

Figure S1. Validation of the expression level of DEGs enriched in cytokine-mediated signaling and immune response. Gene expression quantified by RT-qPCR. DEGs, differentially expressed genes; RT-qPCR, reverse-transcription quantitative PCR.

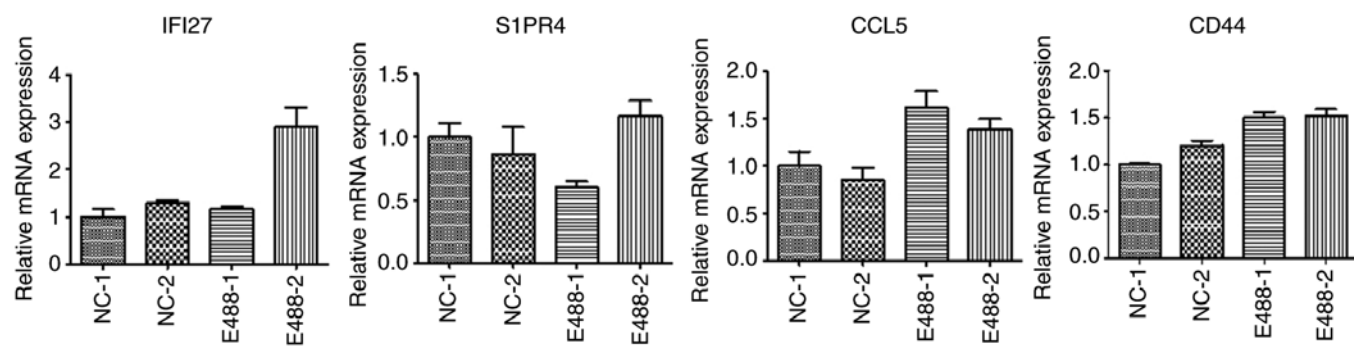


Figure S2. Validation of STAU1-regulated AS events. IGV-Sashimi plot revealed (A-C) three A5SS AS events in three different genes. Reads distribution of each AS event was plotted in the left panel with the transcripts of each gene shown below. The schematic diagrams depict the structures of two AS events, AS1 (purple line) and AS2 (green line). The exon sequences are denoted by black boxes, the intron sequences by a horizontal line (right panel). RNA-seq quantification and RT-qPCR validation of ASEs are presented in the panels on the right. STAU1, double-stranded RNA-binding protein Staufen homolog 1; AS, alternative splicing; A5SS, alternative 5'splice site; RNA-seq, RNA sequencing; RT-qPCR, reverse-transcription quantitative PCR. Error bars represent mean \pm SEM. * $P < 0.05$.

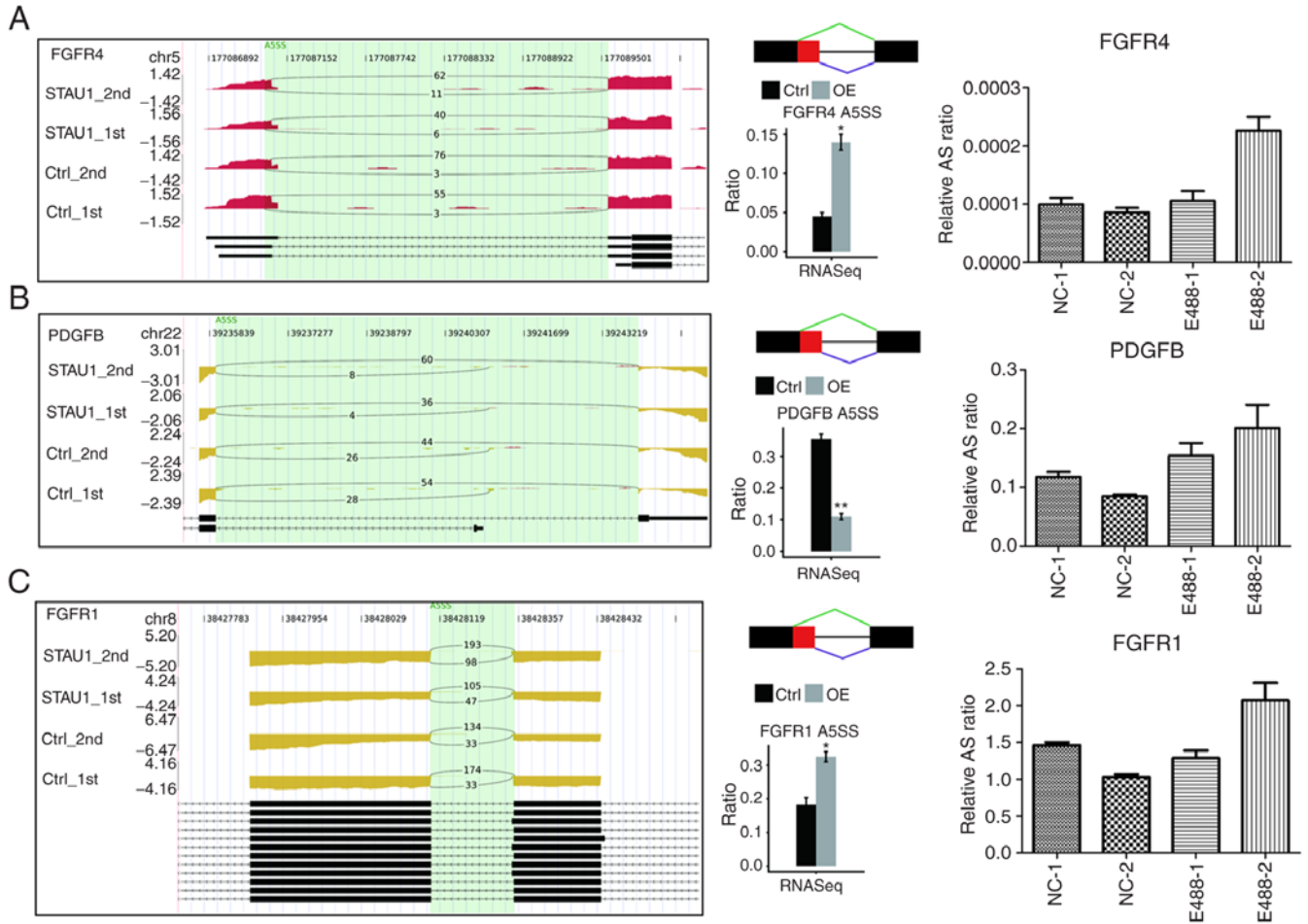


Table SI. Primers used in gene validation experiments.

