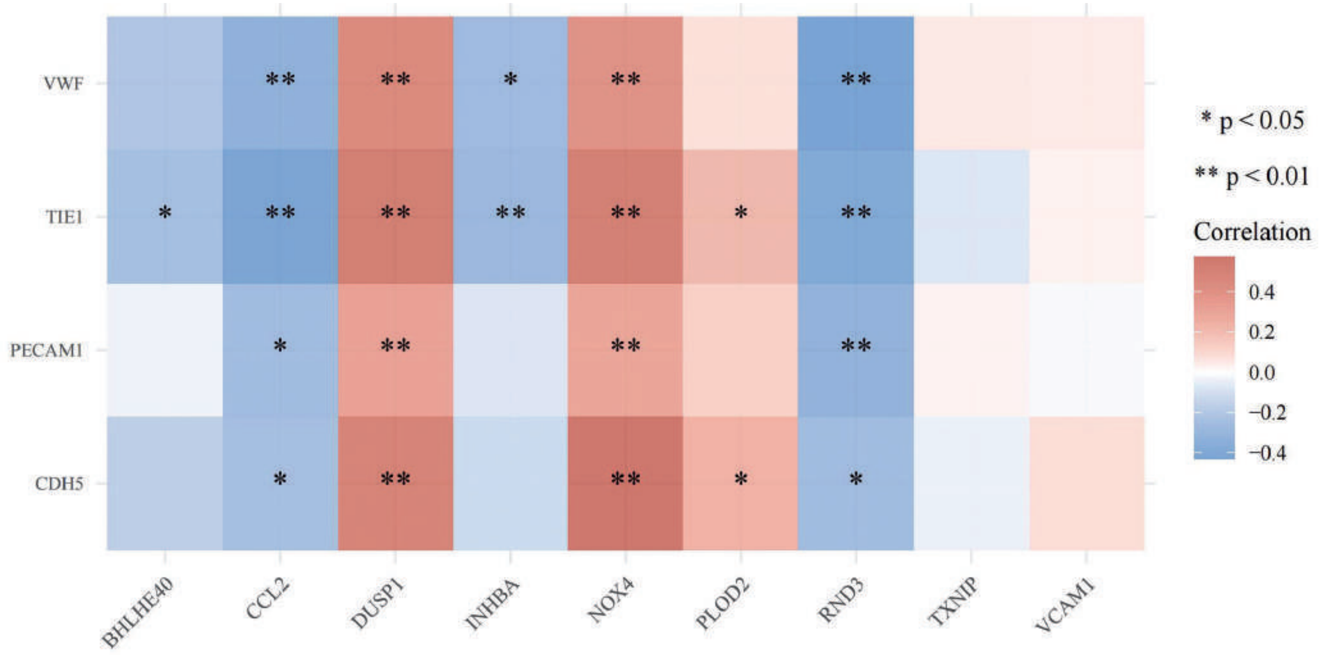
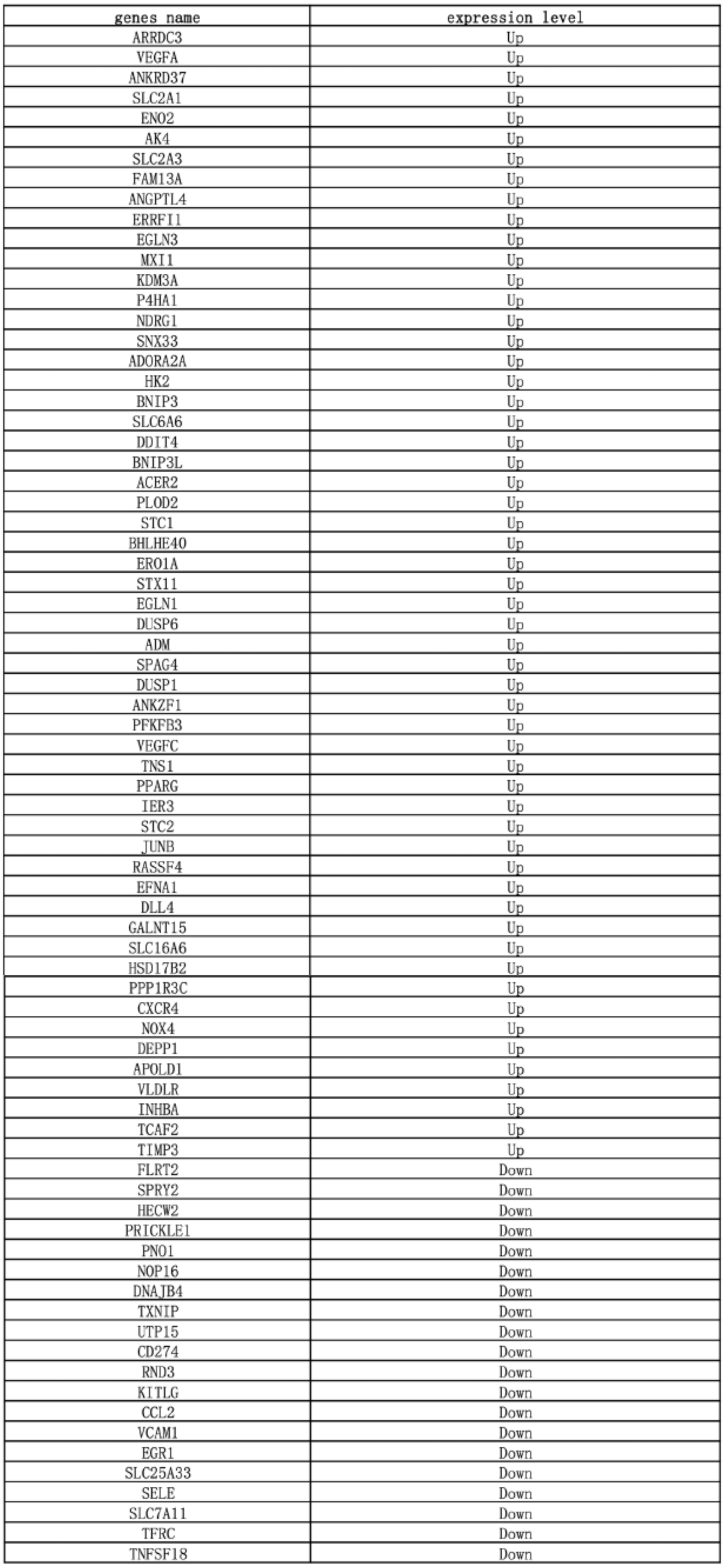


Table S1. The sequence of siRNAs

Gene name	sense（5'-3'）	antisense（5'-3'）
siR-INHBA-1	GCUUUGGCUGAGAGGAUUUTT	AAAUCCUCUCAGCCAAAGCTT
siR-INHBA-2	CCGAGGAAGUGGGCUUAAATT	UUUAAGCCCACUUCCUCGGTT
siR-INHBA-3	UCCACUCAACAGUCAUCAATT	UUGAUGACUGUUGAGUGGATT
siR-DUSP1-1	GCCAUUGACUUCAUAGACUTT	AGUCUAUGAAGUCAAUGGCTT
siR-DUSP1-2	GCAUCACUGCCUUGAUCAATT	UUGAUCAAGGCAGUGAUGCTT
siR-DUSP1-3	GCUUACCUUAUGAGGACUATT	UAGUCCUCAUAAGGUAAGCTT
siR-NOX4-1	CCUCAGCAUCUGUUCUUAATT	UUAAGAACAGAUGCUGAGGTT
siR-NOX4-2	GCAGGAGAACCAGGAGAUUTT	AAUCUCCUGGUUCUCCUGCTT
siR-NOX4-3	CCCUCAACUUCUCAGUGAATT	UUCACUGAGAAGUUGAGGGTT
siR-PLOD2-1	GGAACACUAUGCUGAUCAATT	UUGAUCAGCAUAGUGUUCCTT
siR-PLOD2-2	GCUGCACUCUUUGUGAAUUTT	AAUUCACAAAGAGUGCAGCTT
siR-PLOD2-3	GCUAUUAUCCACUGCUAAUTT	AUUAGCAGUGGAUAAUAGCTT
siR-BHLHE40-1	GGAUGUACCCUGCCCACAUTT	AUGUGGGCAGGGUACAUCCTT
siR-BHLHE40-2	GGACACAGACAGUGGCUAUTT	AUAGCCACUGUCUGUGUCCTT
siR-BHLHE40-3	CCCUCUCUAGCUUCAUGAATT	UUCAUGAAGCUAGAGAGGGTT
siR-VCAM1-1	GCAGAGUACGCAAACACUUTT	AAGUGUUUGCGUACUCUGCTT
siR-VCAM1-2	GCAGAAAGGAAGUGGAAUUTT	AAUUCCACUUCCUUUCUGCTT
siR-VCAM1-3	GGGAGUAUAUGAAUGUGAATT	UUCACAUUCAUAUACUCCCTT
siR-RND3-1	CUAUCAUGGAUCCUAAUCATT	UGAUUAGGAUCCAUGAUAGTT
siR-RND3-2	CAUUAGUAGAGCUCUCCAATT	UUGGAGAGCUCUACUAAUGTT
siR-RND3-3	GCGGAACAAAUCACAGAGATT	UCUCUGUGAUUUGUUCCGCTT
siR-CCL2-1	GAAAGUCUCUGCCGCCCUUTT	AAGGGCGGCAGAGACUUUCTT
siR-CCL2-2	GCAGAGGCUCGCGAGCUAUTT	AUAGCUCGCGAGCCUCUGCTT
siR-CCL2-3	GCAGAAGUGGGUUCAGGAUTT	AUCCUGAACCCACUUCUGCTT
siR-TXNIP-1	GCCUUCGGGUUCAGAAGAUTT	AUCUUCUGAACCCGAAGGCTT
siR-TXNIP-2	GGCAGCAGAUCAGGUCUAATT	UUAGACCUGAUCUGCUGCCTT
siR-TXNIP-3	GGAGGUGUGUGAAGUUACUTT	AGUAACUUCACACACCUCCTT

Table S2. the full list of DEGs in vascular endothelial cells of SSc patients under hypoxic condition



genes name	expression level
ARRDC3	Up
VEGFA	Up
ANKRD37	Up
SLC2A1	Up
ENO2	Up
AK4	Up
SLC2A3	Up
FAM13A	Up
ANGPTL4	Up
ERRFI1	Up
EGLN3	Up
MXI1	Up
KDM3A	Up
P4HA1	Up
NDRG1	Up
SNX33	Up
ADORA2A	Up
HK2	Up
BNIP3	Up
SLC6A6	Up
DDIT4	Up
BNIP3L	Up
ACER2	Up
PLOD2	Up
STC1	Up
BHLHE40	Up
ERO1A	Up
STX11	Up
EGLN1	Up
DUSP6	Up
ADM	Up
SPAG4	Up
DUSP1	Up
ANKZF1	Up
PFKFB3	Up
VEGFC	Up
TNS1	Up
PPARG	Up
IER3	Up
STC2	Up
JUNB	Up
RASSF4	Up
EFNA1	Up
DLL4	Up
GALNT15	Up
SLC16A6	Up
HSD17B2	Up
PPP1R3C	Up
CXCR4	Up
NOX4	Up
DEPP1	Up
APOLD1	Up
VLDLR	Up
INHBA	Up
TCAF2	Up
TIMP3	Up
FLRT2	Down
SPRY2	Down
HECW2	Down
PRICKLE1	Down
PNO1	Down
NOP16	Down
DNAJB4	Down
TXNIP	Down
UTP15	Down
CD274	Down
RND3	Down
KITLG	Down
CCL2	Down
VCAM1	Down
EGR1	Down
SLC25A33	Down
SELE	Down
SLC7A11	Down
TFRC	Down
TNFSF18	Down

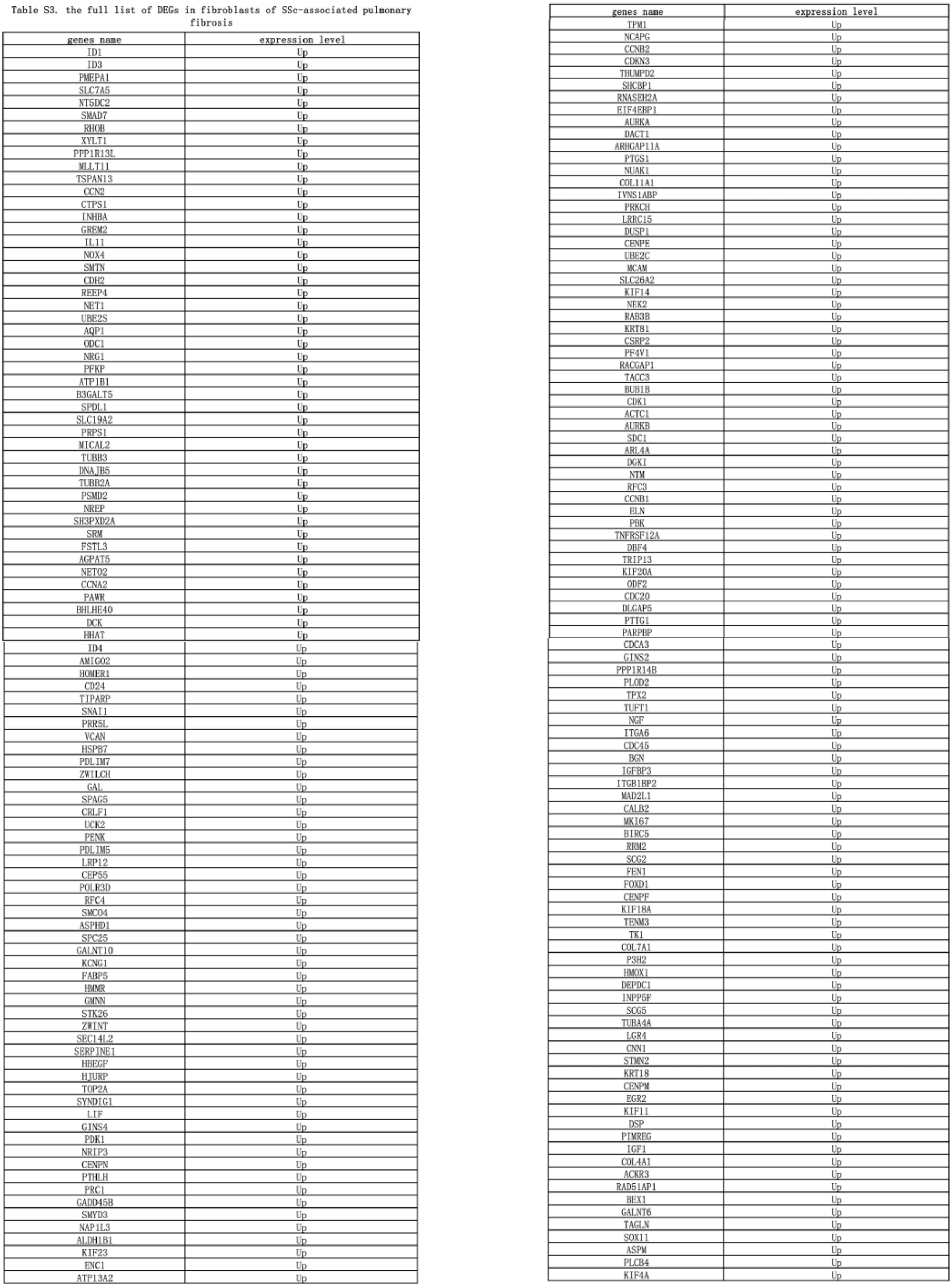
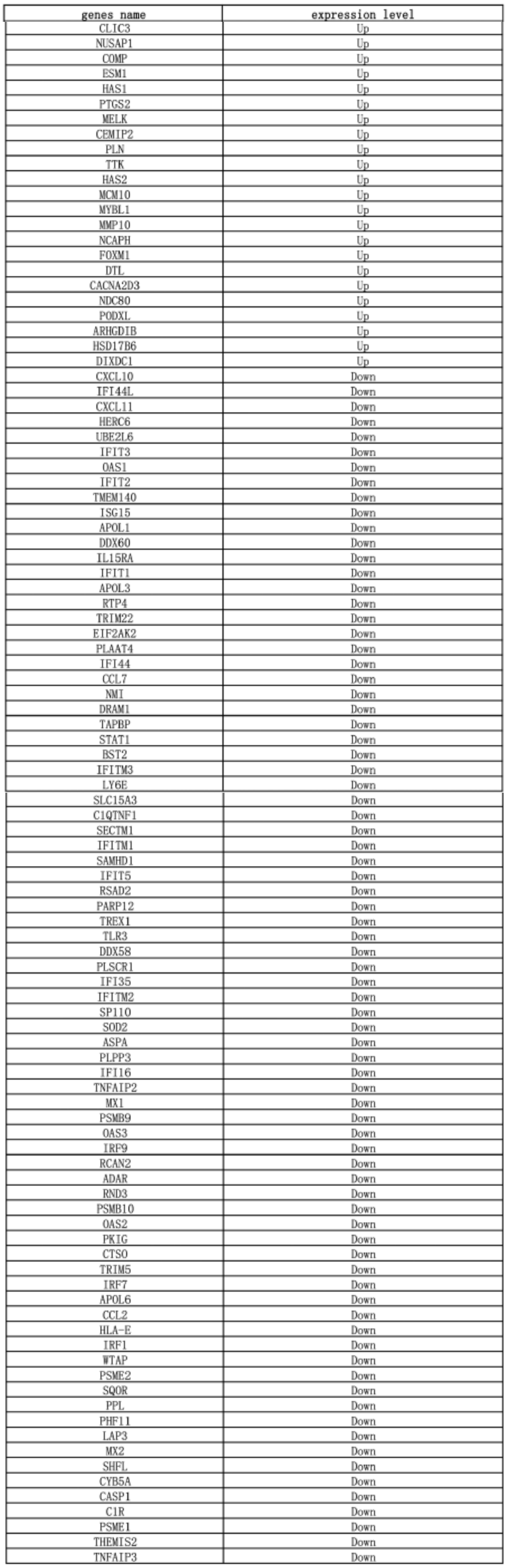
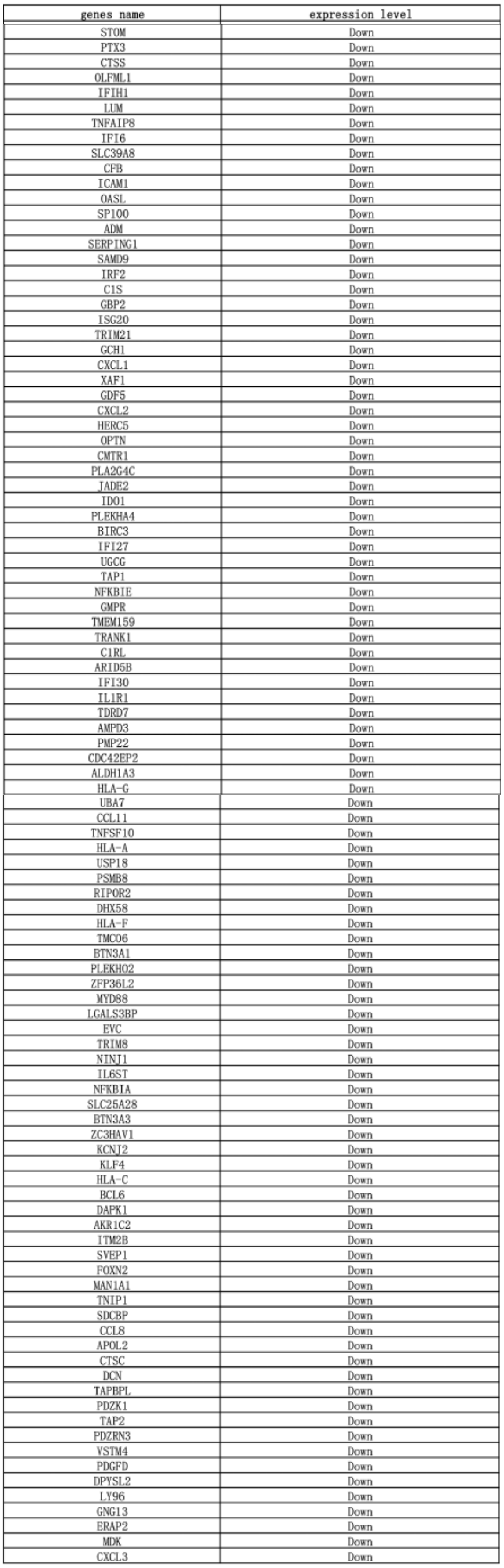


Table S3. the full list of DEGs in fibroblasts of SSc-associated pulmonary fibrosis

genes name	expression level
ID1	Up
ID3	Up
PMEPA1	Up
SLC7A5	Up
NT5DC2	Up
SMAD7	Up
RHOB	Up
XYLT1	Up
PPP1R13L	Up
MLLT11	Up
TSPAN13	Up
CCN2	Up
CTPS1	Up
INHBA	Up
GREM2	Up
IL11	Up
NOX4	Up
SMTN	Up
CDH2	Up
REEP4	Up
NET1	Up
UBE2S	Up
AQP1	Up
ODC1	Up
NRG1	Up
PFKP	Up
ATP1B1	Up
B3GALT5	Up
SPDL1	Up
SLC19A2	Up
PRPS1	Up
MICAL2	Up
TUBB3	Up
DNAJB5	Up
TUBB2A	Up
PSMD2	Up
NREP	Up
SH3PXD2A	Up
SRM	Up
FSTL3	Up
AGPAT5	Up
NETO2	Up
CCNA2	Up
PAWR	Up
BHLHE40	Up
DCK	Up
HHAT	Up
ID4	Up
AMIGO2	Up
HOMER1	Up
CD24	Up
TIPARP	Up
SNAI1	Up
PRR5L	Up
VCAN	Up
HSPB7	Up
PDLIM7	Up
ZWILCH	Up
GAL	Up
SPAG5	Up
CRLF1	Up
UCK2	Up
PENK	Up
PDLIM5	Up
LRP12	Up
CEP55	Up
POLR3D	Up
RFC4	Up
SMCO4	Up
ASPHD1	Up
SPC25	Up
GALNT10	Up
KCNG1	Up
FABP5	Up
HMMR	Up
GMNN	Up
STK26	Up
ZWINT	Up
SEC14L2	Up
SERPINE1	Up
HBEGF	Up
HJURP	Up
TOP2A	Up
SYNDIG1	Up
LIF	Up
GINS4	Up
PDK1	Up
NRIP3	Up
CENPN	Up
PTHLH	Up
PRC1	Up
GADD45B	Up
SMYD3	Up
NAP1L3	Up
ALDH1B1	Up
KIF23	Up
ENC1	Up
ATP13A2	Up
TPM1	Up
NCAPG	Up
CCNB2	Up
CDKN3	Up
THUMPD2	Up
SHCBP1	Up
RNASEH2A	Up
EIF4EBP1	Up
AURKA	Up
DACT1	Up
ARHGAP11A	Up
PTGS1	Up
NUAK1	Up
COL11A1	Up
IVNS1ABP	Up
PRKCH	Up
LRRC15	Up
DUSP1	Up
CENPE	Up
UBE2C	Up
MCAM	Up
SLC26A2	Up
KIF14	Up
NEK2	Up
RAB3B	Up
KRT81	Up
CSRP2	Up
PF4V1	Up
RACGAP1	Up
TACC3	Up
BUB1B	Up
CDK1	Up
ACTC1	Up
AURKB	Up
SDC1	Up
ARL4A	Up
DGKI	Up
NTM	Up
RFC3	Up
CCNB1	Up
ELN	Up
PBK	Up
TNFRSF12A	Up
DBF4	Up
TRIP13	Up
KIF20A	Up
ODF2	Up
CDC20	Up
DLGAP5	Up
PTTG1	Up
PARPBP	Up
CDCA3	Up
GINS2	Up
PPP1R14B	Up
PLOD2	Up
TPX2	Up
TUFT1	Up
NGF	Up
ITGA6	Up
CDC45	Up
BGN	Up
IGFBP3	Up
ITGB1BP2	Up
MAD2L1	Up
CALB2	Up
MKI67	Up
BIRC5	Up
RRM2	Up
SCG2	Up
FEN1	Up
FOXD1	Up
CENPF	Up
KIF18A	Up
TENM3	Up
TK1	Up
COL7A1	Up
P3H2	Up
HMOX1	Up
DEPDC1	Up
INPP5F	Up
SCG5	Up
TUBA4A	Up
LGR4	Up
CNN1	Up
STMN2	Up
KRT18	Up
CENPM	Up
EGR2	Up
KIF11	Up
DSP	Up
PIMREG	Up
IGF1	Up
COL4A1	Up
ACKR3	Up
RAD51AP1	Up
BEX1	Up
GALNT6	Up
TAGLN	Up
SOX11	Up
ASPM	Up
PLCB4	Up
KIF4A	Up

