 CDC42	1.89E-05	GO.0045785
8	GO Process	integrin-mediated signaling pathway	ITGB4 MYH9 PLEK LAMA5 FERMT3 ITGA2 ZFYX CDC42	1.94E-05	GO.0007229
44	GO Process	regulation of cellular protein metabolic process	ARHGEF5 MAP2K5 MYH9 EHD4 CCL2 GAPDH ENO1 CDC25B HSPB1 PDGFRA THBS1 DNAJB6 PRKCG ICAM1 FLT1 APP CSF1R KIT ITGA2 PLK1 CDC25A MMP14 DAB2 CALR CDC25C LCK SNCA CAV1 MAP4K4 ANXA2 FYN FN1 FAS EPHA2 SLK PTPN1 SDC4 TLR4 XRCC5 G6PD BCL2 DYRK1A PBK VIM	2.07E-05	GO.0032268
46	GO Process	regulation of protein metabolic process	ARHGEF5 MAP2K5 MYH9 EHD4 CCL2 GAPDH ENO1 CDC25B HSPB1 PDGFRA THBS1 DNAJB6 PRKCG ICAM1 FLT1 APP CSF1R KIT ITGA2 PLK1 DDB1 CDC25A MMP14 DAB2 CALR CDC25C LCK SNCA CAV1 MAP4K4 ANXA2 FYN FN1 FAS EPHA2 SLK FLNA PTPN1 SDC4 TLR4 XRCC5 G6PD BCL2 DYRK1A PBK VIM	2.22E-05	GO.0051246
18	GO Process	response to wounding	ITGB4 PDGFRA VWF PRKCG ANXA5 ITGA2 ARF4 PRKCH LCK FYN FN1 MYH10 FLNA SDC4 ANXA1 SDC1 BCL2 CDC42	2.25E-05	GO.0009611
19	GO Process	regulation of cell projection organization	NGEF ICAM1 APP KIT ITGA2 BRSK1 CAV1 MAP4K4 FYN FN1 EPHA2 FSCN1 PPP3CA CAMK2B SEPT7 CDC42 CFL1 VIM CAMK1D	2.33E-05	GO.0031344
35	GO Process	regulation of protein modification process	ARHGEF5 MAP2K5 EHD4 CCL2 CDC25B HSPB1 PDGFRA THBS1 PRKCG ICAM1 FLT1 APP CSF1R KIT PLK1 CDC25A DAB2 CDC25C SNCA CAV1 MAP4K4 ANXA2 FYN FN1 FAS EPHA2 SLK PTPN1 SDC4 TLR4 XRCC5 G6PD BCL2 DYRK1A PBK	2.35E-05	GO.0031399
11	GO Process	peptidyl-tyrosine phosphorylation	MAP2K5 PDGFRA FLT1 CSF1R KIT MEK1 LCK FYN EPHA2 DYRK1A WEE1	2.40E-05	GO.0018108
18	GO Process	positive regulation of organelle organization	ARHGEF5 PLEK ICAM1 CCT2 ANXA2 SFPQ MYO1C ARHGEF15 FLNA SDC4 ANXA1 SDC1 FSCN1 XRCC5 BCL2 SEPT7 CDC42 CFL1	2.50E-05	GO.0010638
8	GO Process	regulation of blood vessel endothelial cell migration	MAP2K5 HSPB1 THBS1 AKT3 NOS3 EPHA2 MMPR2 ANXA1	2.59E-05	GO.0043535
11	GO Process	cellular response to steroid hormone stimulus	RORA ICAM1 CALR RORC RARB NR1I2 RXRG RARB ANXA1 RARG NR1H4	2.60E-05	GO.0071383
27	GO Process	positive regulation of protein modification process	ARHGEF5 MAP2K5 EHD4 CCL2 CDC25B PDGFRA THBS1 ICAM1 FLT1 APP CSF1R KIT PLK1 DAB2 SNCA CAV1 MAP4K4 ANXA2 FYN FAS SLK PTPN1 SDC4 TLR4 XRCC5 BCL2 DYRK1A	2.69E-05	GO.0031401
15	GO Process	regulation of apoptotic signaling pathway	MAP2K5 ENO1 HSPB1 BCL2L2 THBS1 ICAM1 NOS3 BCL2L1 LCK CAV1 FYN FAS SFPQ PTPN1 BCL2	2.69E-05	GO.2001233
11	GO Process	actin filament organization	ADD1 ZYX TPM4 TPM3 FLNA TPM2 FSCN1 MYO1B BCL2 CDC42 CFL1	2.93E-05	GO.0007015
23	GO Process	response to organonitrogen compound	MMP2 APLP1 PDGFRA PRKCG ICAM1 APP CAPN2 ITGA2 BCL2L1 SNCA CAV1 FYN PTPN1 DNM1 TLR4 ANXA1 TBC1D4 SDC1 PPP3CA CAMK2A CFL1 NR1H4	2.93E-05	GO.0010243
23	GO Process	positive regulation of cell population proliferation	MAP2K5 MMP2 CDC25B PDGFRA THBS1 AKT3 FLT1 CSF1R KIT ITGA2 BCL2L1 CALR PRKCH RARB ANXA2 FN1 DPP4 TGM2 DLL1 FLNA ANXA1 BCL2 RARG	3.02E-05	GO.0008284
34	GO Process	regulation of cell differentiation	PDGFRA THBS1 RORA NGEF ADD1 APP KIT MMP14 BRSK1 DAB2 CALR RORC PRKCH RARB CAV1 MAP4K4 CDH5 FYN FN1 DLL1 FLNA TLR4 ANXA1 XRCC5 G6PD PPP3CA CAMK2B BCL2 CDC42 RARG CFL1 VIM NUMB CAMK1D	3.20E-05	GO.0045595
17	GO Process	response to growth factor	MAP2K5 EHD4 CCL2 HSPB1 PDGFRA THBS1 CAD FLT1 APP ZYX SNCA CAV1 CDH5 FYN EPHA2 MYO1C ANXA1	3.34E-05	GO.0070848
19	GO Process	positive regulation of transferase activity	ARHGEF5 MAP2K5 CDC25B PDGFRA THBS1 FLT1 APP CSF1R KIT CCT2 PLK1 SNCA MAP4K4 FYN SLK PTPN1 SDC4 TLR4 XRCC5	3.65E-05	GO.0051347
23	GO Process	embryo development	ITGB4 MYH9 MMP2 LAMA5 PDGFRA COL8A1 ADD1 FLT1 KIT CAPN2 ITGA2 NOS3 BCL2L1 MMP14 JAG2 RARB FN1 MYH10 DLL1 SDC4 RARG CFL1 APBA2	3.71E-05	GO.0009790
24	GO Process	positive regulation of intracellular signal transduction	ARHGEF5 MAP2K5 CCL2 PDGFRA THBS1 AKT3 ICAM1 FLT1 APP CSF1R KIT BCL2L1 CALR LCK CAV1 MAP4K4 FYN SFPQ TGM2 GSTO1 PTPN1 TLR4 PPP3CA BCL2	3.73E-05	GO.1902533
17	GO Process	negative regulation of intracellular signal transduction	APLP1 PLEK ENO1 HSPB1 BCL2L2 THBS1 RORA BCL2L1 CAV1 EPHA2 GSTO1 PTPN1 TLR4 BCL2 DYRK1A PBK NR1H4	3.93E-05	GO.1902532
10	GO Process	cell-cell junction organization	LAMA5 TJP1 CSF1R ITGA2 CDH5 FSCN1 BCL2 NR1H4 NUMB TLN2	4.36E-05	GO.0045216
21	GO Process	regulation of cellular localization	APP CCT2 PLK1 BCL2L1 BRSK1 DAB2 PRKCH SNCA CAV1 MAP4K4 ANXA2 FYN EPHA2 MYO1C GSTO1 PTPN1 DNM1 BCL2 CAMK2A NR1H4 NUMB	4.36E-05	GO.0060341
10	GO Process	regulation of reactive oxygen species metabolic process	THBS1 ICAM1 APP ARF4 SNCA CAV1 FYN TLR4 G6PD BCL2	4.57E-05	GO.2000377
9	GO Process	steroid hormone mediated signaling pathway	RORA CALR RORC RARB NR1I2 RXRG RARB RARG NR1H4	4.63E-05	GO.0043401
9	GO Process	male gonad development	BCL2L2 PDGFRA ICAM1 KIT BCL2L1 MMP14 FLNA SDC1 BCL2	4.89E-05	GO.0008584
18	GO Process	cellular response to hormone stimulus	RORA ICAM1 KIT ITGA2 CALR RORC RARB NR1I2 CAV1 FYN RXRG PTPN1 RARB ANXA1 TBC1D4 CAMK2A RARG NR1H4	5.08E-05	GO.0032870
13	GO Process	positive regulation of cell activation	CCL2 PLEK THBS1 APP MMP14 LCK CAV1 FYN DPP4 TLR4 ANXA1 BCL2 CDC42	5.16E-05	GO.0050867
22	GO Process	cell adhesion	ITGB4 APLP1 CCL2 LAMA4 LAMA5 PDGFRA THBS1 COL8A1 VWF ICAM1 FERMT3 APP KIT ITGA2 ZYX CDH5 FN1 EPHA2 MYH10 DPP4 BCL2 TLN2	5.19E-05	GO.0007155
10	GO Process	intracellular receptor signaling pathway	CYP24A1 RORA CALR RORC RARB NR1I2 RXRG RARB RARG NR1H4	5.42E-05	GO.0030522

22	GO Process	regulation of kinase activity	ARHGEF5 MAP2K5 CDC25B HSPB1 PDGFRA THBS1 FLT1 APP CSF1R KIT PLK1 CDC25A CDC25C SNCA CAV1 MAP4K4 FYN SLK PTPN1 SDC4 TLR4 XRC5	5.75E-05	GO.0043549
24	GO Process	response to nitrogen compound	MMP2 APLP1 PDGFRA PRKCG CAD ICAM1 APP CAPN2 ITGA2 BCL2L1 NQO1 SNCA CAV1 FYN PTPN1 DNM1 TLR4 ANXA1 TBC1D4 SDC1 PPP3CA CAMK2A CFL1 NR1H4	5.82E-05	GO.1901698
16	GO Process	cell part morphogenesis	APP CSF1R BCL2L1 BRSK1 MAP4K4 DOK4 FYN MYH10 SPTAN1 BCL2 CAMK2A CDC42 TOP2B WEE1 SPTBN2 NUMB	5.85E-05	GO.0032990
41	GO Process	cellular component assembly	ITGB4 EHD4 LAMA5 PDGFRA VWF TUBB4A ADD1 FERMT3 TJP1 APP KIT ITGA2 CCT2 PLK1 TUBA1A DDB1 CALR ZYX FLNC CAV1 TUBB4B CDH5 ANXA2 ANXA6 FN1 FAS ARHGEF26 RXRG MYH10 TGM2 FLNA DNM1 PSIP1 FSCN1 MYO1B BCL2 SEPT7 CDC42 SPTBN2 NR1H4 TLN2	6.26E-05	GO.0022607
16	GO Process	cellular response to growth factor stimulus	MAP2K5 EHD4 CCL2 HSPB1 PDGFRA THBS1 CAD FLT1 APP ZYX SNCA CAV1 CDH5 FYN MYO1C ANXA1	6.27E-05	GO.0071363
21	GO Process	regulation of protein kinase activity	ARHGEF5 MAP2K5 CDC25B HSPB1 THBS1 FLT1 APP CSF1R KIT PLK1 CDC25A CDC25C SNCA CAV1 MAP4K4 FYN SLK PTPN1 SDC4 TLR4 XRC5	6.29E-05	GO.0045859
8	GO Process	myeloid leukocyte differentiation	MYH9 APP CSF1R KIT ANXA2 EPHA2 PIR G6PD CDC42	6.39E-05	GO.0002573
18	GO Process	regulation of plasma membrane bounded cell projection organization	NGEF ICAM1 APP KIT BRSK1 CAV1 MAP4K4 FYN FN1 EPHA2 FSCN1 PPP3CA CAMK2B SEPT7 CDC42 CFL1 VIM CAMK1D	6.80E-05	GO.0120035
20	GO Process	regulation of neurogenesis	NGEF APP KIT BRSK1 CALR PRKCH RARB MAP4K4 FYN FN1 DLL1 FLNA XRC5 PPP3CA CAMK2B BCL2 CFL1 VIM NUMB CAMK1D	7.23E-05	GO.0050767
10	GO Process	positive regulation of supramolecular fiber organization	ARHGEF5 PLEK ICAM1 APP MYO1C ARHGEF15 FLNA SDC4 CDC42 CFL1	7.23E-05	GO.1902905
8	GO Process	negative regulation of extrinsic apoptotic signaling pathway	MAP2K5 THBS1 ICAM1 NOS3 BCL2L1 FYN FAS BCL2	7.23E-05	GO.2001237
11	GO Process	regulation of muscle system process	ENO1 KIT ITGA2 NOS3 CAV1 ANXA6 GSTO1 FLNA G6PD PPP3CA CAMK2B	7.35E-05	GO.0090257
14	GO Process	response to oxidative stress	PXDN PDGFRA APP NOS3 MELK MMP14 NQO1 SNCA FYN ANXA1 PSIP1 SDC1 G6PD BCL2	7.40E-05	GO.0006979
18	GO Process	microtubule-based process	MYH9 GAPDH HSPB1 TUBB4A APP PLK1 TUBA1A TUBA1C BRSK1 TUBB4B MYO1C MYH10 SLK FLNA MYO1B CDC42 SUN1 WEE1	7.43E-05	GO.0007017
13	GO Process	response to oxygen levels	PLOD1 MMP2 THBS1 RORA ICAM1 PLOD2 CAPN2 ITGA2 MMP14 CAV1 FAS DPP4 BCL2	7.43E-05	GO.0070482
8	GO Process	actin filament-based movement	MYH9 TPM4 MYO1C MYH10 TPM3 TPM2 MYO1B VIM	7.56E-05	GO.0030048
13	GO Process	response to acid chemical	MMP2 PDGFRA ICAM1 CAPN2 ITGA2 BCL2L1 NQO1 PTGES FYN XRC5 RARG CFL1 NR1H4	7.86E-05	GO.0001101
16	GO Process	regulation of protein serine/threonine kinase activity	ARHGEF5 MAP2K5 HSPB1 THBS1 FLT1 APP CSF1R KIT PLK1 CDC25A CDC25C SNCA CAV1 MAP4K4 PTPN1 TLR4	7.90E-05	GO.0071900
6	GO Process	interleukin-12-mediated signaling pathway	CNN2 ANXA2 GSTO1 CDC42 CFL1 ARF1	7.96E-05	GO.0035722
16	GO Process	positive regulation of cell development	ADD1 APP KIT CALR PRKCH RARB CDH5 FYN FN1 FLNA XRC5 CAMK2B BCL2 CDC42 NUMB CAMK1D	8.39E-05	GO.0010720
17	GO Process	positive regulation of kinase activity	ARHGEF5 MAP2K5 CDC25B PDGFRA THBS1 FLT1 APP CSF1R KIT SNCA MAP4K4 FYN SLK PTPN1 SDC4 TLR4 XRC5	8.86E-05	GO.0033674
22	GO Process	positive regulation of immune system process	MMP2 CCL2 THBS1 ICAM1 APP ITGA2 MMP14 CALR PRKCH LCK CAV1 FYN SFPQ MYO1C DPP4 TLR4 ANXA1 XRC5 BCL2 CDC42 NR1H4 CAMK1D	9.49E-05	GO.0002684
31	GO Process	cellular response to stress	MAP2K5 CCL2 BCL2L2 PDGFRA THBS1 RORA ADD1 ICAM1 NRC1L1 NOS3 MELK PLK1 DDB1 BCL2L1 BRSK1 NQO1 CALR CDC25C SNCA CAV1 USP1 FAS SFPQ EPHA2 SLK PTPN1 ANXA1 XRC5 G6PD BCL2 PDIAG	9.49E-05	GO.0033554
18	GO Process	regulation of cellular response to stress	ARHGEF5 ENO1 HSPB1 DNAJB6 PRKCG AKT3 APP BCL2L1 CAV1 USP1 MAP4K4 FYN FAS SFPQ PTPN1 TLR4 DYRK1A PBK	9.49E-05	GO.0080135
7	GO Process	regulation of blood coagulation	PLEK PDGFRA THBS1 NOS3 CAV1 ANXA2 TLR4	9.85E-05	GO.0030193
10	GO Process	regulation of cell-substrate adhesion	THBS1 COL8A1 MMP14 CALR FN1 SLK FLNA SDC4 BCL2 CDC42	1.00E-04	GO.0010810
9	GO Process	regulation of endothelial cell migration	MAP2K5 HSPB1 THBS1 AKT3 NOS3 CALR EPHA2 MMRN2 ANXA1	1.10E-04	GO.0010594
22	GO Process	cell cycle process	MYH9 CDC25B THBS1 TUBB4A MELK PLK1 TUBA1A BCL2L1 CDC25A BRSK1 CDC25C TUBB4B MYH10 FLNA PPP3CA CAMK2A SUN1 TOP2B WEE1 CFL1 ABCB1 MCM3	1.10E-04	GO.0022402
22	GO Process	leukocyte activation	MYH9 RORA CNN2 ICAM1 APP KIT CCT2 RORC JAG2 LCK SNCA TUBB4B ANXA2 FYN DPP4 DLL1 SPTAN1 TLR4 ANXA1 XRC5 PPP3CA BCL2	1.10E-04	GO.0045321
23	GO Process	regulation of transferase activity	ARHGEF5 MAP2K5 CDC25B HSPB1 PDGFRA THBS1 FLT1 APP CSF1R KIT CCT2 PLK1 CDC25A CDC25C SNCA CAV1 MAP4K4 FYN SLK PTPN1 SDC4 TLR4 XRC5	1.10E-04	GO.0051338
11	GO Process	regulation of calcium ion transport	CCL2 ICAM1 NOS3 SNCA CAV1 FYN GSTO1 G6PD CAMK2B BCL2 CAMK2A	1.10E-04	GO.0051924
12	GO Process	response to hypoxia	PLOD1 MMP2 THBS1 RORA ICAM1 PLOD2 CAPN2 ITGA2 MMP14 CAV1 DPP4 BCL2	1.20E-04	GO.0001666
22	GO Process	response to drug	MT2A THBS1 PRKCG CAD ICAM1 NPC1L1 ITGA2 BCL2L1 NQO1 CALR NR1I2 LCK SNCA CAV1 FYN ANXA1 SDC1 XRC5 G6PD PPP3CA BCL2 ABCB1	1.20E-04	GO.0042493
15	GO Process	neuron projection morphogenesis	APP CSF1R BRSK1 MAP4K4 DOK4 FYN MYH10 SPTAN1 BCL2 CAMK2A CDC42 TOP2B WEE1 SPTBN2 NUMB	1.20E-04	GO.0048812
10	GO Process	gonad development	BCL2L2 PDGFRA ICAM1 KIT NOS3 BCL2L1 MMP14 FLNA SDC1 BCL2	1.40E-04	GO.0008406
7	GO Process	multicellular organism growth	ADD1 TENC1 RARB CLIC4 RARG SPTBN2 APBA2	1.40E-04	GO.0035264
16	GO Process	positive regulation of protein kinase activity	ARHGEF5 MAP2K5 CDC25B THBS1 FLT1 APP CSF1R KIT SNCA MAP4K4 FYN SLK PTPN1 SDC4 TLR4 XRC5	1.40E-04	GO.0045860
22	GO Process	negative regulation of developmental process	MAP2K5 THBS1 RORA AKT3 NGEF APP NOS3 CALR RARB CAV1 MAP4K4 ANXA2 ARHGEF15 DLL1 MMRN2 TLR4 ANXA1 G6PD PPP3CA BCL2 RARG VIM	1.40E-04	GO.0051093
38	GO Process	cellular localization	MYH9 EHD4 PPP3R1 PLEK HSPB1 LAMA5 TUBB4A EXOC6B APP KIT CCR5 PLK1 TUBA1A TUBA1C ARF4 BRSK1 CALR STXB6 LCK SNCA CAV1 TUBB4B ANXA2 MYO1C MYH10 COPA FLNA SPTAN1 DNM1 TBC1D4 PSIP1 XRC5 PPP3CA CDC42 SUN1 FLNB SPTBN2 TLN2	1.50E-04	GO.0051641
12	GO Process	positive regulation of leukocyte activation	CCL2 THBS1 APP MMP14 LCK CAV1 FYN DPP4 TLR4 ANXA1 BCL2 CDC42	1.60E-04	GO.0002696
7	GO Process	female gonad development	PDGFRA ICAM1 KIT NOS3 BCL2L1 MMP14 BCL2	1.60E-04	GO.0008585
13	GO Process	signal transduction by protein phosphorylation	MAP2K5 CCL2 PDGFRA KIT CCR5 MAP4K4 FYN SLK PTPN1 SPTAN1 CAMK2B CAMK2A SPTBN2	1.60E-04	GO.0023014
15	GO Process	wound healing	PDGFRA VWF PRKCG ANXA5 ITGA2 PRKCH LCK FYN FN1 MYH10 FLNA SDC4 ANXA1 SDC1 CDC42	1.60E-04	GO.0042060
9	GO Process	regulation of extrinsic apoptotic signaling pathway	MAP2K5 THBS1 ICAM1 NOS3 BCL2L1 CAV1 FYN FAS BCL2	1.60E-04	GO.2001236
9	GO Process	regulation of intrinsic apoptotic signaling pathway	ENO1 HSPB1 BCL2L2 BCL2L1 LCK CAV1 SFPQ PTPN1 BCL2	1.60E-04	GO.2001242
18	GO Process	brain development	RORA AKT3 APP CSF1R CKB ARF4 RARB FYN MYH10 DLL1 FLNA XRC5 PPP3CA BCL2 SUN1 TOP2B SPTBN2 NUMB	1.70E-04	GO.0007420
10	GO Process	myeloid cell differentiation	MYH9 ADD1 APP CSF1R KIT ANXA2 EPHA2 PIR G6PD CDC42	1.70E-04	GO.0030099
24	GO Process	secretion	PLEK THBS1 VWF CNN2 CAD EXOC6B FERMT3 APP KIT ANXA5 CCT2 BRSK1 CAV1 TUBB4B ANXA2 FN1 MYH10 COPA FLNA SPTAN1 TLR4 ANXA1 XRC5 NR1H4	1.80E-04	GO.0046903
15	GO Process	regulation of leukocyte activation	CCL2 THBS1 RORA APP MMP14 LCK SNCA CAV1 FYN DPP4 SDC4 TLR4 ANXA1 BCL2 CDC42	1.90E-04	GO.0002694
6	GO Process	actin cytoskeleton reorganization	MYH9 PLEK KIT FLNA PTPN1 ANXA1	1.90E-04	GO.0031532
13	GO Process	lymphocyte activation	MYH9 RORA ICAM1 KIT RORC JAG2 LCK FYN DPP4 DLL1 ANXA1 PPP3CA BCL2	2.00E-04	GO.0046649
8	GO Process	regulation of wound healing	PLEK PDGFRA THBS1 NOS3 CAV1 ANXA2 TLR4 ANXA1	2.00E-04	GO.0061041
12	GO Process	regulation of vasculature development	MAP2K5 HSPB1 THBS1 AKT3 FLT1 KIT NOS3 CDH5 EPHA2 DLL1 MMRN2 ANXA1	2.00E-04	GO.1901342

21	GO Process	animal organ morphogenesis	ITGB4 MMP2 APLP1 CCL2 LAMA5 PDGFRA COL8A1 AKT3 CSF1R ITGA2 NOS3 MMP14 JAG2 RARB CAV1 EPHA2 TGM2 DLL1 SDC1 BCL2 RARG	2.10E-04	GO.0009887
10	GO Process	regulation of epithelial cell migration	MAP2K5 HSPB1 THBS1 AKT3 ITGA2 NOS3 CALR EPHA2 MMRN2 ANXA1	2.10E-04	GO.0010632
6	GO Process	negative regulation of protein polymerization	TUBB4A ADD1 SNCA SPTAN1 DYRK1A SPTBN2	2.10E-04	GO.0032272
18	GO Process	cellular chemical homeostasis	MT2A PDGFRA ICAM1 APP CCR5 CKB CALR LCK SNCA CAV1 ANXA6 TGM2 GSTO1 CLIC4 PPP3CA BCL2 ARF1 NR1H4	2.20E-04	GO.0055082
9	GO Process	regulation of cell cycle G2/M phase transition	CDC25B TUBB4A APP PLK1 TUBA1A CDC25A BRSK1 CDC25C TUBB4B	2.30E-04	GO.1902749
6	GO Process	positive regulation of actin filament bundle assembly	ARHGEF5 PLEK ARHGEF15 FLNA SDC4 CDC42	2.40E-04	GO.0032233
17	GO Process	regulation of mitotic cell cycle	MAP2K5 CCL2 CDC25B TUBB4A APP PLK1 TUBA1A DDB1 BCL2L1 BRSK1 CDC25C TUBB4B MAP4K4 SLK ANXA1 BCL2 TOP2B	2.50E-04	GO.0007346
8	GO Process	platelet degranulation	PLEK THBS1 VWF FERMT3 APP ANXA5 FN1 FLNA	2.60E-04	GO.0002576
15	GO Process	cellular response to organonitrogen compound	MMP2 APLP1 PDGFRA ICAM1 APP CAPN2 BCL2L1 SNCA CAV1 FYN PTPN1 TLR4 TBC1D4 CAMK2A NR1H4	2.60E-04	GO.0071417
4	GO Process	vascular endothelial growth factor signaling pathway	HSPB1 PDGFRA FLT1 MYO1C	2.70E-04	GO.0038084
7	GO Process	gland morphogenesis	LAMA5 CSF1R CAV1 EPHA2 TGM2 BCL2 RARG	2.80E-04	GO.0022612
15	GO Process	chemotaxis	ARHGEF5 CCL2 PDGFRA FLT1 APP CSF1R KIT CCR5 DOK4 FYN EPHA2 MYH10 SPTAN1 ANXA1 SPTBN2	2.90E-04	GO.0006935
9	GO Process	peptidyl-serine phosphorylation	PRKCG AKT3 PLK1 PRKCH CAMK2B BCL2 CAMK2A DYRK1A CAMK1D	2.90E-04	GO.0018105
17	GO Process	neuron projection development	APP CSF1R ARF4 BRSK1 MAP4K4 DOK4 FYN MYH10 SDC4 SPTAN1 BCL2 CAMK2A CDC42 TOP2B WEE1 SPTBN2 NUMB	2.90E-04	GO.0031175
5	GO Process	cellular response to vascular endothelial growth factor stimulus	HSPB1 PDGFRA FLT1 MYO1C ANXA1	2.90E-04	GO.0035924
9	GO Process	regulation of leukocyte migration	CCL2 THBS1 ICAM1 APP ITGA2 MMP14 CALR ANXA1 CAMK1D	3.10E-04	GO.0002685
12	GO Process	MAPK cascade	MAP2K5 CCL2 PDGFRA KIT CCR5 MAP4K4 FYN PTPN1 SPTAN1 CAMK2B CAMK2A SPTBN2	3.20E-04	GO.0000165
4	GO Process	retinoic acid receptor signaling pathway	RARB RXRG RXRB RARG	3.20E-04	GO.0048384
5	GO Process	regulation of cell migration involved in sprouting angiogenesis	MAP2K5 THBS1 AKT3 MMRN2 ANXA1	3.20E-04	GO.0090049
27	GO Process	reproductive process	MYH9 MMP2 CDC25B BCL2L2 PDGFRA CAD ICAM1 APP KIT ITGA2 NOS3 CCT2 PLK1 BCL2L1 MMP14 CALR CDC25C JAG2 FLNA CLIC4 ANXA1 SDC1 BCL2 SEPT7 SUN1 RARG TOP2B	3.30E-04	GO.0022414
15	GO Process	positive regulation of cellular component biogenesis	ARHGEF5 PLEK ICAM1 KIT DDB1 CAV1 MYO1C ARHGEF15 FLNA SDC4 TLR4 SDC1 FSCN1 SEPT7 CDC42	3.30E-04	GO.0044089
6	GO Process	regulation of sprouting angiogenesis	MAP2K5 THBS1 AKT3 DLL1 MMRN2 ANXA1	3.30E-04	GO.1903670
15	GO Process	transmembrane receptor protein tyrosine kinase signaling pathway	MMP2 HSPB1 PDGFRA NGEF FLT1 CSF1R KIT ARF4 LCK FYN EPHA2 MYO1C PTPN1 DNMT1 CDC42	3.40E-04	GO.0007169
9	GO Process	positive regulation of vasculature development	HSPB1 THBS1 AKT3 FLT1 KIT NOS3 CDH5 DLL1 ANXA1	3.60E-04	GO.1904018
18	GO Process	enzyme linked receptor protein signaling pathway	MMP2 HSPB1 PDGFRA NGEF FLT1 CSF1R KIT ARF4 ZYX LCK CDH5 FYN EPHA2 MYO1C PTPN1 DNMT1 CDC42 VIM	3.70E-04	GO.0007167
6	GO Process	regulation of phospholipase activity	PDGFRA FLT1 KIT ARF4 SNCA ANXA1	3.70E-04	GO.0010517
13	GO Process	regulation of cell cycle phase transition	CCL2 CDC25B TUBB4A APP PLK1 TUBA1A DDB1 CDC25A BRSK1 CDC25C TUBB4B ANXA1 BCL2	3.70E-04	GO.1901987
11	GO Process	regulation of angiogenesis	MAP2K5 HSPB1 THBS1 AKT3 FLT1 NOS3 CDH5 EPHA2 DLL1 MMRN2 ANXA1	3.80E-04	GO.0045765
26	GO Process	positive regulation of developmental process	HSPB1 THBS1 AKT3 ADD1 FLT1 APP KIT NOS3 MMP14 DAB2 CALR PRKCH RARB CDH5 FYN FN1 DLL1 FLNA ANXA1 XRC5 CAMK2B BCL2 CDC42 NR1H4 NUMB CAMK1D	3.90E-04	GO.0051094
9	GO Process	striated muscle cell differentiation	MYH9 PDGFRA CAPN2 CALR FLNC RARB MYH10 SDC1 PPP3CA	4.00E-04	GO.0051146
10	GO Process	muscle cell differentiation	MYH9 PDGFRA RORA CAPN2 CALR FLNC RARB MYH10 SDC1 PPP3CA	4.10E-04	GO.0042692
5	GO Process	cell-substrate junction assembly	ITGB4 LAMA5 ITGA2 FN1 BCL2	4.30E-04	GO.0007044
5	GO Process	regulation of macrophage activation	THBS1 RORA APP SNCA TLR4	4.30E-04	GO.0043030
14	GO Process	negative regulation of transport	THBS1 ICAM1 NOS3 STXBP6 SNCA CAV1 MAP4K4 FN1 GSTO1 ANXA1 TBC1D4 PPP3CA BCL2 NR1H4	4.30E-04	GO.0051051
7	GO Process	response to amino acid	MMP2 PDGFRA ICAM1 CAPN2 BCL2L1 FYN CFL1	4.60E-04	GO.0043200
18	GO Process	regulation of MAPK cascade	ARHGEF5 MAP2K5 CCL2 PDGFRA THBS1 ICAM1 FLT1 APP CSF1R KIT CAV1 MAP4K4 FN1 FAS EPHA2 PTPN1 TLR4 PBK	4.70E-04	GO.0043408
14	GO Process	muscle structure development	MYH9 LAMA5 PDGFRA RORA CAPN2 CALR FLNC RARB CAV1 MYH10 DLL1 SDC1 PPP3CA FLNB	4.90E-04	GO.0061061
13	GO Process	cell morphogenesis involved in neuron differentiation	APP CSF1R BRSK1 DOK4 FYN MYH10 SPTAN1 BCL2 CAMK2A CDC42 TOP2B SPTBN2 NUMB	5.20E-04	GO.0048667
6	GO Process	endothelial cell differentiation	LAMA5 ICAM1 TJP1 ARHGEF26 DLL1 CLIC4	5.30E-04	GO.0045446
8	GO Process	ameboidal-type cell migration	MYH9 LAMA5 KIT NOS3 FN1 DPP4 MMRN2 CFL1	5.40E-04	GO.0001667
9	GO Process	regulation of protein polymerization	TUBB4A ADD1 ICAM1 SNCA MYO1C SPTAN1 DYRK1A SPTBN2 ARF1	5.70E-04	GO.0032271
12	GO Process	positive regulation of proteolysis	MYH9 ENO1 APP PLK1 MMP14 DAB2 LCK SNCA CAV1 FYN FN1 FAS	5.70E-04	GO.0045862
9	GO Process	protein dephosphorylation	PPP3R1 CDC25B CDC25A TENC1 CDC25C LCK PTPN1 PPP3CA BCL2	6.10E-04	GO.0006470
18	GO Process	membrane organization	MYH9 THBS1 CCR5 PLK1 BCL2L1 SDPR DAB2 CALR SNCA CAV1 ANXA2 MYH10 DNMT1 BCL2 CAMK2A CDC42 SUN1 ABCB1	6.10E-04	GO.0061024
17	GO Process	regulation of establishment of protein localization	ARHGEF5 GAPDH APP CSF1R CCT2 MAP4K4 FYN FN1 MYO1C MYH10 DPP4 PTPN1 TLR4 ANXA1 PPP3CA BCL2 NR1H4	6.20E-04	GO.0070201
23	GO Process	negative regulation of multicellular organismal process	MAP2K5 PDGFRA THBS1 NGEF APP ANXA5 NOS3 CALR RARB MAP4K4 ANXA2 FN1 ARHGAP15 DLL1 MMRN2 TLR4 ANXA1 G6PD PPP3CA BCL2 RARG VIM NR1H4	6.50E-04	GO.0051241
11	GO Process	epithelial tube morphogenesis	PPP3R1 LAMA5 CSF1R MMP14 EPHA2 DLL1 SDC4 CLIC4 BCL2 RARG CFL1	6.70E-04	GO.0060562
11	GO Process	urogenital system development	ITGB4 LAMA5 PDGFRA TENC1 RARB DLL1 SDC4 ANXA1 SDC1 BCL2 RARG	6.90E-04	GO.0001655
18	GO Process	regulation of proteolysis	MAP2K5 MYH9 GAPDH ENO1 THBS1 DNAJB6 PRKCG APP PLK1 MMP14 DAB2 LCK SNCA CAV1 FYN FN1 FAS PBK	7.50E-04	GO.0030162
21	GO Process	secretion by cell	PLEK THBS1 VWF CNN2 EXOC68 FERMT3 APP KIT ANXA5 CCT2 BRSK1 TUBB4B ANXA2 FN1 MYH10 FLNA SPTAN1 TLR4 ANXA1 XRC5 NR1H4	7.60E-04	GO.0032940
12	GO Process	regulation of metal ion transport	CCL2 ICAM1 NOS3 SNCA CAV1 FYN GSTO1 FLNA G6PD CAMK2B BCL2 CAMK2A	7.80E-04	GO.0010959
17	GO Process	regulation of defense response	MMP2 RORA APP ITGA2 ZYX SNCA CAV1 CDH5 FYN SFPQ TGM2 PTPN1 TLR4 ANXA1 XRC5 PBK NR1H4	7.80E-04	GO.0031347
6	GO Process	regulation of reactive oxygen species biosynthetic process	ICAM1 APP SNCA CAV1 FYN TLR4	7.80E-04	GO.1903426
15	GO Process	embryonic morphogenesis	ITGB4 MMP2 LAMA5 PDGFRA COL8A1 FLT1 ITGA2 MMP14 JAG2 RARB FN1 DLL1 SDC4 RARG CFL1	8.00E-04	GO.0048598
8	GO Process	interaction with host	GAPDH ICAM1 CCR5 ITGA2 BCL2L1 CAV1 EPHA2 DPP4	8.00E-04	GO.0051701
9	GO Process	positive regulation of cytoskeleton organization	ARHGEF5 PLEK ICAM1 MYO1C ARHGEF15 FLNA SDC4 CDC42 CFL1	8.30E-04	GO.0051495
6	GO Process	ephrin receptor signaling pathway	MMP2 NGEF FYN EPHA2 DNMT1 CDC42	8.70E-04	GO.0048013
13	GO Process	response to radiation	ICAM1 APP KIT DDB1 BCL2L1 CDC25A BRSK1 CYP2R1 USP1 ANXA1 XRC5 BCL2 PBK	8.80E-04	GO.0009314
17	GO Process	regulation of cell cycle process	CCL2 CDC25B TUBB4A APP PLK1 TUBA1A DDB1 BCL2L1 CDC25A BRSK1 CALR CDC25C TUBB4B SFPQ ANXA1 BCL2 CDC42	8.80E-04	GO.0010564
5	GO Process	positive regulation of phospholipid metabolic process	PDGFRA FLT1 APP KIT NR1H4	8.80E-04	GO.1903727
6	GO Process	peptidyl-threonine phosphorylation	CAD CAMK2B BCL2 CAMK2A DYRK1A CAMK1D	9.10E-04	GO.0018107
4	GO Process	cerebellar Purkinje cell layer development	RORA MYH10 DLL1 SPTBN2	9.10E-04	GO.0021680