IFIT2-F	CAGCCTACGGCAACTAAA
IFIT2-R	GAGCCTTCTCAAAGCAC
IFIT3-F	ACACCAAACAATGGCTAC
IFIT3-R	TGGACAAACCTCTAAAC
OASL-F	AATGGTGACCGTGATGGG
OASL-R	ACCTGAGGATGGAGCAGAG
IFI27-F	TTCACTGCGGCGGAATC
IFI27-R	TGGCTGCTATGGAGGACGAG
S1PR4-F	TGCTGAAGACGGTGCTGATG
S1PR4-R	TGCGGAAGGAGTAGATGATGG
CCL5-F	ACGACTGCTGGGTTGGAG
CCL5-R	ACCCTGCTGCTTTGCCTA
CCL2-F	CTAACCCAGAAACATCCAAT
CCL2-R	GCTATGAGCAGCAGGCAC
CD44-F	TGGAGGACAGAAAGCCAAGT
CD44-R	TTCGCAATGAAACAATCAGTAG
PLEKHG2-M/As-F	CCAAAAGTAAGCCTGTCC
PLEKHG2-M-R	GGAGATGGAGCTGTGTTCCCT
PLEKHG2-As-R	TTCACCGGCTCTGTGTTCCCT
ARHGEF11-M/As-F	TATGGAAGATCATGCCACG
ARHGEF11-M-R	AAGGCTACGGGGAAGTCTGCTT
ARHGEF11-As-R	GTGAGAAAAGGGAAGTCTGCTT
PDGFB-M/As-F	AGGAGCGGATCGAGTGGT
PDGFB-M-R	CAGCGCCGAGGGGGACCCCA
PDGFB-As-R	AGCCCTGGAGGGGGACCCCA
FGFR4-M-F	GCCAGGTGAGGAGGAGCCAGG
	AAGGCAGTT
FGFR4-As-F	TGAGGCGGCGGAGGAGCCAGG
	AAGGCAGTT
FGFR4-M/As-R	GCCGCATCTCCTTCTCAC
RALGDS-M/As-F	ATACAGCAGTCGCCCACC
RALGDS-M-R	GGAAAAGAAGTTCTGGGAAT
RALGDS-As-R	TCTCCCTCAGTTCTGGGAAT
FGFR1-M/As-F	CTTGTAGCCTCCAATTCTGT
FGFR1-M-R	AAACCAAACCCCGTAGCTCC
FGFR1-As-R	AACCGTATGCCCGTAGCTCC

CCL2, chemokine (C-C motif) ligand 2; IFIT2, interferon-induced protein with tetratricopeptide repeats 2; IFIT3, interferon-induced protein with tetratricopeptide repeats 3; OASL, 2'-5'-oligoadenylate synthetase-like protein; F, forward; R, reverse; M, model; As, alternative splicing.

Table SII. Analysis of gene GO enrichment.

#Term	ID	Input number	Background number	P-value	Corrected P-value	Input
Retrograde transport, endosome to Golgi transcription, DNA -dependent	GO:0042147	6	33	2.83×10^{-5}	0.002493449	PIKfyve, Wash3p, Wash6p, Arfrp1, Stx16, Gosr1
	GO:0006351	56	1,857	0.000152097	0.00669225	Srcap, Aes, Znf195, Trim33, Znf319, Rbbp5, Cttnnb1, Ezh2, Ikbkg, Znf300, Znf780a, Arntl2, Uimc1, Stat6, Zbtb17, Tcf3, Ncoa4, Chd9, Rora, Apx1, Fhl2, Elof1, Znf266, Pou6f1, Hnrnpul1, Dmap1, Fgfr1, Zbtb34, Yaf2, Rbl1, Znf226, Mier1, Znf48, Znf808, Supt6h, Scml1, Brd2, Hey1, Arid3b, Psip1, Hmbox1, Acad8, Arnt, Rfx2, Zfp62, Nr1i3, Zgpap, Linc00473, Hes6, Hdac10, Mak, Linc54, Nab1, Ewsr1, Zscan31, Zbtb25
Muscle cell differentiation response to hormone stimulus DNA repair	GO:0042692	5	36	0.000502744	0.014747147	Cttnnb1, Syne1, Rora, Cttna1, Tcf3
	GO:0009725	5	40	0.000825985	0.018171669	Fhl2, Snrpn, Mmp19, Ncoa4, Dhcr24
	GO:0006281	13	280	0.00228755	0.036690602	Smug1, Ercc8, Ints3, Rps27l, Cep164, Mutyh, Apx1, Rad52, Dmap1, Usp28, Polk, Fanci, Eme2
Negative regulation of transcription, DNA-dependent	GO:0045892	18	464	0.002690117	0.036690602	Nr1i3, Pdgfb, Zgpap, Hmbox1, Prmt2, Dab2ip, Aes, Fhl2, Trim33, Cttnnb1, Ezh2, Mbd1, Yaf2, Dmap1, Hdac10, Nab1, Uimc1, Hey1
	GO:0016568	7	102	0.002918571	0.036690602	Rbl1, Cabin1, Tlk2, Tdrd3, Chd9, Hdac10, Brd2
Chromatin modification regulation of transcription, DNA-dependent	GO:0006355	38	1,305	0.003673355	0.040406902	Znf195, Rbak-rbakdn, Elof1, Znf319, Sfmtb2, Ezh2, Rfx2, Dnm2, Znf780a, Arntl2, Tcf3, Chd9, Rora, Apx1, Znf266, Zfp62, Znf45, Znf226, Zbtb7b, Znf48, Znf808, Supt6h, Znf300, Hnrnpul1, Hey1, Arid3b, Psip1, Acad8, Rbbp5, Zbtb34, Gon4l, Hdac10, Mak, Linc54, Nab1, Ewsr1, Hes6, Srsf10
	GO:0043627	5	60	0.005074627	0.046649338	Cttnnb1, Rbbp5, Cttna1, Arsb, Cavi
Response to estrogen stimulus Cilium assembly	GO:0042384	6	86	0.005301061	0.046649338	Cep164, Ift81, Snx10, Iqcb1, Fbf1, Tmem107
	GO:0016197	5	64	0.006673011	0.051055288	Anxa8, Wash3p, Chmp2a, Wash6p, Picalm
Muscle contraction Multicellular organism growth	GO:0006936	6	91	0.006962085	0.051055288	Cacna1h, Slmap, Gnao1, Mylk, Myl6, Ttn
	GO:0035264	5	68	0.008594474	0.05772428	Stil, Pde4d, Ggylf2, Slik3, Gpd2
Cell migration mRNA processing	GO:0016477	7	126	0.009183408	0.05772428	Plxnb1, Ptk7, Pip5k1a, Tns3, Fgfr4, Bcari, Fgfr1
	GO:0006397	9	195	0.010804681	0.063387461	Supt6h, Nsrp1, Gemin2, Tsen15, Mettl3, Phrf1, Rnpc3, Ptbp3, Tardbp
Nerve growth factor receptor signaling pathway	GO:0048011	11	273	0.01334861	0.066866514	Plekkg2, Arhgef11, Pdgfb, Ralgds, Nr4a1, Irs1, Ap2b1, Fgfr4, Bcari, Nrg4, Fgfr1
	GO:0006974	8	169	0.013772803	0.066866514	Ercc8, Ints3, Rps27l, Tlk2, Rbbp5, Ikbkg, Usp28, Aptx
Response to DNA damage stimulus Angiogenesis	GO:0001525	9	206	0.015027863	0.066866514	Hey1, Anxa2, Dab2ip, Mmp19, Rora, Pdcdd10, Cavi, Apold1, Fgfr1
	GO:0007067	10	243	0.015660316	0.066866514	Sac3d1, Cdc16, Cep164, Ppp2r2d, Numal1, Dsn1, Arpp19, Skaa2, Nedd1, Anapc11

