Category	Term	Count	P Value	Genes
GOTERM_BP_DIRECT	GO:0002376~immune system process	58	3.76E-22	MASP1, S100A8, LY86, S100A9, TLR2, HP, C1QC, TLR7, CFP, OASL1, CLEC4A2, LBP, MX1, CD300C2, PIK3CG, ADGRE1, SERPING1, CLEC4N, CD84, C1QA, C1QB, CD86, SERPINA3G, H2-AA, MST1R, PRDM1, CD300LB, CLEC5A, CD300LD, TNFAIP8L2, TNFRSF21, HMGB2, IFITM1, C3, FCNA, IL4RA, OAS3, IFI30, ALCAM, PTK2B, PSTPIP1, CSF1R, ZBP1, LGALS3, CFB, HCK, TLR13, CTLA4, ANXA1, H2-AB1, FCGR1, CD180, LCN2, PIRB, IFIT3, IRF7, H2-EB1, CD14
GOTERM_BP_DIRECT	GO:0007155~cell adhesion	55	2.80E-15	MYBPC2, ATP1B2, FERMT3, IGFBP7, POSTN, CDH22, WISP2, CGREF1, WISP1, CTGF, HPSE, TGFBI, CSF3R, COL12A1, CNTNAP1, CDH23, PARVG, PTPRF, PDPN, CERCAM, CD84, NCAM1, SIGLEC1, MFAP4, CYP1B1, TNC, ITGB2, ITGB3, CD24A, ITGAM, ALCAM, LPXN, COL6A6, PTK2B, COMP, ITGB6, PSTPIP1, EMB, GPNMB, COL8A1, SELPLG, THBS3, SPP1, FN1, THBS4, SVEP1, ADAM23, PCDH12, COL16A1, COL5A1, EPHA4, LYVE1, COL14A1, SRPX2, SULF1
GOTERM_BP_DIRECT	GO:0045087~innate immune response	49	6.03E-15	S100A8, MASP1, LY86, S100A9, TLR2, C1QC, TLR7, CFP, ANG, OASL1, CLEC4A2, LBP, MX1, C4B, SERPING1, CLEC4N, C1QA, CD84, C1QB, PRDM1, MST1R, TREM2, CLEC5A, TNFAIP8L2, HMGB2, IFITM1, C3, FCNA, OAS3, PTK2B, PSTPIP1, FCER1G, CSF1R, ZBP1, TYROBP, LGALS3, CFB, HCK, TLR13, ANXA1, FCGR1, CD180, LCN2, IFIT3,

				CYBB, TRIM59, IRF7, CLEC7A, CD14
GOTERM_BP_DIRECT	GO:0006954~inflammatory response	44	3.97E-14	TNFRSF21, C3AR1, HMGB2, S100A8, C3, CCR1, LY86, S100A9, CCL9, TLR2, CCL8, PF4, TLR7, CCL6, CXCL10, S1PR3, SLC11A1, CYP26B1, ITGB6, PSTPIP1, NOS2, ADAM8, CSF1R, SPP1, PIK3CG, BMP2, C5AR1, C4B, NCF1, HCK, TLR13, ANXA1, ACKR2, ECM1, CD180, CD163, CCL12, CYBB, CCR5, CCR2, PLA2G7, CLEC7A, PTAFR, CD14
GOTERM_BP_DIRECT	GO:0007049~cell cycle	44	2.36E-06	E2F1, KIF23, PRC1, DBF4, ANLN, AURKB, CGREF1, NCAPH, CDCA8, HMCN1, NCAPG2, INCENP, FBXO5, CCNA2, ASPM, CKAP2, CDK1, KIF11, MKI67, TRNP1, IKZF1, TPX2, NUSAP1, CENPE, BIRC5, CDC20, RACGAP1, UBE2C, KNSTRN, SMC2, MCM5, SMC4, CDKN1C, UHRF1, CCNB2, MAD2L1, DUSP1, PLK1, SPAG5, RGCC, KIF20B, BUB1B, CHAF1A, SMPD3
GOTERM_BP_DIRECT	GO:0043066~negative regulation of apoptotic process	34	0.00101077	IER3, MMP9, CLU, HSPA1B, TGFB2, TIMP1, GPX1, CASP3, PTK2B, COMP, ANGPT1, SCX, CSF1R, SPP1, ANGPTL4, FN1, BMP4, CDK1, LGALS3, HCK, NCKAP1L, BIRC5, PLAC8, KDR, PLAUR, IFIT3, MAD2L1, SFRP1, DUSP1, BCL2A1B, BTG2, UCP2, PLK1, CLEC5A
GOTERM_BP_DIRECT	GO:0051301~cell division	32	2.19E-06	KIF23, KIFC1, PRC1, ANLN, AURKB, CDCA8, NCAPH, HMCN1, NCAPG2, INCENP, FBXO5, CCNA2, ASPM, CDK1, KIF11, TPX2, NUSAP1, CENPE, CDC20, BIRC5, KNSTRN, UBE2C, RACGAP1, SMC2, MCM5, SMC4, MAD2L1, CCNB2, PLK1, SPAG5, KIF20B, BUB1B

GOTERM_BP_DIRECT	GO:0010628~positive regulation of gene expression	32	8.24E-06	E2F1, HMGB2, LDLR, STAR, TNC, VIM, IQGAP3, TLR2, PF4, ITGB3, TGFB2, ALDH1A2, SLC11A1, CTGF, CD46, CYP26B1, SERPINE1, NFIL3, SCX, FN1, EGR1, BMP4, CDK1, BMP2, IKZF1, RNF207, PLAUR, LCN2, INHBA, CCR5, RGCC, PRDM1
GOTERM_BP_DIRECT	GO:0008284~positive regulation of cell proliferation	32	0.00191316	PRC1, TNC, CRLF1, CLU, CXCL10, TGFB2, TIMP1, ALDH1A2, RAC2, FOLR2, PTK2B, CTGF, PTN, PDGFC, PAK1, SCX, MYC, CSF1R, FN1, BMP4, PTPN6, LGALS3, NTF3, HCK, CDC20, S100A13, PLAC8, KDR, PLA2G4A, SFRP1, KIF20B, HBEGF
GOTERM_BP_DIRECT	GO:0006508~proteolysis	30	0.01655723	AEBP1, MASP1, CNDP2, LGMN, MMP9, UCHL1, PAMR1, HP, ENPEP, MMP3, PCOLCE, ACE, CASP3, CD46, ADAMTS12, ADAM8, DPEP2, CTSZ, ADAM23, CFB, MMP19, ESPL1, KY, CTSS, MMP12, CTSK, ADAM1A, CTSC, CTSB, ADAMTS2
GOTERM_BP_DIRECT	GO:0007067~mitotic nuclear division	29	1.29E-07	KIF23, ANLN, AURKB, CDCA8, NCAPH, NCAPG2, INCENP, FBXO5, CCNA2, ASPM, TUBB3, CDK1, KIF11, TPX2, NUSAP1, CDC20, ESPL1, BIRC5, CENPE, KNSTRN, UBE2C, SMC2, SMC4, MAD2L1, CCNB2, PLK1, SPAG5, KIF20B, BUB1B
GOTERM_BP_DIRECT	GO:0006955~immune response	27	1.06E-06	CCR1, CCL9, OAS3, TLR2, CCL8, PF4, TLR7, CD24A, CCL6, CXCL10, HRH2, OASL1, NFIL3, PRG4, CTLA4, COLEC12, H2-AB1, CTSS, VAV1, WAS, CCL12, CCR5, FCGR2B, CCR2, H2-EB1, H2-AA, LCP2
GOTERM_BP_DIRECT	GO:0043065~positive regulation of apoptotic process	27	4.43E-05	TSPO, CYP1B1, MMP9, CLU, OSGIN1, ANKRD1, TGFB2, ALDH1A2, ACE, CASP3, HMOX1, TGM2, PTN, TOP2A, BMP4, NOX4, BMP2, PTPRF, NTF3,