16	GO Process	regulation of ion transport	CCL2 THBS1 ICAM1 APP NOS3 SNCA CAV1 FYN GSTO1 FLNA CLIC4 G6PD CAMK2B BCL2 CAMK2A ABC1	9.10E-04	GO.0043269
4	GO Process	regulation of long-term neuronal synaptic plasticity	APP KIT SNCA CAMK2B	9.10E-04	GO.0048169
8	GO Process	regulation of actin polymerization or depolymerization	PLEK ADD1 ICAM1 MYO1C SPTAN1 SPTBN2 CFL1 ARF1	9.20E-04	GO.0008064
5	GO Process	ovarian follicle development	ICAM1 KIT BCL2L1 MMP14 BCL2	9.40E-04	GO.0001541
5	GO Process	regulation of actin filament depolymerization	PLEK ADD1 SPTAN1 SPTBN2 CFL1	9.40E-04	GO.0030834
3	GO Process	negative regulation of glial cell apoptotic process	CCL2 PRKCH DLL1	9.80E-04	GO.0034351
8	GO Process	transcription initiation from RNA polymerase II promoter	RORA RORC RARB NR1I2 RXRG RARB RARG NR1H4	9.90E-04	GO.0006367
8	GO Process	cell-substrate adhesion	ITGB4 LAMA5 VWF FERMT3 ITGA2 ZYX FN1 BCL2	9.90E-04	GO.0031589
8	GO Process	positive regulation of angiogenesis	HSPB1 THBS1 AKT3 FLT1 NOS3 CDH5 DLL1 ANXA1	9.90E-04	GO.0045766
8	GO Process	establishment or maintenance of cell polarity	MYH9 ARF4 BRSK1 CLIC4 FSCN1 CDC42 WEE1 CFL1	0.001	GO.0007163
10	GO Process	response to xenobiotic stimulus	RORA PRKCG CAD ICAM1 NQO1 RORC NR1I2 SNCA GSTO1 PPP3CA	0.001	GO.0009410
9	GO Process	response to mechanical stimulus	THBS1 CNN2 KIT ITGA2 MMP14 FYN FAS TLR4 SUN1	0.001	GO.0009612
7	GO Process	platelet activation	PDGFRA VWF PRKCG PRKCH LCK FYN FLNA	0.001	GO.0030168
8	GO Process	regulation of protein localization to membrane	BCL2L1 DAB2 PRKCH FYN EPHA2 MYO1C BCL2 NUMB	0.001	GO.1905475
9	GO Process	DNA-templated transcription, initiation	RORA RORC RARB NR1I2 PTRF RXRG RARB RARG NR1H4	0.0011	GO.0006352
8	GO Process	viral life cycle	CCL2 ICAM1 CCR5 ITGA2 CAV1 EPHA2 DPP4 CDC42	0.0011	GO.0019058
7	GO Process	negative regulation of protein complex assembly	TUBB4A ADD1 SNCA SPTAN1 DYRK1A CDC42 SPTBN2	0.0011	GO.0031333
5	GO Process	regulation of neuronal synaptic plasticity	APP KIT SNCA CAMK2B CAMK2A	0.0011	GO.0048168
5	GO Process	T cell costimulation	LCK CAV1 FYN DPP4 CDC42	0.0012	GO.0031295
98	GO Process	primary metabolic process	RCN1 MAP2K5 PLOD1 MYH9 CYP24A1 MMP2 CCL2 GAPDH RBP1 PPP3R1 PLEK ENO1 CD C25B ARF3 PDGFRA THBS1 VWF RORA PRKCG AKT3 CAD ADD1 FLT1 PLOD2 APP CSF1R KIT NPC1L1 CCR5 CAPN2 NOS3 MELK CKB PLK1 DDB1 CDC25A ARF4 MMP14 BRSK1 TEN C1 CALR CDC25C RORC PRKCH RARB CYP2R1 NR1I2 LCK SNCA CAV1 RGS12 PTGES USP1 MAP4K4 PTMA ANXA2 FYN FN1 PTRF SFPQ EPHA2 RXRG DPP4 TGM2 GSTO1 SLK FLNA PTPN1 SDC4 SPTAN1 TLR4 RARB ANXA1 PIR PSIP1 SDC1 XRCC5 G6PD PPP3CA CAMK2B LDHB BCL2 CAMK2A DYRK1A PAIC5 CDC42 PDIA6 RARG TOP2B WEE1 PBK SPTBN2 CFL1 ARF1 NR1H4 PRKCH CAMK1D MCM3	0.0012	GO.0044238
21	GO Process	chemical homeostasis	RBP1 MT2A PDGFRA RORA ICAM1 APP CCR5 CKB DDB1 CALR LCK SNCA CAV1 ANXA6 T GM2 GSTO1 CLIC4 PPP3CA BCL2 ARF1 NR1H4	0.0012	GO.0048878
31	GO Process	positive regulation of gene expression	MAP2K5 MYH9 PPP3R1 ENO1 THBS1 RORA APP KIT ITGA2 NOS3 ARF4 MMP14 DAB2 CA LR RORC RARB NR1I2 CAV1 FN1 SFPQ MYO1C RXRG DLL1 TLR4 RARB PSIP1 PPP3CA DYR K1A RARG VIM NR1H4	0.0013	GO.0010628
77	GO Process	cellular macromolecule metabolic process	RCN1 MAP2K5 PLOD1 MMP2 CCL2 GAPDH PPP3R1 ENO1 CDC25B PDGFRA THBS1 RORA PRKCG AKT3 CAD ADD1 FLT1 PLOD2 APP CSF1R KIT CCR5 CAPN2 MELK PLK1 DDB1 CDC 25A ARF4 BRSK1 TENC1 CDC25C RORC PRKCH RARB NR1I2 LCK SNCA CAV1 RGS12 USP1 MAP4K4 PTMA FYN FN1 PTRF EPHA2 RXRG TGM2 SLK FLNA PTPN1 SPTAN1 DNM 1 TLR4 RARB ANXA1 PIR PSIP1 XRCC5 PPP3CA CAMK2B BCL2 CAMK2A DYRK1A CDC42 P DIA6 RARG TOP2B WEE1 PBK SPTBN2 CFL1 NR1H4 PRKCH CAMK1D MCM3	0.0013	GO.0044260
4	GO Process	positive regulation of cell cycle G2/M phase transition	CDC25B APP CDC25A CDC25C	0.0013	GO.1902751
7	GO Process	positive regulation of leukocyte migration	THBS1 ICAM1 APP ITGA2 MMP14 CALR CAMK1D	0.0014	GO.0002687
19	GO Process	central nervous system development	RORA AKT3 APP CSF1R CKB ARF4 RARB FYN MYH10 DLL1 FLNA XRCC5 PPP3CA BCL2 SU N1 TOP2B SPTBN2 VIM NUMB	0.0014	GO.0007417
14	GO Process	sensory organ development	PDGFRA COL8A1 KIT JAG2 RARB EPHA2 MYH10 ARHGEF15 DLL1 SDC4 CLIC4 BCL2 RARG VIM	0.0014	GO.0007423
15	GO Process	cellular ion homeostasis	MT2A PDGFRA APP CCR5 CKB CALR LCK SNCA CAV1 ANXA6 TGM2 GSTO1 CLIC4 BCL2 A RF1	0.0015	GO.0006873
11	GO Process	negative regulation of organelle organization	TUBB4A ADD1 APP PLK1 BCL2L1 SNCA SPTAN1 TBC1D4 XRCC5 DYRK1A SPTBN2	0.0015	GO.0010639
20	GO Process	neuron differentiation	RORA APP CSF1R ARF4 BRSK1 JAG2 MAP4K4 DOK4 FYN MYH10 DLL1 SDC4 SPTAN1 BCL 2 CAMK2A CDC42 TOP2B WEE1 SPTBN2 NUMB	0.0015	GO.0030182
11	GO Process	regulation of cellular component size	PLEK AKT3 ADD1 ICAM1 FN1 MYO1C SPTAN1 RARG SPTBN2 CFL1 ARF1	0.0015	GO.0032535
86	GO Process	macromolecule metabolic process	RCN1 MAP2K5 PLOD1 MYH9 MMP2 CCL2 GAPDH PPP3R1 ENO1 CDC25B PDGFRA THBS1 VWF RORA PRKCG AKT3 CAD ADD1 FLT1 PLOD2 APP CSF1R KIT NPC1L1 CCR5 CAPN2 MELK PLK1 DDB1 CDC25A ARF4 MMP14 BRSK1 TENC1 CALR CDC25C RORC PRKCH RARB NR1I2 LCK SNCA CAV1 RGS12 USP1 MAP4K4 PTMA ANXA2 FYN FN1 PTRF SFPQ EPHA2 RXRG DPP4 TGM2 SLK FLNA PTPN1 SDC4 SPTAN1 DNM1 TLR4 RARB ANXA1 PIR PSIP1 SDC1 XRCC5 PPP3CA CAMK2B BCL2 CAMK2A DYRK1A CDC42 PDIA6 RARG TOP2B WEE1 PBK SPTBN2 CFL1 NR1H4 PRKCH CAMK1D MCM3	0.0015	GO.0043170
5	GO Process	positive regulation of blood vessel endothelial cell migration	HSPB1 THBS1 AKT3 NOS3 ANXA1	0.0015	GO.0043536
7	GO Process	response to calcium ion	THBS1 ADD1 CAV1 PTGES CLIC4 SDC1 PPP3CA	0.0015	GO.0051592
11	GO Process	regulation of small molecule metabolic process	PLEK ENO1 RORA KIT NOS3 NQO1 RORC SNCA CAV1 ANXA1 NR1H4	0.0015	GO.0062012
5	GO Process	positive regulation of intrinsic apoptotic signaling pathway	BCL2L1 LCK CAV1 SFPQ BCL2	0.0015	GO.2001244
24	GO Process	cell cycle	MYH9 CDC25B THBS1 TUBB4A MELK PLK1 TUBA1A BCL2L1 CDC25A BRSK1 CDC25C TUBB 4B MYH10 FLNA PPP3CA CAMK2A SEPT7 SUN1 TOP2B WEE1 PBK CFL1 ABC1B MCM3	0.0016	GO.0007049
7	GO Process	T cell differentiation	RORA KIT RORC JAG2 LCK ANXA1 BCL2	0.0016	GO.0030217
19	GO Process	regulation of immune response	MMP2 PPP3R1 ICAM1 APP KIT PRKCH LCK CAV1 FYN SFPQ MYO1C PTPN1 TLR4 ANXA1 XRCC5 PPP3CA BCL2 CDC42 NR1H4	0.0016	GO.0050776
5	GO Process	regulation of extrinsic apoptotic signaling pathway via death domain receptors	THBS1 ICAM1 NOS3 BCL2L1 FAS	0.0016	GO.1902041
4	GO Process	response to amyloid-beta	APP FYN DNM1 TLR4	0.0016	GO.1904645
6	GO Process	viral entry into host cell	ICAM1 CCR5 ITGA2 CAV1 EPHA2 DPP4	0.0017	GO.0046718
11	GO Process	developmental growth	ADD1 APP TENC1 RARB DLL1 CLIC4 ANXA1 BCL2 RARG SPTBN2 APBA2	0.0017	GO.0048589
11	GO Process	regulation of inflammatory response	RORA APP ITGA2 ZYX SNCA CDH5 TGM2 TLR4 ANXA1 PBK NR1H4	0.0017	GO.0050727
11	GO Process	positive regulation of protein serine/threonine kinase activity	ARHGEF5 MAP2K5 THBS1 FLT1 APP CSF1R KIT SNCA MAP4K4 PTPN1 TLR4	0.0017	GO.0071902
15	GO Process	regulation of neuron differentiation	NGEF APP BRSK1 CALR RARB MAP4K4 FYN FN1 DLL1 PPP3CA CAMK2B BCL2 CFL1 VIM C AMK1D	0.0018	GO.0045664
6	GO Process	tissue remodeling	NOS3 MMP14 CAV1 EPHA2 TGM2 ANXA1	0.0018	GO.0048771
12	GO Process	regulation of DNA-binding transcription factor activity	ARHGEF5 MAP2K5 ICAM1 APP KIT PRKCH FLNA TLR4 PPP3CA CAMK2A NR1H4 CAMK1D	0.0018	GO.0051090
13	GO Process	regulation of anatomical structure size	PLEK AKT3 ADD1 ICAM1 NOS3 CAV1 FN1 MYO1C SPTAN1 RARG SPTBN2 CFL1 ARF1	0.0018	GO.0090066
11	GO Process	axonogenesis	APP CSF1R BRSK1 DOK4 FYN MYH10 SPTAN1 BCL2 TOP2B SPTBN2 NUMB	0.0019	GO.0007409
10	GO Process	blood coagulation	PDGFRA VWF PRKCG ANXA5 ITGA2 PRKCH LCK FYN FLNA CDC42	0.0019	GO.0007596
4	GO Process	regulation of platelet activation	PLEK PDGFRA NOS3 TLR4	0.0019	GO.0010543

7	GO Process	positive regulation of epithelial cell migration	HSPB1 THBS1 AKT3 ITGA2 NOS3 CALR ANXA1	0.0019	GO.0010634
3	GO Process	positive regulation of tumor necrosis factor biosynthetic process	HSPB1 THBS1 TLR4	0.0019	GO.0042535
22	GO Process	negative regulation of molecular function	MAP2K5 GAPDH HSPB1 PXDN THBS1 DNAJB6 APP ANXA5 NOS3 PLK1 DAB2 NQO1 SNCA CAV1 ANXA2 GSTO1 FLNA CNN3 PTPN1 ANXA1 PPP3CA NR1H4	0.0019	GO.0044092
12	GO Process	reproductive structure development	BCL2L2 PDGFRA ICAM1 KIT NOS3 BCL2L1 MMP14 FLNA ANXA1 SDC1 BCL2 RARG	0.0019	GO.0048608
7	GO Process	retina development in camera-type eye	PDGFRA RARB MYH10 ARHGEF15 DLL1 CLIC4 RARG	0.0019	GO.0060041
8	GO Process	cell chemotaxis	ARHGEF5 CCL2 PDGFRA FLT1 KIT CCR5 EPHA2 ANXA1	0.0019	GO.0060326
5	GO Process	regulation of postsynapse organization	NGEF APP FYN CAMK2B CFL1	0.0019	GO.0099175
10	GO Process	regulation of neuron death	CCL2 PRKCG APP BCL2L1 NQO1 SNCA FYN TLR4 G6PD BCL2	0.0019	GO.1901214
5	GO Process	regulation of adherens junction organization	THBS1 ADD1 MMP14 SLK SDC4	0.0019	GO.1903391
8	GO Process	phagocytosis	MYH9 THBS1 FYN MYO1C TGM2 ANXA1 CDC42 PDIA6	0.002	GO.0006909
6	GO Process	positive regulation of endothelial cell migration	HSPB1 THBS1 AKT3 NOS3 CALR ANXA1	0.002	GO.0010595
5	GO Process	cellular response to amino acid stimulus	MMP2 PDGFRA CAPN2 BCL2L1 FYN	0.002	GO.0071230
6	GO Process	negative regulation of intrinsic apoptotic signaling pathway	ENO1 HSPB1 BCL2L2 BCL2L1 PTPN1 BCL2	0.002	GO.2001243
6	GO Process	actomyosin structure organization	MYH9 PDGFRA CNN2 ZYX MYH10 CNN3	0.0021	GO.0031032
10	GO Process	camera-type eye development	PDGFRA COL8A1 RARB EPHA2 MYH10 ARHGEF15 DLL1 CLIC4 RARG VIM	0.0021	GO.0043010
22	GO Process	regulation of cell cycle	MAP2K5 CCL2 CDC25B THBS1 TUBB4A APP PLK1 TUBA1A DDB1 BCL2L1 CDC25A BRSK1 CALR CDC25C TUBB4B MAP4K4 SFPQ SLK ANXA1 BCL2 CDC42 TOP2B	0.0021	GO.0051726
11	GO Process	regulation of mitotic cell cycle phase transition	CCL2 TUBB4A APP PLK1 TUBA1A DDB1 BRSK1 CDC25C TUBB4B ANXA1 BCL2	0.0021	GO.1901990
10	GO Process	regulation of neurotransmitter levels	RORA ICAM1 APP NOS3 BRSK1 NQO1 SNCA CAV1 TLR4 CAMK2A	0.0022	GO.0001505
3	GO Process	negative regulation of microtubule polymerization	TUBB4A SNCA DYRK1A	0.0022	GO.0031115
8	GO Process	regulation of chemotaxis	CCL2 HSPB1 PDGFRA THBS1 APP ITGA2 CALR CAMK1D	0.0022	GO.0050920
4	GO Process	positive regulation of phosphatidylinositol 3-kinase activity	PDGFRA FLT1 APP KIT	0.0023	GO.0043552
4	GO Process	homeostasis of number of cells within a tissue	AKT3 ADD1 NOS3 BCL2	0.0023	GO.0048873
14	GO Process	chordate embryonic development	MYH9 PDGFRA ADD1 CAPN2 NOS3 BCL2L1 MMP14 JAG2 MYH10 DLL1 SDC4 RARG CFL1 APBA2	0.0024	GO.0043009
7	GO Process	negative regulation of ion transport	THBS1 ICAM1 NOS3 SNCA CAV1 GSTO1 BCL2	0.0024	GO.0043271
19	GO Process	positive regulation of cell differentiation	ADD1 APP KIT MMP14 DAB2 CALR PRKCH RARB CDH5 FYN FN1 FLNA ANXA1 XRCC5 CAMK2B BCL2 CDC42 NUMB CAMK1D	0.0024	GO.0045597
13	GO Process	cell division	MYH9 CDC25B KIT PLK1 TUBA1A TUBA1C CDC25A CDC25C MYH10 SEPT7 WEE1 CFL1 NUMB	0.0024	GO.0051301
18	GO Process	response to other organism	CCL2 GAPDH ENO1 HSPB1 ICAM1 APP CCR5 NOS3 BCL2L1 SNCA CAV1 PTGES FAS TLR4 BCL2 CFL1 ARF1 NR1H4	0.0024	GO.0051707
7	GO Process	hindbrain development	RORA CKB MYH10 DLL1 FLNA BCL2 SPTBN2	0.0025	GO.0030902
3	GO Process	nitric oxide biosynthetic process	RORA NOS3 NQO1	0.0026	GO.0006809
3	GO Process	cerebellar Purkinje cell layer morphogenesis	RORA DLL1 SPTBN2	0.0026	GO.0021692
6	GO Process	establishment of cell polarity	MYH9 BRSK1 FSCN1 CDC42 WEE1 CFL1	0.0026	GO.0030010
15	GO Process	regulation of protein transport	ARHGEF5 GAPDH APP CSF1R MAP4K4 FYN FN1 MYO1C MYH10 DPP4 PTPN1 TLR4 ANXA1 PPP3CA NR1H4	0.0026	GO.0051223
5	GO Process	regulation of oxidative stress-induced cell death	HSPB1 APP FYN SFPQ TLR4	0.0026	GO.1903201
8	GO Process	regulation of neuron apoptotic process	CCL2 PRKCG BCL2L1 NQO1 SNCA FYN G6PD BCL2	0.0027	GO.0043523
12	GO Process	positive regulation of neurogenesis	APP KIT PRKCH RARB FYN FN1 FLNA XRCC5 CAMK2B BCL2 NUMB CAMK1D	0.0027	GO.0050769
17	GO Process	exocytosis	PLEK THBS1 VWF CNN2 EXOC68 FERMT3 APP KIT ANXA5 CCT2 TUBB4B ANXA2 FN1 MYH10 FLNA SPTAN1 XRCC5	0.0028	GO.0006887
6	GO Process	metencephalon development	RORA CKB MYH10 DLL1 BCL2 SPTBN2	0.0028	GO.0022037
11	GO Process	regulation of cell-cell adhesion	MAP2K5 CCL2 ICAM1 FERMT3 LCK CAV1 FYN DPP4 SDC4 ANXA1 CDC42	0.0028	GO.0022407
11	GO Process	positive regulation of defense response	MMP2 APP ITGA2 SNCA CAV1 FYN SFPQ TGM2 TLR4 XRCC5 NR1H4	0.0028	GO.0031349
8	GO Process	gliogenesis	CCL2 PPP3R1 APP MMP14 DLL1 ANXA1 SUN1 VIM	0.0028	GO.0042063
9	GO Process	positive regulation of DNA-binding transcription factor activity	ARHGEF5 ICAM1 APP KIT PRKCH TLR4 PPP3CA CAMK2A CAMK1D	0.0028	GO.0051091
70	GO Process	regulation of nitrogen compound metabolic process	ARHGEF5 MAP2K5 MYH9 EHD4 CCL2 GAPDH PPP3R1 PLEK ENO1 CDC25B HSPB1 PDGFRA THBS1 RORA DNAJB6 PRKCG ICAM1 FLT1 APP CSF1R KIT ITGA2 NOS3 CCT2 PLK1 DDB1 CDC25A ARF4 MMP14 DAB2 NQO1 CALR CDC25C RORC PRKCH RARB NR12 LCK SNCA CAV1 USP1 MAP4K4 ANXA2 FYN FN1 FAS PTRF SFPQ EPHA2 RXRG DLL1 SLK FLNA PTPN1 SDC4 TLR4 RXRB PIR PSIP1 XRCC5 G6PD PPP3CA BCL2 CAMK2A DYRK1A RARG PBK VIM NR1H4 CAMK1D	0.0028	GO.0051171
8	GO Process	cellular response to acid chemical	MMP2 PDGFRA CAPN2 BCL2L1 FYN XRCC5 RARG NR1H4	0.0028	GO.0071229
10	GO Process	cellular response to external stimulus	CYP24A1 CNN2 ICAM1 ITGA2 CAV1 FYN FAS TLR4 BCL2 NR1H4	0.0028	GO.0071496
99	GO Process	organic substance metabolic process	RCN1 MAP2K5 PLOC1 MYH9 CYP24A1 MMP2 CCL2 GAPDH RBP1 PPP3R1 PLEK ENO1 CDC25B ARF3 PDGFRA THBS1 VWF RORA PRKCG AKT3 CAD ADD1 FLT1 PLOC2 APP CSF1R KIT NPC1L1 CCR5 CAPN2 NOS3 MELK CKB PLK1 DDB1 CDC25A ARF4 MMP14 BRSK1 TEN C1 CALR CDC25C RORC PRKCH RARB CYP2R1 NR12 LCK SNCA CAV1 RG512 PTGES USP1 MAP4K4 PTMA ANXA2 FYN FN1 PTRF SFPQ EPHA2 RXRG DPP4 TGM2 GSTO1 SLK FLNA PTPN1 SDC4 SPTAN1 DNM1 TLR4 RXRB ANXA1 PIR PSIP1 SDC1 XRCC5 G6PD PPP3CA CAMK2B LDHB BCL2 CAMK2A DYRK1A PAICS CDC42 PDIA6 RARG TOP2B WEE1 PBK SPTB N2 CFL1 ARF1 NR1H4 PRKCSH CAMK1D MCM3	0.0028	GO.0071704
5	GO Process	multicellular organismal response to stress	THBS1 PRKCG DPP4 PPP3CA BCL2	0.0029	GO.0033555
11	GO Process	regulation of protein catabolic process	PRKCG APP PLK1 DDB1 DAB2 SNCA CAV1 ANXA2 FYN FLNA PBK	0.0029	GO.0042176
4	GO Process	neuron projection organization	APP FYN CDC42 ARF1	0.0029	GO.0106027
4	GO Process	negative regulation of extrinsic apoptotic signaling pathway via death domain receptors	ICAM1 NOS3 BCL2L1 FAS	0.0029	GO.1902042
3	GO Process	cellular copper ion homeostasis	MT2A APP ARF1	0.003	GO.0006878
3	GO Process	Sertoli cell development	ICAM1 FLNA SDC1	0.003	GO.0060009
5	GO Process	positive regulation of organelle assembly	ARHGEF5 SDC4 SDC1 FSCN1 SEPT7	0.003	GO.1902117
13	GO Process	cellular metal ion homeostasis	MT2A PDGFRA APP CCR5 CALR LCK SNCA CAV1 ANXA6 TGM2 GSTO1 BCL2 ARF1	0.0031	GO.0006875
7	GO Process	cytoskeleton-dependent intracellular transport	HSPB1 APP TUBA1A TUBA1C MYO1C CDC42 SUN1	0.0031	GO.0030705
16	GO Process	ion homeostasis	MT2A PDGFRA APP CCR5 CKB CALR LCK SNCA CAV1 ANXA6 TGM2 GSTO1 CLIC4 BCL2 ARF1 NR1H4	0.0031	GO.0050801
4	GO Process	negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	MAP2K5 BCL2L1 FYN BCL2	0.0031	GO.2001240
7	GO Process	response to unfolded protein	CCL2 HSPB1 THBS1 ADD1 CALR PTPN1 PDIA6	0.0032	GO.0006986
14	GO Process	cellular cation homeostasis	MT2A PDGFRA APP CCR5 CALR LCK SNCA CAV1 ANXA6 TGM2 GSTO1 CLIC4 BCL2 ARF1	0.0032	GO.0030003
5	GO Process	regulation of phagocytosis	CCL2 PRKCG ITGA2 CALR CAMK1D	0.0032	GO.0050764
72	GO Process	regulation of macromolecule metabolic process	ARHGEF5 MAP2K5 MYH9 EHD4 CCL2 GAPDH PPP3R1 PLEK ENO1 CDC25B HSPB1 PDGFRA THBS1 RORA DNAJB6 PRKCG ICAM1 FLT1 APP CSF1R KIT ITGA2 NOS3 CCT2 PLK1 DDB1 CDC25A ARF4 MMP14 DAB2 CALR CDC25C RORC PRKCH RARB NR12 LCK SNCA CAV1 USP1 MAP4K4 ANXA2 FYN FN1 FAS PTRF SFPQ EPHA2 MYO1C RXRG DLL1 SLK FLNA PTPN1 SDC4 TLR4 RXRB PIR PSIP1 XRCC5 G6PD PPP3CA BCL2 CAMK2A DYRK1A RARG PBK ARF1 VIM NR1H4 APBA2 CAMK1D	0.0032	GO.0060255