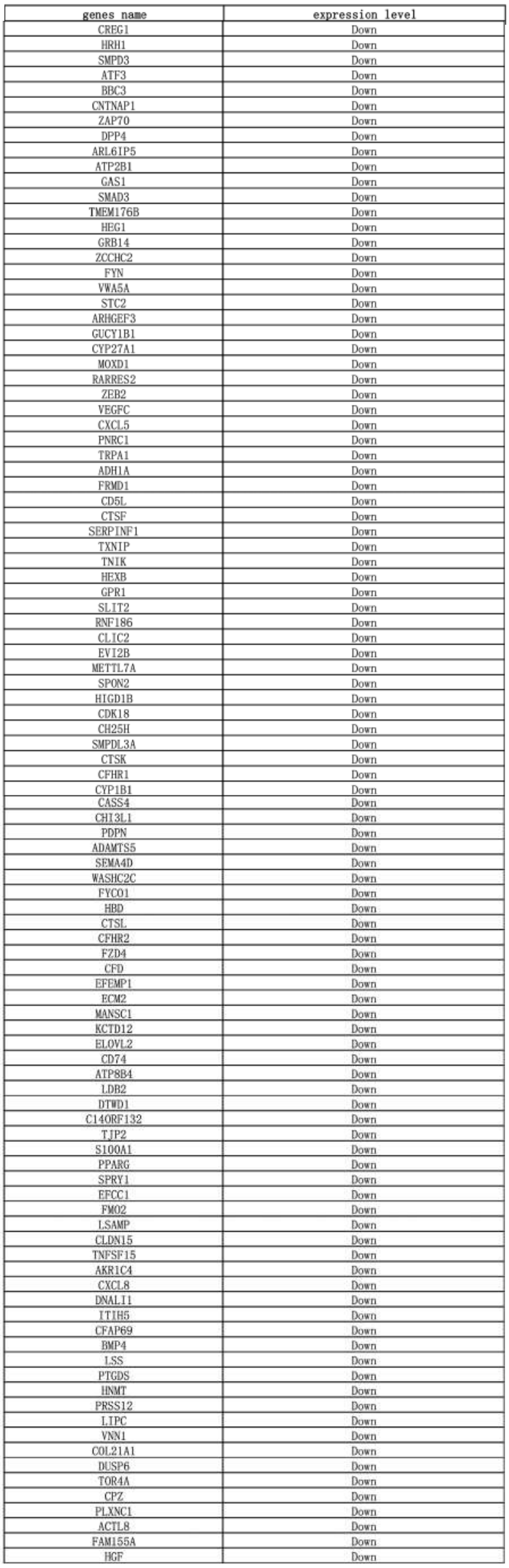


genes name	expression level
CLIC3	Up
NUSAP1	Up
COMP	Up
ESM1	Up
HAS1	Up
PTGS2	Up
MELK	Up
CEMIP2	Up
PLN	Up
TTK	Up
HAS2	Up
MCM10	Up
MYBL1	Up
MMP10	Up
NCAPH	Up
FOXM1	Up
DTL	Up
CACNA2D3	Up
NDC80	Up
PODXL	Up
ARHGDIB	Up
HSD17B6	Up
DIXDC1	Up
CXCL10	Down
IFI44L	Down
CXCL11	Down
HERC6	Down
UBE2L6	Down
IFIT3	Down
OAS1	Down
IFIT2	Down
TMEM140	Down
ISG15	Down
APOL1	Down
DDX60	Down
IL15RA	Down
IFIT1	Down
APOL3	Down
RTP4	Down
TRIM22	Down
EIF2AK2	Down
PLAAT4	Down
IFI44	Down
CCL7	Down
NMI	Down
DRAM1	Down
TAPBP	Down
STAT1	Down
BST2	Down
IFITM3	Down
LY6E	Down
SLC15A3	Down
C1QTNF1	Down
SECTM1	Down
IFITM1	Down
SAMHD1	Down
IFIT5	Down
RSAD2	Down
PARP12	Down
TREX1	Down
TLR3	Down
DDX58	Down
PLSCR1	Down
IFI35	Down
IFITM2	Down
SP110	Down
SOD2	Down
ASPA	Down
PLPP3	Down
IFI16	Down
TNFAIP2	Down
MX1	Down
PSMB9	Down
OAS3	Down
IRF9	Down
RCAN2	Down
ADAR	Down
RND3	Down
PSMB10	Down
OAS2	Down
PKIG	Down
CTSO	Down
TRIM5	Down
IRF7	Down
APOL6	Down
CCL2	Down
HLA-E	Down
IRF1	Down
WTAP	Down
PSME2	Down
SQOR	Down
PPL	Down
PHF11	Down
LAP3	Down
MX2	Down
SHFL	Down
CYB5A	Down
CASP1	Down
C1R	Down
PSME1	Down
THEMIS2	Down
TNFAIP3	Down



genes name	expression level
STOM	Down
PTX3	Down
CTSS	Down
OLFML1	Down
IFIH1	Down
LUM	Down
TNFAIP8	Down
IFI6	Down
SLC39A8	Down
CFB	Down
ICAM1	Down
OASL	Down
SP100	Down
ADM	Down
SERPING1	Down
SAMD9	Down
IRF2	Down
C1S	Down
GBP2	Down
ISG20	Down
TRIM21	Down
GCH1	Down
CXCL1	Down
XAF1	Down
GDF5	Down
CXCL2	Down
HERC5	Down
OPTN	Down
CMTR1	Down
PLA2G4C	Down
JADE2	Down
IDO1	Down
PLEKHA4	Down
BIRC3	Down
IFI27	Down
UGCG	Down
TAP1	Down
NFKBIE	Down
GMPR	Down
TMEM159	Down
TRANK1	Down
C1RL	Down
ARID5B	Down
IFI30	Down
IL1R1	Down
TDRD7	Down
AMPD3	Down
PMP22	Down
CDC42EP2	Down
ALDH1A3	Down
HLA-G	Down
UBA7	Down
CCL11	Down
TNFSF10	Down
HLA-A	Down
USP18	Down
PSMB8	Down
RIPOR2	Down
DHX58	Down
HLA-F	Down
TMCO6	Down
BTN3A1	Down
PLEKHO2	Down
ZFP36L2	Down
MYD88	Down
LGALS3BP	Down
EVC	Down
TRIM8	Down
NINJ1	Down
IL6ST	Down
NFKBIA	Down
SLC25A28	Down
BTN3A3	Down
ZC3HAV1	Down
KCNJ2	Down
KLF4	Down
HLA-C	Down
BCL6	Down
DAPK1	Down
AKR1C2	Down
ITM2B	Down
SVEP1	Down
FOXN2	Down
MAN1A1	Down
TNIP1	Down
SDCBP	Down
CCL8	Down
APOL2	Down
CTSC	Down
DCN	Down
TAPBPL	Down
PDZK1	Down
TAP2	Down
PDZRN3	Down
VSTM4	Down
PDGFD	Down
DPYSL2	Down
LY96	Down
GNG13	Down
ERAP2	Down
MDK	Down
CXCL3	Down

genes name	expression level
TNFRSF11B	Down
NFE2L3	Down
PTGES	Down
AKR1C3	Down
VCAM1	Down
AKR1C1	Down
TRIM38	Down
TGFBR3	Down
PMAIP1	Down
SCPEP1	Down
KIT	Down
C3	Down
BDKRB2	Down
PLSCR4	Down
RAB29	Down
MAP3K5	Down
CEMIP	Down
FCGRT	Down
HLA-B	Down
FTH1	Down
RBCK1	Down
BTN3A2	Down
NAMPT	Down
AKR1B1	Down
EPB41L2	Down
CHI3L2	Down
GRN	Down
VAMP5	Down
PLPP1	Down
FAM110B	Down
LGALS9	Down
DEPP1	Down
REV3L	Down
LHFPL6	Down
GASK1B	Down
MAP3K8	Down
ACSL5	Down
CYP3A7	Down
HEBP1	Down
CXCL6	Down
OSR2	Down
TNFAIP6	Down
MAN1C1	Down
ZC3H12A	Down
AHR	Down
RGCC	Down
DDIT3	Down
KAT2B	Down
PTGFR	Down
SELENOP	Down
ARNT2	Down
LY75	Down
EPAS1	Down
DPYD	Down
KIAA0513	Down
CAMK2N1	Down
VGLL3	Down
TNFRSF21	Down
NUAK2	Down
SGCE	Down
OLFML2A	Down
PSAP	Down
CCN3	Down
TRIM34	Down
TNFRSF1B	Down
TMEM176A	Down
PLSCR2	Down
MYLIP	Down
LAMB1	Down
GLRX	Down
WDR19	Down
MFAP4	Down
DGLUCY	Down
IGFBP6	Down
SLC43A3	Down
CCL5	Down
AOX1	Down
GYPC	Down
GBP1	Down
CCDC102B	Down
PTN	Down
SQSTM1	Down
IL6	Down
HSD11B1	Down
ADD3	Down
IL32	Down
ADGRA2	Down
ADH1B	Down
CLEC2B	Down
GRK5	Down
PLAAT3	Down
NIBAN1	Down
SLC22A18	Down
G0S2	Down
PDGFRL	Down
CITED2	Down
IRAK3	Down
BDKRB1	Down
MITF	Down
TNS3	Down
CEBPD	Down
MXRA5	Down



genes name	expression level
CREG1	Down
HRH1	Down
SMPD3	Down
ATF3	Down
BBC3	Down
CNTNAP1	Down
ZAP70	Down
DPP4	Down
ARL6IP5	Down
ATP2B1	Down
GAS1	Down
SMAD3	Down
TMEM176B	Down
HEG1	Down
GRB14	Down
ZCCHC2	Down
FYN	Down
VWA5A	Down
STC2	Down
ARHGEF3	Down
GUCY1B1	Down
CYP27A1	Down
MOXD1	Down
RARRES2	Down
ZEB2	Down
VEGFC	Down
CXCL5	Down
PNRC1	Down
TRPA1	Down
ADH1A	Down
FRMD1	Down
CD5L	Down
CTSF	Down
SERPINF1	Down
TXNIP	Down
TNIK	Down
HEXB	Down
GPR1	Down
SLIT2	Down
RNF186	Down
CLIC2	Down
EVI2B	Down
METTL7A	Down
SPON2	Down
HIGD1B	Down
CDK18	Down
CH25H	Down
SMPDL3A	Down
CTSK	Down
CFHR1	Down
CYP1B1	Down
CASS4	Down
CHI3L1	Down
PDPN	Down
ADAMTS5	Down
SEMA4D	Down
WASHC2C	Down
FYCO1	Down
HBD	Down
CTSL	Down
CFHR2	Down
FZD4	Down
CFD	Down
EFEMP1	Down
ECM2	Down
MANSC1	Down
KCTD12	Down
ELOVL2	Down
CD74	Down
ATP8B4	Down
LDB2	Down
DTWD1	Down
C14ORF132	Down
TJP2	Down
S100A1	Down
PPARG	Down
SPRY1	Down
EFCC1	Down
FMO2	Down
LSAMP	Down
CLDN15	Down
TNFSF15	Down
AKR1C4	Down
CXCL8	Down
DNALI1	Down
ITIH5	Down
CFAP69	Down
BMP4	Down
LSS	Down
PTGDS	Down
HNMT	Down
PRSS12	Down
LIPC	Down
VNN1	Down
COL21A1	Down
DUSP6	Down
TOR4A	Down
CPZ	Down
PLXNC1	Down
ACTL8	Down
FAM155A	Down
HGF	Down

genes name	expression level
IL12A	Down
KIR3DL3	Down
ASTN1	Down
ADGRL2	Down
IL7	Down
FGF9	Down
C7	Down
TMEM158	Down
GRIK3	Down
ADAMTS8	Down
S100A4	Down
GPNMB	Down
COLEC12	Down
CD68	Down
TFPI	Down
CFH	Down
QSOX1	Down
PRKAR2B	Down
CRYBG1	Down
NFIX	Down
SLC22A11	Down
ACKR4	Down
RAB11FIP1	Down
SLC12A8	Down
CTSV	Down
SULF1	Down
IL7R	Down
ISOC1	Down
FGF14	Down
CLDN11	Down
MME	Down
IQGAP2	Down
CCN5	Down
SLC16A4	Down
RASL12	Down
EVI2A	Down
DOCK4	Down
FGF7	Down

Table S4. the full list of KEGG analysis and GO analysis for CCL2

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0019221	Cytokine-mediated signaling pathway	21	678	1.46	3.84E-27	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000227752, 9606.ENSP00000263341, 9606.ENSP00000290200, 9606.ENSP00000292301, 9606.ENSP00000292303, 9606.ENSP00000295683, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000314807, 9606.ENSP00000319635, 9606.ENSP00000330959, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL10RA, IL1B, IL10RB, CCR2, CCR5, CXCR1, CSF2, CXCL10, CXCL8, IL1RAP, CXCR2, IL1R2, TRADD, IL6R, CXCL1, IL6, TNF, IL10
GO:0030595	Leukocyte chemotaxis	12	142	1.9	3.21E-17	9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000292303, 9606.ENSP00000295683, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000357470, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000412237	CCL2, IL1B, CCR2, CCR5, CXCR1, CXCL10, CXCL8, CXCR2, IL6R, CXCL1, IL6, IL10
GO:0050900	Leukocyte migration	13	316	1.58	1.94E-15	9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000292303, 9606.ENSP00000295683, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000357470, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CCL2, IL1B, CCR2, CCR5, CXCR1, CXCL10, CXCL8, CXCR2, IL6R, CXCL1, IL6, TNF, IL10
GO:0006954	Inflammatory response	14	515	1.4	1.16E-14	9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000290200, 9606.ENSP00000292301, 9606.ENSP00000292303, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000314807, 9606.ENSP00000319635, 9606.ENSP00000357470, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698	TNFRSF1A, CCL2, IL1B, IL10RB, CCR2, CCR5, CXCL10, CXCL8, IL1RAP, CXCR2, IL6R, CXCL1, IL6, TNF
GO:0006955	Immune response	18	1588	1.02	2.88E-14	9606.ENSP00000011653, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000290200, 9606.ENSP00000292301, 9606.ENSP00000292303, 9606.ENSP00000295683, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000314807, 9606.ENSP00000319635, 9606.ENSP00000330959, 9606.ENSP00000357470, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, CCL2, IL1B, IL10RB, CCR2, CCR5, CXCR1, CSF2, CXCL10, CXCL8, IL1RAP, CXCR2, IL1R2, IL6R, CXCL1, IL6, TNF, IL10
GO:0097529	Myeloid leukocyte migration	10	123	1.88	4.83E-14	9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000295683, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000357470, 9606.ENSP00000379110, 9606.ENSP00000385675	CCL2, IL1B, CCR2, CXCR1, CXCL10, CXCL8, CXCR2, IL6R, CXCL1, IL6
GO:0009617	Response to bacterium	14	634	1.31	1.41E-13	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000227752, 9606.ENSP00000263341, 9606.ENSP00000292303, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000357470, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL10RA, IL1B, CCR5, CSF2, CXCL10, CXCL8, IL6R, CXCL1, IL6, TNF, IL10
GO:0009605	Response to external stimulus	19	634	0.88	3.57E-13	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000227752, 9606.ENSP00000263341, 9606.ENSP00000290200, 9606.ENSP00000292301, 9606.ENSP00000292303, 9606.ENSP00000295683, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000314807, 9606.ENSP00000319635, 9606.ENSP00000357470, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL10RA, IL1B, IL10RB, CCR2, CCR5, CXCR1, CSF2, CXCL10, CXCL8, IL1RAP, CXCR2, IL6R, CXCL1, IL6, TNF, IL10
GO:0051707	Response to other organism	16	1256	1.07	1.10E-12	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000227752, 9606.ENSP00000263341, 9606.ENSP00000290200, 9606.ENSP00000292303, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000314807, 9606.ENSP00000357470, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL10RA, IL1B, IL10RB, CCR5, CSF2, CXCL10, CXCL8, IL1RAP, IL6R, CXCL1, IL6, TNF, IL10
GO:0006952	Defense response	16	1296	1.06	1.50E-12	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000290200, 9606.ENSP00000292301, 9606.ENSP00000292303, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000314807, 9606.ENSP00000319635, 9606.ENSP00000357470, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL1B, IL10RB, CCR2, CCR5, CXCL10, CXCL8, IL1RAP, CXCR2, IL6R, CXCL1, IL6, TNF, IL10
GO:0071222	Cellular response to lipopolysaccharide	10	185	1.7	1.56E-12	9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292303, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CCL2, IL1B, CCR5, CSF2, CXCL10, CXCL8, CXCL1, IL6, TNF, IL10

Table S4. the full list of KEGG analysis and GO analysis for CCL2

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0032496	Response to lipopolysaccharide	11	313	1.52	3.81E-12	9606.ENSP00000225831, 9606.ENSP00000227752, 9606.ENSP00000263341, 9606.ENSP00000292303, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CCL2, IL10RA, IL1B, CCR5, CSF2, CXCL10, CXCL8, CXCL1, IL6, TNF, IL10
GO:0070098	Chemokine-mediated signaling pathway	8	80	1.97	1.15E-11	9606.ENSP00000225831, 9606.ENSP00000292301, 9606.ENSP00000292303, 9606.ENSP00000295683, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000379110	CCL2, CCR2, CCR5, CXCR1, CXCL10, CXCL8, CXCR2, CXCL1
GO:0044419	Interspecies interaction between organisms	17	1899	0.92	1.25E-11	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000227752, 9606.ENSP00000263341, 9606.ENSP00000290200, 9606.ENSP00000292301, 9606.ENSP00000292303, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000314807, 9606.ENSP00000357470, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL10RA, IL1B, IL10RB, CCR2, CCR5, CSF2, CXCL10, CXCL8, IL1RAP, IL6R, CXCL1, IL6, TNF, IL10
GO:0046427	Positive regulation of receptor signaling pathway via jak-stat	8	85	1.94	1.69E-11	9606.ENSP00000162749, 9606.ENSP00000227752, 9606.ENSP00000290200, 9606.ENSP00000296871, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	TNFRSF1A, IL10RA, IL10RB, CSF2, IL6R, IL6, TNF, IL10
GO:0030593	Neutrophil chemotaxis	7	74	1.95	5.52E-10	9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000295683, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000379110	CCL2, IL1B, CXCR1, CXCL10, CXCL8, CXCR2, CXCL1
GO:0032101	Regulation of response to external stimulus	13	1013	1.08	8.73E-10	9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000330959, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	TNFRSF1A, CCL2, IL1B, CCR2, CXCL10, CXCL8, CXCR2, IL1R2, TRADD, IL6R, IL6, TNF, IL10
GO:0033993	Response to lipid	12	858	1.11	2.98E-09	9606.ENSP00000011653, 9606.ENSP00000225831, 9606.ENSP00000227752, 9606.ENSP00000263341, 9606.ENSP00000292303, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, CCL2, IL10RA, IL1B, CCR5, CSF2, CXCL10, CXCL8, CXCL1, IL6, TNF, IL10
GO:0048584	Positive regulation of response to stimulus	16	2257	0.82	3.10E-09	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000227752, 9606.ENSP00000263341, 9606.ENSP00000290200, 9606.ENSP00000292301, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL10RA, IL1B, IL10RB, CCR2, CSF2, CXCL10, CXCL8, CXCR2, TRADD, IL6R, IL6, TNF, IL10
GO:0002685	Regulation of leukocyte migration	8	209	1.55	9.22E-09	9606.ENSP00000225831, 9606.ENSP00000292301, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698	CCL2, CCR2, CXCL10, CXCL8, CXCR2, IL6R, IL6, TNF
GO:1901342	Regulation of vasculature development	9	336	1.4	9.22E-09	9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	IL1B, CCR2, CXCL10, CXCL8, CXCR2, IL6R, IL6, TNF, IL10
GO:0032103	Positive regulation of response to external stimulus	10	511	1.26	1.07E-08	9606.ENSP00000162749, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698	TNFRSF1A, IL1B, CCR2, CXCL10, CXCL8, CXCR2, TRADD, IL6R, IL6, TNF
GO:0002688	Regulation of leukocyte chemotaxis	7	124	1.72	1.30E-08	9606.ENSP00000225831, 9606.ENSP00000292301, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000357470, 9606.ENSP00000385675	CCL2, CCR2, CXCL10, CXCL8, CXCR2, IL6R, IL6
GO:0051094	Positive regulation of developmental process	13	1389	0.94	3.27E-08	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000296871, 9606.ENSP00000306512, 9606.ENSP00000314807, 9606.ENSP00000319635, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, IL1B, CCR2, CSF2, CXCL8, IL1RAP, CXCR2, TRADD, IL6R, IL6, TNF, IL10
GO:0002687	Positive regulation of leukocyte migration	7	144	1.66	3.31E-08	9606.ENSP00000292301, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698	CCR2, CXCL10, CXCL8, CXCR2, IL6R, IL6, TNF
GO:0006950	Response to stress	17	3485	0.66	1.16E-07	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000290200, 9606.ENSP00000292301, 9606.ENSP00000292303, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000314807, 9606.ENSP00000319635, 9606.ENSP00000357470, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL1B, IL10RB, CCR2, CCR5, CSF2, CXCL10, CXCL8, IL1RAP, CXCR2, IL6R, CXCL1, IL6, TNF, IL10
GO:0001819	Positive regulation of cytokine production	9	461	1.26	1.17E-07	9606.ENSP00000011653, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000296871, 9606.ENSP00000314807, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, IL1B, CCR2, CSF2, IL1RAP, IL6R, IL6, TNF, IL10

Table S4. the full list of KEGG analysis and GO analysis for CCL2

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0045765	Regulation of angiogenesis	8	303	1.39	1.30E-07	9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	IL1B, CCR2, CXCL10, CXCL8, CXCR2, IL6, TNF, IL10
GO:0002684	Positive regulation of immune system process	11	949	1.03	1.70E-07	9606.ENSP00000011653, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, CCL2, IL1B, CCR2, CXCL10, CXCL8, CXCR2, IL6R, IL6, TNF, IL10
GO:0002690	Positive regulation of leukocyte chemotaxis	6	98	1.76	1.98E-07	9606.ENSP00000292301, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000357470, 9606.ENSP00000385675	CCR2, CXCL10, CXCL8, CXCR2, IL6R, IL6
GO:0042127	Regulation of cell population proliferation	13	1642	0.87	2.26E-07	9606.ENSP00000011653, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000357470, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, CCL2, IL1B, CCR2, CSF2, CXCL10, CXCL8, CXCR2, IL6R, CXCL1, IL6, TNF, IL10
GO:0009967	Positive regulation of signal transduction	13	1654	0.86	2.43E-07	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000227752, 9606.ENSP00000263341, 9606.ENSP00000290200, 9606.ENSP00000292301, 9606.ENSP00000296871, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL10RA, IL1B, IL10RB, CCR2, CSF2, TRADD, IL6R, IL6, TNF, IL10
GO:2000026	Regulation of multicellular organismal development	14	2096	0.79	2.91E-07	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000314807, 9606.ENSP00000319635, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, IL1B, CCR2, CSF2, CXCL10, CXCL8, IL1RAP, CXCR2, TRADD, IL6R, IL6, TNF, IL10
GO:0001817	Regulation of cytokine production	10	742	1.1	2.98E-07	9606.ENSP00000011653, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000296871, 9606.ENSP00000314807, 9606.ENSP00000330959, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, IL1B, CCR2, CSF2, IL1RAP, IL1R2, IL6R, IL6, TNF, IL10
GO:0030335	Positive regulation of cell migration	9	522	1.21	3.03E-07	9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698	IL1B, CCR2, CXCL10, CXCL8, CXCR2, TRADD, IL6R, IL6, TNF
GO:0035556	Intracellular signal transduction	13	1712	0.85	3.49E-07	9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000292303, 9606.ENSP00000295683, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000341268, 9606.ENSP00000379110, 9606.ENSP00000398698	TNFRSF1A, CCL2, IL1B, CCR2, CCR5, CXCR1, CSF2, CXCL10, CXCL8, CXCR2, TRADD, CXCL1, TNF
GO:0050727	Regulation of inflammatory response	8	351	1.33	3.52E-07	9606.ENSP00000162749, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000330959, 9606.ENSP00000341268, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	TNFRSF1A, IL1B, CCR2, IL1R2, TRADD, IL6, TNF, IL10
GO:0050793	Regulation of developmental process	15	2648	0.72	4.16E-07	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000314807, 9606.ENSP00000319635, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL1B, CCR2, CSF2, CXCL10, CXCL8, IL1RAP, CXCR2, TRADD, IL6R, IL6, TNF, IL10
GO:0001775	Cell activation	11	1075	0.98	5.18E-07	9606.ENSP00000011653, 9606.ENSP00000263341, 9606.ENSP00000295683, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, IL1B, CXCR1, CSF2, CXCL10, CXCL8, CXCR2, CXCL1, IL6, TNF, IL10
GO:0030334	Regulation of cell migration	10	865	1.03	1.09E-06	9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698	CCL2, IL1B, CCR2, CXCL10, CXCL8, CXCR2, TRADD, IL6R, IL6, TNF
GO:0002682	Regulation of immune system process	12	1514	0.87	1.15E-06	9606.ENSP00000011653, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, CCL2, IL1B, CCR2, CSF2, CXCL10, CXCL8, CXCR2, IL6R, IL6, TNF ,IL10

Table S4. the full list of KEGG analysis and GO analysis for CCL2

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0048583	Regulation of response to stimulus	17	4114	0.59	1.22E-06	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000227752, 9606.ENSP00000263341, 9606.ENSP00000290200, 9606.ENSP00000292301, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000330959, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL10RA, IL1B, IL10RB, CCR2, CSF2, CXCL10, CXCL8, CXCR2, IL1R2, TRADD, IL6R, IL6, TNF, IL10
GO:0032675	Regulation of interleukin-6 production	6	142	1.6	1.27E-06	9606.ENSP00000263341, 9606.ENSP00000314807, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	IL1B, IL1RAP, IL6R, IL6, TNF, IL10
GO:0002407	Dendritic cell chemotaxis	4	19	2.29	1.29E-06	9606.ENSP00000292301, 9606.ENSP00000292303, 9606.ENSP00000295683, 9606.ENSP00000319635	CCR2, CCR5, CXCR1, CXCR2
GO:0050729	Positive regulation of inflammatory response	6	144	1.59	1.35E-06	9606.ENSP00000162749, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000341268, 9606.ENSP00000385675, 9606.ENSP00000398698	TNFRSF1A, IL1B, CCR2, TRADD, IL6, TNF
GO:0098542	Defense response to other organism	10	900	1.02	1.46E-06	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000290200, 9606.ENSP00000305651, 9606.ENSP00000314807, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL10RB, CXCL10, IL1RAP, IL6R, IL6, TNF, IL10
GO:0022409	Positive regulation of cell-cell adhesion	7	272	1.38	1.54E-06	9606.ENSP00000011653, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, CCL2, IL1B, CCR2, IL6, TNF, IL10
GO:1901700	Response to oxygen-containing compound	12	1567	0.85	1.54E-06	9606.ENSP00000011653, 9606.ENSP00000225831, 9606.ENSP00000227752, 9606.ENSP00000263341, 9606.ENSP00000292303, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, CCL2, IL10RA, IL1B, CCR5, CSF2, CXCL10, CXCL8, CXCL1, IL6, TNF, IL10
GO:0002822	e response based on somatic recombination of immune receptors built from immun	6	150	1.57	1.61E-06	9606.ENSP00000011653, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, IL1B, CCR2, IL6, TNF, IL10
GO:0006959	Humoral immune response	7	275	1.38	1.63E-06	9606.ENSP00000225831, 9606.ENSP00000292301, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698	CCL2, CCR2, CXCL10, CXCL8, CXCL1, IL6, TNF
GO:0008284	Positive regulation of cell population proliferation	10	919	1.01	1.66E-06	9606.ENSP00000011653, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000319635, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, IL1B, CCR2, CSF2, CXCL10, CXCR2, IL6R, IL6, TNF, IL10
GO:0042531	Positive regulation of tyrosine phosphorylation of stat protein	5	68	1.84	1.66E-06	9606.ENSP00000162749, 9606.ENSP00000296871, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698	TNFRSF1A, CSF2, IL6R, IL6, TNF
GO:0009966	Regulation of signal transduction	15	3107	0.65	2.84E-06	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000227752, 9606.ENSP00000263341, 9606.ENSP00000290200, 9606.ENSP00000292301, 9606.ENSP00000296871, 9606.ENSP00000306512, 9606.ENSP00000330959, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL10RA, IL1B, IL10RB, CCR2, CSF2, CXCL8, IL1R2, TRADD, IL6R, IL6, TNF, IL10
GO:1903037	Regulation of leukocyte cell-cell adhesion	7	315	1.32	3.69E-06	9606.ENSP00000011653, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, CCL2, IL1B, CCR2, IL6, TNF, IL10
GO:0032642	Regulation of chemokine production	5	84	1.74	4.14E-06	9606.ENSP00000263341, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	IL1B, IL6R, IL6, TNF, IL10
GO:0051239	Regulation of multicellular organismal process	15	3227	0.64	4.58E-06	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000314807, 9606.ENSP00000319635, 9606.ENSP00000330959, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, IL1B, CCR2, CSF2, CXCL10, CXCL8, IL1RAP, CXCR2, IL1R2, TRADD, IL6R, IL6, TNF, IL10
GO:0051240	Positive regulation of multicellular organismal process	12	1770	0.8	5.11E-06	9606.ENSP00000011653, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000296871, 9606.ENSP00000306512, 9606.ENSP00000314807, 9606.ENSP00000319635, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, IL1B, CCR2, CSF2, CXCL8, IL1RAP, CXCR2, TRADD, IL6R, IL6, TNF, IL10
GO:0002718	Regulation of cytokine production involved in immune response	5	89	1.72	5.31E-06	9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	IL1B, CCR2, IL6, TNF, IL10
GO:0032879	Regulation of localization	14	2740	0.68	5.97E-06	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000292303, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL1B, CCR2, CCR5, CXCL10, CXCL8, CXCR2, TRADD, IL6R, IL6, TNF, IL10

