Supplementary material

Table S1. Grouping information for the combination among the expression of p53,p21,nm23,and VEGF.

Group	Score=0	Score=1	Score=2	Score=3	Score=4
p53/p21	+/-	+/+;-/-	-/+		
p53/nm23	+/-	+/+;-/-	-/+		
p53/VEGF	+/+	+/-;-/+	-/-		
p21/nm23	-/-	-/+;+/-	+/+		
p21/VEGF	-/+	+/+;-/-	+/-		
nm23/VEGF	-/+	+/+;-/-	+/-		
p53/p21/nm23	+/-/-	-/-/-;+/+/-;+/-/+	+/+/+;-/-/+;-/+/-	-/+/+	
p53/p21/VEGF	+/-/+	-/-/+;+/+/+;+/-/-	+/+/-;-/-/-;-/+/+	-/+/-	
p53/nm23/VEGF	+/-/+	-/-/+;+/+/+;+/-/-	+/+/-;-/-/-;-/+/+	-/+/-	
p21/nm23/VEGF	-/-/+	+/-/+;-/+/+;-/-/-	-/+/-;+/-/-;+/+/+	+/+/-	
p53/p21/nm23/VEGF	+/-/-/+	-/-/-/+;+/+/-/+; +/-/+/+;+/-/-/-	-/+/-/+;+/+/+/+;+/-/+/-; -/-/-/-;-/-/+/+;+/+/-/-	+/+/+/-;-/-/+/-; -/+/-/-;-/+/+/+	-/+/+/-

Notes: According to previous studies show the role of these proteins,defined p53 positive =0, p53 negative =1, p21 positive =1, p21 negative =0, nm23 positive =1, nm23 negative =0, VEGF positive =0, VEGF negative =1.

Table S2. Clinical parameters of 212 HBV-related HCC in GSE14520 database

Variables		**Patients(n=212)**	OS			
			No. of events	**MST(months)**	**HR (95% CI)**	***P***
Age**(year)**						
	≤60	175	69	NA	1	
	>60	37	13	NA	0.864(0.478-1.564)	0.63
Gender						
	Female	29	8	NA	1	
	Male	183	74	NA	1.704(0.821-3.534)	0.152
Multinodular						
	Single	167	59	NA	1	
	Multiple	45	23	47	1.607(0.992-2.604)	0.054
Tumor Size[₤]						
	≤5	137	46	NA	1	
	>5	74	36	53	1.975(1.274-3.060)	**0.002**
Cirrhosis						
	NO	17	2	NA	1	
	Yes	195	80	NA	4.335(1.065-17.638)	**0.041**
BCLC stage[£]						
	0	20	2	NA	1	
	A	74	48	NA	4.119(1.001-16.951)	**0.05**
	B	22	12	46	8.992(2.005-40.320)	0.004
	C	27	20	13	18.993(4.419-81.632)	<0.001
AFP**(ng/ml)**[Ψ]						
	≤300	115	39	NA	1	
	>300	94	43	NA	1.546(1.002-2.385)	**0.049**

Notes: [₤] information regarding Tumor Size was unavailable for 1 patients; [£] information regarding BCLC stage was unavailable for 69 patients; [Ψ] information regarding AFP level was unavailable for 3 patients;

Table S3. GO and KEGG enrichment results of VEGF and its co-expression genes

Category	Term	Count	%	P Value	Genes
GOTERM_MF_DIRECT	GO:0005515~protein binding	562	0.392694	5.46E-13	LDHA, XRCC3, XRCC2, EHHADH, RUSC1, PPP2R5D, RUSC2, VPS52, CXORF40A, INTS3, MYLIP, KIAA0319L, SSR1, TMEM140, CUL3, CDCA8, HTR1B, CLK2, INTS7, INCENP, MAP3K9, SERPINE1, LSM2, LSM1, DDAH2, PCBD1, MPDZ, CRYAB, PTBP1, ESPL1, PTPRO, MARK2, GRB10, ZNF783, SPAG4, UBL4A, MAPK7, MYBBP1A, ADAMTS5, SH3GL1, HSD17B10, KIAA1109, PPP2R3B, NFKBIE, ERBB3, HFE, HSPA1A, NAGK, VPS72, PPP1R3C, IL23A, RAC1, MKI67, HGD, UBE2L6, TMEM110, GAS1, DVL1, SYNE1, UPF3B, WDR61, FNBP4, H3F3A, HGS, TNK1, POP7, RERE, ELF3, MARCKSL1, GRIP1, EZH2, BNIP3, RNF187, PDIA4, RASSF7, DAXX, DGCR14, GTSE1, RTN3, IL4R, SPG21, USP11, MAGEH1, ANGPT2, SLC22A1, FMNL1, CDC6, ARHGEF2, SH3PXD2A, CLIC1, MMP15, WAS, TTF2, CARD10, KLHDC3, TAF11, INHBB, INHBA, DOK2, MAST2, USP22, THOC2, TBC1D9, MKNK2, HK2, FPR1, FHL2, ITM2C, SF3B4, SF3B2, NPDC1, SORBS3, EXOC4, WIPF2, SERPINC1, DHX16, PPP3CA, ARMCX1, EXOC2, RASA1, FLRT3, SSRP1, SHMT2, BRD2, BRD3, SELL, PAK1IP1, PPP1R11, CSNK2B, AXL, TRIM27, ZNF26, TRIM22, MTTP, RLF, CSNK1D, SFPQ, ZNF460, MAT2B, BARD1, RALY, RNASEL, PRPF4B, LMO2, STK38, ATOX1, ZNF451, RBM4, KNTC1, SLC7A8, ADH1A, CRADD, RCBTB2, GHITM, CDKN2A, APOA1, CDKN2C, SLC2A1, SMARCD1, LONRF3, FBXO24, ANKZF1, FBXO22, DDOST, ATG9A, ACTN4, DFFA, STK24, PCTP, TACC3, TMEM106C, NFU1, DCUN1D1, MAD2L1BP, HIF1A, THBD, TIMELESS, HSPB6, FBXO17, IGBP1, PRCP, VAMP5, ZNF587, MFAP4, SPTB, PHKA2, TRAF2, HMGB3, CCDC90B, ADORA2A, ADAMTSL4, ZNF330, TUBB, MEIS2, FBXW4, HIST1H4C, ASF1B, MRC1, TAF6, C14ORF159, SMG5, MEA1, EFEMP1, BRIP1, WHSC1, TEAD3, EHMT2, CDKN1C, EPS15, APEH, ATF5, CDKN1B, CRBN, HDAC1, TRAF3IP3, PTTG1IP, TDG, TBXA2R, ABL1, NOMO2, ZNF410, IER3, E2F3, LEPR, CLSTN1, DPH1, C1ORF35, NDUFAF1, SPRY4, SLC1A5, KIF2C, ALAS1, MAZ, HEY1, CASP1, LOXL2, SUCLA2, CASP2, ANKS1A, MID1IP1, SLC9A3R1, CCNL2, LCK, NCOA6, MAPRE2, ZFPM2, JAM2, CA1, EGLN3, RAG1, CDC73, NFYA, DCN, PIPOX, ANXA6, CHD1L, TSC22D4, TMED1, CD2, GPSM2, CD4, SELPLG, HSPA8, CEBPA, FLT1, GMDS, SNX27, VHL, CEBPG, ANXA1, SAMHD1, DPYSL4, BCS1L, COTL1, UBE2Q1, IFIT1, NEB, HBZ, GDF15, DMBT1, MRPL40, ATP1B1, EFNA1, STAT5A, U2AF2, ZNRF4, RAB1B, PTPN21, CD53, CD2AP, SHH, CD48, KIF13A, HOOK1, DDX11, HOMER3, KIFAP3, RAPGEF6, C7ORF49, RARA, CRY1, BCL7A, GTPBP2, F12, POLH, BYSL, STRN4, RAP1GDS1, RAD9A, TAF6L, HES1, LILRB2, VEGFC, KRT17, BAZ1B, CCR5, ABT1, TXNDC5, VEGFA, EFNA4, ALDOA, FIP1L1, CLCN3, ELL, FCER2, KEL, TAF9B, BANF1, TJAP1, TIPRL, TK1, SLC4A1AP, FBXO3, FBXO9, CDC37L1, KLF5, NOTCH2NL, CDC23, NCKAP1L, CDC20, YTHDC2, RAD54L, EPHA3, CCT7, YY1AP1, TULP3, NUP62, ATP2A2, PTCD3, ETS2, AIRE, POMP, RIT1, CLEC7A, KLF2, NCOR2, PPARD, HIP1R, COPS4, GJA1, GJA4, RBM4B, TNFRSF11A, CEP250, COX17, TOP2A, ICAM1, CCNK, POGZ, CCNH, GZMA, ATP4B, VIL1, FLOT1, POLR1C, GTF2B, RBBP6, CD163, MED4, CKM, G6PD, ADM, SIAH1, REV3L, PRF1, THAP7, PPFIA4, RAP1GAP, SHFM1, LANCL1, ZBTB16, SEC14L4, SFN, CYLD, LPXN, MDC1, NCAPG, FAT4, ETV1, BCL3, CD24, PEX12, BCAS3, GDI1, PLEK, NASP, GMNN, BCKDHB, ATP1A1, ITPR3, HYI, SLC16A3, UBTF, MAPK13, FYN, MAPK14, PHF21A, PGK1, PYGB, CRABP1, TUFT1, CHMP4A, MORF4L2, CBX4, PKMYT1, APOBEC3G, SAE1, ITPKB, TLR6, FLCN, MRPS31, KLHL3, MMP2, PDHB, KLHL2, TTR, PTGIS, TBC1D17, RBCK1, SRRM1, CUTA, DTL, TRIM36, TNS1, TRIM33, RIOK3, FNBP1L, SNRPB, RNF24, SNRPA, SNRPF, DYNLRB1, PRPS2, IFIH1, TSHZ2, FGFR3, SNX2, COPS7A, SOX4, NEDD9, MAP4K1, ENSA, SRF, FXYD6,