8	GO Process	positive regulation of leukocyte cell-cell adhesion	CCL2 ICAM1 LCK CAV1 FYN DPP4 ANXA1 CDC42	0.0032	GO.1903039
4	GO Process	negative regulation of endothelial cell proliferation	CCL2 THBS1 FLT1 CAV1	0.0033	GO.0001937
6	GO Process	positive regulation of cell-substrate adhesion	COL8A1 CALR FN1 FLNA SDC4 CDC42	0.0033	GO.0010811
4	GO Process	muscle filament sliding	TPM4 TPM3 TPM2 VIM	0.0033	GO.0030049
72	GO Process	regulation of cellular metabolic process	ARHGEF5 MAP2K5 MYH9 EHD4 CCL2 GAPDH PPP3R1 PLEK ENO1 CDC25B HSPB1 PDGFRA THBS1 RORA DNAJB6 PRKCG ICAM1 FLT1 APP CSF1R KIT ITGA2 NOS3 CCT2 PLK1 BCL2L1 CDC25A ARF4 MMP14 DAB2 NQO1 CALR CDC25C RORC PRKCH RARB NR1I2 LCK SNCA CAV1 USP1 MAP4K4 ANXA2 FYN FN1 FAS PTRF SFPQ EPHA2 RXRG DLL1 SLK FLNA PTPN1 SDC4 TLR4 RXRB ANXA1 PIR PSIP1 XRCC5 G6PD PPP3CA BCL2 CAMK2A DYRK1A RARG PBK ARF1 VIM NR1H4 CAMK1D	0.0033	GO.0031323
15	GO Process	inorganic ion homeostasis	MT2A PDGFRA APP CCR5 CKB CALR LCK SNCA CAV1 ANXA6 TGM2 GSTO1 CLIC4 BCL2 ARF1	0.0033	GO.0098771
14	GO Process	organelle localization	MYH9 PLEK TUBB4A EXOC6B KIT PLK1 TUBA1A SNCA TUBB4B MYO1C MYH10 DNM1 CDC42 SUN1	0.0034	GO.0051640
2	GO Process	cellular response to norepinephrine stimulus	APLP1 APP	0.0034	GO.0071874
2	GO Process	T cell extravasation	CCL2 ICAM1	0.0034	GO.0072683
71	GO Process	regulation of primary metabolic process	ARHGEF5 MAP2K5 MYH9 EHD4 CCL2 GAPDH PPP3R1 PLEK ENO1 CDC25B HSPB1 PDGFRA THBS1 RORA DNAJB6 PRKCG ICAM1 FLT1 APP CSF1R KIT ITGA2 NOS3 CCT2 PLK1 DDB1 CDC25A ARF4 MMP14 DAB2 NQO1 CALR CDC25C RORC PRKCH RARB NR1I2 LCK SNCA CAV1 USP1 MAP4K4 ANXA2 FYN FN1 FAS PTRF SFPQ EPHA2 RXRG DLL1 SLK FLNA PTPN1 SDC4 TLR4 RXRB ANXA1 PIR PSIP1 XRCC5 G6PD PPP3CA BCL2 CAMK2A DYRK1A RARG PBK VIM NR1H4 CAMK1D	0.0034	GO.0080090
3	GO Process	negative regulation of cell migration involved in sprouting angiogenesis	MAP2K5 THBS1 MMR2	0.0034	GO.0090051
7	GO Process	regulation of muscle contraction	ENO1 KIT ITGA2 CAV1 ANXA6 GSTO1 FLNA	0.0035	GO.0006937
9	GO Process	positive regulation of lymphocyte activation	CCL2 MMP14 LCK CAV1 FYN DPP4 ANXA1 BCL2 CDC42	0.0035	GO.0051251
102	GO Process	metabolic process	RCN1 MAP2K5 PLOD1 ITGB4 MYH9 CYP24A1 MMP2 CCL2 GAPDH RBP1 PPP3R1 PLEK ENO1 CDC25B PXDN ARF3 PDGFRA THBS1 VWF RORA PRKCG AKT3 CAD ADD1 FLT1 PLOD2 APP CSF1R KIT NPC1L1 CCR5 CAPN2 NOS3 MELK CKB PLK1 DDB1 CDC25A ARF4 MMP14 BRSK1 TENC1 NQO1 CALR CDC25C RORC PRKCH RARB CYP2R1 NR1I2 LCK SNCA CAV1 RGS12 PTGES USP1 MAP4K4 PTMA ANXA2 FYN FN1 PTRF SFPQ EPHA2 RXRG DPP4 TGM2 GSTO1 SLK FLNA PTPN1 SDC4 SPTAN1 DNM1 TLR4 RXRB ANXA1 PIR PSIP1 SDC1 XRCC5 G6PD PPP3CA CAMK2B LDHB BCL2 CAMK2A DYRK1A PAICS CDC42 PDIA6 RARG TOP2B WEE1 PBK SPTBN2 CFL1 ARF1 NR1H4 PRKCSH CAMK1D MCM3	0.0036	GO.0008152
30	GO Process	positive regulation of biosynthetic process	MAP2K5 CCL2 PPP3R1 ENO1 HSPB1 THBS1 RORA ICAM1 APP ITGA2 NOS3 CCT2 ARF4 DAB2 RORC RARB NR1I2 SNCA SFPQ RXRG DLL1 TLR4 RXRB ANXA1 PSIP1 XRCC5 PPP3CA RARG VIM NR1H4	0.0037	GO.0009891
9	GO Process	regulation of cell morphogenesis involved in differentiation	NGEF BRSK1 CALR FN1 FLNA PPP3CA CAMK2B CDC42 CFL1	0.0037	GO.0010769
13	GO Process	positive regulation of MAPK cascade	ARHGEF5 MAP2K5 CCL2 PDGFRA THBS1 ICAM1 FLT1 APP CSF1R KIT MAP4K4 PTPN1 TLR4	0.0037	GO.0043410
9	GO Process	positive regulation of MAP kinase activity	ARHGEF5 MAP2K5 THBS1 FLT1 APP KIT MAP4K4 PTPN1 TLR4	0.0038	GO.0043406
13	GO Process	regulation of system process	ENO1 ICAM1 APP KIT ITGA2 NOS3 CAV1 ANXA6 GSTO1 FLNA G6PD PPP3CA CAMK2B	0.0039	GO.0044057
4	GO Process	neuron apoptotic process	GAPDH APP BCL2L1 BCL2	0.0039	GO.0051402
3	GO Process	retina vasculature development in camera-type eye	PDGFRA ARHGEF15 CLIC4	0.0039	GO.0061298
3	GO Process	positive regulation of oxidative stress-induced cell death	APP SFPQ TLR4	0.0039	GO.1903209
8	GO Process	phosphatidylinositol metabolic process	PLEK ARF3 PDGFRA CSF1R KIT LCK FYN ARF1	0.004	GO.0046488
7	GO Process	morphogenesis of a branching epithelium	PPP3R1 LAMA5 MMP14 EPHA2 TGM2 CLIC4 BCL2	0.004	GO.0061138
6	GO Process	formation of primary germ layer	ITGB4 MMP2 COL8A1 ITGA2 MMP14 FN1	0.0041	GO.0001704
11	GO Process	cellular calcium ion homeostasis	PDGFRA APP CCR5 CALR LCK SNCA CAV1 ANXA6 TGM2 GSTO1 BCL2	0.0041	GO.0006874
5	GO Process	adherens junction organization	LAMA5 ITGA2 CDH5 BCL2 NUMB	0.0041	GO.0034332
4	GO Process	endodermal cell differentiation	MMP2 COL8A1 MMP14 FN1	0.0041	GO.0035987
7	GO Process	regulation of synapse organization	NGEF APP SNCA FYN ARHGEF15 CAMK2B CFL1	0.0041	GO.0050807
6	GO Process	positive regulation of calcium ion transport	CCL2 SNCA CAV1 GSTO1 G6PD CAMK2A	0.0041	GO.0051928
9	GO Process	renal system development	ITGB4 LAMA5 PDGFRA TENC1 RARB DLL1 SDC4 SDC1 BCL2	0.0041	GO.0072001
6	GO Process	negative regulation of supramolecular fiber organization	TUBB4A ADD1 SNCA SPTAN1 DYRK1A SPTBN2	0.0041	GO.1902904
5	GO Process	interaction with symbiont	GAPDH DDB1 ANXA2 FN1 CFL1	0.0042	GO.0051702
7	GO Process	regulation of plasma membrane bounded cell projection assembly	ICAM1 KIT CAV1 EPHA2 FSCN1 SEPT7 CDC42	0.0043	GO.0120032
5	GO Process	cell-cell junction assembly	TJP1 CDH5 FSCN1 NR1H4 TLN2	0.0044	GO.0007043
3	GO Process	nitric oxide metabolic process	RORA NOS3 NQO1	0.0045	GO.0046209
7	GO Process	regulation of synaptic plasticity	APP KIT BRSK1 SNCA CAMK2B CAMK2A ARF1	0.0045	GO.0048167
15	GO Process	negative regulation of cell population proliferation	CCL2 THBS1 FLT1 APP CSF1R NOS3 TENC1 RARB CAV1 PTGES CDH5 DLL1 SDC4 BCL2 RARG	0.0046	GO.0008285
95	GO Process	cellular metabolic process	RCN1 MAP2K5 PLOD1 ITGB4 CYP24A1 MMP2 CCL2 GAPDH RBP1 PPP3R1 PLEK ENO1 CDC25B PXDN ARF3 PDGFRA THBS1 RORA PRKCG AKT3 CAD ADD1 FLT1 PLOD2 APP CSF1R KIT CCR5 CAPN2 NOS3 MELK CKB PLK1 DDB1 CDC25A ARF4 BRSK1 TENC1 NQO1 CDC25C RORC PRKCH RARB CYP2R1 NR1I2 LCK SNCA CAV1 RGS12 PTGES USP1 MAP4K4 PTMA FYN FN1 PTRF SFPQ EPHA2 RXRG TGM2 GSTO1 SLK FLNA PTPN1 SDC4 SPTAN1 DNM1 TLR4 RXRB ANXA1 PIR PSIP1 SDC1 XRCC5 G6PD PPP3CA CAMK2B LDHB BCL2 CAMK2A DYRK1A PAICS CDC42 PDIA6 RARG TOP2B WEE1 PBK SPTBN2 CFL1 ARF1 NR1H4 PRKCSH CAMK1D MCM3	0.0046	GO.0044237
11	GO Process	gland development	LAMA5 PDGFRA CAD CSF1R ITGA2 CAV1 EPHA2 TGM2 ANXA1 BCL2 RARG	0.0046	GO.0048732
4	GO Process	endothelial cell development	ICAM1 TJP1 ARHGEF26 CLIC4	0.0047	GO.0001885
6	GO Process	cell-matrix adhesion	ITGB4 LAMA5 ITGA2 ZFY FN1 BCL2	0.0047	GO.0007160
4	GO Process	establishment or maintenance of apical/basal cell polarity	ARF4 CLIC4 FSCN1 CDC42	0.0047	GO.0035088
4	GO Process	negative regulation of G protein-coupled receptor signaling pathway	APLP1 PLEK SNCA DNM1	0.0047	GO.0045744
9	GO Process	regulation of ERK1 and ERK2 cascade	CCL2 PDGFRA ICAM1 APP CSF1R FN1 EPHA2 PTPN1 TLR4	0.0047	GO.0070372
15	GO Process	regulation of secretion by cell	GAPDH CSF1R STXBP6 SNCA MAP4K4 FN1 MYH10 DPP4 SDC4 TLR4 ANXA1 SDC1 PPP3CA CAMK2A NR1H4	0.0047	GO.1903530
11	GO Process	positive regulation of establishment of protein localization	ARHGEF5 GAPDH APP CSF1R CCT2 FYN MYO1C MYH10 TLR4 BCL2 NR1H4	0.0047	GO.1904951
12	GO Process	regulation of cellular protein localization	APP CCT2 PLK1 BCL2L1 DAB2 PRKCH FYN EPHA2 MYO1C PTPN1 BCL2 NUMB	0.0049	GO.1903827
3	GO Process	glandular epithelial cell development	RARB DLL1 RARG	0.005	GO.0002068

91	GO Process	nitrogen compound metabolic process	RCN1 MAP2K5 PLOD1 MYH9 MMP2 CCL2 GAPDH PPP3R1 ENO1 CDC25B PDGFRA THBS1 VWVF RORA PRKCG AKT3 CAD ADD1 FLT1 PLOD2 APP CSF1R KIT NPC1L1 CCR5 CAPN2 NOS3 MELK CKB PLK1 DDB1 CDC25A ARF4 MMP14 BRSK1 TENC1 NQO1 CALR CDC25C RORC PRKCH RARB NR1I2 LCK SNCA RG512 USP1 MAP4K4 PTMA ANXA2 FYN FN1 PTRF SFPQ EPHA2 RXRG DPP4 TGM2 GSTO1 SLK FLNA PTPN1 SDC4 SPTAN1 TLR4 RXRB ANXA1 PIR PSIP1 SDC1 XRCC5 G6PD PPP3CA CAMK2B LDHB BCL2 CAMK2A DYRK1A PAICS CDC42 PDIA6 RARG TOP2B WEE1 PBK SPTBN2 CFL1 NR1H4 PRKCSH CAMK1D MCM3	0.005	GO.0006807
2	GO Process	regulation of nitrogen utilization	BCL2 NR1H4	0.005	GO.0006808
12	GO Process	response to toxic substance	PXDN ICAM1 NOS3 BCL2L1 NQO1 FYN GSTO1 ANXA1 SDC1 G6PD PPP3CA BCL2	0.005	GO.0009636
4	GO Process	response to amine	CAD ICAM1 ITGA2 PPP3CA	0.005	GO.0014075
75	GO Process	regulation of metabolic process	ARHGEF5 MAP2K5 MYH9 EHD4 CCL2 GAPDH PPP3R1 PLEK ENO1 CDC25B HSPB1 PDGFRA THBS1 RORA DNAJB6 PRKCG ICAM1 FLT1 APP CSF1R KIT ITGA2 NOS3 CCT2 PLK1 DDB1 BCL2L1 CDC25A ARF4 MMP14 DAB2 NQO1 CALR CDC25C RORC PRKCH RARB NR1I2 LCK SNCA CAV1 USP1 MAP4K4 ANXA2 FYN FN1 FAS PTRF SFPQ EPHA2 MYO1C RXRG DLL1 SLK FLNA PTPN1 SDC4 TLR4 RXRB ANXA1 PIR PSIP1 XRCC5 G6PD PPP3CA BCL2 CAMK2A DYRK1A RARG PBK ARF1 VIM NR1H4 APBA2 CAMK1D	0.005	GO.0019222
7	GO Process	membrane docking	PLEK TUBB4A ICAM1 EXOC6B PLK1 TUBA1A TUBB4B	0.005	GO.0022406
3	GO Process	monocyte differentiation	MYH9 CSF1R PIR	0.005	GO.0030224
8	GO Process	cellular response to oxidative stress	PDGFRA NOS3 MELK NQO1 SNCA ANXA1 G6PD BCL2	0.005	GO.0034599
6	GO Process	negative regulation of protein catabolic process	PRKCG SNCA ANXA2 FYN FLNA PBK	0.005	GO.0042177
10	GO Process	regulation of MAP kinase activity	ARHGEF5 MAP2K5 THBS1 FLT1 APP KIT CAV1 MAP4K4 PTPN1 TLR4	0.005	GO.0043405
2	GO Process	hydroxylysine metabolic process	PLOD1 PLOD2	0.005	GO.0046946
2	GO Process	hydroxylysine biosynthetic process	PLOD1 PLOD2	0.005	GO.0046947
6	GO Process	negative regulation of cytoskeleton organization	TUBB4A ADD1 SNCA SPTAN1 DYRK1A SPTBN2	0.005	GO.0051494
9	GO Process	regulation of leukocyte cell-cell adhesion	CCL2 ICAM1 LCK CAV1 FYN DPP4 SDC4 ANXA1 CDC42	0.005	GO.1903037
3	GO Process	regulation of vascular endothelial cell proliferation	CCL2 AKT3 FLT1	0.005	GO.1905562
3	GO Process	negative regulation of anoliks	BCL2L1 CAV1 BCL2	0.005	GO.2000811
5	GO Process	hematopoietic progenitor cell differentiation	PLEK PDGFRA KIT XRCC5 BCL2	0.0052	GO.0002244
5	GO Process	epithelial cell migration	MYH9 KIT NOS3 DPP4 MMRN2	0.0052	GO.0010631
9	GO Process	negative regulation of response to external stimulus	CCL2 PDGFRA THBS1 RORA NOS3 CDH5 ANXA2 PBK NR1H4	0.0053	GO.0032102
15	GO Process	negative regulation of cell differentiation	RORA NGEF APP CALR RARB CAV1 MAP4K4 DLL1 TLR4 ANXA1 G6PD PPP3CA BCL2 RARG VIM	0.0053	GO.0045596
7	GO Process	positive regulation of apoptotic signaling pathway	THBS1 BCL2L1 LCK CAV1 FAS SFPQ BCL2	0.0053	GO.2001235
20	GO Process	cell-cell signaling	PPP3R1 PRKCG TJP1 CCR5 DDB1 BRSK1 DAB2 NQO1 ZYZ SNCA CAV1 DLL1 DNM1 ANXA1 SDC1 PPP3CA CAMK2A CDC42 RARG APBA2	0.0054	GO.0007267
13	GO Process	behavior	THBS1 PRKCG APP KIT ARF4 BRSK1 SNCA FYN DPP4 DNM1 BCL2 SPTBN2 APBA2	0.0054	GO.0007610
29	GO Process	positive regulation of cellular biosynthetic process	MAP2K5 PPP3R1 ENO1 HSPB1 THBS1 RORA ICAM1 APP ITGA2 NOS3 CCT2 ARF4 DAB2 RORC RARB NR1I2 SNCA SFPQ RXRG DLL1 TLR4 RXRB ANXA1 PSIP1 XRCC5 PPP3CA RARG VIM NR1H4	0.0054	GO.0031328
9	GO Process	cellular response to abiotic stimulus	CNN2 ITGA2 DDB1 BCL2L1 CDC25A FAS TLR4 XRCC5 PBK	0.0054	GO.0071214
5	GO Process	positive regulation of cell cycle phase transition	CDC25B APP CDC25A CDC25C ANXA1	0.0054	GO.1901989
8	GO Process	lymphocyte differentiation	RORA KIT RORC JAG2 LCK DLL1 ANXA1 BCL2	0.0055	GO.0030098
17	GO Process	regulation of catabolic process	GAPDH HSPB1 PRKCG APP PLK1 DDB1 BCL2L1 DAB2 SNCA CAV1 ANXA2 FYN FLNA PTPN1 BCL2 PBK VIM	0.0056	GO.0009894
6	GO Process	Fc receptor signaling pathway	PPP3R1 KIT FYN MYO1C PPP3CA CDC42	0.0058	GO.0038093
15	GO Process	regulated exocytosis	PLEK THBS1 VWF CNN2 FERMT3 APP KIT ANXA5 CCT2 TUBB4B ANXA2 FN1 FLNA SPTAN1 XRCC5	0.0058	GO.0045055
5	GO Process	epithelial cell proliferation	BCL2L2 COL8A1 KIT MMP14 EPHA2	0.0058	GO.0050673
18	GO Process	multi-organism reproductive process	MMP2 CDC25B BCL2L2 CAD APP KIT ITGA2 NOS3 CCT2 PLK1 BCL2L1 CALR CDC25C JAG2 CLIC4 BCL2 SEPT7 SUN1	0.0059	GO.0044703
4	GO Process	positive regulation of muscle contraction	ENO1 KIT ITGA2 GSTO1	0.0059	GO.0045933
4	GO Process	positive regulation of phagocytosis	CCL2 ITGA2 CALR CAMK1D	0.0059	GO.0050766
11	GO Process	plasma membrane bounded cell projection assembly	LAMA5 TUBB4A KIT PLK1 TUBA1A TUBB4B ARHGEF26 MYH10 FLNA FSCN1 SEPT7	0.0059	GO.0120031
3	GO Process	regulation of bicellular tight junction assembly	TJP1 PRKCH MYO1C	0.0061	GO.2000810
4	GO Process	actin filament bundle assembly	ADD1 ZYZ FSCN1 MYO1B	0.0062	GO.0051017
6	GO Process	kidney epithelium development	LAMA5 RARB DLL1 SDC4 SDC1 BCL2	0.0062	GO.0072073
7	GO Process	positive regulation of peptidase activity	APP LCK SNCA CAV1 FYN FN1 FAS	0.0063	GO.0010952
9	GO Process	positive regulation of response to external stimulus	HSPB1 THBS1 APP ITGA2 CALR SNCA TGM2 TLR4 CAMK1D	0.0063	GO.0032103
5	GO Process	positive regulation of neuron death	APP NQO1 SNCA FYN TLR4	0.0063	GO.1901216
7	GO Process	negative regulation of secretion by cell	STXBP6 SNCA MAP4K4 FN1 ANXA1 PPP3CA NR1H4	0.0063	GO.1903531
5	GO Process	ureteric bud development	LAMA5 RARB SDC4 SDC1 BCL2	0.0066	GO.0001657
6	GO Process	leukocyte chemotaxis	ARHGEF5 CCL2 FLT1 KIT CCR5 ANXA1	0.0066	GO.0030595
7	GO Process	positive regulation of peptidyl-tyrosine phosphorylation	EHD4 ICAM1 APP CSF1R KIT FYN PTPN1	0.0066	GO.0050731
11	GO Process	regulation of peptidase activity	MAP2K5 GAPDH THBS1 DNAJB6 APP LCK SNCA CAV1 FYN FN1 FAS	0.0066	GO.0052547
3	GO Process	macrophage differentiation	APP CSF1R CDC42	0.0067	GO.0030225
2	GO Process	positive regulation of extracellular exosome assembly	SDC4 SDC1	0.0067	GO.1903553
2	GO Process	negative regulation of vascular endothelial cell proliferation	CCL2 FLT1	0.0067	GO.1905563
9	GO Process	apoptotic signaling pathway	BCL2L2 MELK BCL2L1 CAV1 ANXA6 FAS EPHA2 TLR4 BCL2	0.0068	GO.0097190
5	GO Process	regulation of protein localization to plasma membrane	BCL2L1 DAB2 PRKCH EPHA2 NUMB	0.0068	GO.1903076
4	GO Process	alpha-beta T cell differentiation	RORA RORC ANXA1 BCL2	0.0069	GO.0046632
8	GO Process	regulation of peptidyl-tyrosine phosphorylation	EHD4 ICAM1 APP CSF1R KIT CAV1 FYN PTPN1	0.0069	GO.0050730
4	GO Process	positive regulation of stress fiber assembly	ARHGEF5 ARHGEF15 SDC4 CDC42	0.0069	GO.0051496
4	GO Process	negative regulation of reactive oxygen species metabolic process	CAV1 FYN G6PD BCL2	0.0069	GO.2000378
9	GO Process	negative regulation of cell development	NGEF APP CALR MAP4K4 DLL1 G6PD PPP3CA BCL2 VIM	0.0072	GO.0010721
9	GO Process	response to lipopolysaccharide	CCL2 ICAM1 CCR5 NOS3 SNCA PTGES FAS TLR4 NR1H4	0.0072	GO.0032496
21	GO Process	lipid metabolic process	CYP24A1 RBP1 PLEK ARF3 PDGFRA APP CSF1R KIT NPC1L1 CYP2R1 NR1I2 LCK SNCA CAV1 PTGES FYN SDC4 SDC1 G6PD ARF1 NR1H4	0.0074	GO.0006629
6	GO Process	branching morphogenesis of an epithelial tube	PPP3R1 LAMA5 MMP14 EPHA2 CLIC4 BCL2	0.0074	GO.0048754
4	GO Process	negative regulation of coagulation	PDGFRA ANXA5 NOS3 ANXA2	0.0074	GO.0050819
4	GO Process	positive regulation of wound healing	PLEK THBS1 TLR4 ANXA1	0.0074	GO.0090303
3	GO Process	negative regulation of synapse organization	NGEF FYN ARHGEF15	0.0074	GO.1905809
5	GO Process	dendrite development	APP ARF4 FYN CAMK2A CDC42	0.0076	GO.0016358

6	GO Process	positive regulation of lipid metabolic process	PDGFRA FLT1 APP KIT ANXA1 NR1H4	0.0076	GO.0045834
5	GO Process	regulation of protein tyrosine kinase activity	APP CSF1R CAV1 FYN PTPN1	0.0076	GO.0061097
10	GO Process	immune response-regulating signaling pathway	PPP3R1 KIT LCK FYN MYO1C TLR4 PPP3CA BCL2 CDC42 NR1H4	0.0077	GO.0002764
11	GO Process	response to peptide	CAD ICAM1 APP CAV1 FYN PTPN1 DNM1 TLR4 ANXA1 TBC1D4 CAMK2A	0.0077	GO.1901652
9	GO Process	Wnt signaling pathway	PPP3R1 DDB1 DAB2 CAV1 SDC1 PPP3CA CAMK2A CDC42 RARG	0.0078	GO.0016055
8	GO Process	regulation of cysteine-type endopeptidase activity	MAP2K5 THBS1 DNAJB6 APP LCK SNCA FYN FAS	0.0078	GO.2000116
7	GO Process	response to reactive oxygen species	PDGFRA NOS3 NQO1 FYN ANXA1 SDC1 BCL2	0.0081	GO.0000302
3	GO Process	ruffle organization	PLEK CSF1R ARHGEF26	0.0081	GO.0031529
3	GO Process	endoplasmic reticulum calcium ion homeostasis	APP TGM2 BCL2	0.0081	GO.0032469
3	GO Process	positive regulation of macrophage activation	THBS1 APP TLR4	0.0081	GO.0043032
7	GO Process	synapse organization	APP SNCA FYN MYH10 CDC42 SPTBN2 ARF1	0.0081	GO.0050808
3	GO Process	negative regulation of protein localization to plasma membrane	BCL2L1 DAB2 NUMB	0.0081	GO.1903077
9	GO Process	in utero embryonic development	MYH9 PDGFRA ADD1 CAPN2 NOS3 BCL2L1 JAG2 MYH10 APBA2	0.0082	GO.0001701
6	GO Process	negative regulation of neuron apoptotic process	CCL2 PRKCG BCL2L1 SNCA FYN BCL2	0.0082	GO.0043524
6	GO Process	positive regulation of chemotaxis	HSPB1 THBS1 APP ITGA2 CALR CAMK1D	0.0082	GO.0050921
6	GO Process	response to UV	DDB1 CDC25A BRSK1 USP1 BCL2 PBK	0.0085	GO.0009411
7	GO Process	negative regulation of neuron death	CCL2 PRKCG APP BCL2L1 SNCA FYN BCL2	0.0085	GO.1901215
8	GO Process	steroid metabolic process	CYP24A1 PDGFRA APP NPC1L1 CYP2R1 NR1I2 G6PD NR1H4	0.0086	GO.0008202
4	GO Process	regulation of nitric oxide biosynthetic process	ICAM1 APP CAV1 TLR4	0.0086	GO.0045428
4	GO Process	myeloid cell development	APP KIT ANXA2 G6PD	0.0086	GO.0061515
2	GO Process	positive regulation of platelet activation	PLEK TLR4	0.0087	GO.0010572
10	GO Process	regulation of lipid metabolic process	PDGFRA RORA FLT1 APP KIT RORC SNCA CAV1 ANXA1 NR1H4	0.0087	GO.0019216
3	GO Process	focal adhesion assembly	LAMA5 ITGA2 BCL2	0.0087	GO.0048041
2	GO Process	establishment of Sertoli cell barrier	ICAM1 FLNA	0.0087	GO.0097368
2	GO Process	positive regulation of establishment of endothelial barrier	ADD1 CDH5	0.0087	GO.1903142
2	GO Process	positive regulation of oxidative stress-induced neuron death	APP TLR4	0.0087	GO.1903223
5	GO Process	positive regulation of reactive oxygen species metabolic process	THBS1 ICAM1 APP SNCA TLR4	0.0087	GO.2000379
6	GO Process	regulation of actin filament polymerization	ADD1 ICAM1 MYO1C SPTAN1 SPTBN2 ARF1	0.0088	GO.0030833
16	GO Process	negative regulation of catalytic activity	MAP2K5 GAPDH HSPB1 THBS1 DNAJB6 APP ANXA5 NOS3 PLK1 NQO1 SNCA CAV1 ANXA2 CNN3 PTPN1 ANXA1	0.0088	GO.0043086
8	GO Process	rhythmic process	PDGFRA RORA PRKCG NOS3 RORC SFPQ ANXA1 DYRK1A	0.0088	GO.0048511
7	GO Process	homeostasis of number of cells	AKT3 ADD1 KIT NOS3 ANXA1 G6PD BCL2	0.0088	GO.0048872
7	GO Process	positive regulation of T cell activation	CCL2 LCK CAV1 FYN DPP4 ANXA1 CDC42	0.0088	GO.0050870
8	GO Process	kidney development	LAMA5 PDGFRA TENC1 RARB DLL1 SDC4 SDC1 BCL2	0.009	GO.0001822
8	GO Process	positive regulation of cytosolic calcium ion concentration	PDGFRA APP CCR5 LCK SNCA CAV1 TGM2 GSTO1	0.009	GO.0007204
6	GO Process	regulation of G protein-coupled receptor signaling pathway	APLP1 PLEK APP SNCA RGS12 DNM1	0.0091	GO.0008277
8	GO Process	positive regulation of ion transport	CCL2 SNCA CAV1 GSTO1 FLNA G6PD CAMK2A ABCB1	0.0092	GO.0043270
4	GO Process	positive regulation of phospholipase activity	PDGFRA FLT1 KIT ARF4	0.0094	GO.0010518
5	GO Process	cerebellum development	RORA CKB MYH10 DLL1 SPTBN2	0.0094	GO.0021549
5	GO Process	maintenance of protein location	CAV1 FLNA SUN1 FLNB TLN2	0.0094	GO.0045185
4	GO Process	regulation of focal adhesion assembly	THBS1 MMP14 SLK SDC4	0.0094	GO.0051893
3	GO Process	positive regulation of protein processing	MYH9 ENO1 MMP14	0.0095	GO.0010954
13	GO Process	positive regulation of immune response	MMP2 PRKCH LCK CAV1 FYN SFPQ MYO1C TLR4 ANXA1 XRCC5 BCL2 CDC42 NR1H4	0.0095	GO.0050778
8	GO Process	regulation of cellular response to growth factor stimulus	THBS1 FLT1 DAB2 CAV1 MYO1C DLL1 PTPN1 MMRN2	0.0095	GO.0090287
5	GO Process	regulation of calcium ion transport into cytosol	SNCA CAV1 FYN GSTO1 BCL2	0.0096	GO.0010522
10	GO Process	cell surface receptor signaling pathway involved in cell-cell signaling	PPP3R1 DDB1 DAB2 SNCA CAV1 SDC1 PPP3CA CAMK2A CDC42 RARG	0.0101	GO.1905114
6	GO Process	cellular response to lipopolysaccharide	CCL2 ICAM1 CCR5 NOS3 TLR4 NR1H4	0.0102	GO.0071222
3	GO Process	positive regulation of blood coagulation	PLEK THBS1 TLR4	0.0104	GO.0030194
3	GO Process	detection of mechanical stimulus involved in sensory perception	KIT ITGA2 FYN	0.0104	GO.0050974
4	GO Process	negative regulation of response to cytokine stimulus	MAP2K5 PXDN CAV1 NR1H4	0.0104	GO.0060761
12	GO Process	regulation of transmembrane transport	THBS1 APP SNCA CAV1 FYN GSTO1 FLNA CLIC4 G6PD BCL2 NR1H4 ABCB1	0.0105	GO.0034762
11	GO Process	response to nutrient levels	CYP24A1 CAD ICAM1 ITGA2 NQO1 CAV1 FYN FAS G6PD BCL2 NR1H4	0.0107	GO.0031667
6	GO Process	regulation of muscle cell differentiation	KIT MMP14 DLL1 G6PD BCL2 CDC42	0.0107	GO.0051147
6	GO Process	activation of MAPK activity	MAP2K5 THBS1 APP KIT PTPN1 TLR4	0.0109	GO.0000187
2	GO Process	regulation of the force of heart contraction by chemical signal	NOS3 CAV1	0.0109	GO.0003057
2	GO Process	retinal pigment epithelium development	RARB RARG	0.0109	GO.0003406
6	GO Process	response to ionizing radiation	ICAM1 BCL2L1 CYP2R1 ANXA1 XRCC5 BCL2	0.0109	GO.0010212
6	GO Process	regulation of G2/M transition of mitotic cell cycle	TUBB4A APP PLK1 TUBA1A BRSK1 TUBB4B	0.0109	GO.0010389
4	GO Process	peptide cross-linking	THBS1 FN1 TGM2 ANXA1	0.0109	GO.0018149
2	GO Process	astrocyte cell migration	CCL2 MMP14	0.0109	GO.0043615
7	GO Process	regulation of protein kinase B signaling	PDGFRA THBS1 APP KIT LCK FYN EPHA2	0.0109	GO.0051896
2	GO Process	modulation by symbiont of host programmed cell death	GAPDH BCL2L1	0.0109	GO.0052040
2	GO Process	modulation by organism of apoptotic process in other organism involved in symbiotic interaction	GAPDH BCL2L1	0.0109	GO.0052433
3	GO Process	response to sterol	RORA CCR5 RORC	0.0111	GO.0036314
6	GO Process	maintenance of location	CALR CAV1 FLNA SUN1 FLNB TLN2	0.0112	GO.0051235
17	GO Process	apoptotic process	APLP1 GAPDH BCL2L2 APP MEK BCL2L1 DAB2 JAG2 SNCA CAV1 ANXA6 FAS EPHA2 SLK TLR4 BCL2 CAMK2A	0.0113	GO.0006915
4	GO Process	positive regulation of protein tyrosine kinase activity	APP CSF1R FYN PTPN1	0.0113	GO.0061098
29	GO Process	protein localization	MYH9 PPP3R1 PLEK HSPB1 LAMA5 ARF3 EXOC6B ITGA2 PLK1 ARF4 DAB2 CALR STXBP6 CAV1 ANXA2 MYO1C COPA FLNA TLR4 ANXA1 TBC1D4 XRCC5 PPP3CA SUN1 FLNB ARF1 NR1H4 APBA2 TLN2	0.0114	GO.0008104
7	GO Process	negative regulation of neuron differentiation	NGEF APP CALR MAP4K4 DLL1 PPP3CA VIM	0.0114	GO.0045665
7	GO Process	cellular response to nutrient levels	CYP24A1 ICAM1 CAV1 FYN FAS BCL2 NR1H4	0.0116	GO.0031669
5	GO Process	endoplasmic reticulum unfolded protein response	CCL2 ADD1 CALR PTPN1 PDIA6	0.0118	GO.0030968
4	GO Process	endothelial cell migration	MYH9 NOS3 DPP4 MMRN2	0.0118	GO.0043542
5	GO Process	reactive oxygen species metabolic process	PXDN RORA NOS3 NQO1 BCL2	0.0118	GO.0072593