Table S4. the full list of KEGG analysis and GO analysis for CCL2

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0050731	Positive regulation of peptidyl-tyrosine phosphorylation	6	196	1.46	6.28E-06	9606. ENSP00000011653, 9606. ENSP00000162749, 9606. ENSP00000296871, 9606. ENSP00000357470, 9606. ENSP00000385675, 9606. ENSP00000398698	CD4, TNFRSF1A, CSF2, IL6R, IL6, TNF
GO:0032755	Positive regulation of interleukin-6 production	5	94	1.7	6.64E-06	9606. ENSP00000263341, 9606. ENSP00000314807, 9606. ENSP00000357470, 9606. ENSP00000385675, 9606. ENSP00000398698	IL1B, IL1RAP, IL6R, IL6, TNF
GO:0022603	Regulation of anatomical structure morphogenesis	10	1095	0.93	7.23E-06	9606. ENSP00000162749, 9606. ENSP00000225831, 9606. ENSP00000263341, 9606. ENSP00000292301, 9606. ENSP00000305651, 9606. ENSP00000306512, 9606. ENSP00000319635, 9606. ENSP00000385675, 9606. ENSP00000398698, 9606. ENSP00000412237	TNFRSF1A, CCL2, IL1B, CCR2, CXCL10, CXCL8, CXCR2, IL6, TNF, IL10
GO:0097191	Extrinsic apoptotic signaling pathway	5	100	1.67	8.77E-06	9606. ENSP00000162749, 9606. ENSP00000263341, 9606. ENSP00000341268, 9606. ENSP00000357470, 9606. ENSP00000398698	TNFRSF1A, IL1B, TRADD, IL6R, TNF
GO:0002824	mmune response based on somatic recombination of immune receptors built from i	5	101	1.66	9.12E-06	9606. ENSP00000011653, 9606. ENSP00000263341, 9606. ENSP00000292301, 9606. ENSP00000385675, 9606. ENSP00000398698	CD4, IL1B, CCR2, IL6, TNF
GO:0043112	Receptor metabolic process	5	105	1.65	1.09E-05	9606. ENSP00000295683, 9606. ENSP00000306512, 9606. ENSP00000319635, 9606. ENSP00000398698, 9606. ENSP00000412237	CXCR1, CXCL8, CXCR2, TNF, IL10
GO:1903039	Positive regulation of leukocyte cell-cell adhesion	6	228	1.39	1.40E-05	9606. ENSP00000011653, 9606. ENSP00000225831, 9606. ENSP00000263341, 9606. ENSP00000292301, 9606. ENSP00000385675, 9606. ENSP00000398698	CD4, CCL2, IL1B, CCR2, IL6, TNF
GO:0042981	Regulation of apoptotic process	11	1550	0.82	1.44E-05	9606. ENSP00000162749, 9606. ENSP00000225831, 9606. ENSP00000263341, 9606. ENSP00000292303, 9606. ENSP00000296871, 9606. ENSP00000305651, 9606. ENSP00000319635, 9606. ENSP00000341268, 9606. ENSP00000385675, 9606. ENSP00000398698, 9606. ENSP00000412237	TNFRSF1A, CCL2, IL1B, CCR5, CSF2, CXCL10, CXCR2, TRADD, IL6, TNF, IL10
GO:0043066	Negative regulation of apoptotic process	9	893	0.97	1.69E-05	9606. ENSP00000225831, 9606. ENSP00000263341, 9606. ENSP00000292303, 9606. ENSP00000296871, 9606. ENSP00000319635, 9606. ENSP00000341268, 9606. ENSP00000385675, 9606. ENSP00000398698, 9606. ENSP00000412237	CCL2, IL1B, CCR5, CSF2, CXCR2, TRADD, IL6, TNF, IL10
GO:0002548	Monocyte chemotaxis	4	43	1.94	1.78E-05	9606. ENSP00000225831, 9606. ENSP00000292301, 9606. ENSP00000357470, 9606. ENSP00000385675	CCL2, CCR2, IL6R, IL6
GO:0071550	Death-inducing signaling complex assembly	3	8	2.54	1.82E-05	9606. ENSP00000162749, 9606. ENSP00000341268, 9606. ENSP00000398698	TNFRSF1A, TRADD, TNF
GO:0045321	Leukocyte activation	9	929	0.96	2.25E-05	9606. ENSP00000011653, 9606. ENSP00000295683, 9606. ENSP00000296871, 9606. ENSP00000306512, 9606. ENSP00000319635, 9606. ENSP00000379110, 9606. ENSP00000385675, 9606. ENSP00000398698, 9606. ENSP00000412237	CD4, CXCR1, CSF2, CXCL8, CXCR2, CXCL1, IL6, TNF, IL10
GO:0048585	Negative regulation of response to stimulus	11	1636	0.8	2.30E-05	9606. ENSP00000162749, 9606. ENSP00000225831, 9606. ENSP00000263341, 9606. ENSP00000292301, 9606. ENSP00000296871, 9606. ENSP00000306512, 9606. ENSP00000330959, 9606. ENSP00000341268, 9606. ENSP00000385675, 9606. ENSP00000398698, 9606. ENSP00000412237	TNFRSF1A, CCL2, IL1B, CCR2, CSF2, CXCL8, IL1R2, TRADD, IL6, TNF, IL10
GO:0051091	Positive regulation of dna-binding transcription factor activity	6	271	1.31	3.32E-05	9606. ENSP00000263341, 9606. ENSP00000314807, 9606. ENSP00000341268, 9606. ENSP00000385675, 9606. ENSP00000398698, 9606. ENSP00000412237	IL1B, IL1RAP, TRADD, IL6, TNF, IL10
GO:0042742	Defense response to bacterium	6	277	1.3	3.74E-05	9606. ENSP00000011653, 9606. ENSP00000162749, 9606. ENSP00000357470, 9606. ENSP00000385675, 9606. ENSP00000398698, 9606. ENSP00000412237	CD4, TNFRSF1A, IL6R, IL6, TNF, IL10
GO:0030155	Regulation of cell adhesion	8	712	1.02	4.03E-05	9606. ENSP00000011653, 9606. ENSP00000225831, 9606. ENSP00000263341, 9606. ENSP00000292301, 9606. ENSP00000306512, 9606. ENSP00000385675, 9606. ENSP00000398698, 9606. ENSP00000412237	CD4, CCL2, IL1B, CCR2, CXCL8, IL6, TNF, IL10
GO:0048519	Negative regulation of biological process	17	5389	0.47	5.18E-05	9606. ENSP00000162749, 9606. ENSP00000225831, 9606. ENSP00000227752, 9606. ENSP00000263341, 9606. ENSP00000292301, 9606. ENSP00000292303, 9606. ENSP00000296871, 9606. ENSP00000305651, 9606. ENSP00000306512, 9606. ENSP00000319635, 9606. ENSP00000330959, 9606. ENSP00000341268, 9606. ENSP00000357470, 9606. ENSP00000379110, 9606. ENSP00000385675, 9606. ENSP00000398698, 9606. ENSP00000412237	TNFRSF1A, CCL2, IL10RA, IL1B, CCR2, CCR5, CSF2, CXCL10, CXCL8, CXCR2, IL1R2, TRADD, IL6R, CXCL1, IL6, TNF, IL10
GO:0002706	Regulation of lymphocyte mediated immunity	5	152	1.49	5.30E-05	9606. ENSP00000263341, 9606. ENSP00000292301, 9606. ENSP00000385675, 9606. ENSP00000398698, 9606. ENSP00000412237	IL1B, CCR2, IL6, TNF, IL10
GO:0007204	Positive regulation of cytosolic calcium ion concentration	6	297	1.27	5.34E-05	9606. ENSP00000011653, 9606. ENSP00000292301, 9606. ENSP00000292303, 9606. ENSP00000295683, 9606. ENSP00000305651, 9606. ENSP00000319635	CD4, CCR2, CCR5, CXCR1, CXCL10, CXCR2
GO:0032722	Positive regulation of chemokine production	4	61	1.79	5.77E-05	9606. ENSP00000263341, 9606. ENSP00000357470, 9606. ENSP00000385675, 9606. ENSP00000398698	IL1B, IL6R, IL6, TNF
GO:0044093	Positive regulation of molecular function	11	1842	0.75	6.87E-05	9606. ENSP00000011653, 9606. ENSP00000225831, 9606. ENSP00000263341, 9606. ENSP00000292301, 9606. ENSP00000314807, 9606. ENSP00000341268, 9606. ENSP00000357470, 9606. ENSP00000379110, 9606. ENSP00000385675, 9606. ENSP00000398698, 9606. ENSP00000412237	CD4, CCL2, IL1B, CCR2, IL1RAP, TRADD, IL6R, CXCL1, IL6, TNF, IL10
GO:0001959	Regulation of cytokine-mediated signaling pathway	5	163	1.46	7.15E-05	9606. ENSP00000162749, 9606. ENSP00000330959, 9606. ENSP00000341268, 9606. ENSP00000385675, 9606. ENSP00000398698	TNFRSF1A, IL1R2, TRADD, IL6, TNF
GO:0019722	Calcium-mediated signaling	5	165	1.45	7.53E-05	9606. ENSP00000292301, 9606. ENSP00000292303, 9606. ENSP00000295683, 9606. ENSP00000306512, 9606. ENSP00000319635	CCR2, CCR5, CXCR1, CXCL8, CXCR2
GO:0042129	Regulation of t cell proliferation	5	165	1.45	7.53E-05	9606. ENSP00000011653, 9606. ENSP00000263341, 9606. ENSP00000292301, 9606. ENSP00000385675, 9606. ENSP00000412237	CD4, IL1B, CCR2, IL6, IL10

Table S4. the full list of KEGG analysis and GO analysis for CCL2

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0060252	Positive regulation of glial cell proliferation	3	15	2.27	7.55E-05	9606.ENSP00000263341, 9606.ENSP00000385675, 9606.ENSP00000398698	IL1B, IL6, TNF
GO:1903140	Regulation of establishment of endothelial barrier	3	15	2.27	7.55E-05	9606.ENSP00000162749, 9606.ENSP00000263341, 9606.ENSP00000398698	TNFRSF1A, IL1B, TNF
GO:0048522	Positive regulation of cellular process	17	5579	0.45	8.16E-05	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000227752, 9606.ENSP00000263341, 9606.ENSP00000290200, 9606.ENSP00000292301, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000314807, 9606.ENSP00000319635, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL10RA, IL1B, IL10RB, CCR2, CSF2, CXCL10, CXCL8, IL1RAP, CXCR2, TRADD, IL6R, IL6, TNF, IL10
GO:0051179	Localization	17	5591	0.45	8.38E-05	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000227752, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000292303, 9606.ENSP00000295683, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000357470, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL10RA, IL1B, CCR2, CCR5, CXCR1, CSF2, CXCL10, CXCL8, CXCR2, IL6R, CXCL1, IL6, TNF, IL10
GO:0034116	Positive regulation of heterotypic cell-cell adhesion	3	16	2.24	8.66E-05	9606.ENSP00000263341, 9606.ENSP00000398698, 9606.ENSP00000412237	IL1B, TNF, IL10
GO:0050863	Regulation of t cell activation	6	329	1.23	8.84E-05	9606.ENSP00000011653, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000385675, 9606.ENSP00000412237	CD4, CCL2, IL1B, CCR2, IL6, IL10
GO:0071347	Cellular response to interleukin-1	5	174	1.43	9.15E-05	9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000306512, 9606.ENSP00000314807, 9606.ENSP00000330959	CCL2, IL1B, CXCL8, IL1RAP, IL1R2
GO:0002696	Positive regulation of leukocyte activation	6	332	1.23	9.19E-05	9606.ENSP00000011653, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000385675, 9606.ENSP00000412237	CD4, CCL2, IL1B, CCR2, IL6, IL10
GO:0014015	Positive regulation of gliogenesis	4	72	1.71	9.81E-05	9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000385675, 9606.ENSP00000398698	IL1B, CCR2, IL6, TNF
GO:0048523	Negative regulation of cellular process	16	4874	0.49	9.83E-05	9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000227752, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000292303, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000330959, 9606.ENSP00000341268, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	TNFRSF1A, CCL2, IL10RA, IL1B, CCR2, CCR5, CSF2, CXCL10, CXCL8, CXCR2, IL1R2, TRADD, CXCL1, IL6, TNF, IL10
GO:0002526	Acute inflammatory response	4	74	1.7	0.00011	9606.ENSP00000263341, 9606.ENSP00000319635, 9606.ENSP00000357470, 9606.ENSP00000385675	IL1B, CXCR2, IL6R, IL6
GO:0032677	Regulation of interleukin-8 production	4	76	1.69	0.00012	9606.ENSP00000263341, 9606.ENSP00000357470, 9606.ENSP00000398698, 9606.ENSP00000412237	IL1B, IL6R, TNF, IL10
GO:0019932	Second-messenger-mediated signaling	6	354	1.2	0.00013	9606.ENSP00000292301, 9606.ENSP00000292303, 9606.ENSP00000295683, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635	CCR2, CCR5, CXCR1, CXCL10, CXCL8, CXCR2
GO:1904018	Positive regulation of vasculature development	5	189	1.39	0.00013	9606.ENSP00000263341, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000357470, 9606.ENSP00000412237	IL1B, CXCL8, CXCR2, IL6R, IL10
GO:0043123	Positive regulation of i-kappab kinase/nf-kappab signaling	5	194	1.38	0.00014	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000263341, 9606.ENSP00000341268, 9606.ENSP00000398698	CD4, TNFRSF1A, IL1B, TRADD, TNF
GO:1904996	Positive regulation of leukocyte adhesion to vascular endothelial cell	3	20	2.15	0.00014	9606.ENSP00000292301, 9606.ENSP00000385675, 9606.ENSP00000398698	CCR2, IL6, TNF
GO:0019725	Cellular homeostasis	8	895	0.92	0.00018	9606.ENSP00000011653, 9606.ENSP00000225831, 9606.ENSP00000292301, 9606.ENSP00000292303, 9606.ENSP00000295683, 9606.ENSP00000305651, 9606.ENSP00000319635, 9606.ENSP00000385675	CD4, CCL2, CCR2, CCR5, CXCR1, CXCL10, CXCR2, IL6
GO:0051241	Negative regulation of multicellular organismal process	9	1231	0.83	0.00018	9606.ENSP00000162749, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000305651, 9606.ENSP00000330959, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	TNFRSF1A, IL1B, CCR2, CXCL10, IL1R2, IL6R, IL6, TNF, IL10
GO:0048661	Positive regulation of smooth muscle cell proliferation	4	88	1.63	0.00019	9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	IL6R, IL6, TNF, IL10
GO:0014070	Response to organic cyclic compound	8	911	0.91	0.0002	9606.ENSP00000011653, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292303, 9606.ENSP00000305651, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, CCL2, IL1B, CCR5, CXCL10, IL6, TNF, IL10
GO:0050870	Positive regulation of t cell activation	5	209	1.35	0.0002	9606.ENSP00000011653, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000385675	CD4, CCL2, IL1B, CCR2, IL6
GO:0051043	Regulation of membrane protein ectodomain proteolysis	3	24	2.07	0.00022	9606.ENSP00000263341, 9606.ENSP00000398698, 9606.ENSP00000412237	IL1B, TNF, IL10
GO:0051050	Positive regulation of transport	8	923	0.91	0.00022	9606.ENSP00000011653, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000305651, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, CCL2, IL1B, CCR2, CXCL10, IL6, TNF, IL10
GO:0042102	Positive regulation of t cell proliferation	4	97	1.58	0.00027	9606.ENSP00000011653, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000385675	CD4, IL1B, CCR2, IL6
GO:0043065	Positive regulation of apoptotic process	7	660	0.99	0.00028	9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000319635, 9606.ENSP00000341268, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	TNFRSF1A, CCL2, CXCR2, TRADD, IL6, TNF, IL10

Table S4. the full list of KEGG analysis and GO analysis for CCL2

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0032268	Regulation of cellular protein metabolic process	12	2693	0.62	0.00029	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000330959, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL1B, CSF2, CXCL10, IL1R2, TRADD, IL6R, IL6, TNF, IL10
GO:0071677	Positive regulation of mononuclear cell migration	3	27	2.02	0.00029	9606.ENSP00000292301, 9606.ENSP00000305651, 9606.ENSP00000398698	CCR2, CXCL10, TNF
GO:1901623	Regulation of lymphocyte chemotaxis	3	27	2.02	0.00029	9606.ENSP00000225831, 9606.ENSP00000292301, 9606.ENSP00000305651	CCL2, CCR2, CXCL10
GO:0002675	Positive regulation of acute inflammatory response	3	29	1.98	0.00035	9606.ENSP00000263341, 9606.ENSP00000385675, 9606.ENSP00000398698	IL1B, IL6, TNF
GO:0032649	Regulation of interferon-gamma production	4	106	1.55	0.00035	9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000398698, 9606.ENSP00000412237	IL1B, CCR2, TNF, IL10
GO:2001237	Negative regulation of extrinsic apoptotic signaling pathway	4	106	1.55	0.00035	9606.ENSP00000263341, 9606.ENSP00000296871, 9606.ENSP00000341268, 9606.ENSP00000398698	IL1B, CSF2, TRADD, TNF
GO:0008285	Negative regulation of cell population proliferation	7	696	0.97	0.00037	9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000306512, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CCL2, IL1B, CXCL8, CXCL1, IL6, TNF, IL10
GO:0071356	Cellular response to tumor necrosis factor	5	245	1.28	0.00037	9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000306512, 9606.ENSP00000341268, 9606.ENSP00000398698	TNFRSF1A, CCL2, CXCL8, TRADD, TNF
GO:0001934	Positive regulation of protein phosphorylation	8	1019	0.86	0.0004	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000296871, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698	CD4, TNFRSF1A, CCL2, IL1B, CSF2, IL6R, IL6, TNF
GO:0002384	Hepatic immune response	2	2	2.97	0.00042	9606.ENSP00000357470, 9606.ENSP00000385675	IL6R, IL6
GO:0002724	Regulation of t cell cytokine production	3	32	1.94	0.00043	9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000385675	IL1B, CCR2, IL6
GO:0010574	Regulation of vascular endothelial growth factor production	3	32	1.94	0.00043	9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000385675	IL1B, CCR2, IL6
GO:0032743	Positive regulation of interleukin-2 production	3	32	1.94	0.00043	9606.ENSP00000011653, 9606.ENSP00000263341, 9606.ENSP00000292301	CD4, IL1B, CCR2
GO:0072678	T cell migration	3	32	1.94	0.00043	9606.ENSP00000225831, 9606.ENSP00000292301, 9606.ENSP00000305651	CCL2, CCR2, CXCL10
GO:1902533	Positive regulation of intracellular signal transduction	8	1041	0.85	0.00044	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698	CD4, TNFRSF1A, CCL2, IL1B, TRADD, IL6R, IL6, TNF
GO:0010628	Positive regulation of gene expression	11	2337	0.64	0.00049	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000314807, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, IL1B, CCR2, CSF2, CXCL10, IL1RAP, IL6R, IL6, TNF, IL10
GO:0031663	Lipopolysaccharide-mediated signaling pathway	3	34	1.91	0.00049	9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000398698	CCL2, IL1B, TNF
GO:0008625	Extrinsic apoptotic signaling pathway via death domain receptors	3	35	1.9	0.00052	9606.ENSP00000162749, 9606.ENSP00000341268, 9606.ENSP00000398698	TNFRSF1A, TRADD, TNF
GO:0001932	Regulation of protein phosphorylation	9	1459	0.76	0.00055	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698	CD4, TNFRSF1A, CCL2, IL1B, CSF2, CXCL10, IL6R, IL6, TNF
GO:0002437	Inflammatory response to antigenic stimulus	3	37	1.88	0.0006	9606.ENSP00000263341, 9606.ENSP00000319635, 9606.ENSP00000398698	IL1B, CXCR2, TNF
GO:2001240	egative regulation of extrinsic apoptotic signaling pathway in absence of ligar	3	37	1.88	0.0006	9606.ENSP00000263341, 9606.ENSP00000296871, 9606.ENSP00000398698	IL1B, CSF2, TNF
GO:0001818	Negative regulation of cytokine production	5	280	1.22	0.00061	9606.ENSP00000330959, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	IL1R2, IL6R, IL6, TNF, IL10
GO:0002874	Regulation of chronic inflammatory response to antigenic stimulus	2	3	2.79	0.00063	9606.ENSP00000398698, 9606.ENSP00000412237	TNF, IL10
GO:0043491	Protein kinase b signaling	3	38	1.87	0.00063	9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000398698	CCL2, IL1B, TNF
GO:0060559	Positive regulation of calcidiol 1-monooxygenase activity	2	3	2.79	0.00063	9606.ENSP00000263341, 9606.ENSP00000398698	IL1B, TNF
GO:0043270	Positive regulation of ion transport	5	285	1.21	0.00064	9606.ENSP00000011653, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000305651	CD4, CCL2, IL1B, CCR2, CXCL10
GO:0010604	Positive regulation of macromolecule metabolic process	13	3600	0.53	0.00071	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000314807, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL1B, CCR2, CSF2, CXCL10, IL1RAP, TRADD, IL6R, IL6, TNF, IL10
GO:0045123	Cellular extravasation	3	42	1.82	0.00079	9606.ENSP00000225831, 9606.ENSP00000292301, 9606.ENSP00000398698	CCL2, CCR2, TNF
GO:0030730	Sequestering of triglyceride	2	4	2.67	0.00087	9606.ENSP00000263341, 9606.ENSP00000398698	IL1B, TNF
GO:0006953	Acute-phase response	3	44	1.8	0.00088	9606.ENSP00000263341, 9606.ENSP00000357470, 9606.ENSP00000385675	IL1B, IL6R, IL6
GO:0043410	Positive regulation of mapk cascade	6	543	1.01	0.00094	9606.ENSP00000011653, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698	CD4, CCL2, IL1B, IL6R, IL6, TNF