Table SII. Continued.

#Term	ID	Input number	Background number	P-value	Corrected P-value	Input
Viral reproduction	GO:0016032	18	555	0.015896711	0.066866514	SRCAP, RBCK1, IFIH1, SUPT6H, RBL1, PSIP1, DDX11, EIF4G1, CD46, CFLAR, CHMP2A, IKBKKG, AP1S2, KLCL1, SEPT6, AP2B1, F11R, CAV1
RNA splicing	GO:0008380	10	247	0.017353123	0.066866514	NHP2L1, SUPT6H, NSRPI, GEMIN2, HNRNPA3, SNRPN, RNPC3, PTBP3, HNRNPUL1, TARDBP
Cell-matrix adhesion	GO:0007160	5	81	0.017413059	0.066866514	CTNNB1, SGCE, PKD1, THBS3, ITGA10
G2/M transition of mitotic cell cycle	GO:0000086	7	143	0.017476475	0.066866514	CEP164, DDX11, NEDD1, NUMA1, ARPP19, DNMM2, LIN54
Positive regulation of transcription, DNA-dependent	GO:0045893	16	503	0.026084584	0.092281731	ARHGFEF1, PDGFB, ZBTB17, NCOA4, TCF3, ARNT, PRMT2, HMBOX1, RORA, FHL2, CTNNB1, YAF2, DNMM2, ARNTL2, ELF4, PICALM
Epidermal growth factor receptor signaling pathway	GO:0007173	8	191	0.026519644	0.092281731	PDGFB, NR4A1, IRS1, NRG4, FGFR4, BCAR1, AP2B1, FGFR1
Peptidyl-tyrosine phosphorylation	GO:0018108	5	91	0.027265057	0.092281731	PDGFB, FGFR4, PTK7, YES1, FGFR1
Endocytosis	GO:0006897	6	125	0.029238983	0.09434093	GAPVD1, FNBP1, LRP8, LRP8, ITS2, DNMM2, AP2B1
Regulation of small GTPase-mediated signal transduction	GO:0051056	7	160	0.030017569	0.09434093	PLEKHG2, GAPVD1, RALGDS, ARHGFEF1, ARHGAP33, ARHGAPI2, RAPIGAP2
Fibroblast growth factor receptor signaling pathway	GO:0008543	7	163	0.032731157	0.099322132	PDGFB, NR4A1, MKNK1, IRS1, FGFR4, NRG4, FGFR1
Negative regulation of transcription from RNA polymerase II promoter	GO:0000122	17	565	0.035181361	0.103198659	CTNNB1, AES, RBL1, HEY1, STAT6, TRIM33, LRP8, PKIG, DAB2IP, FHL2, EZH2, DMAP1, SAMD11, HDAC10, RITA1, FGFR1, CAV1
Vesicle-mediated transport	GO:0016192	7	169	0.038639358	0.107642319	GGA3, AP1S2, STX16, KXDI, SPTBN4, AP2B1, PICALM
Regulation of transcription from RNA polymerase II promoter	GO:0006357	10	283	0.039142662	0.107642319	SRCAP, STAT6, AES, RBL1, TRAK1, FHL2, TARBPI, HES6, ARNTL2, BRD2
Phosphatidylinositol-mediated signaling	GO:0048015	6	137	0.042774244	0.11137954	PDGFB, NR4A1, IRS1, FGFR4, NRG4, FGFR1
Response to oxidative stress	GO:0006979	5	103	0.043033004	0.11137954	ERCC8, HMOX2, PSIP1, MSRB3, DHCR24
Axon guidance	GO:0007411	11	334	0.048104698	0.120948955	CACNA1H, ARHGFEF1, PLXNB1, ROBO3, SPTB, MYL6, ITGA10, NUMB, SPTBN4, AP2B1, FGFR1
Insulin receptor signaling pathway	GO:0008286	6	149	0.059703568	0.145578054	CAB39L, EIF4G1, IRS1, FGFR4, BCAR1, FGFR1
Response to virus	GO:0009615	5	114	0.061466992	0.145578054	IFIH1, IFITM1, IKBKKG, HNRNPUL1, TPT1
Cellular lipid metabolic process	GO:0044255	6	151	0.062863251	0.145578054	CHD9, FHL2, AGPAT3, GPD2, FDFI1, TXNRD1
Metabolic process	GO:0008152	5	116	0.06523212	0.147190424	MYL6, KLCL1, DNAH17, MYO1B, PITPNM2
Phospholipid metabolic process	GO:0006644	6	157	0.072924698	0.160434336	PIKFYVE, PIP5K1A, PLD3, CHPT1, AGPAT3, SACMIL
Sensory perception of sound	GO:0007605	5	121	0.075197154	0.16139877	EML2, NAV2, SPTBN4, DIAPH1, FGFR1
Signal transduction	GO:0007165	26	1,045	0.078561317	0.164604664	PTK7, ARFRP1, DNMM2, GAPVD1, PLXNB1, PRMT2, MIER1, TXNRD1, NPR2, CLIC1, MTSSL, PPP2R2D, NR4A1, STAT6, AGAP3, CHRNA3, PDE10A, NFAT5, IL15RA, PIP5K1A, PKIG,

Table SII. Continued.