					LLGL2, RASAL2, UBE2D3, MTCH1, SCARB1, UBAP2L, NDRG1, ARL6IP5, RNF13, SREBF1, MRPS27, PTPN6, TMEM97, CSTF3, GABARAPL1, MAFB, CPS1, REEP5, CORO1A, C2ORF42, GCM2, PLEKHA5, PHF1, NEDD4, PPID, LAGE3, TROAP, HOXB6, RFX1, KCTD17, SPCS1, CD79A, SCMH1, KCTD13, PLEKHA1, ARHGAP10, TACR3, FOXK2, HPS4, SLA, AKT1, ACVR1B, TDO2, GSN, POU5F1, KLHL22, SHC1, PLCB1, SHC3, PHC2, KHDRBS1, KIAA0907, NOL3, PFKL, RING1, LDB2, MCM3, UBE2B, NLRP1, UBE2O, DDR1, ALDH7A1, CRKL, BTG2, C1QBP, LARP7, CFL1, TNNI3K, KPNA3, PPP1R15A, C1D, CXORF57, HCFC1, TRIB3, NPAS2, ENO2, SLC25A46, SLC39A7, YES1, ENO1, TNPO3, EPO, DCTD, PTPRC, ZBTB7A, IL2RB, NUP153, GIMAP5, MSH5, PSRC1, CEP63, RACGAP1, UBL5, WSB1, TRPC4AP, IGFBP2, IGFBP3, ATP8A1
GOTERM_CC_DIRECT	GO:0005829~cytosol	253	0.176782	1.02E-12	LDHA, STAT5A, EHHADH, PPP2R5D, RUSC2, VPS52, MYLIP, SHH, HOOK1, CUL3, CDCA8, HOMER3, KIFAP3, INCENP, CH25H, RPL26L1, RAPGEF6, SMOX, LSM2, LSM1, DDAH2, CRYAB, PCBD1, BYSL, RAP1GDS1, ESPL1, RIC8B, FARP2, GRB10, ALOX15B, CCR2, UBL4A, HARS, MAPK7, MPST, ALDOA, CHKA, NFKBIE, PFKFB3, HSPA1A, NAGK, BANF1, CAPZB, TK1, PPP1R3C, RAC2, RAC1, FBXO3, CDC42EP3, ARHGEF10L, MOCS1, CDC23, UBE2L6, HGD, NCKAP1L, CDC20, GAS2, ARFIP1, DVL1, CCT7, UPF3B, POMP, HGS, TNK1, GRIP1, COPS4, GJA1, DAXX, GTSE1, MSRA, CEP250, SPG21, LMOD1, FMNL1, CDC6, ARHGEF2, POLR1C, GRHPR, RBBP6, MORC2, WAS, KLHDC3, DOK2, CKM, G6PD, OTOF, ADK, SIAH1, TPH1, PPFIA4, RAP1GAP, HK2, DPYS, ZBTB16, SFN, CYLD, SORBS3, CBR1, MTMR1, NCAPG, PDE1A, EXOC4, WIPF2, PPP3CA, EXOC2, RASA1, GDI1, PLEK, GMNN, CSNK2B, TRIM27, TRIM22, PCK1, CSNK1D, MAPK13, FYN, MAPK14, MAT2B, PGK1, DUSP6, RNASEL, ALDH1L1, IL16, CRABP1, ATOX1, CHMP4A, KNTC1, PKMYT1, ADH1B, SAE1, ITPKB, ADH1A, APOBEC3G, ITPKA, KLHL3, KLHL2, CRADD, TBC1D17, CDKN2A, APOA1, CDKN2C, SLC2A1, RGN, RBCK1, SRRM1, ITPK1, SAR1B, STK24, DFFA, NUDT3, PCTP, TAZ, PDE4C, PNPLA4, DDIT4, NFU1, HIF1A, TRIM36, RIOK3, TRIM34, IGBP1, SNRPB, SNRPF, PCCB, SPTB, PHKA2, TRAF2, FGD1, IFIH1, SNX2, RASAL2, UBE2D3, GALE, GLO1, NDRG1, SREBF1, PTPN6, GABARAPL1, SMG5, FN3KRP, EPS15, APEH, PDE7B, CORO1A, CDKN1B, PLEKHA5, HDAC1, NEDD4, FABP4, ABL1, ARHGAP10, IER3, METAP1, DPH1, ARHGAP15, AKT1, KIF2C, CRYL1, TDO2, AKR1C4, GSN, POU5F1, SHC1, CAT, PLCB1, SHC3, CASP1, CASP2, HPD, KHDRBS1, NOL3, PFKL, NUP88, MID1IP1, NLRP1, ARHGAP25, UBE2O, ALDH7A1, CAPN10, CRKL, C1QBP, BTG2, LCK, KPNA3, CA1, PPP1R15A, LCP1, CPLX3, ADH5, EGLN3, ADH6, TRIB3, NPAS2, ENO2, PNPO, YES1, HSPA8, ENO1, DCTD, CENPM, GIMAP4, GMDS, GIMAP6, VHL, SNX27, PSRC1, DPYSL4, CEP63, RACGAP1, UBE2Q1, WSB1, IFIT1, NEB
GOTERM_CC_DIRECT	GO:0005737~cytoplasm	341	0.238272	1.25E-08	HMGN1, LDHA, XRCC3, XRCC2, STAT5A, EHHADH, PTPN21, AQP7, CD2AP, HTR1B, DDX11, HOMER3, C7ORF49, ZNF395, RARA, SMOX, DDAH2, LSM1, PDPR, ARC, POLH, CRYAB, MPDZ, PCBD1, BYSL, STRN4, ESPL1, RAD9A, RIC8B, ERMAP, FARP2, HES1, LILRB2, GRB10, KRT17, CCR5, MTF2, ALOX15B, SPAG4, CCR2, VEGFA, HARS, UBL4A, STC1, MAPK7, NEK4, DOC2B, MYBBP1A, SH3GL1, HSD17B10, NFKBIE, ELL, HSPA1A, CAPZB, BANF1, TIPRL, RAC2, RAC1, SLC4A1AP, FBXO3, CDC42EP3, CDC37L1, FBXO9, ARHGEF10L, KLF5, MSTO1, MKI67, NOTCH2NL, CDC20, CD5L, CCT7, SYNE1, YY1AP1, TULP3, UPF3B, NUP62, WDR61, ETS2, POMP, AIRE, HGS, TNK1, CLEC7A, POP7, PLCXD1, BMP6, ELF3, HIP1R, MARCKSL1, UBE2G1, EZH2, BNIP3, RNF187, TTLL7, RASSF7, DAXX, MSRA, ZNF146, SPG21, USP11, LMOD1, USP16, COX17, TOP2A, MAGEH1, CDC6, ARHGEF2, SH3PXD2A, POGZ, LPGAT1, VIL1, TTF1, GRHPR, DECR1, CLIC1, MORC2, TTF2, CARD10, KLHDC3, PJA2, MAST2, G6PD, ADM, PFDN6, ADK, SIAH1, TRIOBP, MKNK2, C11ORF21, LANCL1, SFN, LOC440434,

					LPXN, MTMR1, FAM117A, NCAPG, EXOC4, DHX16, BCL3, PPP3CA, LECT2, BCAS3, RASA1, FLRT3, SSRP1, FLRT2, GDI1, BRD2, SHMT2, NBPF10, PLEK, NASP, GMNN, NBPF11, CSNK2B, TRIM27, PPP1R11, ITPR3, TRIM22, PCK1, CLEC3B, MAPK14, SFPQ, USP48, PYGB, DUSP6, BARD1, ALDH1L1, CRABP1, STK38, IL16, TUFT1, CHMP4A, RBM4, KNTC1, SLC7A8, APOBEC3G, FLCN, CRADD, KLHL2, TTR, CDKN2A, CDKN2C, SLC2A2, RGN, RBMS3, ACTN4, NUDT3, DTL, STK24, DFFA, PNPLA4, TACC3, DDIT4, NFU1, RNF130, MAD2L1BP, TNS1, HIF1A, HSPB6, FNBP1L, TRIM34, IGBP1, CSTB, SNRPA, DYNLRB1, SPTB, TRAF2, FGD1, HMGB3, LST1, SSH3, HDGF, SNX2, TFEB, COPS7A, SOX4, NEDD9, MAP4K1, ENSA, BICC1, SRF, LLGL2, RASAL2, TUBB, SRR, SCARB1, NDRG1, GLO1, UBAP2L, SDF4, IFT140, SREBF1, PTPN6, PHACTR4, TAF6, SMG5, MEA1, MTHFSD, BRIP1, MTRF1L, WHSC1, CDKN1C, EPS15, P2RX5, FBXO38, APEH, ATF5, CORO1A, CDKN1B, CRBN, PLEKHA5, PHF1, HDAC1, THSD1, NEDD4, PPID, TROAP, KCTD17, PTTG1IP, FABP4, ZNF318, CD79A, ABL1, PLEKHA1, CYB5R3, METAP1, E2F3, TACR3, HPS4, NDUFAF1, SPRY4, AKT1, CCHCR1, CRYL1, ALAS1, AKR1C4, HEY1, GSN, POU5F1, NBPF1, KLHL22, PLCB1, PPP1R14B, CASP2, ANKS1A, ZCCHC2, NOL3, PFKL, RING1, UBE2NL, SLC9A3R1, UBE2B, LAP3, UBE2O, LARP6, ALDH7A1, C1QBP, FRMD4A, LARP7, TBCC, CFL1, TNNI3K, ZFPM2, MAPRE2, KPNA3, CA1, PPP1R15A, LCP1, C1D, EGLN3, HCFC1, CDC73, DCN, IVNS1ABP, NPAS2, CHD1L, RGS12, TSC22D4, CYP26B1, PNPO, GPSM2, YES1, ENO1, TNPO3, DCTD, NUP153, MBTPS2, GMDS, SNX27, PSRC1, GRSF1, ANXA1, DPYSL4, COTL1, RACGAP1, UBL5, CYP4A11, IFIT1, GDF15, DMBT1
GOTERM_CC_DIRECT	GO:0005654~nucleoplasm	203	0.141845	2.06E-08	HMGN1, XRCC3, XRCC2, STAT5A, U2AF2, PPP2R5D, INTS3, CUL3, CDCA8, DDX11, CLK2, INCENP, INTS7, RARA, LSM2, RPP21, POLH, PCBD1, CRYAB, BYSL, LIG1, PTBP1, RAD9A, HES1, BAZ1B, MTF2, MAPK7, MYBBP1A, PPP2R3B, FIP1L1, ELL, PFKFB3, TAF9B, HSPA1A, BANF1, VPS72, TCF20, SLC4A1AP, FBXO3, KLF5, UBE2L6, CDC23, CDC20, RAD54L, SYNE1, UPF3B, WDR61, ETS2, FNBP4, POMP, H3F3A, CLEC7A, POP7, NCOR2, GTF3A, PPARD, COPS4, EZH2, BNIP3, RNF187, DAXX, GTSE1, MSRA, FANCE, TOP2A, CDC6, CCNK, POGZ, SNAPC1, CCNH, VIL1, TTF1, POLR1C, DECR1, RBBP6, GTF2B, TAF11, MED4, ADK, THOC2, REV3L, SKIV2L, MKNK2, FHL2, SF3B4, SF3B2, MDC1, BCL3, DHX16, PPP3CA, SSRP1, JARID2, GMNN, NASP, PAK1IP1, CSNK2B, TRIM27, ITPR3, TRIM22, CSNK1D, UBTF, SFPQ, MAPK14, PHF21A, USP48, BARD1, DUSP6, PRPF4B, RBM4, MORF4L2, CBX4, PKMYT1, SAE1, PDHB, CDKN2A, RGN, SRRM1, STK24, DTL, DFFA, NFU1, RCL1, HIF1A, TIMELESS, TRIM33, SNRPB, SNRPA, SNRPF, HDGF, SOX4, COPS7A, ENSA, SRF, LLGL2, UBE2D3, HIST1H4C, ASF1B, SREBF1, CSTF3, TAF6, BRIP1, WHSC1, TEAD3, EHMT2, ATF5, PLEKHA5, CDKN1B, PHF1, HDAC1, PPID, RFX1, TDG, ZNF318, SCMH1, ABL1, KCTD13, PLEKHA1, E2F3, FOXK2, DEK, AKT1, ALAS1, HEY1, POU5F1, LOXL2, PHC2, KHDRBS1, ANKS1A, NUP88, RING1, MCM3, MSC, UBE2B, CCNL2, LAP3, LARP7, NCOA6, ZFPM2, KPNA3, C1D, RAG1, EGLN3, TRIB3, HCFC1, CDC73, NFYA, IVNS1ABP, RPA4, NPAS2, CHD1L, SLC39A7, PNPO, HSPA8, TSEN34, FAM50A, NUP153, CENPM, VHL, SNX27, CEBPG, ANXA1, SAMHD1, RACGAP1
GOTERM_MF_DIRECT	GO:0019899~enzyme binding	40	0.02795	1.99E-06	TRAF2, ADORA2A, U2AF2, EHHADH, CBX4, HSPA1A, DAXX, BANF1, TSPYL1, AKT1, APOA1, RAC1, RARA, SLC4A2, CD4, CAT, PPP3CA, YES1, PLCB1, TOP2A, CASP2, HSPA8, CUTA, VHL, LDB2, RAD9A, CDC20, COTL1, NLRP1, DVL1, HIF1A, TULP3, ATP2A2, HDAC1, FYN, MAPK14, NCOA6, MAT2B, USP22, SLC27A2
GOTERM_CC_DIRECT	GO:0070062~extracellular exosome	194	0.135556	2.33E-06	ATP1B1, LDHA, EFNA1, RUSC2, RAB1B, CD53, KIAA0319L, CD2AP, CUL3, CD48, DDX11, PLOD1, PLOD2, KIFAP3, SERPINE1, RPL26L1, IGLL1, DDAH2, GNG7, ITFG1, F12, CLCA4, PTPRF, PCBD1, CRYAB, PTBP1, RAP1GDS1, F9, TAF6L, PTPRO, PRELP, KRT17, ALOX15B,