Table S4. the full list of KEGG analysis and GO analysis for CCL2

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:1900015	Regulation of cytokine production involved in inflammatory response	3	46	1.78	0.00099	9606.ENSP00000330959, 9606.ENSP00000385675, 9606.ENSP00000398698	IL1R2, IL6, TNF
GO:0048731	System development	14	4426	0.47	0.0011	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000357470, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL1B, CCR2, CSF2, CXCL10, CXCL8, CXCR2, IL6R, CXCL1, IL6, TNF, IL10
GO:0001816	Cytokine production	4	158	1.37	0.0012	9606.ENSP00000011653, 9606.ENSP00000263341, 9606.ENSP00000314807, 9606.ENSP00000398698	CD4, IL1B, IL1RAP, TNF
GO:0030097	Hemopoiesis	6	570	0.99	0.0012	9606.ENSP00000011653, 9606.ENSP00000292301, 9606.ENSP00000296871, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, CCR2, CSF2, IL6, TNF, IL10
GO:0032270	Positive regulation of cellular protein metabolic process	9	1635	0.71	0.0012	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000296871, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698	CD4, TNFRSF1A, CCL2, IL1B, CSF2, TRADD, IL6R, IL6, TNF
GO:0032800	Receptor biosynthetic process	2	5	2.57	0.0012	9606.ENSP00000398698, 9606.ENSP00000412237	TNF, IL10
GO:0048247	Lymphocyte chemotaxis	3	50	1.75	0.0012	9606.ENSP00000225831, 9606.ENSP00000292301, 9606.ENSP00000305651	CCL2, CCR2, CXCL10
GO:0048513	Animal organ development	12	3197	0.54	0.0012	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000292301, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, CCR2, CSF2, CXCL10, CXCL8, CXCR2, IL6R, IL6, TNF, IL10
GO:0051092	Positive regulation of nf-kappab transcription factor activity	4	158	1.37	0.0012	9606.ENSP00000263341, 9606.ENSP00000314807, 9606.ENSP00000341268, 9606.ENSP00000398698	IL1B, IL1RAP, TRADD, TNF
GO:2000660	Negative regulation of interleukin-1-mediated signaling pathway	2	5	2.57	0.0012	9606.ENSP00000330959, 9606.ENSP00000385675	IL1R2, IL6
GO:0002274	Myeloid leukocyte activation	6	585	0.98	0.0013	9606.ENSP00000295683, 9606.ENSP00000296871, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000379110, 9606.ENSP00000398698	CXCR1, CSF2, CXCL8, CXCR2, CXCL1, TNF
GO:0002521	Leukocyte differentiation	5	338	1.14	0.0013	9606.ENSP00000011653, 9606.ENSP00000296871, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, CSF2, IL6, TNF, IL10
GO:0007186	G protein-coupled receptor signaling pathway	8	1255	0.77	0.0013	9606.ENSP00000225831, 9606.ENSP00000292301, 9606.ENSP00000292303, 9606.ENSP00000295683, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000379110	CCL2, CCR2, CCR5, CXCR1, CXCL10, CXCL8, CXCR2, CXCL1
GO:0051235	Maintenance of location	4	161	1.36	0.0013	9606.ENSP00000011653, 9606.ENSP00000263341, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, IL1B, TNF, IL10
GO:0006968	Cellular defense response	3	54	1.71	0.0014	9606.ENSP00000292301, 9606.ENSP00000292303, 9606.ENSP00000319635	CCR2, CCR5, CXCR2
GO:0009968	Negative regulation of signal transduction	8	1271	0.77	0.0014	9606.ENSP00000263341, 9606.ENSP00000296871, 9606.ENSP00000306512, 9606.ENSP00000330959, 9606.ENSP00000341268, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	IL1B, CSF2, CXCL8, IL1R2, TRADD, IL6, TNF, IL10
GO:0042592	Homeostatic process	9	1676	0.7	0.0014	9606.ENSP00000011653, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000292303, 9606.ENSP00000295683, 9606.ENSP00000305651, 9606.ENSP00000319635, 9606.ENSP00000385675	CD4, CCL2, IL1B, CCR2, CCR5, CXCR1, CXCL10, CXCR2, IL6
GO:1904783	Positive regulation of nmda glutamate receptor activity	2	6	2.49	0.0014	9606.ENSP00000225831, 9606.ENSP00000292301	CCL2, CCR2
GO:0045766	Positive regulation of angiogenesis	4	169	1.34	0.0015	9606.ENSP00000263341, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000412237	IL1B, CXCL8, CXCR2, IL10
GO:0006915	Apoptotic process	7	918	0.85	0.0016	9606.ENSP00000162749, 9606.ENSP00000263341, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	TNFRSF1A, IL1B, TRADD, IL6R, IL6, TNF, IL10
GO:0007159	Leukocyte cell-cell adhesion	3	56	1.7	0.0016	9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000398698	IL1B, CCR2, TNF
GO:0010803	Regulation of tumor necrosis factor-mediated signaling pathway	3	57	1.69	0.0016	9606.ENSP00000162749, 9606.ENSP00000341268, 9606.ENSP00000398698	TNFRSF1A, TRADD, TNF
GO:0032102	Negative regulation of response to external stimulus	5	367	1.1	0.0017	9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000330959, 9606.ENSP00000398698, 9606.ENSP00000412237	TNFRSF1A, CCL2, IL1R2, TNF, IL10
GO:0000165	MAPK cascade	5	370	1.1	0.0018	9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292303, 9606.ENSP00000296871, 9606.ENSP00000398698	CCL2, IL1B, CCR5, CSF2, TNF
GO:0019064	Fusion of virus membrane with host plasma membrane	2	7	2.43	0.0018	9606.ENSP00000011653, 9606.ENSP00000292303	CD4, CCR5
GO:0031622	Positive regulation of fever generation	2	7	2.43	0.0018	9606.ENSP00000263341, 9606.ENSP00000398698	IL1B, TNF
GO:1903530	Regulation of secretion by cell	6	630	0.95	0.0018	9606.ENSP00000162749, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	TNFRSF1A, IL1B, CCR2, IL6, TNF, IL10
GO:0045428	Regulation of nitric oxide biosynthetic process	3	61	1.66	0.0019	9606.ENSP00000263341, 9606.ENSP00000398698, 9606.ENSP00000412237	IL1B, TNF, IL10
GO:0051049	Regulation of transport	9	1776	0.67	0.002	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000305651, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL1B, CCR2, CXCL10, IL6, TNF, IL10
GO:0002252	Immune effector process	7	969	0.83	0.0021	9606.ENSP00000290200, 9606.ENSP00000295683, 9606.ENSP00000305651, 9606.ENSP00000319635, 9606.ENSP00000357470, 9606.ENSP00000379110, 9606.ENSP00000385675	IL10RB, CXCR1, CXCL10, CXCR2, IL6R, CXCL1, IL6

Table S4. the full list of KEGG analysis and GO analysis for CCL2

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:1900015	Regulation of cytokine production involved in inflammatory response	3	46	1.78	0.00099	9606.ENSP00000330959, 9606.ENSP00000385675, 9606.ENSP00000398698	IL1R2, IL6, TNF
GO:0048731	System development	14	4426	0.47	0.0011	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000357470, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL1B, CCR2, CSF2, CXCL10, CXCL8, CXCR2, IL6R, CXCL1, IL6, TNF, IL10
GO:0001816	Cytokine production	4	158	1.37	0.0012	9606.ENSP00000011653, 9606.ENSP00000263341, 9606.ENSP00000314807, 9606.ENSP00000398698	CD4, IL1B, IL1RAP, TNF
GO:0030097	Hemopoiesis	6	570	0.99	0.0012	9606.ENSP00000011653, 9606.ENSP00000292301, 9606.ENSP00000296871, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, CCR2, CSF2, IL6, TNF, IL10
GO:0032270	Positive regulation of cellular protein metabolic process	9	1635	0.71	0.0012	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000296871, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698	CD4, TNFRSF1A, CCL2, IL1B, CSF2, TRADD, IL6R, IL6, TNF
GO:0032800	Receptor biosynthetic process	2	5	2.57	0.0012	9606.ENSP00000398698, 9606.ENSP00000412237	TNF, IL10
GO:0048247	Lymphocyte chemotaxis	3	50	1.75	0.0012	9606.ENSP00000225831, 9606.ENSP00000292301, 9606.ENSP00000305651	CCL2, CCR2, CXCL10
GO:0048513	Animal organ development	12	3197	0.54	0.0012	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000292301, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, CCR2, CSF2, CXCL10, CXCL8, CXCR2, IL6R, IL6, TNF, IL10
GO:0051092	Positive regulation of nf-kappab transcription factor activity	4	158	1.37	0.0012	9606.ENSP00000263341, 9606.ENSP00000314807, 9606.ENSP00000341268, 9606.ENSP00000398698	IL1B, IL1RAP, TRADD, TNF
GO:2000660	Negative regulation of interleukin-1-mediated signaling pathway	2	5	2.57	0.0012	9606.ENSP00000330959, 9606.ENSP00000385675	IL1R2, IL6
GO:0002274	Myeloid leukocyte activation	6	585	0.98	0.0013	9606.ENSP00000295683, 9606.ENSP00000296871, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000379110, 9606.ENSP00000398698	CXCR1, CSF2, CXCL8, CXCR2, CXCL1, TNF
GO:0002521	Leukocyte differentiation	5	338	1.14	0.0013	9606.ENSP00000011653, 9606.ENSP00000296871, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, CSF2, IL6, TNF, IL10
GO:0007186	G protein-coupled receptor signaling pathway	8	1255	0.77	0.0013	9606.ENSP00000225831, 9606.ENSP00000292301, 9606.ENSP00000292303, 9606.ENSP00000295683, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000379110	CCL2, CCR2, CCR5, CXCR1, CXCL10, CXCL8, CXCR2, CXCL1
GO:0051235	Maintenance of location	4	161	1.36	0.0013	9606.ENSP00000011653, 9606.ENSP00000263341, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, IL1B, TNF, IL10
GO:0006968	Cellular defense response	3	54	1.71	0.0014	9606.ENSP00000292301, 9606.ENSP00000292303, 9606.ENSP00000319635	CCR2, CCR5, CXCR2
GO:0009968	Negative regulation of signal transduction	8	1271	0.77	0.0014	9606.ENSP00000263341, 9606.ENSP00000296871, 9606.ENSP00000306512, 9606.ENSP00000330959, 9606.ENSP00000341268, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	IL1B, CSF2, CXCL8, IL1R2, TRADD, IL6, TNF, IL10
GO:0042592	Homeostatic process	9	1676	0.7	0.0014	9606.ENSP00000011653, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000292303, 9606.ENSP00000295683, 9606.ENSP00000305651, 9606.ENSP00000319635, 9606.ENSP00000385675	CD4, CCL2, IL1B, CCR2, CCR5, CXCR1, CXCL10, CXCR2, IL6
GO:1904783	Positive regulation of nmda glutamate receptor activity	2	6	2.49	0.0014	9606.ENSP00000225831, 9606.ENSP00000292301	CCL2, CCR2
GO:0045766	Positive regulation of angiogenesis	4	169	1.34	0.0015	9606.ENSP00000263341, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000412237	IL1B, CXCL8, CXCR2, IL10
GO:0006915	Apoptotic process	7	918	0.85	0.0016	9606.ENSP00000162749, 9606.ENSP00000263341, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	TNFRSF1A, IL1B, TRADD, IL6R, IL6, TNF, IL10
GO:0007159	Leukocyte cell-cell adhesion	3	56	1.7	0.0016	9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000398698	IL1B, CCR2, TNF
GO:0010803	Regulation of tumor necrosis factor-mediated signaling pathway	3	57	1.69	0.0016	9606.ENSP00000162749, 9606.ENSP00000341268, 9606.ENSP00000398698	TNFRSF1A, TRADD, TNF
GO:0032102	Negative regulation of response to external stimulus	5	367	1.1	0.0017	9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000330959, 9606.ENSP00000398698, 9606.ENSP00000412237	TNFRSF1A, CCL2, IL1R2, TNF, IL10
GO:0000165	MAPK cascade	5	370	1.1	0.0018	9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292303, 9606.ENSP00000296871, 9606.ENSP00000398698	CCL2, IL1B, CCR5, CSF2, TNF
GO:0019064	Fusion of virus membrane with host plasma membrane	2	7	2.43	0.0018	9606.ENSP00000011653, 9606.ENSP00000292303	CD4, CCR5
GO:0031622	Positive regulation of fever generation	2	7	2.43	0.0018	9606.ENSP00000263341, 9606.ENSP00000398698	IL1B, TNF
GO:1903530	Regulation of secretion by cell	6	630	0.95	0.0018	9606.ENSP00000162749, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	TNFRSF1A, IL1B, CCR2, IL6, TNF, IL10
GO:0045428	Regulation of nitric oxide biosynthetic process	3	61	1.66	0.0019	9606.ENSP00000263341, 9606.ENSP00000398698, 9606.ENSP00000412237	IL1B, TNF, IL10
GO:0051049	Regulation of transport	9	1776	0.67	0.002	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000305651, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL1B, CCR2, CXCL10, IL6, TNF, IL10
GO:0002252	Immune effector process	7	969	0.83	0.0021	9606.ENSP00000290200, 9606.ENSP00000295683, 9606.ENSP00000305651, 9606.ENSP00000319635, 9606.ENSP00000357470, 9606.ENSP00000379110, 9606.ENSP00000385675	IL10RB, CXCR1, CXCL10, CXCR2, IL6R, CXCL1, IL6

Table S4. the full list of KEGG analysis and GO analysis for CCL2

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0010829	Negative regulation of glucose transmembrane transport	2	17	2.04	0.0064	9606.ENSP00000263341, 9606.ENSP00000398698	IL1B, TNF
GO:0002708	Positive regulation of lymphocyte mediated immunity	3	104	1.43	0.0067	9606.ENSP00000263341, 9606.ENSP00000385675, 9606.ENSP00000398698	IL1B, IL6, TNF
GO:0051023	Regulation of immunoglobulin secretion	2	18	2.02	0.007	9606.ENSP00000385675, 9606.ENSP00000398698	IL6, TNF
GO:1902105	Regulation of leukocyte differentiation	4	285	1.12	0.0076	9606.ENSP00000011653, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000398698	CD4, IL1B, CCR2, TNF
GO:1905517	Macrophage migration	2	19	1.99	0.0076	9606.ENSP00000225831, 9606.ENSP00000292301	CCL2, CCR2
GO:0051962	Positive regulation of nervous system development	5	547	0.93	0.0081	9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000314807, 9606.ENSP00000385675, 9606.ENSP00000398698	IL1B, CCR2, IL1RAP, IL6, TNF
GO:0002573	Myeloid leukocyte differentiation	3	113	1.39	0.0082	9606.ENSP00000011653, 9606.ENSP00000296871, 9606.ENSP00000398698	CD4, CSF2, TNF
GO:0002726	Positive regulation of t cell cytokine production	2	20	1.97	0.0082	9606.ENSP00000263341, 9606.ENSP00000385675	IL1B, IL6
GO:0002827	Positive regulation of t-helper 1 type immune response	2	20	1.97	0.0082	9606.ENSP00000263341, 9606.ENSP00000292301	IL1B, CCR2
GO:0009615	Response to virus	4	293	1.1	0.0082	9606.ENSP00000290200, 9606.ENSP00000305651, 9606.ENSP00000385675, 9606.ENSP00000398698	IL10RB, CXCL10, IL6, TNF
GO:0032682	Negative regulation of chemokine production	2	20	1.97	0.0082	9606.ENSP00000385675, 9606.ENSP00000412237	IL6, IL10
GO:0032717	Negative regulation of interleukin-8 production	2	20	1.97	0.0082	9606.ENSP00000357470, 9606.ENSP00000412237	IL6R, IL10
GO:0048143	Astrocyte activation	2	20	1.97	0.0082	9606.ENSP00000263341, 9606.ENSP00000398698	IL1B, TNF
GO:0061844	Antimicrobial humoral immune response mediated by antimicrobial peptide	3	113	1.39	0.0082	9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000379110	CXCL10, CXCL8, CXCL1
GO:0070372	Regulation of erk1 and erk2 cascade	4	292	1.11	0.0082	9606.ENSP00000011653, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000398698	CD4, CCL2, IL1B, TNF
GO:0010888	Negative regulation of lipid storage	2	21	1.95	0.0087	9606.ENSP00000385675, 9606.ENSP00000398698	IL6, TNF
GO:0016525	Negative regulation of angiogenesis	3	117	1.38	0.0087	9606.ENSP00000292301, 9606.ENSP00000305651, 9606.ENSP00000398698	CCR2, CXCL10, TNF
GO:0034762	Regulation of transmembrane transport	5	560	0.92	0.0087	9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000305651, 9606.ENSP00000398698	CCL2, IL1B, CCR2, CXCL10, TNF
GO:0045667	Regulation of osteoblast differentiation	3	117	1.38	0.0087	9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698	IL6R, IL6, TNF
GO:0061756	Leukocyte adhesion to vascular endothelial cell	2	21	1.95	0.0087	9606.ENSP00000292301, 9606.ENSP00000398698	CCR2, TNF
GO:0090026	Positive regulation of monocyte chemotaxis	2	21	1.95	0.0087	9606.ENSP00000292301, 9606.ENSP00000305651	CCR2, CXCL10
GO:1900017	Positive regulation of cytokine production involved in inflammatory response	2	21	1.95	0.0087	9606.ENSP00000385675, 9606.ENSP00000398698	IL6, TNF
GO:0031325	Positive regulation of cellular metabolic process	11	3413	0.48	0.009	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL1B, CSF2, CXCL10, TRADD, IL6R, IL6, TNF, IL10
GO:0050830	Defense response to gram-positive bacterium	3	119	1.37	0.009	9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698	IL6R, IL6, TNF
GO:0010468	Regulation of gene expression	13	4813	0.4	0.0098	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000314807, 9606.ENSP00000330959, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, IL1B, CCR2, CSF2, CXCL10, IL1RAP, IL1R2, TRADD, IL6R, IL6, TNF, IL10
GO:1903532	Positive regulation of secretion by cell	4	312	1.08	0.0099	9606.ENSP00000263341, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	IL1B, IL6, TNF, IL10
GO:0002698	Negative regulation of immune effector process	3	125	1.35	0.0103	9606.ENSP00000292301, 9606.ENSP00000398698, 9606.ENSP00000412237	CCR2, TNF, IL10
GO:0007155	Cell adhesion	6	925	0.78	0.0103	9606.ENSP00000011653, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000314807, 9606.ENSP00000398698	CD4, CCL2, IL1B, CCR2, IL1RAP, TNF
GO:0009895	Negative regulation of catabolic process	4	316	1.07	0.0103	9606.ENSP00000227752, 9606.ENSP00000263341, 9606.ENSP00000398698, 9606.ENSP00000412237	IL10RA, IL1B, TNF, IL10
GO:0033209	Tumor necrosis factor-mediated signaling pathway	3	125	1.35	0.0103	9606.ENSP00000162749, 9606.ENSP00000341268, 9606.ENSP00000398698	TNFRSF1A, TRADD, TNF
GO:0051928	Positive regulation of calcium ion transport	3	125	1.35	0.0103	9606.ENSP00000011653, 9606.ENSP00000225831, 9606.ENSP00000305651	CD4, CCL2, CXCL10
GO:0050995	Negative regulation of lipid catabolic process	2	24	1.89	0.0106	9606.ENSP00000263341, 9606.ENSP00000398698	IL1B, TNF
GO:0002719	Negative regulation of cytokine production involved in immune response	2	25	1.87	0.0114	9606.ENSP00000398698, 9606.ENSP00000412237	TNF, IL10
GO:0001936	Regulation of endothelial cell proliferation	3	134	1.32	0.0121	9606.ENSP00000225831, 9606.ENSP00000398698, 9606.ENSP00000412237	CCL2, TNF, IL10
GO:0009889	Regulation of biosynthetic process	12	4210	0.42	0.0121	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000314807, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL1B, CSF2, CXCL10, IL1RAP, TRADD, IL6R, IL6, TNF, IL10
GO:0030225	Macrophage differentiation	2	26	1.86	0.0121	9606.ENSP00000011653, 9606.ENSP00000296871	CD4, CSF2
GO:0050708	Regulation of protein secretion	4	333	1.05	0.0121	9606.ENSP00000263341, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	IL1B, IL6, TNF, IL10
GO:0051968	Positive regulation of synaptic transmission, glutamatergic	2	26	1.86	0.0121	9606.ENSP00000225831, 9606.ENSP00000292301	CCL2, CCR2
GO:0090023	Positive regulation of neutrophil chemotaxis	2	26	1.86	0.0121	9606.ENSP00000306512, 9606.ENSP00000319635	CXCL8, CXCR2
GO:0045662	Negative regulation of myoblast differentiation	2	27	1.84	0.0128	9606.ENSP00000305651, 9606.ENSP00000398698	CXCL10, TNF
GO:0050790	Regulation of catalytic activity	9	2386	0.55	0.0129	9606.ENSP00000011653, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000305651, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000379110, 9606.ENSP00000398698	CD4, CCL2, IL1B, CCR2, CXCL10, TRADD, IL6R, CXCL1, TNF

Table S4. the full list of KEGG analysis and GO analysis for CCL2

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0050728	Negative regulation of inflammatory response	3	139	1.3	0.0131	9606. ENSP00000162749, 9606. ENSP00000330959, 9606. ENSP00000412237	TNFRSF1A, IL1R2, IL10
GO:0010575	Positive regulation of vascular endothelial growth factor production	2	28	1.82	0.0135	9606. ENSP00000263341, 9606. ENSP00000385675	IL1B, IL6
GO:0051128	Regulation of cellular component organization	9	2402	0.54	0.0135	9606. ENSP00000162749, 9606. ENSP00000227752, 9606. ENSP00000263341, 9606. ENSP00000296871, 9606. ENSP00000305651, 9606. ENSP00000314807, 9606. ENSP00000385675, 9606. ENSP00000398698, 9606. ENSP00000412237	TNFRSF1A, IL10RA, IL1B, CSF2, CXCL10, IL1RAP, IL6, TNF, IL10
GO:0033280	Response to vitamin d	2	29	1.81	0.0144	9606. ENSP00000011653, 9606. ENSP00000305651	CD4, CXCL10
GO:0051222	Positive regulation of protein transport	4	352	1.02	0.0144	9606. ENSP00000263341, 9606. ENSP00000385675, 9606. ENSP00000398698, 9606. ENSP00000412237	IL1B, IL6, TNF, IL10
GO:1904064	Positive regulation of cation transmembrane transport	3	145	1.29	0.0144	9606. ENSP00000225831, 9606. ENSP00000292301, 9606. ENSP00000305651	CCL2, CCR2, CXCL10
GO:0010557	Positive regulation of macromolecule biosynthetic process	8	1906	0.59	0.0147	9606. ENSP00000011653, 9606. ENSP00000162749, 9606. ENSP00000225831, 9606. ENSP00000263341, 9606. ENSP00000305651, 9606. ENSP00000385675, 9606. ENSP00000398698, 9606. ENSP00000412237	CD4, TNFRSF1A, CCL2, IL1B, CXCL10, IL6, TNF, IL10
GO:0050806	Positive regulation of synaptic transmission	3	147	1.28	0.0149	9606. ENSP00000225831, 9606. ENSP00000292301, 9606. ENSP00000398698	CCL2, CCR2, TNF
GO:0051384	Response to glucocorticoid	3	147	1.28	0.0149	9606. ENSP00000385675, 9606. ENSP00000398698, 9606. ENSP00000412237	IL6, TNF, IL10
GO:0050715	Positive regulation of cytokine secretion	2	30	1.79	0.015	9606. ENSP00000398698, 9606. ENSP00000412237	TNF, IL10
GO:0002828	Regulation of type 2 immune response	2	31	1.78	0.0158	9606. ENSP00000292301, 9606. ENSP00000385675	CCR2, IL6
GO:1905952	Regulation of lipid localization	3	151	1.27	0.0158	9606. ENSP00000263341, 9606. ENSP00000385675, 9606. ENSP00000398698	IL1B, IL6, TNF
GO:2000406	Positive regulation of t cell migration	2	31	1.78	0.0158	9606. ENSP00000292301, 9606. ENSP00000305651	CCR2, CXCL10
GO:0060341	Regulation of cellular localization	6	1027	0.74	0.016	9606. ENSP00000011653, 9606. ENSP00000263341, 9606. ENSP00000292301, 9606. ENSP00000292303, 9606. ENSP00000305651, 9606. ENSP00000398698	CD4, IL1B, CCR2, CCR5, CXCL10, TNF
GO:1903531	Negative regulation of secretion by cell	3	153	1.26	0.0163	9606. ENSP00000162749, 9606. ENSP00000263341, 9606. ENSP00000292301	TNFRSF1A, IL1B, CCR2
GO:1903900	Regulation of viral life cycle	3	153	1.26	0.0163	9606. ENSP00000011653, 9606. ENSP00000306512, 9606. ENSP00000398698	CD4, CXCL8, TNF
GO:0050777	Negative regulation of immune response	3	154	1.26	0.0164	9606. ENSP00000292301, 9606. ENSP00000398698, 9606. ENSP00000412237	CCR2, TNF, IL10
GO:1901889	Negative regulation of cell junction assembly	2	32	1.77	0.0164	9606. ENSP00000263341, 9606. ENSP00000398698	IL1B, TNF
GO:1902107	Positive regulation of leukocyte differentiation	3	156	1.25	0.017	9606. ENSP00000011653, 9606. ENSP00000263341, 9606. ENSP00000398698	CD4, IL1B, TNF
GO:0043085	Positive regulation of catalytic activity	7	1489	0.64	0.018	9606. ENSP00000011653, 9606. ENSP00000225831, 9606. ENSP00000263341, 9606. ENSP00000341268, 9606. ENSP00000357470, 9606. ENSP00000379110, 9606. ENSP00000398698	CD4, CCL2, IL1B, TRADD, IL6R, CXCL1, TNF
GO:0032692	Negative regulation of interleukin-1 production	2	34	1.74	0.0181	9606. ENSP00000330959, 9606. ENSP00000412237	IL1R2, IL10
GO:0048566	Embryonic digestive tract development	2	34	1.74	0.0181	9606. ENSP00000306512, 9606. ENSP00000398698	CXCL8, TNF
GO:0034250	Positive regulation of cellular amide metabolic process	3	162	1.24	0.0186	9606. ENSP00000162749, 9606. ENSP00000385675, 9606. ENSP00000398698	TNFRSF1A, IL6, TNF
GO:1901031	Regulation of response to reactive oxygen species	2	35	1.73	0.0189	9606. ENSP00000398698, 9606. ENSP00000412237	TNF, IL10
GO:1904707	Positive regulation of vascular associated smooth muscle cell proliferation	2	35	1.73	0.0189	9606. ENSP00000398698, 9606. ENSP00000412237	TNF, IL10
GO:0050714	Positive regulation of protein secretion	3	167	1.22	0.02	9606. ENSP00000385675, 9606. ENSP00000398698, 9606. ENSP00000412237	IL6, TNF, IL10
GO:0007259	Receptor signaling pathway via jak-stat	2	38	1.69	0.0215	9606. ENSP00000225831, 9606. ENSP00000292301	CCL2, CCR2
GO:0032501	Multicellular organismal process	15	6933	0.3	0.0221	9606. ENSP00000011653, 9606. ENSP00000162749, 9606. ENSP00000225831, 9606. ENSP00000263341, 9606. ENSP00000292301, 9606. ENSP00000296871, 9606. ENSP00000305651, 9606. ENSP00000306512, 9606. ENSP00000314807, 9606. ENSP00000319635, 9606. ENSP00000357470, 9606. ENSP00000379110, 9606. ENSP00000385675, 9606. ENSP00000398698, 9606. ENSP00000412237	CD4, TNFRSF1A, CCL2, IL1B, CCR2, CSF2, CXCL10, CXCL8, IL1RAP, CXCR2, IL6R, CXCL1, IL6, TNF, IL10
GO:0010469	Regulation of signaling receptor activity	3	176	1.2	0.0225	9606. ENSP00000225831, 9606. ENSP00000292301, 9606. ENSP00000412237	CCL2, CCR2, IL10
GO:0019222	Regulation of metabolic process	15	6948	0.3	0.0225	9606. ENSP00000011653, 9606. ENSP00000162749, 9606. ENSP00000225831, 9606. ENSP00000227752, 9606. ENSP00000263341, 9606. ENSP00000292301, 9606. ENSP00000296871, 9606. ENSP00000305651, 9606. ENSP00000314807, 9606. ENSP00000330959, 9606. ENSP00000341268, 9606. ENSP00000357470, 9606. ENSP00000385675, 9606. ENSP00000398698, 9606. ENSP00000412237	CD4, TNFRSF1A, CCL2, IL10RA, IL1B, CCR2, CSF2, CXCL10, IL1RAP, IL1R2, TRADD, IL6R, IL6, TNF, IL10
GO:0031018	Endocrine pancreas development	2	39	1.68	0.0225	9606. ENSP00000357470, 9606. ENSP00000385675	IL6R, IL6
GO:0045058	T cell selection	2	40	1.67	0.0233	9606. ENSP00000011653, 9606. ENSP00000385675	CD4, IL6
GO:1902895	Positive regulation of pri-mirna transcription by rna polymerase ii	2	40	1.67	0.0233	9606. ENSP00000398698, 9606. ENSP00000412237	TNF, IL10
GO:1903053	Regulation of extracellular matrix organization	2	41	1.66	0.0242	9606. ENSP00000162749, 9606. ENSP00000385675	TNFRSF1A, IL6
GO:1904037	Positive regulation of epithelial cell apoptotic process	2	41	1.66	0.0242	9606. ENSP00000225831, 9606. ENSP00000385675	CCL2, IL6
GO:0045893	Positive regulation of transcription, dna-templated	7	1587	0.61	0.0243	9606. ENSP00000011653, 9606. ENSP00000162749, 9606. ENSP00000263341, 9606. ENSP00000305651, 9606. ENSP00000385675, 9606. ENSP00000398698, 9606. ENSP00000412237	CD4, TNFRSF1A, IL1B, CXCL10, IL6, TNF, IL10
GO:0030162	Regulation of proteolysis	5	747	0.79	0.0249	9606. ENSP00000263341, 9606. ENSP00000330959, 9606. ENSP00000341268, 9606. ENSP00000398698, 9606. ENSP00000412237	IL1B, IL1R2, TRADD, TNF, IL10
GO:0052372	Modulation by symbiont of entry into host	2	42	1.65	0.0249	9606. ENSP00000011653, 9606. ENSP00000306512	CD4, CXCL8
GO:0001937	Negative regulation of endothelial cell proliferation	2	43	1.64	0.0259	9606. ENSP00000225831, 9606. ENSP00000398698	CCL2, TNF