				CTLA4, ANXA1, FRZB, PLA2G4A, NUPR1, SFRP1, DUSP1, BCL2A1B
GOTERM_BP_DIRECT	GO:0001525~angiogenesis	26	3.18E-07	RTN4, CYP1B1, ENPEP, CTGF, PTK2B, ANG, HMOX1, TGFBI, SERPINE1, ANGPT1, COL8A1, ADAM8, FN1, ANGPTL4, PIK3CG, BMP4, MMP19, CCDC80, ECM1, ANXA2, KDR, CCL12, SRPX2, PLXDC1, CCR2, HBEGF
GOTERM_BP_DIRECT	GO:0006915~apoptotic process	26	0.08454444	E2F1, TNFRSF21, S100A8, S100A9, GPR65, GPX1, CASP3, DYNLL1, COMP, HMOX1, PAK1, AATK, CKAP2, CDK1, C5AR1, NCF1, LGALS1, TPX2, BIRC5, TOX3, LSP1, LCN2, RASSF5, SERPINA3G, SULF1, BUB1B
GOTERM_BP_DIRECT	GO:0030335~positive regulation of cell migration	25	5.49E-08	C3AR1, FERMT3, CCR1, ITGB3, MMP3, LGR6, TGFB2, CXCL10, PTK2B, PDGFC, RHOD, PAK1, GPNMB, CSF1R, FN1, BMP4, BMP2, NTF3, PDPN, MYO1F, KDR, CORO1A, CARMIL1, HBEGF, COL1A1
GOTERM_BP_DIRECT	GO:0042493~response to drug	25	3.44E-04	PAM, CDK1, TSPO, HMGB2, HSP90AA1, STAR, LGALS1, MMP9, ANXA1, NCKAP1L, AQP7, TGFB2, KDR, LCN2, NCAM1, INHBA, CYBB, CD86, SFRP1, APOD, PTK2B, PTN, COL1A1, LOX, NNMT
GOTERM_BP_DIRECT	GO:0008285~negative regulation of cell proliferation	25	0.0019405	BMP4, CEBPA, NOX4, BMP2, CYP1B1, PTPRF, IFITM1, CLMN, TLR2, FRZB, SLFN1, TGFB2, IFIT3, HIST1H2AP, ALDH1A2, INHBA, RASSF5, WISP2, SFRP1, SERPINE2, BTG2, PTK2B, HMOX1, RGCC, CSF1R
GOTERM_BP_DIRECT	GO:0006935~chemotaxis	22	2.20E-10	PIK3CG, C3AR1, HMGB2, C5AR1, S100A8, CCR1, S100A9, CCL9, CCL8, ACKR2, NCKAP1L, PF4, ACKR4, CCL6, CXCL10, LSP1, CCL12, DOCK2, CCR5, RAC2, CCR2, PTAFR
GOTERM_BP_DIRECT	GO:0001666~response to hypoxia	22	1.35E-06	EGR1, NOX4, PAM, BMP2, TLR2, POSTN, KCNA5, TACC3,

				CD24A, KDR, TGFB2, PTGIS, ALAS2, PENK, PTK2B, UCP2, ANG, HMOX1, PAK1, NOS2, NPPA, ANGPTL4
GOTERM_BP_DIRECT	GO:0070374~positive regulation of ERK1 and ERK2 cascade	21	3.70E-06	NOX4, BMP4, BMP2, C5AR1, C3, CCR1, CCL9, TLR2, CCL8, ITGB3, CCL6, KDR, GLIPR2, CCL12, CTGF, PTK2B, ANGPT1, PDGFC, TREM2, GPNMB, CSF1R
GOTERM_BP_DIRECT	GO:0007568~aging	18	5.43E-05	NOX4, TSPO, COL3A1, ITGB2, SERPING1, AURKB, TIMP1, NCAM1, CDKN1C, CD86, PPP1R9A, APOD, PENK, SERPINF1, CTGF, UCP2, IFI27L2A, CTSC
GOTERM_BP_DIRECT	GO:0042127~regulation of cell proliferation	18	0.00132829	CEBPA, TRNP1, PRG4, HCK, TNC, IL4RA, ANXA1, S100A11, NR3C2, PF4, SPARC, TGFB2, CXCL10, PLA2G4A, PTK2B, SERPINE1, PRDM1, NOS2
GOTERM_BP_DIRECT	GO:0030593~neutrophil chemotaxis	17	5.32E-10	C5AR1, S100A8, LGALS3, S100A9, CCL9, CCL8, NCKAP1L, ITGB2, VAV1, ITGAM, CCL6, TGFB2, FCGR3, CCL12, FCER1G, CSF3R, SPP1
GOTERM_BP_DIRECT	GO:0045766~positive regulation of angiogenesis	17	2.07E-06	C3AR1, CYP1B1, C5AR1, LGALS3, C3, MMP9, ITGB2, ITGB3, ECM1, KDR, CYBB, PTGIS, PTK2B, LRG1, HMOX1, SERPINE1, HSPB1
GOTERM_BP_DIRECT	GO:0043524~negative regulation of neuron apoptotic process	17	7.25E-05	C5AR1, STAR, NTF3, LGMN, CRLF1, PRKCG, BIRC5, TOX3, KDR, CCL12, CORO1A, BTG2, PTK2B, HMOX1, MT1, ANGPT1, ADAM8
GOTERM_BP_DIRECT	GO:0032496~response to lipopolysaccharide	17	7.75E-04	TNFRSF21, HMGB2, C5AR1, S100A8, NCF2, TLR2, ACP5, PF4, SPARC, CXCL10, SLC11A1, ACE, PENK, LBP, NOS2, LOXL1, PTAFR
GOTERM_BP_DIRECT	GO:0071222~cellular response to lipopolysaccharide	17	0.00145026	ZFP36, MRC1, TSPO, HMGB2, STAR, FCGR4, ANKRD1, CD180, CXCL10, LCN2, CD86, NR1D1, SERPINE1, LBP, NOS2, CD300LB, CD14
GOTERM_BP_DIRECT	GO:0008283~cell proliferation	17	0.00244731	PTPN6, CDK1, MKI67, CFB, PDPN, NCF1, UCHL1, DACH1,

				ENPEP, AURKB, TACC3, GPX1, GLUL, UHRF1, TGFBI, MYC, CSF1R
GOTERM_BP_DIRECT	GO:0050729~positive regulation of inflammatory response	16	1.25E-09	S100A8, LDLR, S100A9, TLR2, CCL9, CCL8, CTSS, CCL6, CCL12, ACE, PLA2G4A, CCR5, SERPINE1, CCR2, TGM2, ADAM8
GOTERM_BP_DIRECT	GO:0016477~cell migration	16	0.0015656	PTPRF, ENPEP, ITGB3, SIRPA, CD24A, COL5A1, TGFB2, KDR, CORO1A, CTGF, ANG, CARMIL1, PSTPIP1, HBEGF, ADAMTS12, LCP1
GOTERM_BP_DIRECT	GO:0010629~negative regulation of gene expression	16	0.02825209	BMP4, HMGB2, BMP2, LDLR, CCR1, IQGAP3, TGFB2, ACE, SFRP1, SERPINF1, CTGF, CD46, SERPINE1, PRDM1, NOS2, MYC
GOTERM_BP_DIRECT	GO:0042060~wound healing	15	2.14E-06	S100A8, TNC, COL3A1, FCGR4, SPARC, MMP12, TGFB2, TIMP1, SLC11A1, HPSE, SERPINE1, COL1A1, LOX, PAK1, FN1
GOTERM_BP_DIRECT	GO:0001503~ossification	15	2.76E-06	BMP4, BMP2, IFITM1, CTGF, MMP9, FSTL3, MGP, PTN, SPARC, TMEM119, COL11A2, ECM1, COL5A2, SPP1, AHSG
GOTERM_BP_DIRECT	GO:0008360~regulation of cell shape	15	1.87E-04	PDPN, PLXNB1, HCK, ANXA1, RHOU, S100A13, KDR, CCL12, MYO10, CORO1A, PTK2B, PTN, PAKAP, CSF1R, FN1
GOTERM_BP_DIRECT	GO:0071356~cellular response to tumor necrosis factor	14	6.19E-05	CEBPA, ZFP36, TNFRSF21, CCL9, CCL8, POSTN, ANKRD1, CCL6, LCN2, CCL12, SFRP1, COL1A1, ADAMTS12, DBN1
GOTERM_BP_DIRECT	GO:0002250~adaptive immune response	14	6.43E-04	TNFRSF21, ADGRE1, CTLA4, ANXA1, CTSS, CLEC4N, CD84, PIRB, ALCAM, CD86, PTK2B, SERPINA3G, CLEC4A2, PRDM1
GOTERM_BP_DIRECT	GO:0007507~heart development	14	0.08797785	BMP4, ALDH1A2, PAM, CASP3, BMP2, DNAAF3, XIRP2, MMP9, COL3A1, PTN, SPARC, LOX, TGFB2, IFT74
GOTERM_BP_DIRECT	GO:0030199~collagen fibril organization	13	2.32E-09	COL14A1, CYP1B1, COL3A1, COL1A2, COL1A1, LOX, COL11A2, SCX, ADAMTS2, COL5A2, COL5A1, TGFB2, ANXA2