					TXNDC5, MPST, ALDOA, FCER2, NAGK, BANF1, CAPZB, RAC2, RAC1, FGL2, SPP2, HGD, NCKAP1L, CD5L, KRT35, CCT7, HYOU1, H3F3A, HGS, MARCKSL1, UBE2G1, COPS4, GJA1, RTN3, MSRA, CEP250, SEMA3G, CETP, VWA1, SCN10A, FMNL1, ICAM1, CAMP, VIL1, FLOT1, CLIC1, DECR1, GRHPR, WAS, G6PD, SLC27A2, C7, GANAB, LANCL1, DPYS, SFN, ITM2C, LOC440434, CBR1, FAT4, SERPINC1, C2, FLRT2, SHMT2, AXL, CSNK2B, ATP1A1, PCK1, TMEM2, CLEC3B, MAPK14, MAT2B, PGK1, PYGB, ALDH1L1, CHMP4A, SLC7A8, CXCL12, PDHB, TTR, APOA1, GHITM, SLC2A1, CUTA, ACTN4, STK24, NUDT3, TRIM36, FNBP1L, PRCP, VAMP5, SNRPB, CSTB, NEU1, MFAP4, PRPS2, SNX2, TUBB, UBE2D3, HIST1H4C, GALE, GLO1, NDRG1, SCARB1, SDF4, ARL6IP5, PTPN6, EFEMP1, REEP5, APEH, OMD, CORO1A, NEDD4, PTTG1IP, FABP4, PLEKHA1, KCTD12, CYB5R3, CLSTN1, CLDN5, IGFBP6, SLC1A5, ACVR1B, CRYL1, AKR1C4, GSN, ACYP1, CAT, SUCLA2, PLCB1, HPD, PFKL, UBE2NL, SLC9A3R1, LAP3, DDR1, ALDH7A1, CRKL, BTG2, CFL1, LCK, CA1, PROS1, LCP1, ADH5, ADH6, ANXA6, ENO2, PNPO, YES1, HSPA8, DPT, ENO1, DCTD, PTPRC, LIPA, GMDS, TMC5, ANXA1, RACGAP1, COTL1, UBL3, HPR, CYP4A11, NEB, HBZ, GDF15, IGFBP2, IGFBP3, DMBT1, ATP8A1
GOTERM_BP_DIRECT	GO:0001666~response to hypoxia	25	0.017469	9.71E-06	LDHA, ATP1B1, EGLN3, BNIP3, CXCL12, SRF, MMP2, PLOD1, PLOD2, CAT, CD24, CASP1, LOXL2, ANGPT2, EPO, NOL3, ACTN4, CRYAB, DDIT4, VEGFC, CDKN1B, HIF1A, ADM, CA9, VEGFA
GOTERM_BP_DIRECT	GO:0050900~leukocyte migration	20	0.013975	1.69E-05	ICAM1, PTPN6, ATP1B1, SELL, SLC7A8, FPR1, MMP1, SLC16A3, CD48, DOK2, THBD, FYN, LCK, CD2, SHC1, JAM2, YES1, SELPLG, ANGPT2, PROS1
GOTERM_BP_DIRECT	GO:0006464~cellular protein modification process	18	0.012577	2.78E-05	PHKA2, STK38, UBE2L6, SAE1, MMP15, TTLL7, UBL5, AKT1, MSRA, UBE2D3, ST3GAL2, PLOD1, PLOD2, UBL4A, ABL1, LOXL2, YES1, FBXO22
GOTERM_BP_DIRECT	GO:0006461~protein complex assembly	19	0.013276	2.94E-05	TRAF2, IL2RB, GMNN, VIL1, KNTC1, HFE, NCKAP1L, SLC9A3R1, NDUFAF1, CD2AP, WAS, CARD10, HES1, LPXN, CLGN, KIFAP3, PPID, SLC2A1, KPNA3
GOTERM_MF_DIRECT	GO:0042802~identical protein binding	66	0.046117	3.70E-05	LDHA, CHMP4A, CLDN5, BNIP3, KLHL2, HOOK1, AKT1, TTR, TDO2, ALAS1, APOA1, CLK2, SLC2A1, VWA1, CASP2, PHC2, KHDRBS1, PCDHB8, NOL3, PFKL, PCBD1, CRYAB, VIL1, WAS, INHBA, G6PD, ZNF783, LCK, VEGFA, SNRPA, SIAH1, MAPRE2, LCP1, PRPS2, MPST, SH3GL1, ALDOA, TRAF2, THAP7, ERBB3, ADORA2A, FHL2, HCFC1, SFN, ZBTB16, TK1, GPSM2, GALE, LECT2, SDF4, TNPO3, DCTD, SHMT2, NUP153, GMDS, TRIM27, CSNK2B, HGD, DVL1, EPS15, CCT7, APEH, FYN, KCTD17, AIRE, KCTD13
GOTERM_CC_DIRECT	GO:0016020~membrane	151	0.10551	5.74E-05	KIFC1, ATP1B1, LDHA, EFNA1, TNFSF15, VPS52, SLC7A8, PKMYT1, ITPKB, CD48, CUL3, GLT8D1, SLC2A6, SLC2A2, SLC2A1, DHX34, IGLL1, SLC4A2, ANKZF1, DDOST, CUTA, ATG9A, STK24, BYSL, PTBP1, STRN4, PNPLA4, MARK2, OGFRL1, TMEM106C, VEGFC, LILRB2, ALOX15B, VEGFA, UBL4A, NEU1, DOC2B, MYBBP1A, DYNLRB1, ALDOA, CLCN3, KIAA1109, LST1, ADORA2A, MMD, LRBA, SNX2, MAP4K1, SFXN1, CAPZB, SLCO2A1, SLC29A1, RAC2, FOLR2, MTCH1, RAC1, HIST1H4C, ARL6IP5, SDF4, GAL3ST1, CSF1R, PTPN6, MKI67, NCKAP1L, GAS2, CD5L, EPS15, HYOU1, CORO1A, CRBN, PLEKHA5, ATP2A2, PTTG1IP, RIT1, TNK1, NCOR2, CYB5R3, SLC20A1, LEPR, HPS4, CYC1, MAN1B1, ALG5, NUP188, ARHGAP15, GTSE1, SPRY4, SLC1A5, ACVR1B, KIF2C, MSRA, SLC1A3, PIGG, LMOD1, CAT, LOXL2, CASP2, SLC22A1, FMNL1, KHDRBS1, ICAM1, NOL3, LPGAT1, PFKL, FLOT1, CLIC1, MCM3, SLC9A3R1, CD163, DDR1, SLC26A6, MED4, G6PD, C1QBP, CFL1, PPP1R15A, DEGS1, PRF1, GANAB, RAP1GAP, TBC1D8, HK2, HCFC1, ANXA6, LPXN, NCAPG, FAT4, EXOC4, SLC39A7,

					CD4, PPP3CA, CD24, SELPLG, EXOC2, HSPA8, SLC39A1, ENO1, PTPRC, IL2RB, PLEK, VHL, RRBP1, SELL, TRIM27, ATP1A1, ITPR3, SLC16A3, PGK1, DMBT1, ATP8A1, PYGB
GOTERM_BP_DIRECT	GO:0090023~positive regulation of neutrophil chemotaxis	8	0.00559	8.59E-05	CCR7, IL23A, C1QBP, RAC2, CCL21, RAC1, NCKAP1L, CCL19
GOTERM_BP_DIRECT	GO:0007165~signal transduction	90	0.062887	1.30E-04	SLC20A1, CRABP1, PPP2R5D, IGFBP6, TNFSF15, GJA1, ITPKB, DEK, CD53, RASSF7, TLR6, ARHGAP15, CXCL12, CD2AP, ITPKA, CRADD, CD48, AKT1, ACVR1B, TNFRSF11A, EVI2A, KIFAP3, IL4R, SHC1, RARA, CASP1, PLCB1, SHC3, ITPK1, ANGPT2, KHDRBS1, DFFA, STK24, PDE4C, CLIC1, ARHGAP25, VEGFC, LILRB2, GRB10, DOK2, HIF1A, THBD, KRT17, ADM, IGBP1, MAPRE2, MAPK7, CLEC5A, SH3GL1, TRAF2, FGD1, CHKA, RAP1GAP, ERBB3, HDGF, FPR1, NEDD9, SP110, SFN, OR1G1, RASAL2, LPXN, RGS12, RAC2, PDE1A, TMED1, CD4, CDC42EP3, RASA1, CSF1R, EPO, CREBL2, MRC1, GDI1, GABRE, IL2RB, SNX27, CSNK2B, AXL, ANXA1, RACGAP1, P2RX5, PDE7B, CSNK1D, MAPK14, HGS, RIT1, IGFBP2, GDF15, ARHGAP10
GOTERM_MF_DIRECT	GO:0008134~transcription factor binding	31	0.021661	1.96E-04	PPARD, TAF9B, FHL2, DAXX, SRF, SORBS3, MEIS2, CDKN2A, HEY1, POU5F1, BCL3, RARA, BCAS3, CRY1, CEBPA, KLF5, ARHGEF2, VHL, MAFB, CEBPG, CSNK2B, GTF2B, HES1, HIF1A, HDAC1, C1QBP, PPID, TDG, ZFPM2, MYBBP1A, NCOR2
GOTERM_MF_DIRECT	GO:0004842~ubiquitin-protein transferase activity	34	0.023757	2.53E-04	TRAF2, UBE2G1, RAG1, RNF187, MYLIP, KLHL3, KLHL2, CUL3, UBE2D3, KLHL22, RBCK1, FBXO24, FBXO3, PEX12, FBXO9, FBXO22, RNF13, DTL, VHL, TRIM27, UBE2L6, CDC23, RBBP6, UBE2B, WSB1, PJA2, UBE2O, RNF130, TRIM36, TRIM33, NEDD4, SIAH1, KCTD13, BARD1
GOTERM_CC_DIRECT	GO:0015629~actin cytoskeleton	25	0.017469	2.79E-04	ALDOA, TRIOBP, ARC, ACTN4, ELL, KNTC1, FHL2, IVNS1ABP, SLC9A3R1, WAS, CAPZB, CD2AP, KLHL2, SLC16A3, MSRA, CORO1A, NEB, NCAPG, GSN, CFL1, RARA, ABL1, CDC42EP3, LCP1, SPTB
GOTERM_BP_DIRECT	GO:0045638~negative regulation of myeloid cell differentiation	7	0.004891	2.94E-04	MEIS2, HMGB3, WDR61, GPR171, CDC73, ITPKB, ZBTB16
GOTERM_BP_DIRECT	GO:0016925~protein sumoylation	17	0.011879	3.61E-04	NUP153, IFIH1, NUP88, ZNF451, CBX4, RING1, SAE1, NUP188, CDCA8, CDKN2A, NUP62, MDC1, INCENP, TDG, SCMH1, TOP2A, PHC2
GOTERM_BP_DIRECT	GO:0006513~protein monoubiquitination	8	0.00559	4.54E-04	CUL3, UBE2O, UBE2D3, NEDD4, DTL, KLHL22, PEX12, UBE2B
GOTERM_BP_DIRECT	GO:0031529~ruffle organization	6	0.004192	5.07E-04	CCR7, PLEK, CCL21, RAC1, CSF1R, PLEKHA1
GOTERM_BP_DIRECT	GO:0006974~cellular response to DNA damage stimulus	24	0.01677	5.27E-04	CCNK, XRCC3, DTL, EGLN3, RAD9A, INTS3, RBBP6, UBE2B, AKT1, NPAS2, CHD1L, TIMELESS, BAZ1B, PHF1, BTG2, DDX11, NCOA6, BCL3, NEK4, ABL1, USP16, TOP2A, PPP1R15A, BARD1
GOTERM_MF_DIRECT	GO:0008022~protein C-terminus binding	22	0.015372	5.44E-04	ATP1B1, MKI67, GRIP1, MPDZ, SAE1, CDC20, MID1IP1, ZBTB16, BANF1, CD2AP, CORO1A, CEP250, ATP2A2, MDC1, HOMER3, LCK, TNNI3K, SIAH1, PEX12, ABL1, KPNA3, TOP2A
GOTERM_MF_DIRECT	GO:0016597~amino acid binding	7	0.004891	7.21E-04	SHMT2, TDO2, SLC1A3, OTC, DPYS, TPH1, DDAH2
GOTERM_MF_DIRECT	GO:0042826~histone deacetylase binding	15	0.010481	8.25E-04	SMG5, GMNN, CDC20, HSPA1A, RAD9A, SRF, HES1, HIF1A, HDAC1, SFPQ, RAC1, RARA, CRY1, TOP2A, NCOR2
GOTERM_BP_DIRECT	GO:0008360~regulation of cell shape	18	0.012577	9.64E-04	FMNL1, ALDOA, ICAM1, FGD1, LST1, VIL1, ANXA1, GAS2, SLC9A3R1, ARHGAP15, CORO1A, CSNK1D, FYN, VEGFA, WIPF2, CDC42EP3, RASA1, CSF1R
GOTERM_BP_DIRECT	GO:0051289~protein homotetramerization	11	0.007686	9.68E-04	ALDOA, SHMT2, PFKL, PCBD1, SRR, SAMHD1, DPYS, CAT, DECR1, USP16, TK1