5	GO Process	myeloid leukocyte migration	ARHGEF5 CCL2 FLT1 KIT ANXA1	0.0118	GO.0097529
8	GO Process	immune response-regulating cell surface receptor signaling pathway	PPP3R1 KIT LCK FYN MYO1C PPP3CA BCL2 CDC42	0.0119	GO.0002768
3	GO Process	regulation of myeloid cell apoptotic process	CCR5 ANXA1 BCL2	0.012	GO.0033032
15	GO Process	sexual reproduction	CDC25B BCL2L2 APP KIT NOS3 CCT2 PLK1 BCL2L1 CALR CDC25C JAG2 CLIC4 BCL2 SEPT7 SUN1	0.0122	GO.0019953
4	GO Process	mesenchymal cell development	LAMA5 FN1 BCL2 CFL1	0.0124	GO.0014031
7	GO Process	regulation of cysteine-type endopeptidase activity involved in apoptotic process	MAP2K5 THBS1 DNAJB6 APP LCK SNCA FAS	0.0125	GO.0043281
15	GO Process	multicellular organismal reproductive process	CDC25B BCL2L2 PDGFRA APP KIT NOS3 PLK1 BCL2L1 CALR CDC25C JAG2 ANXA1 BCL2 SEPT7 SUN1	0.0125	GO.0048609
5	GO Process	regulation of cell-matrix adhesion	THBS1 MMP14 SLK SDC4 BCL2	0.0126	GO.0001952
25	GO Process	establishment of localization in cell	MYH9 EHD4 PPP3R1 HSPB1 APP KIT CCR5 TUBA1A TUBA1C ARF4 BRSK1 CALR LCK SNCA MYO1C MYH10 COPA SPTAN1 DNM1 TBC1D4 PSIP1 PPP3CA CDC42 SUN1 SPTBN2	0.0126	GO.0051649
32	GO Process	macromolecule localization	MYH9 PPP3R1 PLEK HSPB1 LAMA5 ARF3 EXOC6B NPC1L1 ITGA2 CCT2 PLK1 ARF4 DAB2 CALR STXB6 CAV1 ANXA2 MYO1C COPA FLNA TLR4 ANXA1 TBC1D4 XRCC5 PPP3CA SUN1 FLNB ARF1 NR1H4 APBA2 TLN2 ABC1	0.0129	GO.0033036
3	GO Process	astrocyte development	APP DLL1 VIM	0.013	GO.0014002
8	GO Process	striated muscle tissue development	PDGFRA CALR RARB CAV1 MYH10 DLL1 PPP3CA FLNB	0.013	GO.0014706
3	GO Process	apoptotic cell clearance	THBS1 TGM2 PDIA6	0.013	GO.0043277
5	GO Process	response to alkaloid	PRKCG CAD ICAM1 BCL2L1 SNCA	0.013	GO.0043279
10	GO Process	regulation of lymphocyte activation	CCL2 MMP14 LCK CAV1 FYN DPP4 SDC4 ANXA1 BCL2 CDC42	0.013	GO.0051249
3	GO Process	dendritic spine organization	FYN CDC42 ARF1	0.013	GO.0097061
2	GO Process	cellular response to erythropoietin	MT2A KIT	0.0131	GO.0036018
2	GO Process	positive regulation of cell migration by vascular endothelial growth factor signaling pathway	HSPB1 MYO1C	0.0131	GO.0038089
2	GO Process	cellular response to hyperoxia	CAV1 FAS	0.0131	GO.0071455
6	GO Process	positive regulation of protein kinase B signaling	PDGFRA THBS1 APP KIT LCK FYN	0.0134	GO.0051897
6	GO Process	cellular response to xenobiotic stimulus	RORA ICAM1 NQO1 RORC NR1I2 GSTO1	0.0134	GO.0071466
4	GO Process	maintenance of protein location in cell	CAV1 SUN1 FLNB TLN2	0.0135	GO.0032507
7	GO Process	regulation of protein binding	ADD1 APP PLK1 DAB2 CAV1 ANXA2 BCL2	0.0135	GO.0043393
8	GO Process	negative regulation of catabolic process	PRKCG BCL2L1 SNCA ANXA2 FYN FLNA BCL2 PBK	0.0137	GO.0009895
13	GO Process	developmental process involved in reproduction	CDC25B BCL2L2 PDGFRA ICAM1 KIT NOS3 BCL2L1 MMP14 FLNA ANXA1 SDC1 BCL2 RARG	0.0138	GO.0003006
5	GO Process	xenobiotic metabolic process	RORA NQO1 RORC NR1I2 GSTO1	0.0138	GO.0006805
3	GO Process	regulation of lamellipodium assembly	EPHA2 FSCN1 CDC42	0.0139	GO.0010591
3	GO Process	regulation of vascular endothelial growth factor receptor signaling pathway	FLT1 PTPN1 MMRN2	0.0139	GO.0030947
3	GO Process	negative regulation of exocytosis	STXB6 SNCA ANXA1	0.0139	GO.0045920
3	GO Process	regulation of defense response to virus by virus	LCK FYN ARF1	0.0139	GO.0050690
6	GO Process	organelle localization by membrane tethering	PLEK TUBB4A EXOC6B PLK1 TUBA1A TUBB4B	0.014	GO.0140056
4	GO Process	positive regulation of phosphatidylinositol 3-kinase signaling	PDGFRA FLT1 KIT FYN	0.0141	GO.0014068
4	GO Process	negative regulation of calcium ion transport	ICAM1 NOS3 GSTO1 BCL2	0.0141	GO.0051926
8	GO Process	microtubule-based movement	MYH9 HSPB1 APP MYO1C MYH10 MYO1B CDC42 SUN1	0.0142	GO.0007018
3	GO Process	epithelial cell morphogenesis	ARHGEF26 CLIC4 FLNB	0.0149	GO.0003382
3	GO Process	phagocytosis, engulfment	MYH9 THBS1 CDC42	0.0149	GO.0006911
9	GO Process	positive regulation of cell projection organization	KIT ITGA2 FYN FN1 FSCN1 CAMK2B SEPT7 CDC42 CAMK1D	0.0149	GO.0031346
3	GO Process	lipopolysaccharide-mediated signaling pathway	CCL2 NOS3 TLR4	0.0149	GO.0031663
8	GO Process	negative regulation of nervous system development	NGEF APP CALR MAP4K4 ARHGEF15 DLL1 PPP3CA VIM	0.0149	GO.0051961
3	GO Process	extrinsic apoptotic signaling pathway in absence of ligand	BCL2L2 BCL2L1 BCL2	0.0149	GO.0097192
6	GO Process	regulation of response to cytokine stimulus	MAP2K5 PXDN CAV1 PTPN1 TLR4 NR1H4	0.0151	GO.0060759
6	GO Process	cellular response to metal ion	MT2A ADD1 NQO1 CALR SNCA CLIC4	0.0151	GO.0071248
4	GO Process	vascular endothelial growth factor receptor signaling pathway	HSPB1 FLT1 FYN CDC42	0.0153	GO.0048010
2	GO Process	blood vessel maturation	MMP2 CDH5	0.0156	GO.0001955
5	GO Process	regulation of leukocyte chemotaxis	CCL2 THBS1 APP CALR CAMK1D	0.0156	GO.0002688
7	GO Process	axon guidance	APP CSF1R DOK4 FYN MYH10 SPTAN1 SPTBN2	0.0156	GO.0007411
2	GO Process	peptidyl-lysine hydroxylation	PLOD1 PLOD2	0.0156	GO.0017185
2	GO Process	positive regulation of vesicle fusion	ANXA2 ANXA1	0.0156	GO.0031340
2	GO Process	regulation of cell-cell adhesion mediated by integrin	FERMT3 DPP4	0.0156	GO.0033632
5	GO Process	response to hydrogen peroxide	NQO1 FYN ANXA1 SDC1 BCL2	0.0156	GO.0042542
5	GO Process	negative regulation of protein secretion	MAP4K4 FN1 ANXA1 PPP3CA NR1H4	0.0156	GO.0050709
2	GO Process	T-helper 17 cell differentiation	RORA RORC	0.0156	GO.0072539
2	GO Process	establishment of integrated proviral latency	PSIP1 XRCC5	0.0156	GO.0075713
2	GO Process	regulation of membrane repolarization during action potential	CAV1 FLNA	0.0156	GO.0098903
3	GO Process	response to iron ion	SNCA G6PD BCL2	0.0158	GO.0010039
5	GO Process	odontogenesis	ITGB4 LAMA5 PDGFRA JAG2 SDC1	0.0158	GO.0042476
3	GO Process	actin filament capping	ADD1 SPTAN1 SPTBN2	0.0158	GO.0051693
3	GO Process	positive regulation of substrate adhesion-dependent cell spreading	CALR FLNA CDC42	0.0158	GO.1900026
18	GO Process	programmed cell death	APLP1 GAPDH BCL2L2 APP KIT MEK1 BCL2L1 DAB2 JAG2 SNCA CAV1 ANXA6 FAS EPHA2 SLK TLR4 BCL2 CAMK2A	0.0163	GO.0012501
4	GO Process	interferon-gamma-mediated signaling pathway	MT2A ICAM1 CAMK2B CAMK2A	0.0165	GO.0060333
4	GO Process	body fluid secretion	CAD CAV1 ANXA2 COPA	0.0172	GO.0007589
4	GO Process	regulation of interleukin-1 production	HSPB1 TLR4 ANXA1 NR1H4	0.0172	GO.0032652
4	GO Process	regulation of tyrosine phosphorylation of STAT protein	CSF1R KIT CAV1 FYN	0.0172	GO.0042509
10	GO Process	regulation of protein secretion	GAPDH CSF1R MAP4K4 FN1 MYH10 DPP4 TLR4 ANXA1 PPP3CA NR1H4	0.0172	GO.0050708
6	GO Process	regulation of organelle assembly	ARHGEF5 PLK1 SDC4 SDC1 FSCN1 SEPT7	0.0172	GO.1902115
4	GO Process	cytokinesis	MYH9 PLK1 MYH10 CFL1	0.0179	GO.0000910
4	GO Process	intrinsic apoptotic signaling pathway in response to DNA damage	BCL2L2 BCL2L1 EPHA2 BCL2	0.0179	GO.0008630
8	GO Process	response to light stimulus	APP KIT DDB1 CDC25A BRSK1 USP1 BCL2 PBK	0.0179	GO.0009416
4	GO Process	regulation of vesicle fusion	STXB6 ANXA2 ANXA1 TBC1D4	0.0179	GO.0031338
4	GO Process	organ growth	RARB DLL1 BCL2 RARG	0.0179	GO.0035265
9	GO Process	regulation of binding	ADD1 APP ITGA2 PLK1 DAB2 CAV1 ANXA2 PPP3CA BCL2	0.0179	GO.0051098
5	GO Process	positive regulation of protein localization to membrane	PRKCH FYN EPHA2 MYO1C BCL2	0.0179	GO.1905477
2	GO Process	integrin activation	FERMT3 FN1	0.0181	GO.0033622

2	GO Process	retina vasculature morphogenesis in camera-type eye	ARHGEF15 CLIC4	0.0181	GO.0061299
3	GO Process	neural crest cell migration	LAMA5 FN1 CFL1	0.0193	GO.0001755
3	GO Process	fat-soluble vitamin metabolic process	CYP24A1 RBP1 CYP2R1	0.0193	GO.0006775
3	GO Process	Wnt signaling pathway, calcium modulating pathway	PPP3R1 PPP3CA CAMK2A	0.0193	GO.0007223
3	GO Process	regulation of cellular amine metabolic process	NQO1 SNCA NR1H4	0.0193	GO.0033238
9	GO Process	regulation of innate immune response	MMP2 APP CAV1 FYN SFPQ PTPN1 TLR4 XRCC5 NR1H4	0.0193	GO.0045088
3	GO Process	cellular response to catecholamine stimulus	APLP1 APP SNCA	0.0193	GO.0071870
3	GO Process	regulation of actin cytoskeleton reorganization	PDGFRA CSF1R CDC42	0.0193	GO.2000249
5	GO Process	positive regulation of inflammatory response	APP ITGA2 SNCA TGM2 TLR4	0.0195	GO.0050729
6	GO Process	regulation of cytokine secretion	GAPDH CSF1R FN1 TLR4 ANXA1 NR1H4	0.0198	GO.0050707
7	GO Process	response to alcohol	CAD ICAM1 CCR5 BCL2L1 NQO1 FYN G6PD	0.0198	GO.0097305
4	GO Process	regulation of chemokine production	MAP2K5 CSF1R TLR4 NR1H4	0.0201	GO.0032642
10	GO Process	regulation of ion transmembrane transport	THBS1 APP SNCA CAV1 FYN GSTO1 FLNA CLIC4 G6PD ABC81	0.0201	GO.0034765
5	GO Process	striated muscle cell development	PDGFRA FLNC MYH10 SDC1 PPP3CA	0.0201	GO.0055002
5	GO Process	anatomical structure maturation	MMP2 CDC25B APP CDH5 G6PD	0.0201	GO.0071695
9	GO Process	positive regulation of protein transport	ARHGEF5 GAPDH APP CSF1R FYN MYO1C MYH10 TLR4 NR1H4	0.0204	GO.0051222
3	GO Process	regulation of dendritic spine morphogenesis	NGEF CAMK2B CFL1	0.0204	GO.0061001
5	GO Process	regulation of endothelial cell proliferation	CCL2 THBS1 AKT3 FLT1 CAV1	0.0206	GO.0001936
5	GO Process	regulation of cellular ketone metabolic process	NQO1 SNCA CAV1 ANXA1 NR1H4	0.0206	GO.0010565
9	GO Process	forebrain development	APP CSF1R RARB FYN MYH10 FLNA SUN1 TOP2B NUMB	0.0206	GO.0030900
5	GO Process	G1/S transition of mitotic cell cycle	CDC25A PPP3CA CAMK2A WEE1 MCM3	0.021	GO.0000082
2	GO Process	membrane raft assembly	CAV1 ANXA2	0.021	GO.0001765
2	GO Process	endothelial cell morphogenesis	ARHGEF26 CLIC4	0.021	GO.0001886
2	GO Process	cytoskeletal anchoring at plasma membrane	FLNB TLN2	0.021	GO.0007016
2	GO Process	regulation of low-density lipoprotein particle clearance	ANXA2 NR1H4	0.021	GO.0010988
2	GO Process	lateral ventricle development	MYH10 NUMB	0.021	GO.0021670
7	GO Process	negative regulation of cell migration	MAP2K5 CCL2 THBS1 CALR MMP2 CLIC4 BCL2	0.021	GO.0030336
5	GO Process	mammary gland development	CAD CSF1R ITGA2 CAV1 EPHA2	0.021	GO.0030879
2	GO Process	negative regulation of vascular endothelial growth factor receptor signaling pathway	PTPN1 MMP2	0.021	GO.0030948
14	GO Process	regulation of cellular catabolic process	GAPDH HSPB1 PRKCG APP PLK1 BCL2L1 DAB2 SNCA CAV1 ANXA2 PTPN1 BCL2 PBK VIM	0.021	GO.0031329
2	GO Process	calcineurin-NFAT signaling cascade	PPP3R1 PPP3CA	0.021	GO.0033173
2	GO Process	xenobiotic transport	NR1I2 ABC81	0.021	GO.0042908
18	GO Process	negative regulation of protein metabolic process	MAP2K5 GAPDH HSPB1 THBS1 DNAJB6 PRKCG APP PLK1 CALR SNCA CAV1 ANXA2 FYN FLNA PTPN1 TLR4 G6PD PBK	0.021	GO.0051248
2	GO Process	establishment of endothelial intestinal barrier	ICAM1 TJP1	0.021	GO.0090557
2	GO Process	positive regulation of receptor binding	APP ANXA2	0.021	GO.1900122
2	GO Process	regulation of receptor catabolic process	ANXA2 PTPN1	0.021	GO.2000644
3	GO Process	morphogenesis of a polarized epithelium	LAMA5 BRSK1 CDC42	0.0213	GO.0001738
3	GO Process	positive regulation of response to endoplasmic reticulum stress	APP CAV1 PTPN1	0.0213	GO.1905898
8	GO Process	regulation of T cell activation	CCL2 LCK CAV1 FYN DPP4 SDC4 ANXA1 CDC42	0.0214	GO.0050863
5	GO Process	regulation of embryonic development	MAP2K5 LAMA4 LAMA5 DLL1 SEPT7	0.0221	GO.0045995
7	GO Process	response to endoplasmic reticulum stress	CCL2 THBS1 ADD1 CALR PTPN1 BCL2 PDIA6	0.0222	GO.0034976
4	GO Process	regulation of dendrite morphogenesis	NGEF PPP3CA CAMK2B CFL1	0.0222	GO.0048814
10	GO Process	regulation of neuron projection development	NGEF BRSK1 MAP4K4 FYN FN1 PPP3CA CAMK2B CFL1 VIM CAMK1D	0.0223	GO.0010975
9	GO Process	skin development	ITGB4 LAMA5 ITGA2 EPHA2 DLL1 CLIC4 ANXA1 BCL2 FLNB	0.0225	GO.0043588
8	GO Process	response to antibiotic	ICAM1 BCL2L1 NQO1 FYN ANXA1 SDC1 G6PD BCL2	0.0225	GO.0046677
3	GO Process	glial cell migration	CCL2 MMP14 SUN1	0.0226	GO.0008347
3	GO Process	osteoclast differentiation	CSF1R ANXA2 EPHA2	0.0226	GO.0030316
7	GO Process	positive regulation of protein complex assembly	ARHGEF5 PLEK ICAM1 DDB1 MYO1C TLR4 FSCN1	0.0226	GO.0031334
3	GO Process	substrate adhesion-dependent cell spreading	LAMA5 FERMT3 FN1	0.0226	GO.0034446
5	GO Process	digestive tract development	ITGB4 PDGFRA KIT RARB BCL2	0.0226	GO.0048565
5	GO Process	regulation of smooth muscle cell proliferation	MMP2 THBS1 ITGA2 TGM2 XRCC5	0.0226	GO.0048660
3	GO Process	positive regulation of sprouting angiogenesis	AKT3 DLL1 ANXA1	0.0226	GO.1903672
7	GO Process	calcium ion transport	CCR5 LCK CAV1 ANXA6 FYN PPP3CA CAMK2A	0.0228	GO.0006816
4	GO Process	odontogenesis of dentin-containing tooth	ITGB4 LAMA5 PDGFRA JAG2	0.0228	GO.0042475
4	GO Process	cellular response to mechanical stimulus	CNN2 ITGA2 FAS TLR4	0.0228	GO.0071260
7	GO Process	negative regulation of mitotic cell cycle	CCL2 PLK1 BCL2L1 BRSK1 CDC25C BCL2 TOP2B	0.0232	GO.0045930
2	GO Process	lymphoid progenitor cell differentiation	KIT BCL2	0.0235	GO.0002320
2	GO Process	detection of mechanical stimulus involved in sensory perception of pain	ITGA2 FYN	0.0235	GO.0050966
4	GO Process	cardiac muscle cell differentiation	PDGFRA CALR RARB MYH10	0.0235	GO.0055007
2	GO Process	hepatocyte differentiation	ITGA2 ANXA1	0.0235	GO.0070365
2	GO Process	positive regulation of podosome assembly	ARHGEF5 FSCN1	0.0235	GO.0071803
2	GO Process	regulation of synapse maturation	ARHGEF15 CAMK2B	0.0235	GO.0090128
6	GO Process	response to ketone	THBS1 CAD ICAM1 BCL2L1 CALR CAV1	0.0235	GO.1901654
3	GO Process	response to ischemia	CAV1 BCL2 CAMK2A	0.0236	GO.0002931
7	GO Process	negative regulation of cytokine production	MAP2K5 THBS1 FN1 DLL1 TLR4 ANXA1 NR1H4	0.024	GO.0001818
9	GO Process	regulation of cellular amide metabolic process	GAPDH HSPB1 THBS1 APP ITGA2 CALR SNCA VIM NR1H4	0.0242	GO.0034248
5	GO Process	positive regulation of small molecule metabolic process	ENO1 NOS3 SNCA ANXA1 NR1H4	0.0242	GO.0062013
4	GO Process	positive regulation of smooth muscle cell proliferation	MMP2 THBS1 ITGA2 TGM2	0.0243	GO.0048661
17	GO Process	organophosphate metabolic process	GAPDH PLEK ENO1 ARF3 PDGFRA RORA CAD CSF1R KIT LCK SNCA FYN EPHA2 G6PD LDHB PAICS ARF1	0.0245	GO.0019637
16	GO Process	immune effector process	RORA CNN2 ICAM1 APP KIT CCT2 RORC TUBB4B ANXA2 FYN MYO1C DLL1 SPTAN1 XRCC5 BCL2 CDC42	0.0246	GO.0002252
5	GO Process	mesenchymal cell differentiation	PPP3R1 LAMA5 FN1 BCL2 CFL1	0.0248	GO.0048762
3	GO Process	positive regulation of phospholipase C activity	PDGFRA FLT1 KIT	0.0249	GO.0010863
17	GO Process	negative regulation of cellular protein metabolic process	MAP2K5 GAPDH HSPB1 THBS1 DNAJB6 PRKCG APP PLK1 CALR SNCA CAV1 ANXA2 FYN PTPN1 TLR4 G6PD PBK	0.0251	GO.0032269
4	GO Process	regulation of muscle adaptation	NOS3 G6PD PPP3CA CAMK2B	0.0252	GO.0043502
4	GO Process	regulation of receptor-mediated endocytosis	APP DAB2 ANXA2 ARF1	0.0252	GO.0048259
6	GO Process	mesenchyme development	PPP3R1 LAMA5 NOS3 FN1 BCL2 CFL1	0.0254	GO.0060485
5	GO Process	stem cell differentiation	LAMA5 KIT FN1 XRCC5 CFL1	0.0255	GO.0048863
5	GO Process	regulation of dendrite development	NGEF PPP3CA CAMK2B CFL1 CAMK1D	0.0255	GO.0050773
6	GO Process	respiratory system development	PPP3R1 LAMA5 PDGFRA NOS3 MMP14 RARG	0.0259	GO.0060541
3	GO Process	monocyte chemotaxis	CCL2 FLT1 ANXA1	0.0262	GO.0002548
2	GO Process	regulation of plasminogen activation	ENO1 THBS1	0.0262	GO.0010755
5	GO Process	calcium-mediated signaling	PPP3R1 APP CCR5 GSTO1 PPP3CA	0.0262	GO.0019722
7	GO Process	regulation of protein stability	GAPDH CCT2 PLK1 CALR SNCA FLNA BCL2	0.0262	GO.0031647

2	GO Process	negative regulation of monooxygenase activity	SNCA CAV1	0.0262	GO.0032769
3	GO Process	response to testosterone	THBS1 CAD CALR	0.0262	GO.0033574
3	GO Process	regulation of cell adhesion mediated by integrin	FERMT3 EPAH2 DPP4	0.0262	GO.0033628
2	GO Process	angiotensin-activated signaling pathway	CAV1 CAMK2A	0.0262	GO.0038166
3	GO Process	macrophage activation	APP SNCA TLR4	0.0262	GO.0042116
2	GO Process	regulation of interleukin-8 biosynthetic process	MAP2K5 TLR4	0.0262	GO.0045414
8	GO Process	modulation of chemical synaptic transmission	APP KIT BRSK1 SNCA PPP3CA CAMK2B CAMK2A ARF1	0.0262	GO.0050804
3	GO Process	mammary gland morphogenesis	CSF1R CAV1 EPAH2	0.0262	GO.0060443
2	GO Process	regulation of dendritic spine maintenance	APP FYN	0.0262	GO.1902950
2	GO Process	regulation of bile acid metabolic process	KIT NR1H4	0.0262	GO.1904251
3	GO Process	positive regulation of nitric oxide biosynthetic process	ICAM1 APP TLR4	0.0274	GO.0045429
3	GO Process	positive regulation of nitric oxide metabolic process	ICAM1 APP TLR4	0.0274	GO.1904407
12	GO Process	regulation of cytokine production	MAP2K5 GAPDH HSPB1 THBS1 RORA CSF1R FN1 DLL1 TLR4 ANXA1 XRCC5 NR1H4	0.0275	GO.0001817
4	GO Process	regulation of cytokinesis	CDC25B PLK1 BCL2L1 CDC42	0.0275	GO.0032465
4	GO Process	positive regulation of muscle cell differentiation	KIT MMP14 BCL2 CDC42	0.0285	GO.0051149
5	GO Process	positive regulation of cell morphogenesis involved in differentiation	CALR FN1 FLNA CAMK2B CDC42	0.0286	GO.0010770
9	GO Process	activation of immune response	LCK FYN SFPQ MYO1C TLR4 XRCC5 BCL2 CDC42 NR1H4	0.0288	GO.0002253
9	GO Process	regulation of endopeptidase activity	MAP2K5 GAPDH THBS1 DNAJB6 APP LCK SNCA FYN FAS	0.0288	GO.0052548
25	GO Process	positive regulation of macromolecule biosynthetic process	MAP2K5 CCL2 PPP3R1 HSPB1 THBS1 RORA APP ITGA2 CCT2 ARF4 DAB2 RORC RARB NR112 SFPQ RXRG DLL1 TLR4 RXRB PSIP1 XRCC5 PPP3CA RARG VIM NR1H4	0.0289	GO.0010557
6	GO Process	positive regulation of transmembrane transport	SNCA GSTO1 FLNA G6PD NR1H4 ABCB1	0.0289	GO.0034764
12	GO Process	cell activation involved in immune response	RORA CNN2 ICAM1 APP KIT CCT2 RORC TUBB4B ANXA2 DLL1 SPTAN1 XRCC5	0.029	GO.0002263
2	GO Process	chronic inflammatory response	THBS1 PTGES	0.0292	GO.0002544
2	GO Process	growth plate cartilage development	RARB RARG	0.0292	GO.0003417
5	GO Process	learning	APP KIT ARF4 BRSK1 FYN	0.0292	GO.0007612
2	GO Process	regulation of skeletal muscle adaptation	PPP3CA CAMK2B	0.0292	GO.0014733
2	GO Process	removal of superoxide radicals	NOS3 NQO1	0.0292	GO.0019430
2	GO Process	positive regulation of actin filament depolymerization	PLEK CFL1	0.0292	GO.0030836
5	GO Process	regulation of epithelial cell differentiation	ADD1 PRKCH CAV1 CDH5 DLL1	0.0292	GO.0030856
2	GO Process	positive regulation of pseudopodium assembly	KIT CDC42	0.0292	GO.0031274
21	GO Process	intracellular transport	EHD4 PPP3R1 HSPB1 APP KIT TUBA1A TUBA1C ARF4 CALR SNCA MYO1C MYH10 COPA1 SPTAN1 DNM1 TBC1D4 PSIP1 PPP3CA CDC42 SUN1 SPTBN2	0.0292	GO.0046907
2	GO Process	lens fiber cell development	EPAH2 VIM	0.0292	GO.0070307
2	GO Process	positive regulation of phospholipid biosynthetic process	APP NR1H4	0.0292	GO.0071073
4	GO Process	cellular oxidant detoxification	PXDN NOS3 NQO1 GSTO1	0.0292	GO.0098869
5	GO Process	response to glucocorticoid	CAD ICAM1 ANXA1 SDC1 BCL2	0.0296	GO.0051384
7	GO Process	positive regulation of innate immune response	MMP2 CAV1 FYN SFPQ TLR4 XRCC5 NR1H4	0.0297	GO.0045089
4	GO Process	non-canonical Wnt signaling pathway	PPP3R1 PPP3CA CAMK2A CDC42	0.03	GO.0035567
5	GO Process	positive regulation of cysteine-type endopeptidase activity	APP LCK SNCA FYN FAS	0.0304	GO.2001056
10	GO Process	regulation of GTPase activity	ARHGEF5 CCL2 NGEF ARHGAP31 ICAM1 RGS12 EPAH2 ARHGEF15 ARHGAP30 TBC1D4	0.0314	GO.0043087
9	GO Process	glycerolipid metabolic process	PLEK ARF3 PDGFRA CSF1R KIT LCK CAV1 FYN ARF1	0.0316	GO.0046486
9	GO Process	phospholipid metabolic process	PLEK ARF3 PDGFRA CSF1R KIT LCK SNCA FYN ARF1	0.032	GO.0006644
5	GO Process	morphogenesis of embryonic epithelium	LAMA5 JAG2 SDC4 RARG CFL1	0.032	GO.0016331
2	GO Process	positive regulation of receptor recycling	SNCA ANXA2	0.0323	GO.0001921
12	GO Process	gamete generation	CDC25B BCL2L2 KIT NOS3 PLK1 BCL2L1 CALR CDC25C JAG2 BCL2 SEPT7 SUN1	0.0323	GO.0007276
9	GO Process	epidermis development	PLOD1 LAMA5 JAG2 EPAH2 DLL1 CLIC4 ANXA1 BCL2 FLNB	0.0323	GO.0008544
2	GO Process	vitamin D metabolic process	CYP24A1 CYP2R1	0.0323	GO.0042359
2	GO Process	protein kinase C signaling	PLEK PRKCH	0.0323	GO.0070528
2	GO Process	positive regulation of exosomal secretion	SDC4 SDC1	0.0323	GO.1903543
2	GO Process	negative regulation of cardiac muscle cell differentiation	DLL1 G6PD	0.0323	GO.2000726
5	GO Process	positive regulation of ion transmembrane transport	SNCA GSTO1 FLNA G6PD ABCB1	0.0325	GO.0034767
5	GO Process	positive regulation of NF-kappaB transcription factor activity	ICAM1 APP PRKCH TLR4 CAMK2A	0.0325	GO.0051092
11	GO Process	response to bacterium	CCL2 ICAM1 APP CCR5 NOS3 SNCA CAV1 PTGES FAS TLR4 NR1H4	0.0328	GO.0009617
3	GO Process	sprouting angiogenesis	THBS1 DLL1 MMRN2	0.0329	GO.0002040
32	GO Process	negative regulation of cellular metabolic process	MAP2K5 GAPDH PLEK ENO1 HSPB1 THBS1 DNAJB6 PRKCG APP PLK1 BCL2L1 DAB2 CALR RORC RARB NR112 SNCA CAV1 ANXA2 FYN SFPQ FLNA PTPN1 TLR4 XRCC5 G6PD PPP3CA BCL2 DYRK1A RARG PBK NR1H4	0.0329	GO.0031324
4	GO Process	positive regulation of protein binding	ADD1 APP CAV1 ANXA2	0.0329	GO.0032092
3	GO Process	regulation of synaptic vesicle cycle	BRSK1 SNCA DNM1	0.0329	GO.0098693
3	GO Process	regulation of endothelial cell apoptotic process	CCL2 THBS1 ICAM1	0.0329	GO.2000351
9	GO Process	positive regulation of GTPase activity	ARHGEF5 CCL2 ARHGAP31 ICAM1 RGS12 EPAH2 ARHGEF15 ARHGAP30 TBC1D4	0.0333	GO.0043547
6	GO Process	regulation of symbiosis, encompassing mutualism through parasitism	GAPDH DDB1 CAV1 ANXA2 BCL2 CFL1	0.0337	GO.0043903
4	GO Process	columnar/cuboidal epithelial cell differentiation	JAG2 RARB DLL1 RARG	0.0338	GO.0002065
4	GO Process	positive regulation of leukocyte chemotaxis	THBS1 APP CALR CAMK1D	0.0338	GO.0002690
4	GO Process	regulation of Notch signaling pathway	KIT MMP14 JAG2 DLL1	0.0338	GO.0008593
4	GO Process	glial cell development	PPP3R1 APP DLL1 VIM	0.0338	GO.0021782
4	GO Process	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	MAP2K5 THBS1 DNAJB6 SNCA	0.0338	GO.0043154
5	GO Process	eye morphogenesis	COL8A1 RARB EPAH2 DLL1 RARG	0.0346	GO.0048592
2	GO Process	regulation of extracellular matrix disassembly	DPP4 FSCN1	0.0353	GO.0010715
2	GO Process	regulation of inositol phosphate biosynthetic process	PLEK SNCA	0.0353	GO.0010919
2	GO Process	negative regulation of myeloid cell apoptotic process	CCR5 BCL2	0.0353	GO.0033033
2	GO Process	negative regulation of dendrite morphogenesis	NGEF PPP3CA	0.0353	GO.0050774
2	GO Process	negative regulation of focal adhesion assembly	THBS1 MMP14	0.0353	GO.0051895
2	GO Process	positive regulation of macrophage migration	THBS1 MMP14	0.0353	GO.1905523
3	GO Process	negative regulation of blood coagulation	PDGFRA NOS3 ANXA2	0.0356	GO.0030195
3	GO Process	peptidyl-tyrosine autophosphorylation	LCK FYN DYRK1A	0.0356	GO.0038083
3	GO Process	positive regulation of Notch signaling pathway	KIT JAG2 DLL1	0.0356	GO.0045747
3	GO Process	face development	MMP2 PDGFRA RARG	0.0356	GO.0060324