#Term	ID	Input number	Background number	P-value	Corrected P-value	Input
Post-translational protein modification	GO:0043687	7	201	0.081647632	0.167092829	IRS1, NR1I3, ARHGAP33, PDE4D, LRP8
Positive regulation of NF- κ B transcription factor activity	GO:0051092	5	127	0.088181668	0.17527579	PIGB, ARSB, MGAT1, PIGO, FIGQ, MPI, UGGT2 CFLAR, CARD14, IKBKG, RBCK1, ANKRD42
Regulation of apoptotic process	GO:0042981	6	166	0.089644533	0.17527579	IFIH1, TPT1, CFLAR, CARD14, PEA15, BCAR1
Nuclear mRNA splicing, via spliceosome	GO:0000398	6	167	0.091621436	0.17527579	NHP2L1, HNRNPA3, GEMIN7, SRSF10, TRA2B, HNRNPUL1
Positive regulation of cell migration	GO:0030335	5	130	0.095084898	0.178031299	PDGFB, BCAR1, DIAPH1, IRS1, MYLK
Blood coagulation	GO:0007596	13	469	0.099037025	0.179297313	PDGFB, ANXA8, LRP8, CD59, ITGA10, TTN, YES1, KLC1, DGKA, BCAR1, PDE10A, F11R, CAV1
Cell cycle arrest	GO:0007050	5	132	0.099836004	0.179297313	CAB39L, CDKN3, PKD1, DST, DHCR24
<i>In utero</i> embryonic development	GO:0001701	7	220	0.116558884	0.205143635	STIL, PKD1, LY6E, CTNNB1, MGAT1, TTN, FGFR1
Mitotic cell cycle	GO:0000278	11	403	0.131831936	0.22596403	CEP164, CDC16, RBL1, NUMA1, PPP2R2D, DSN1, ARPP19, SKA2, NEDD1, LINS4, ANAPC11
Transcription initiation from RNA polymerase II promoter	GO:0006367	6	186	0.1335242	0.22596403	ZNF45, RBL1, TRIM33, NR4A1, RORA, NR1I3
Positive regulation of I- κ B kinase/NF- κ B cascade	GO:0043123	5	153	0.156415751	0.259709171	CTNNB1, MIER1, IKBKG, RBCK1, CFLAR
Intracellular signal transduction	GO:0035556	10	379	0.169368266	0.272304588	MINK1, NPR2, PLXNB1, PIKFYVE, RGS11, IFITM1, TLK2, TNS3, MKNK1, DGKA
Response to hypoxia	GO:0001666	5	159	0.174599086	0.272304588	HMOX2, PDGFB, ARNT, APOLD1, CAV1
Cell surface receptor signaling pathway	GO:0007166	5	160	0.177706085	0.272304588	NPR2, CD59, IFITM1, LY6E, CABIN1
Protein autophosphorylation	GO:0046777	5	161	0.180833969	0.272304588	MINK1, FGFR4, MAK, YES1, FGFR1
Positive regulation of apoptotic process	GO:0043065	8	294	0.182342257	0.272304588	PLEKHG2, ARHGEF11, PRMT2, NR4A1, DAB2IP, CTNNB1, RBCK1, DNMT2
Gene expression	GO:0010467	16	672	0.186307214	0.272304588	GEMIN2, ZNF45, METTL3, SLBP, RBL1, TRIM33, HNRNPA3, EIF4G1, NR4A1, GEMIN7, RORA, NR1I3, EDC3, NHP2L1, HNRNPUL1, ZBTB25
Cell death	GO:0008219	6	207	0.188519893	0.272304588	GIGYF2, EIF4G1, DNMT2, SYNE1, APTX, TARDBP
Cellular protein metabolic process	GO:0044267	13	530	0.188850344	0.272304588	PIGB, ZBTB17, GIGYF2, ARSB, FIGQ, EIF4G1, EXTL3, DDX11, PIKFYVE, PIGO, MGAT1, MPI, UGGT2
Protein phosphorylation	GO:0006468	9	344	0.19185096	0.272304588	MINK1, PDGFB, SIK3, TLK2, MKNK1, PHKA1, MYLK, MAK, FGFR1
Ubiquitin-dependent protein catabolic process	GO:0006511	5	174	0.223227764	0.31181021	NUB1, FBXO4, USP14, USP36, USP28
Positive regulation of transcription from RNA polymerase II promoter	GO:0045944	17	749	0.230697951	0.317209683	NFAT5, PSIP1, RBL1, TCF3, ARNT, PKD1, BCL2L12, DAB2IP, STAT6, RORA, CTNNB1, CAPRIN2, DCAF6, IKBKG, ARNTL2,

Table SII. Continued.