Table S4. the full list of KEGG analysis and GO analysis for CCL2

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0006897	Endocytosis	4	433	0.93	0.0265	9606.ENSP00000227752, 9606.ENSP00000295683, 9606.ENSP00000306512, 9606.ENSP00000319635	IL10RA, CXCR1, CXCL8, CXCR2
GO:0032715	Negative regulation of interleukin-6 production	2	44	1.63	0.0269	9606.ENSP00000398698, 9606.ENSP00000412237	TNF, IL10
GO:0045429	Positive regulation of nitric oxide biosynthetic process	2	44	1.63	0.0269	9606.ENSP00000263341, 9606.ENSP00000398698	IL1B, TNF
GO:1902115	Regulation of organelle assembly	3	191	1.17	0.0271	9606.ENSP00000296871, 9606.ENSP00000314807, 9606.ENSP00000398698	CSF2, IL1RAP, TNF
GO:0010556	Regulation of macromolecule biosynthetic process	11	3976	0.41	0.0273	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000314807, 9606.ENSP00000341268, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL1B, CSF2, CXCL10, IL1RAP, TRADD, IL6, TNF, IL10
GO:0031323	Regulation of cellular metabolic process	14	6239	0.32	0.0274	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000227752, 9606.ENSP00000263341, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000314807, 9606.ENSP00000330959, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL10RA, IL1B, CSF2, CXCL10, IL1RAP, IL1R2, TRADD, IL6R, IL6, TNF, IL10
GO:0050850	Positive regulation of calcium-mediated signaling	2	45	1.62	0.0278	9606.ENSP00000011653, 9606.ENSP00000398698	CD4, TNF
GO:0051051	Negative regulation of transport	4	443	0.92	0.0283	9606.ENSP00000162749, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000398698	TNFRSF1A, IL1B, CCR2, TNF
GO:0016032	Viral process	5	776	0.78	0.0285	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000292301, 9606.ENSP00000292303	CD4, TNFRSF1A, CCL2, CCR2, CCR5
GO:0050999	Regulation of nitric-oxide synthase activity	2	46	1.61	0.0287	9606.ENSP00000263341, 9606.ENSP00000398698	IL1B, TNF
GO:0050804	Modulation of chemical synaptic transmission	4	446	0.92	0.0288	9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000398698	CCL2, IL1B, CCR2, TNF
GO:0048568	Embryonic organ development	4	448	0.92	0.0291	9606.ENSP00000296871, 9606.ENSP00000306512, 9606.ENSP00000398698, 9606.ENSP00000412237	CSF2, CXCL8, TNF, IL10
GO:0010718	Positive regulation of epithelial to mesenchymal transition	2	47	1.6	0.0296	9606.ENSP00000263341, 9606.ENSP00000385675	IL1B, IL6
GO:1901888	Regulation of cell junction assembly	3	199	1.15	0.0296	9606.ENSP00000263341, 9606.ENSP00000314807, 9606.ENSP00000398698	IL1B, IL1RAP, TNF
GO:0045599	Negative regulation of fat cell differentiation	2	48	1.59	0.0305	9606.ENSP00000385675, 9606.ENSP00000398698	IL6, TNF
GO:0019058	Viral life cycle	3	202	1.14	0.0307	9606.ENSP00000011653, 9606.ENSP00000225831, 9606.ENSP00000292303	CD4, CCL2, CCR5
GO:0006355	Regulation of transcription, dna-templated	10	3388	0.44	0.0311	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000263341, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000314807, 9606.ENSP00000341268, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, IL1B, CSF2, CXCL10, IL1RAP, TRADD, IL6, TNF, IL10
GO:2000107	Negative regulation of leukocyte apoptotic process	2	49	1.58	0.0315	9606.ENSP00000292303, 9606.ENSP00000319635	CCR5, CXCR2
GO:2000351	Regulation of endothelial cell apoptotic process	2	50	1.57	0.0327	9606.ENSP00000225831, 9606.ENSP00000398698	CCL2, TNF
GO:0070374	Positive regulation of erk1 and erk2 cascade	3	209	1.13	0.0333	9606.ENSP00000011653, 9606.ENSP00000225831, 9606.ENSP00000398698	CD4, CCL2, TNF
GO:0045859	Regulation of protein kinase activity	5	812	0.76	0.0335	9606.ENSP00000011653, 9606.ENSP00000263341, 9606.ENSP00000305651, 9606.ENSP00000357470, 9606.ENSP00000398698	CD4, IL1B, CXCL10, IL6R, TNF
GO:0051607	Defense response to virus	3	210	1.12	0.0336	9606.ENSP00000290200, 9606.ENSP00000305651, 9606.ENSP00000385675	IL10RB, CXCL10, IL6
GO:0009612	Response to mechanical stimulus	3	212	1.12	0.0343	9606.ENSP00000162749, 9606.ENSP00000263341, 9606.ENSP00000305651	TNFRSF1A, IL1B, CXCL10
GO:0043523	Regulation of neuron apoptotic process	3	212	1.12	0.0343	9606.ENSP00000225831, 9606.ENSP00000398698, 9606.ENSP00000412237	CCL2, TNF, IL10
GO:0060255	Regulation of macromolecule metabolic process	14	6407	0.31	0.0345	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000314807, 9606.ENSP00000330959, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL1B, CCR2, CSF2, CXCL10, IL1RAP, IL1R2, TRADD, IL6R, IL6, TNF, IL10
GO:0042116	Macrophage activation	2	53	1.55	0.0354	9606.ENSP00000296871, 9606.ENSP00000398698	CSF2, TNF
GO:0045944	Positive regulation of transcription by rna polymerase ii	6	1253	0.65	0.0367	9606.ENSP00000162749, 9606.ENSP00000263341, 9606.ENSP00000305651, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	TNFRSF1A, IL1B, CXCL10, IL6, TNF, IL10
GO:0032757	Positive regulation of interleukin-8 production	2	55	1.53	0.0378	9606.ENSP00000263341, 9606.ENSP00000398698	IL1B, TNF
GO:0043030	Regulation of macrophage activation	2	55	1.53	0.0378	9606.ENSP00000385675, 9606.ENSP00000412237	IL6, IL10
GO:0002889	Regulation of immunoglobulin mediated immune response	2	56	1.52	0.0388	9606.ENSP00000398698, 9606.ENSP00000412237	TNF, IL10
GO:0042119	Neutrophil activation	4	497	0.87	0.0396	9606.ENSP00000295683, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000379110	CXCR1, CXCL8, CXCR2, CXCL1
GO:0010524	Positive regulation of calcium ion transport into cytosol	2	57	1.51	0.0398	9606.ENSP00000011653, 9606.ENSP00000305651	CD4, CXCL10
GO:0042063	Gliogenesis	3	228	1.09	0.0404	9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000398698	CCL2, IL1B, TNF
GO:0002763	Positive regulation of myeloid leukocyte differentiation	2	58	1.51	0.0408	9606.ENSP00000011653, 9606.ENSP00000398698	CD4, TNF
GO:0098609	Cell-cell adhesion	4	505	0.87	0.0413	9606.ENSP00000263341, 9606.ENSP00000292301, 9606.ENSP00000314807, 9606.ENSP00000398698	IL1B, CCR2, IL1RAP, TNF
GO:0045669	Positive regulation of osteoblast differentiation	2	60	1.49	0.0432	9606.ENSP00000357470, 9606.ENSP00000385675	IL6R, IL6
GO:0031329	Regulation of cellular catabolic process	5	875	0.73	0.0436	9606.ENSP00000227752, 9606.ENSP00000263341, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	IL10RA, IL1B, IL6, TNF, IL10
GO:0030098	Lymphocyte differentiation	3	242	1.06	0.0468	9606.ENSP00000011653, 9606.ENSP00000385675, 9606.ENSP00000412237	CD4, IL6, IL10

Table S4. the full list of KEGG analysis and GO analysis for CCL2

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0051171	Regulation of nitrogen compound metabolic process	13	5836	0.32	0.0497	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000314807, 9606.ENSP00000330959, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL1B, CSF2, CXCL10, IL1RAP, IL1R2, TRADD, IL6R, IL6, TNF, IL10
hsa04060	Cytokine-cytokine receptor interaction	19	282	1.8	1.36E-30	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000227752, 9606.ENSP00000263341, 9606.ENSP00000290200, 9606.ENSP00000292301, 9606.ENSP00000292303, 9606.ENSP00000295683, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000330959, 9606.ENSP00000357470, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, TNFRSF1A, CCL2, IL10RA, IL1B, IL10RB, CCR2, CCR5, CXCR1, CSF2, CXCL10, CXCL8, CXCR2, IL1R2, IL6R, CXCL1, IL6, TNF, IL10
hsa04061	Viral protein interaction with cytokine and cytokine receptor	15	96	2.16	6.61E-28	9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000227752, 9606.ENSP00000290200, 9606.ENSP00000292301, 9606.ENSP00000292303, 9606.ENSP00000295683, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000357470, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	TNFRSF1A, CCL2, IL10RA, IL10RB, CCR2, CCR5, CXCR1, CXCL10, CXCL8, CXCR2, IL6R, CXCL1, IL6, TNF, IL10
hsa05163	Human cytomegalovirus infection	12	218	1.71	1.54E-16	9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000227752, 9606.ENSP00000263341, 9606.ENSP00000290200, 9606.ENSP00000292303, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000341268, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698	TNFRSF1A, CCL2, IL10RA, IL1B, IL10RB, CCR5, CXCL8, CXCR2, TRADD, IL6R, IL6, TNF
hsa04657	IL-17 signaling pathway	9	92	1.96	4.20E-14	9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000341268, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698	CCL2, IL1B, CSF2, CXCL10, CXCL8, TRADD, CXCL1, IL6, TNF
hsa04668	TNF signaling pathway	9	112	1.87	1.80E-13	9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000296871, 9606.ENSP00000305651, 9606.ENSP00000341268, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698	TNFRSF1A, CCL2, IL1B, CSF2, CXCL10, TRADD, CXCL1, IL6, TNF
hsa05146	Amoebiasis	8	100	1.87	7.05E-12	9606.ENSP00000263341, 9606.ENSP00000296871, 9606.ENSP00000306512, 9606.ENSP00000330959, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	IL1B, CSF2, CXCL8, IL1R2, CXCL1, IL6, TNF, IL10
hsa05323	Rheumatoid arthritis	7	85	1.88	2.11E-10	9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000296871, 9606.ENSP00000306512, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698	CCL2, IL1B, CSF2, CXCL8, CXCL1, IL6, TNF
hsa05164	Influenza A	8	165	1.65	2.44E-10	9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000341268, 9606.ENSP00000385675, 9606.ENSP00000398698	TNFRSF1A, CCL2, IL1B, CXCL10, CXCL8, TRADD, IL6, TNF
hsa04640	Hematopoietic cell lineage	7	91	1.86	2.49E-10	9606.ENSP00000011653, 9606.ENSP00000263341, 9606.ENSP00000296871, 9606.ENSP00000330959, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698	CD4, IL1B, CSF2, IL1R2, IL6R, IL6, TNF
hsa05152	Tuberculosis	8	168	1.65	2.49E-10	9606.ENSP00000162749, 9606.ENSP00000227752, 9606.ENSP00000263341, 9606.ENSP00000290200, 9606.ENSP00000341268, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	TNFRSF1A, IL10RA, IL1B, IL10RB, TRADD, IL6, TNF, IL10
hsa05142	Chagas disease	7	99	1.82	3.71E-10	9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000306512, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	TNFRSF1A, CCL2, IL1B, CXCL8, IL6, TNF, IL10
hsa04062	Chemokine signaling pathway	8	186	1.6	3.83E-10	9606.ENSP00000225831, 9606.ENSP00000292301, 9606.ENSP00000292303, 9606.ENSP00000295683, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000379110	CCL2, CCR2, CCR5, CXCR1, CXCL10, CXCL8, CXCR2, CXCL1
hsa05144	Malaria	6	46	2.08	3.83E-10	9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000306512, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CCL2, IL1B, CXCL8, IL6, TNF, IL10
hsa05135	Yersinia infection	7	125	1.72	1.39E-09	9606.ENSP00000011653, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000306512, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, CCL2, IL1B, CXCL8, IL6, TNF, IL10
hsa05167	Kaposi sarcoma-associated herpesvirus infection	7	187	1.54	1.94E-08	9606.ENSP00000162749, 9606.ENSP00000292303, 9606.ENSP00000296871, 9606.ENSP00000306512, 9606.ENSP00000341268, 9606.ENSP00000379110, 9606.ENSP00000385675	TNFRSF1A, CCR5, CSF2, CXCL8, TRADD, CXCL1, IL6
hsa04064	NF-kappa B signaling pathway	6	101	1.74	2.46E-08	9606.ENSP00000162749, 9606.ENSP00000263341, 9606.ENSP00000306512, 9606.ENSP00000341268, 9606.ENSP00000379110, 9606.ENSP00000398698	TNFRSF1A, IL1B, CXCL8, TRADD, CXCL1, TNF
hsa05145	Toxoplasmosis	6	105	1.73	2.89E-08	9606.ENSP00000162749, 9606.ENSP00000227752, 9606.ENSP00000290200, 9606.ENSP00000292303, 9606.ENSP00000398698, 9606.ENSP00000412237	TNFRSF1A, IL10RA, IL10RB, CCR5, TNF, IL10
hsa05134	Legionellosis	5	55	1.93	8.32E-08	9606.ENSP00000263341, 9606.ENSP00000306512, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698	IL1B, CXCL8, CXCL1, IL6, TNF

Table S4. the full list of KEGG analysis and GO analysis for CCL2

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
hsa04932	Non-alcoholic fatty liver disease	6	148	1.58	1.86E-07	9606.ENSP00000162749, 9606.ENSP00000263341, 9606.ENSP00000306512, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000398698	TNFRSF1A, IL1B, CXCL8, IL6R, IL6, TNF
hsa04630	JAK-STAT signaling pathway	6	160	1.54	2.78E-07	9606.ENSP00000227752, 9606.ENSP00000290200, 9606.ENSP00000296871, 9606.ENSP00000357470, 9606.ENSP00000385675, 9606.ENSP00000412237	IL10RA, IL10RB, CSF2, IL6R, IL6, IL10
hsa05133	Pertussis	5	74	1.8	2.91E-07	9606.ENSP00000263341, 9606.ENSP00000306512, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	IL1B, CXCL8, IL6, TNF, IL10
hsa04621	NOD-like receptor signaling pathway	6	174	1.51	4.10E-07	9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000306512, 9606.ENSP00000379110, 9606.ENSP00000385675, 9606.ENSP00000398698	CCL2, IL1B, CXCL8, CXCL1, IL6, TNF
hsa05130	Pathogenic Escherichia coli infection	6	187	1.48	5.93E-07	9606.ENSP00000162749, 9606.ENSP00000263341, 9606.ENSP00000306512, 9606.ENSP00000341268, 9606.ENSP00000385675, 9606.ENSP00000398698	TNFRSF1A, IL1B, CXCL8, TRADD, IL6, TNF
hsa04933	AGE-RAGE signaling pathway in diabetic complications	5	98	1.68	9.71E-07	9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000306512, 9606.ENSP00000385675, 9606.ENSP00000398698	CCL2, IL1B, CXCL8, IL6, TNF
hsa04620	Toll-like receptor signaling pathway	5	101	1.66	1.04E-06	9606.ENSP00000263341, 9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000385675, 9606.ENSP00000398698	IL1B, CXCL10, CXCL8, IL6, TNF
hsa05132	Salmonella infection	6	209	1.43	1.04E-06	9606.ENSP00000162749, 9606.ENSP00000263341, 9606.ENSP00000306512, 9606.ENSP00000341268, 9606.ENSP00000385675, 9606.ENSP00000398698	TNFRSF1A, IL1B, CXCL8, TRADD, IL6, TNF
hsa05143	African trypanosomiasis	4	36	2.02	1.04E-06	9606.ENSP00000263341, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	IL1B, IL6, TNF, IL10
hsa05166	Human T-cell leukemia virus 1 infection	6	211	1.42	1.04E-06	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000296871, 9606.ENSP00000330959, 9606.ENSP00000385675, 9606.ENSP00000398698	CD4, TNFRSF1A, CSF2, IL1R2, IL6, TNF
hsa05131	Shigellosis	6	218	1.41	1.14E-06	9606.ENSP00000162749, 9606.ENSP00000263341, 9606.ENSP00000296871, 9606.ENSP00000306512, 9606.ENSP00000341268, 9606.ENSP00000398698	TNFRSF1A, IL1B, CSF2, CXCL8, TRADD, TNF
hsa05418	Fluid shear stress and atherosclerosis	5	130	1.55	3.01E-06	9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000330959, 9606.ENSP00000398698	TNFRSF1A, CCL2, IL1B, IL1R2, TNF
hsa05321	Inflammatory bowel disease	4	60	1.79	6.45E-06	9606.ENSP00000263341, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	IL1B, IL6, TNF, IL10
hsa05120	Epithelial cell signaling in Helicobacter pylori infection	4	67	1.75	9.51E-06	9606.ENSP00000295683, 9606.ENSP00000306512, 9606.ENSP00000319635, 9606.ENSP00000379110	CXCR1, CXCL8, CXCR2, CXCL1
hsa04622	RIG-I-like receptor signaling pathway	4	70	1.73	1.09E-05	9606.ENSP00000305651, 9606.ENSP00000306512, 9606.ENSP00000341268, 9606.ENSP00000398698	CXCL10, CXCL8, TRADD, TNF
hsa05170	Human immunodeficiency virus 1 infection	5	204	1.36	2.31E-05	9606.ENSP00000011653, 9606.ENSP00000162749, 9606.ENSP00000292303, 9606.ENSP00000341268, 9606.ENSP00000398698	CD4, TNFRSF1A, CCR5, TRADD, TNF
hsa04625	C-type lectin receptor signaling pathway	4	102	1.56	4.18E-05	9606.ENSP00000263341, 9606.ENSP00000385675, 9606.ENSP00000398698, 9606.ENSP00000412237	IL1B, IL6, TNF, IL10
hsa04659	Th17 cell differentiation	4	101	1.57	4.18E-05	9606.ENSP00000011653, 9606.ENSP00000263341, 9606.ENSP00000357470, 9606.ENSP00000385675	CD4, IL1B, IL6R, IL6
hsa04660	T cell receptor signaling pathway	4	101	1.57	4.18E-05	9606.ENSP00000011653, 9606.ENSP00000296871, 9606.ENSP00000398698, 9606.ENSP00000412237	CD4, CSF2, TNF, IL10
hsa01523	Antifolate resistance	3	31	1.96	5.50E-05	9606.ENSP00000263341, 9606.ENSP00000385675, 9606.ENSP00000398698	IL1B, IL6, TNF
hsa05168	Herpes simplex virus 1 infection	6	479	1.07	7.61E-05	9606.ENSP00000162749, 9606.ENSP00000225831, 9606.ENSP00000263341, 9606.ENSP00000341268, 9606.ENSP00000385675, 9606.ENSP00000398698	TNFRSF1A, CCL2, IL1B, TRADD, IL6, TNF
hsa05332	Graft-versus-host disease	3	36	1.89	7.95E-05	9606.ENSP00000263341, 9606.ENSP00000385675, 9606.ENSP00000398698	IL1B, IL6, TNF
hsa04217	Necroptosis	4	149	1.4	0.00016	9606.ENSP00000162749, 9606.ENSP00000263341, 9606.ENSP00000341268, 9606.ENSP00000398698	TNFRSF1A, IL1B, TRADD, TNF
hsa05160	Hepatitis C	4	156	1.38	0.00018	9606.ENSP00000162749, 9606.ENSP00000305651, 9606.ENSP00000341268, 9606.ENSP00000398698	TNFRSF1A, CXCL10, TRADD, TNF
hsa05202	Transcriptional misregulation in cancer	4	171	1.34	0.00026	9606.ENSP00000296871, 9606.ENSP00000306512, 9606.ENSP00000330959, 9606.ENSP00000385675	CSF2, CXCL8, IL1R2, IL6
hsa04623	Cytosolic DNA-sensing pathway	3	62	1.65	0.00034	9606.ENSP00000263341, 9606.ENSP00000305651, 9606.ENSP00000385675	IL1B, CXCL10, IL6
hsa05169	Epstein-Barr virus infection	4	193	1.29	0.00039	9606.ENSP00000305651, 9606.ENSP00000341268, 9606.ENSP00000385675, 9606.ENSP00000398698	CXCL10, TRADD, IL6, TNF
hsa04920	Adipocytokine signaling pathway	3	69	1.61	0.00044	9606.ENSP00000162749, 9606.ENSP00000341268, 9606.ENSP00000398698	TNFRSF1A, TRADD, TNF
hsa05140	Leishmaniasis	3	70	1.6	0.00045	9606.ENSP00000263341, 9606.ENSP00000398698, 9606.ENSP00000412237	IL1B, TNF, IL10
hsa04931	Insulin resistance	3	107	1.42	0.0015	9606.ENSP00000162749, 9606.ENSP00000385675, 9606.ENSP00000398698	TNFRSF1A, IL6, TNF
hsa04010	MAPK signaling pathway	4	288	1.11	0.0016	9606.ENSP00000162749, 9606.ENSP00000263341, 9606.ENSP00000341268, 9606.ENSP00000398698	TNFRSF1A, IL1B, TRADD, TNF
hsa04071	Sphingolipid signaling pathway	3	116	1.38	0.0018	9606.ENSP00000162749, 9606.ENSP00000341268, 9606.ENSP00000398698	TNFRSF1A, TRADD, TNF
hsa04380	Osteoclast differentiation	3	122	1.36	0.002	9606.ENSP00000162749, 9606.ENSP00000263341, 9606.ENSP00000398698	TNFRSF1A, IL1B, TNF
hsa04210	Apoptosis	3	132	1.33	0.0025	9606.ENSP00000162749, 9606.ENSP00000341268, 9606.ENSP00000398698	TNFRSF1A, TRADD, TNF

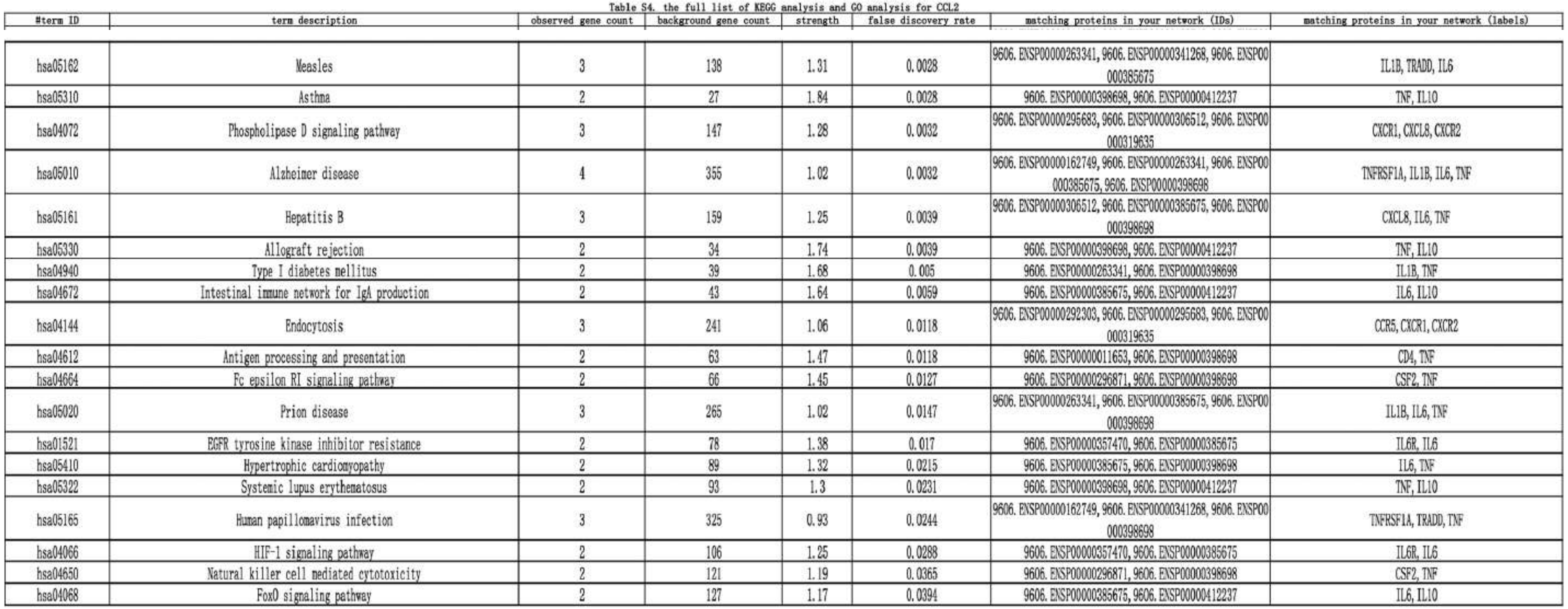


Table S4. the full list of KEGG analysis and GO analysis for CCL2

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
hsa05162	Measles	3	138	1.31	0.0028	9606. ENSP00000263341, 9606. ENSP00000341268, 9606. ENSP00000385675	IL1B, TRADD, IL6
hsa05310	Asthma	2	27	1.84	0.0028	9606. ENSP00000398698, 9606. ENSP00000412237	TNF, IL10
hsa04072	Phospholipase D signaling pathway	3	147	1.28	0.0032	9606. ENSP00000295683, 9606. ENSP00000306512, 9606. ENSP00000319635	CXCR1, CXCL8, CXCR2
hsa05010	Alzheimer disease	4	355	1.02	0.0032	9606. ENSP00000162749, 9606. ENSP00000263341, 9606. ENSP00000385675, 9606. ENSP00000398698	TNFRSF1A, IL1B, IL6, TNF
hsa05161	Hepatitis B	3	159	1.25	0.0039	9606. ENSP00000306512, 9606. ENSP00000385675, 9606. ENSP00000398698	CXCL8, IL6, TNF
hsa05330	Allograft rejection	2	34	1.74	0.0039	9606. ENSP00000398698, 9606. ENSP00000412237	TNF, IL10
hsa04940	Type I diabetes mellitus	2	39	1.68	0.005	9606. ENSP00000263341, 9606. ENSP00000398698	IL1B, TNF
hsa04672	Intestinal immune network for IgA production	2	43	1.64	0.0059	9606. ENSP00000385675, 9606. ENSP00000412237	IL6, IL10
hsa04144	Endocytosis	3	241	1.06	0.0118	9606. ENSP00000292303, 9606. ENSP00000295683, 9606. ENSP00000319635	CCR5, CXCR1, CXCR2
hsa04612	Antigen processing and presentation	2	63	1.47	0.0118	9606. ENSP00000011653, 9606. ENSP00000398698	CD4, TNF
hsa04664	Fc epsilon RI signaling pathway	2	66	1.45	0.0127	9606. ENSP00000296871, 9606. ENSP00000398698	CSF2, TNF
hsa05020	Prion disease	3	265	1.02	0.0147	9606. ENSP00000263341, 9606. ENSP00000385675, 9606. ENSP00000398698	IL1B, IL6, TNF
hsa01521	EGFR tyrosine kinase inhibitor resistance	2	78	1.38	0.017	9606. ENSP00000357470, 9606. ENSP00000385675	IL6R, IL6
hsa05410	Hypertrophic cardiomyopathy	2	89	1.32	0.0215	9606. ENSP00000385675, 9606. ENSP00000398698	IL6, TNF
hsa05322	Systemic lupus erythematosus	2	93	1.3	0.0231	9606. ENSP00000398698, 9606. ENSP00000412237	TNF, IL10
hsa05165	Human papillomavirus infection	3	325	0.93	0.0244	9606. ENSP00000162749, 9606. ENSP00000341268, 9606. ENSP00000398698	TNFRSF1A, TRADD, TNF
hsa04066	HIF-1 signaling pathway	2	106	1.25	0.0288	9606. ENSP00000357470, 9606. ENSP00000385675	IL6R, IL6
hsa04650	Natural killer cell mediated cytotoxicity	2	121	1.19	0.0365	9606. ENSP00000296871, 9606. ENSP00000398698	CSF2, TNF
hsa04068	FoxO signaling pathway	2	127	1.17	0.0394	9606. ENSP00000385675, 9606. ENSP00000412237	IL6, IL10