GOTERM_BP_DIRECT	GO:0071347~cellular response to interleukin-1	13	1.05E-05	LCN2, CCL12, PTGIS, SFRP1, SERPINE1, CCL9, SAA3, CCL8, ANKRD1, ADAMTS12, MYC, CCL6, FN1
GOTERM_BP_DIRECT	GO:0009615~response to virus	13	1.75E-05	IFITM1, TLR13, CLU, OAS3, CXCL10, IFIT3, LCN2, IFI27L2A, OASL1, HSPB1, STMN1, MST1R, MX1
GOTERM_BP_DIRECT	GO:0007229~integrin-mediated signaling pathway	13	4.95E-05	PLEK, FERMT3, COL3A1, ITGB2, ITGB3, VAV1, ITGAM, CTGF, PTK2B, ITGB6, FCER1G, ADAM8, TYROBP
GOTERM_BP_DIRECT	GO:0030324~lung development	13	7.58E-04	BMP4, CEBPA, PDPN, FSTL3, MGP, SPARC, KDR, ALDH1A2, EIF4EBP1, CTGF, PTN, LOX, ADAMTS2
GOTERM_BP_DIRECT	GO:0001934~positive regulation of protein phosphorylation	13	0.0180186	BMP4, BMP2, C3, MMP9, IQGAP3, PLAUR, ANXA2, KDR, CTGF, AKAP5, PAK1, GPNMB, CSF1R
GOTERM_BP_DIRECT	GO:0002244~hematopoietic progenitor cell differentiation	12	3.54E-04	BMP4, PTPN6, INHBA, SFRP1, PLEK, KCNAB2, PLD4, FSTL3, ANLN, SIRPA, TOP2A, SMPD3
GOTERM_BP_DIRECT	GO:0032355~response to estradiol	12	4.60E-04	ALDH1A2, PAM, PENK, DUSP1, CTGF, GRN, ANXA1, PTN, POSTN, COL1A1, FCGR1, MYC
GOTERM_BP_DIRECT	GO:0030198~extracellular matrix organization	12	0.00127236	NEPN, LGALS3, ADAMTSL2, HPSE, SPOCK2, MMP9, COMP, TGFBI, CCDC80, POSTN, TGFB2, FN1
GOTERM_BP_DIRECT	GO:0045471~response to ethanol	12	0.00157181	CDK1, EIF4EBP1, TBXAS1, S100A8, STAR, PENK, PTK2B, TNC, SPARC, CDO1, MYC, CD14
GOTERM_BP_DIRECT	GO:0010976~positive regulation of neuron projection development	12	0.00565902	BMP4, PPP1R9A, SCN1B, SERPINE2, SERPINF1, PTK2B, GRN, PTN, HSPB1, ANKRD1, CD24A, DBN1
GOTERM_BP_DIRECT	GO:0019221~cytokine-mediated signaling pathway	12	0.0085385	CEBPA, PIRB, ASPN, CCL12, PTPN6, BGN, CSF2RB2, CCR2, CSF2RB, PF4, PTPRN, CSF1R
GOTERM_BP_DIRECT	GO:0051607~defense response to virus	12	0.02149471	IFIT3, CD86, ISG15, IFITM1, SLFN9, OASL1, OAS3, IFIT3B, MX1, TLR7, ZBP1, CXCL10
GOTERM_BP_DIRECT	GO:0051260~protein homooligomerization	12	0.05927259	IKBKE, PAM, GLUL, P2RX6, HMOX1, TGM2, ANGPT1, KCNA5, SLC1A1, KCNV2, THBS4, ANGPTL4

GOTERM_BP_DIRECT	GO:0007160~cell-matrix adhesion	11	2.20E-04	SNED1, CTGF, HPSE, COL3A1, ITGB6, ITGB2, ITGB3, ADAMTS12, ADAM8, SIRPA, FN1
GOTERM_BP_DIRECT	GO:0048661~positive regulation of smooth muscle cell proliferation	11	2.71E-04	EGR1, BMP4, C3AR1, WISP1, HMOX1, SULF1, TGM2, HBEGF, ITGB3, MYC, PTAFR
GOTERM_BP_DIRECT	GO:0030308~negative regulation of cell growth	11	0.00794321	RTN4, INHBA, CGREF1, SFRP1, SERPINE2, FHL1, OSGIN1, FRZB, NPPA, TGFB2, AHSG
GOTERM_BP_DIRECT	GO:0007411~axon guidance	11	0.02462752	ALCAM, NCAM1, EPHA4, ENAH, SCN1B, EFNB3, NTF3, CD24A, TUBB3, CSF1R, TGFB2
GOTERM_BP_DIRECT	GO:0071560~cellular response to transforming growth factor beta stimulus	10	1.52E-04	NOX4, STAR, SFRP1, PENK, SERPINE1, POSTN, COL1A1, ANKRD1, SCX, DBN1
GOTERM_BP_DIRECT	GO:0071407~cellular response to organic cyclic compound	10	7.37E-04	CEBPA, CCL12, P2RY6, BMP2, MSR1, CYP1B1, LGALS1, NOS2, PAK1, ANKRD1
GOTERM_BP_DIRECT	GO:0007015~actin filament organization	10	0.00153125	ENAH, CORO1A, PPP1R9A, RAC2, PTK2B, ACTN1, SIRPA, WAS, DBN1, PAKAP
GOTERM_BP_DIRECT	GO:0030097~hemopoiesis	10	0.00196546	SFRP1, IKZF1, CCR2, ANGPT1, HBB-BS, HBB-BT, TACC3, CSF1R, TGFB2, KDR
GOTERM_BP_DIRECT	GO:0050830~defense response to Gram-positive bacterium	10	0.00336374	LYZ2, HMGB2, C5AR1, ANG, NCF1, HCK, TLR2, MYO1F, ACP5, LBP
GOTERM_BP_DIRECT	GO:0071456~cellular response to hypoxia	10	0.00659666	E2F1, EIF4EBP1, PTGIS, SFRP1, HMOX1, RGCC, PTN, ANKRD1, ADAM8, CCNA2
GOTERM_BP_DIRECT	GO:0001501~skeletal system development	10	0.00840981	BMP4, CDKN1C, LGALS3, MMP9, COL3A1, COL1A2, COL1A1, COL11A2, COL5A2, TGFB2
GOTERM_BP_DIRECT	GO:0008584~male gonad development	10	0.01118095	INHBA, HMGB2, NUPR1, STAR, SFRP1, FSTL3, ASPM, TGFB2, AHSG, KDR
GOTERM_BP_DIRECT	GO:0001649~osteoblast differentiation	10	0.01180868	BMP4, BMP2, SFRP1, PENK, TNC, MRC2, COL1A1, GPNMB, TMEM119, SPP1
GOTERM_BP_DIRECT	GO:0010466~negative regulation of peptidase activity	10	0.01458521	SERPINA3N, SERPINE2, SERPINA3G, SERPINE1, SERPINB1A, BIRC5, SERPING1, PAPLN, ECM1, TIMP1

GOTERM_BP_DIRECT	GO:0001822~kidney development	10	0.0269396	BMP4, CDKN1C, ALDH1A2, ACE, SERPINF1, SULF1, WNT9B, FSTL3, CYS1, TGFB2
GOTERM_BP_DIRECT	GO:0034765~regulation of ion transmembrane transport	10	0.03323139	CLCN1, KCNQ4, CYBB, SCN1B, KCNAB2, SCN4B, KCNA5, CLIC1, KCNV2, SCN4A
GOTERM_BP_DIRECT	GO:0030036~actin cytoskeleton organization	10	0.04364645	GAS2L3, CORO2A, ENAH, CORO1A, DOCK2, SFRP1, RAC2, XIRP2, PAK1, RHOU
GOTERM_BP_DIRECT	GO:0000281~mitotic cytokinesis	9	3.85E-06	CKAP2, KIF23, PLK1, KIF4, NUSAP1, ANLN, STMN1, RACGAP1, KIF20A
GOTERM_BP_DIRECT	GO:0050766~positive regulation of phagocytosis	9	1.48E-04	SLC11A1, DOCK2, FCGR2B, C3, FCER1G, FCGR1, SIRPA, FCGR3, AHSG
GOTERM_BP_DIRECT	GO:0070098~chemokine-mediated signaling pathway	9	3.90E-04	CCL12, PTK2B, CCR1, CCR2, CCL9, CCL8, PF4, CCL6, CXCL10
GOTERM_BP_DIRECT	GO:0042542~response to hydrogen peroxide	9	5.64E-04	GPX1, CASP3, STAR, DUSP1, PTK2B, HMOX1, HP, COL1A1, KCNA5
GOTERM_BP_DIRECT	GO:0032760~positive regulation of tumor necrosis factor production	9	6.34E-04	CCR5, CLU, TLR2, FCER1G, PF4, LBP, SASH3, PTAFR, CD14
GOTERM_BP_DIRECT	GO:0048839~inner ear development	9	0.00134487	CEBPA, C1QB, BMP2, IGFBP7, SPARC, CYS1, CDH23, TGFB2, IFI204
GOTERM_BP_DIRECT	GO:0001938~positive regulation of endothelial cell proliferation	9	0.00148439	BMP4, BMP2, HMGB2, ANG, LRG1, ITGB3, ECM1, THBS4, KDR
GOTERM_BP_DIRECT	GO:0071346~cellular response to interferon-gamma	9	0.00163515	MRC1, CCL12, STAR, CCL9, CCL8, H2-AB1, NOS2, MYC, CCL6
GOTERM_BP_DIRECT	GO:0016525~negative regulation of angiogenesis	9	0.00236329	SERPINF1, CCR2, RGCC, SULF1, PTN, PF4, SPARC, THBS4, CXCL10
GOTERM_BP_DIRECT	GO:0043627~response to estrogen	9	0.00305956	ARPC1B, HSP90AA1, STAR, HMOX1, IL4RA, RCAN1, PTPRN, CD24A, TGFB2
GOTERM_BP_DIRECT	GO:0007018~microtubule-based movement	9	0.00390584	KIF23, KIF22, KIFC1, KIF11, KIF6, KIF4, KIF20B, CENPE, KIF20A
GOTERM_BP_DIRECT	GO:0060326~cell chemotaxis	9	0.00390584	CCL12, HMGB2, CCL9, SAA3, CCL8, HBEGF, BIN2, CCL6, CXCL10
GOTERM_BP_DIRECT	GO:0060548~negative regulation of cell death	9	0.00456329	NCAM1, BMP4, NPAS2, WISP2, WISP1, CTGF, CTSB, ITGB3, MYC