GOTERM_CC_DIRECT	GO:0005884~actin filament	11	0.007686	0.00145379	CORO1A, RAC2, FYN, RAC1, WIPF2, GAS2, LMOD1, YES1, CAPZB, LCP1, MARK2
GOTERM_BP_DIRECT	GO:0006469~negative regulation of protein kinase activity	14	0.009782	0.0018197	FLRT3, PTPRC, FLRT2, ADORA2A, TRIM27, TRIB3, SFN, DCN, CAMK2N1, DVL1, AKT1, CDKN2A, FABP4, RGN
GOTERM_BP_DIRECT	GO:0061621~canonical glycolysis	7	0.004891	0.00182358	ALDOA, PFKL, PFKFB3, ENO2, HK2, PGK1, ENO1
GOTERM_CC_DIRECT	GO:0043234~protein complex	36	0.025155	0.00185196	SNX2, VPS72, CD48, AKT1, TTR, CDCA8, TUBB, CDKN2A, CEP250, INCENP, BCL3, HIST1H4C, ASF1B, TOP2A, DDOST, HIGD1A, SREBF1, GDI1, ARHGEF2, ACTN4, NASP, STRN4, ANXA1, CDC20, ATP1A1, CPS1, GNAT3, CORO1A, CDKN1B, ATP2A2, HDAC1, NEB, H3F3A, PRPS2, SLC27A5, SPTB
GOTERM_CC_DIRECT	GO:0005634~nucleus	314	0.219406	0.00194505	MRPL40, HMGN1, KIFC1, LDHA, XRCC3, STAT5A, RUSC1, U2AF2, PPP2R5D, INTS3, DNASE1L3, CUL3, CDCA8, DDX11, CLK2, ZNF248, DHX34, C7ORF49, ZNF395, RARA, SMOX, LSM1, CRY1, CRYAB, PMCH, LIG1, BYSL, PTBP1, ESPL1, RAD9A, TAF6L, HES1, ZNF787, SPAG7, ABT1, ZNF783, MTF2, ALOX15B, UBL4A, STC1, MAPK7, MYBBP1A, ZNF613, ALDOA, PPP2R3B, KIAA1109, PUS1, ELL, BANF1, VPS72, TCF20, ZNF225, RAC1, ZNF222, SLC4A1AP, MOCS1, MKI67, CDC20, YTHDC2, RAD54L, SYNE1, YY1AP1, TULP3, UPF3B, WDR61, ETS2, POMP, AIRE, H3F3A, KLF2, RERE, NCOR2, POP7, GTF3A, HLF, PPARD, ELF3, PCDHA2, ZNF532, COPS4, EZH2, BNIP3, RNF187, DGCR14, DAXX, MBTD1, ZNF146, USP11, FANCE, USP16, TOP2A, ANGPT2, CDC6, CCNK, POGZ, CCNH, SNAPC1, GZMA, TTF1, DECR1, CLIC1, RBBP6, MORC2, GTF2B, MED4, G6PD, ZNF692, ADK, SIAH1, REV3L, TRIOBP, SKIV2L, MKNK2, FHL2, ZBTB16, SFN, SORBS3, LPXN, MDC1, NCAPG, PDE1A, DHX16, BCL3, ETV1, MEIS3P1, PPP3CA, BCAS3, SSRP1, BRD2, SHMT2, BRD3, JARID2, NASP, GMNN, CSNK2B, TRIM27, PPP1R11, ZNF26, TRIM22, RLF, CSNK1D, UBTF, FYN, MAPK14, SFPQ, ZNF460, MAT2B, REPIN1, BARD1, RALY, LMO2, STK38, IL16, CHMP4A, MORF4L2, RBM4, ZNF451, KNTC1, CBX4, SAE1, ITPKB, FLCN, MMP2, PDHB, CRADD, APOA1, CDKN2A, PTGIS, CDKN2C, RGN, SRRM1, FBXO22, ACTN4, NUDT3, DTL, STK24, DFFA, TAZ, RNF130, NFU1, DCUN1D1, MAD2L1BP, HIF1A, TRIM33, HSPB6, TIMELESS, SNRPB, ZNF587, TSHZ2, IFIH1, FGFR3, HMGB3, SSH3, TFEB, SOX4, NEDD9, SP110, SRF, ZNF330, TUBB, MEIS2, NDRG1, HIST1H4C, ASF1B, STK19, CREBL2, SREBF1, PTPN6, CSTF3, TAF6, SMG5, MAFB, BRIP1, WHSC1, TEAD3, EHMT2, CDKN1C, FBXO38, ATF5, CORO1A, GCM2, C2ORF42, CDKN1B, CRBN, PHF1, HDAC1, NEDD4, PPID, LAGE3, HOXB6, RFX1, TDG, PTTG1IP, FABP4, ABL1, SCMH1, ZNF410, IER3, METAP1, E2F3, TACR3, CYC1, CLSTN1, FOXK2, DPH1, DEK, AKT1, CCHCR1, KIF2C, CRYL1, MAZ, HEY1, GSN, POU5F1, S100PBP, PLCB1, LOXL2, CASP2, PHC2, KHDRBS1, KIAA0907, RING1, LDB2, UBE2NL, MID1IP1, MCM3, SLC9A3R1, UBE2B, MSC, NLRP1, CCNL2, LAP3, UBE2O, LARP6, ALDH7A1, C1QBP, LARP7, CFL1, NCOA6, TNNI3K, ZFPM2, KPNA3, C1D, TRA2A, RAG1, EGLN3, HCFC1, TRIB3, CDC73, NFYA, RPA4, TSPYL1, NPAS2, FAM107A, CHD1L, RGS12, TSC22D4, HSPA8, TSEN34, ENO1, FAM50A, CEBPA, ZBTB7A, VHL, CEBPG, ANXA1, SAMHD1, COTL1, RACGAP1, UBE2Q1, UBL5, F8A1, GDF15, IGFBP3
GOTERM_BP_DIRECT	GO:0042493~response to drug	29	0.020264	0.00247375	LDHA, ADORA2A, HTR1B, SLC1A3, APOA1, SRR, CAT, HTR1F, SREBF1, ICAM1, RPP21, OTC, ANXA1, NCKAP1L, ATP1A1, CPS1, RAD54L, UBE2B, INHBA, VEGFC, CDKN1B, HDAC1, CA9, FYN, LCK, TBXA2R, ABL1, IGFBP2, DUSP6
GOTERM_BP_DIRECT	GO:2000107~negative regulation of leukocyte apoptotic process	4	0.002795	0.00248796	CCR7, CCL21, CCL19, CXCL12
GOTERM_BP_DIRECT	GO:0001768~establishment of T cell polarity	4	0.002795	0.00248796	CCR7, CCL21, CYP26B1, CCL19

GOTERM_BP_DIRECT	GO:0070534~protein K63-linked ubiquitination	8	0.00559	0.00262429	TRAF2, UBE2O, CDKN2A, NEDD4, UBE2G1, TRIM27, UBE2NL, UBE2B
GOTERM_BP_DIRECT	GO:0061418~regulation of transcription from RNA polymerase II promoter in response to hypoxia	7	0.004891	0.00273085	UBE2D3, HIF1A, CA9, VHL, VEGFA, EGLN3, EPO
GOTERM_BP_DIRECT	GO:0046718~viral entry into host cell	12	0.008385	0.00276396	EPS15, MRC1, ICAM1, SLC1A5, NUP153, AXL, SCARB1, HSPA1A, KPNA3, CLEC5A, SELPLG, SLC10A1
GOTERM_BP_DIRECT	GO:0042326~negative regulation of phosphorylation	6	0.004192	0.00302689	CDKN1C, INHBA, GRB10, CDKN2A, CDKN1B, CDKN2C
GOTERM_BP_DIRECT	GO:0044267~cellular protein metabolic process	15	0.010481	0.00324631	ADORA2A, IGFBP6, UBE2L6, TTF1, MMP2, MMP1, TTR, APOA1, GSN, H3F3A, HIST1H4C, SIAH1, IGFBP2, IGFBP3, DMBT1
GOTERM_MF_DIRECT	GO:0001618~virus receptor activity	11	0.007686	0.00328402	MRC1, ICAM1, SLC1A5, CCR5, AXL, SCARB1, CD4, HSPA1A, CLEC5A, SELPLG, SLC10A1
GOTERM_MF_DIRECT	GO:0019888~protein phosphatase regulator activity	7	0.004891	0.00335774	PPP2R3B, PPP1R3C, PPME1, PPP2R5D, IGBP1, ENSA, PPP1R15A
GOTERM_BP_DIRECT	GO:0006919~activation of cysteine-type endopeptidase activity involved in apoptotic process	12	0.008385	0.00369932	TRAF2, CDKN2A, CDKN1B, HIP1R, MTCH1, LCK, TNFSF15, EGLN3, CASP1, CASP2, NLRP1, CRADD
GOTERM_BP_DIRECT	GO:0000077~DNA damage checkpoint	7	0.004891	0.00393967	MAPK14, INTS7, BRIP1, RAD9A, CEP63, RPA4, TIPRL
GOTERM_MF_DIRECT	GO:0005524~ATP binding	102	0.071272	0.0040464	KIFC1, ATP1B1, XRCC3, RNASEL, PRPF4B, XRCC2, ADCY7, STK38, PKMYT1, ITPKB, ITPKA, KIF13A, DDX11, CLK2, MAP3K9, DHX34, ITPK1, STK24, LIG1, ABCC10, MARK2, BAZ1B, RIOK3, HARS, MAPK7, NEK4, PCCB, PRPS2, CHKA, ABCA7, IFIH1, CLCN3, FGFR3, PFKFB3, ERBB3, MAP4K1, HSPA1A, NAGK, TK1, UBE2D3, SRR, STK19, CSF1R, MKI67, BRIP1, UBE2L6, YTHDC2, CPS1, RAD54L, EPHA3, CCT7, P2RX5, HYOU1, ATP2A2, KCNJ8, ATP2A3, TNK1, ABL1, UBE2G1, TTLL7, AKT1, ACVR1B, KIF2C, SUCLA2, TOP2A, ATP8B4, CDC6, PFKL, MCM3, UBE2B, NLRP1, TTF2, DDR1, UBE2O, MAST2, CKM, ADK, LCK, TNNI3K, SLC27A2, SLC27A5, SKIV2L, MKNK2, HK2, TRIB3, ITM2C, CHD1L, DHX16, YES1, HSPA8, FLT1, MSH5, AXL, BCS1L, ATP1A1, UBE2Q1, CSNK1D, FYN, MAPK13, MAPK14, PGK1, ATP8A1
GOTERM_BP_DIRECT	GO:0000122~negative regulation of transcription from RNA polymerase II promoter	55	0.038431	0.00445331	PPARD, EFNA1, EZH2, CBX4, FLCN, SHH, CUL3, HEY1, POU5F1, RARA, CRY1, MSC, HES1, TIMELESS, TRIM33, BTG2, C1QBP, MTF2, IGBP1, VEGFA, ZFPM2, ZNF613, TSHZ2, TAF9B, HDGF, FHL2, TRIB3, HCFC1, CDC73, ZBTB16, VPS72, SORBS3, UBE2D3, MEIS2, EPO, KLF5, SREBF1, CEBPA, ZBTB7A, JARID2, VHL, TRIM27, WHSC1, EHMT2, CDKN1C, HDAC1, SFPQ, PPID, ETS2, HBZ, TDG, PHF21A, NCOR2, RERE, BMP6
GOTERM_MF_DIRECT	GO:0003682~chromatin binding	34	0.023757	0.00457878	HMGN1, TSHZ2, EZH2, CBX4, HCFC1, DEK, DDX11, SMARCD1, BCAS3, LOXL2, TOP2A, SREBF1, SSRP1, SHMT2, BRD2, BRD3, JARID2, CSNK2B, RING1, TTF1, WHSC1, KLHDC3, ATF5, BAZ1B, HDAC1, UBTF, PHF1, NUP62, SFPQ, NCOA6, AIRE, PHF21A, RERE, NCOR2
GOTERM_BP_DIRECT	GO:0050821~protein stabilization	16	0.01118	0.00474973	ATP1B1, VHL, HIP1R, HPS4, TAF9B, HCFC1, SOX4, HSPA1A, UBE2B, GTSE1, DVL1, CCT7, APOA1, CDKN2A, CDC37L1, CREBL2
GOTERM_BP_DIRECT	GO:0051209~release of sequestered calcium ion into cytosol	8	0.00559	0.00478655	PTPRC, HTR1B, CCR7, CCL21, LCK, CCL19, ITPR3, HTR1F
GOTERM_BP_DIRECT	GO:0008285~negative regulation of cell proliferation	34	0.023757	0.00525086	ADORA2A, IGFBP6, SOX4, CDC73, ZBTB16, SRF, CDKN2A, CDKN2C, KIFAP3, NDRG1, RARA, DPT, CSF1R, CEBPA, CDC6, PTPN6, TAF6, JARID2, VHL, CSNK2B, BRIP1, SLC9A3R1, ATF5, DDR1, VEGFC, INHBA, CDKN1B, NUP62, BTG2, ADM, HDAC1, ALOX15B, HGS, IGFBP3
GOTERM_BP_DIRECT	GO:0002548~monocyte chemotaxis	8	0.00559	0.0054917	TNFRSF11A, FLT1, FOLR2, CCL21, ANXA1, CCL19, CCL16, PTPRO
GOTERM_BP_DIRECT	GO:0007595~lactation	8	0.00559	0.0054917	SLC29A1, DDR1, HIF1A, STAT5A, VEGFA, HK2, SERPINC1, NCOR2
GOTERM_BP_DIRECT	GO:0007566~embryo implantation	8	0.00559	0.0054917	DDR1, PPARD, PTGIS, H3F3A, STC1, UBE2Q1, MMP2, EPO