Table S5. the full list of KEGG analysis and GO analysis for RND3

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0007264	Small gtpase mediated signal transduction	10	316	1.47	5.48E-09	9606.ENSP00000172229, 9606.ENSP00000269321, 9606.ENSP00000308461, 9606.ENSP00000317985, 9606.ENSP00000348461, 9606.ENSP00000364886, 9606.ENSP00000371897, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000400175	NGFR, ARHGDIA, RND1, ROCK2, RAC1, RND3, ARHGAP5, ROCK1, CDC42, RHOA
GO:0007266	Rho protein signal transduction	7	62	2.02	5.48E-09	9606.ENSP00000172229, 9606.ENSP00000269321, 9606.ENSP00000317985, 9606.ENSP00000371897, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000400175	NGFR, ARHGDIA, ROCK2, ARHGAP5, ROCK1, CDC42, RHOA
GO:0035556	Intracellular signal transduction	15	1712	0.91	1.99E-08	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000269321, 9606.ENSP00000274376, 9606.ENSP00000308461, 9606.ENSP00000317985, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000364886, 9606.ENSP00000371897, 9606.ENSP00000379287, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385824, 9606.ENSP00000400175	NGFR, RAF1, ARHGDIA, RASA1, RND1, ROCK2, RAC1, PLXNB1, RND3, ARHGAP5, YWHAZ, ROCK1, CDC42, FOXO3, RHOA
GO:0007165	Signal transduction	20	4876	0.58	4.53E-08	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000269321, 9606.ENSP00000274376, 9606.ENSP00000308461, 9606.ENSP00000317985, 9606.ENSP00000329380, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000364886, 9606.ENSP00000371897, 9606.ENSP00000379287, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000385824, 9606.ENSP00000400175, 9606.ENSP00000409171, 9606.ENSP00000439625	NGFR, RAF1, ARHGDIA, RASA1, RND1, ROCK2, RAC1, PLXNB1, RND3, ARHGAP5, YWHAZ, ROCK1, CDC42, FOXO3, RHOA
GO:0051056	Regulation of small gtpase mediated signal transduction	9	320	1.42	6.04E-08	9606.ENSP00000251849, 9606.ENSP00000269321, 9606.ENSP00000274376, 9606.ENSP00000348461, 9606.ENSP00000371897, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000400175, 9606.ENSP00000439625	RAF1, ARHGDIA, RASA1, RAC1, ARHGAP5, CDC42, ARHGAP35, RHOA, PLEKHG5
GO:0060284	Regulation of cell development	12	956	1.07	8.27E-08	9606.ENSP00000172229, 9606.ENSP00000269321, 9606.ENSP00000317985, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000385824, 9606.ENSP00000400175, 9606.ENSP00000409171	NGFR, ARHGDIA, ROCK2, CTNNB1, RAC1, PLXNB1, ROCK1, CDC42, ARHGAP35, FOXO3, RHOA, PLXNB2
GO:0007265	Ras protein signal transduction	8	230	1.51	1.20E-07	9606.ENSP00000172229, 9606.ENSP00000269321, 9606.ENSP00000317985, 9606.ENSP00000348461, 9606.ENSP00000371897, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000400175	NGFR, ARHGDIA, ROCK2, RAC1, ARHGAP5, ROCK1, CDC42, RHOA
GO:0051493	Regulation of cytoskeleton organization	10	546	1.23	1.20E-07	9606.ENSP00000269321, 9606.ENSP00000274376, 9606.ENSP00000317985, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000400175	ARHGDIA, RASA1, ROCK2, CTNNB1, RAC1, PLXNB1, ROCK1, CDC42, ARHGAP35, RHOA
GO:0050793	Regulation of developmental process	16	2648	0.75	1.59E-07	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000269321, 9606.ENSP00000274376, 9606.ENSP00000317985, 9606.ENSP00000329380, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000379287, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000385824, 9606.ENSP00000400175, 9606.ENSP00000409171	NGFR, RAF1, ARHGDIA, RASA1, ROCK2, GP1BA, CTNNB1, RAC1, PLXNB1, YWHAZ, ROCK1, CDC42, ARHGAP35, FOXO3, RHOA, PLXNB2
GO:0022603	Regulation of anatomical structure morphogenesis	12	1095	1.01	1.96E-07	9606.ENSP00000172229, 9606.ENSP00000269321, 9606.ENSP00000274376, 9606.ENSP00000317985, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000400175, 9606.ENSP00000409171	NGFR, ARHGDIA, RASA1, ROCK2, CTNNB1, RAC1, PLXNB1, ROCK1, CDC42, ARHGAP35, RHOA, PLXNB2
GO:0048666	Neuron development	11	827	1.09	1.96E-07	9606.ENSP00000172229, 9606.ENSP00000308461, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000379287, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000400175, 9606.ENSP00000409171	NGFR, RND1, CTNNB1, RAC1, PLXNB1, YWHAZ, ROCK1, CDC42, ARHGAP35, RHOA, PLXNB2

Table S5. the full list of KEGG analysis and GO analysis for RND3

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:1902531	Regulation of intracellular signal transduction	14	1807	0.86	1.96E-07	9606.ENSP00000251849, 9606.ENSP00000269321, 9606.ENSP00000274376, 9606.ENSP00000317985, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000371897, 9606.ENSP00000379287, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000400175, 9606.ENSP00000439625	RAF1, ARHGDIA, RASA1, ROCK2, CTNNB1, RAC1, PLXNB1, ARHGAP5, YWHAZ, ROCK1, CDC42, ARHGAP35, RHOA, PLEKHG5
GO:0010770	Positive regulation of cell morphogenesis involved in differentiation	7	159	1.61	2.49E-07	9606.ENSP00000172229, 9606.ENSP00000269321, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000383118, 9606.ENSP00000400175, 9606.ENSP00000409171	NGFR, ARHGDIA, RAC1, PLXNB1, CDC42, RHOA, PLXNB2
GO:0045595	Regulation of cell differentiation	14	1874	0.84	2.78E-07	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000269321, 9606.ENSP00000317985, 9606.ENSP00000329380, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000385824, 9606.ENSP00000400175, 9606.ENSP00000409171	NGFR, RAF1, ARHGDIA, ROCK2, GP1BA, CTNNB1, RAC1, PLXNB1, ROCK1, CDC42, ARHGAP35, FOXO3, RHOA, PLXNB2
GO:0007166	Cell surface receptor signaling pathway	15	2325	0.78	2.80E-07	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000269321, 9606.ENSP00000274376, 9606.ENSP00000317985, 9606.ENSP00000329380, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000379287, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385824, 9606.ENSP00000400175, 9606.ENSP00000409171	NGFR, RAF1, ARHGDIA, RASA1, ROCK2, GP1BA, CTNNB1, RAC1, PLXNB1, YWHAZ, ROCK1, CDC42, FOXO3, RHOA, PLXNB2
GO:0048013	Ephrin receptor signaling pathway	6	86	1.81	3.33E-07	9606.ENSP00000274376, 9606.ENSP00000317985, 9606.ENSP00000348461, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000400175	RASA1, ROCK2, RAC1, ROCK1, CDC42, RHOA
GO:0048699	Generation of neurons	13	1551	0.89	3.83E-07	9606.ENSP00000172229, 9606.ENSP00000269321, 9606.ENSP00000308461, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000379287, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000385824, 9606.ENSP00000400175, 9606.ENSP00000409171	NGFR, ARHGDIA, RND1, CTNNB1, RAC1, PLXNB1, YWHAZ, ROCK1, CDC42, ARHGAP35, FOXO3, RHOA, PLXNB2
GO:0051130	Positive regulation of cellular component organization	12	1209	0.97	3.83E-07	9606.ENSP00000172229, 9606.ENSP00000269321, 9606.ENSP00000317985, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000379287, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000400175, 9606.ENSP00000409171	NGFR, ARHGDIA, ROCK2, CTNNB1, RAC1, PLXNB1, YWHAZ, ROCK1, CDC42, ARHGAP35, RHOA, PLXNB2
GO:0010769	Regulation of cell morphogenesis involved in differentiation	8	309	1.38	4.47E-07	9606.ENSP00000172229, 9606.ENSP00000269321, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000400175, 9606.ENSP00000409171	NGFR, ARHGDIA, RAC1, PLXNB1, CDC42, ARHGAP35, RHOA, PLXNB2
GO:0022604	Regulation of cell morphogenesis	9	498	1.23	6.01E-07	9606.ENSP00000172229, 9606.ENSP00000269321, 9606.ENSP00000274376, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000400175, 9606.ENSP00000409171	NGFR, ARHGDIA, RASA1, RAC1, PLXNB1, CDC42, ARHGAP35, RHOA, PLXNB2
GO:0030155	Regulation of cell adhesion	10	712	1.12	6.01E-07	9606.ENSP00000269321, 9606.ENSP00000274376, 9606.ENSP00000308461, 9606.ENSP00000317985, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000400175, 9606.ENSP00000409171	ARHGDIA, RASA1, RND1, ROCK2, RAC1, PLXNB1, ROCK1, CDC42, RHOA, PLXNB2
GO:0048812	Neuron projection morphogenesis	9	495	1.23	6.01E-07	9606.ENSP00000172229, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000400175, 9606.ENSP00000409171	NGFR, CTNNB1, RAC1, PLXNB1, ROCK1, CDC42, ARHGAP35, RHOA, PLXNB2
GO:0000902	Cell morphogenesis	10	726	1.11	6.07E-07	9606.ENSP00000172229, 9606.ENSP00000329380, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000400175, 9606.ENSP00000409171	NGFR, GP1BA, CTNNB1, RAC1, PLXNB1, ROCK1, CDC42, ARHGAP35, RHOA, PLXNB2
GO:0007169	Transmembrane receptor protein tyrosine kinase signaling pathway	9	518	1.21	6.73E-07	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000274376, 9606.ENSP00000317985, 9606.ENSP00000348461, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385824, 9606.ENSP00000400175	NGFR, RAF1, RASA1, ROCK2, RAC1, ROCK1, CDC42, FOXO3, RHOA

Table S5. the full list of KEGG analysis and GO analysis for RND3

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0009966	Regulation of signal transduction	16	3107	0.68	6.73E-07	9606.ENSP0000172229, 9606.ENSP0000251849, 9606.ENSP0000269321, 9606.ENSP0000274376, 9606.ENSP0000317985, 9606.ENSP0000344456, 9606.ENSP0000348461, 9606.ENSP0000351338, 9606.ENSP0000371897, 9606.ENSP0000379287, 9606.ENSP0000382697, 9606.ENSP0000383118, 9606.ENSP0000385720, 9606.ENSP0000385824, 9606.ENSP0000400175, 9606.ENSP0000439625	NGFR, RAF1, ARHGDIA, RASA1, ROCK2, CTNNB1, RAC1, PLXNB1, ARHGAP5, YWHAZ, ROCK1, CDC42, ARHGAP35, FOXO3, RHOA, PLEKHG5
GO:2000026	Regulation of multicellular organismal development	14	2096	0.79	6.73E-07	9606.ENSP0000172229, 9606.ENSP0000269321, 9606.ENSP0000317985, 9606.ENSP0000329380, 9606.ENSP0000344456, 9606.ENSP0000348461, 9606.ENSP0000351338, 9606.ENSP0000379287, 9606.ENSP0000382697, 9606.ENSP0000383118, 9606.ENSP0000385720, 9606.ENSP0000385824, 9606.ENSP0000400175, 9606.ENSP0000409171	NGFR, ARHGDIA, ROCK2, GP1BA, CTNNB1, RAC1, PLXNB1, YWHAZ, ROCK1, CDC42, ARHGAP35, FOXO3, RHOA, PLXNB2
GO:0032956	Regulation of actin cytoskeleton organization	8	348	1.33	6.89E-07	9606.ENSP0000269321, 9606.ENSP0000274376, 9606.ENSP0000317985, 9606.ENSP0000348461, 9606.ENSP0000382697, 9606.ENSP0000383118, 9606.ENSP0000385720, 9606.ENSP0000400175	ARHGDIA, RASA1, ROCK2, RAC1, ROCK1, CDC42, ARHGAP35, RHOA
GO:0009653	Anatomical structure morphogenesis	14	2165	0.78	8.54E-07	9606.ENSP0000172229, 9606.ENSP0000274376, 9606.ENSP0000317985, 9606.ENSP0000329380, 9606.ENSP0000344456, 9606.ENSP0000348461, 9606.ENSP0000351338, 9606.ENSP0000379287, 9606.ENSP0000382697, 9606.ENSP0000383118, 9606.ENSP0000385720, 9606.ENSP0000385824, 9606.ENSP0000400175, 9606.ENSP0000409171	NGFR, RASA1, ROCK2, GP1BA, CTNNB1, RAC1, PLXNB1, YWHAZ, ROCK1, CDC42, ARHGAP35, FOXO3, RHOA, PLXNB2
GO:0010720	Positive regulation of cell development	9	556	1.18	9.99E-07	9606.ENSP0000172229, 9606.ENSP0000269321, 9606.ENSP0000344456, 9606.ENSP0000348461, 9606.ENSP0000351338, 9606.ENSP0000383118, 9606.ENSP0000385720, 9606.ENSP0000400175, 9606.ENSP0000409171	NGFR, ARHGDIA, CTNNB1, RAC1, PLXNB1, CDC42, ARHGAP35, RHOA, PLXNB2
GO:0000904	Cell morphogenesis involved in differentiation	9	566	1.17	1.13E-06	9606.ENSP0000172229, 9606.ENSP0000344456, 9606.ENSP0000348461, 9606.ENSP0000351338, 9606.ENSP0000382697, 9606.ENSP0000383118, 9606.ENSP0000385720, 9606.ENSP0000400175, 9606.ENSP0000409171	NGFR, CTNNB1, RAC1, PLXNB1, ROCK1, CDC42, ARHGAP35, RHOA, PLXNB2
GO:0031346	Positive regulation of cell projection organization	8	391	1.28	1.44E-06	9606.ENSP0000172229, 9606.ENSP0000269321, 9606.ENSP0000348461, 9606.ENSP0000351338, 9606.ENSP0000383118, 9606.ENSP0000385720, 9606.ENSP0000400175, 9606.ENSP0000409171	NGFR, ARHGDIA, RAC1, PLXNB1, CDC42, ARHGAP35, RHOA, PLXNB2
GO:0048583	Regulation of response to stimulus	17	4114	0.59	2.38E-06	9606.ENSP0000172229, 9606.ENSP0000251849, 9606.ENSP0000269321, 9606.ENSP0000274376, 9606.ENSP0000317985, 9606.ENSP0000329380, 9606.ENSP0000344456, 9606.ENSP0000348461, 9606.ENSP0000351338, 9606.ENSP0000371897, 9606.ENSP0000379287, 9606.ENSP0000382697, 9606.ENSP0000383118, 9606.ENSP0000385720, 9606.ENSP0000385824, 9606.ENSP0000400175, 9606.ENSP0000439625	NGFR, RAF1, ARHGDIA, RASA1, ROCK2, GP1BA, CTNNB1, RAC1, PLXNB1, ARHGAP5, YWHAZ, ROCK1, CDC42, ARHGAP35, FOXO3, RHOA, PLEKHG5
GO:0051128	Regulation of cellular component organization	14	2402	0.73	2.71E-06	9606.ENSP0000172229, 9606.ENSP0000251849, 9606.ENSP0000269321, 9606.ENSP0000274376, 9606.ENSP0000317985, 9606.ENSP0000344456, 9606.ENSP0000348461, 9606.ENSP0000351338, 9606.ENSP0000379287, 9606.ENSP0000382697, 9606.ENSP0000383118, 9606.ENSP0000385720, 9606.ENSP0000400175, 9606.ENSP0000409171	NGFR, RAF1, ARHGDIA, RASA1, ROCK2, CTNNB1, RAC1, PLXNB1, YWHAZ, ROCK1, CDC42, ARHGAP35, RHOA, PLXNB2
GO:0110053	Regulation of actin filament organization	7	273	1.38	3.17E-06	9606.ENSP0000274376, 9606.ENSP0000317985, 9606.ENSP0000348461, 9606.ENSP0000382697, 9606.ENSP0000383118, 9606.ENSP0000385720, 9606.ENSP0000400175	RASA1, ROCK2, RAC1, ROCK1, CDC42, ARHGAP35, RHOA
GO:0008360	Regulation of cell shape	6	153	1.56	3.49E-06	9606.ENSP0000274376, 9606.ENSP0000348461, 9606.ENSP0000351338, 9606.ENSP0000383118, 9606.ENSP0000385720, 9606.ENSP0000409171	RASA1, RAC1, PLXNB1, CDC42, ARHGAP35, PLXNB2
GO:0048010	Vascular endothelial growth factor receptor signaling pathway	5	69	1.83	3.49E-06	9606.ENSP0000317985, 9606.ENSP0000348461, 9606.ENSP0000382697, 9606.ENSP0000383118, 9606.ENSP0000400175	ROCK2, RAC1, ROCK1, CDC42, RHOA
GO:0051960	Regulation of nervous system development	10	942	1	3.98E-06	9606.ENSP0000172229, 9606.ENSP0000269321, 9606.ENSP0000344456, 9606.ENSP0000351338, 9606.ENSP0000379287, 9606.ENSP0000382697, 9606.ENSP0000385720, 9606.ENSP0000385824, 9606.ENSP0000400175, 9606.ENSP0000409171	NGFR, ARHGDIA, CTNNB1, PLXNB1, YWHAZ, ROCK1, ARHGAP35, FOXO3, RHOA, PLXNB2

Table S5. the full list of KEGG analysis and GO analysis for RND3

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0048468	Cell development	12	1629	0.84	4.16E-06	9606. ENSP00000172229, 9606. ENSP00000308461, 9606. ENSP00000344456, 9606. ENSP00000348461, 9606. ENSP00000351338, 9606. ENSP00000379287, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000385720, 9606. ENSP00000385824, 9606. ENSP00000400175, 9606. ENSP00000409171	NGFR, RND1, CTNNB1, RAC1, PLXNB1, YWHAZ, ROCK1, CDC42, ARHGAP35, FOXO3, RHOA, PLXNB2
GO:0051336	Regulation of hydrolase activity	11	1284	0.9	4.76E-06	9606. ENSP00000172229, 9606. ENSP00000251849, 9606. ENSP00000269321, 9606. ENSP00000274376, 9606. ENSP00000317985, 9606. ENSP00000351338, 9606. ENSP00000371897, 9606. ENSP00000382697, 9606. ENSP00000385720, 9606. ENSP00000400175, 9606. ENSP00000409171	NGFR, RAF1, ARHGDIA, RASA1, ROCK2, PLXNB1, ARHGAP5, ROCK1, ARHGAP35, RHOA, PLXNB2
GO:0033043	Regulation of organelle organization	11	1306	0.89	5.56E-06	9606. ENSP00000269321, 9606. ENSP00000274376, 9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000348461, 9606. ENSP00000351338, 9606. ENSP00000379287, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000385720, 9606. ENSP00000400175	ARHGDIA, RASA1, ROCK2, CTNNB1, RAC1, PLXNB1, YWHAZ, ROCK1, CDC42, ARHGAP35, RHOA
GO:0045597	Positive regulation of cell differentiation	10	993	0.97	5.94E-06	9606. ENSP00000172229, 9606. ENSP00000269321, 9606. ENSP00000344456, 9606. ENSP00000348461, 9606. ENSP00000351338, 9606. ENSP00000383118, 9606. ENSP00000385720, 9606. ENSP00000385824, 9606. ENSP00000400175, 9606. ENSP00000409171	NGFR, ARHGDIA, CTNNB1, RAC1, PLXNB1, CDC42, ARHGAP35, FOXO3, RHOA, PLXNB2
GO:0048731	System development	17	4426	0.55	5.94E-06	9606. ENSP00000172229, 9606. ENSP00000251849, 9606. ENSP00000269321, 9606. ENSP00000274376, 9606. ENSP00000308461, 9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000348461, 9606. ENSP00000351338, 9606. ENSP00000371897, 9606. ENSP00000379287, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000385720, 9606. ENSP00000385824, 9606. ENSP00000400175, 9606. ENSP00000409171	NGFR, RAF1, ARHGDIA, RASA1, RND1, ROCK2, CTNNB1, RAC1, PLXNB1, ARHGAP5, YWHAZ, ROCK1, CDC42, ARHGAP35, FOXO3, RHOA, PLXNB2
GO:0030036	Actin cytoskeleton organization	8	516	1.16	8.40E-06	9606. ENSP00000308461, 9606. ENSP00000317985, 9606. ENSP00000348461, 9606. ENSP00000364886, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000385720, 9606. ENSP00000400175	RND1, ROCK2, RAC1, RND3, ROCK1, CDC42, ARHGAP35, RHOA
GO:0050770	Regulation of axonogenesis	6	187	1.48	9.00E-06	9606. ENSP00000172229, 9606. ENSP00000269321, 9606. ENSP00000351338, 9606. ENSP00000385720, 9606. ENSP00000400175, 9606. ENSP00000409171	NGFR, ARHGDIA, PLXNB1, ARHGAP35, RHOA, PLXNB2
GO:0050772	Positive regulation of axonogenesis	5	89	1.72	9.53E-06	9606. ENSP00000172229, 9606. ENSP00000269321, 9606. ENSP00000351338, 9606. ENSP00000400175, 9606. ENSP00000409171	NGFR, ARHGDIA, PLXNB1, RHOA, PLXNB2
GO:0051492	Regulation of stress fiber assembly	5	89	1.72	9.53E-06	9606. ENSP00000317985, 9606. ENSP00000348461, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000400175	ROCK2, RAC1, ROCK1, CDC42, RHOA
GO:0048856	Anatomical structure development	18	5402	0.49	1.00E-05	9606. ENSP00000172229, 9606. ENSP00000251849, 9606. ENSP00000269321, 9606. ENSP00000274376, 9606. ENSP00000308461, 9606. ENSP00000317985, 9606. ENSP00000329380, 9606. ENSP00000344456, 9606. ENSP00000348461, 9606. ENSP00000351338, 9606. ENSP00000371897, 9606. ENSP00000379287, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000385720, 9606. ENSP00000385824, 9606. ENSP00000400175, 9606. ENSP00000409171	NGFR, RAF1, ARHGDIA, RASA1, RND1, ROCK2, GP1BA, CTNNB1, RAC1, PLXNB1, ARHGAP5, YWHAZ, ROCK1, CDC42, ARHGAP35, FOXO3, RHOA, PLXNB2
GO:0007010	Cytoskeleton organization	10	1126	0.92	1.63E-05	9606. ENSP00000251849, 9606. ENSP00000308461, 9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000348461, 9606. ENSP00000364886, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000385720, 9606. ENSP00000400175	RAF1, RND1, ROCK2, CTNNB1, RAC1, RND3, ROCK1, CDC42, ARHGAP35, RHOA
GO:0010810	Regulation of cell-substrate adhesion	6	212	1.42	1.63E-05	9606. ENSP00000274376, 9606. ENSP00000317985, 9606. ENSP00000348461, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000400175	RASA1, ROCK2, RAC1, ROCK1, CDC42, RHOA
GO:0043523	Regulation of neuron apoptotic process	6	212	1.42	1.63E-05	9606. ENSP00000274376, 9606. ENSP00000344456, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000385824, 9606. ENSP00000400175	RASA1, CTNNB1, ROCK1, CDC42, FOXO3, RHOA
GO:0050767	Regulation of neurogenesis	9	828	1.01	1.63E-05	9606. ENSP00000172229, 9606. ENSP00000269321, 9606. ENSP00000344456, 9606. ENSP00000351338, 9606. ENSP00000382697, 9606. ENSP00000385720, 9606. ENSP00000385824, 9606. ENSP00000400175, 9606. ENSP00000409171	NGFR, ARHGDIA, CTNNB1, PLXNB1, ROCK1, ARHGAP35, FOXO3, RHOA, PLXNB2