GOTERM_BP_DIRECT	GO:0051897~positive regulation of protein kinase B signaling	9	0.01410039	NOX4, PIK3CG, GPX1, HPSE, HBEGF, ANGPT1, PIK3R5, MST1R, ADAM8
GOTERM_BP_DIRECT	GO:0031175~neuron projection development	9	0.08593406	NCAM1, EFHD1, PPP1R9A, BTG2, PTK2B, CLMN, TNC, CNTNAP1, CD24A
GOTERM_BP_DIRECT	GO:0030574~collagen catabolic process	8	8.20E-06	CTSK, MMP9, MRC2, MMP19, CTSB, CTSS, MMP3, ADAMTS2
GOTERM_BP_DIRECT	GO:0042130~negative regulation of T cell proliferation	8	2.80E-04	TNFRSF21, PTPN6, CTLA4, H2-AA, H2-AB1, GPNMB, VSIG4, SLFN1
GOTERM_BP_DIRECT	GO:0051496~positive regulation of stress fiber assembly	8	5.15E-04	NOX4, PPM1E, CTGF, CARMIL1, RGCC, GPR65, S100A10, PAK1
GOTERM_BP_DIRECT	GO:0006909~phagocytosis	8	0.00143536	SLC11A1, CORO1A, HCK, PLD4, ANXA1, ITGB2, VAV1, CD302
GOTERM_BP_DIRECT	GO:0043408~regulation of MAPK cascade	8	0.00300835	INHBB, INHBA, BMP2, TLR13, PAK1, GDF15, CD24A, TGFB2
GOTERM_BP_DIRECT	GO:0009612~response to mechanical stimulus	8	0.0043632	INHBB, BTG2, PTK2B, TNC, COL3A1, RCAN1, POSTN, KCNA5
GOTERM_BP_DIRECT	GO:0048812~neuron projection morphogenesis	8	0.0043632	NBL1, PLXNB1, CLU, KIF20B, CNTNAP1, PAK1, THBS4, KDR
GOTERM_BP_DIRECT	GO:0048146~positive regulation of fibroblast proliferation	8	0.00519255	E2F1, SERPINE1, PDGFC, ITGB3, MYC, CCNA2, FN1, ANXA2
GOTERM_BP_DIRECT	GO:0006461~protein complex assembly	8	0.00564905	CDK1, NUPR1, TSPAN4, SLC2A1, NCKAP1L, MGP, PF4, AHSG
GOTERM_BP_DIRECT	GO:0000165~MAPK cascade	8	0.00719928	ZFP36, SLC11A1, CCL12, DOK1, PTK2B, PLVAP, ITPKB, MYC
GOTERM_BP_DIRECT	GO:0001568~blood vessel development	8	0.00839454	BMP4, ALDH1A2, COL3A1, COL1A2, COL1A1, LOX, COL5A1, TGFB2
GOTERM_BP_DIRECT	GO:0043434~response to peptide hormone	8	0.00972965	SERPINA3N, BTG2, CTGF, SERPINA3G, ANXA1, COL1A1, SPARC, TIMP1
GOTERM_BP_DIRECT	GO:0009749~response to glucose	8	0.0137369	EGR1, CASP3, GLUL, NCF2, CTGF, PTK2B, ILDR2, PTPRN
GOTERM_BP_DIRECT	GO:0034097~response to cytokine	8	0.01664292	ALDH1A2, CORO1A, SERPINA3N, SERPINA3G, COL3A1, ACP5, SPARC, TIMP1
GOTERM_BP_DIRECT	GO:0050728~negative regulation of inflammatory response	8	0.02370972	ZFP36, TNFAIP8L2, IER3, PTGIS, SERPINF1, AOAH, ACP5, CTLA2A
GOTERM_BP_DIRECT	GO:0007059~chromosome segregation	8	0.02646389	KIF11, SPAG5, INCENP, BIRC5, CENPE, ESPL1, KNSTRN, TOP2A

GOTERM_BP_DIRECT	GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway	8	0.04551826	DOK1, EPHA4, NTF3, HCK, ANGPT1, CSF1R, LCP2, KDR
GOTERM_BP_DIRECT	GO:0050731~positive regulation of peptidyl-tyrosine phosphorylation	8	0.04759506	NTF3, PTK2B, HBEGF, ANGPT1, ITGB3, TREM2, CD24A, THBS4
GOTERM_BP_DIRECT	GO:0030336~negative regulation of cell migration	8	0.05887707	CYP1B1, SFRP1, CCR5, IFITM1, SERPINE1, SULF1, PTN, DACH1
GOTERM_BP_DIRECT	GO:0000070~mitotic sister chromatid segregation	7	7.46E-05	CDCA8, MAD2L1, PLK1, SPAG5, NUSAP1, ESPL1, KNSTRN
GOTERM_BP_DIRECT	GO:0050715~positive regulation of cytokine secretion	7	7.32E-04	CD300C2, PANX1, RGCC, TLR2, CLEC5A, CLEC4N, CD14
GOTERM_BP_DIRECT	GO:0006953~acute-phase response	7	8.60E-04	SERPINA3N, SAA3, HP, LBP, FN1, AHSG, CD163
GOTERM_BP_DIRECT	GO:0000910~cytokinesis	7	0.00116499	KIF23, PRC1, PLK1, INCENP, PSTPIP1, BIRC5, KIF20A
GOTERM_BP_DIRECT	GO:0014911~positive regulation of smooth muscle cell migration	7	0.00154717	NOX4, EGR1, P2RY6, CYP1B1, POSTN, ITGB3, MYC
GOTERM_BP_DIRECT	GO:0002548~monocyte chemotaxis	7	0.00177071	CCL12, LGALS3, CCR2, ANXA1, CCL9, CCL8, CCL6
GOTERM_BP_DIRECT	GO:0010811~positive regulation of cell-substrate adhesion	7	0.0022903	FBLN2, SPOCK2, CCDC80, PTN, COL8A1, DBN1, SPP1
GOTERM_BP_DIRECT	GO:0045429~positive regulation of nitric oxide biosynthetic process	7	0.00327461	HSP90AA1, ASS1, PTK2B, CLU, TLR2, ITGB2, SMPD3
GOTERM_BP_DIRECT	GO:0006911~phagocytosis, engulfment	7	0.00327461	FCGR2B, FCER1G, TREM2, FCGR1, SIRPA, BIN2, FCGR3
GOTERM_BP_DIRECT	GO:0032956~regulation of actin cytoskeleton organization	7	0.00557039	PAM, CORO1A, MYO1F, SH3BGRL3, PAK1, ITGB3, TGFB2
GOTERM_BP_DIRECT	GO:0051591~response to cAMP	7	0.00614278	DUSP1, PTK2B, MMP19, COL1A1, SPARC, PTPRN, CDO1
GOTERM_BP_DIRECT	GO:0031100~organ regeneration	7	0.00966194	CDK1, ACE, C5AR1, MKI67, CCNA2, LCP1, NNMT
GOTERM_BP_DIRECT	GO:0051603~proteolysis involved in cellular protein catabolic process	7	0.01050857	CTSZ, CTSK, LGMN, CTSC, CTSB, CTSS, ADAMTS12
GOTERM_BP_DIRECT	GO:0009611~response to wounding	7	0.01140648	ZFP36, GPX1, CASP3, SERPINE2, MYC, LCP1, TGFB2
GOTERM_BP_DIRECT	GO:0008217~regulation of blood pressure	7	0.01554111	C3AR1, ACE, CYP4F18, HMOX1, COL1A2, ENPEP, NPPA
GOTERM_BP_DIRECT	GO:0071300~cellular response to retinoic acid	7	0.01925211	ALDH1A2, SERPINF1, PTK2B, TNC, CYP26B1, COL1A1, MYC