4	GO Process	extrinsic apoptotic signaling pathway	BCL2L2 BCL2L1 FAS BCL2	0.0356	GO.0097191
4	GO Process	positive regulation of plasma membrane bounded cell projection assembly	KIT FSCN1 SEPT7 CDC42	0.0356	GO.0120034
5	GO Process	response to interleukin-1	CCL2 RORA ICAM1 SNCA ANXA1	0.0358	GO.0070555
6	GO Process	regulation of stress-activated MAPK cascade	ARHGEF5 APP MAP4K4 FAS PTPN1 PBK	0.0366	GO.0032872
7	GO Process	positive regulation of cell cycle process	CDC25B APP CDC25A CDC25C SFPQ ANXA1 CDC42	0.0366	GO.0090068
3	GO Process	endochondral bone morphogenesis	MMP14 RAR B RARG	0.0372	GO.0060350
6	GO Process	receptor-mediated endocytosis	DAB2 CALR SNCA CAV1 DLL1 DNM1	0.0373	GO.0006898
4	GO Process	ciliary basal body-plasma membrane docking	TUBB4A PLK1 TUBA1A TUBB4B	0.0377	GO.0097711
2	GO Process	regulation of cellular amino acid metabolic process	NQO1 NR1H4	0.0386	GO.0006521
2	GO Process	regulation of developmental pigmentation	KIT BCL2	0.0386	GO.0048070
2	GO Process	positive regulation of nitric-oxide synthase biosynthetic process	CCL2 TLR4	0.0386	GO.0051770
2	GO Process	cardiac myofibril assembly	PDGFRA MYH10	0.0386	GO.0055003
2	GO Process	branching involved in salivary gland morphogenesis	LAMA5 TGM2	0.0386	GO.0060445
2	GO Process	epithelial cell fate commitment	JAG2 DLL1	0.0386	GO.0072148
2	GO Process	regulation of vascular endothelial growth factor signaling pathway	MYO1C DLL1	0.0386	GO.1900746
3	GO Process	mitotic cytokinesis	PLK1 MYH10 CFL1	0.0387	GO.0000281
4	GO Process	regulation of cytokine biosynthetic process	MAP2K5 HSPB1 THBS1 TLR4	0.0387	GO.0042035
3	GO Process	positive regulation of receptor-mediated endocytosis	APP DAB2 ANXA2	0.0387	GO.0048260
4	GO Process	regulation of striated muscle cell differentiation	MMP14 DLL1 G6PD BCL2	0.0387	GO.0051153
8	GO Process	activation of protein kinase activity	MAP2K5 THBS1 APP KIT MAP4K4 SLK PTPN1 TLR4	0.0389	GO.0032147
9	GO Process	organic hydroxy compound metabolic process	CYP24A1 APP NPC1L1 CYP2R1 SNCA G6PD LDHB BCL2 NR1H4	0.0389	GO.1901615
8	GO Process	negative regulation of proteolysis	MAP2K5 GAPDH THBS1 DNAJB6 PRKCG APP SNCA PBK	0.04	GO.0045861
6	GO Process	protein folding	GNB4 HSPB1 DNAJB6 CCT2 CALR PDIA6	0.0406	GO.0006457
5	GO Process	mitotic cell cycle checkpoint	PLK1 BCL2L1 BRSK1 CDC25C TOP2B	0.0409	GO.0007093
4	GO Process	regulation of circadian rhythm	RORA PRKCG RORC SFPQ	0.0409	GO.0042752
5	GO Process	cellular response to radiation	DDDB1 BCL2L1 CDC25A XRCC5 PBK	0.0409	GO.0071478
25	GO Process	system process	PRKCG ICAM1 APP KIT NPC1L1 ITGA2 NOS3 ARF4 BRSK1 JAG2 SNCA CAV1 TPM4 FYN M YH10 DLL1 COPA TPM3 DNM1 TLR4 TPM2 PPP3CA LTB4R BCL2 VIM	0.0412	GO.0003008
6	GO Process	ossification	CYP24A1 MMP2 MMP14 EPHA2 BCL2 SUN1	0.0413	GO.0001503
2	GO Process	arginine metabolic process	CAD NOS3	0.0419	GO.0006525
2	GO Process	intrinsic apoptotic signaling pathway in response to oxidative stress	MELK BCL2	0.0419	GO.0008631
2	GO Process	regulation of hydrogen peroxide metabolic process	SNCA FYN	0.0419	GO.0010310
3	GO Process	myotube differentiation	MYH9 CAPN2 PPP3CA	0.0419	GO.0014902
2	GO Process	melanocyte differentiation	KIT BCL2	0.0419	GO.0030318
2	GO Process	cell adhesion mediated by integrin	ICAM1 ITGA2	0.0419	GO.0033627
2	GO Process	toll-like receptor 4 signaling pathway	TLR4 NR1H4	0.0419	GO.0034142
2	GO Process	establishment of apical/basal cell polarity	FSCN1 CDC42	0.0419	GO.0035089
3	GO Process	IRE1-mediated unfolded protein response	ADD1 PTPN1 PDIA6	0.0419	GO.0036498
4	GO Process	cellular transition metal ion homeostasis	MT2A APP LCK ARF1	0.0419	GO.0046916
2	GO Process	regulation of transcription involved in cell fate commitment	RORA RORC	0.0419	GO.0060850
7	GO Process	multicellular organismal homeostasis	AKT3 ADD1 NOS3 TENC1 DLL1 TLR4 BCL2	0.042	GO.0048871
5	GO Process	tissue homeostasis	AKT3 ADD1 NOS3 TLR4 BCL2	0.0422	GO.0001894
4	GO Process	peptidyl-tyrosine dephosphorylation	CDC25B CDC25A CDC25C PTPN1	0.043	GO.0035335
15	GO Process	oxidation-reduction process	PLOD1 CYP24A1 GAPDH ENO1 PXDN PLOD2 NOS3 NQO1 CYP2R1 SNCA GSTO1 PIR G6PD LDHB PDIA6	0.0449	GO.0055114
7	GO Process	positive regulation of cellular protein localization	CCT2 PLK1 PRKCH FYN EPHA2 MYO1C BCL2	0.0449	GO.1903829
5	GO Process	intrinsic apoptotic signaling pathway	BCL2L2 MELK BCL2L1 EPHA2 BCL2	0.0452	GO.0097193
3	GO Process	negative regulation of cytokine-mediated signaling pathway	PXDN CAV1 NR1H4	0.0454	GO.0001960
4	GO Process	myeloid cell homeostasis	ADD1 KIT ANXA1 G6PD	0.0454	GO.0002262
2	GO Process	nuclear migration	MYH10 SUN1	0.0454	GO.0007097
2	GO Process	negative regulation of calcium ion transport into cytosol	GSTO1 BCL2	0.0454	GO.0010523
2	GO Process	negative regulation of platelet activation	PDGFRA NOS3	0.0454	GO.0010544
2	GO Process	positive regulation of lamellipodium assembly	FSCN1 CDC42	0.0454	GO.0010592
2	GO Process	response to magnesium ion	THBS1 SNCA	0.0454	GO.0032026
2	GO Process	negative regulation of chemokine production	MAP2K5 NR1H4	0.0454	GO.0032682
3	GO Process	collagen metabolic process	MMP2 MMP14 TENC1	0.0454	GO.0032963
2	GO Process	cellular response to sterol	RORA RORC	0.0454	GO.0036315
21	GO Process	establishment of protein localization	MYH9 PPP3R1 PLEK HSPB1 ARF3 EXOGB8 ITGA2 PLK1 ARF4 DAB2 CALR MYO1C COPA FL NA TLR4 ANXA1 TBC1D4 PPP3CA ARF1 NR1H4 APBA2	0.0454	GO.0045184
2	GO Process	nucleobase biosynthetic process	CAD PAICS	0.0454	GO.0046112
3	GO Process	positive regulation of fibroblast proliferation	PDGFRA ANXA2 FN1	0.0454	GO.0048146
3	GO Process	dendrite morphogenesis	FYN CAMK2A CDC42	0.0454	GO.0048813
2	GO Process	regulation of synaptic vesicle recycling	SNCA DNM1	0.0454	GO.1903421
2	GO Process	positive regulation of endothelial cell apoptotic process	CCL2 THBS1	0.0454	GO.2000353
5	GO Process	regulation of cell size	PLEK AKT3 ADD1 FN1 RARG	0.0455	GO.0008361
5	GO Process	positive regulation of cell growth	MAP2K5 MMP14 FN1 BCL2 CDC42	0.0455	GO.0030307
10	GO Process	protein complex oligomerization	EHD4 VWF APP CAV1 ANXA2 ANXA6 RXRG TGM2 DNM1 SEPT7	0.0455	GO.0051259
7	GO Process	cellular response to peptide	APP CAV1 FYN PTPN1 TLR4 TBC1D4 CAMK2A	0.0455	GO.1901653
4	GO Process	phosphatidylinositol phosphorylation	PDGFRA KIT LCK FYN	0.046	GO.0046854
5	GO Process	negative regulation of mitotic cell cycle phase transition	CCL2 PLK1 BRSK1 CDC25C BCL2	0.0463	GO.1901991
8	GO Process	response to peptide hormone	CAD ICAM1 CAV1 FYN PTPN1 ANXA1 TBC1D4 CAMK2A	0.0464	GO.0043434
7	GO Process	muscle system process	NOS3 TPM4 TPM3 TPM2 PPP3CA LTB4R VIM	0.0467	GO.0003012
3	GO Process	response to gamma radiation	BCL2L1 XRCC5 BCL2	0.0467	GO.0010332
3	GO Process	positive regulation of calcium ion transport into cytosol	SNCA CAV1 GSTO1	0.0467	GO.0010524
3	GO Process	monosaccharide biosynthetic process	GAPDH ENO1 G6PD	0.0467	GO.0046364
4	GO Process	lymphocyte activation involved in immune response	RORA ICAM1 RORC DLL1	0.0471	GO.0002285
4	GO Process	digestion	NPC1L1 COPA TLR4 PIR	0.0471	GO.0007586
9	GO Process	negative regulation of hydrolase activity	MAP2K5 GAPDH THBS1 DNAJB6 APP NOS3 SNCA CNN3 ANXA1	0.0471	GO.0051346
5	GO Process	meiotic cell cycle process	MYH9 CDC25B PLK1 SUN1 TOP2B	0.0471	GO.1903046
8	GO Process	positive regulation of secretion by cell	GAPDH CSF1R SNCA MYH10 SDC4 TLR4 SDC1 NR1H4	0.0474	GO.1903532

5	GO Process	lung development	PPP3R1 LAMA5 PDGFRA NOS3 MMP14	0.0481	GO.0030324
2	GO Process	activation of MAPKKK activity	APP MAP4K4	0.0482	GO.0000185
2	GO Process	dendritic cell chemotaxis	ARHGEF5 CCR5	0.0482	GO.0002407
2	GO Process	myoblast fusion	MYH9 CAPN2	0.0482	GO.0007520
3	GO Process	receptor internalization	SNCA CAV1 DNM1	0.0482	GO.0031623
2	GO Process	negative regulation of chondrocyte differentiation	RARB RARG	0.0482	GO.0032331
2	GO Process	negative regulation of interleukin-8 production	MAP2K5 ANXA1	0.0482	GO.0032717
3	GO Process	regulation of monooxygenase activity	NOS3 SNCA CAV1	0.0482	GO.0032768
4	GO Process	positive regulation of peptidyl-serine phosphorylation	APP SNCA CAV1 BCL2	0.0482	GO.0033138
2	GO Process	positive regulation of circadian rhythm	RORA RORC	0.0482	GO.0042753
2	GO Process	ventricular cardiac muscle cell differentiation	RARB MYH10	0.0482	GO.0055012
7	GO Process	regulation of cation transmembrane transport	APP SNCA CAV1 FYN GSTO1 FLNA G6PD	0.0482	GO.1904062
5	GO Process	negative regulation of cell projection organization	NGEF MAP4K4 FYN PPP3CA VIM	0.0486	GO.0031345
5	GO Process	sensory perception of mechanical stimulus	ICAM1 KIT ITGA2 FYN DNM1	0.0486	GO.0050954
4	GO Process	meiosis I	CDC25B PLK1 SUN1 TOP2B	0.0492	GO.0007127
24	GO Process	positive regulation of nucleobase-containing compound metabolic process	MAP2K5 PPP3R1 ENO1 RORA PRKCG APP NOS3 CCT2 ARF4 DAB2 RORC RARB NR12 SFPQ RXRG DLL1 TLR4 RXRB PSIP1 XRCC5 PPP3CA DYRK1A RARG NR1H4	0.0492	GO.0045935
5	GO Process	protein localization to nucleus	PPP3R1 PLK1 CALR PPP3CA SUN1	0.0496	GO.0034504
5	GO Process	cellular response to oxygen levels	RORA ICAM1 CAV1 FAS BCL2	0.0496	GO.0071453
21	InterPro Domains	Protein kinase, ATP binding site	MAP2K5 PDGFRA PRKCG AKT3 FLT1 CSF1R KIT MELK PLK1 BRSK1 PRKCH LCK MAP4K4 FYN EPHA2 SLK CAMK2B CAMK2A DYRK1A WEE1 CAMK1D	1.10E-08	IPR017441
22	InterPro Domains	Protein kinase domain	MAP2K5 PDGFRA PRKCG AKT3 FLT1 CSF1R KIT MELK PLK1 BRSK1 PRKCH LCK MAP4K4 FYN EPHA2 SLK CAMK2B CAMK2A DYRK1A WEE1 PBK CAMK1D	6.60E-08	IPR000719
22	InterPro Domains	Protein kinase-like domain superfamily	MAP2K5 PDGFRA PRKCG AKT3 FLT1 CSF1R KIT MELK PLK1 BRSK1 PRKCH LCK MAP4K4 FYN EPHA2 SLK CAMK2B CAMK2A DYRK1A WEE1 PBK CAMK1D	2.09E-07	IPR011009
8	InterPro Domains	Nuclear hormone receptor, ligand-binding domain	RORA RORC RARB NR1I2 RXRG RXRB RARG NR1H4	1.95E-06	IPR000536
8	InterPro Domains	Zinc finger, nuclear hormone receptor-type	RORA RORC RARB NR1I2 RXRG RXRB RARG NR1H4	1.95E-06	IPR001628
8	InterPro Domains	Nuclear hormone receptor	RORA RORC RARB NR1I2 RXRG RXRB RARG NR1H4	1.95E-06	IPR001723
18	InterPro Domains	PH-like domain superfamily	ARHGEF5 PLEK AKT3 NGEF FERMT3 APP DAB2 TENC1 RGS12 DOK4 ARHGEF26 ARHGEF15 DNM1 TBC1D4 SPTBN2 NUMB APBA2 TLN2	1.95E-06	IPR011993
8	InterPro Domains	Nuclear hormone receptor-like domain superfamily	RORA RORC RARB NR1I2 RXRG RXRB RARG NR1H4	1.95E-06	IPR035500
8	InterPro Domains	Zinc finger, NHR/GATA-type	RORA RORC RARB NR1I2 RXRG RXRB RARG NR1H4	3.43E-06	IPR013088
15	InterPro Domains	Serine/threonine-protein kinase, active site	MAP2K5 PRKCG AKT3 MELK PLK1 BRSK1 PRKCH MAP4K4 SLK CAMK2B CAMK2A DYRK1A WEE1 PBK CAMK1D	5.05E-06	IPR008271
4	InterPro Domains	Tyrosine-protein kinase, receptor class III, conserved site	PDGFRA FLT1 CSF1R KIT	1.10E-04	IPR001824
6	InterPro Domains	PTB/PI domain	DAB2 TENC1 RGS12 TBC1D4 NUMB APBA2	1.10E-04	IPR006020
7	InterPro Domains	Tyrosine-protein kinase, catalytic domain	PDGFRA FLT1 CSF1R KIT LCK FYN EPHA2	3.10E-04	IPR020635
3	InterPro Domains	M-phase inducer phosphatase	CDC25B CDC25A CDC25C	3.90E-04	IPR000751
4	InterPro Domains	Annexin	ANXA5 ANXA2 ANXA6 ANXA1	3.90E-04	IPR001464
3	InterPro Domains	Apoptosis regulator, Bcl-2 protein, BH4	BCL2L2 BCL2L1 BCL2	3.90E-04	IPR003093
4	InterPro Domains	Annexin repeat, conserved site	ANXA5 ANXA2 ANXA6 ANXA1	3.90E-04	IPR018252
4	InterPro Domains	Annexin repeat	ANXA5 ANXA2 ANXA6 ANXA1	3.90E-04	IPR018502
3	InterPro Domains	Apoptosis regulator, Bcl-2, BH4 motif, conserved site	BCL2L2 BCL2L1 BCL2	3.90E-04	IPR020731
4	InterPro Domains	Annexin superfamily	ANXA5 ANXA2 ANXA6 ANXA1	3.90E-04	IPR037104
3	InterPro Domains	Tropomyosin	TPM4 TPM3 TPM2	5.00E-04	IPR000533
7	InterPro Domains	Tyrosine-protein kinase, active site	PDGFRA FLT1 CSF1R KIT LCK FYN EPHA2	5.60E-04	IPR008266
4	InterPro Domains	Tubulin/FtsZ, C-terminal domain superfamily	TUBB4A TUBA1A TUBA1C TUBB4B	0.0012	IPR037103
4	InterPro Domains	Tubulin/FtsZ, 2-layer sandwich domain	TUBB4A TUBA1A TUBA1C TUBB4B	0.0013	IPR018316
4	InterPro Domains	Tubulin	TUBB4A TUBA1A TUBA1C TUBB4B	0.0015	IPR000217
4	InterPro Domains	Actinin-type actin-binding domain, conserved site	FLNC FLNA FLNB SPTBN2	0.0015	IPR001589
6	InterPro Domains	Calponin homology domain	CNN2 FLNC FLNA CNN3 FLNB SPTBN2	0.0015	IPR001715
4	InterPro Domains	Tubulin/FtsZ, GTPase domain	TUBB4A TUBA1A TUBA1C TUBB4B	0.0015	IPR003008
4	InterPro Domains	Tubulin/FtsZ, C-terminal	TUBB4A TUBA1A TUBA1C TUBB4B	0.0015	IPR008280
4	InterPro Domains	Tubulin, conserved site	TUBB4A TUBA1A TUBA1C TUBB4B	0.0015	IPR017975
3	InterPro Domains	Apoptosis regulator, Bcl-2, BH1 motif, conserved site	BCL2L2 BCL2L1 BCL2	0.0015	IPR020717
3	InterPro Domains	Apoptosis regulator, Bcl-2, BH2 motif, conserved site	BCL2L2 BCL2L1 BCL2	0.0015	IPR020726
4	InterPro Domains	Tubulin, C-terminal	TUBB4A TUBA1A TUBA1C TUBB4B	0.0015	IPR023123
4	InterPro Domains	Tubulin/FtsZ, GTPase domain superfamily	TUBB4A TUBA1A TUBA1C TUBB4B	0.0015	IPR036525
6	InterPro Domains	CH domain superfamily	CNN2 FLNC FLNA CNN3 FLNB SPTBN2	0.0016	IPR036872
3	InterPro Domains	Filamin/ABP280 repeat	FLNC FLNA FLNB	0.0018	IPR001298
7	InterPro Domains	Serine-threonine/tyrosine-protein kinase, catalytic domain	PDGFRA FLT1 CSF1R KIT LCK FYN EPHA2	0.0022	IPR001245
3	InterPro Domains	Bcl2 family	BCL2L2 BCL2L1 BCL2	0.0022	IPR026298
3	InterPro Domains	Bcl2-like	BCL2L2 BCL2L1 BCL2	0.0027	IPR002475
3	InterPro Domains	Filamin/ABP280 repeat-like	FLNC FLNA FLNB	0.0027	IPR017868
3	InterPro Domains	Bcl2-like superfamily	BCL2L2 BCL2L1 BCL2	0.0046	IPR036834
4	InterPro Domains	VWFC domain	PXDN THBS1 VWF JAG2	0.0052	IPR001007
4	InterPro Domains	Myosin head, motor domain	MYH9 MYO1C MYH10 MYO1B	0.0052	IPR001609
2	InterPro Domains	Apoptosis regulator, Bcl-2/ BclX	BCL2L1 BCL2	0.0052	IPR004725
9	InterPro Domains	Pleckstrin homology domain	ARHGEF5 PLEK AKT3 NGEF FERMT3 DOK4 ARHGEF26 DNM1 SPTBN2	0.0064	IPR001849
2	InterPro Domains	Procollagen-lysine 5-dioxygenase, conserved site	PLOD1 PLOD2	0.0079	IPR001006
2	InterPro Domains	Nuclear receptor ROR	RORA RORC	0.0079	IPR003079
2	InterPro Domains	Amyloidogenic glycoprotein, extracellular	APLP1 APP	0.0079	IPR008154
2	InterPro Domains	Amyloidogenic glycoprotein	APLP1 APP	0.0079	IPR008155
2	InterPro Domains	Amyloidogenic glycoprotein, copper-binding	APLP1 APP	0.0079	IPR011178
2	InterPro Domains	Amyloidogenic glycoprotein, heparin-binding	APLP1 APP	0.0079	IPR015849
2	InterPro Domains	Beta-amyloid precursor protein C-terminal	APLP1 APP	0.0079	IPR019543
2	InterPro Domains	Amyloidogenic glycoprotein, extracellular domain conserved site	APLP1 APP	0.0079	IPR019744
2	InterPro Domains	Amyloidogenic glycoprotein, intracellular domain, conserved site	APLP1 APP	0.0079	IPR019745
2	InterPro Domains	Amyloidogenic glycoprotein, E2 domain	APLP1 APP	0.0079	IPR024329
2	InterPro Domains	E2 domain superfamily	APLP1 APP	0.0079	IPR036176
2	InterPro Domains	Amyloidogenic glycoprotein, heparin-binding domain superfamily	APLP1 APP	0.0079	IPR036454

2	InterPro Domains	Amyloidogenic glycoprotein, copper-binding domain superfamily	APLP1 APP	0.0079	IPR036669
2	InterPro Domains	Retinoid X receptor/HNF4	RXRG RXRB	0.0092	IPR000003
2	InterPro Domains	Syndecan	SDC4 SDC1	0.0092	IPR001050
2	InterPro Domains	Delta/Serrate/lag-2 (DSL) protein	JAG2 DLL1	0.0092	IPR001774
2	InterPro Domains	Calponin/LIMCH1	CNN2 CNN3	0.0092	IPR001997
2	InterPro Domains	Retinoic acid receptor	RARB RARG	0.0092	IPR003078
2	InterPro Domains	Notch ligand, N-terminal domain	JAG2 DLL1	0.0092	IPR011651
2	InterPro Domains	Calcium/calmodulin-dependent protein kinase II, association-domain	CAMK2B CAMK2A	0.0092	IPR013543
2	InterPro Domains	Cavin family	SDPR PTRF	0.0092	IPR026752
2	InterPro Domains	Syndecan, conserved site	SDC4 SDC1	0.0092	IPR030479
2	InterPro Domains	Calcium/calmodulin-dependent protein kinase type II	CAMK2B CAMK2A	0.0092	IPR039071
3	InterPro Domains	Rhodanese-like domain	CDC25B CDC25A CDC25C	0.01	IPR001763
3	InterPro Domains	Rhodanese-like domain superfamily	CDC25B CDC25A CDC25C	0.01	IPR036873
2	InterPro Domains	Laminin alpha, domain I	LAMA4 LAMA5	0.0107	IPR009254
2	InterPro Domains	Laminin domain II	LAMA4 LAMA5	0.0107	IPR010307
2	InterPro Domains	Calponin repeat	CNN2 CNN3	0.0138	IPR000557
3	InterPro Domains	Protein kinase, C-terminal	PRKCG AKT3 PRKCH	0.0171	IPR017892
2	InterPro Domains	Syndecan/Neurexin domain	SDC4 SDC1	0.0171	IPR027789
7	InterPro Domains	SH3-like domain superfamily	ARHGEF5 NGEF TJP1 LCK FYN ARHGEF26 SPTAN1	0.0171	IPR036028
7	InterPro Domains	SH3 domain	ARHGEF5 NGEF TJP1 LCK FYN ARHGEF26 SPTAN1	0.0207	IPR001452
2	InterPro Domains	Alpha tubulin	TUBA1A TUBA1C	0.0207	IPR002452
3	InterPro Domains	Small GTPase superfamily, ARF/SAR type	ARF3 ARF4 ARF1	0.0207	IPR006689
2	InterPro Domains	Class I myosin tail homology domain	MYO1C MYO1B	0.0207	IPR010926
2	InterPro Domains	Apoptosis regulator, Bcl-2, BH3 motif, conserved site	BCL2L1 BCL2	0.0207	IPR020728
2	InterPro Domains	Class I myosin, motor domain	MYO1C MYO1B	0.0207	IPR036072
2	InterPro Domains	PGBD superfamily	MMP2 MMP14	0.0207	IPR036366
4	InterPro Domains	Dbl homology (DH) domain	ARHGEF5 NGEF ARHGEF26 ARHGEF15	0.0227	IPR000219
4	InterPro Domains	Dbl homology (DH) domain superfamily	ARHGEF5 NGEF ARHGEF26 ARHGEF15	0.0236	IPR035899
6	InterPro Domains	EF-Hand 1, calcium-binding site	RCN1 EHD4 PPP3R1 CAPN2 SPTAN1 PRKCSH	0.0237	IPR018247
2	InterPro Domains	Beta tubulin, autoregulation binding site	TUBB4A TUBB4B	0.0266	IPR013838
2	InterPro Domains	Flavoprotein-like superfamily	NOS3 NQO1	0.0266	IPR029039
2	InterPro Domains	Beta tubulin	TUBB4A TUBB4B	0.0306	IPR002453
2	InterPro Domains	Smooth muscle protein/calponin	CNN2 CNN3	0.0306	IPR003096
4	InterPro Domains	Kinesin motor domain superfamily	MYH9 MYO1C MYH10 MYO1B	0.0306	IPR036961
4	InterPro Domains	IQ motif, EF-hand binding site	MYH9 MYO1C MYH10 MYO1B	0.0324	IPR000048
13	InterPro Domains	Immunoglobulin-like fold	ITGB4 PXDND PDGFRA ICAM1 FLT1 CSF1R KIT FLNC FN1 EPHA2 TGM2 FLNA FLNB	0.0424	IPR013783
2	InterPro Domains	Neurexin/syndecan/glycophorin C	SDC4 SDC1	0.0439	IPR003585
2	InterPro Domains	Dynamin-type guanine nucleotide-binding (G) domain	EHD4 DNM1	0.0439	IPR030381
2	InterPro Domains	Peptidase M10A, cysteine switch, zinc binding site	MMP2 MMP14	0.0484	IPR021158
2	InterPro Domains	Dynamin superfamily	EHD4 DNM1	0.0484	IPR022812
20	KEGG Pathways	Focal adhesion	ITGB4 LAMA4 LAMA5 PDGFRA THBS1 VWF PRKCG AKT3 FLT1 CAPN2 ITGA2 ZYX FLNC CAV1 FYN FLNA BCL2 CDC42 FLNB TLN2	3.60E-13	hsa04510
24	KEGG Pathways	Pathways in cancer	MMP2 LAMA4 GNB4 LAMA5 PDGFRA PRKCG AKT3 CSF1R KIT ITGA2 BCL2L1 NQO1 JAG2 RARB FAS RXRG DLL1 TPM3 GSTO1 RXRB CAMK2B BCL2 CAMK2A CDC42	2.16E-09	hsa05200
16	KEGG Pathways	Proteoglycans in cancer	MMP2 THBS1 PRKCG AKT3 ITGA2 FLNC CAV1 FAS FLNA SDC4 TLR4 SDC1 CAMK2B CAMK2A CDC42 FLNB	2.16E-09	hsa05205
18	KEGG Pathways	MAPK signaling pathway	MAP2K5 PPP3R1 CDC25B HSPB1 PDGFRA PRKCG AKT3 FLT1 CSF1R KIT FLNC MAP4K4 FAS EPHA2 FLNA PPP3CA CDC42 FLNB	6.49E-09	hsa04010
13	KEGG Pathways	Fluid shear stress and atherosclerosis	MAP2K5 MMP2 CCL2 AKT3 ICAM1 NOS3 NQO1 CAV1 CDH5 GSTO1 SDC4 SDC1 BCL2	1.17E-08	hsa05418
17	KEGG Pathways	PI3K-Akt signaling pathway	ITGB4 LAMA4 GNB4 LAMA5 PDGFRA THBS1 VWF AKT3 FLT1 CSF1R KIT ITGA2 NOS3 BCL2L1 EPHA2 TLR4 BCL2	3.70E-07	hsa04151
12	KEGG Pathways	MicroRNAs in cancer	CYP24A1 CDC25B BCL2L2 PDGFRA THBS1 PRKCG CDC25A CDC25C FSCN1 BCL2 VIM ABCB1	3.70E-07	hsa05206
10	KEGG Pathways	HIF-1 signaling pathway	GAPDH ENO1 PRKCG AKT3 FLT1 NOS3 TLR4 CAMK2B BCL2 CAMK2A	6.15E-07	hsa04066
9	KEGG Pathways	Small cell lung cancer	LAMA4 LAMA5 AKT3 ITGA2 BCL2L1 RARB RXRG RXRB BCL2	3.93E-06	hsa05222
7	KEGG Pathways	Pathogenic Escherichia coli infection	TUBB4A TUBA1A TUBA1C TUBB4B FYN TLR4 CDC42	1.38E-05	hsa05130
8	KEGG Pathways	ECM-receptor interaction	ITGB4 LAMA4 LAMA5 THBS1 VWF ITGA2 SDC4 SDC1	1.49E-05	hsa04512
8	KEGG Pathways	Salmonella infection	MYH9 TJP1 FLNC MYH10 FLNA TLR4 CDC42 FLNB	1.76E-05	hsa05132
7	KEGG Pathways	VEGF signaling pathway	PPP3R1 HSPB1 PRKCG AKT3 NOS3 PPP3CA CDC42	2.05E-05	hsa04370
8	KEGG Pathways	Gap junction	MAP2K5 PDGFRA PRKCG TUBB4A TJP1 TUBA1A TUBA1C TUBB4B	2.05E-05	hsa04540
10	KEGG Pathways	Rap1 signaling pathway	PDGFRA THBS1 PRKCG AKT3 FLT1 CSF1R KIT EPHA2 CDC42 TLN2	1.70E-04	hsa04015
9	KEGG Pathways	Axon guidance	PPP3R1 NGEF FYN EPHA2 PPP3CA CAMK2B CAMK2A CDC42 CFL1	2.90E-04	hsa04360
8	KEGG Pathways	Apoptosis	AKT3 CAPN2 TUBA1A TUBA1C BCL2L1 FAS SPTAN1 BCL2	3.30E-04	hsa04210
7	KEGG Pathways	AGE-RAGE signaling pathway in diabetic complications	MMP2 CCL2 AKT3 ICAM1 NOS3 BCL2 CDC42	3.30E-04	hsa04933
10	KEGG Pathways	Ras signaling pathway	GNB4 PDGFRA PRKCG AKT3 FLT1 CSF1R KIT BCL2L1 EPHA2 CDC42	3.50E-04	hsa04014
7	KEGG Pathways	Th17 cell differentiation	PPP3R1 RORA RORC LCK RXRG RXRB PPP3CA	3.80E-04	hsa04659
6	KEGG Pathways	Platinum drug resistance	AKT3 BCL2L1 FAS GSTO1 BCL2 TOP2B	4.10E-04	hsa01524
8	KEGG Pathways	Phagosome	THBS1 TUBB4A ITGA2 TUBA1A TUBA1C CALR TUBB4B TLR4	4.20E-04	hsa04145
8	KEGG Pathways	Oxytocin signaling pathway	MAP2K5 PPP3R1 PRKCG NOS3 PPP3CA CAMK2B CAMK2A CAMK1D	4.80E-04	hsa04921
7	KEGG Pathways	Toxoplasmosis	LAMA4 LAMA5 AKT3 CCR5 BCL2L1 TLR4 BCL2	4.80E-04	hsa05145
7	KEGG Pathways	Cholinergic synapse	GNB4 PRKCG AKT3 FYN CAMK2B BCL2 CAMK2A	5.00E-04	hsa04725
5	KEGG Pathways	Malaria	CCL2 THBS1 ICAM1 TLR4 SDC1	5.80E-04	hsa05144
7	KEGG Pathways	Oocyte meiosis	PPP3R1 PLK1 CDC25C SLK PPP3CA CAMK2B CAMK2A	6.10E-04	hsa04114
7	KEGG Pathways	Platelet activation	VWF AKT3 FERMT3 ITGA2 NOS3 FYN TLN2	8.30E-04	hsa04611
7	KEGG Pathways	Natural killer cell mediated cytotoxicity	PPP3R1 PRKCG ICAM1 LCK FYN FAS PPP3CA	8.40E-04	hsa04650
9	KEGG Pathways	Endocytosis	EHD4 ARF3 PDGFRA CCR5 DAB2 CAV1 DNM1 CDC42 ARF1	0.0018	hsa04144
6	KEGG Pathways	T cell receptor signaling pathway	PPP3R1 AKT3 LCK FYN PPP3CA CDC42	0.0018	hsa04660
5	KEGG Pathways	Long-term potentiation	PPP3R1 PRKCG PPP3CA CAMK2B CAMK2A	0.0018	hsa04720
6	KEGG Pathways	Glucagon signaling pathway	PPP3R1 AKT3 PPP3CA CAMK2B LDHB CAMK2A	0.0018	hsa04922
5	KEGG Pathways	Amphetamine addiction	PPP3R1 PRKCG PPP3CA CAMK2B CAMK2A	0.0018	hsa05031
4	KEGG Pathways	African trypanosomiasis	LAMA4 PRKCG ICAM1 FAS	0.0018	hsa05143
9	KEGG Pathways	HTLV-1 infection	PPP3R1 PDGFRA AKT3 ICAM1 BCL2L1 CALR LCK PPP3CA TLN2	0.0019	hsa05166
5	KEGG Pathways	Non-small cell lung cancer	PRKCG AKT3 RARB RXRG RXRB	0.0019	hsa05223
5	KEGG Pathways	Glioma	PDGFRA PRKCG AKT3 CAMK2B CAMK2A	0.002	hsa05214
6	KEGG Pathways	Neurotrophin signaling pathway	MAP2K5 AKT3 CAMK2B BCL2 CAMK2A CDC42	0.003	hsa04722
5	KEGG Pathways	EGFR tyrosine kinase inhibitor resistance	PDGFRA PRKCG AKT3 BCL2L1 BCL2	0.0034	hsa01521
7	KEGG Pathways	Alzheimer's disease	GAPDH PPP3R1 APP CAPN2 SNCA FAS PPP3CA	0.0035	hsa05010
6	KEGG Pathways	Cell cycle	CDC25B PLK1 CDC25A CDC25C WEE1 MCM3	0.0038	hsa04110
6	KEGG Pathways	Osteoclast differentiation	PPP3R1 AKT3 CSF1R LCK FYN PPP3CA	0.0038	hsa04380