Table S5. the full list of KEGG analysis and GO analysis for RND3

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0043085	Positive regulation of catalytic activity	11	1489	0.84	1.64E-05	9606. ENSP00000172229, 9606. ENSP00000251849, 9606. ENSP00000269321, 9606. ENSP00000274376, 9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000351338, 9606. ENSP00000371897, 9606. ENSP00000383118, 9606. ENSP00000385720, 9606. ENSP00000400175	NGFR, RAF1, ARHGDIA, RASA1, ROCK2, CTNNB1, PLXNB1, ARHGAP5, CDC42, ARHGAP35, RHOA
GO:0071526	Semaphorin-plexin signaling pathway	4	37	2	1.77E-05	9606. ENSP00000269321, 9606. ENSP00000348461, 9606. ENSP00000351338, 9606. ENSP00000409171	ARHGDIA, RAC1, PLXNB1, PLXNB2
GO:0050790	Regulation of catalytic activity	13	2386	0.71	1.89E-05	9606. ENSP00000172229, 9606. ENSP00000251849, 9606. ENSP00000269321, 9606. ENSP00000274376, 9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000351338, 9606. ENSP00000371897, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000385720, 9606. ENSP00000400175, 9606. ENSP00000409171	NGFR, RAF1, ARHGDIA, RASA1, ROCK2, CTNNB1, PLXNB1, ARHGAP5, ROCK1, CDC42, ARHGAP35, RHOA, PLXNB2
GO:0042981	Regulation of apoptotic process	11	1550	0.82	2.30E-05	9606. ENSP00000172229, 9606. ENSP00000251849, 9606. ENSP00000269321, 9606. ENSP00000274376, 9606. ENSP00000344456, 9606. ENSP00000379287, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000385824, 9606. ENSP00000400175, 9606. ENSP00000439625	NGFR, RAF1, ARHGDIA, RASA1, CTNNB1, YWHAZ, ROCK1, CDC42, FOXO3, RHOA, PLEKHG5
GO:0016525	Negative regulation of angiogenesis	5	117	1.6	2.74E-05	9606. ENSP00000172229, 9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000382697, 9606. ENSP00000400175	NGFR, ROCK2, CTNNB1, ROCK1, RHOA
GO:0001952	Regulation of cell-matrix adhesion	5	120	1.59	3.02E-05	9606. ENSP00000274376, 9606. ENSP00000317985, 9606. ENSP00000348461, 9606. ENSP00000382697, 9606. ENSP00000400175	RASA1, ROCK2, RAC1, ROCK1, RHOA
GO:0040011	Locomotion	10	1251	0.87	3.43E-05	9606. ENSP00000172229, 9606. ENSP00000344456, 9606. ENSP00000348461, 9606. ENSP00000351338, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000385720, 9606. ENSP00000400175, 9606. ENSP00000409171, 9606. ENSP00000439625	NGFR, CTNNB1, RAC1, PLXNB1, ROCK1, CDC42, ARHGAP35, RHOA, PLXNB2, PLEKHG5
GO:0030154	Cell differentiation	15	3702	0.58	3.85E-05	9606. ENSP00000172229, 9606. ENSP00000251849, 9606. ENSP00000269321, 9606. ENSP00000274376, 9606. ENSP00000308461, 9606. ENSP00000344456, 9606. ENSP00000348461, 9606. ENSP00000351338, 9606. ENSP00000379287, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000385720, 9606. ENSP00000385824, 9606. ENSP00000400175, 9606. ENSP00000409171	NGFR, RAF1, ARHGDIA, RASA1, RND1, CTNNB1, RAC1, PLXNB1, YWHAZ, ROCK1, CDC42, ARHGAP35, FOXO3, RHOA, PLXNB2
GO:0009967	Positive regulation of signal transduction	11	1654	0.79	3.90E-05	9606. ENSP00000172229, 9606. ENSP00000251849, 9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000348461, 9606. ENSP00000351338, 9606. ENSP00000379287, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000400175, 9606. ENSP00000439625	NGFR, RAF1, ROCK2, CTNNB1, RAC1, PLXNB1, YWHAZ, ROCK1, CDC42, RHOA, PLEKHG5
GO:0032501	Multicellular organismal process	19	6933	0.41	3.90E-05	9606. ENSP00000172229, 9606. ENSP00000251849, 9606. ENSP00000269321, 9606. ENSP00000274376, 9606. ENSP00000308461, 9606. ENSP00000317985, 9606. ENSP00000329380, 9606. ENSP00000344456, 9606. ENSP00000348461, 9606. ENSP00000351338, 9606. ENSP00000371897, 9606. ENSP00000379287, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000385720, 9606. ENSP00000385824, 9606. ENSP00000400175, 9606. ENSP00000409171, 9606. ENSP00000439625	NGFR, RAF1, ARHGDIA, RASA1, RND1, ROCK2, GP1BA, CTNNB1, RAC1, PLXNB1, ARHGAP5, YWHAZ, ROCK1, CDC42, ARHGAP35, FOXO3, RHOA, PLXNB2, PLEKHG5
GO:0045664	Regulation of neuron differentiation	8	665	1.05	3.90E-05	9606. ENSP00000172229, 9606. ENSP00000269321, 9606. ENSP00000351338, 9606. ENSP00000382697, 9606. ENSP00000385720, 9606. ENSP00000385824, 9606. ENSP00000400175, 9606. ENSP00000409171	NGFR, ARHGDIA, PLXNB1, ROCK1, ARHGAP35, FOXO3, RHOA, PLXNB2
GO:0042060	Wound healing	7	439	1.17	3.95E-05	9606. ENSP00000251849, 9606. ENSP00000329380, 9606. ENSP00000348461, 9606. ENSP00000379287, 9606. ENSP00000383118, 9606. ENSP00000385720, 9606. ENSP00000400175	RAF1, GP1BA, RAC1, YWHAZ, CDC42, ARHGAP35, RHOA
GO:0120035	Regulation of plasma membrane bounded cell projection organization	8	687	1.04	4.65E-05	9606. ENSP00000172229, 9606. ENSP00000269321, 9606. ENSP00000348461, 9606. ENSP00000351338, 9606. ENSP00000383118, 9606. ENSP00000385720, 9606. ENSP00000400175, 9606. ENSP00000409171	NGFR, ARHGDIA, RAC1, PLXNB1, CDC42, ARHGAP35, RHOA, PLXNB2
GO:0030865	Cortical cytoskeleton organization	4	53	1.85	5.13E-05	9606. ENSP00000317985, 9606. ENSP00000348461, 9606. ENSP00000382697, 9606. ENSP00000383118	ROCK2, RAC1, ROCK1, CDC42
GO:0051496	Positive regulation of stress fiber assembly	4	53	1.85	5.13E-05	9606. ENSP00000317985, 9606. ENSP00000348461, 9606. ENSP00000383118, 9606. ENSP00000400175	ROCK2, RAC1, CDC42, RHOA
GO:0007162	Negative regulation of cell adhesion	6	280	1.3	5.56E-05	9606. ENSP00000269321, 9606. ENSP00000274376, 9606. ENSP00000308461, 9606. ENSP00000351338, 9606. ENSP00000400175, 9606. ENSP00000409171	ARHGDIA, RASA1, RND1, PLXNB1, RHOA, PLXNB2

Table S5. the full list of KEGG analysis and GO analysis for RND3

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0051129	Negative regulation of cellular component organization	8	713	1.02	5.71E-05	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000269321, 9606.ENSP00000317985, 9606.ENSP00000348461, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000400175	NGFR, RAF1, ARHGDIA, ROCK2, RAC1, ROCK1, CDC42, RHOA
GO:0050769	Positive regulation of neurogenesis	7	479	1.13	6.25E-05	9606.ENSP00000172229, 9606.ENSP00000269321, 9606.ENSP00000344456, 9606.ENSP00000351338, 9606.ENSP00000385720, 9606.ENSP00000400175, 9606.ENSP00000409171	NGFR, ARHGDIA, CTNNB1, PLXNB1, ARHGAP35, RHOA, PLXNB2
GO:0010976	Positive regulation of neuron projection development	6	288	1.29	6.33E-05	9606.ENSP00000172229, 9606.ENSP00000269321, 9606.ENSP00000351338, 9606.ENSP00000385720, 9606.ENSP00000400175, 9606.ENSP00000409171	NGFR, ARHGDIA, PLXNB1, ARHGAP35, RHOA, PLXNB2
GO:0051240	Positive regulation of multicellular organismal process	11	1770	0.76	6.53E-05	9606.ENSP00000172229, 9606.ENSP00000269321, 9606.ENSP00000317985, 9606.ENSP00000344456, 9606.ENSP00000351338, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000385824, 9606.ENSP00000400175, 9606.ENSP00000409171	NGFR, ARHGDIA, ROCK2, CTNNB1, PLXNB1, ROCK1, CDC42, ARHGAP35, FOXO3, RHOA, PLXNB2
GO:0043525	Positive regulation of neuron apoptotic process	4	58	1.81	6.65E-05	9606.ENSP00000344456, 9606.ENSP00000383118, 9606.ENSP00000385824, 9606.ENSP00000400175	CTNNB1, CDC42, FOXO3, RHOA
GO:0048519	Negative regulation of biological process	17	5389	0.47	6.96E-05	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000269321, 9606.ENSP00000274376, 9606.ENSP00000308461, 9606.ENSP00000317985, 9606.ENSP00000329380, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000379287, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000385824, 9606.ENSP00000400175, 9606.ENSP00000409171	NGFR, RAF1, ARHGDIA, RASA1, RND1, ROCK2, GP1BA, CTNNB1, RAC1, PLXNB1, YWHAZ, ROCK1, CDC42, ARHGAP35, FOXO3, RHOA, PLXNB2
GO:1902533	Positive regulation of intracellular signal transduction	9	1041	0.91	7.15E-05	9606.ENSP00000251849, 9606.ENSP00000317985, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000400175, 9606.ENSP00000439625	RAF1, ROCK2, CTNNB1, RAC1, PLXNB1, ROCK1, CDC42, RHOA, PLEKHG5
GO:0048584	Positive regulation of response to stimulus	12	2257	0.69	7.46E-05	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000317985, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000379287, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385824, 9606.ENSP00000400175, 9606.ENSP00000439625	NGFR, RAF1, ROCK2, CTNNB1, RAC1, PLXNB1, YWHAZ, ROCK1, CDC42, FOXO3, RHOA, PLEKHG5
GO:0051893	Regulation of focal adhesion assembly	4	63	1.77	8.58E-05	9606.ENSP00000317985, 9606.ENSP00000348461, 9606.ENSP00000382697, 9606.ENSP00000400175	ROCK2, RAC1, ROCK1, RHOA
GO:0051345	Positive regulation of hydrolase activity	8	772	0.98	8.90E-05	9606.ENSP00000172229, 9606.ENSP00000269321, 9606.ENSP00000274376, 9606.ENSP00000317985, 9606.ENSP00000351338, 9606.ENSP00000371897, 9606.ENSP00000385720, 9606.ENSP00000400175	NGFR, ARHGDIA, RASA1, ROCK2, PLXNB1, ARHGAP5, ARHGAP35, RHOA
GO:0065008	Regulation of biological quality	15	4042	0.54	9.16E-05	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000274376, 9606.ENSP00000317985, 9606.ENSP00000329380, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000379287, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000385824, 9606.ENSP00000400175, 9606.ENSP00000409171	NGFR, RAF1, RASA1, ROCK2, GP1BA, CTNNB1, RAC1, PLXNB1, YWHAZ, ROCK1, CDC42, ARHGAP35, FOXO3, RHOA, PLXNB2
GO:0070848	Response to growth factor	7	524	1.1	9.58E-05	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000317985, 9606.ENSP00000344456, 9606.ENSP00000382697, 9606.ENSP00000385824, 9606.ENSP00000400175	NGFR, RAF1, ROCK2, CTNNB1, ROCK1, FOXO3, RHOA
GO:0000281	Mitotic cytokinesis	4	70	1.73	0.00012	9606.ENSP00000274376, 9606.ENSP00000317985, 9606.ENSP00000382697, 9606.ENSP00000400175	RASA1, ROCK2, ROCK1, RHOA
GO:0006928	Movement of cell or subcellular component	10	1501	0.79	0.00012	9606.ENSP00000172229, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000400175, 9606.ENSP00000409171, 9606.ENSP00000439625	NGFR, CTNNB1, RAC1, PLXNB1, ROCK1, CDC42, ARHGAP35, RHOA, PLXNB2, PLEKHG5
GO:0006935	Chemotaxis	7	545	1.08	0.00012	9606.ENSP00000172229, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000385720, 9606.ENSP00000400175, 9606.ENSP00000409171, 9606.ENSP00000439625	NGFR, RAC1, PLXNB1, ARHGAP35, RHOA, PLXNB2, PLEKHG5

Table S5. the full list of KEGG analysis and GO analysis for RND3

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0048523	Negative regulation of cellular process	16	4874	0.49	0.00012	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000269321, 9606.ENSP00000274376, 9606.ENSP00000308461, 9606.ENSP00000317985, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000379287, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000385824, 9606.ENSP00000400175, 9606.ENSP00000409171	NGFR, RAF1, ARHGDIA, RASA1, RND1, ROCK2, CTNNB1, RAC1, PLXNB1, YWHAZ, ROCK1, CDC42, ARHGAP35, FOXO3, RHOA, PLXNB2
GO:0046578	Regulation of ras protein signal transduction	5	191	1.39	0.00017	9606.ENSP00000251849, 9606.ENSP00000269321, 9606.ENSP00000274376, 9606.ENSP00000348461, 9606.ENSP00000385720	RAF1, ARHGDIA, RASA1, RAC1, ARHGAP35
GO:0070507	Regulation of microtubule cytoskeleton organization	5	192	1.38	0.00018	9606.ENSP00000317985, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000382697, 9606.ENSP00000400175	ROCK2, CTNNB1, RAC1, ROCK1, RHOA
GO:0072359	Circulatory system development	8	872	0.93	0.00019	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000274376, 9606.ENSP00000317985, 9606.ENSP00000344456, 9606.ENSP00000379287, 9606.ENSP00000382697, 9606.ENSP00000383118	NGFR, RAF1, RASA1, ROCK2, CTNNB1, YWHAZ, ROCK1, CDC42
GO:0071695	Anatomical structure maturation	5	200	1.37	0.00021	9606.ENSP00000308461, 9606.ENSP00000344456, 9606.ENSP00000351338, 9606.ENSP00000385824, 9606.ENSP00000400175	RND1, CTNNB1, PLXNB1, FOXO3, RHOA
GO:0016477	Cell migration	8	896	0.92	0.00023	9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000400175, 9606.ENSP00000439625	CTNNB1, RAC1, PLXNB1, ROCK1, CDC42, ARHGAP35, RHOA, PLEKHG5
GO:0043066	Negative regulation of apoptotic process	8	893	0.92	0.00023	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000269321, 9606.ENSP00000274376, 9606.ENSP00000344456, 9606.ENSP00000379287, 9606.ENSP00000382697, 9606.ENSP00000400175	NGFR, RAF1, ARHGDIA, RASA1, CTNNB1, YWHAZ, ROCK1, RHOA
GO:0051241	Negative regulation of multicellular organismal process	9	1231	0.83	0.00023	9606.ENSP00000172229, 9606.ENSP00000269321, 9606.ENSP00000317985, 9606.ENSP00000329380, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000382697, 9606.ENSP00000385824, 9606.ENSP00000400175	NGFR, ARHGDIA, ROCK2, GP1BA, CTNNB1, RAC1, ROCK1, FOXO3, RHOA
GO:0035023	Regulation of rho protein signal transduction	4	88	1.63	0.00025	9606.ENSP00000251849, 9606.ENSP00000269321, 9606.ENSP00000348461, 9606.ENSP00000385720	RAF1, ARHGDIA, RAC1, ARHGAP35
GO:0045682	Regulation of epidermis development	4	88	1.63	0.00025	9606.ENSP00000172229, 9606.ENSP00000317985, 9606.ENSP00000344456, 9606.ENSP00000382697	NGFR, ROCK2, CTNNB1, ROCK1
GO:0007155	Cell adhesion	8	925	0.91	0.00028	9606.ENSP00000329380, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000364886, 9606.ENSP00000371897, 9606.ENSP00000382697, 9606.ENSP00000400175, 9606.ENSP00000409171	GP1BA, CTNNB1, RAC1, RND3, ARHGAP5, ROCK1, RHOA, PLXNB2
GO:0010638	Positive regulation of organelle organization	7	633	1.01	0.00028	9606.ENSP00000317985, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000379287, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000400175	ROCK2, CTNNB1, RAC1, YWHAZ, CDC42, ARHGAP35, RHOA
GO:2000145	Regulation of cell motility	8	929	0.9	0.00029	9606.ENSP00000251849, 9606.ENSP00000317985, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000382697, 9606.ENSP00000385824, 9606.ENSP00000400175, 9606.ENSP00000409171	RAF1, ROCK2, RAC1, PLXNB1, ROCK1, FOXO3, RHOA, PLXNB2
GO:0048513	Animal organ development	13	3197	0.58	0.0003	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000317985, 9606.ENSP00000344456, 9606.ENSP00000351338, 9606.ENSP00000371897, 9606.ENSP00000379287, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000385824, 9606.ENSP00000400175, 9606.ENSP00000409171	NGFR, RAF1, ROCK2, CTNNB1, PLXNB1, ARHGAP5, YWHAZ, ROCK1, CDC42, ARHGAP35, FOXO3, RHOA, PLXNB2
GO:1903426	Regulation of reactive oxygen species biosynthetic process	4	95	1.59	0.00031	9606.ENSP00000317985, 9606.ENSP00000348461, 9606.ENSP00000385824, 9606.ENSP00000400175	ROCK2, RAC1, FOXO3, RHOA
GO:0035239	Tube morphogenesis	7	656	1	0.00034	9606.ENSP00000274376, 9606.ENSP00000344456, 9606.ENSP00000379287, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000400175, 9606.ENSP00000409171	RASA1, CTNNB1, YWHAZ, CDC42, ARHGAP35, RHOA, PLXNB2
GO:0043065	Positive regulation of apoptotic process	7	660	0.99	0.00035	9606.ENSP00000172229, 9606.ENSP00000344456, 9606.ENSP00000379287, 9606.ENSP00000383118, 9606.ENSP00000385824, 9606.ENSP00000400175, 9606.ENSP00000439625	NGFR, CTNNB1, YWHAZ, CDC42, FOXO3, RHOA, PLEKHG5
GO:0044087	Regulation of cellular component biogenesis	8	971	0.89	0.00037	9606.ENSP00000251849, 9606.ENSP00000274376, 9606.ENSP00000317985, 9606.ENSP00000348461, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000400175	RAF1, RASA1, ROCK2, RAC1, ROCK1, CDC42, ARHGAP35, RHOA

Table S5. the full list of KEGG analysis and GO analysis for RND3

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0032879	Regulation of localization	12	2740	0.61	0.00042	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000317985, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000379287, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385824, 9606.ENSP00000400175, 9606.ENSP00000409171	NGFR, RAF1, ROCK2, CTNNB1, RAC1, PLXNB1, YWHAZ, ROCK1, CDC42, FOXO3, RHOA, PLXNB2
GO:0002009	Morphogenesis of an epithelium	6	435	1.11	0.00043	9606.ENSP00000172229, 9606.ENSP00000344456, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000400175, 9606.ENSP00000409171	NGFR, CTNNB1, CDC42, ARHGAP35, RHOA, PLXNB2
GO:0048667	Cell morphogenesis involved in neuron differentiation	6	445	1.1	0.00048	9606.ENSP00000172229, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000409171	NGFR, RAC1, PLXNB1, CDC42, ARHGAP35, PLXNB2
GO:0110061	Regulation of angiotensin-activated signaling pathway	2	2	2.97	0.00053	9606.ENSP00000317985, 9606.ENSP00000382697	ROCK2, ROCK1
GO:0051246	Regulation of protein metabolic process	12	2828	0.6	0.00055	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000317985, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000379287, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385824, 9606.ENSP00000400175, 9606.ENSP00000409171, 9606.ENSP00000439625	NGFR, RAF1, ROCK2, CTNNB1, RAC1, YWHAZ, ROCK1, CDC42, FOXO3, RHOA, PLXNB2, PLEKHG5
GO:2000027	Regulation of animal organ morphogenesis	5	257	1.26	0.00055	9606.ENSP00000172229, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000383118, 9606.ENSP00000400175	NGFR, CTNNB1, RAC1, CDC42, RHOA
GO:0045601	Regulation of endothelial cell differentiation	3	34	1.91	0.00063	9606.ENSP00000317985, 9606.ENSP00000344456, 9606.ENSP00000382697	ROCK2, CTNNB1, ROCK1
GO:0043087	Regulation of gtpase activity	6	480	1.07	0.0007	9606.ENSP00000269321, 9606.ENSP00000274376, 9606.ENSP00000351338, 9606.ENSP00000371897, 9606.ENSP00000385720, 9606.ENSP00000409171	ARHGDIA, RASA1, PLXNB1, ARHGAP5, ARHGAP35, PLXNB2
GO:0001932	Regulation of protein phosphorylation	9	1459	0.76	0.00072	9606.ENSP00000251849, 9606.ENSP00000317985, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000379287, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000400175, 9606.ENSP00000409171	RAF1, ROCK2, CTNNB1, RAC1, YWHAZ, ROCK1, CDC42, RHOA, PLXNB2
GO:0007411	Axon guidance	5	275	1.23	0.00075	9606.ENSP00000172229, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000385720, 9606.ENSP00000409171	NGFR, RAC1, PLXNB1, ARHGAP35, PLXNB2
GO:0034329	Cell junction assembly	5	280	1.22	0.0008	9606.ENSP00000344456, 9606.ENSP00000351338, 9606.ENSP00000383118, 9606.ENSP00000400175, 9606.ENSP00000409171	CTNNB1, PLXNB1, CDC42, RHOA, PLXNB2
GO:0065009	Regulation of molecular function	15	4913	0.45	0.00083	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000269321, 9606.ENSP00000274376, 9606.ENSP00000317985, 9606.ENSP00000344456, 9606.ENSP00000351338, 9606.ENSP00000371897, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000385824, 9606.ENSP00000400175, 9606.ENSP00000409171, 9606.ENSP00000439625	NGFR, RAF1, ARHGDIA, RASA1, ROCK2, CTNNB1, PLXNB1, ARHGAP5, ROCK1, CDC42, ARHGAP35, FOXO3, RHOA, PLXNB2, PLEKHG5
GO:1905205	Positive regulation of connective tissue replacement	2	3	2.79	0.00083	9606.ENSP00000317985, 9606.ENSP00000382697	ROCK2, ROCK1
GO:0035567	Non-canonical wnt signaling pathway	4	130	1.46	0.00086	9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000383118, 9606.ENSP00000400175	CTNNB1, RAC1, CDC42, RHOA
GO:0050768	Negative regulation of neurogenesis	5	287	1.21	0.00088	9606.ENSP00000172229, 9606.ENSP00000269321, 9606.ENSP00000344456, 9606.ENSP00000385824, 9606.ENSP00000400175	NGFR, ARHGDIA, CTNNB1, FOXO3, RHOA
GO:0060322	Head development	7	788	0.92	0.00092	9606.ENSP00000251849, 9606.ENSP00000344456, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000385824, 9606.ENSP00000400175, 9606.ENSP00000409171	RAF1, CTNNB1, CDC42, ARHGAP35, FOXO3, RHOA, PLXNB2
GO:0090066	Regulation of anatomical structure size	6	516	1.03	0.00098	9606.ENSP00000274376, 9606.ENSP00000317985, 9606.ENSP00000348461, 9606.ENSP00000382697, 9606.ENSP00000385720, 9606.ENSP00000400175	RASA1, ROCK2, RAC1, ROCK1, ARHGAP35, RHOA
GO:0007596	Blood coagulation	5	303	1.19	0.0011	9606.ENSP00000251849, 9606.ENSP00000329380, 9606.ENSP00000348461, 9606.ENSP00000379287, 9606.ENSP00000383118	RAF1, GP1BA, RAC1, YWHAZ, CDC42
GO:0042221	Response to chemical	14	4333	0.48	0.0011	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000317985, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000379287, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000385824, 9606.ENSP00000400175, 9606.ENSP00000409171, 9606.ENSP00000439625	NGFR, RAF1, ROCK2, CTNNB1, RAC1, PLXNB1, YWHAZ, ROCK1, CDC42, ARHGAP35, FOXO3, RHOA, PLXNB2, PLEKHG5
GO:0044089	Positive regulation of cellular component biogenesis	6	542	1.01	0.0012	9606.ENSP00000317985, 9606.ENSP00000348461, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000400175	ROCK2, RAC1, ROCK1, CDC42, ARHGAP35, RHOA
GO:1903347	Negative regulation of bicellular tight junction assembly	2	4	2.67	0.0012	9606.ENSP00000317985, 9606.ENSP00000382697	ROCK2, ROCK1
GO:0035148	Tube formation	4	147	1.4	0.0013	9606.ENSP00000344456, 9606.ENSP00000379287, 9606.ENSP00000385720, 9606.ENSP00000409171	CTNNB1, YWHAZ, ARHGAP35, PLXNB2