GOTERM_BP_DIRECT	GO:0045669~positive regulation of osteoblast differentiation	7	0.02352531	CEBPA, BMP4, BMP2, IFITM1, CLIC1, TMEM119, IFI204
GOTERM_BP_DIRECT	GO:0050679~positive regulation of epithelial cell proliferation	7	0.03789315	BMP4, GLUL, C5AR1, SFRP1, GRN, MYC, KDR
GOTERM_BP_DIRECT	GO:0060395~SMAD protein signal transduction	7	0.04000908	BMP4, INHBB, INHBA, BMP2, VIM, GDF15, TGFB2
GOTERM_BP_DIRECT	GO:0006821~chloride transport	7	0.04679943	CLCN1, TSPO, CLCA3A1, GABRA3, ANO1, ANO5, CLIC1
GOTERM_BP_DIRECT	GO:0051216~cartilage development	7	0.05169963	BMP4, BMP2, SULF1, MGP, COL11A2, SCX, TIMP1
GOTERM_BP_DIRECT	GO:0042535~positive regulation of tumor necrosis factor biosynthetic process	6	3.80E-05	CYBB, CCR2, TLR2, HSPB1, LBP, FCGR3
GOTERM_BP_DIRECT	GO:0002523~leukocyte migration involved in inflammatory response	6	3.80E-05	S100A8, S100A9, ITGB2, ADAM8, CD24A, ITGAM
GOTERM_BP_DIRECT	GO:0019886~antigen processing and presentation of exogenous peptide antigen via MHC class II	6	5.75E-05	FCGR2B, H2-EB1, IFI30, FCER1G, H2-AA, H2-AB1
GOTERM_BP_DIRECT	GO:0033630~positive regulation of cell adhesion mediated by integrin	6	8.39E-05	PTPN6, NCKAP1L, ITGB3, CD24A, TGFB2, IFT74
GOTERM_BP_DIRECT	GO:0030261~chromosome condensation	6	1.19E-04	CDK1, NCAPH, NCAPG2, SMC2, TOP2A, SMC4
GOTERM_BP_DIRECT	GO:2000573~positive regulation of DNA biosynthetic process	6	2.21E-04	NOX4, C3AR1, CYP1B1, PTK2B, RGCC, MYC
GOTERM_BP_DIRECT	GO:0030889~negative regulation of B cell proliferation	6	2.21E-04	TNFRSF21, CASP3, FCGR2B, CTLA4, PRDM1, CD24A
GOTERM_BP_DIRECT	GO:0010575~positive regulation of vascular endothelial growth factor production	6	9.30E-04	C3AR1, C5AR1, CYP1B1, HPSE, C3, SULF1
GOTERM_BP_DIRECT	GO:0045453~bone resorption	6	0.00113194	NOX4, CTSK, RAC2, PTK2B, ACP5, CTSS
GOTERM_BP_DIRECT	GO:0090023~positive regulation of neutrophil chemotaxis	6	0.00193139	C3AR1, C5AR1, RAC2, NCKAP1L, LBP, THBS4
GOTERM_BP_DIRECT	GO:0044344~cellular response to fibroblast growth factor stimulus	6	0.00265402	ZFP36, STAR, SFRP1, POSTN, COL1A1, MYC

GOTERM_BP_DIRECT	GO:0048147~negative regulation of fibroblast proliferation	6	0.00355456	NUPR1, SFRP1, MMP9, IFI30, DACH1, MYC
GOTERM_BP_DIRECT	GO:0009617~response to bacterium	6	0.00528822	SLC11A1, FCGR2B, NCF1, TLR2, FCGR1, CD14
GOTERM_BP_DIRECT	GO:0045786~negative regulation of cell cycle	6	0.00597932	CEBPA, BMP4, INHBA, CASP3, BMP2, NUPR1
GOTERM_BP_DIRECT	GO:0040007~growth	6	0.00597932	BMP4, INHBB, INHBA, BMP2, CCNB2, TGFB2
GOTERM_BP_DIRECT	GO:0070527~platelet aggregation	6	0.00754759	PTPN6, PLEK, FERMT3, HSPB1, ITGB3, CLIC1
GOTERM_BP_DIRECT	GO:0010595~positive regulation of endothelial cell migration	6	0.01040402	BMP4, PTK2B, ANGPT1, SPARC, ITGB3, KDR
GOTERM_BP_DIRECT	GO:0006879~cellular iron ion homeostasis	6	0.01525487	LCN2, SLC11A1, ALAS2, FTL1, HMOX1, MYC
GOTERM_BP_DIRECT	GO:0010862~positive regulation of pathway-restricted SMAD protein phosphorylation	6	0.01975028	BMP4, INHBB, INHBA, BMP2, GDF15, TGFB2
GOTERM_BP_DIRECT	GO:0045600~positive regulation of fat cell differentiation	6	0.02142213	CEBPA, ZFP36, BMP2, MEDAG, SFRP1, FRZB
GOTERM_BP_DIRECT	GO:0031532~actin cytoskeleton reorganization	6	0.02698024	PARVG, PLEK, S100A9, ANXA1, GPR65, PAK1
GOTERM_BP_DIRECT	GO:0032755~positive regulation of interleukin-6 production	6	0.02698024	RAB7B, CCR5, TLR2, FCER1G, LBP, TLR7
GOTERM_BP_DIRECT	GO:0008630~intrinsic apoptotic signaling pathway in response to DNA damage	6	0.03115125	E2F1, IER3, IKBKE, BCL2A1B, HMOX1, MYC
GOTERM_BP_DIRECT	GO:0043406~positive regulation of MAP kinase activity	6	0.03115125	NOX4, PIK3CG, PIK3R5, PDGFC, MST1R, CD24A
GOTERM_BP_DIRECT	GO:0006958~complement activation, classical pathway	6	0.03337987	C1QA, C1QB, C4B, C3, SERPING1, C1QC
GOTERM_BP_DIRECT	GO:0035914~skeletal muscle cell differentiation	6	0.03337987	EGR1, NUPR1, BTG2, ANKRD1, SCX, MYC
GOTERM_BP_DIRECT	GO:0045785~positive regulation of cell adhesion	6	0.03570516	TGM2, ANGPT1, RHOD, ADAM8, VAV1, APBB1IP
GOTERM_BP_DIRECT	GO:0001541~ovarian follicle development	6	0.03812791	BMP4, INHBA, MMP19, ANGPT1, MYC, KDR
GOTERM_BP_DIRECT	GO:0001558~regulation of cell growth	6	0.0406488	WISP2, WISP1, CTGF, IGFBP7, IGFBP6, CSF2RB

GOTERM_BP_DIRECT	GO:0006898~receptor-mediated endocytosis	6	0.04598713	MRC1, MSR1, FTL1, FCGR2B, FCGR1, CD14
GOTERM_BP_DIRECT	GO:0000082~G1/S transition of mitotic cell cycle	6	0.05172326	INHBA, EIF4EBP1, RGCC, IQGAP3, TCF19, RHOU
GOTERM_BP_DIRECT	GO:0042102~positive regulation of T cell proliferation	6	0.0578585	CORO1A, CD86, CD46, ANXA1, NCKAP1L, SASH3
GOTERM_BP_DIRECT	GO:0014068~positive regulation of phosphatidylinositol 3-kinase signaling	6	0.0578585	PTPN6, PLXNB1, ANGPT1, PDGFC, TGFB2, KDR
GOTERM_BP_DIRECT	GO:0018108~peptidyl-tyrosine phosphorylation	6	0.06107569	PTPN6, EPHA4, PTK2B, HCK, CSF1R, KDR
GOTERM_BP_DIRECT	GO:0010033~response to organic substance	6	0.06107569	PLA2G4A, CASP3, CTSC, KCNA5, PAK1, SPP1
GOTERM_BP_DIRECT	GO:0051592~response to calcium ion	6	0.07132267	PLA2G4A, TRPC3, PENK, DUSP1, PTK2B, SPARC
GOTERM_BP_DIRECT	GO:0071333~cellular response to glucose stimulus	6	0.08245271	NOX4, GPX1, STAR, SERPINF1, UCP2, LGALS1
GOTERM_BP_DIRECT	GO:0045165~cell fate commitment	6	0.08635583	BMP4, CASP3, BMP2, WNT9B, PRDM1, KDR
GOTERM_BP_DIRECT	GO:0050680~negative regulation of epithelial cell proliferation	6	0.08635583	BMP4, CDKN1C, SFRP1, PTN, TGFB2, IFT74
GOTERM_BP_DIRECT	GO:0006812~cation transport	6	0.09035408	PANX1, SLC24A3, SLC41A2, ANO1, SLC41A3, SCN4A
GOTERM_BP_DIRECT	GO:0051384~response to glucocorticoid	6	0.09863193	PAM, PTGDS, DUSP1, ASS1, SPARC, CDO1
GOTERM_BP_DIRECT	GO:0043206~extracellular fibril organization	5	3.10E-04	LTBP2, COL3A1, MFAP4, MFAP5, COL5A1
GOTERM_BP_DIRECT	GO:0035457~cellular response to interferon-alpha	5	4.54E-04	IFIT3, STAR, IFIT3B, MYC, IFI204
GOTERM_BP_DIRECT	GO:0045576~mast cell activation	5	6.38E-04	CD48, FCGR2B, FCER1G, FCGR3, LCP2
GOTERM_BP_DIRECT	GO:0090026~positive regulation of monocyte chemotaxis	5	8.71E-04	CCR1, CCR2, SERPINE1, PLA2G7, CXCL10
GOTERM_BP_DIRECT	GO:0006956~complement activation	5	0.00115659	MASP1, C4B, C3, CFB, RGCC
GOTERM_BP_DIRECT	GO:0006693~prostaglandin metabolic process	5	0.00115659	TBXAS1, PTGIS, PTGDS, PDPN, HPGDS
GOTERM_BP_DIRECT	GO:0007051~spindle organization	5	0.00150254	KIF11, SPAG5, AURKB, KNSTRN, ASPM