7	KEGG Pathways	Tuberculosis	PPP3R1 AKT3 TLR4 PPP3CA CAMK2B BCL2 CAMK2A	0.0038	hsa05152
6	KEGG Pathways	Dopaminergic synapse	GNB4 PRKCG AKT3 PPP3CA CAMK2B CAMK2A	0.0043	hsa04728
7	KEGG Pathways	Calcium signaling pathway	PPP3R1 PDGFRA PRKCG NOS3 PPP3CA CAMK2B CAMK2A	0.0044	hsa04020
5	KEGG Pathways	Th1 and Th2 cell differentiation	PPP3R1 JAG2 LCK DLL1 PPP3CA	0.0048	hsa04658
5	KEGG Pathways	GnRH signaling pathway	MMP2 MMP14 CAMK2B CAMK2A CDC42	0.0048	hsa04912
4	KEGG Pathways	Amyotrophic lateral sclerosis (ALS)	PPP3R1 BCL2L1 PPP3CA BCL2	0.0048	hsa05014
7	KEGG Pathways	Kaposi's sarcoma-associated herpesvirus infection	GNB4 PPP3R1 AKT3 ICAM1 CCR5 FAS PPP3CA	0.0048	hsa05167
5	KEGG Pathways	NF-kappa B signaling pathway	ICAM1 BCL2L1 LCK TLR4 BCL2	0.0057	hsa04064
5	KEGG Pathways	Endocrine resistance	MMP2 AKT3 JAG2 DLL1 BCL2	0.0059	hsa01522
5	KEGG Pathways	Progesterone-mediated oocyte maturation	CDC25B AKT3 PLK1 CDC25A CDC25C	0.0059	hsa04914
5	KEGG Pathways	Amoebiasis	LAMA4 HSPB1 LAMA5 PRKCG TLR4	0.0059	hsa05146
6	KEGG Pathways	Hepatitis B	PRKCG AKT3 DDI1 FAS TLR4 BCL2	0.0059	hsa05161
6	KEGG Pathways	Phospholipase D signaling pathway	PDGFRA AKT3 KIT FYN DNM1 ARF1	0.0063	hsa04072
9	KEGG Pathways	Human papillomavirus infection	ITGB4 LAMA4 LAMA5 THBS1 VWF AKT3 ITGA2 FAS CDC42	0.0063	hsa05165
6	KEGG Pathways	Gastric cancer	AKT3 RARB RXRG RXRB BCL2 ABCB1	0.0066	hsa05226
5	KEGG Pathways	Chagas disease (American trypanosomiasis)	CCL2 AKT3 CALR FAS TLR4	0.007	hsa05142
7	KEGG Pathways	Regulation of actin cytoskeleton	ITGB4 MYH9 PDGFRA ITGA2 MYH10 CDC42 CFL1	0.0072	hsa04810
6	KEGG Pathways	Necroptosis	CAPN2 FAS TLR4 CAMK2B BCL2 CAMK2A	0.0081	hsa04217
5	KEGG Pathways	TNF signaling pathway	CCL2 AKT3 ICAM1 MMP14 FAS	0.0088	hsa04668
4	KEGG Pathways	Central carbon metabolism in cancer	PDGFRA AKT3 KIT G6PD	0.0089	hsa05230
5	KEGG Pathways	Leukocyte transendothelial migration	MMP2 PRKCG ICAM1 CDH5 CDC42	0.0099	hsa04670
6	KEGG Pathways	Tight junction	MYH9 TJP1 TUBA1A TUBA1C MYH10 CDC42	0.0108	hsa04530
5	KEGG Pathways	Thyroid hormone signaling pathway	PRKCG AKT3 RXRG RXRB TBC1D4	0.0108	hsa04919
5	KEGG Pathways	Sphingolipid signaling pathway	PRKCG AKT3 NOS3 FYN BCL2	0.0109	hsa04071
4	KEGG Pathways	Adherens junction	TJP1 FYN PTPN1 CDC42	0.0111	hsa04520
4	KEGG Pathways	Bacterial invasion of epithelial cells	CAV1 ARHGEF26 DNM1 CDC42	0.0115	hsa05100
3	KEGG Pathways	Thyroid cancer	RXRG TPM3 RXRB	0.0136	hsa05216
4	KEGG Pathways	ErbB signaling pathway	PRKCG AKT3 CAMK2B CAMK2A	0.0181	hsa04012
4	KEGG Pathways	Rheumatoid arthritis	CCL2 ICAM1 FLT1 TLR4	0.0186	hsa05323
6	KEGG Pathways	Epstein-Barr virus infection	HSPB1 AKT3 ICAM1 PTMA BCL2 VIM	0.0194	hsa05169
5	KEGG Pathways	Adrenergic signaling in cardiomyocytes	AKT3 TPM3 CAMK2B BCL2 CAMK2A	0.0206	hsa04261
7	KEGG Pathways	Cytokine-cytokine receptor interaction	CCL2 PDGFRA FLT1 CSF1R KIT CCR5 FAS	0.0214	hsa04060
4	KEGG Pathways	Fc gamma R-mediated phagocytosis	PRKCG AKT3 CDC42 CFL1	0.0214	hsa04666
5	KEGG Pathways	Wnt signaling pathway	PPP3R1 PRKCG PPP3CA CAMK2B CAMK2A	0.0221	hsa04310
4	KEGG Pathways	Inflammatory mediator regulation of TRP channels	PRKCG PRKCH CAMK2B CAMK2A	0.0232	hsa04750
3	KEGG Pathways	Notch signaling pathway	JAG2 DLL1 NUMB	0.0237	hsa04330
4	KEGG Pathways	Circadian entrainment	GNB4 PRKCG CAMK2B CAMK2A	0.0237	hsa04713
4	KEGG Pathways	Aldosterone synthesis and secretion	PRKCG CAMK2B CAMK2A CAMK1D	0.0237	hsa04925
5	KEGG Pathways	Melanogenesis	PRKCG KIT CAMK2B CAMK2A	0.0272	hsa04916
5	KEGG Pathways	Cellular senescence	PPP3R1 AKT3 CAPN2 CDC25A PPP3CA	0.0289	hsa04218
2	KEGG Pathways	Protein processing in endoplasmic reticulum	CAPN2 CALR BCL2 PDIA6 PRKCSH	0.0322	hsa04141
2	KEGG Pathways	Steroid biosynthesis	CYP24A1 CYP2R1	0.0327	hsa00100
5	KEGG Pathways	Hepatocellular carcinoma	PRKCG AKT3 BCL2L1 NQO1 GSTO1	0.0327	hsa05225
3	KEGG Pathways	Viral myocarditis	ICAM1 CAV1 FYN	0.0327	hsa05416
4	KEGG Pathways	Insulin resistance	AKT3 NOS3 PTPN1 TBC1D4	0.0337	hsa04931
5	KEGG Pathways	Influenza A	CCL2 AKT3 ICAM1 FAS TLR4	0.0358	hsa05164
5	KEGG Pathways	Transcriptional misregulation in cancer	FLT1 CSF1R BCL2L1 RXRG RXRB	0.0362	hsa05202
4	KEGG Pathways	Glutamatergic synapse	GNB4 PPP3R1 PRKCG PPP3CA	0.0378	hsa04724
3	KEGG Pathways	Inflammatory bowel disease (IBD)	RORA RORC TLR4	0.0393	hsa05321
5	KEGG Pathways	Chemokine signaling pathway	CCL2 GNB4 AKT3 CCR5 CDC42	0.0454	hsa04062
3	KEGG Pathways	Acute myeloid leukemia	AKT3 CSF1R KIT	0.0454	hsa05221
3	KEGG Pathways	Glycolysis / Gluconeogenesis	GAPDH ENO1 LDHB	0.0481	hsa00010
3	KEGG Pathways	Adipocytokine signaling pathway	AKT3 RXRG RXRB	0.0494	hsa04920
22	Pfam	Protein kinase domain	MAP2K5 PDGFRA PRKCG AKT3 FLT1 CSF1R KIT MLK PLK1 BRSK1 PRKCH LCK MAP4K4 FYN EPHA2 SLK CAMK2B CAMK2A DYRK1A WEE1 PBK CAMK1D	5.39E-08	PF00069
22	Pfam	Protein tyrosine kinase	MAP2K5 PDGFRA PRKCG AKT3 FLT1 CSF1R KIT MLK PLK1 BRSK1 PRKCH LCK MAP4K4 FYN EPHA2 SLK CAMK2B CAMK2A DYRK1A WEE1 PBK CAMK1D	5.39E-08	PF07714
8	Pfam	Zinc finger, C4 type (two domains)	RORA RORC RARB NR1I2 RXRG RXRB RARG NR1H4	1.23E-06	PF00105
8	Pfam	Ligand-binding domain of nuclear hormone receptor	RORA RORC RARB NR1I2 RXRG RXRB RARG NR1H4	1.24E-06	PF00104
4	Pfam	Annexin	ANXA5 ANXA2 ANXA6 ANXA1	5.70E-04	PF00191
3	Pfam	M-phase inducer phosphatase	CDC25B CDC25A CDC25C	5.70E-04	PF06617
3	Pfam	Tropomyosin	TPM4 TPM3 TPM2	7.00E-04	PF00261
3	Pfam	Bcl-2 homology region 4	BCL2L2 BCL2L1 BCL2	7.00E-04	PF02180
3	Pfam	Tropomyosin like	TPM4 TPM3 TPM2	7.00E-04	PF12718
6	Pfam	Calponin homology (CH) domain	CNN2 FLNC FLNA CNN3 FLNB SPTBN2	8.30E-04	PF00307
4	Pfam	Tubulin C-terminal domain	TUBB4A TUBA1A TUBA1C TUBB4B	0.0016	PF03953
4	Pfam	Tubulin/FtsZ family, GTPase domain	TUBB4A TUBA1A TUBA1C TUBB4B	0.002	PF00091
3	Pfam	Filamin/ABP280 repeat	FLNC FLNA FLNB	0.003	PF00630
4	Pfam	Phosphotyrosine interaction domain (PTB/PID)	DAB2 TBC1D4 NUMB APBA2	0.003	PF00640
3	Pfam	Apoptosis regulator proteins, Bcl-2 family	BCL2L2 BCL2L1 BCL2	0.0033	PF00452
4	Pfam	Myosin head (motor domain)	MYH9 MYO1C MYH10 MYO1B	0.0064	PF00063
2	Pfam	Amyloid A4 N-terminal heparin-binding	APLP1 APP	0.0102	PF02177
7	Pfam	Variant SH3 domain	ARHGEF5 NGEF TJP1 LCK FYN ARHGEF26 SPTAN1	0.0102	PF07653
2	Pfam	beta-amyloid precursor protein C-terminus	APLP1 APP	0.0102	PF10515
2	Pfam	Copper-binding of amyloid precursor, CuBD	APLP1 APP	0.0102	PF12924
2	Pfam	E2 domain of amyloid precursor protein	APLP1 APP	0.0102	PF12925
3	Pfam	Rhodanese-like domain	CDC25B CDC25A CDC25C	0.0117	PF00581
2	Pfam	Delta serrate ligand	JAG2 DLL1	0.0117	PF01414
2	Pfam	N terminus of Notch ligand	JAG2 DLL1	0.0117	PF07657
2	Pfam	Calcium/calmodulin dependent protein kinase II association domain	CAMK2B CAMK2A	0.0117	PF08332
2	Pfam	Snoal-like domain	CAMK2B CAMK2A	0.0117	PF13474
2	Pfam	Domain of unknown function (DUF4440)	CAMK2B CAMK2A	0.0117	PF14534
2	Pfam	PTRF/SDPR family	SDPR PTRF	0.0117	PF15237
2	Pfam	Laminin Domain I	LAMA4 LAMA5	0.0124	PF06008
2	Pfam	Laminin Domain II	LAMA4 LAMA5	0.0124	PF06009
3	Pfam	von Willebrand factor type C domain	PXDN THBS1 VWF	0.0154	PF00093
2	Pfam	Calponin family repeat	CNN2 CNN3	0.0154	PF00402
2	Pfam	C-terminal leucine zipper domain of cyclic nucleotide-gated channels	TPM4 TPM3	0.0154	PF16526
6	Pfam	Variant SH3 domain	ARHGEF5 NGEF LCK FYN ARHGEF26 SPTAN1	0.0163	PF14604
2	Pfam	Syndecan domain	SDC4 SDC1	0.0174	PF01034
2	Pfam	2OG-Fe(II) oxygenase superfamily	PLOD1 PLOD2	0.0174	PF03171
3	Pfam	Protein kinase C terminal domain	PRKCG AKT3 PRKCH	0.0177	PF00433

2	Pfam	Unconventional myosin tail, actin- and lipid-binding	MYO1C MYO1B	0.0199	PF06017
6	Pfam	SH3 domain	ARHGEF5 NGEF LYN ARHGEF26 SPTAN1	0.0216	PF00018
4	Pfam	RhoGEF domain	ARHGEF5 NGEF ARHGEF26 ARHGEF15	0.0226	PF00621
4	Pfam	Kinase-like	AKT3 MLK PLK1 CAMK1D	0.0317	PF14531
3	Pfam	IQ calmodulin-binding motif	MYO1C MYH10 MYO1B	0.0378	PF00612
6	Pfam	PH domain	PLEK AKT3 NGEF FERMT3 DNM1 SPTBN2	0.0394	PF00169
2	Pfam	Fibronectin type II domain	MMP2 FN1	0.0444	PF00040
2	Pfam	Myosin N-terminal SH3-like domain	MYH9 MYH10	0.0444	PF02736
2	Pfam	Phosphotyrosine-binding domain	TENC1 NUMB	0.0444	PF08416
3	Pfam	Signal recognition particle receptor beta subunit	ARF3 ARF4 ARF1	0.0444	PF09439
4	Pfam	EF hand	RCN1 PPP3R1 SPTAN1 PRKCSH	0.0444	PF13202
2	Pfam	Glutathione S-transferase, C-terminal domain	GSTO1 CLIC4	0.0444	PF13410
2	Pfam	Pleckstrin homology domain	PLEK SPTBN2	0.0444	PF15410
2	Pfam	Dynamin family	EHD4 DNM1	0.0483	PF00350
64	Reactome Pathways	Signal Transduction	ARHGEF5 MAP2K5 MYH9 LAMA4 RBP1 GNB4 PPP3R1 HSPB1 LAMA5 PDGFRA THBS1 VWF PRKCG AKT3 NGEF TUBB4A ARHGAP31 TJP1 FLT1 APP KIT CCR5 ITGA2 NOS3 PLK1 TUBA1A TUBA1C CDC25C JAG2 PRKCH RAR CAV1 JRG512 TUBB4B CDH5 FYN FAS ARHGEF26 SFPQ RXRG MYH10 ARHGEF15 DLL1 ARHGAP30 FLNA PTPN1 SDC4 SPTAN1 DNM1 RXRB ANXA1 SDC1 PPP3CA CAMK2B LTB4R BCL2 CAMK2A SEPT7 CDC42 RARG SPTBN2 CFL1 NUMB	2.03E-13	HSA-162582
29	Reactome Pathways	Cytokine Signaling in Immune system	MMP2 CCL2 MTA2 LAMA5 RORA CNN2 ICAM1 APP CSF1R CCR5 BCL2L1 RORC LCK ANXA2 FYN GSTO1 FLNA PTPN1 ANXA1 SDC1 FSCN1 CAMK2B BCL2 CAMK2A CDC42 FLNB CFL1 ARF1 VIM	1.37E-10	HSA-1280215
23	Reactome Pathways	Signaling by Interleukins	MMP2 CCL2 LAMA5 RORA CNN2 ICAM1 APP CSF1R CCR5 BCL2L1 RORC LCK ANXA2 FYN GSTO1 ANXA1 SDC1 FSCN1 BCL2 CDC42 CFL1 ARF1 VIM	1.30E-09	HSA-449147
26	Reactome Pathways	Hemostasis	GNB4 PLEK THBS1 VWF PRKCG TUBB4A FERMT3 APP ANXA5 ITGA2 NOS3 TUBA1A TUBA1C PRKCH LCK CAV1 TUBB4B ANXA2 FYN FLNA PTPN1 SDC4 SDC1 CDC42 WEE1 CFL1	2.20E-09	HSA-109582
47	Reactome Pathways	Immune System	MYH9 MMP2 CCL2 PPP3R1 MTA2 LAMA5 RORA CNN2 AKT3 TUBB4A ICAM1 APP CSF1R CCR5 NOS3 CCT2 TUBA1A TUBA1C BCL2L1 CALR RORC LCK TUBB4B ANXA2 FYN MYO1C GSTO1 FLNA PTPN1 SPTAN1 DNM1 TLR4 ANXA1 SDC1 FSCN1 XRCC5 PPP3CA CAMK2B BCL2 CAMK2A CDC42 FLNB SPTBN2 CFL1 ARF1 VIM PRKCSH	2.20E-09	HSA-168256
17	Reactome Pathways	Extracellular matrix organization	PLOD1 ITGB4 MMP2 LAMA4 PXDN LAMA5 THBS1 COL8A1 VWF ICAM1 PLOD2 APP CAPN2 ITGA2 MMP14 SDC4 SDC1	1.33E-07	HSA-1474244
11	Reactome Pathways	Interleukin-4 and Interleukin-13 signaling	MMP2 CCL2 LAMA5 RORA ICAM1 BCL2L1 RORC ANXA1 FSCN1 BCL2 VIM	3.62E-07	HSA-6785807
15	Reactome Pathways	Platelet activation, signaling and aggregation	GNB4 PLEK THBS1 VWF PRKCG FERMT3 APP ANXA5 PRKCH LCK FYN FLNA PTPN1 CDC42 CFL1	7.04E-07	HSA-76002
10	Reactome Pathways	COPI-mediated anterograde transport	ARF3 TUBB4A TUBA1A TUBA1C ARF4 TUBB4B COPA SPTAN1 SPTBN2 ARF1	1.87E-06	HSA-6807878
18	Reactome Pathways	Signaling by Receptor Tyrosine Kinases	MAP2K5 LAMA4 HSPB1 LAMA5 PDGFRA THBS1 AKT3 FLT1 KIT ITGA2 NOS3 LCK CAV1 CDH5 FYN PTPN1 DNM1 CDC42	3.22E-06	HSA-9006934
17	Reactome Pathways	Signaling by Rho GTPases	ARHGEF5 MYH9 NGEF TUBB4A ARHGAP31 PLK1 TUBA1A TUBA1C CDC25C TUBB4B ARHGAP26 MYH10 ARHGEF15 ARHGAP30 FLNA CDC42 CFL1	4.93E-06	HSA-194315
9	Reactome Pathways	EPH-Ephrin signaling	MYH9 MMP2 NGEF FYN EPHA2 MYH10 DNM1 CDC42 CFL1	8.43E-06	HSA-2682334
7	Reactome Pathways	Gap junction trafficking and regulation	TUBB4A TJP1 TUBA1A TUBA1C DAB2 TUBB4B DNM1	1.58E-05	HSA-157858
7	Reactome Pathways	Non-integrin membrane-ECM interactions	ITGB4 LAMA4 LAMA5 THBS1 ITGA2 SDC4 SDC1	4.71E-05	HSA-3000171
9	Reactome Pathways	L1CAM interactions	TUBB4A ITGA2 TUBA1A TUBA1C TUBB4B SPTAN1 DNM1 SPTBN2 NUMB	4.71E-05	HSA-373760
18	Reactome Pathways	Axon guidance	MYH9 MMP2 NGEF TUBB4A ITGA2 TUBA1A TUBA1C TUBB4B DOK4 FYN EPHA2 MYH10 SPTAN1 DNM1 CDC42 SPTBN2 CFL1 NUMB	4.71E-05	HSA-422475
10	Reactome Pathways	Apoptosis	PPP3R1 AKT3 ADD1 TJP1 BCL2L1 FAS SPTAN1 TLR4 BCL2 VIM	6.07E-05	HSA-109581
25	Reactome Pathways	Disease	CYP24A1 RBP1 CDC25B PDGFRA THBS1 VWF AKT3 APP KIT CCR5 CAPN2 CDC25A CALR CDC25C JAG2 CYP2R1 LCK FYN DLL1 SDC4 TLR4 PSIP1 SDC1 XRCC5 ARF1	6.07E-05	HSA-1643685
6	Reactome Pathways	Nuclear Receptor transcription pathway	RORA RORC RAR RARG RXRG RXRB RARG	6.07E-05	HSA-383280
6	Reactome Pathways	Gene and protein expression by JAK-STAT signaling after Interleukin-12 stimulation	CNN2 ANXA2 GSTO1 CDC42 CFL1 ARF1	6.07E-05	HSA-8950505
8	Reactome Pathways	COPI-dependent Golgi-to-ER retrograde traffic	ARF3 TUBB4A TUBA1A TUBA1C ARF4 TUBB4B COPA ARF1	7.19E-05	HSA-6811434
9	Reactome Pathways	Response to elevated platelet cytosolic Ca2+	PLEK THBS1 VWF PRKCG FERMT3 APP ANXA5 FLNA CFL1	7.19E-05	HSA-76005
5	Reactome Pathways	Deregulated CDK5 triggers multiple neurodegenerative pathways in Alzheimer's disease models	CDC25B APP CAPN2 CDC25A CDC25C	7.19E-05	HSA-8862803
7	Reactome Pathways	Translocation of SLC2A4 (GLUT4) to the plasma membrane	MYH9 TUBB4A TUBA1A TUBA1C TUBB4B MYO1C TBC1D4	7.58E-05	HSA-1445148
5	Reactome Pathways	Formation of tubulin folding intermediates by CCT/Tric	TUBB4A CCT2 TUBA1A TUBA1C TUBB4B	7.58E-05	HSA-389960
19	Reactome Pathways	Vesicle-mediated transport	MYH9 ARF3 AKT3 TUBB4A TJP1 APP TUBA1A TUBA1C ARF4 DAB2 CALR TUBB4B MYO1C COPA SPTAN1 DNM1 TBC1D4 SPTBN2 ARF1	7.58E-05	HSA-5653656
6	Reactome Pathways	Recycling pathway of L1	TUBB4A TUBA1A TUBA1C TUBB4B DNM1 NUMB	8.86E-05	HSA-437239
6	Reactome Pathways	Gap junction trafficking	TUBB4A TUBA1A TUBA1C DAB2 TUBB4B DNM1	9.46E-05	HSA-190828
8	Reactome Pathways	Signaling by VEGF	HSPB1 AKT3 FLT1 NOS3 CAV1 CDH5 FYN CDC42	9.46E-05	HSA-194138
5	Reactome Pathways	Cyclin A/B1/B2 associated events during G2/M transition	CDC25B PLK1 CDC25A CDC25C WEE1	9.46E-05	HSA-69273
18	Reactome Pathways	Membrane Trafficking	MYH9 ARF3 AKT3 TUBB4A TJP1 APP TUBA1A TUBA1C ARF4 DAB2 TUBB4B MYO1C COPA SPTAN1 DNM1 TBC1D4 SPTBN2 ARF1	9.88E-05	HSA-199991
5	Reactome Pathways	Syndecan interactions	ITGB4 THBS1 ITGA2 SDC4 SDC1	9.88E-05	HSA-3000170
5	Reactome Pathways	Prefoldin mediated transfer of substrate to CCT/Tric	TUBB4A CCT2 TUBA1A TUBA1C TUBB4B	9.88E-05	HSA-389957
5	Reactome Pathways	EPHA-mediated growth cone collapse	MYH9 NGEF FYN EPHA2 MYH10	1.30E-04	HSA-3928663
5	Reactome Pathways	RHO GTPases activate IQGAPs	TUBB4A TUBA1A TUBA1C TUBB4B CDC42	1.40E-04	HSA-5626467
12	Reactome Pathways	Asparagine N-linked glycosylation	ARF3 TUBB4A TUBA1A TUBA1C ARF4 CALR TUBB4B COPA SPTAN1 SPTBN2 ARF1 PRKCSH	1.80E-04	HSA-446203
8	Reactome Pathways	Platelet degranulation	PLEK THBS1 VWF FERMT3 APP ANXA5 FLNA CFL1	2.40E-04	HSA-114608
4	Reactome Pathways	Polo-like kinase mediated events	PLK1 CDC25A CDC25C WEE1	2.90E-04	HSA-156711
7	Reactome Pathways	VEGFA-VEGFR2 Pathway	HSPB1 AKT3 NOS3 CAV1 CDH5 FYN CDC42	3.30E-04	HSA-4420097
4	Reactome Pathways	Microtubule-dependent trafficking of connexons from Golgi to the plasma membrane	TUBB4A TUBA1A TUBA1C TUBB4B	3.40E-04	HSA-190840
11	Reactome Pathways	RHO GTPase Effectors	MYH9 TUBB4A PLK1 TUBA1A TUBA1C CDC25C TUBB4B MYH10 FLNA CDC42 CFL1	3.60E-04	HSA-195258
11	Reactome Pathways	MAPK family signaling cascades	HSPB1 PDGFRA VWF KIT FYN SPTAN1 CAMK2B CAMK2A SEPT7 CDC42 SPTBN2	3.60E-04	HSA-5683057
4	Reactome Pathways	Post-chaperonin tubulin folding pathway	TUBB4A TUBA1A TUBA1C TUBB4B	5.50E-04	HSA-389977
4	Reactome Pathways	RHO GTPases activate PAKs	MYH9 MYH10 FLNA CDC42	5.50E-04	HSA-5627123
9	Reactome Pathways	G2/M Transition	CDC25B TUBB4A PLK1 TUBA1A TUBA1C CDC25A CDC25C TUBB4B WEE1	5.50E-04	HSA-69275
7	Reactome Pathways	MHC class II antigen presentation	TUBB4A TUBA1A TUBA1C TUBB4B DNM1 SPTBN2 ARF1	0.0011	HSA-2132295
4	Reactome Pathways	VEGFR2 mediated vascular permeability	AKT3 NOS3 CAV1 CDH5	0.0014	HSA-5218920
21	Reactome Pathways	Innate Immune System	MYH9 PPP3R1 CNN2 APP NOS3 CCT2 BCL2L1 LCK TUBB4B ANXA2 FYN MYO1C SPTAN1 DNM1 TLR4 XRCC5 PPP3CA BCL2 CDC42 CFL1 PRKCSH	0.0016	HSA-168249

21	Reactome Pathways	Developmental Biology	MYH9 MMP2 AKT3 NGEF TUBB4A ITGA2 TUBA1A TUBA1C RARB TUBB4B DOK4 FYN EPH A2 MYH10 SPTAN1 DNM1 CDC42 RARG SPTBN2 CFL1 NUMB	0.0018	HSA-1266738
4	Reactome Pathways	Laminin interactions	ITGB4 LAMA4 LAMA5 ITGA2	0.0019	HSA-3000157
6	Reactome Pathways	Chaperonin-mediated protein folding	GNB4 TUBB4A CCT2 TUBA1A TUBA1C TUBB4B	0.0019	HSA-390466
4	Reactome Pathways	CD28 co-stimulation	AKT3 LCK FYN CDC42	0.0021	HSA-389356
3	Reactome Pathways	CD28 dependent Vav1 pathway	LCK FYN CDC42	0.0021	HSA-389359
7	Reactome Pathways	Rho GTPase cycle	ARHGEF5 NGEF ARHGAP31 ARHGEF26 ARHGEF15 ARHGAP30 CDC42	0.0023	HSA-194840
4	Reactome Pathways	Smooth Muscle Contraction	ANXA2 ANXA6 TPM3 ANXA1	0.0023	HSA-445355
3	Reactome Pathways	Caspase-mediated cleavage of cytoskeletal proteins	ADD1 SPTAN1 VIM	0.0024	HSA-264870
3	Reactome Pathways	Regulation of KIT signaling	KIT LCK FYN	0.0029	HSA-1433559
3	Reactome Pathways	Early Phase of HIV Life Cycle	CCR5 PSIP1 XRCC5	0.0033	HSA-162594
4	Reactome Pathways	Apoptotic cleavage of cellular proteins	ADD1 TP1 SPTAN1 VIM	0.0034	HSA-111465
3	Reactome Pathways	Activation of BAD and translocation to mitochondria	PPP3R1 AKT3 BCL2	0.0038	HSA-111447
3	Reactome Pathways	Platelet Adhesion to exposed collagen	VWF ITGA2 FYN	0.0038	HSA-75892
4	Reactome Pathways	Carboxyterminal post-translational modifications of tubulin	TUBB4A TUBA1A TUBA1C TUBB4B	0.0039	HSA-8955332
5	Reactome Pathways	The role of GTSE1 in G2/M progression after G2 checkpoint	TUBB4A PLK1 TUBA1A TUBA1C TUBB4B	0.0042	HSA-8852276
11	Reactome Pathways	G alpha (i) signalling events	RBP1 GNB4 PPP3R1 PRKCG APP CCR5 RGS12 SDC4 ANXA1 SDC1 PPP3CA	0.0044	HSA-418594
16	Reactome Pathways	Adaptive Immune System	PPP3R1 AKT3 TUBB4A ICAM1 TUBA1A TUBA1C CALR LCK TUBB4B FYN DNM1 TLR4 PPP3 CA CDC42 SPTBN2 ARF1	0.0045	HSA-1280218
4	Reactome Pathways	Intrinsic Pathway for Apoptosis	PPP3R1 AKT3 BCL2L1 BCL2	0.0053	HSA-109606
5	Reactome Pathways	G alpha (12/13) signalling events	ARHGEF5 GNB4 NGEF ARHGEF26 ARHGEF15	0.0053	HSA-416482
4	Reactome Pathways	Signaling by Retinoic Acid	RARB RXRG RXRB RARG	0.0053	HSA-5362517
2	Reactome Pathways	The NLRP1 inflammasome	BCL2L1 BCL2	0.0055	HSA-844455
3	Reactome Pathways	RHO GTPases Activate ROCKs	MYH9 MYH10 CFL1	0.0062	HSA-5627117
6	Reactome Pathways	Cell-Cell communication	ITGB4 FLNC CDH5 FYN FLNA SPTAN1	0.0067	HSA-1500931
5	Reactome Pathways	Integrin cell surface interactions	THBS1 COL8A1 VWF ICAM1 ITGA2	0.0067	HSA-216083
8	Reactome Pathways	RAF/MAP kinase cascade	PDGFRA VWF KIT FYN SPTAN1 CAMK2B CAMK2A SPTBN2	0.0067	HSA-5673001
5	Reactome Pathways	Fc gamma receptor (FCGR) dependent phagocytosis	MYH9 FYN MYO1C CDC42 CFL1	0.0068	HSA-2029480
5	Reactome Pathways	PI3K/AKT Signaling in Cancer	PDGFRA AKT3 KIT LCK FYN	0.0068	HSA-2219528
3	Reactome Pathways	CTLA4 inhibitory signaling	AKT3 LCK FYN	0.0068	HSA-389513
3	Reactome Pathways	Inflammasomes	APP BCL2L1 BCL2	0.0068	HSA-622312
12	Reactome Pathways	Cell Cycle, Mitotic	CDC25B AKT3 TUBB4A PLK1 TUBA1A TUBA1C CDC25A CDC25C TUBB4B DYRK1A WEE1 M CM3	0.0068	HSA-69278
4	Reactome Pathways	COPI-independent Golgi-to-ER retrograde traffic	TUBB4A TUBA1A TUBA1C TUBB4B	0.007	HSA-6811436
5	Reactome Pathways	Interferon gamma signaling	MT2A ICAM1 PTPN1 CAMK2B CAMK2A	0.007	HSA-877300
2	Reactome Pathways	NOSTRIN mediated eNOS trafficking	NOS3 CAV1	0.0071	HSA-203641
6	Reactome Pathways	RHO GTPases Activate Formins	TUBB4A PLK1 TUBA1A TUBA1C TUBB4B CDC42	0.0071	HSA-5663220
4	Reactome Pathways	EPH-ephrin mediated repulsion of cells	MMP2 FYN EPHA2 DNM1	0.0073	HSA-3928665
4	Reactome Pathways	Intraflagellar transport	TUBB4A TUBA1A TUBA1C TUBB4B	0.0073	HSA-5620924
5	Reactome Pathways	Collagen formation	PLOD1 ITGB4 PXDN COL8A1 PLOD2	0.0076	HSA-1474290
3	Reactome Pathways	CD28 dependent PI3K/Akt signaling	AKT3 LCK FYN	0.0076	HSA-389357
5	Reactome Pathways	Recruitment of NuMA to mitotic centrosomes	TUBB4A PLK1 TUBA1A TUBA1C TUBB4B	0.0081	HSA-380320
5	Reactome Pathways	Negative regulation of the PI3K/AKT network	PDGFRA AKT3 KIT LCK FYN	0.0083	HSA-199418
4	Reactome Pathways	HSP90 chaperone cycle for steroid hormone receptors (SHR)	TUBB4A TUBA1A TUBA1C TUBB4B	0.0083	HSA-3371497
7	Reactome Pathways	Interferon Signaling	MT2A ICAM1 FLNA PTPN1 CAMK2B CAMK2A FLNB	0.0083	HSA-913531
13	Reactome Pathways	Cell Cycle	CDC25B AKT3 TUBB4A PLK1 TUBA1A TUBA1C CDC25A CDC25C TUBB4B DYRK1A SUN1 W EE1 MCM3	0.0096	HSA-1640170
7	Reactome Pathways	Cilium Assembly	TUBB4A CCT2 PLK1 TUBA1A TUBA1C ARF4 TUBB4B	0.0096	HSA-5617833
7	Reactome Pathways	Muscle contraction	ANXA2 ANXA6 TPM3 ANXA1 CAMK2B CAMK2A VIM	0.0103	HSA-397014
3	Reactome Pathways	The role of Nef in HIV-1 replication and disease pathogenesis	LCK FYN ARF1	0.0108	HSA-164952
4	Reactome Pathways	NRAGE signals death through JNK	ARHGEF5 NGEF ARHGEF26 ARHGEF15	0.0108	HSA-193648
4	Reactome Pathways	Constitutive Signaling by Aberrant PI3K in Cancer	PDGFRA KIT LCK FYN	0.0108	HSA-2219530
4	Reactome Pathways	Transcriptional Regulation by MECP2	DL1 PTPN1 CAMK2B CAMK2A	0.0108	HSA-8986944
4	Reactome Pathways	Kinesins	TUBB4A TUBA1A TUBA1C TUBB4B	0.0108	HSA-983189
2	Reactome Pathways	Vitamins	CYP24A1 CYP2R1	0.0109	HSA-211916
4	Reactome Pathways	Ca2+ pathway	GNB4 PPP3R1 PPP3CA CAMK2A	0.0109	HSA-4086398
4	Reactome Pathways	Regulation of actin dynamics for phagocytic cup formation	MYH9 MYO1C CDC42 CFL1	0.0112	HSA-2029482
3	Reactome Pathways	Trafficking of AMPA receptors	PRKCG CAMK2B CAMK2A	0.0112	HSA-399719
6	Reactome Pathways	Factors involved in megakaryocyte development and platelet production	TUBB4A TUBA1A TUBA1C TUBB4B CDC42 WEE1	0.012	HSA-983231
2	Reactome Pathways	2-LTR circle formation	PSIP1 XRCC5	0.0129	HSA-164843
2	Reactome Pathways	Nef and signal transduction	LCK FYN	0.0129	HSA-164944
2	Reactome Pathways	Constitutive Signaling by NOTCH1 t(7;9)(NOTCH1:M1580_K2555) Translocation Mutant	JAG2 DLL1	0.0129	HSA-2660826
4	Reactome Pathways	Semaphorin interactions	MYH9 FYN MYH10 CFL1	0.0129	HSA-373755
2	Reactome Pathways	Formyl peptide receptors bind formyl peptides and many other ligands	APP ANXA1	0.0129	HSA-444473
3	Reactome Pathways	MET activates PTK2 signaling	LAMA4 LAMA5 ITGA2	0.0129	HSA-8874081
5	Reactome Pathways	Hedgehog 'off' state	TUBB4A TUBA1A TUBA1C TUBB4B NUMB	0.0132	HSA-5610787
3	Reactome Pathways	Activated NOTCH1 Transmits Signal to the Nucleus	JAG2 DLL1 NUMB	0.0144	HSA-2122948
2	Reactome Pathways	BH3-only proteins associate with and inactivate anti-apoptotic BCL-2 members	BCL2L1 BCL2	0.0151	HSA-111453
4	Reactome Pathways	Loss of Nlp from mitotic centrosomes	TUBB4A PLK1 TUBA1A TUBB4B	0.0154	HSA-380259
3	Reactome Pathways	GPVI-mediated activation cascade	LCK FYN CDC42	0.0176	HSA-114604
4	Reactome Pathways	AURKA Activation by TPX2	TUBB4A PLK1 TUBA1A TUBB4B	0.0176	HSA-8854518
2	Reactome Pathways	Nef Mediated CD4 Down-regulation	LCK ARF1	0.0177	HSA-167590
2	Reactome Pathways	Calcineurin activates NFAT	PPP3R1 PPP3CA	0.0177	HSA-2025928
5	Reactome Pathways	Resolution of Sister Chromatid Cohesion	TUBB4A PLK1 TUBA1A TUBA1C TUBB4B	0.0177	HSA-2500257
9	Reactome Pathways	Diseases of signal transduction	RBP1 PDGFRA VWF AKT3 KIT JAG2 LCK FYN DLL1	0.0181	HSA-5663202
4	Reactome Pathways	ECM proteoglycans	LAMA4 LAMA5 APP ITGA2	0.0202	HSA-3000178
5	Reactome Pathways	Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)	RCN1 MMP2 APP PDIA6 PRKCSH	0.0203	HSA-381426
3	Reactome Pathways	Activation of ATR in response to replication stress	CDC25A CDC25C MCM3	0.0206	HSA-176187