#Term	ID	Input number	Background number	P-value	Corrected P-value	Input
Small molecule metabolic process	GO:0044281	30	1,413	0.24633959	0.333505907	ELF4, HEY1 GALT,ALAD,GPD2,ATP5J,DNM2,PYCR1,CAV1,CTPS2,CHD9, FHL2,CHPT1,SACMIL,GMPR2,FDFT1,TXNRD1,ISCU,CA5B, PIKFYVE,PHKA1,SULT1A2,GGT1,GUK1,DHCR24,ARSB, PLD3,ACAD8,PIP5K1A,HMOX2,SLC35B3,AGPAT3 PDGFB,NR4A1,IRS1,IKBK,FGFR4,NRG4,FGFR1 COL7A1,PTK7,DST,PPFIBP1,THBS3,CTNNB1,ITGA10, GGA3,STX16,AP2B1,AP1S2,SNX10 PDGFB,DGKA,BCAR1,TTN,ENTPD2 GALT,ARSB,MGAT1,GNPDA2,PHKA1,MPI,PIGQ,SLC35B3 APEX1,PDGFB,TCF3,GNAO1,LRP8,CTNNB1,EI24 NFAT5,HEY1,SLBP,ZBTB7B,PHRF1,MBD1,ARNTL2,ELF4, TARDBP PDGFB,COL7A1,DST,MMP19,ITGA10,SERPINH1,F11R ARHGFEF11,ENTPD2,RGS11,GNAO1,LPAR2,BCAR1,GPR176
Fc-ε receptor signaling pathway	GO:0038095	7	294	0.306542492	0.407725091	
Cell adhesion	GO:0007155	10	445	0.314952374	0.407725091	
BCAR1, CTNNA1, F11R						
Intracellular protein transport	GO:0006886	5	200	0.315060297	0.407725091	
Platelet activation	GO:0030168	5	204	0.329690677	0.420475066	
Carbohydrate metabolic process	GO:0005975	8	354	0.337348716	0.420678889	
Response to drug	GO:0042493	7	305	0.339411376	0.420678889	
Transcription from RNA polymerase II promoter	GO:0006366	9	407	0.345274489	0.422002153	
Extracellular matrix organization	GO:0030198	7	312	0.360573101	0.434663464	
G-protein coupled receptor signaling pathway	GO:0007186	7	317	0.375760234	0.446850008	
Protein ubiquitination	GO:0016567	6	269	0.383784467	0.450307108	
Synaptic transmission	GO:0007268	8	389	0.436053161	0.50490366	NUB1,ANAPC11,TRIM33,FBXO4,DCAF6,RNF34 MINK1,GRIK1,USP14,CHRNA3,GABBR1,GRIP2,AP2B1, GPR176
Cell differentiation	GO:0030154	8	395	0.452954867	0.513629259	ARNT,ZBTB7B,MMP19,APOLD1,MAK,SEMA6B,ELF4,HES6
Cell proliferation	GO:0008283	7	344	0.457760096	0.513629259	STIL,CDC16,IL15RA,USP28,BCAR1,PICALM,TXNRD1
Small GTPase mediated signal transduction	GO:0007264	7	348	0.46977759	0.513629259	PLEKHG2,ARHGFEF11,RALGDS,ARFRP1,AGAP3,ARHGAP12, ARHGAP33
Protein transport	GO:0015031	8	402	0.472565415	0.513629259	SEC22C,COG8,XPO4,MAMDC4,CHMP2A,TM9SF1,GOSR1, ARHGAP33
Transport	GO:0006810	7	349	0.472772386	0.513629259	SEC22C,CACNA1H,GRIK1,PEA15,ACBD5,PITPNM2,ABCD4
Negative regulation of apoptotic Process	GO:0043066	9	475	0.524136464	0.562487913	STIL,TPT1,CD59,CARD14,FHL2,CFLAR,PDCD10,CTNNA1, DHCR24
Innate immune response	GO:0045087	14	754	0.540532156	0.573094334	STAT6,PDGFB,NR4A1,CD46,DAB2IP,IRS1,IFIH1,CTNNB1, CD59,IKBK,FGFR4,NRG4,YES1,FGFR1
Apoptotic process	GO:0006915	11	605	0.573079394	0.600368889	TJP2,CTNNB1,CFLAR,PTPRH,CARD14,EI24,PEA15,IKBK, PDCD10,DHCR24,EMC4
Positive regulation of cell proliferation	GO:0008284	7	429	0.689002497	0.713320232	PDGFB,DDX11,IRS1,TNS3,PDCD10,FGFR4,FGFR1
Negative regulation of cell proliferation	GO:0008285	6	378	0.708075842	0.724542722	IFITM1,CDKN3,CDK10,DAB2IP,CTNNB1,DHCR24
Transmembrane transport	GO:0055085	7	578	0.916342696	0.926875371	SLC9A3,ANO4,SLC9A8,HMOX2,SLC35B3,SLC29A1,ABCD4
Multicellular organismal development	GO:0007275	5	474	0.942707711	0.942707711	MINK1,ZNF45,MAK,AES,ZBTB7B

Table SIII. Analysis of gene KEGG pathway enrichment.