GOTERM_BP_DIRECT	GO:0016064~immunoglobulin mediated immune response	5	0.00517019	FCGR2B, C4B, IRF7, IL4RA, FCER1G
GOTERM_BP_DIRECT	GO:1902042~negative regulation of extrinsic apoptotic signaling pathway via death domain receptors	5	0.00827626	GPX1, HMGB2, TNFRSF23, HMOX1, SERPINE1
GOTERM_BP_DIRECT	GO:0034341~response to interferon-gamma	5	0.009533	SLC11A1, CD86, IFITM1, H2-EB1, H2-AA
GOTERM_BP_DIRECT	GO:0048821~erythrocyte development	5	0.01090747	HBA-A1, HBA-A2, NCKAP1L, HBB-BS, HBB-BT
GOTERM_BP_DIRECT	GO:0035987~endodermal cell differentiation	5	0.01090747	INHBA, MMP9, COL12A1, COL8A1, FN1
GOTERM_BP_DIRECT	GO:0048247~lymphocyte chemotaxis	5	0.02181893	CCL12, CCL9, CCL8, ADAM8, CCL6
GOTERM_BP_DIRECT	GO:0010718~positive regulation of epithelial to mesenchymal transition	5	0.02410738	GLIPR2, BMP2, RGCC, COL1A1, TGFB2
GOTERM_BP_DIRECT	GO:0090307~mitotic spindle assembly	5	0.02653566	KIFC1, KIF11, TPX2, BIRC5, CDC20
GOTERM_BP_DIRECT	GO:0071773~cellular response to BMP stimulus	5	0.02653566	BMP4, BMP2, SFRP1, ADAMTS12, SCX
GOTERM_BP_DIRECT	GO:0048754~branching morphogenesis of an epithelial tube	5	0.02910521	BMP4, WNT9B, MGP, PAK1, KDR
GOTERM_BP_DIRECT	GO:0002931~response to ischemia	5	0.02910521	EGR1, EIF4EBP1, PANX1, UCHL1, RCAN1
GOTERM_BP_DIRECT	GO:0007346~regulation of mitotic cell cycle	5	0.03181716	CDKN1C, PLK1, FBXO5, BIRC5, MYC
GOTERM_BP_DIRECT	GO:0030177~positive regulation of Wnt signaling pathway	5	0.03181716	BMP2, SFRP1, SULF1, TLR2, LGR6
GOTERM_BP_DIRECT	GO:0006910~phagocytosis, recognition	5	0.03467241	COLEC12, CLEC7A, FCGR1, SIRPA, FCGR3
GOTERM_BP_DIRECT	GO:0048873~homeostasis of number of cells within a tissue	5	0.03467241	CORO1A, COL14A1, CCR2, ILDR2, SASH3
GOTERM_BP_DIRECT	GO:0034605~cellular response to heat	5	0.03767154	MKI67, HMOX1, ANO1, MYOF, CXCL10
GOTERM_BP_DIRECT	GO:0007162~negative regulation of cell adhesion	5	0.04753436	LPXN, PLXNB1, TNC, MYO1F, ANGPT1
GOTERM_BP_DIRECT	GO:0048706~embryonic skeletal system development	5	0.0548285	BMP4, SULF1, ETL4, COL1A1, SCX
GOTERM_BP_DIRECT	GO:0002062~chondrocyte differentiation	5	0.06269133	BMP4, BMP2, TGFBI, COL11A2, SCX

GOTERM_BP_DIRECT	GO:0007265~Ras protein signal transduction	5	0.0668332	CNKSR1, DOK1, DOK3, IQGAP3, CCNA2
GOTERM_BP_DIRECT	GO:0010942~positive regulation of cell death	5	0.07111347	EGR1, BMP4, CTGF, UCP2, HP
GOTERM_BP_DIRECT	GO:0030218~erythrocyte differentiation	5	0.07111347	BMP4, CASP3, ALAS2, IKZF1, SPI1
GOTERM_BP_DIRECT	GO:0009725~response to hormone	5	0.07111347	PTK2B, ANG, MMP19, LOX, TIMP1
GOTERM_BP_DIRECT	GO:0060291~long-term synaptic potentiation	5	0.07553047	SERPINE2, RASGRF2, PTK2B, SYT12, PTN
GOTERM_BP_DIRECT	GO:0071320~cellular response to cAMP	5	0.08008239	NOX4, PIK3CG, STAR, PENK, PTAFR
GOTERM_BP_DIRECT	GO:0006936~muscle contraction	5	0.08008239	CLCN1, MYBPC2, ANXA1, MYH7, ANXA2
GOTERM_BP_DIRECT	GO:0019882~antigen processing and presentation	5	0.09959688	RAB32, H2-EB1, H2-AA, H2-AB1, CTSS
GOTERM_BP_DIRECT	GO:0048002~antigen processing and presentation of peptide antigen	4	1.36E-04	SLC11A1, H2-AA, H2-AB1, CTSS
GOTERM_BP_DIRECT	GO:0098869~cellular oxidant detoxification	4	3.31E-04	HBA-A1, HBA-A2, HBB-BS, HBB-BT
GOTERM_BP_DIRECT	GO:0042590~antigen processing and presentation of exogenous peptide antigen via MHC class I	4	3.31E-04	IFI30, FCER1G, FCGR1, FCGR3
GOTERM_BP_DIRECT	GO:0051256~mitotic spindle midzone assembly	4	6.45E-04	KIF23, KIF4, AURKB, RACGAP1
GOTERM_BP_DIRECT	GO:0045730~respiratory burst	4	0.00110195	SLC11A1, CYBB, NCF1, CD24A
GOTERM_BP_DIRECT	GO:0001798~positive regulation of type IIa hypersensitivity	4	0.00172039	C3, FCER1G, FCGR1, FCGR3
GOTERM_BP_DIRECT	GO:0071223~cellular response to lipoteichoic acid	4	0.00251816	TLR2, LBP, TREM2, CD14
GOTERM_BP_DIRECT	GO:0071305~cellular response to vitamin D	4	0.00351048	SFRP1, PENK, TNC, PTN
GOTERM_BP_DIRECT	GO:0008347~glial cell migration	4	0.00471053	EPHA4, TSPO, TGFB2, FN1
GOTERM_BP_DIRECT	GO:0042554~superoxide anion generation	4	0.00471053	NOX4, CYBB, NCF2, NCF1
GOTERM_BP_DIRECT	GO:0050777~negative regulation of immune response	4	0.00471053	FCGR2B, COL3A1, CTLA4, TGFB2

GOTERM_BP_DIRECT	GO:0071276~cellular response to cadmium ion	4	0.00612954	CYBB, STAR, HMOX1, MT2
GOTERM_BP_DIRECT	GO:0010447~response to acidic pH	4	0.00612954	SERPINF1, LGMN, GPR65, CTSS
GOTERM_BP_DIRECT	GO:0007076~mitotic chromosome condensation	4	0.00777693	NCAPH, NUSAP1, SMC2, SMC4
GOTERM_BP_DIRECT	GO:0033690~positive regulation of osteoblast proliferation	4	0.00777693	BMP2, HPSE, ITGB3, TMEM119
GOTERM_BP_DIRECT	GO:0051279~regulation of release of sequestered calcium ion into cytosol	4	0.00966049	PTPN6, CORO1A, PTK2B, ITGB3
GOTERM_BP_DIRECT	GO:2000249~regulation of actin cytoskeleton reorganization	4	0.01178647	PTK2B, GMFG, RHOD, CSF1R
GOTERM_BP_DIRECT	GO:0045019~negative regulation of nitric oxide biosynthetic process	4	0.01178647	TSPO, PTGIS, DYNLL1, ACP5
GOTERM_BP_DIRECT	GO:0030502~negative regulation of bone mineralization	4	0.01178647	PTK2B, CCR1, ECM1, AHSG
GOTERM_BP_DIRECT	GO:0050918~positive chemotaxis	4	0.01178647	BMP4, CORO1A, LGALS3, ANGPT1
GOTERM_BP_DIRECT	GO:0055008~cardiac muscle tissue morphogenesis	4	0.01415968	BMP2, XIRP2, ANGPT1, ANKRD1
GOTERM_BP_DIRECT	GO:0001516~prostaglandin biosynthetic process	4	0.01415968	TBXAS1, PTGIS, PTGDS, HPGDS
GOTERM_BP_DIRECT	GO:0002224~toll-like receptor signaling pathway	4	0.01678365	CD86, TLR2, TLR7, CD180
GOTERM_BP_DIRECT	GO:0007094~mitotic spindle assembly checkpoint	4	0.01966068	MAD2L1, PLK1, BUB1B, CENPE
GOTERM_BP_DIRECT	GO:0070542~response to fatty acid	4	0.02279199	TBXAS1, CTGF, UCP2, TLR2
GOTERM_BP_DIRECT	GO:0016339~calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules	4	0.02279199	CDH22, PCDHGA12, PCDH12, CDH23
GOTERM_BP_DIRECT	GO:0006801~superoxide metabolic process	4	0.02279199	NOX4, CYBB, NCF2, NOS2
GOTERM_BP_DIRECT	GO:1901741~positive regulation of myoblast fusion	4	0.02279199	IL4RA, CCL8, CD53, GDF15
GOTERM_BP_DIRECT	GO:0007088~regulation of mitotic nuclear division	4	0.02617776	MKI67, KIF20B, FBXO5, CENPE