4	Reactome Pathways	Signaling by MET	LAMA4 LAMA5 ITGA2 PTPN1	0.0206	HSA-6806834
18	Reactome Pathways	GPCR downstream signalling	ARHGEF5 RBP1 GNB4 PPP3R1 PRKCG AKT3 NGEF APP CCR5 PRKCH RG512 ARHGEF26 ARHGEF15 SDC4 ANXA1 SDC1 PPP3CA LTB4R	0.0213	HSA-388396
2	Reactome Pathways	Formation of annular gap junctions	DAB2 DNM1	0.0229	HSA-196025
2	Reactome Pathways	Vitamin D (calciferol) metabolism	CYP24A1 CYP2R1	0.0229	HSA-196791
2	Reactome Pathways	eNOS activation	NOS3 CAV1	0.0229	HSA-203615
2	Reactome Pathways	PECAM1 interactions	LCK FYN	0.0229	HSA-210990
4	Reactome Pathways	Recruitment of mitotic centrosome proteins and complexes	TUBB4A PLK1 TUBA1A TUBB4B	0.0229	HSA-380270
2	Reactome Pathways	GP1b-IX-V activation signalling	VWF FLNA	0.0229	HSA-430116
2	Reactome Pathways	CLEC7A (Dectin-1) induces NFAT activation	PPP3R1 PPP3CA	0.0229	HSA-5607763
4	Reactome Pathways	Opioid Signalling	GNB4 PPP3R1 PRKCG PPP3CA	0.0245	HSA-111885
3	Reactome Pathways	EPHB-mediated forward signaling	FYN CDC42 CFL1	0.0245	HSA-3928662
4	Reactome Pathways	Cyclin A:Cdk2-associated events at S phase entry	CDC25B AKT3 CDC25A WEE1	0.0245	HSA-69656
5	Reactome Pathways	Cell surface interactions at the vascular wall	LCK CAV1 FYN SDC4 SDC1	0.0263	HSA-202733
4	Reactome Pathways	Regulation of PLK1 Activity at G2/M Transition	TUBB4A PLK1 TUBA1A TUBB4B	0.0268	HSA-2565942
4	Reactome Pathways	PI3P, PP2A and IER3 Regulate PI3K/AKT Signaling	PDGFR4 KIT LCK FYN	0.0268	HSA-6811558
27	Reactome Pathways	Metabolism of proteins	RCN1 MMP2 CCL2 GNB4 ARF3 THBS1 RORA TUBB4A ADD1 APP CCT2 TUBA1A TUBA1C DDB1 CDC25A ARF4 CALR SNCA TUBB4B DPP4 COPA SPTAN1 PDIA6 TOP2B SPTBN2 ARF1 PRKCSH	0.0271	HSA-392499
2	Reactome Pathways	Chk1/Chk2(Cds1) mediated inactivation of Cyclin B:Cdk1 complex	CDC25C WEE1	0.0272	HSA-75035
2	Reactome Pathways	Advanced glycosylation endproduct receptor signaling	APP PRKCSH	0.0272	HSA-879415
3	Reactome Pathways	Retinoid metabolism and transport	RBP1 SDC4 SDC1	0.028	HSA-975634
5	Reactome Pathways	Degradation of the extracellular matrix	MMP2 LAMA5 COL8A1 CAPN2 MMP14	0.0283	HSA-1474228
5	Reactome Pathways	Death Receptor Signalling	ARHGEF5 NGEF FAS ARHGEF26 ARHGEF15	0.0283	HSA-73887
5	Reactome Pathways	Beta-catenin independent WNT signaling	GNB4 PPP3R1 PRKCG PPP3CA CAMK2A	0.0288	HSA-3858494
3	Reactome Pathways	Interleukin-10 signaling	CCL2 ICAM1 CCR5	0.029	HSA-6783783
2	Reactome Pathways	Defective EXT2 causes exostoses 2	SDC4 SDC1	0.0296	HSA-3656237
2	Reactome Pathways	Defective EXT1 causes exostoses 1, TRPS2 and CHDS	SDC4 SDC1	0.0296	HSA-3656253
4	Reactome Pathways	Cell junction organization	ITGB4 FLNC CDH5 FLNA	0.0306	HSA-446728
3	Reactome Pathways	G alpha (z) signalling events	GNB4 PRKCG PRKCH	0.031	HSA-418597
5	Reactome Pathways	Mitotic G1-G1/S phases	AKT3 CDC25A DYRK1A WEE1 MCM3	0.031	HSA-453279
2	Reactome Pathways	Caspase activation via Death Receptors in the presence of ligand	FAS TLR4	0.0316	HSA-140534
2	Reactome Pathways	Constitutive Signaling by NOTCH1 HD Domain Mutants	JAG2 DLL1	0.0316	HSA-2691232
2	Reactome Pathways	Nucleobase biosynthesis	CAD PAICS	0.0316	HSA-8956320
4	Reactome Pathways	Unfolded Protein Response (UPR)	CCL2 ADD1 CALR PDIA6	0.0326	HSA-381119
2	Reactome Pathways	Sema3A PAK dependent Axon repulsion	FYN CFL1	0.0344	HSA-399954
4	Reactome Pathways	Anchoring of the basal body to the plasma membrane	TUBB4A PLK1 TUBA1A TUBB4B	0.0346	HSA-5620912
20	Reactome Pathways	Post-translational protein modification	RCN1 ARF3 THBS1 RORA TUBB4A APP TUBA1A TUBA1C DDB1 CDC25A ARF4 CALR TUBB4B COPA SPTAN1 PDIA6 TOP2B SPTBN2 ARF1 PRKCSH	0.0393	HSA-597592
5	Reactome Pathways	S Phase	CDC25B AKT3 CDC25A WEE1 MCM3	0.0393	HSA-69242
2	Reactome Pathways	Synthesis of PIPs at the Golgi membrane	ARF3 ARF1	0.0409	HSA-1660514
2	Reactome Pathways	CREB phosphorylation through the activation of CaMKII	CAMK2B CAMK2A	0.0409	HSA-442729
2	Reactome Pathways	Cell-extracellular matrix interactions	FLNC FLNA	0.0409	HSA-446353
6	Reactome Pathways	HIV Infection	CCR5 LCK FYN PSIP1 XRCC5 ARF1	0.0428	HSA-162906
17	Reactome Pathways	Generic Transcription Pathway	THBS1 RORA AKT3 TJP1 KIT CDC25C RORC RARB FAS RXRG DLL1 PTPN1 RXRB G6PD CAMK2B CAMK2A RARG	0.0436	HSA-212436
2	Reactome Pathways	RHO GTPases activate CIT	MYH9 MYH10	0.0436	HSA-5625900
4	Reactome Pathways	Post-translational protein phosphorylation	RCN1 APP PDIA6 PRKCSH	0.0449	HSA-8957275
2	Reactome Pathways	Defective B4GALT7 causes EDS, progeroid type	SDC4 SDC1	0.0473	HSA-3560783
2	Reactome Pathways	Defective B3GAT3 causes JDSSDHD	SDC4 SDC1	0.0473	HSA-3560801
2	Reactome Pathways	Sema4D induced cell migration and growth-cone collapse	MYH9 MYH10	0.0473	HSA-416572
2	Reactome Pathways	Unblocking of NMDA receptors, glutamate binding and activation	CAMK2B CAMK2A	0.0473	HSA-438066
2	Reactome Pathways	Defective B3GALT6 causes EDSP2 and SEMD11	SDC4 SDC1	0.0473	HSA-4420332
2	Reactome Pathways	Ras activation upon Ca2+ influx through NMDA receptor	CAMK2B CAMK2A	0.0473	HSA-442982
5	Reactome Pathways	Signaling by Nuclear Receptors	RARB RXRG RXRB BCL2 RARG	0.0473	HSA-9006931
3	Reactome Pathways	Assembly of collagen fibrils and other multimeric structures	ITGB4 PXDN COL8A1	0.0497	HSA-2022090
3	Reactome Pathways	NCAM signaling for neurite out-growth	FYN SPTAN1 SPTBN2	0.0497	HSA-375165
15	Reference publications	(2014) Interaction of membranelipid rafts with the cytoskeleton: impact on signaling and function: membranelipid rafts, mediators of cytoskeletal arrangement and cell signaling.	APP ANXA5 NOS3 SDPR LCK CAV1 ANXA2 ANXA6 FYN FN1 PTRF DPP4 FLNA ANXA1 CDC42	8.40E-11	PMID.23899502
16	Reference publications	(2018) A multi-step transcriptional cascade underlies vascular regeneration in vivo.	MMP2 LAMA4 PXDN THBS1 COL8A1 VWF ICAM1 FLT1 CSF1R NOS3 BCL2L1 MMP14 DAB2 CDH5 CLIC4 ANXA1	1.08E-10	PMID.29615716
12	Reference publications	(2016) Prostate stromal cell proteomics analysis discriminates normal from tumour reactive stromal phenotypes.	MYH9 GAPDH ANXA5 TUBA1A CAV1 TPM4 FN1 FLNA ANXA1 TPM2 CFL1 VIM	1.91E-09	PMID.26934553
11	Reference publications	(2016) Mechanism of Fibronectin Binding to Human Trabecular Meshwork Exosomes and Its Modulation by Dexamethasone.	MMP2 CCL2 ANXA5 SDPR MMP14 ANXA2 ANXA6 FN1 DPP4 ANXA1 SDC1	1.91E-09	PMID.27783649
14	Reference publications	(2012) A proteomic view at T cell costimulation.	MYH9 GAPDH ICAM1 ANXA5 TUBA1A TUBA1C BCL2L1 CALR LCK TUBB4B FYN TPM3 FLNA LDHB	1.16E-08	PMID.22539942
13	Reference publications	(2013) Annexin A2 heterotetramer: structure and function.	FLT1 ANXA5 CALR CDH5 ANXA2 ANXA6 FN1 TLR4 ANXA1 SDC1 FSCN1 CDC42 CFL1	1.16E-08	PMID.23519104
17	Reference publications	(2012) Quantitative proteomics of extracellular vesicles derived from human primary and metastatic colorectal cancer cells.	ITGB4 MYH9 EHD4 GAPDH ENO1 ARF3 ICAM1 ANXA5 ITGA2 LCK ANXA2 ANXA6 MYH10 ANXA1 FSCN1 MYO1B VIM	1.16E-08	PMID.24009881
15	Reference publications	(2016) Secreted primary human malignant mesothelioma exosome signature reflects oncogenic cargo.	MMP2 ENO1 THBS1 TUBB4A CCT2 MMP14 CALR TUBB4B ANXA2 ANXA6 FN1 DNM1 ANXA1 G6PD VIM	1.16E-08	PMID.27605433
13	Reference publications	(2014) Quantification of pancreatic cancer proteome and phosphorylome: indicates molecular events likely contributing to cancer and activity of drug targets.	ITGB4 MYH9 GAPDH ARHGAP31 ZYX FLNC FYN FN1 MYH10 FLNA CDC42 FLNB TLN2	2.31E-08	PMID.24670416

12	Reference publications	(2014) PPARGamma activation but not PPARGamma haplo deficiency affects proangiogenic potential of endothelial cells and bone marrow-derived progenitors.	MMP2 THBS1 VWF NGEF ICAM1 FLT1 KIT NOS3 CCT2 MMP14 CAV1 FN1	2.31E-08	PMID.25361524
12	Reference publications	(2016) ISN Forefronts Symposium 2015: Nuclear Receptors and Diabetic Nephropathy.	CCL2 RORA ICAM1 RORC RARB NR1I2 PTGES FYN FN1 RXRG RARG NR1H4	2.39E-08	PMID.28932823
14	Reference publications	(2010) Comprehensive identification and modified-site mapping of S-nitrosylated targets in prostate epithelial cells.	ITGB4 GAPDH ENO1 NOS3 FLNC TUBB4B ANXA2 FLNA CLIC4 ANXA1 XRCC5 PDIA6 FLNB VIM	4.86E-08	PMID.20140087
15	Reference publications	(2010) Molecular characterization of c-Abl-Scr kinase inhibitors targeted against murine tumour progenitor cells that express stem cell markers.	ITGB4 CDC25B THBS1 KIT PLK1 TUBA1A BCL2L1 CDC25C FLNC LCK CAV1 FYN FN1 TLR4 VIM	5.83E-08	PMID.21152443
13	Reference publications	(2014) Plasma membrane proteomics of human breast cancer cell lines identifies potential targets for breast cancer diagnosis and treatment.	MYH9 ICAM1 FLT1 KIT FLNC TPM4 EPHA2 MYO1C MYH10 TPM3 FLNA TPM2 FLNB	8.25E-08	PMID.25029196
13	Reference publications	(2016) More Than Tiny Sacks: Stem Cell Exosomes as Cell-Free Modality for Cardiac Repair.	CCL2 GAPDH ICAM1 KIT ANXA5 NOS3 BCL2L1 ANXA2 ANXA6 FLNA PTPN1 TLR4 ANXA1	1.14E-07	PMID.26838317
11	Reference publications	(2008) Proteomic profiling of neuromas reveals alterations in protein composition and local protein synthesis in hyper-excitability nerves.	ENO1 ANXA5 CKB CCT2 CALR SNCA ANXA2 ANXA6 ANXA1 FSCN1 LDHB	1.84E-07	PMID.18700027
14	Reference publications	(2011) Proteomic analysis of endothelial cold-adaptation.	GAPDH ENO1 THBS1 FERMT3 PLOC2 CCT2 CALR FN1 FLNA ANXA1 FSCN1 G6PD CDC42 VIM	2.50E-07	PMID.22192797
10	Reference publications	(2009) Comparative proteomic analysis of malformed umbilical cords from somatic cell nuclear transfer-derived piglets: implications for early postnatal death.	HSPB1 VWF FLT1 ANXA5 TPM4 ANXA2 ANXA1 TPM2 LDHB CFL1	2.55E-07	PMID.19889237
10	Reference publications	(2011) Analysis of the myosin-II-responsive focal adhesion proteome reveals a role for Beta-Pix in negative regulation of focal adhesion maturation.	GAPDH CAPN2 DAB2 ZYX FLNC CAV1 FN1 FLNA FLNB CFL1	2.55E-07	PMID.21423176
10	Reference publications	(2011) Potential Agents against Plasma Leakage.	ICAM1 TJP1 ZYX CAV1 CDH5 FYN FN1 SDC1 CDC42 CFL1	2.55E-07	PMID.22084722
10	Reference publications	(2012) Novel processed form of syndecan-1 shed from SCC-9 cells plays a role in cell migration.	MMP2 GAPDH LAMA5 THBS1 ANXA5 MMP14 FN1 SDC4 ANXA1 SDC1	2.55E-07	PMID.22905270
10	Reference publications	(2012) The Cytotoxicity Mechanism of 6-Shogaol-Treated HeLa Human Cervical Cancer Cells Revealed by Label-Free Shotgun Proteomics and Bioinformatics Analysis.	MYH9 ENO1 ANXA5 CALR CDC25C TUBB4B ANXA2 ANXA1 CFL1 VIM	2.55E-07	PMID.23243437
12	Reference publications	(2011) Pathophysiological mechanisms in antiphospholipid syndrome.	MMP2 CCL2 VWF ICAM1 FLT1 ANXA5 ITGA2 NR1I2 ANXA2 ANXA6 TLR4 ANXA1	2.55E-07	PMID.23487578
10	Reference publications	(2014) Tumor-derived exosomes: A message delivery system for tumor progression.	MMP2 PDGFRA KIT ANXA5 BCL2L1 ANXA2 ANXA6 FN1 ANXA1 VIM	3.61E-07	PMID.24778765
10	Reference publications	(2016) Endothelial Mechanosignaling: Does One Sensor Fit All?	ICAM1 NOS3 CDH5 FYN FN1 PTRF SDC4 DNM1 SDC1 CDC42	4.24E-07	PMID.27027326
10	Reference publications	(2017) Differential Impact of Single-Dose Fe Ion and X-Ray Irradiation on Endothelial Cell Transcriptomic and Proteomic Responses.	CCL2 VWF ICAM1 NOS3 ARF4 FLNC CAV1 CDH5 FN1 PTPN1	4.24E-07	PMID.28993729
11	Reference publications	(2012) Comparative expression profiling of distinct T cell subsets undergoing oxidative stress.	ENO1 ANXA5 TUBA1A LCK TPM4 TPM3 GSTO1 FLNA TPM2 G6PD CFL1	4.78E-07	PMID.22911781
10	Reference publications	(2015) Novel human-derived extracellular matrix induces in vitro and in vivo vascularization and inhibits fibrosis.	MMP2 LAMA4 LAMA5 THBS1 ICAM1 ANXA5 ANXA2 ANXA6 FN1 ANXA1	4.78E-07	PMID.25725553
11	Reference publications	(2007) The extracellular matrix and blood vessel formation: not just a scaffold.	MMP2 LAMA4 THBS1 VWF TJP1 FLT1 MMP14 CDH5 FN1 SDC4 SDC1	5.30E-07	PMID.17488472
8	Reference publications	(2016) ARHGAP10, downregulated in ovarian cancer, suppresses tumorigenicity of ovarian cancer cells.	GAPDH PLEK ANXA5 PLK1 FN1 CDC42 ARF1 MCM3	5.30E-07	PMID.27010858
9	Reference publications	(2016) Proteome analysis of human amniotic mesenchymal stem cells (hA-MSCs) reveals impaired antioxidant ability, cytoskeleton and metabolic functionality in maternal obesity.	GAPDH ENO1 HSPB1 ICAM1 ANXA5 ANXA2 ANXA6 ANXA1 VIM	5.30E-07	PMID.27125468
10	Reference publications	(2016) Progressive muscle proteome changes in a clinically relevant pig model of Duchenne muscular dystrophy.	ANXA5 FLNC CAV1 TPM4 ANXA2 ANXA6 TPM3 ANXA1 TPM2 VIM	5.30E-07	PMID.27634466
10	Reference publications	(2009) Molecular mechanisms of endothelial hyperpermeability: implications in inflammation.	MMP2 ICAM1 TJP1 FLT1 NR1I2 LCK CAV1 CDH5 FYN CDC42	6.29E-07	PMID.19563700
11	Reference publications	(2011) Blood-brain barrier pathophysiology in traumatic brain injury.	MMP2 CCL2 THBS1 ICAM1 TJP1 FLT1 APP NR1I2 CDH5 TLR4 ABCB1	6.29E-07	PMID.22299022
11	Reference publications	(2015) Neutrophil migration under normal and sepsis conditions.	MYH9 MMP2 CCL2 ICAM1 TJP1 KIT NOS3 CAV1 CDH5 TLR4 ANXA1	6.29E-07	PMID.25567338
13	Reference publications	(2016) Extracellular Vesicles in Physiology, Pathology, and Therapy of the Immune and Central Nervous System, with Focus on Extracellular Vesicles Derived from Mesenchymal Stem Cells as Therapeutic Tools.	MMP2 GAPDH ICAM1 APP CCR5 ANXA5 SNCA ANXA2 ANXA6 FN1 ANXA1 CDC42 CFL1	6.29E-07	PMID.27199663
8	Reference publications	(2016) Quantitative proteomics reveals FLNC as a potential progression marker for the development of hepatocellular carcinoma.	GAPDH HSPB1 ITGA2 FLNC CAV1 FLNA CDC42 FLNB	6.29E-07	PMID.27626164
11	Reference publications	(2017) Multiple therapeutic effect of endothelial progenitor cell regulated by drugs in diabetes and diabetes related disorder.	MMP2 CCL2 VWF ICAM1 FLT1 KIT NOS3 CDH5 DPP4 DLL1 SDC4	6.29E-07	PMID.28859673
16	Reference publications	(2012) Amniotic fluid and amniotic membrane stem cells: marker discovery.	CCL2 THBS1 VWF ICAM1 KIT PLK1 CAV1 TPM4 ANXA2 FN1 TGM2 TPM3 CLIC4 TPM2 CFL1 VIM	6.56E-07	PMID.22701492
14	Reference publications	(2010) Comparative proteomics of human embryonic stem cells and embryonal carcinoma cells.	GAPDH MT2A HSPB1 APP ARF4 ZYX FLNC CAV1 FLNA ANXA1 PSIP1 LDHB CDC42 FLNB	6.99E-07	PMID.20104618
13	Reference publications	(2014) Discovery of new glomerular disease-relevant genes by translational profiling of podocytes in vivo.	MYH9 GAPDH PLEK THBS1 VWF ITGA2 FN1 MYH10 SDC4 TLR4 MYO1B FLNB CFL1	7.09E-07	PMID.24940801

10	Reference publications	(2015) Exosomes serve as tumour markers for personalized diagnostics owing to their important role in cancer metastasis.	CCL2 VWF ICAM1 TJP1 ANXA5 CDH5 ANXA2 ANXA6 FN1 ANXA1	7.64E-07	PMID.26095380
11	Reference publications	(....) Systems biology from virus to humans.	CCL2 GAPDH ENO1 ANXA5 CAV1 ANXA2 ANXA6 FLNA TLR4 ANXA1 CFL1	7.64E-07	PMID.26269748
12	Reference publications	(2014) Rho GAPs and GEFs: controlling switches in endothelial cell adhesion.	PLEK VWF ARHGAP31 ICAM1 TJP1 CDH5 FN1 ARHGEF26 EPHA2 ARHGEF15 FLNA CDC42	8.12E-07	PMID.24622613
14	Reference publications	(2016) Protein Co-Expression Analysis as a Strategy to Complement a Standard Quantitative Proteomics Approach: Case of a Glioblastoma Multiforme Study.	MYH9 ANXA5 CALR SNCA FN1 SFPQ FLNA DNM1 ANXA1 XRCC5 CAMK2A PDIA6 VIM PRKCSH	8.12E-07	PMID.27571357
10	Reference publications	(2011) Proteomic and transcriptomic analysis of heart failure due to volume overload in a rat aorto-caval fistula model provides support for new potential therapeutic targets - monoamine oxidase A and transglutaminase 2.	GAPDH ENO1 HSPB1 ANXA5 CKB CALR ANXA2 ANXA6 TGM2 ANXA1	8.48E-07	PMID.22078724
9	Reference publications	(2010) Endocytosis of nanomedicines.	ICAM1 APP NOS3 CALR LCK CAV1 FN1 PTRF CDC42	1.34E-06	PMID.20226220
9	Reference publications	(2010) The PI3K p110alpha isoform regulates endothelial adherens junctions via Pyk2 and Rac1.	CCL2 GAPDH PLEK ICAM1 TJP1 CDH5 FYN FN1 CDC42	1.34E-06	PMID.20308428
9	Reference publications	(2011) The physics of cancer: the role of physical interactions and mechanical forces in metastasis.	ICAM1 MMP14 ZFYX TPM4 FN1 TPM3 TPM2 FSCN1 SUN1	1.34E-06	PMID.21701513
11	Reference publications	(2011) Polymicrobial periodontal pathogen transcriptomes in calvarial bone and soft tissue.	MMP2 CCL2 THBS1 VWF APP MMP14 CDH5 FN1 SDC4 SDC1 LTB4R	1.34E-06	PMID.21896157
10	Reference publications	(2016) Stress-Induced Premature Senescence of Endothelial and Endothelial Progenitor Cells.	VWF ICAM1 FLT1 KIT NOS3 TENC1 CDH5 FN1 TGM2 DLL1	1.34E-06	PMID.27451101
9	Reference publications	(2017) Talin Modulation by a Synthetic N-Acylurea Derivative Reduces Angiogenesis in Human Endothelial Cells.	GAPDH VWF ICAM1 FLT1 ANXA5 NOS3 CDH5 FN1 TLN2	1.34E-06	PMID.28117756
13	Reference publications	(2017) Distinct proteome pathology of circulating microparticles in systemic lupus erythematosus.	MYH9 GAPDH PLEK ENO1 CAPN2 ANXA5 ITGA2 CALR ANXA2 ANXA1 G6PD CDC42 ARF1	1.34E-06	PMID.28649187
9	Reference publications	(1995) Identification of proteins that are abnormally regulated in differentiated cultured human keratinocytes.	ENO1 HSPB1 ANXA5 TPM4 ANXA2 ANXA6 TPM3 ANXA1 TPM2	1.34E-06	PMID.8824783
10	Reference publications	(2009) The role of tenascin-C in tissue injury and tumorigenesis.	MMP2 CCL2 THBS1 ICAM1 APP ANXA2 FN1 FAS SDC4 TLR4	1.38E-06	PMID.19838819
8	Reference publications	(2016) The protein kinase promiscuities in the cancer preventive mechanisms of NSAIDs.	FLT1 CSF1R KIT FYN EPHA2 RXRG RXRB RARG	1.42E-06	PMID.25714784
9	Reference publications	(2017) Perspective Insights of Exosomes in Neurodegenerative Diseases: A Critical Appraisal.	GAPDH ICAM1 APP ANXA5 SNCA ANXA2 ANXA6 DPP4 ANXA1	1.42E-06	PMID.29033828
9	Reference publications	(2018) Proteomic Analysis of Secretomes of Oncolytic Herpes Simplex Virus-Infected Squamous Cell Carcinoma Cells.	MMP2 THBS1 CALR FLNC ANXA2 FN1 COPA ANXA1 FSCN1	1.42E-06	PMID.29360750
16	Reference publications	(2009) Proteomic analysis of blastema formation in regenerating axolotl limbs.	MYH9 EHD4 HSPB1 PXDN ANXA5 CCT2 PLK1 TUBB4B CDH5 ANXA2 ANXA6 FN1 MYO1C ANXA1 PDIA6 FLNB	1.51E-06	PMID.19948009
11	Reference publications	(2013) The hCMECD3 cell line as a model of the human blood brain barrier.	CCL2 VWF ICAM1 TJP1 ANXA5 NR1I2 CDH5 ANXA2 ANXA6 ANXA1 ABCB1	1.51E-06	PMID.23531482
10	Reference publications	(2016) Mining kidney toxicogenomic data by using gene co-expression modules.	CCL2 ICAM1 LCK MAP4K4 ANXA2 FN1 FLNA TLR4 SDC1 VIM	1.51E-06	PMID.27724849
10	Reference publications	(2017) Caveolin-1 and Caveolin-2 Can Be Antagonistic Partners in Inflammation and Beyond.	MMP2 CCL2 NOS3 MMP14 CAV1 CDH5 FN1 PTRF TLR4 CDC42	1.51E-06	PMID.29250058
9	Reference publications	(2017) The molecular biology in wound healing & non-healing wound.	MMP2 CCL2 VWF ICAM1 NOS3 MMP14 CDH5 FN1 PRKCSH	1.55E-06	PMID.28712679
8	Reference publications	(2013) Interaction of proteins identified in human thyroid cells.	MYH9 CAPN2 ANXA5 ANXA2 FN1 FLNA ANXA1 CFL1	1.65E-06	PMID.23303277
8	Reference publications	(2015) Identification of proteins responsible for adriamycin resistance in breast cancer cells using proteomics analysis.	HSPB1 ANXA5 ANXA2 ANXA6 ANXA1 G6PD LDHB ABCB1	1.65E-06	PMID.25818003
11	Reference publications	(2015) Integrin traffic - the update.	ARF4 MMP14 DAB2 ZFYX CAV1 MAP4K4 FN1 SDC4 SDC1 CDC42 NUMB	1.81E-06	PMID.25663697
9	Reference publications	(2018) STAT3-RXR-Nrf2 activates systemic redox and energy homeostasis upon steep decline in pO2 gradient.	CCL2 GAPDH PPP3R1 CAPN2 ANXA5 ANXA2 ANXA6 ANXA1 VIM	1.81E-06	PMID.29078168
12	Reference publications	(2018) Exosome-Based Cell-Cell Communication in the Tumor Microenvironment.	MMP2 CCL2 ICAM1 TJP1 KIT ANXA5 BCL2L1 ANXA2 FN1 EPHA2 TLR4 SDC1	1.94E-06	PMID.29515996
8	Reference publications	(2015) Microparticles as novel biomarkers and therapeutic targets in coronary heart disease.	MMP2 CCL2 VWF ICAM1 FLT1 CSF1R ANXA5 NOS3	2.00E-06	PMID.25591573
10	Reference publications	(2013) Signaling pathways in exosomes biogenesis, secretion and fate.	GAPDH ENO1 ICAM1 APP ANXA5 SNCA ANXA2 ANXA6 ANXA1 CFL1	2.03E-06	PMID.24705158
9	Reference publications	(2016) Genome-wide analysis of Musashi-2 targets reveals novel functions in governing epithelial cell migration.	ITGB4 GAPDH LAMA4 THBS1 ANXA5 ITGA2 DLL1 FLNB NUMB	2.05E-06	PMID.27034466
9	Reference publications	(2017) Protein and chemotherapy profiling of extracellular vesicles harvested from therapeutic induced senescent triple negative breast cancer cells.	GAPDH LAMA5 ANXA5 ANXA2 ANXA6 FN1 ANXA1 NR1H4 ABCB1	2.44E-06	PMID.28991260
8	Reference publications	(2005) Proteomic analysis of cellular response to osmotic stress in thick ascending limb of Henle's loop (TALH) cells.	GAPDH ENO1 ANXA5 CALR TPM4 ANXA2 ANXA6 ANXA1	2.45E-06	PMID.15975915
12	Reference publications	(2009) Inhibitor of DASH proteases affects expression of adhesion molecules in osteoclasts and reduces myeloma growth and bone disease.	ITGB4 MMP2 GAPDH LAMA4 THBS1 COL8A1 ICAM1 ITGA2 MMP14 FN1 DPP4 SDC1	2.45E-06	PMID.19388929
8	Reference publications	(2012) Cytoskeleton as an emerging target of anthrax toxins.	PLEK HSPB1 TJP1 FLT1 CDH5 FYN CDC42 CFL1	2.45E-06	PMID.22474568
10	Reference publications	(2011) Quantitative proteomic and interaction network analysis of cisplatin resistance in HeLa cells.	ANXA5 DDB1 CALR ANXA2 ANXA6 GSTO1 ANXA1 XRCC5 G6PD PDIA6	2.51E-06	PMID.21637840
10	Reference publications	(2016) The biology of extracellular vesicles with focus on platelet microparticles and their role in cancer development and progression.	GAPDH CCR5 ANXA5 ITGA2 MMP14 ANXA2 ANXA6 DPP4 ANXA1 ABCB1	2.51E-06	PMID.27629289