Term	ID	Input number	Background number	P-value	Corrected P-value	Input
Bacterial invasion of epithelial cells	hsa05100	6	76	0.00495373	0.814390314	CTNNB1, DNM2, SEPT6, BCAR1, CTNNA1, CAV1
	hsa04810	10	215	0.014367305	0.814390314	PDGFB, DIAPH1, PIKFYVE, PIP5K1A, MYLK, ITGA10, SSH2, FGFR4, BCAR1, FGFR1
Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	hsa00563	3	25	0.014717897	0.814390314	PIGQ, PIGB, PIGO
	hsa03410	3	33	0.030942694	0.938081005	SMUG1, MUTYH, APEX1
Base excision repair	hsa00564	5	91	0.041429974	0.938081005	CHPT1, DGKA, AGPAT3, GPD2, PLD3
	hsa00920	2	18	0.053429525	0.938081005	MPST, SULT1A2
Sulfur metabolism	hsa04530	6	134	0.061435758	0.938081005	TJP2, PPP2R2D, CTNNB1, YES1, CTNNA1, F11R
	hsa04144	8	203	0.062169263	0.938081005	SMAP1, PIP5K1A, CHMP2A, AGAP3, DNM2, FGFR4, AP2B1, CAV1
Endocytosis	hsa00230	7	169	0.063523767	0.938081005	NPR2, ENTPD4, ENTPD2, GUK1, GMPR2, PDE4D, PDE10A
	hsa04520	4	73	0.066043255	0.938081005	CTNNB1, CTNNA1, YES1, FGFR1
Purine metabolism	hsa04510	8	207	0.068065279	0.938081005	PDGFB, DIAPH1, THBS3, MYLK, CTNNB1, ITGA10, BCAR1, CAV1
	hsa00520	3	49	0.082332063	0.938081005	GNPDA2, GALT, MPI
Amino sugar and nucleotide sugar metabolism	hsa00534	2	24	0.088929836	0.938081005	EXTL2, EXTL3
	hsa03460	3	54	0.10297988	0.938081005	POLK, FANCI, EME2
heparan sulfate/heparin	hsa03440	2	28	0.115488835	0.938081005	SSBP1, RAD52
	hsa05215	4	89	0.11553549	0.938081005	CTNNB1, PDGFB, IKKBKG, FGFR1
Fanconi anemia pathway	hsa05216	2	29	0.122413217	0.938081005	CTNNB1, NCOA4
	hsa05032	4	93	0.129901669	0.938081005	GNAO1, PDE4D, PDE10A, GABBR1
Homologous recombination	hsa00460	1	7	0.137628514	0.938081005	GGT1
	hsa04130	2	36	0.173269803	0.938081005	GOSR1, STX16
Prostate cancer	hsa05142	4	105	0.177014231	0.938081005	GNAO1, IKKBKG, PPP2R2D, CFLAR
	hsa04151	10	346	0.187249902	0.938081005	PDGFB, PPP2R2D, NR4A1, IRS1, THBS3, ITGA10, IKKBKG, LPAR2, FGFR4, FGFR1
Thyroid cancer	hsa00430	1	10	0.190691957	0.938081005	GGT1
	hsa04122	1	10	0.190691957	0.938081005	MPST
Morphine addiction	hsa01100	29	1182	0.197063181	0.938081005	ALAD, CTPS2, GNPDA2, HY1, ATP5J, COX6B2, PYCR1, MGAT1, PANK4, ACSM3, MPST, CHPT1, DGKA, FDF1, GALT, PIGB, EXTL2, EXTL3, PIGO, PIGQ, GGT1, GUK1, DHCR24, ARSB, PLD3, ACAD8, PIP5K1A, MPL, AGPAT3
	hsa05412	3	75	0.206831238	0.938081005	CTNNB1, ITGA10, CTNNA1
Cyanoamino acid metabolism	hsa00460	1	7	0.137628514	0.938081005	GGT1
	hsa04130	2	36	0.173269803	0.938081005	GOSR1, STX16
SNARE interactions in vesicular transport	hsa05142	4	105	0.177014231	0.938081005	GNAO1, IKKBKG, PPP2R2D, CFLAR
	hsa04151	10	346	0.187249902	0.938081005	PDGFB, PPP2R2D, NR4A1, IRS1, THBS3, ITGA10, IKKBKG, LPAR2, FGFR4, FGFR1
Chagas disease (American trypanosomiasis)	hsa00430	1	10	0.190691957	0.938081005	GGT1
	hsa04122	1	10	0.190691957	0.938081005	MPST
PI3K-Akt signaling pathway	hsa01100	29	1182	0.197063181	0.938081005	ALAD, CTPS2, GNPDA2, HY1, ATP5J, COX6B2, PYCR1, MGAT1, PANK4, ACSM3, MPST, CHPT1, DGKA, FDF1, GALT, PIGB, EXTL2, EXTL3, PIGO, PIGQ, GGT1, GUK1, DHCR24, ARSB, PLD3, ACAD8, PIP5K1A, MPL, AGPAT3
	hsa05412	3	75	0.206831238	0.938081005	CTNNB1, ITGA10, CTNNA1
Taurine and hypotaurine metabolism	hsa00430	1	10	0.190691957	0.938081005	GGT1
	hsa04122	1	10	0.190691957	0.938081005	MPST
Sulfur relay system	hsa01100	29	1182	0.197063181	0.938081005	ALAD, CTPS2, GNPDA2, HY1, ATP5J, COX6B2, PYCR1, MGAT1, PANK4, ACSM3, MPST, CHPT1, DGKA, FDF1, GALT, PIGB, EXTL2, EXTL3, PIGO, PIGQ, GGT1, GUK1, DHCR24, ARSB, PLD3, ACAD8, PIP5K1A, MPL, AGPAT3
	hsa05412	3	75	0.206831238	0.938081005	CTNNB1, ITGA10, CTNNA1
Metabolic pathways	hsa01100	29	1182	0.197063181	0.938081005	ALAD, CTPS2, GNPDA2, HY1, ATP5J, COX6B2, PYCR1, MGAT1, PANK4, ACSM3, MPST, CHPT1, DGKA, FDF1, GALT, PIGB, EXTL2, EXTL3, PIGO, PIGQ, GGT1, GUK1, DHCR24, ARSB, PLD3, ACAD8, PIP5K1A, MPL, AGPAT3
	hsa05412	3	75	0.206831238	0.938081005	CTNNB1, ITGA10, CTNNA1
Arrhythmogenic right ventricular cardiomyopathy (ARVC)	hsa00430	1	10	0.190691957	0.938081005	GGT1
	hsa04122	1	10	0.190691957	0.938081005	MPST

Table SIII. Continued.

Term	ID	Input number	Background number	P-value	Corrected P-value	Input
Ether lipid metabolism	hsa00565	2	42	0.219075376	0.938081005	CHPT1, PLD3
Porphyryn and chlorophyll metabolism	hsa00860	2	43	0.226821797	0.938081005	ALAD, HMOX2
Leukocyte transendothelial migration	hsa04670	4	118	0.233475234	0.938081005	CTNNA1, BCAR1, CTNNA1, F11R
Phosphatidylinositol signaling system	hsa04070	3	81	0.239950091	0.938081005	PIP5K1A, DGKA, PIKFYVE
Vascular smooth muscle contraction	hsa04270	4	121	0.247102593	0.938081005	MYL6, ARHGEF11, NPR2, MYLK
Lysosome	hsa04142	4	122	0.251684586	0.938081005	GGA3, ENTPD4, AP1S2, ARSB
Cell cycle	hsa04110	4	124	0.260902516	0.938081005	ANAPC11, CDC16, ZBTB17, RBL1
Endocrine and other factor-regulated calcium reabsorption	hsa04961	2	48	0.265770196	0.938081005	AP2B1, DNM2
Mineral absorption	hsa04978	2	51	0.289175828	0.938081005	SLC9A3, HMOX2
Spliceosome	hsa03040	4	131	0.29363952	0.938081005	HNRNPA3, NHP2L1, SRSF10, TRA2B
Endometrial cancer	hsa05213	2	52	0.296963296	0.938081005	CTNNA1, CTNNA1
MAPK signaling pathway	hsa04010	7	260	0.30167936	0.938081005	CACNA1H, PDGFB, NR4A1, MKNK1, IKBKKG, FGFR4, FGFR1
Selenocompound metabolism	hsa00450	1	17	0.302223331	0.938081005	TXNRD1
Pantothenate and CoA biosynthesis	hsa00770	1	17	0.302223331	0.938081005	PANK4
HTLV-I infection	hsa05166	7	264	0.315163394	0.938081005	PDGFB, CDC16, TCF3, ANAPC11, CTNNA1, IKBKKG, IL15RA
Steroid biosynthesis	hsa00100	1	18	0.316868827	0.938081005	DHCR24
Glycerolipid metabolism	hsa00561	2	55	0.320240377	0.938081005	DGKA, AGPAT3
Ubiquitin mediated proteolysis	hsa04120	4	138	0.326891763	0.938081005	ERCC8, ANAPC11, CDC16, FBXO4
Glycosaminoglycan degradation	hsa00531	1	19	0.331199529	0.938081005	ARSB
NOD-like receptor signaling pathway	hsa04621	2	57	0.335660095	0.938081005	CARD8, IKBKKG
mTOR signaling pathway	hsa04150	2	60	0.358592933	0.938081005	CAB39L, IRS1
Shigellosis	hsa05131	2	61	0.366175886	0.938081005	DIAPH1, IKBKKG
Inositol phosphate metabolism	hsa00562	2	61	0.366175886	0.938081005	PIP5K1A, PIKFYVE
Colorectal cancer	hsa05210	2	62	0.373724781	0.938081005	CTNNA1, RALGDS
Pathways in cancer	hsa05200	8	327	0.376662316	0.938081005	PDGFB, RALGDS, NCOA4, ARNT, CTNNA1, IKBKKG, CTNNA1, FGFR1
Pyrimidine metabolism	hsa00240	3	105	0.37733411	0.938081005	ENTPD4, CTPS2, TXNRD1
Synaptic vesicle cycle	hsa04721	2	63	0.381237727	0.938081005	AP2B1, DNM2
Mismatch repair	hsa03430	1	23	0.385598334	0.938081005	SSBPI
Proximal tubule bicarbonate reclamation	hsa04964	1	23	0.385598334	0.938081005	SLC9A3
Glyoxylate and dicarboxylate metabolism	hsa00630	1	24	0.398496964	0.938081005	HYI
Renal cell carcinoma	hsa05211	2	66	0.403543339	0.938081005	PDGFB, ARNT
Pancreatic cancer	hsa05212	2	66	0.403543339	0.938081005	IKBKKG, RALGDS
Inflammatory bowel disease (IBD)	hsa05321	2	66	0.403543339	0.938081005	STAT6, RORA