GOTERM_BP_DIRECT	GO:0022409~positive regulation of cell-cell adhesion	4	0.02617776	MYO10, CCR5, FSTL3, CD24A
GOTERM_BP_DIRECT	GO:0045780~positive regulation of bone resorption	4	0.02617776	ITGB3, ADAM8, SPP1, AHSG
GOTERM_BP_DIRECT	GO:0030517~negative regulation of axon extension	4	0.02617776	RTN4, CCR5, FSTL4, AATK
GOTERM_BP_DIRECT	GO:0071398~cellular response to fatty acid	4	0.02981726	E2F1, OLFR78, LDLR, PTAFR
GOTERM_BP_DIRECT	GO:0045648~positive regulation of erythrocyte differentiation	4	0.02981726	INHBA, HMGB2, ISG15, NCKAP1L
GOTERM_BP_DIRECT	GO:0090280~positive regulation of calcium ion import	4	0.02981726	CCL12, LGALS3, SERPINE1, GM34302
GOTERM_BP_DIRECT	GO:0048870~cell motility	4	0.02981726	MYO10, SRPX2, PDPN, CCDC80
GOTERM_BP_DIRECT	GO:0022617~extracellular matrix disassembly	4	0.0337089	MMP19, MMP3, MMP12, LCP1
GOTERM_BP_DIRECT	GO:0002687~positive regulation of leukocyte migration	4	0.0337089	CCL12, MMP9, TLR2, ITGB3
GOTERM_BP_DIRECT	GO:0030595~leukocyte chemotaxis	4	0.0337089	CORO1A, CCR1, S100A9, PF4
GOTERM_BP_DIRECT	GO:0032733~positive regulation of interleukin-10 production	4	0.03785034	CD46, TLR2, FCER1G, SASH3
GOTERM_BP_DIRECT	GO:0036120~cellular response to platelet-derived growth factor stimulus	4	0.03785034	PTN, ITGB3, MYC, CCNA2
GOTERM_BP_DIRECT	GO:0007159~leukocyte cell-cell adhesion	4	0.0422385	FERMT3, ITGB2, CD24A, ITGAM
GOTERM_BP_DIRECT	GO:0030833~regulation of actin filament polymerization	4	0.0422385	ARPC1B, CORO1A, PPP1R9A, DBN1
GOTERM_BP_DIRECT	GO:0050850~positive regulation of calcium-mediated signaling	4	0.0422385	NCAM1, TREM2, CD24A, KDR
GOTERM_BP_DIRECT	GO:0032757~positive regulation of interleukin-8 production	4	0.04686972	SERPINE1, TLR2, LBP, TLR7
GOTERM_BP_DIRECT	GO:0048010~vascular endothelial growth factor receptor signaling pathway	4	0.04686972	PTK2B, SULF1, VAV1, KDR

GOTERM_BP_DIRECT	GO:0045662~negative regulation of myoblast differentiation	4	0.05173973	BMP4, CCL9, NMRK2, CXCL10
GOTERM_BP_DIRECT	GO:0032967~positive regulation of collagen biosynthetic process	4	0.05173973	BMP4, CTGF, RGCC, SCX
GOTERM_BP_DIRECT	GO:0030325~adrenal gland development	4	0.05684376	CDKN1C, DKK3, TSPO, FSTL3
GOTERM_BP_DIRECT	GO:0042476~odontogenesis	4	0.05684376	MYO5A, BMP4, INHBA, PAM
GOTERM_BP_DIRECT	GO:0030099~myeloid cell differentiation	4	0.05684376	CEBPA, CDKN1C, CCR1, CLEC5A
GOTERM_BP_DIRECT	GO:2000352~negative regulation of endothelial cell apoptotic process	4	0.06217659	SERPINE1, ANGPT1, ANGPTL4, KDR
GOTERM_BP_DIRECT	GO:0007052~mitotic spindle organization	4	0.06217659	WDR62, GPSM2, STMN1, AURKB
GOTERM_BP_DIRECT	GO:0031214~biomineral tissue development	4	0.0677326	ASPN, TMEM119, ECM1, SPP1
GOTERM_BP_DIRECT	GO:0032570~response to progesterone	4	0.07350579	TSPO, TLR2, PTN, TGFB2
GOTERM_BP_DIRECT	GO:0031663~lipopolysaccharide-mediated signaling pathway	4	0.07948988	CCL12, LBP, TREM2, CD14
GOTERM_BP_DIRECT	GO:2000379~positive regulation of reactive oxygen species metabolic process	4	0.07948988	NOX4, TSPO, CYP1B1, PTK2B
GOTERM_BP_DIRECT	GO:0043029~T cell homeostasis	4	0.07948988	CORO1A, CASP3, CCNB2, NCKAP1L
GOTERM_BP_DIRECT	GO:0043388~positive regulation of DNA binding	4	0.08567828	HMGB2, MMP9, MYC, PLAUR
GOTERM_BP_DIRECT	GO:0061077~chaperone-mediated protein folding	4	0.08567828	FKBP5, CLU, TTC9, FKBP11
GOTERM_BP_DIRECT	GO:2000134~negative regulation of G1/S transition of mitotic cell cycle	4	0.08567828	FHL1, SLFN9, GPNMB, SLFN1
GOTERM_BP_DIRECT	GO:0045071~negative regulation of viral genome replication	4	0.08567828	ISG15, IFITM1, OASL1, OAS3
GOTERM_BP_DIRECT	GO:0050776~regulation of immune response	4	0.08567828	CLEC12A, FCER1G, FCGR1, FCGR3
GOTERM_BP_DIRECT	GO:0032147~activation of protein kinase activity	4	0.09206422	SLC11A1, TPX2, ITGB3, TGFB2
GOTERM_BP_DIRECT	GO:0032467~positive regulation of cytokinesis	4	0.09206422	KIF23, KIF20B, AURKB, RACGAP1

GOTERM_BP_DIRECT	GO:1900026~positive regulation of substrate adhesion-dependent cell spreading	4	0.09206422	CARMIL1, S100A10, ITGB3, DBN1
GOTERM_BP_DIRECT	GO:0071310~cellular response to organic substance	4	0.09206422	EGR1, CD68, CASP3, IQGAP3
GOTERM_BP_DIRECT	GO:0042110~T cell activation	4	0.09864069	CD48, DOCK2, VAV1, WAS
GOTERM_BP_DIRECT	GO:0007080~mitotic metaphase plate congression	4	0.09864069	KIF22, KIFC1, CDCA8, CENPE
GOTERM_BP_DIRECT	GO:0050769~positive regulation of neurogenesis	4	0.09864069	ACE, BMP2, STAR, SERPINF1
GOTERM_BP_DIRECT	GO:0001805~positive regulation of type III hypersensitivity	3	0.00612458	FCER1G, FCGR1, FCGR3
GOTERM_BP_DIRECT	GO:0060244~negative regulation of cell proliferation involved in contact inhibition	3	0.00612458	SRPX, DACH1, PAK1
GOTERM_BP_DIRECT	GO:0014012~peripheral nervous system axon regeneration	3	0.00998715	TSPO, APOD, TNC
GOTERM_BP_DIRECT	GO:0018119~peptidyl-cysteine S-nitrosylation	3	0.00998715	S100A8, S100A9, NOS2
GOTERM_BP_DIRECT	GO:0002693~positive regulation of cellular extravasation	3	0.01465805	PLVAP, ADAM8, PTAFR
GOTERM_BP_DIRECT	GO:0001936~regulation of endothelial cell proliferation	3	0.01465805	BMP4, ALDH1A2, KDR
GOTERM_BP_DIRECT	GO:0033622~integrin activation	3	0.02008049	FERMT3, COL16A1, FN1
GOTERM_BP_DIRECT	GO:0051988~regulation of attachment of spindle microtubules to kinetochore	3	0.02008049	SPAG5, KNSTRN, RACGAP1
GOTERM_BP_DIRECT	GO:0051549~positive regulation of keratinocyte migration	3	0.02620052	MMP9, SERPINE1, HBEGF
GOTERM_BP_DIRECT	GO:0002223~stimulatory C-type lectin receptor signaling pathway	3	0.02620052	FCER1G, CLEC7A, CLEC4N
GOTERM_BP_DIRECT	GO:0006691~leukotriene metabolic process	3	0.02620052	NCF1, ALOX5AP, TLR2

GOTERM_BP_DIRECT	GO:0002446~neutrophil mediated immunity	3	0.02620052	ACE, MYO1F, CD300LB
GOTERM_BP_DIRECT	GO:0050810~regulation of steroid biosynthetic process	3	0.02620052	TSPO, STAR, IGFBP7
GOTERM_BP_DIRECT	GO:0002675~positive regulation of acute inflammatory response	3	0.02620052	PIK3CG, ALOX5AP, ADAM8
GOTERM_BP_DIRECT	GO:0019227~neuronal action potential propagation	3	0.02620052	CLCN1, SCN1B, CNTNAP1
GOTERM_BP_DIRECT	GO:0001878~response to yeast	3	0.02620052	CD86, ANG, NCF1
GOTERM_BP_DIRECT	GO:0032680~regulation of tumor necrosis factor production	3	0.03296691	ZFP36, ANGPT1, CD300LD
GOTERM_BP_DIRECT	GO:0060346~bone trabecula formation	3	0.03296691	SFRP1, COL1A1, THBS3
GOTERM_BP_DIRECT	GO:0042308~negative regulation of protein import into nucleus	3	0.03296691	APOD, CABP1, ANGPT1
GOTERM_BP_DIRECT	GO:0031340~positive regulation of vesicle fusion	3	0.03296691	PLA2G4A, ANXA1, ANXA2
GOTERM_BP_DIRECT	GO:0030071~regulation of mitotic metaphase/anaphase transition	3	0.03296691	PLK1, CENPE, UBE2C
GOTERM_BP_DIRECT	GO:0060452~positive regulation of cardiac muscle contraction	3	0.03296691	HSP90AA1, CTGF, NPPA
GOTERM_BP_DIRECT	GO:0002504~antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	3	0.03296691	H2-EB1, H2-AA, H2-AB1
GOTERM_BP_DIRECT	GO:0034501~protein localization to kinetochore	3	0.04033102	CDK1, BUB1B, AURKB
GOTERM_BP_DIRECT	GO:0002827~positive regulation of T-helper 1 type immune response	3	0.04033102	SLC11A1, CCR2, H2-AB1
GOTERM_BP_DIRECT	GO:0043534~blood vessel endothelial cell migration	3	0.04033102	GPX1, PTK2B, ADAM8
GOTERM_BP_DIRECT	GO:0006957~complement activation, alternative pathway	3	0.04033102	CFP, C3, CFB
GOTERM_BP_DIRECT	GO:0060055~angiogenesis involved in wound healing	3	0.04033102	GPX1, HPSE, ITGB3