GOTERM_BP_DIRECT	GO:0006369~termination of RNA polymerase II transcription	10	0.006987	0.00560942	FIP1L1, CSTF3, MAZ, UPF3B, U2AF2, SNRPB, SRRM1, THOC2, SNRPF, TTF2
GOTERM_MF_DIRECT	GO:0005102~receptor binding	31	0.021661	0.00604068	ACOX2, NXPH4, EFNA1, EHHADH, IGFBP6, TNFSF15, GJA1, HFE, HSPA1A, ENSA, CXCL12, PIPOX, TMED1, SERPINE1, SMARCD1, CD2, RARA, CAT, YES1, ANGPT2, SELPLG, RASA1, SLC39A1, ANXA1, CSNK2B, SLC9A3R1, ADM, TNK1, ABL1, IGFBP2, SLC27A2
GOTERM_BP_DIRECT	GO:0048538~thymus development	8	0.00559	0.00627184	HES1, CRKL, JARID2, MAFB, RAG1, ABL1, SRF, SHH
GOTERM_BP_DIRECT	GO:0030850~prostate gland development	4	0.002795	0.0064402	ALOX15B, ANXA1, RARA, SHH
GOTERM_BP_DIRECT	GO:2001020~regulation of response to DNA damage stimulus	4	0.002795	0.0064402	IER3, NPAS2, NEK4, ABL1
GOTERM_BP_DIRECT	GO:0045737~positive regulation of cyclin-dependent protein serine/threonine kinase activity	6	0.004192	0.00698531	CDC6, CCNK, CDKN1B, CCNH, PSRC1, CCNL2
GOTERM_BP_DIRECT	GO:0045892~negative regulation of transcription, DNA-templated	40	0.02795	0.00730767	THAP7, PPARD, ELF3, EZH2, CBX4, FHL2, TRIB3, ZBTB16, DAXX, CDKN2A, HEY1, TSC22D4, BCL3, RARA, BCL7A, LOXL2, PLCB1, CRY1, HSPA8, ENO1, KHDRBS1, CEBPA, ZBTB7A, JARID2, GMNN, RING1, CDKN1C, HES1, ATF5, YY1AP1, CDKN1B, TIMELESS, HDAC1, TRIM33, SFPQ, FABP4, ZFPM2, SCMH1, MYBBP1A, C1D
GOTERM_BP_DIRECT	GO:0006096~glycolytic process	7	0.004891	0.00748113	ALDOA, LDHA, PFKL, ENO2, HK2, PGK1, ENO1
GOTERM_BP_DIRECT	GO:0043065~positive regulation of apoptotic process	27	0.018866	0.00761465	FGD1, LDHA, HIP1R, ADAMTSL4, BNIP3, SOX4, ZBTB16, FLCN, AKT1, CDKN2A, MAP3K9, MTCH1, RAC1, CASP2, ARL6IP5, TOP2A, ARHGEF2, DFFA, GZMA, ADM, C1QBP, PPID, SIAH1, ABL1, IGFBP3, DUSP6, BARD1
GOTERM_BP_DIRECT	GO:0008203~cholesterol metabolic process	10	0.006987	0.00835315	CEBPA, SREBF1, PPARD, APOA1, MBTPS2, LEPR, CH25H, CETP, CAT, LIPC
GOTERM_BP_DIRECT	GO:0006915~apoptotic process	44	0.030745	0.00853161	IER3, PACS2, PRF1, PPARD, HIP1R, ADORA2A, LY86, ADAMTSL4, GPR65, EGLN3, GJA1, BNIP3, ZBTB16, RASSF7, DAXX, RTN3, UBE2D3, GHITM, CDKN2A, MAP3K9, MTCH1, CD2, CASP1, CASP2, MAGEH1, EBAG9, EPO, PTPN6, DFFA, GZMA, VIL1, ESPL1, GAS2, CD5L, NLRP1, RNF130, C1QBP, ALOX15B, PPID, MAPK14, SIAH1, IGFBP3, PPP1R15A, C1D
GOTERM_CC_DIRECT	GO:0005925~focal adhesion	32	0.02236	0.00877184	TRIOBP, FGFR3, FHL2, NEDD9, GJA1, HSPA1A, SPRY4, ANXA6, LPXN, SORBS3, RAC2, GSN, MDC1, RAC1, SLC4A2, CAT, YES1, HSPA8, FLRT3, ICAM1, PTPRC, FLRT2, ARHGEF2, FLT1, ACTN4, FLOT1, ANXA1, LAP3, HYOU1, TNS1, CFL1, LCP1
GOTERM_BP_DIRECT	GO:0070301~cellular response to hydrogen peroxide	9	0.006289	0.00890559	IL18RAP, EZH2, ANXA1, AXL, BNIP3, MAPK7, ABL1, KLF2, PLEKHA1
GOTERM_MF_DIRECT	GO:0042803~protein homodimerization activity	54	0.037732	0.00928428	HIP1R, CHMP4A, HPS4, BNIP3, APOBEC3G, DAXX, CUL3, CRYL1, PLOD1, MAP3K9, CAT, PLCB1, TOP2A, SLC22A1, ACTN4, GZMA, CRYAB, VIL1, GRHPR, PTPRO, HES1, INHBB, G6PD, TIMELESS, HSPB6, CCR2, VEGFA, PRPS2, CHKA, CLCN3, RAP1GAP, ERBB3, ADH5, RAG1, SNX2, ZBTB16, BANF1, SRF, ANXA6, MTMR1, CD2, SRR, CD4, SCARB1, GALE, CSF1R, FLRT3, CEBPA, PLEK, ANXA1, SYNE1, CORO1A, TDG, BARD1
GOTERM_MF_DIRECT	GO:0044822~poly(A) RNA binding	78	0.054502	0.00929732	MRPL40, RALY, PRPF4B, U2AF2, RBM4, DEK, PDIA4, C1ORF35, MRPS31, RBM4B, MAZ, CDKN2A, POU5F1, DHX34, SRRM1, LSM2, LSM1, TOP2A, FNDC3B, KHDRBS1, MRPL2, ACTN4, BYSL, PTBP1, RBBP6, MARK2, UBE2O, TNS1, CRKL, ABT1, LARP7, ADK, CSTB, SNRPB, SNRPA, MYBBP1A, ALDOA, HSD17B10, FIP1L1, CXORF57, GANAB, HMGB3, PUS1, TRA2A, HDGF, BICC1, DCN, SF3B4, SF3B2, TCF20,

					DHX16, HIST1H4C, UBAP2L, HSPA8, ENO1, FAM50A, SSRP1, CSTF3, MRPS28, NBPF10, MKI67, RRBP1, GRSF1, MTHFSD, YTHDC2, SLC16A3, APEH, CORO1A, MRPL22, SYNE1, UPF3B, UBTF, PTCD3, SFPQ, HOXB6, POP7, KCTD12, REPIN1
GOTERM_BP_DIRECT	GO:1901741~positive regulation of myoblast fusion	5	0.003494	0.01002924	IL4R, MAPK14, FLOT1, CD53, GDF15
GOTERM_BP_DIRECT	GO:0042789~mRNA transcription from RNA polymerase II promoter	5	0.003494	0.01002924	SREBF1, HIF1A, LMO2, POU5F1, SRF
GOTERM_BP_DIRECT	GO:0002407~dendritic cell chemotaxis	5	0.003494	0.01002924	CCR7, CCR5, CCL21, CCR2, CCL19
GOTERM_MF_DIRECT	GO:0051020~GTPase binding	6	0.004192	0.0100796	FNBP1L, BNIP3, RASA1, LCP1, SH3GL1, ENO1
GOTERM_BP_DIRECT	GO:0042110~T cell activation	8	0.00559	0.01023512	CD48, NEDD4, FYN, CD2, PPP3CA, CLEC7A, DDOST, WAS
GOTERM_BP_DIRECT	GO:0031100~organ regeneration	8	0.00559	0.01023512	APOA1, ADM, MKI67, AXL, ANGPT2, CXCL12, PRPS2, LCP1
GOTERM_BP_DIRECT	GO:0071456~cellular response to hypoxia	12	0.008385	0.0110152	SLC29A1, AKT1, ICAM1, HYOU1, PPARD, HIF1A, PTGIS, VEGFA, BNIP3, STC1, NDRG1, PCK1
GOTERM_BP_DIRECT	GO:0007080~mitotic metaphase plate congression	7	0.004891	0.01133659	CUL3, KIFC1, KIF2C, CDCA8, CHMP4A, PSRC1, CDC23
GOTERM_BP_DIRECT	GO:0010862~positive regulation of pathway-restricted SMAD protein phosphorylation	8	0.00559	0.01145966	INHBB, ACVR1B, INHBA, INHBE, CSNK2B, HFE, GDF15, BMP6
GOTERM_CC_DIRECT	GO:0031464~Cul4A-RING E3 ubiquitin ligase complex	4	0.002795	0.01174741	CRBN, CDKN1B, DTL, TRPC4AP
GOTERM_MF_DIRECT	GO:0051721~protein phosphatase 2A binding	6	0.004192	0.01185066	AKT1, PPME1, SMG5, IGBP1, STRN4, ENSA
GOTERM_BP_DIRECT	GO:0042102~positive regulation of T cell proliferation	9	0.006289	0.01203866	HES1, PTPRC, LILRB2, CORO1A, IL23A, ANXA1, NCKAP1L, CCL19, CD4
GOTERM_BP_DIRECT	GO:0042267~natural killer cell mediated cytotoxicity	5	0.003494	0.01237363	PTPN6, TUBB, MICB, CEBPG, SLAMF7
GOTERM_BP_DIRECT	GO:0001771~immunological synapse formation	4	0.002795	0.0127639	PRF1, CORO1A, CCL21, CCL19
GOTERM_BP_DIRECT	GO:0008380~RNA splicing	17	0.011879	0.01283801	NOL3, PRPF4B, PTBP1, RBM4, IVNS1ABP, SF3B4, TTF2, SF3B2, RBM4B, C1QBP, SFPQ, SNRPB, SRRM1, DHX16, SNRPF, THOC2, LSM1
GOTERM_BP_DIRECT	GO:0043066~negative regulation of apoptotic process	36	0.025155	0.01340703	IER3, PPARD, TAF9B, CBX4, FHL2, BNIP3, SHH, AKT1, KIFAP3, BCL3, RGN, GLO1, RARA, CAT, DDAH2, HIGD1A, CSF1R, IL2RB, NOL3, VHL, CRYAB, PRG1, ANXA1, NCKAP1L, UBE2B, ATF5, CDKN1B, NUP62, HDAC1, TXNDC5, CFL1, VEGFA, MAPK7, CLEC5A, ARHGAP10, BARD1
GOTERM_CC_DIRECT	GO:0001891~phagocytic cup	5	0.003494	0.01357143	ABCA7, CORO1A, RAC1, ANXA1, LCP1
GOTERM_BP_DIRECT	GO:0071222~cellular response to lipopolysaccharide	13	0.009084	0.01444348	MRC1, ICAM1, PPARD, CAMP, AXL, CDC73, LILRB2, CCR5, MAPK14, SERPINE1, TBXA2R, RARA, ABL1
GOTERM_BP_DIRECT	GO:0016569~covalent chromatin modification	13	0.009084	0.01444348	BRD2, MBTD1, BRD3, PHF1, JARID2, MTF2, SMARCD1, TDG, CBX4, DEK, ASF1B, DAXX, VPS72
GOTERM_BP_DIRECT	GO:0000079~regulation of cyclin-dependent protein serine/threonine kinase activity	7	0.004891	0.01457704	CDC6, CCNK, CDKN1B, CDKN2C, PKMYT1, SFN, CCNL2
GOTERM_BP_DIRECT	GO:0043536~positive regulation of blood vessel endothelial cell migration	5	0.003494	0.01504115	AKT1, VEGFC, MAPK14, STAT5A, VEGFA
GOTERM_BP_DIRECT	GO:0051882~mitochondrial depolarization	3	0.002096	0.01510083	CDKN2A, ABL1, CASP1