Table SIII. Continued.

Term	ID	Input number	Background number	P-value	Corrected P-value	Input
Epithelial cell signaling in Helicobacter pylori infection	hsa05120	2	68	0.418203376	0.938081005	IKBKG, F11R
Complement and coagulation cascades	hsa04610	2	69	0.425465912	0.938081005	CD46, CD59
Nitrogen metabolism	hsa00910	1	27	0.435601699	0.938081005	CA5B
Adipocytokine signaling pathway	hsa04920	2	71	0.439849508	0.938081005	IRS1, IKBKG
Melanoma	hsa05218	2	71	0.439849508	0.938081005	PDGFB, FGFR1
Viral myocarditis	hsa05416	2	71	0.439849508	0.938081005	EIF4G1, CAV1
RIG-I-like receptor signaling pathway	hsa04622	2	71	0.439849508	0.938081005	IFIH1, IKBKG
Butanoate metabolism	hsa00650	1	29	0.459066464	0.938081005	ACSM3
B cell receptor signaling pathway	hsa04662	2	74	0.461053841	0.938081005	IFITM1, IKBKG
Galactose metabolism	hsa00052	1	30	0.470433019	0.938081005	GALT
Circadian rhythm	hsa04710	1	31	0.481562413	0.938081005	RORA
Axon guidance	hsa04360	3	129	0.509545851	0.938081005	ROBO3, PLXNB1, SEMA6B
Cysteine and methionine metabolism	hsa00270	1	34	0.513576255	0.938081005	MPST
Chemical carcinogenesis	hsa05204	2	83	0.521763977	0.938081005	SULT1A2, ARNT
Hypertrophic cardiomyopathy (HCM)	hsa05410	2	84	0.528225544	0.938081005	ITGA10, TTN
Primary immunodeficiency	hsa05340	1	36	0.533820431	0.938081005	IKBKG
Fructose and mannose metabolism	hsa00051	1	36	0.533820431	0.938081005	MPI
DNA replication	hsa03030	1	36	0.533820431	0.938081005	SSBP1
Progesterone-mediated oocyte maturation	hsa04914	2	86	0.540972134	0.938081005	CDC16, ANAPC11
ECM-receptor interaction	hsa04512	2	87	0.547256424	0.938081005	ITGA10, THBS3
Apoptosis	hsa04210	2	88	0.553480959	0.938081005	CFLAR, IKBKG
Protein digestion and absorption	hsa04974	2	88	0.553480959	0.938081005	COL7A1, SLC9A3
Aldosterone-regulated sodium reabsorption	hsa04960	1	39	0.562628632	0.938081005	IRS1
GABAergic synapse	hsa04727	2	90	0.565749733	0.938081005	GNAO1, GABBR1
Dilated cardiomyopathy	hsa05414	2	91	0.571793549	0.938081005	ITGA10, TTN
Fc gamma R-mediated phagocytosis	hsa04666	2	91	0.571793549	0.938081005	PIP5K1A, DNM2
Insulin signaling pathway	hsa04910	3	142	0.574906826	0.938081005	MKNK1, PHKAI, IRS1
NF-κB signaling pathway	hsa04064	2	92	0.57777676	0.938081005	CFLAR, IKBKG
Hepatitis B	hsa05161	3	147	0.598577721	0.938081005	STAT6, IFIH1, IKBKG
ABC transporters	hsa02010	1	44	0.606766418	0.938081005	ABCD4
Valine, leucine and isoleucine degradation	hsa00280	1	44	0.606766418	0.938081005	ACAD8
Circadian entrainment	hsa04713	2	97	0.606780374	0.938081005	CACNA1H, GNAO1
Estrogen signaling pathway	hsa04915	2	100	0.623451759	0.938081005	GNAO1, GABBR1
Melanogenesis	hsa04916	2	101	0.628887351	0.938081005	CTNNB1, GNAO1

Table SIII. Continued.