GOTERM_BP_DIRECT	GO:0006809~nitric oxide biosynthetic process	3	0.04033102	HSP90AA1, CYP1B1, NOS2
GOTERM_BP_DIRECT	GO:0060100~positive regulation of phagocytosis, engulfment	3	0.04824669	NCKAP1L, LBP, FCGR1
GOTERM_BP_DIRECT	GO:0000050~urea cycle	3	0.04824669	CEBPA, ASS1, GM5424
GOTERM_BP_DIRECT	GO:0045577~regulation of B cell differentiation	3	0.04824669	PTPN6, NFAM1, CD24A
GOTERM_BP_DIRECT	GO:0051639~actin filament network formation	3	0.04824669	CARMIL1, ACTN1, LCP1
GOTERM_BP_DIRECT	GO:0007252~I-kappaB phosphorylation	3	0.05667012	SAA3, TLR2, TLR7
GOTERM_BP_DIRECT	GO:0071294~cellular response to zinc ion	3	0.05667012	TSPO, MT2, MT1
GOTERM_BP_DIRECT	GO:0001542~ovulation from ovarian follicle	3	0.05667012	PLA2G4A, MMP19, NOS2
GOTERM_BP_DIRECT	GO:0035313~wound healing, spreading of epidermal cells	3	0.05667012	HBEGF, COL5A1, MMP12
GOTERM_BP_DIRECT	GO:0002237~response to molecule of bacterial origin	3	0.06555979	TLR2, CD24A, CD14
GOTERM_BP_DIRECT	GO:0060317~cardiac epithelial to mesenchymal transition	3	0.06555979	RTN4, BMP2, TGFB2
GOTERM_BP_DIRECT	GO:0010524~positive regulation of calcium ion transport into cytosol	3	0.06555979	BMP4, TRPC3, AKAP5
GOTERM_BP_DIRECT	GO:0032743~positive regulation of interleukin-2 production	3	0.07487634	CCR2, ANXA1, SASH3
GOTERM_BP_DIRECT	GO:2000279~negative regulation of DNA biosynthetic process	3	0.07487634	DUSP1, DACH1, ANKRD1
GOTERM_BP_DIRECT	GO:0030194~positive regulation of blood coagulation	3	0.07487634	HPSE, S100A9, SERPINE1
GOTERM_BP_DIRECT	GO:0001775~cell activation	3	0.07487634	CD24A, FN1, TIMP1
GOTERM_BP_DIRECT	GO:0043267~negative regulation of potassium ion transport	3	0.07487634	PTK2B, AKAP5, KCNA5
GOTERM_BP_DIRECT	GO:0051489~regulation of filopodium assembly	3	0.07487634	MYO10, PPP1R9A, DBN1
GOTERM_BP_DIRECT	GO:0060252~positive regulation of glial cell proliferation	3	0.07487634	TSPO, VIM, MYC

GOTERM_BP_DIRECT	GO:0030225~macrophage differentiation	3	0.07487634	CEBPA, BMP4, SPI1
GOTERM_BP_DIRECT	GO:0006518~peptide metabolic process	3	0.07487634	PAM, ACE, AEBP1
GOTERM_BP_DIRECT	GO:0030949~positive regulation of vascular endothelial growth factor receptor signaling pathway	3	0.07487634	BMP4, ANGPT1, KDR
GOTERM_BP_DIRECT	GO:0042573~retinoic acid metabolic process	3	0.08458247	ALDH1A2, RBP1, CYP26B1
GOTERM_BP_DIRECT	GO:0033627~cell adhesion mediated by integrin	3	0.08458247	ITGB6, ITGB3, COL16A1
GOTERM_BP_DIRECT	GO:0061351~neural precursor cell proliferation	3	0.08458247	TRNP1, GRN, DBN1
GOTERM_BP_DIRECT	GO:2001241~positive regulation of extrinsic apoptotic signaling pathway in absence of ligand	3	0.08458247	INHBA, SRPX, TGFB2
GOTERM_BP_DIRECT	GO:0007263~nitric oxide mediated signal transduction	3	0.08458247	MT2, MT1, NOS2
GOTERM_BP_DIRECT	GO:2000649~regulation of sodium ion transmembrane transporter activity	3	0.09464287	SCN1B, SCN4B, FXYD5
GOTERM_BP_DIRECT	GO:0002755~MyD88-dependent toll-like receptor signaling pathway	3	0.09464287	TLR13, TLR2, TLR7
GOTERM_BP_DIRECT	GO:0010288~response to lead ion	3	0.09464287	NCAM1, STAR, SPARC
GOTERM_BP_DIRECT	GO:2000406~positive regulation of T cell migration	3	0.09464287	ITGB3, ADAM8, CXCL10
GOTERM_BP_DIRECT	GO:0061036~positive regulation of cartilage development	3	0.09464287	BMP4, BMP2, SCX
GOTERM_BP_DIRECT	GO:0032270~positive regulation of cellular protein metabolic process	3	0.09464287	INHBA, UHRF1, PTK2B
GOTERM_BP_DIRECT	GO:0031529~ruffle organization	3	0.09464287	PLEK, CARMIL1, CSF1R
GOTERM_BP_DIRECT	GO:0070488~neutrophil aggregation	2	0.06430235	S100A8, S100A9
GOTERM_BP_DIRECT	GO:2000098~negative regulation of smooth muscle cell-matrix adhesion	2	0.06430235	APOD, SERPINE1

GOTERM_BP_DIRECT	GO:0003130~BMP signaling pathway involved in heart induction	2	0.06430235	BMP4, BMP2
GOTERM_BP_DIRECT	GO:0071373~cellular response to luteinizing hormone stimulus	2	0.06430235	STAR, CCNA2
GOTERM_BP_DIRECT	GO:0000915~actomyosin contractile ring assembly	2	0.06430235	KIF23, RACGAP1
GOTERM_BP_DIRECT	GO:0031449~regulation of slow-twitch skeletal muscle fiber contraction	2	0.06430235	GM34302, MYH7
GOTERM_BP_DIRECT	GO:1903225~negative regulation of endodermal cell differentiation	2	0.06430235	COL5A2, COL5A1
GOTERM_BP_DIRECT	GO:0051383~kinetochore organization	2	0.09488849	SMC2, SMC4
GOTERM_BP_DIRECT	GO:0031577~spindle checkpoint	2	0.09488849	BIRC5, AURKB
GOTERM_BP_DIRECT	GO:0002246~wound healing involved in inflammatory response	2	0.09488849	HMOX1, CCR2
GOTERM_BP_DIRECT	GO:0035993~deltoid tuberosity development	2	0.09488849	BMP4, SCX
GOTERM_BP_DIRECT	GO:0010046~response to mycotoxin	2	0.09488849	LCN2, ASS1
GOTERM_BP_DIRECT	GO:0035989~tendon development	2	0.09488849	SCX, COL5A1
GOTERM_BP_DIRECT	GO:0071603~endothelial cell-cell adhesion	2	0.09488849	CYP1B1, THBS4
GOTERM_BP_DIRECT	GO:0072138~mesenchymal cell proliferation involved in ureteric bud development	2	0.09488849	BMP4, BMP2
GOTERM_BP_DIRECT	GO:0000053~argininosuccinate metabolic process	2	0.09488849	ASS1, GM5424
GOTERM_BP_DIRECT	GO:1901509~regulation of endothelial tube morphogenesis	2	0.09488849	ADAMTS12, CXCL10
GOTERM_BP_DIRECT	GO:0071378~cellular response to growth hormone stimulus	2	0.09488849	STAR, MYC
GOTERM_BP_DIRECT	GO:0002924~negative regulation of humoral immune response mediated by circulating immunoglobulin	2	0.09488849	PTPN6, FCGR2B

GOTERM_BP_DIRECT	GO:2001180~negative regulation of interleukin-10 secretion	2	0.09488849	CD84, TNFRSF21
GOTERM_BP_DIRECT	GO:0042376~phylloquinone catabolic process	2	0.09488849	CYP4F18, CBR3
GOTERM_BP_DIRECT	GO:0009609~response to symbiotic bacterium	2	0.09488849	GPX1, PTAFR
GOTERM_BP_DIRECT	GO:0071727~cellular response to triacyl bacterial lipopeptide	2	0.09488849	TLR2, CD14
GOTERM_BP_DIRECT	GO:0061035~regulation of cartilage development	2	0.09488849	BMP4, SCX