GOTERM_MF_DIRECT	GO:0043548~phosphatidylinositol 3-kinase binding	5	0.003494	0.01523732	CORO1A, FYN, LCK, AXL, ATP1A1
GOTERM_BP_DIRECT	GO:0034976~response to endoplasmic reticulum stress	10	0.006987	0.01545759	HYOU1, TRAF2, MBTPS2, ATP2A2, TXNDC5, FLOT1, TRIB3, PDIA4, ABL1, PPP1R15A
GOTERM_BP_DIRECT	GO:0000082~G1/S transition of mitotic cell cycle	12	0.008385	0.01684198	CUL3, ACVR1B, INHBA, CDC6, CDKN2A, CDKN1B, CDKN2C, CCNH, PKMYT1, PPP3CA, MCM3, RPA4
GOTERM_BP_DIRECT	GO:0043249~erythrocyte maturation	4	0.002795	0.01688127	G6PD, HBZ, KLF2, EPO
GOTERM_MF_DIRECT	GO:0004861~cyclin-dependent protein serine/threonine kinase inhibitor activity	4	0.002795	0.01705622	CDKN1C, CDKN2A, CDKN1B, CDKN2C
GOTERM_BP_DIRECT	GO:0042632~cholesterol homeostasis	9	0.006289	0.01738668	TMEM97, APOA1, FABP4, SCARB1, CETP, MYLIP, CD24, LIPC, MTTP
GOTERM_CC_DIRECT	GO:0005739~mitochondrion	85	0.059393	0.01826027	MRPL40, CYB5R3, ACOX2, XRCC3, ALDH1L1, HIP1R, EHHADH, CYC1, BNIP3, GJA1, RAB1B, MMP2, MRPS31, PDHB, AKT1, ALAS1, MSRA, NDUFS4, CDKN2A, DHX34, CAT, DDAH2, CASP1, CRY1, SUCLA2, COX17, CASP2, NOL3, CRYAB, LIG1, OTC, TAZ, RAP1GDS1, CLIC1, DECR1, PNPLA4, DDIT4, MARK2, LAP3, NFU1, ALDH7A1, CAPN10, C1QBP, HARS, PCCB, PPP1R15A, SLC27A2, DEGS1, MPST, HSD17B10, PACS2, CCDC90B, PUS1, MRPS10, ADH5, SOX4, HCFC1, SFXN1, HSPA1A, SFN, ANXA6, MTCH1, MTCP1, PPP3CA, MRPS27, GCDH, SHMT2, GABARAPL1, MRPS28, C14ORF159, VHL, BCKDHB, GRSF1, MTRF1L, BCS1L, CCT7, MRPL22, FYN, PTCD3, KCNJ8, MAPK14, SDHD, MAT2B, USP48, ABL1
GOTERM_BP_DIRECT	GO:0031295~T cell costimulation	10	0.006987	0.01957787	AKT1, PTPN6, FYN, CCL21, LCK, RAC1, CCL19, CD4, CD24, YES1
GOTERM_BP_DIRECT	GO:0032355~response to estradiol	11	0.007686	0.01959793	CDKN1B, TACR3, CRYAB, EZH2, ANXA1, CD4, RARA, CAT, MMP15, IGFBP2, NCOR2
GOTERM_MF_DIRECT	GO:0008270~zinc ion binding	78	0.054502	0.01968289	PPARD, LMO2, RBM4, ADH1B, ZNRF4, ADH1A, APOBEC3G, RNF187, MYLIP, MMP2, MMP1, SHH, RBM4B, MBTD1, ZNF146, RGN, RBCK1, LONRF3, RARA, USP16, PHC2, ARHGEF2, ZCCHC2, RING1, MMP15, RBBP6, GTF2B, MORC2, TTF2, PJA2, RNF130, TRIM36, TRIM33, CA9, BAZ1B, TRIM34, MTF2, RNF24, ZFPM2, SIAH1, USP22, CA1, ADAMTS2, ADAMTS5, TRAF2, IFIH1, ZFAND3, RAG1, LANCL1, ADH5, FHL2, DPYS, ADH6, SP110, ZNF330, TK1, LOC440434, CYLD, TCF20, LPXN, CD4, GLO1, PEX12, RNF13, DCTD, NUP153, TRIM27, SAMHD1, WHSC1, EHMT2, TRIM22, RLF, PHF1, AIRE, PHF21A, ZNF318, RERE, BARD1
GOTERM_BP_DIRECT	GO:0043547~positive regulation of GTPase activity	42	0.029347	0.01974397	FGD1, FGFR3, RAP1GAP, ERBB3, HPS4, EZH2, ARHGAP15, FLCN, LLGL2, RASAL2, RCBTB2, TBC1D17, RGS12, RAC1, RAPGEF6, RGN, SHC1, BCAS3, PLCB1, SHC3, CDC42EP3, RASA1, ARHGEF10L, TBC1D3, ICAM1, GDI1, IL2RB, ARHGEF2, DENND1A, RAP1GDS1, NCKAP1L, CCL19, RACGAP1, RIC8B, CCL16, ARHGAP25, FARP2, FNBP1L, FYN, TBXA2R, SPTB, ARHGAP10
GOTERM_CC_DIRECT	GO:0016323~basolateral plasma membrane	17	0.011879	0.01999301	ATP1B1, AQP9, ERBB3, LEPR, FLOT1, ANXA1, SLC7A8, ATP1A1, MTTP, SLC10A1, SLC29A1, SLC26A6, CA9, OTOF, SLC2A1, SLC4A2, SLC22A1
GOTERM_BP_DIRECT	GO:0043552~positive regulation of phosphatidylinositol 3-kinase activity	6	0.004192	0.0207106	CCR7, FGFR3, FLT1, CCL21, RAC1, CCL19
GOTERM_BP_DIRECT	GO:0050853~B cell receptor signaling pathway	8	0.00559	0.02111083	PTPRC, PTPN6, LCK, NCKAP1L, IGLL1, CD79A, ABL1, PLEKHA1
GOTERM_BP_DIRECT	GO:0019835~cytolysis	5	0.003494	0.02139523	PRF1, C7, MICB, GZMA, MMD
GOTERM_BP_DIRECT	GO:0006699~bile acid biosynthetic process	5	0.003494	0.02139523	ACOX2, AKR1C4, CH25H, SLC27A2, SLC27A5

GOTERM_BP_DIRECT	GO:1900182~positive regulation of protein localization to nucleus	5	0.003494	0.02139523	AKT1, CDKN2A, FYN, CD2AP, GTSE1
GOTERM_BP_DIRECT	GO:2000378~negative regulation of reactive oxygen species metabolic process	5	0.003494	0.02139523	HIF1A, G6PD, CRYAB, HK2, BNIP3
GOTERM_BP_DIRECT	GO:0006069~ethanol oxidation	4	0.002795	0.02165271	ADH5, ADH6, ADH1B, ADH1A
GOTERM_BP_DIRECT	GO:0000050~urea cycle	4	0.002795	0.02165271	CEBPA, OTC, CPS1, SLC25A15
GOTERM_MF_DIRECT	GO:0008601~protein phosphatase type 2A regulator activity	5	0.003494	0.02166747	PPP2R3B, PPME1, PPP2R5D, IGBP1, ENSA
GOTERM_CC_DIRECT	GO:0005789~endoplasmic reticulum membrane	58	0.040527	0.02231353	CYB5R3, CYB5R4, CLSTN1, MAN1B1, PKMYT1, ALG5, GJA1, RAB1B, ZNRF4, ALG8, RTN3, SSR1, PTGIS, PLOD1, PLOD2, PIGG, CH25H, SAR1B, DDOST, AGPAT2, HPD, ATG9A, LPGAT1, PGAP1, PIGP, TMEM106C, PJA2, OTOF, ORMDL2, PPP1R15A, SLC27A2, PROS1, SLC27A5, DEGS1, FAM69A, TMCC1, CYP26B1, TMED1, RAC1, SLC39A7, CD4, ARL6IP5, RNF13, SLC39A1, FLRT3, SREBF1, FLRT2, CYP21A2, TMEM110, ITPR3, TMPRSS3, CYP4A11, CLGN, ATP2A2, ATP2A3, SPCS1, NOMO2, MGST2
GOTERM_CC_DIRECT	GO:0016324~apical plasma membrane	24	0.01677	0.02249683	ABCA7, ATP1B1, CLCA4, ERBB3, MPDZ, FLOT1, ANXA1, DUOX1, GJA1, ATP1A1, SLC9A3R1, PTPRO, GNAT3, SLC29A1, EPS15, CYP4A11, SLC26A6, SLC2A2, SLC2A1, RAPGEF6, SLC4A2, STC1, IGFBP2, ITPK1
GOTERM_CC_DIRECT	GO:0012506~vesicle membrane	5	0.003494	0.02273101	TRAF2, CLCN3, SLC26A6, ATP2A2, WAS
GOTERM_BP_DIRECT	GO:0001558~regulation of cell growth	10	0.006987	0.02273237	TMEM97, DDR1, KIAA1109, FAM107A, CLSTN1, IGFBP6, ESM1, IGFBP2, IGFBP3, EBAG9
GOTERM_BP_DIRECT	GO:0000398~mRNA splicing, via spliceosome	20	0.013975	0.02285597	RALY, CSTF3, FIP1L1, PRPF4B, U2AF2, PTBP1, TRA2A, DGCR14, SF3B4, SF3B2, UBL5, UPF3B, SNRPB, SRRM1, DHX16, SNRPA, GPATCH1, LSM2, SNRPF, HSPA8
GOTERM_CC_DIRECT	GO:0005887~integral component of plasma membrane	89	0.062188	0.02312833	AQP9, PCDHA2, TACR3, SLC20A1, EFNA1, TNFSF15, SLC7A8, GJA1, AQP7, CD53, TLR6, GJA4, CD48, ACVR1B, SLC1A5, HTR1B, SLC2A6, TNFRSF11A, SLC2A2, IL4R, SLC2A1, KCNK5, SLC4A2, EVI2B, HTR1F, SLC22A1, ICAM1, PTPRF, CLCA4, GPR171, RXFP3, MMP15, PTPRO, CD163, LILRB2, DDR1, SLC26A6, THBD, CCR5, CCR2, SIGLEC7, VAMP5, EFNA4, JAM2, CLEC5A, DEGS1, SLC38A4, FGFR3, ERBB3, ADORA2A, FCER2, MMD, GPR65, LANCL1, FPR1, HFE, SLCO2A1, SLC29A1, CD2, SCARB1, SLC31A2, SELPLG, GAL3ST1, CSF1R, FLRT3, MRC1, PTPRC, FLRT2, IL2RB, FLT1, SELL, AXL, CD1C, TRIM27, NCKAP1L, SLC6A15, ITPR3, EPHA3, SLC10A1, SLC16A3, P2RX5, P2RY10, ATP2A2, ATP2A3, SLC6A8, SLC6A5, TBXA2R, SLC13A1, CD79A
GOTERM_BP_DIRECT	GO:0016032~viral process	25	0.017469	0.02363009	CEBPA, PACS2, IL2RB, NUP153, MICB, IL16, MPDZ, NUP88, NUP188, SP110, DAXX, GTF2B, MMP1, SF3B2, RTN3, C1QBP, NUP62, HDAC1, DDX11, FYN, CCR2, LCK, RBCK1, SHC1, HSPA8
GOTERM_MF_DIRECT	GO:0008094~DNA-dependent ATPase activity	6	0.004192	0.02387567	XRCC3, XRCC2, DDX11, CCNH, TOP2A, TTF2
GOTERM_BP_DIRECT	GO:0032496~response to lipopolysaccharide	16	0.01118	0.02399506	ATP4B, ADH5, DCN, CPS1, PCK1, CCR7, THBD, TNFRSF11A, ADM, HDAC1, KCNJ8, SRR, CASP1, LOXL1, EPO, MGST2
GOTERM_BP_DIRECT	GO:0042541~hemoglobin biosynthetic process	3	0.002096	0.02430539	INHBA, HIF1A, EPO
GOTERM_MF_DIRECT	GO:0042609~CD4 receptor binding	3	0.002096	0.02448274	FYN, LCK, SPG21
GOTERM_MF_DIRECT	GO:0019904~protein domain specific binding	19	0.013276	0.02462117	CSNK2B, ATP1A1, SFN, ZBTB16, ARFIP1, MRPS31, NLRP1, TUBB, CEP250, NEDD4, GSN, HOMER3, IGBP1, TDG, HGS, RARA, HIST1H4C,