9	Reference publications	(2016) Differentiation of Human Embryonic Stem Cells to Endothelial Progenitor Cells on Laminins in Defined and Xeno-free Systems.	MMP2 GAPDH LAMA4 VWF FLT1 ITGA2 MMP14 CDH5 FN1	2.72E-06	PMID.27693424
12	Reference publications	(2015) Human miR-221222 in Physiological and Atherosclerotic Vascular Remodeling.	MMP2 CCL2 ICAM1 KIT NOS3 CAV1 CDH5 TPM4 TPM3 TLR4 TPM2 CDC42	2.76E-06	PMID.26221589
9	Reference publications	(2016) A genome landscape of SRSF3-regulated splicing events and gene expression in human osteosarcoma U2OS cells.	GAPDH CDC25B MELK PLK1 MAP4K4 CDH5 ANXA1 G6PD NUMB	3.18E-06	PMID.26704980
9	Reference publications	(2016) Functional and Biological Role of Endothelial Precursor Cells in Tumour Progression: A New Potential Therapeutic Target in Haematological Malignancies.	CCL2 VWF FLT1 KIT NOS3 JAG2 CDH5 FN1 DLL1	3.18E-06	PMID.26788072
10	Reference publications	(2017) Platelets and cancer angiogenesis nexus.	MMP2 THBS1 VWF ICAM1 FLT1 KIT ITGA2 NOS3 MMP14 FN1	3.18E-06	PMID.28681240
8	Reference publications	(2010) PPARalpha is essential for microparticle-induced differentiation of mouse bone marrow-derived endothelial progenitor cells and angiogenesis.	THBS1 ICAM1 FLT1 CSF1R ANXA5 NOS3 CDH5 FN1	3.51E-06	PMID.20811625
10	Reference publications	(2012) Endothelial progenitor cells in atherosclerosis.	CCL2 VWF ICAM1 FLT1 KIT CCR5 NOS3 CDH5 FN1 DPP4	3.51E-06	PMID.22652782
12	Reference publications	(2015) Endothelial progenitor cells in ischemic stroke: an exploration from hypothesis to therapy.	MMP2 CCL2 THBS1 VWF ICAM1 FLT1 KIT CCR5 NOS3 FN1 DPP4 CDC42	3.51E-06	PMID.25888494
11	Reference publications	(2013) Systems biology analysis of Brucella infected Peyer's patch reveals rapid invasion with modest transient perturbations of the host transcriptome.	MYH9 GAPDH PRKCG AKT3 FLT1 KIT BCL2L1 MYH10 SPTAN1 SDC1 CDC42	3.54E-06	PMID.24349118
9	Reference publications	(2014) Comparative proteomic profiling of pancreatic ductal adenocarcinoma cell lines.	ITGB4 MYH9 GAPDH CAV1 FN1 FLNA SDC1 FLNB VIM	3.54E-06	PMID.25518923
9	Reference publications	(2016) Microarray analyses to quantify advantages of 2D and 3D hydrogel culture systems in maintaining the native valvular interstitial cell phenotype.	MMP2 GAPDH LAMA4 KIT ITGA2 MMP14 FN1 TPM2 FLNB	3.54E-06	PMID.26433490
10	Reference publications	(2013) Quantitative proteomic analysis of gingival crevicular fluid in different periodontal conditions.	MYH9 HSPB1 ANXA5 TPM4 ANXA2 ANXA6 TPM3 ANXA1 TPM2 CFL1	3.78E-06	PMID.24098404
11	Reference publications	(2011) Acute lung injury: how macrophages orchestrate resolution of inflammation and tissue repair.	ITGB4 CCL2 THBS1 ICAM1 TJP1 KIT CDH5 FN1 TLR4 ANXA1 LTB4R	3.86E-06	PMID.22566854
11	Reference publications	(2012) Motility, survival, and proliferation.	PLEK HSPB1 BCL2L1 CAV1 TPM4 FN1 FAS TPM3 TPM2 CDC42 CFL1	3.86E-06	PMID.23728975
9	Reference publications	(2013) A bright monomeric green fluorescent protein derived from Branchiostoma lanceolatum.	CCL2 TJP1 CALR ZYX CAV1 CDH5 FLNA FSCN1 VIM	3.95E-06	PMID.23524392
12	Reference publications	(2009) Bone marrow microenvironment and the identification of new targets for myeloma therapy.	MMP2 HSPB1 ICAM1 FLT1 KIT BCL2L1 JAG2 CAV1 FN1 DLL1 SDC1 XRCC5	4.02E-06	PMID.18843284
8	Reference publications	(2012) The tipping point for combination therapy: cancer vaccines with radiation, chemotherapy, or targeted small molecule inhibitors.	BCL2L2 ICAM1 FLT1 KIT BCL2L1 CALR FAS TLR4	4.02E-06	PMID.22595055
8	Reference publications	(2012) The Rho-guanine nucleotide exchange factor Trio controls leukocyte transendothelial migration by promoting docking structure formation.	ICAM1 FLNC CDH5 FN1 ARHGEF26 FLNA CDC42 FLNB	4.02E-06	PMID.22696684
8	Reference publications	(2016) A humanized anti-CD26 monoclonal antibody inhibits cell growth of malignant mesothelioma via retarded G2M cell cycle transition.	GAPDH CDC25B KIT CDC25A CDC25C CAV1 FN1 DPP4	4.02E-06	PMID.27134571
14	Reference publications	(2015) Emerging risk biomarkers in cardiovascular diseases and disorders.	MMP2 CCL2 HSPB1 VWF ICAM1 CCR5 ANXA5 CDH5 ANXA2 ANXA6 DPP4 TLR4 ANXA1 ARF1	4.06E-06	PMID.25949827
9	Reference publications	(2011) Purification of tropomyosin, paramyosin, actin, tubulin, troponin and kinases for chemoproteomics and its application to different scientific fields.	MYH9 ANXA5 TPM4 ANXA2 ANXA6 MYH10 TPM3 ANXA1 TPM2	4.40E-06	PMID.21876731
10	Reference publications	(2010) Proteomic study of activated Taenia solium oncospheres.	GAPDH CSF1R ANXA5 TPM4 ANXA2 ANXA6 FN1 TPM3 ANXA1 TPM2	4.45E-06	PMID.20144663
7	Reference publications	(2017) SR-BI Mediated Transcytosis of HDL in Brain Microvascular Endothelial Cells Is Independent of Caveolin, Clathrin, and PDZK1.	GAPDH TJP1 NOS3 CAV1 CDH5 PTPN1 CDC42	4.59E-06	PMID.29163190
8	SMART Domains	c4 zinc finger in nuclear hormone receptors	RORA RORC RARB NR1I2 RXRG RXRB RARG NR1H4	1.69E-06	SM00399
8	SMART Domains	Ligand binding domain of hormone receptors	RORA RORC RARB NR1I2 RXRG RXRB RARG NR1H4	1.69E-06	SM00430
13	SMART Domains	Serine/Threonine protein kinases, catalytic domain	MAP2K5 PRKCG AKT3 MELK PLK1 BRSK1 PRKCH MAP4K4 SLK CAMK2B CAMK2A DYRK1A CAMK1D	2.20E-05	SM00220
6	SMART Domains	Phosphotyrosine-binding domain, phosphotyrosine-interaction (PI) domain	DAB2 TENC1 RGS12 TBC1D4 NUMB APBA2	2.20E-05	SM00462
7	SMART Domains	Tyrosine kinase, catalytic domain	PDGFRA FLT1 CSF1R KIT LCK FYN EPHA2	3.00E-04	SM00219
4	SMART Domains	Annexin repeats	ANXA5 ANXA2 ANXA6 ANXA1	3.00E-04	SM00335
3	SMART Domains	BH4 Bcl-2 homology region 4	BCL2L2 BCL2L1 BCL2	3.20E-04	SM00265
6	SMART Domains	Calponin homology domain	CNN2 FLNC FLNA CNN3 FLNB SPTBN2	3.70E-04	SM00033
4	SMART Domains	Tubulin/FtsZ family, C-terminal domain	TUBB4A TUBA1A TUBA1C TUBB4B	9.00E-04	SM00865
4	SMART Domains	Tubulin/FtsZ family, GTPase domain	TUBB4A TUBA1A TUBA1C TUBB4B	9.40E-04	SM00864
3	SMART Domains	Filamin-type immunoglobulin domains	FLNC FLNA FLNB	0.0016	SM00557
4	SMART Domains	von Willebrand factor (vWF) type C domain	PXDN THBS1 VWF JAG2	0.0028	SM00214
3	SMART Domains	BCL (B-Cell lymphoma)	BCL2L2 BCL2L1 BCL2	0.0028	SM00337
4	SMART Domains	Myosin. Large ATPases.	MYH9 MYO1C MYH10 MYO1B	0.0034	SM00242
2	SMART Domains	amyloid A4	APLP1 APP	0.0053	SM00006
9	SMART Domains	Pleckstrin homology domain.	ARHGEF5 PLEK AKT3 NGEF FERMT3 DOK4 ARHGEF26 DNM1 SPTBN2	0.0053	SM00233
2	SMART Domains	delta serrate ligand	JAG2 DLL1	0.0069	SM00051
3	SMART Domains	ARF-like small GTPases	ARF3 ARF4 ARF1	0.0074	SM00177
3	SMART Domains	Rhodanese Homology Domain	CDC25B CDC25A CDC25C	0.0074	SM00450
4	SMART Domains	Guanine nucleotide exchange factor for Rho/Rac/Cdc42-like GTPases	ARHGEF5 NGEF ARHGEF26 ARHGEF15	0.0152	SM00325
7	SMART Domains	Src homology 3 domains	ARHGEF5 NGEF TJP1 LCK FYN ARHGEF26 SPTAN1	0.0152	SM00326
4	SMART Domains	Short calmodulin-binding motif containing conserved Ile and Gln residues.	MYH9 MYO1C MYH10 MYO1B	0.0319	SM00015
4	SMART Domains	von Willebrand factor (vWF) type A domain	ITGB4 VWF ITGA2 XRCC5	0.0331	SM00327
4	SMART Domains	Immunoglobulin like	PDGFRA ICAM1 CSF1R KIT	0.0356	SM00410

2	SMART Domains	Fibronectin type 2 domain	MMP2 FN1	0.0357	SM00059
2	SMART Domains	putative band 4.1 homologues' binding motif	SDC4 SDC1	0.0357	SM00294
2	SMART Domains	Phosphotyrosine-binding domain	DOK4 TLN2	0.0357	SM01244
2	SMART Domains	Prolyl 4-hydroxylase alpha subunit homologues.	PLOD1 PLOD2	0.0402	SM00702
130	UniProt Keywords	Phosphoprotein	RCN1 ARHGEF5 MAP2K5 ITGB4 MYH9 MMP2 EHD4 GAPDH GNB4 PPP3R1 PLEK ENO1 MT2A CDC25B HSPB1 BCL2L2 PXDN PDGFRA RORA DNAJB6 CNN2 PRKCG AKT3 NGEF TUBB4A ARHGAP31 CAD ADD1 ICAM1 FERMT3 TJP1 FLT1 PLOD2 APP CSF1R KIT CCRS5 ANXA5 NOS3 MELK CKB CCT2 PLK1 TUBA1A TUBA1C DDB1 BCL2L1 CDC25A SDPR ARF4 MMP14 BRSK1 DAB2 TENC1 NQO1 CDC25C ZYX FLNC JAG2 PRKCH RARB LCK SNCA CAV1 RG512 TUBB4B USP1 MAP4K4 CDH5 DOK4 PTMA ANXA2 ANXA6 FYN FAS ARHGEF26 PTRF SFPQ EPHA2 MYO1C MYH10 ARHGEF15 TGM2 DLL1 ARHGAP30 COPA TPM3 GSTO1 SLK FLNA CNN3 PTPN1 SPTAN1 DNM1 CLIC4 ANXA1 TBC1D4 PSIP1 SDC1 FSCN1 XRCC5 MYO1B G6PD PPP3CA CAMK2B LDHB LTB4R BCL2 CAMK2A DYRK1A SEPT7 PAICS CDC42 SUN1 PDIA6 TOP2B WEE1 FLNB PBK SPTBN2 CFL1 VIM NR1H4 NUMB APBA2 TLN2 PRKCSH ABCB1 CAMK1D MCM3	1.12E-20	KW-0597
15	UniProt Keywords	Calmodulin-binding	MYH9 CNN2 ADD1 TJP1 NOS3 FAS MYO1C MYH10 CNN3 SPTAN1 MYO1B PPP3CA CAMK2B CAMK2A CAMK1D	1.28E-09	KW-0112
45	UniProt Keywords	Nucleotide-binding	MAP2K5 MYH9 EHD4 ARF3 PDGFRA PRKCG AKT3 TUBB4A CAD FLT1 CSF1R KIT MELK CKB CCT2 PLK1 TUBA1A TUBA1C ARF4 BRSK1 PRKCH LCK TUBB4B MAP4K4 FYN EPHA2 MYO1C MYH10 SLK DNM1 XRCC5 MYO1B CAMK2B CAMK2A DYRK1A SEPT7 PAICS CDC42 TOP2B WEE1 PBK ARF1 ABCB1 CAMK1D MCM3	1.28E-09	KW-0547
64	UniProt Keywords	Acetylation	MAP2K5 MYH9 EHD4 GAPDH GNB4 PLEK ENO1 MT2A HSPB1 BCL2L2 CNN2 AKT3 CAD ADD1 CAPN2 ANXA5 CCT2 PLK1 TUBA1A TUBA1C DDB1 SDPR DAB2 CALR CDC25C STXB6 ZYX SNCA CAV1 TUBB4B MAP4K4 PTMA ANXA2 ANXA6 PTRF SFPQ MYO1C MYH10 TGM2 TPM3 GSTO1 FLNA CNN3 PTPN1 SPTAN1 CLIC4 ANXA1 TBC1D4 FSCN1 XRCC5 G6PD PPP3CA LDHB SEPT7 PAICS TOP2B FLNB PBK SPTBN2 CFL1 ARF1 VIM NR1H4 MCM3	1.73E-09	KW-0007
16	UniProt Keywords	Actin-binding	MYH9 CNN2 ADD1 FLNC MYO1C MYH10 TPM3 FLNA CNN3 SPTAN1 FSCN1 MYO1B CAMK2B FLNB SPTBN2 CFL1	8.64E-08	KW-0009
49	UniProt Keywords	Ubl conjugation	MYH9 GAPDH ENO1 PDGFRA RORA PRKCG AKT3 ICAM1 FLT1 APP CSF1R KIT ANXA5 CCT2 PLK1 DDB1 BCL2L1 CDC25A NQO1 FLNC SNCA CAV1 RG512 USP1 PTMA ANXA2 PTRF SFPQ EPHA2 ARHGEF15 DLL1 FLNA ANXA1 PSIP1 FSCN1 XRCC5 MYO1B BCL2 SUN1 RARG TOP2B WEE1 FLNB PBK CFL1 VIM NR1H4 NUMB CAMK1D	8.64E-08	KW-0832
65	UniProt Keywords	Disease	ARHGEF5 PLOD1 ITGB4 MYH9 CYP24A1 MMP2 APLP1 LAMA4 GNB4 HSPB1 PXDN PDGFRA VWF RORA DNAJB6 PRKCG AKT3 TUBB4A CAD FERMT3 PLOD2 APP CSF1R KIT CCRS5 TUBA1A MMP14 DAB2 RORC FLNC RARB CYP2R1 LCK SNCA CAV1 TUBB4B FYN FAS PTRF EPHA2 MYH10 COPA TPM3 FLNA SPTAN1 DNM1 TLR4 TBC1D4 XRCC5 G6PD PPP3CA CAMK2B LDHB BCL2 CAMK2A DYRK1A CDC42 TOP2B FLNB SPTBN2 ARF1 VIM NR1H4 TLN2 PRKCSH	8.64E-08	KW-9995
35	UniProt Keywords	ATP-binding	MAP2K5 MYH9 EHD4 PDGFRA PRKCG AKT3 CAD FLT1 CSF1R KIT MELK CKB CCT2 PLK1 BRSK1 PRKCH LCK MAP4K4 FYN EPHA2 MYO1C MYH10 SLK XRCC5 MYO1B CAMK2B CAMK2A DYRK1A PAICS TOP2B WEE1 PBK ABCB1 CAMK1D MCM3	1.12E-07	KW-0067
23	UniProt Keywords	Kinase	MAP2K5 PDGFRA PRKCG AKT3 FLT1 CSF1R KIT MELK CKB PLK1 BRSK1 PRKCH LCK MAP4K4 FYN EPHA2 SLK CAMK2B CAMK2A DYRK1A WEE1 PBK CAMK1D	1.56E-07	KW-0418
76	UniProt Keywords	Cytoplasm	ARHGEF5 MYH9 MMP2 APLP1 GAPDH RBP1 PPP3R1 ENO1 CDC25B HSPB1 ARF3 DNAJB6 PRKCG AKT3 NGEF TUBB4A CAD ADD1 FLT1 APP KIT CAPN2 NOS3 CKB CCT2 PLK1 TUBA1A TUBA1C DDB1 BCL2L1 SDPR MMP14 BRSK1 DAB2 NQO1 CALR STXB6 ZYX FLNC PRKCH RARB LCK SNCA RG512 TUBB4B MAP4K4 ANXA6 FYN PTRF SFPQ MYO1C COPA TPM3 GSTO1 SLK FLNA SPTAN1 DNM1 CLIC4 ANXA1 TBC1D4 PIR FSCN1 PPP3CA CAMK2B LDHB SEPT7 CDC42 TOP2B FLNB SPTBN2 CFL1 ARF1 VIM TLN2 CAMK1D	1.80E-07	KW-0963
53	UniProt Keywords	Disease mutation	PLOD1 ITGB4 MYH9 CYP24A1 MMP2 LAMA4 GNB4 HSPB1 PXDN VWF RORA DNAJB6 PRKCG AKT3 TUBB4A CAD FERMT3 PLOD2 APP CSF1R KIT TUBA1A MMP14 RORC FLNC RARB CYP2R1 LCK SNCA CAV1 TUBB4B FAS EPHA2 MYH10 COPA TPM3 FLNA SPTAN1 DNM1 G6PD PPP3CA LDHB BCL2 CAMK2A CDC42 TOP2B FLNB SPTBN2 ARF1 VIM NR1H4 TLN2 PRKCSH	7.32E-07	KW-0225
10	UniProt Keywords	Tyrosine-protein kinase	MAP2K5 PDGFRA FLT1 CSF1R KIT LCK FYN EPHA2 DYRK1A WEE1	1.40E-06	KW-0829
26	UniProt Keywords	Methylation	ARHGEF5 MYH9 GAPDH RBP1 HSPB1 BCL2L2 RORA DNAJB6 TUBA1A TUBA1C BRSK1 TENC1 ZYX FLNC RG512 SFPQ MYO1C MYH10 COPA CNN3 DNM1 RXRB TBC1D4 CDC42 RARG NR1H4	3.38E-06	KW-0488
29	UniProt Keywords	Cytoskeleton	MYH9 GAPDH CDC25B HSPB1 TUBB4A ADD1 NOS3 PLK1 TUBA1A TUBA1C BCL2L1 BRSK1 ZYX FLNC TUBB4B TPM3 FLNA SPTAN1 DNM1 CLIC4 FSCN1 CAMK2B SEPT7 CDC42 FLNB SPTBN2 CFL1 VIM TLN2	5.71E-06	KW-0206
22	UniProt Keywords	Cell junction	ARHGEF5 ITGB4 PRKCG ARHGAP31 FERMT3 TJP1 BCL2L1 BRSK1 TENC1 ZYX SNCA RG512 CDH5 EPHA2 DPP4 DLL1 CLIC4 FSCN1 CAMK2B CAMK2A ARF1 TLN2	5.84E-06	KW-0965
17	UniProt Keywords	Cell adhesion	ITGB4 MYH9 APLP1 LAMA4 LAMA5 THBS1 COL8A1 VWF ICAM1 FERMT3 APP ITGA2 ZYX CDH5 EPHA2 MYH10 DPP4	1.32E-05	KW-0130
23	UniProt Keywords	Calcium	RCN1 MMP2 EHD4 PPP3R1 PXDN THBS1 PRKCG CAPN2 ANXA5 ITGA2 NOS3 MELK MMP14 CALR JAG2 CDH5 ANXA2 ANXA6 TGM2 SPTAN1 ANXA1 PRKCSH CAMK1D	2.04E-05	KW-0106
34	UniProt Keywords	Isopeptide bond	GAPDH ENO1 RORA TUBB4A APP ANXA5 CCT2 PLK1 TUBA1A DDB1 NQO1 CAV1 RG512 TUBB4B PTMA ANXA2 PTRF SFPQ DLL1 FLNA ANXA1 PSIP1 FSCN1 XRCC5 MYO1B SUN1 RARG TOP2B FLNB PBK CFL1 VIM NR1H4 CAMK1D	3.25E-05	KW-1017
14	UniProt Keywords	Serine/threonine-protein kinase	MAP2K5 PRKCG AKT3 MELK PLK1 BRSK1 PRKCH MAP4K4 SLK CAMK2B CAMK2A DYRK1A PBK CAMK1D	9.51E-05	KW-0723
4	UniProt Keywords	Annexin	ANXA5 ANXA2 ANXA6 ANXA1	1.30E-04	KW-0041
113	UniProt Keywords	Alternative splicing	RCN1 ARHGEF5 MAP2K5 PLOD1 ITGB4 MYH9 CYP24A1 MMP2 APLP1 GAPDH LAMA4 RBP1 CDC25B BCL2L2 PXDN LAMA5 ARF3 PDGFRA THBS1 VWF RORA DNAJB6 CNN2 PRKCG AKT3 NGEF ADD1 EXOC68 FERMT3 TJP1 FLT1 PLOD2 APP CSF1R KIT NPC1L1 CAPN2 NOS3 MELK CCT2 TUBA1A DDB1 BCL2L1 CDC25A BRSK1 DAB2 TENC1 NQO1 CDC25C STXB6 ZYX FLNC JAG2 PRKCH RARB NR12 LCK SNCA RG512 MAP4K4 CDH5 PTMA ANXA2 ANXA6 FYN FAS ARHGEF26 PTRF SFPQ EPHA2 MYO1C MYH10 TGM2 DLL1 ARHGAP30 COPA TPM3 GSTO1 SLK FLNA CNN3 SDC4 SPTAN1 DNM1 TLR4 RXRB TBC1D4 PSIP1 MYO1B G6PD PPP3CA CAMK2B BCL2 CAMK2A DYRK1A SEPT7 PAICS CDC42 SUN1 PDIA6 RARG TOP2B WEE1 FLNB PBK SPTBN2 NR1H4 NUMB APBA2 PRKCSH ABCB1 CAMK1D MCM3	1.50E-04	KW-0025
4	UniProt Keywords	Calcium/phospholipid-binding	ANXA5 ANXA2 ANXA6 ANXA1	1.50E-04	KW-0111
14	UniProt Keywords	Host-virus interaction	PDGFRA ICAM1 CCR5 ITGA2 DDB1 CDC25C ZYX LCK CAV1 FYN EPHA2 PSIP1 DYRK1A VIM	2.60E-04	KW-0945
21	UniProt Keywords	Cell projection	ARHGEF5 PDGFRA PRKCG NGEF ARHGAP31 FERMT3 TJP1 APP RG512 ARHGEF26 EPHA2 MYO1C MYH10 DPP4 ARHGEF15 ANXA1 FSCN1 PPP3CA CAMK2A SEPT7 CFL1	3.40E-04	KW-0966
5	UniProt Keywords	Nitration	CKB TUBA1A TUBA1C DNM1 PPP3CA	7.50E-04	KW-0944
10	UniProt Keywords	Extracellular matrix	MMP2 LAMA4 PXDN LAMA5 THBS1 COL8A1 VWF CALR ANXA2 MMRN2	0.001	KW-0272
9	UniProt Keywords	Proto-oncogene	ARHGEF5 PDGFRA CSF1R KIT RARB LCK FYN TPM3 BCL2	0.0017	KW-0656

4	UniProt Keywords	Basement membrane	LAMA4 LAMA5 COL8A1 ANXA2	0.0046	KW-0084
10	UniProt Keywords	GTP-binding	ARF3 TUBB4A TUBA1A TUBA1C ARF4 TUBB4B DNM1 SEPT7 CDC42 ARF1	0.0062	KW-0342
6	UniProt Keywords	Protein phosphatase	CDC25B CDC25A TENC1 CDC25C PTPN1 PPP3CA	0.0079	KW-0904
7	UniProt Keywords	Myristate	PPP3R1 ARF3 NOS3 ARF4 LCK FYN ARF1	0.0084	KW-0519
4	UniProt Keywords	Myosin	MYH9 MYO1C MYH10 MYO1B	0.0087	KW-0518
9	UniProt Keywords	Iron	PLOD1 CYP24A1 PXDN PLOD2 APP NOS3 CYP2R1 PIR PPP3CA	0.0103	KW-0408
4	UniProt Keywords	S-nitrosylation	GAPDH ANXA5 PTPN1 VIM	0.0114	KW-0702
57	UniProt Keywords	Repeat	RCN1 ITGB4 MMP2 LAMA4 GNB4 PPP3R1 PLEK PXDN LAMA5 PDGFRA THBS1 COL8A1 VWF CNN2 PRKCG CAD ICAM1 TJP1 FLT1 CSF1R KIT CAPN2 ANXA5 ITGA2 PLK1 DDB1 MP14 CALR ZYG FLNC JAG2 PRKCH SNCA RGS12 CDH5 ANXA2 ANXA6 FAS PTRF SFPQ EPHA2 MYO1C DLL1 COPA FLNA CNN3 SPTAN1 TLR4 ANXA1 TBC1D4 MYO1B PDIA6 FLNB SPTBN2 APBA2 PRKCSH ABCB1	0.0133	KW-0677
2	UniProt Keywords	Congenital generalized lipodystrophy	CAV1 PTRF	0.0137	KW-1022
46	UniProt Keywords	Metal-binding	RCN1 MAP2K5 PLOD1 CYP24A1 MMP2 EHD4 APLP1 PPP3R1 ENO1 MT2A PXDN RORA PRKCG CAD PLOD2 APP KIT CAPN2 ITGA2 NOS3 MMP14 BRSK1 TENC1 CALR ZYG RORC PRKCH RARB CYP2R1 NR1I2 SNCA CDH5 FYN RXRG TGM2 SPTAN1 RXRB ANXA1 PIR PPP3CA CAMK2A RARG TOP2B WEE1 NR1H4 PRKCSH	0.0147	KW-0479
27	UniProt Keywords	Transferase	MAP2K5 GAPDH PDGFRA PRKCG AKT3 CAD FLT1 CSF1R KIT MELK CKB PLK1 BRSK1 PRKCH LCK MAP4K4 FYN EPHA2 TGM2 GSTO1 SLK CAMK2B CAMK2A DYRK1A WEE1 PBK CAMK1D	0.0156	KW-0808
6	UniProt Keywords	Inflammatory response	CCL2 CSF1R TLR4 ANXA1 NR1H4 CAMK1D	0.0161	KW-0395
3	UniProt Keywords	Oxidation	GAPDH APP PTPN1	0.017	KW-0558
12	UniProt Keywords	Oxidoreductase	PLOD1 CYP24A1 GAPDH PXDN PLOD2 NOS3 NQO1 CYP2R1 PIR G6PD LDHB	0.0188	KW-0560
7	UniProt Keywords	SH3 domain	ARHGEF5 NGEF TJP1 LCK FYN ARHGEF26 SPTAN1	0.019	KW-0728
4	UniProt Keywords	Host cell receptor for virus entry	ICAM1 CCR5 ITGA2 EPHA2	0.019	KW-1183
41	UniProt Keywords	Cell membrane	ITGB4 EHD4 APLP1 PPP3R1 ENO1 PDGFRA PRKCG ADD1 TJP1 FLT1 APP CSF1R KIT NPC1L1 CCR5 CAPN2 NOS3 MELK TENC1 LCK CAV1 CDH5 FYN FAS PTRF EPHA2 MYO1C DPP4 DLL1 TLR4 CLIC4 ANXA1 PPP3CA LTB4R CAMK2A CDC42 PDIA6 CFL1 ARF1 TLN2 ABCB1	0.0197	KW-1003
5	UniProt Keywords	Endocytosis	APLP1 APP BCL2L1 DAB2 DNM1	0.0265	KW-0254
4	UniProt Keywords	Diabetes mellitus	CCR5 CAV1 PTRF TBC1D4	0.0268	KW-0219
5	UniProt Keywords	Angiogenesis	MMP2 COL8A1 FLT1 EPHA2 MMRN2	0.0297	KW-0037
11	UniProt Keywords	Apoptosis	APLP1 GAPDH BCL2L2 APP MELK BCL2L1 DAB2 FAS EPHA2 SLK BCL2	0.031	KW-0053
5	UniProt Keywords	Motor protein	MYH9 MYO1C MYH10 DNM1 MYO1B	0.031	KW-0505
9	UniProt Keywords	Synapse	PRKCG BCL2L1 BRSK1 SNCA RGS12 CAMK2B CAMK2A ARF1 TLN2	0.0383	KW-0770
3	UniProt Keywords	Sarcoplasmic reticulum	THBS1 CALR CAMK2B	0.0385	KW-0703
4	UniProt Keywords	ER-Golgi transport	ARF3 ARF4 COPA ARF1	0.0401	KW-0931
21	UniProt Keywords	Receptor	ITGB4 PDGFRA RORA ICAM1 FLT1 CSF1R KIT CCR5 ITGA2 RORC RARB NR1I2 FAS EPHA2 RXRG DPP4 TLR4 RXRB LTB4R RARG NR1H4	0.0432	KW-0675
3	UniProt Keywords	Notch signaling pathway	APP JAG2 DLL1	0.0454	KW-0914
2	UniProt Keywords	Heparan sulfate	SDC4 SDC1	0.0464	KW-0357

Supplemental Table 3B. Altered genes in CCM models with 2 validations enrichment data. An enrichment category was exported along with Figure 1 that detailed altered pathways involved with the identified 152 genes. Information provided in the table includes the number of enriched genes in each enrichment category, description of the category, genes specifically involved, FDR value, and the term name for each category (which includes GO terms if applicable). Among the exported pathways identified in this group, a filter search was applied to identify all enrichment data involved with angiogenesis specifically which are bolded and re-summarized in Table 1.