Term	ID	Input number	Background number	P-value	Corrected P-value	Input
Nucleotide excision repair	hsa03420	1	47	0.631095658	0.938081005	ERCC8
Notch signaling pathway	hsa04330	1	48	0.63886854	0.938081005	NUMB
Intestinal immune network for IgA production	hsa04672	1	48	0.63886854	0.938081005	IL15RA
Type II diabetes mellitus	hsa04930	1	48	0.63886854	0.938081005	IRS1
Hippo signaling pathway	hsa04390	3	156	0.63898995	0.938081005	CTNNB1, PPP2R2D, CTNNA1
N-Glycan biosynthesis	hsa00510	1	49	0.646478799	0.938081005	MGAT1
Malaria	hsa05144	1	49	0.646478799	0.938081005	THBS3
HIF-1 signaling pathway	hsa04066	2	106	0.655159434	0.938081005	MKNK1, ARNT
Glutathione metabolism	hsa00480	1	51	0.661224895	0.938081005	GGT1
RNA transport	hsa03013	3	164	0.67247998	0.938081005	GEMIN2, EIF4G1, GEMIN7
TNF signaling pathway	hsa04668	2	110	0.67510148	0.938081005	CFLAR, IKBKKG
<i>Vibrio cholerae</i> infection	hsa05110	1	54	0.682206589	0.938081005	TJP2
Oocyte meiosis	hsa04114	2	112	0.684719302	0.938081005	CDC16, ANAPC11
Pathogenic <i>Escherichia coli</i> infection	hsa05130	1	55	0.688909667	0.938081005	CTNNB1
Basal cell carcinoma	hsa05217	1	55	0.688909667	0.938081005	CTNNB1
Cholinergic synapse	hsa04725	2	113	0.689440924	0.938081005	GNAO1, CHRNA3
Acute myeloid leukemia	hsa05221	1	57	0.701897575	0.938081005	IKBKKG
Arginine and proline metabolism	hsa00330	1	57	0.701897575	0.938081005	PYCR1
Glutamatergic synapse	hsa04724	2	118	0.712189245	0.938081005	GRIK1, GNAO1
Toxoplasmosis	hsa05145	2	119	0.71656942	0.938081005	GNAO1, IKBKKG
Long-term depression	hsa04730	1	60	0.720376711	0.938081005	GNAO1
Transcriptional misregulation in cancer	hsa05202	3	179	0.729063434	0.938081005	ZBTB17, EWSR1, TCF3
Alcoholism	hsa05034	3	180	0.732551027	0.938081005	GNAO1, SLC29A1, HDAC10
Cytosolic DNA-sensing pathway	hsa04623	1	63	0.737718071	0.938081005	IKBKKG
Calcium signaling pathway	hsa04020	3	183	0.742804232	0.938081005	CACNA1H, PHKA1, MYLK
Huntington's disease	hsa05016	3	183	0.742804232	0.938081005	ATP5J, COX6B2, AP2B1
Glioma	hsa05214	1	65	0.748681416	0.938081005	PDGFB
Arachidonic acid metabolism	hsa00590	1	68	0.764279002	0.938081005	GGT1
p53 signaling pathway	hsa04115	1	68	0.764279002	0.938081005	EI24
Parkinson's disease	hsa05012	2	131	0.764909622	0.938081005	ATP5J, COX6B2
Dopaminergic synapse	hsa04728	2	131	0.764909622	0.938081005	GNAO1, PPP2R2D
Hepatitis C	hsa05160	2	133	0.772238555	0.938081005	PPP2R2D, IKBKKG
Oxidative phosphorylation	hsa00190	2	133	0.772238555	0.938081005	ATP5J, COX6B2
Osteoclast differentiation	hsa04380	2	134	0.77582841	0.938081005	FHL2, IKBKKG
Measles	hsa05162	2	134	0.77582841	0.938081005	IFIH1, CD46
Ribosome	hsa03010	2	136	0.782861216	0.938081005	MRPS11, RPS27L

Table SIII. Continued.

Term	ID	Input number	Background number	P-value	Corrected P-value	Input
Bile secretion	hsa04976	1	72	0.783590396	0.938081005	SLC9A3
RNA degradation	hsa03018	1	72	0.783590396	0.938081005	EDC3
Biosynthesis of amino acids	hsa01230	1	72	0.783590396	0.938081005	PYCR1
Prolactin signaling pathway	hsa04917	1	72	0.783590396	0.938081005	GALT
Chronic myeloid leukemia	hsa05220	1	73	0.788167531	0.938081005	IKBK
Gastric acid secretion	hsa04971	1	75	0.797035429	0.938081005	MYLK
Wnt signaling pathway	hsa04310	2	141	0.799608176	0.938081005	CTNNB1, DAAMI
Cardiac muscle contraction	hsa04260	1	77	0.805534651	0.938081005	COX6B2
Antigen processing and presentation	hsa04612	1	78	0.809650789	0.938081005	HSPA4
Viral carcinogenesis	hsa05203	3	207	0.81399599	0.938081005	HDAC10, IKBKG, RBL1
TGF-beta signaling pathway	hsa04350	1	80	0.817625341	0.938081005	RBL1
Peroxisome	hsa04146	1	81	0.821487327	0.938081005	ABCD4
Ribosome biogenesis in eukaryotes	hsa03008	1	84	0.832592797	0.938081005	NHP2L1
Neuroactive ligand-receptor interaction	hsa04080	4	275	0.83409593	0.938081005	LPAR2, GRIK1, GABBR1, CHRNA3
Phagosome	hsa04145	2	154	0.837936959	0.938081005	THBS3, PIKFYVE
Small cell lung cancer	hsa05222	1	86	0.839612556	0.938081005	IKBK
Salmonella infection	hsa05132	1	87	0.843012046	0.938081005	KLC1
Jak-STAT signaling pathway	hsa04630	2	157	0.845792141	0.938081005	STAT6, IL15RA
ErbB signaling pathway	hsa04012	1	88	0.846339989	0.938081005	NRG4
Hematopoietic cell lineage	hsa04640	1	88	0.846339989	0.938081005	CD59
Gap junction	hsa04540	1	89	0.849597881	0.938081005	PDGFB
Proteoglycans in cancer	hsa05205	3	225	0.855872188	0.938081005	CTNNB1, CAV1, FGFR1
mRNA surveillance pathway	hsa03015	1	92	0.85896574	0.938081005	PPP2R2D
Protein processing in endoplasmic reticulum	hsa04141	2	167	0.869555897	0.940400026	NPLOC4, UGGT2
Alzheimer's disease	hsa05010	2	170	0.876005469	0.940400026	ATP5J, COX6B2
Influenza A	hsa05164	2	176	0.888037452	0.940400026	IFIH1, HNRNPUL1
Retrograde endocannabinoid signaling	hsa04723	1	103	0.888620213	0.940400026	GNAO1
T cell receptor signaling pathway	hsa04660	1	106	0.895572082	0.940400026	IKBK
Toll-like receptor signaling pathway	hsa04620	1	107	0.897792253	0.940400026	IKBK
Herpes simplex infection	hsa05168	2	185	0.90408302	0.940400026	IFIH1, IKBKG
Chemokine signaling pathway	hsa04062	2	189	0.910507192	0.940400026	BCAR1, IKBKG
Serotonergic synapse	hsa04726	1	114	0.912074724	0.940400026	GNAO1
Neurotrophin signaling pathway	hsa04722	1	120	0.922727343	0.945510734	IRS1
MicroRNAs in cancer	hsa05206	3	296	0.95140418	0.964573693	PDGFB, EZH2, IRS1
Cell adhesion molecules (CAMs)	hsa04514	1	143	0.952952323	0.964573693	F11R
Cytokine-cytokine receptor interaction	hsa04060	2	266	0.977749173	0.983674926	PDGFB, IL15RA
Epstein-Barr virus infection	hsa05169	1	202	0.986931612	0.986931612	IKBK