					KCTD13, CASP2
GOTERM_CC_DIRECT	GO:0043231~intracellular membrane-bounded organelle	40	0.02795	0.02476833	ACOX2, ABCA7, AQP9, HIP1R, TRA2A, FOXK2, VGF, TIPRL, LLGL2, SPG21, SLC4A1AP, SCARB1, CAT, DDOST, EXOC2, TNPO3, GTPBP2, KLF5, DTL, SNAPC1, LIG1, BYSL, ATP1A1, SLC9A3R1, MCM3, CCNL2, EPS15, CYP4A11, G6PD, NUP62, TRIM33, NCOA6, RFX1, HGS, NEU1, CLEC7A, MYBBP1A, MGST2, ATP8A1, BARD1
GOTERM_BP_DIRECT	GO:0006094~gluconeogenesis	7	0.004891	0.02536809	ALDOA, GPD2, ENO2, CRY1, PGK1, PCK1, ENO1
GOTERM_BP_DIRECT	GO:0098609~cell-cell adhesion	23	0.016071	0.025842	FLRT3, ALDOA, LDHA, PPME1, STK38, STK24, SNX2, HCFC1, HSPA1A, ARFIP1, SFN, CAPZB, MARK2, TMEM2, EPS15, TMEM47, CRKL, CSNK1D, FNBP1L, NDRG1, HSPA8, SH3GL1, ENO1
GOTERM_MF_DIRECT	GO:0016874~ligase activity	23	0.016071	0.02605356	TRAF2, LIG1, ZNF451, TRIM27, RAG1, CBX4, RING1, ZNRF4, RNF187, MYLIP, TRIM22, RBBP6, PJA2, RNF130, TRIM36, TRIM33, NEDD4, RBCK1, SIAH1, SUCLA2, PCCB, RNF13, BARD1
GOTERM_BP_DIRECT	GO:0015758~glucose transport	6	0.004192	0.02657803	AKT1, PPARD, SLC2A2, SLC2A1, HK2, YES1
GOTERM_CC_DIRECT	GO:0001772~immunological synapse	6	0.004192	0.0266368	ICAM1, CORO1A, SNX27, GZMA, LCK, CD53
GOTERM_BP_DIRECT	GO:0071285~cellular response to lithium ion	4	0.002795	0.02708158	CEBPA, CDKN1B, FABP4, SHH
GOTERM_BP_DIRECT	GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway	11	0.007686	0.02735221	DDR1, DOK2, FLT1, FYN, ERBB3, LCK, CD4, TNK1, YES1, SHC3, CSF1R
GOTERM_BP_DIRECT	GO:0030838~positive regulation of actin filament polymerization	7	0.004891	0.02802846	ICAM1, CCR7, CCL21, RAC1, NCKAP1L, LMOD1, CDC42EP3
GOTERM_BP_DIRECT	GO:0035924~cellular response to vascular endothelial growth factor stimulus	5	0.003494	0.02917086	AKT1, FLT1, MAPK14, VEGFA, GAS1
GOTERM_BP_DIRECT	GO:0030316~osteoclast differentiation	5	0.003494	0.02917086	TNFRSF11A, MAPK14, GLO1, CSF1R, FARP2
GOTERM_BP_DIRECT	GO:0007507~heart development	17	0.011879	0.02927915	FLRT3, PPARD, ERBB3, TAZ, SOX4, GJA1, BICC1, SRF, SHH, DVL1, CRKL, ADM, KCNJ8, NCOA6, SHC1, COX17, IFT140
GOTERM_BP_DIRECT	GO:0045893~positive regulation of transcription, DNA-templated	38	0.026552	0.02947753	E2F3, PPARD, ELF3, GRIP1, TFEB, FHL2, SOX4, RNF187, NFYA, ZBTB16, SHH, NPAS2, CDKN2A, BCL3, RARA, USP16, PLCB1, CREBL2, EPO, KLF5, PCBD1, VHL, PSRC1, DVL1, CDKN1C, RLF, ATF5, INHBA, MED4, HIF1A, NUP62, HDAC1, ETS2, NCOA6, AIRE, USP22, KLF2, NEK4
GOTERM_CC_DIRECT	GO:0030496~midbody	13	0.009084	0.02979538	TRIOBP, GDI1, CHMP4A, PSRC1, RACGAP1, FLCN, ZNF330, KIF13A, CYLD, CDCA8, DDX11, INCENP, SLC2A1
GOTERM_BP_DIRECT	GO:0006606~protein import into nucleus	8	0.00559	0.03003183	NUP153, NUP62, NUP88, CFL1, PTTG1IP, NUP188, PPP3CA, KPNA3
GOTERM_CC_DIRECT	GO:0002102~podosome	5	0.003494	0.03050669	LPXN, SH3PXD2A, GSN, LCP1, SH3GL1
GOTERM_BP_DIRECT	GO:0071260~cellular response to mechanical stimulus	9	0.006289	0.0305232	AKT1, RAC1, BNIP3, GJA1, ATP1A1, CASP1, CASP2, CRADD, BMP6
GOTERM_BP_DIRECT	GO:0071347~cellular response to interleukin-1	9	0.006289	0.0305232	ICAM1, HIF1A, PTGIS, CCL21, CAMP, CCL19, KLF2, CCL16, PCK1
GOTERM_MF_DIRECT	GO:0098641~cadherin binding involved in cell-cell adhesion	24	0.01677	0.03055112	ALDOA, LDHA, PPME1, STK38, STK24, SNX2, ANXA1, HCFC1, HSPA1A, ARFIP1, SFN, CLIC1, CAPZB, CD2AP, MARK2, TMEM2, EPS15, CRKL, CSNK1D, FNBP1L, NDRG1, HSPA8, SH3GL1, ENO1

GOTERM_BP_DIRECT	GO:0007596~blood coagulation	17	0.011879	0.03058646	ADORA2A, HPS4, F9, CAPZB, WAS, SHH, P2RX5, THBD, HDAC1, FYN, RAC1, SERPINC1, H3F3A, PHF21A, ZFPM2, ITPK1, PROS1
GOTERM_BP_DIRECT	GO:0006260~DNA replication	15	0.010481	0.03132115	CDC6, SSRP1, POLH, DTL, NASP, LIG1, BRIP1, RAD9A, MCM3, RBBP6, TIMELESS, NCOA6, KCTD13, REPIN1, BARD1
GOTERM_BP_DIRECT	GO:0048010~vascular endothelial growth factor receptor signaling pathway	9	0.006289	0.03283699	VEGFC, FLT1, FYN, MAPK13, MAPK14, VEGFA, RAC1, AXL, NCKAP1L
GOTERM_BP_DIRECT	GO:0051016~barbed-end actin filament capping	4	0.002795	0.03316484	TRIOBP, GSN, VIL1, CAPZB
GOTERM_BP_DIRECT	GO:2000147~positive regulation of cell motility	4	0.002795	0.03316484	CCR7, CCL21, CCL19, CSF1R
GOTERM_BP_DIRECT	GO:0031648~protein destabilization	6	0.004192	0.03340889	CDKN2A, GSN, CDC73, SIAH1, MYLIP, NOMO2
GOTERM_BP_DIRECT	GO:0045648~positive regulation of erythrocyte differentiation	5	0.003494	0.03360797	ACVR1B, INHBA, HIF1A, MAPK14, NCKAP1L
GOTERM_BP_DIRECT	GO:0030099~myeloid cell differentiation	5	0.003494	0.03360797	CDKN1C, CEBPA, NCOA6, ZBTB16, CLEC5A
GOTERM_BP_DIRECT	GO:0045860~positive regulation of protein kinase activity	7	0.004891	0.03388565	PTPRC, CCR7, CCL21, MMD, CCL19, CD4, DAXX
GOTERM_BP_DIRECT	GO:0045600~positive regulation of fat cell differentiation	7	0.004891	0.03388565	KLF5, CEBPA, AKT1, PPARD, ZBTB16, TPH1, CREBL2
GOTERM_BP_DIRECT	GO:0006338~chromatin remodeling	10	0.006987	0.03434945	CHD1L, HDAC1, MORF4L2, SMARCD1, TTF1, DEK, TAF6L, SCMH1, DAXX, RERE
GOTERM_BP_DIRECT	GO:0070126~mitochondrial translational termination	10	0.006987	0.03434945	MRPL40, MRPL2, MRPS27, MRPL22, MRPS28, MRPS18A, PTCD3, MRPS10, MTRF1L, MRPS31
GOTERM_BP_DIRECT	GO:0007067~mitotic nuclear division	21	0.014674	0.03484801	CDC6, TRIOBP, ARHGEF2, CCNK, NUP88, KNTC1, PKMYT1, NEDD9, CDC23, CDC20, ENSA, CEP63, CD2AP, KIF2C, TIMELESS, NUP62, INCENP, MAPRE2, NEK4, ABL1, USP16
GOTERM_BP_DIRECT	GO:0006406~mRNA export from nucleus	11	0.007686	0.03496558	FIP1L1, NUP153, UPF3B, NUP62, NUP88, SMG5, U2AF2, SHFM1, SRRM1, NUP188, THOC2
GOTERM_BP_DIRECT	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	65	0.045418	0.0351061	HLF, RNASEL, ELF3, LMO2, FOXK2, MORF4L2, FLCN, SHH, AKT1, ACVR1B, CDKN2A, HEY1, POU5F1, SERPINE1, RARA, USP16, TOP2A, ARHGEF2, CCNK, CCNH, LDB2, CCNL2, HES1, INHBA, HIF1A, MTF2, IGBP1, NCOA6, VEGFA, ZFPM2, MAPK7, ZNF613, TAF9B, TFEB, SOX4, HCFC1, CDC73, DCN, SRF, NPAS2, TCF20, IL23A, MEIS2, BCL3, ETV1, PPP3CA, BCAS3, YES1, KLF5, SREBF1, CEBPA, MAFB, CEBPG, TEAD3, RLF, ATF5, GCM2, WDR61, HDAC1, ETS2, MAPK14, AIRE, KLF2, RERE, BMP6
GOTERM_BP_DIRECT	GO:0006360~transcription from RNA polymerase I promoter	3	0.002096	0.0352141	CEBPA, UBTF, POLR1C
GOTERM_BP_DIRECT	GO:0010324~membrane invagination	3	0.002096	0.0352141	FNBP1L, CHMP4A, HGS
GOTERM_BP_DIRECT	GO:0006929~substrate-dependent cell migration	3	0.002096	0.0352141	FMNL1, VEGFC, ANKS1A
GOTERM_BP_DIRECT	GO:0021930~cerebellar granule cell precursor proliferation	3	0.002096	0.0352141	ATF5, RERE, SHH
GOTERM_CC_DIRECT	GO:0000790~nuclear chromatin	17	0.011879	0.03523282	PPARD, POGZ, DFFA, NASP, EZH2, EHMT2, UBE2B, SRF, KLHDC3, TIMELESS, HDAC1, DDX11, POU5F1, RARA, PLCB1, ASF1B, NCOR2
GOTERM_BP_DIRECT	GO:0045444~fat cell differentiation	9	0.006289	0.03526736	INHBB, CEBPA, SREBF1, ATF5, RNASEL, OSBPL11, PLCB1, FBXO9, SDF4
GOTERM_MF_DIRECT	GO:0004872~receptor activity	19	0.013276	0.03544819	MRC1, ICAM1, IL18RAP, SLC20A1, RRBP1, MMD, TLR6, PAQR4, CD48, OGFRL1, LILRB2, SLC1A5, MED4, THBD, TNFRSF11A, SIGLEC7, CD2, CD4, TNPO3

GOTERM_MF_DIRECT	GO:0004024~alcohol dehydrogenase activity, zinc-dependent	3	0.002096	0.03546629	ADH6, ADH1B, ADH1A
GOTERM_BP_DIRECT	GO:0048469~cell maturation	6	0.004192	0.03719681	HES1, CEBPA, CCL21, VEGFA, AXL, CCL19
GOTERM_MF_DIRECT	GO:0019901~protein kinase binding	29	0.020264	0.03761202	TRAF2, PPME1, TRIB3, SFN, DAXX, CYLD, CDKN2A, CEP250, CDKN2C, RAC1, CD4, CD24, CRY1, EXOC2, SREBF1, PTPN6, PTPRC, CCNK, RAD9A, ATP1A1, RACGAP1, TRIM22, WAS, CAMK2N1, CCNL2, DVL1, HIF1A, LCK, PPP1R15A
GOTERM_CC_DIRECT	GO:0005913~cell-cell adherens junction	25	0.017469	0.03776838	ALDOA, LDHA, PPME1, STK38, SNX2, HCFC1, HSPA1A, SFN, CD2AP, CAPZB, NDRG1, HSPA8, ENO1, STK24, FLOT1, ANXA1, ARFIP1, CLIC1, TMEM2, MARK2, EPS15, CRKL, CSNK1D, FNBP1L, SH3GL1
GOTERM_BP_DIRECT	GO:0019433~triglyceride catabolic process	5	0.003494	0.03841615	APOA1, FABP4, PNPLA4, CPS1, LIPC
GOTERM_CC_DIRECT	GO:0005694~chromosome	11	0.007686	0.03909356	THAP7, SSRP1, PRPF4B, HMGB3, MDC1, DTL, INTS7, WHSC1, EHMT2, LOXL2, RBBP6
GOTERM_CC_DIRECT	GO:0005730~nucleolus	56	0.03913	0.03946703	MRPL40, MORF4L2, RBM4, DAXX, CD2AP, MRPS31, RBM4B, CRYL1, CDCA8, CDKN2A, DDX11, ZNF146, TOP2A, NOL3, SNAPC1, DTL, STK24, BYSL, PTBP1, TTF1, RBBP6, GTF2B, RCL1, TIMELESS, CA9, C1QBP, ABT1, CSTB, SNRPA, MYBBP1A, C1D, REV3L, TRA2A, MKNK2, TRIB3, SP110, ZBTB16, ZNF330, TSPYL1, BCAS3, HSPA8, TSEN34, CEBPA, SSRP1, PTPN6, NUP153, MKI67, PAK1IP1, CPS1, ITPR3, TULP3, CRBN, UPF3B, UBTF, PPID, ABL1
GOTERM_BP_DIRECT	GO:0006954~inflammatory response	29	0.020264	0.03978671	ELF3, ADORA2A, LY86, FPR1, TLR6, CXCL12, AKT1, TNFRSF11A, IL23A, FOLR2, CCL21, CYP26B1, RAC1, CSF1R, IL18RAP, LIPA, ANXA1, AXL, CCL19, CD5L, CCL16, NLRP1, SIGLEC1, CCR7, CCR5, CCR2, TBXA2R, CLEC7A, BMP6
GOTERM_BP_DIRECT	GO:0034375~high-density lipoprotein particle remodeling	4	0.002795	0.03989397	APOA1, SCARB1, CETP, LIPC
GOTERM_BP_DIRECT	GO:0050930~induction of positive chemotaxis	4	0.002795	0.03989397	VEGFC, IL16, VEGFA, CXCL12
GOTERM_BP_DIRECT	GO:0007623~circadian rhythm	9	0.006289	0.04048613	SREBF1, ATF5, RBM4B, NPAS2, TIMELESS, HS3ST2, SERPINE1, TPH1, MTTP
GOTERM_BP_DIRECT	GO:0000902~cell morphogenesis	8	0.00559	0.04119318	ARHGEF2, LST1, LIPA, VHL, MAPK14, TBCC, KLF2, PTPRO
GOTERM_CC_DIRECT	GO:0005615~extracellular space	83	0.057996	0.04119367	IL16, KERA, LY86, IGFBP6, TNFSF15, LRRC17, VGF, MMP2, CXCL12, SHH, RTN3, TTR, APOA1, PTGIS, SEMA3G, GSN, IL4R, SERPINE1, CETP, CAT, VWA1, LOXL2, ANGPT2, LOXL1, ICAM1, F12, ACTN4, CAMP, F9, PDE4C, CLIC1, PRELP, INHBB, VEGFC, LILRB2, DDR1, THBD, C1QBP, ADM, INHBE, CTSO, CFL1, VEGFA, CSTB, STC1, TNFAIP2, PROS1, LCP1, ADAMTS5, ALDOA, ERBB3, HDGF, HFE, DCN, SFN, CCL27, CCL21, ENO2, SERPINC1, C2, LECT2, HSPA8, DPT, EPO, ENO1, FLRT3, FLRT2, FLT1, EFEMP1, AXL, ANXA1, CCL19, CD5L, CCL16, KRT35, OMD, CLEC3B, LIPC, IGFBP2, GDF15, IGFBP3, BMP6, DMBT1
GOTERM_BP_DIRECT	GO:0002576~platelet degranulation	11	0.007686	0.04156579	ALDOA, VEGFC, APOA1, PLEK, ACTN4, CLEC3B, VEGFA, SERPINE1, PROS1, CDC37L1, SPP2
GOTERM_MF_DIRECT	GO:0051015~actin filament binding	13	0.009084	0.04324063	FMNL1, TRIOBP, ACTN4, HIP1R, VIL1, CAPZB, SYNE1, CORO1A, CFL1, WIPF2, ABL1, LCP1, SPTB
GOTERM_BP_DIRECT	GO:0030324~lung development	9	0.006289	0.0432783	HES1, CEBPA, SREBF1, LIPA, TIMELESS, VEGFA, ZFPM2, ADAMTS2, SHH
GOTERM_BP_DIRECT	GO:0051301~cell division	27	0.018866	0.04353138	KIFC1, TRIOBP, KNTC1, NEDD9, CDC73, ENSA, CD2AP, LLGL2, KIF2C, CDCA8, TUBB, NCAPG, KLHL22, USP16, CDC6, CCNK, ARHGEF2, POGZ, LIG1, PSRC1, CDC23, CDC20, CEP63, TACC3, TIMELESS, MAPRE2, NEK4
GOTERM_BP_DIRECT	GO:0051491~positive regulation of filopodium assembly	5	0.003494	0.04359681	CCR7, FNBP1L, CCL21, BCAS3, SRF

GOTERM_BP_DIRECT	GO:0030041~actin filament polymerization	5	0.003494	0.04359681	GSN, VIL1, RAC1, ABL1, WAS
GOTERM_CC_DIRECT	GO:0035098~ESC/E(Z) complex	4	0.002795	0.04379141	PHF1, JARID2, MTF2, EZH2
GOTERM_BP_DIRECT	GO:0045814~negative regulation of gene expression, epigenetic	7	0.004891	0.04406128	PHF1, JARID2, MTF2, EZH2, TRIM27, H3F3A, HIST1H4C
GOTERM_MF_DIRECT	GO:0046875~ephrin receptor binding	5	0.003494	0.04411751	ANKS1A, FYN, EFNA1, SHC1, EFNA4
GOTERM_CC_DIRECT	GO:0015630~microtubule cytoskeleton	13	0.009084	0.04422338	AKT1, KIF2C, SHMT2, MAST2, TIMELESS, CRYAB, RUSC1, KIFAP3, PSRC1, MAPRE2, NDRG1, MID1IP1, TACC3
GOTERM_CC_DIRECT	GO:0031519~PcG protein complex	5	0.003494	0.04477217	RING1, CSNK2B, CBX4, UBAP2L, PHC2
GOTERM_MF_DIRECT	GO:0004713~protein tyrosine kinase activity	13	0.009084	0.04537694	FGFR3, FLT1, ERBB3, STAT5A, AXL, BAZ1B, FYN, CLK2, MAP3K9, LCK, TNK1, ABL1, YES1
GOTERM_BP_DIRECT	GO:0042517~positive regulation of tyrosine phosphorylation of Stat3 protein	6	0.004192	0.0455332	HES1, FGFR3, IL23A, HDAC1, VEGFA, CSF1R
GOTERM_MF_DIRECT	GO:0004714~transmembrane receptor protein tyrosine kinase activity	6	0.004192	0.04616505	DDR1, FLT1, ERBB3, TRIM27, AXL, CSF1R
GOTERM_BP_DIRECT	GO:0006397~mRNA processing	16	0.01118	0.0466179	KHDRBS1, RNASEL, U2AF2, RBM4, PTBP1, RBBP6, SF3B4, TTF2, SF3B2, RBM4B, C1QBP, SFPQ, SRRM1, GPATCH1, LSM1, TSEN34
GOTERM_BP_DIRECT	GO:0008209~androgen metabolic process	4	0.002795	0.04725571	AKR1C4, ADM, SHH, PLEKHA1
GOTERM_BP_DIRECT	GO:0030949~positive regulation of vascular endothelial growth factor receptor signaling pathway	4	0.002795	0.04725571	GRB10, HIF1A, FLT1, VEGFA
GOTERM_CC_DIRECT	GO:0005681~spliceosomal complex	10	0.006987	0.04738458	U2AF2, SNRPB, SNRPA, DHX16, IVNS1ABP, SNRPF, SF3B4, TTF2, HSPA8, SF3B2
GOTERM_BP_DIRECT	GO:0002606~positive regulation of dendritic cell antigen processing and presentation	3	0.002096	0.04762532	CCR7, CCL21, CCL19
GOTERM_BP_DIRECT	GO:0032515~negative regulation of phosphoprotein phosphatase activity	3	0.002096	0.04762532	PPP1R11, RGN, PPP1R15A
GOTERM_BP_DIRECT	GO:0043567~regulation of insulin-like growth factor receptor signaling pathway	3	0.002096	0.04762532	IGFBP6, IGFBP2, IGFBP3
GOTERM_BP_DIRECT	GO:0051014~actin filament severing	3	0.002096	0.04762532	FMNL1, GSN, VIL1
GOTERM_BP_DIRECT	GO:0030856~regulation of epithelial cell differentiation	3	0.002096	0.04762532	KIAA1109, ALOX15B, CD24
GOTERM_MF_DIRECT	GO:0004022~alcohol dehydrogenase (NAD) activity	3	0.002096	0.04796	ADH5, ADH6, ADH1A
GOTERM_CC_DIRECT	GO:0000922~spindle pole	11	0.007686	0.04843568	CDC6, NUP62, DDX11, MAPK14, PSRC1, KNTC1, NEDD9, GPSM2, CDC20, CEP63, TACC3
GOTERM_MF_DIRECT	GO:0001047~core promoter binding	8	0.00559	0.04848689	E2F3, NPAS2, HDAC1, SFPQ, EZH2, CRY1, MYBBP1A, GTF2B
GOTERM_BP_DIRECT	GO:0007568~aging	15	0.010481	0.04890511	SREBF1, TACR3, CRYAB, DCN, PCK1, AKT1, CDKN1C, ADM, SRR, RGN, CAT, IGFBP2, LOXL2, CASP2, EPO
GOTERM_BP_DIRECT	GO:0009653~anatomical structure morphogenesis	10	0.006987	0.04951861	MRPL40, IER3, LST1, POU5F1, LIG1, RAC1, SIAH1, WHSC1, SCMH1, KRT35

GOTERM_MF_DIRECT	GO:0046966~thyroid hormone receptor binding	5	0.003494	0.04972913	TAF11, MED4, NUP62, NCOA6, GTF2B
GOTERM_MF_DIRECT	GO:0051879~Hsp90 protein binding	5	0.003494	0.04972913	NPAS2, HIF1A, NUP62, NASP, PPID
KEGG_PATHWAY	hsa00010:Glycolysis / Gluconeogenesis	14	0.009782	2.42E-04	ALDOA, LDHA, PFKL, HK2, ADH5, ADH6, ADH1B, ADH1A, PDHB, PCK1, ALDH7A1, ENO2, PGK1, ENO1
KEGG_PATHWAY	hsa04066:HIF-1 signaling pathway	17	0.011879	3.08E-04	FLT1, PFKFB3, VHL, MKNK2, HK2, EGLN3, PDHB, AKT1, HIF1A, CDKN1B, SERPINE1, VEGFA, SLC2A1, ENO2, ANGPT2, EPO, ENO1
KEGG_PATHWAY	hsa01200:Carbon metabolism	18	0.012577	6.94E-04	ALDOA, SHMT2, PFKL, EHHADH, HK2, ADH5, CPS1, PDHB, G6PD, SDHD, ENO2, RGN, CAT, PGK1, SUCLA2, PCCB, PRPS2, ENO1
KEGG_PATHWAY	hsa05230:Central carbon metabolism in cancer	11	0.007686	0.00650896	SLC16A3, AKT1, SLC1A5, HIF1A, FGFR3, G6PD, PFKL, SLC2A2, SLC2A1, HK2, PDHB
KEGG_PATHWAY	hsa01130:Biosynthesis of antibiotics	24	0.01677	0.00770224	ALDOA, GCDH, HSD17B10, SHMT2, LDHA, PFKL, EHHADH, OTC, BCKDHB, HK2, ADH5, PDHB, PCK1, ALDH7A1, G6PD, SDHD, ENO2, RGN, CAT, PGK1, SUCLA2, PCCB, PRPS2, ENO1
KEGG_PATHWAY	hsa03320:PPAR signaling pathway	10	0.006987	0.02454067	ACOX2, PPARD, APOA1, EHHADH, FABP4, AQP7, SLC27A2, SLC27A5, MMP1, PCK1
KEGG_PATHWAY	hsa04110:Cell cycle	15	0.010481	0.02464567	CDC6, E2F3, CCNH, PKMYT1, CDC23, CDC20, ESPL1, SFN, MCM3, CDKN1C, CDKN1B, CDKN2A, HDAC1, CDKN2C, ABL1
KEGG_PATHWAY	hsa04976:Bile secretion	10	0.006987	0.0291234	ATP1B1, AQP9, ADCY7, SLC2A1, SLC4A2, SCARB1, ATP1A1, SLC27A5, SLC22A1, SLC10A1
KEGG_PATHWAY	hsa04520:Adherens junction	10	0.006987	0.03427458	PTPN6, RAC2, PTPRF, ACTN4, FYN, RAC1, CSNK2B, YES1, WAS, FARP2
KEGG_PATHWAY	hsa01230:Biosynthesis of amino acids	10	0.006987	0.03707214	ALDOA, SHMT2, PFKL, OTC, ENO2, MAT2B, CPS1, PGK1, PRPS2, ENO1
KEGG_PATHWAY	hsa05220:Chronic myeloid leukemia	10	0.006987	0.03707214	AKT1, E2F3, CDKN2A, CDKN1B, CRKL, HDAC1, STAT5A, SHC1, ABL1, SHC3
KEGG_PATHWAY	hsa00620:Pyruvate metabolism	7	0.004891	0.03842471	LDHA, ALDH7A1, ACYP1, GLO1, GRHPR, PDHB, PCK1
KEGG_PATHWAY	hsa04015:Rap1 signaling pathway	21	0.014674	0.04343441	FLT1, FGFR3, ADCY7, RAP1GAP, EFNA1, ADORA2A, FPR1, FARP2, AKT1, VEGFC, CRKL, RAC2, MAPK13, MAPK14, RAC1, VEGFA, RAPGEF6, EFNA4, PLCB1, ANGPT2, CSF1R
KEGG_PATHWAY	hsa00310:Lysine degradation	8	0.00559	0.04426413	GCDH, ALDH7A1, PLOD1, PLOD2, EHHADH, WHSC1, EHMT2, PIPOX
KEGG_PATHWAY	hsa00071:Fatty acid degradation	7	0.004891	0.04727144	GCDH, ALDH7A1, EHHADH, ADH5, ADH6, ADH1B, ADH1A

Notes: GO, Gene ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; BP, biological process; CC, cell component; MF, molecular function.

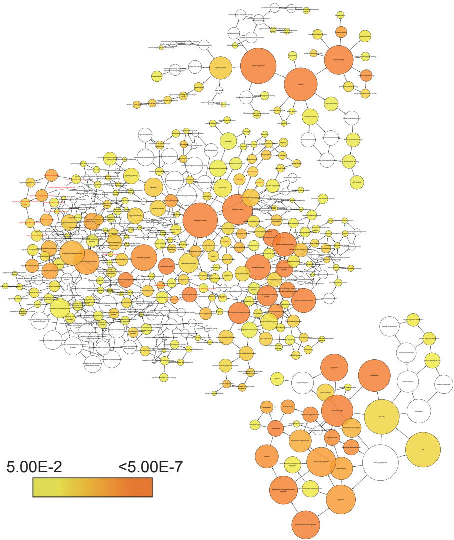

Figure S1. BinGO enrichment results of VEGF and its co-expression genes