Table S5. the full list of KEGG analysis and GO analysis for RND3

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0030334	Regulation of cell migration	7	865	0.88	0.0015	9606.ENSP00000317985, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000382697, 9606.ENSP00000385824, 9606.ENSP00000400175, 9606.ENSP00000409171	ROCK2, RAC1, PLXNB1, ROCK1, FOXO3, RHOA, PLXNB2
GO:0035509	Negative regulation of myosin-light-chain-phosphatase activity	2	5	2.57	0.0015	9606.ENSP00000317985, 9606.ENSP00000382697	ROCK2, ROCK1
GO:0010608	Posttranscriptional regulation of gene expression	6	574	0.99	0.0016	9606.ENSP00000317985, 9606.ENSP00000379287, 9606.ENSP00000382697, 9606.ENSP00000385824, 9606.ENSP00000400175, 9606.ENSP00000409171	ROCK2, YWHAZ, ROCK1, FOXO3, RHOA, PLXNB2
GO:0032270	Positive regulation of cellular protein metabolic process	9	1635	0.71	0.0016	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000317985, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000400175, 9606.ENSP00000409171	NGFR, RAF1, ROCK2, CTNNB1, RAC1, ROCK1, CDC42, RHOA, PLXNB2
GO:0048585	Negative regulation of response to stimulus	9	1636	0.71	0.0016	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000274376, 9606.ENSP00000329380, 9606.ENSP00000344456, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000385824, 9606.ENSP00000400175	NGFR, RAF1, RASA1, GP1BA, CTNNB1, CDC42, ARHGAP35, FOXO3, RHOA
GO:0099024	Plasma membrane invagination	3	52	1.73	0.0018	9606.ENSP00000348461, 9606.ENSP00000383118, 9606.ENSP00000400175	RAC1, CDC42, RHOA
GO:0009968	Negative regulation of signal transduction	8	1271	0.77	0.002	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000274376, 9606.ENSP00000344456, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000385824, 9606.ENSP00000400175	NGFR, RAF1, RASA1, CTNNB1, CDC42, ARHGAP35, FOXO3, RHOA
GO:0032268	Regulation of cellular protein metabolic process	11	2693	0.58	0.002	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000317985, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000379287, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385824, 9606.ENSP00000400175, 9606.ENSP00000409171	NGFR, RAF1, ROCK2, CTNNB1, RAC1, YWHAZ, ROCK1, CDC42, FOXO3, RHOA, PLXNB2
GO:1905330	Regulation of morphogenesis of an epithelium	4	180	1.32	0.0025	9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000383118, 9606.ENSP00000400175	CTNNB1, RAC1, CDC42, RHOA
GO:0016043	Cellular component organization	15	5447	0.41	0.0027	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000274376, 9606.ENSP00000308461, 9606.ENSP00000317985, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000364886, 9606.ENSP00000379287, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000400175, 9606.ENSP00000409171	NGFR, RAF1, RASA1, RND1, ROCK2, CTNNB1, RAC1, PLXNB1, RND3, YWHAZ, ROCK1, CDC42, ARHGAP35, RHOA, PLXNB2
GO:0003018	Vascular process in circulatory system	4	185	1.3	0.0028	9606.ENSP00000317985, 9606.ENSP00000382697, 9606.ENSP00000385720, 9606.ENSP00000400175	ROCK2, ROCK1, ARHGAP35, RHOA
GO:0051683	Establishment of golgi localization	2	8	2.37	0.003	9606.ENSP00000379287, 9606.ENSP00000383118	YWHAZ, CDC42
GO:0007417	Central nervous system development	7	988	0.82	0.0032	9606.ENSP00000172229, 9606.ENSP00000344456, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000385824, 9606.ENSP00000400175, 9606.ENSP00000409171	NGFR, CTNNB1, CDC42, ARHGAP35, FOXO3, RHOA, PLXNB2
GO:0008015	Blood circulation	5	394	1.07	0.0032	9606.ENSP00000317985, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000400175	ROCK2, ROCK1, CDC42, ARHGAP35, RHOA
GO:0051093	Negative regulation of developmental process	7	983	0.82	0.0032	9606.ENSP00000172229, 9606.ENSP00000269321, 9606.ENSP00000317985, 9606.ENSP00000344456, 9606.ENSP00000382697, 9606.ENSP00000385824, 9606.ENSP00000400175	NGFR, ARHGDIA, ROCK2, CTNNB1, ROCK1, FOXO3, RHOA
GO:0006417	Regulation of translation	5	398	1.07	0.0033	9606.ENSP00000317985, 9606.ENSP00000382697, 9606.ENSP00000385824, 9606.ENSP00000400175, 9606.ENSP00000409171	ROCK2, ROCK1, FOXO3, RHOA, PLXNB2
GO:0007163	Establishment or maintenance of cell polarity	4	197	1.28	0.0033	9606.ENSP00000348461, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000400175	RAC1, CDC42, ARHGAP35, RHOA
GO:0009605	Response to external stimulus	10	2310	0.61	0.0033	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000385824, 9606.ENSP00000400175, 9606.ENSP00000409171, 9606.ENSP00000439625	NGFR, RAF1, RAC1, PLXNB1, CDC42, ARHGAP35, FOXO3, RHOA, PLXNB2, PLEKHG5
GO:0048522	Positive regulation of cellular process	15	5579	0.4	0.0034	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000269321, 9606.ENSP00000317985, 9606.ENSP00000344456, 9606.ENSP00000348461, 9606.ENSP00000351338, 9606.ENSP00000379287, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000385720, 9606.ENSP00000385824, 9606.ENSP00000400175, 9606.ENSP00000409171, 9606.ENSP00000439625	NGFR, RAF1, ARHGDIA, ROCK2, CTNNB1, RAC1, PLXNB1, YWHAZ, ROCK1, CDC42, ARHGAP35, FOXO3, RHOA, PLXNB2, PLEKHG5
GO:0099159	Regulation of modification of postsynaptic structure	2	9	2.32	0.0035	9606.ENSP00000383118, 9606.ENSP00000400175	CDC42, RHOA
GO:0050771	Negative regulation of axonogenesis	3	70	1.6	0.0036	9606.ENSP00000172229, 9606.ENSP00000269321, 9606.ENSP00000400175	NGFR, ARHGDIA, RHOA

Table S5. the full list of KEGG analysis and GO analysis for RND3

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0001934	Positive regulation of protein phosphorylation	7	1019	0.81	0.0037	9606. ENSP00000251849, 9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000348461, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000400175	RAF1, ROCK2, CTNNB1, RAC1, ROCK1, CDC42, RHOA
GO:0048732	Gland development	5	410	1.06	0.0037	9606. ENSP00000251849, 9606. ENSP00000344456, 9606. ENSP00000371897, 9606. ENSP00000383118, 9606. ENSP00000385720	RAF1, CTNNB1, ARHGAP5, CDC42, ARHGAP35
GO:0060341	Regulation of cellular localization	7	1027	0.8	0.0038	9606. ENSP00000172229, 9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000348461, 9606. ENSP00000379287, 9606. ENSP00000382697, 9606. ENSP00000383118	NGFR, ROCK2, CTNNB1, RAC1, YWHAZ, ROCK1, CDC42
GO:0052548	Regulation of endopeptidase activity	5	418	1.05	0.0039	9606. ENSP00000172229, 9606. ENSP00000251849, 9606. ENSP00000317985, 9606. ENSP00000382697, 9606. ENSP00000400175	NGFR, RAF1, ROCK2, ROCK1, RHOA
GO:1901215	Negative regulation of neuron death	4	211	1.25	0.004	9606. ENSP00000274376, 9606. ENSP00000344456, 9606. ENSP00000382697, 9606. ENSP00000400175	RASA1, CTNNB1, ROCK1, RHOA
GO:0043408	Regulation of mapk cascade	6	725	0.89	0.0048	9606. ENSP00000251849, 9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000379287, 9606. ENSP00000382697, 9606. ENSP00000383118	RAF1, ROCK2, CTNNB1, YWHAZ, ROCK1, CDC42
GO:0045665	Negative regulation of neuron differentiation	4	222	1.22	0.0048	9606. ENSP00000172229, 9606. ENSP00000269321, 9606. ENSP00000385824, 9606. ENSP00000400175	NGFR, ARHGDIA, FOXO3, RHOA
GO:0001775	Cell activation	7	1075	0.78	0.0049	9606. ENSP00000251849, 9606. ENSP00000329380, 9606. ENSP00000344456, 9606. ENSP00000348461, 9606. ENSP00000379287, 9606. ENSP00000382697, 9606. ENSP00000400175	RAF1, GP1BA, CTNNB1, RAC1, YWHAZ, ROCK1, RHOA
GO:0043254	Regulation of protein-containing complex assembly	5	451	1.01	0.0053	9606. ENSP00000251849, 9606. ENSP00000274376, 9606. ENSP00000348461, 9606. ENSP00000383118, 9606. ENSP00000400175	RAF1, RASA1, RAC1, CDC42, RHOA
GO:0043502	Regulation of muscle adaptation	3	82	1.53	0.0053	9606. ENSP00000317985, 9606. ENSP00000382697, 9606. ENSP00000385824	ROCK2, ROCK1, FOXO3
GO:0061154	Endothelial tube morphogenesis	2	12	2.19	0.0053	9606. ENSP00000344456, 9606. ENSP00000400175	CTNNB1, RHOA
GO:1902287	Semaphorin-plexin signaling pathway involved in axon guidance	2	12	2.19	0.0053	9606. ENSP00000351338, 9606. ENSP00000409171	PLXNB1, PLXNB2
GO:0007420	Brain development	6	745	0.88	0.0054	9606. ENSP00000344456, 9606. ENSP00000383118, 9606. ENSP00000385720, 9606. ENSP00000385824, 9606. ENSP00000400175, 9606. ENSP00000409171	CTNNB1, CDC42, ARHGAP35, FOXO3, RHOA, PLXNB2
GO:0090257	Regulation of muscle system process	4	231	1.21	0.0054	9606. ENSP00000317985, 9606. ENSP00000382697, 9606. ENSP00000385824, 9606. ENSP00000400175	ROCK2, ROCK1, FOXO3, RHOA
GO:0060429	Epithelium development	7	1109	0.77	0.0057	9606. ENSP00000172229, 9606. ENSP00000344456, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000385720, 9606. ENSP00000400175, 9606. ENSP00000409171	NGFR, CTNNB1, ROCK1, CDC42, ARHGAP35, RHOA, PLXNB2
GO:0039694	Viral rna genome replication	2	13	2.16	0.0059	9606. ENSP00000317985, 9606. ENSP00000383118	ROCK2, CDC42
GO:0030901	Midbrain development	3	88	1.5	0.0062	9606. ENSP00000344456, 9606. ENSP00000383118, 9606. ENSP00000400175	CTNNB1, CDC42, RHOA
GO:2000177	Regulation of neural precursor cell proliferation	3	88	1.5	0.0062	9606. ENSP00000344456, 9606. ENSP00000385824, 9606. ENSP00000400175	CTNNB1, FOXO3, RHOA
GO:0110110	Positive regulation of animal organ morphogenesis	3	89	1.5	0.0063	9606. ENSP00000172229, 9606. ENSP00000344456, 9606. ENSP00000383118	NGFR, CTNNB1, CDC42
GO:0001678	Cellular glucose homeostasis	3	90	1.49	0.0065	9606. ENSP00000172229, 9606. ENSP00000251849, 9606. ENSP00000385824	NGFR, RAF1, FOXO3
GO:0043931	Ossification involved in bone maturation	2	14	2.12	0.0065	9606. ENSP00000351338, 9606. ENSP00000400175	PLXNB1, RHOA
GO:0007015	Actin filament organization	4	254	1.17	0.0073	9606. ENSP00000308461, 9606. ENSP00000348461, 9606. ENSP00000383118, 9606. ENSP00000400175	RND1, RAC1, CDC42, RHOA
GO:0045198	Establishment of epithelial cell apical/basal polarity	2	15	2.09	0.0073	9606. ENSP00000383118, 9606. ENSP00000400175	CDC42, RHOA
GO:1903140	Regulation of establishment of endothelial barrier	2	15	2.09	0.0073	9606. ENSP00000317985, 9606. ENSP00000382697	ROCK2, ROCK1
GO:0071363	Cellular response to growth factor stimulus	5	494	0.97	0.0074	9606. ENSP00000172229, 9606. ENSP00000251849, 9606. ENSP00000344456, 9606. ENSP00000385824, 9606. ENSP00000400175	NGFR, RAF1, CTNNB1, FOXO3, RHOA
GO:0060071	Wnt signaling pathway, planar cell polarity pathway	3	96	1.46	0.0075	9606. ENSP00000348461, 9606. ENSP00000383118, 9606. ENSP00000400175	RAC1, CDC42, RHOA
GO:0001568	Blood vessel development	5	500	0.97	0.0077	9606. ENSP00000172229, 9606. ENSP00000274376, 9606. ENSP00000344456, 9606. ENSP00000379287, 9606. ENSP00000383118	NGFR, RASA1, CTNNB1, YWHAZ, CDC42
GO:0007507	Heart development	5	522	0.95	0.0092	9606. ENSP00000251849, 9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000382697, 9606. ENSP00000383118	RAF1, ROCK2, CTNNB1, ROCK1, CDC42
GO:0120034	Positive regulation of plasma membrane bounded cell projection assembly	3	104	1.43	0.0092	9606. ENSP00000348461, 9606. ENSP00000383118, 9606. ENSP00000385720	RAC1, CDC42, ARHGAP35
GO:0050808	Synapse organization	4	283	1.12	0.0103	9606. ENSP00000344456, 9606. ENSP00000351338, 9606. ENSP00000383118, 9606. ENSP00000409171	CTNNB1, PLXNB1, CDC42, PLXNB2
GO:0031032	Actomyosin structure organization	3	111	1.4	0.0108	9606. ENSP00000317985, 9606. ENSP00000382697, 9606. ENSP00000400175	ROCK2, ROCK1, RHOA
GO:0043410	Positive regulation of mapk cascade	5	543	0.93	0.0108	9606. ENSP00000251849, 9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000382697, 9606. ENSP00000383118	RAF1, ROCK2, CTNNB1, ROCK1, CDC42

Table S5. the full list of KEGG analysis and GO analysis for RND3

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0048011	Neurotrophin trk receptor signaling pathway	2	20	1.97	0.0113	9606. ENSP00000172229, 9606. ENSP00000251849	NGFR, RAF1
GO:0051797	Regulation of hair follicle development	2	21	1.95	0.0123	9606. ENSP00000172229, 9606. ENSP00000344456	NGFR, CTNNB1
GO:1903827	Regulation of cellular protein localization	5	568	0.91	0.013	9606. ENSP00000172229, 9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000379287, 9606. ENSP00000383118	NGFR, ROCK2, CTNNB1, YWHAZ, CDC42
GO:0048598	Embryonic morphogenesis	5	571	0.91	0.0132	9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000382697, 9606. ENSP00000385720, 9606. ENSP00000409171	ROCK2, CTNNB1, ROCK1, ARHGAP35, PLXNB2
GO:2000114	Regulation of establishment of cell polarity	2	22	1.93	0.0132	9606. ENSP00000317985, 9606. ENSP00000382697	ROCK2, ROCK1
GO:0060562	Epithelial tube morphogenesis	4	307	1.08	0.0133	9606. ENSP00000344456, 9606. ENSP00000385720, 9606. ENSP00000400175, 9606. ENSP00000409171	CTNNB1, ARHGAP35, RHOA, PLXNB2
GO:0001838	Embryonic epithelial tube formation	3	123	1.36	0.0139	9606. ENSP00000344456, 9606. ENSP00000385720, 9606. ENSP00000409171	CTNNB1, ARHGAP35, PLXNB2
GO:0006996	Organelle organization	11	3450	0.47	0.0139	9606. ENSP00000251849, 9606. ENSP00000308461, 9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000348461, 9606. ENSP00000364886, 9606. ENSP00000379287, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000385720, 9606. ENSP00000400175	RAF1, RND1, ROCK2, CTNNB1, RAC1, RND3, YWHAZ, ROCK1, CDC42, ARHGAP35, RHOA
GO:0010811	Positive regulation of cell-substrate adhesion	3	124	1.35	0.0141	9606. ENSP00000348461, 9606. ENSP00000382697, 9606. ENSP00000383118	RAC1, ROCK1, CDC42
GO:0045453	Bone resorption	2	23	1.91	0.0141	9606. ENSP00000344456, 9606. ENSP00000348461	CTNNB1, RAC1
GO:0007160	Cell-matrix adhesion	3	127	1.34	0.015	9606. ENSP00000344456, 9606. ENSP00000348461, 9606. ENSP00000400175	CTNNB1, RAC1, RHOA
GO:0032880	Regulation of protein localization	6	934	0.78	0.0151	9606. ENSP00000172229, 9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000348461, 9606. ENSP00000379287, 9606. ENSP00000383118	NGFR, ROCK2, CTNNB1, RAC1, YWHAZ, CDC42
GO:0033688	Regulation of osteoblast proliferation	2	24	1.89	0.0151	9606. ENSP00000351338, 9606. ENSP00000400175	PLXNB1, RHOA
GO:0010592	Positive regulation of lamellipodium assembly	2	25	1.87	0.0161	9606. ENSP00000348461, 9606. ENSP00000383118	RAC1, CDC42
GO:0051894	Positive regulation of focal adhesion assembly	2	25	1.87	0.0161	9606. ENSP00000348461, 9606. ENSP00000382697	RAC1, ROCK1
GO:0050863	Regulation of t cell activation	4	329	1.05	0.0164	9606. ENSP00000344456, 9606. ENSP00000348461, 9606. ENSP00000383118, 9606. ENSP00000400175	CTNNB1, RAC1, CDC42, RHOA
GO:0070887	Cellular response to chemical stimulus	10	2919	0.5	0.0166	9606. ENSP00000172229, 9606. ENSP00000251849, 9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000348461, 9606. ENSP00000379287, 9606. ENSP00000383118, 9606. ENSP00000385824, 9606. ENSP00000400175, 9606. ENSP00000439625	NGFR, RAF1, ROCK2, CTNNB1, RAC1, YWHAZ, CDC42, FOXO3, RHOA, PLEKHG5
GO:0022607	Cellular component assembly	9	2359	0.55	0.017	9606. ENSP00000251849, 9606. ENSP00000344456, 9606. ENSP00000348461, 9606. ENSP00000351338, 9606. ENSP00000379287, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000400175, 9606. ENSP00000409171	RAF1, CTNNB1, RAC1, PLXNB1, YWHAZ, ROCK1, CDC42, RHOA, PLXNB2
GO:0044319	Wound healing, spreading of cells	2	26	1.86	0.017	9606. ENSP00000385720, 9606. ENSP00000400175	ARHGAP35, RHOA
GO:0019827	Stem cell population maintenance	3	135	1.32	0.0171	9606. ENSP00000251849, 9606. ENSP00000344456, 9606. ENSP00000385824	RAF1, CTNNB1, FOXO3
GO:0030168	Platelet activation	3	135	1.32	0.0171	9606. ENSP00000251849, 9606. ENSP00000329380, 9606. ENSP00000379287	RAF1, GP1BA, YWHAZ
GO:0009749	Response to glucose	3	138	1.31	0.0179	9606. ENSP00000251849, 9606. ENSP00000385824, 9606. ENSP00000400175	RAF1, FOXO3, RHOA
GO:1903671	Negative regulation of sprouting angiogenesis	2	27	1.84	0.0179	9606. ENSP00000172229, 9606. ENSP00000400175	NGFR, RHOA
GO:1990776	Response to angiotensin	2	27	1.84	0.0179	9606. ENSP00000317985, 9606. ENSP00000382697	ROCK2, ROCK1
GO:0097746	Regulation of blood vessel diameter	3	139	1.3	0.0182	9606. ENSP00000317985, 9606. ENSP00000382697, 9606. ENSP00000400175	ROCK2, ROCK1, RHOA
GO:1903829	Positive regulation of cellular protein localization	4	342	1.04	0.0182	9606. ENSP00000172229, 9606. ENSP00000317985, 9606. ENSP00000379287, 9606. ENSP00000383118	NGFR, ROCK2, YWHAZ, CDC42
GO:0003180	Aortic valve morphogenesis	2	28	1.82	0.0187	9606. ENSP00000317985, 9606. ENSP00000382697	ROCK2, ROCK1
GO:0010243	Response to organonitrogen compound	6	987	0.75	0.0187	9606. ENSP00000172229, 9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000382697, 9606. ENSP00000385824, 9606. ENSP00000400175	NGFR, ROCK2, CTNNB1, ROCK1, FOXO3, RHOA
GO:0010613	Positive regulation of cardiac muscle hypertrophy	2	28	1.82	0.0187	9606. ENSP00000317985, 9606. ENSP00000382697	ROCK2, ROCK1
GO:0031069	Hair follicle morphogenesis	2	28	1.82	0.0187	9606. ENSP00000172229, 9606. ENSP00000344456	NGFR, CTNNB1
GO:0070168	Negative regulation of biomineral tissue development	2	28	1.82	0.0187	9606. ENSP00000317985, 9606. ENSP00000382697	ROCK2, ROCK1
GO:0010557	Positive regulation of macromolecule biosynthetic process	8	1906	0.59	0.0199	9606. ENSP00000172229, 9606. ENSP00000251849, 9606. ENSP00000344456, 9606. ENSP00000348461, 9606. ENSP00000383118, 9606. ENSP00000385824, 9606. ENSP00000400175, 9606. ENSP00000409171	NGFR, RAF1, CTNNB1, RAC1, CDC42, FOXO3, RHOA, PLXNB2
GO:0043524	Negative regulation of neuron apoptotic process	3	148	1.28	0.0205	9606. ENSP00000274376, 9606. ENSP00000382697, 9606. ENSP00000400175	RASA1, ROCK1, RHOA
GO:1903427	Negative regulation of reactive oxygen species biosynthetic process	2	31	1.78	0.0214	9606. ENSP00000317985, 9606. ENSP00000400175	ROCK2, RHOA
GO:0040036	Regulation of fibroblast growth factor receptor signaling pathway	2	32	1.77	0.0225	9606. ENSP00000172229, 9606. ENSP00000344456	NGFR, CTNNB1
GO:0061157	mRNA destabilization	2	32	1.77	0.0225	9606. ENSP00000317985, 9606. ENSP00000382697	ROCK2, ROCK1
GO:1902003	Regulation of amyloid-beta formation	2	32	1.77	0.0225	9606. ENSP00000317985, 9606. ENSP00000382697	ROCK2, ROCK1
GO:0071559	Response to transforming growth factor beta	3	156	1.25	0.0231	9606. ENSP00000317985, 9606. ENSP00000382697, 9606. ENSP00000400175	ROCK2, ROCK1, RHOA

Table S5. the full list of KEGG analysis and GO analysis for RND3

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0048469	Cell maturation	3	158	1.25	0.0237	9606. ENSP00000308461, 9606. ENSP00000344456, 9606. ENSP00000385824	RND1, CTNNB1, FOXO3
GO:1901701	Cellular response to oxygen-containing compound	6	1055	0.72	0.0243	9606. ENSP00000172229, 9606. ENSP00000251849, 9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000385824, 9606. ENSP00000400175	NGFR, RAF1, ROCK2, CTNNB1, FOXO3, RHOA
GO:0032535	Regulation of cellular component size	4	383	0.99	0.0249	9606. ENSP00000274376, 9606. ENSP00000348461, 9606. ENSP00000385720, 9606. ENSP00000400175	RASA1, RAC1, ARHGAP35, RHOA
GO:0034250	Positive regulation of cellular amide metabolic process	3	162	1.24	0.0252	9606. ENSP00000317985, 9606. ENSP00000400175, 9606. ENSP00000409171	ROCK2, RHOA, PLXNB2
GO:0031328	Positive regulation of cellular biosynthetic process	8	2005	0.57	0.0261	9606. ENSP00000172229, 9606. ENSP00000251849, 9606. ENSP00000344456, 9606. ENSP00000348461, 9606. ENSP00000383118, 9606. ENSP00000385824, 9606. ENSP00000400175, 9606. ENSP00000409171	NGFR, RAF1, CTNNB1, RAC1, CDC42, FOXO3, RHOA, PLXNB2
GO:0002682	Regulation of immune system process	7	1514	0.63	0.0263	9606. ENSP00000251849, 9606. ENSP00000329380, 9606. ENSP00000344456, 9606. ENSP00000348461, 9606. ENSP00000383118, 9606. ENSP00000385824, 9606. ENSP00000400175	RAF1, GP1BA, CTNNB1, RAC1, CDC42, FOXO3, RHOA
GO:0030521	Androgen receptor signaling pathway	2	36	1.71	0.0267	9606. ENSP00000344456, 9606. ENSP00000400175	CTNNB1, RHOA
GO:1900026	Positive regulation of substrate adhesion-dependent cell spreading	2	38	1.69	0.0293	9606. ENSP00000348461, 9606. ENSP00000383118	RAC1, CDC42
GO:0010950	Positive regulation of endopeptidase activity	3	176	1.2	0.0305	9606. ENSP00000172229, 9606. ENSP00000317985, 9606. ENSP00000400175	NGFR, ROCK2, RHOA
GO:0030866	Cortical actin cytoskeleton organization	2	39	1.68	0.0305	9606. ENSP00000317985, 9606. ENSP00000382697	ROCK2, ROCK1
GO:0048514	Blood vessel morphogenesis	4	410	0.96	0.0305	9606. ENSP00000274376, 9606. ENSP00000344456, 9606. ENSP00000379287, 9606. ENSP00000383118	RASA1, CTNNB1, YWHAZ, CDC42
GO:0048599	Oocyte development	2	39	1.68	0.0305	9606. ENSP00000344456, 9606. ENSP00000385824	CTNNB1, FOXO3
GO:1904646	Cellular response to amyloid-beta	2	39	1.68	0.0305	9606. ENSP00000172229, 9606. ENSP00000385824	NGFR, FOXO3
GO:2000249	Regulation of actin cytoskeleton reorganization	2	39	1.68	0.0305	9606. ENSP00000269321, 9606. ENSP00000383118	ARHGDIA, CDC42
GO:2001233	Regulation of apoptotic signaling pathway	4	409	0.96	0.0305	9606. ENSP00000172229, 9606. ENSP00000251849, 9606. ENSP00000344456, 9606. ENSP00000379287	NGFR, RAF1, CTNNB1, YWHAZ
GO:1901700	Response to oxygen-containing compound	7	1567	0.62	0.0309	9606. ENSP00000172229, 9606. ENSP00000251849, 9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000382697, 9606. ENSP00000385824, 9606. ENSP00000400175	NGFR, RAF1, ROCK2, CTNNB1, ROCK1, FOXO3, RHOA
GO:0032467	Positive regulation of cytokinesis	2	40	1.67	0.0312	9606. ENSP00000383118, 9606. ENSP00000400175	CDC42, RHOA
GO:0045740	Positive regulation of dna replication	2	40	1.67	0.0312	9606. ENSP00000348461, 9606. ENSP00000383118	RAC1, CDC42
GO:1902895	Positive regulation of pri-mirna transcription by rna polymerase ii	2	40	1.67	0.0312	9606. ENSP00000172229, 9606. ENSP00000385824	NGFR, FOXO3
GO:0051173	Positive regulation of nitrogen compound metabolic process	10	3239	0.46	0.0313	9606. ENSP00000172229, 9606. ENSP00000251849, 9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000348461, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000385824, 9606. ENSP00000400175, 9606. ENSP00000409171	NGFR, RAF1, ROCK2, CTNNB1, RAC1, ROCK1, CDC42, FOXO3, RHOA, PLXNB2
GO:0045216	Cell-cell junction organization	3	180	1.19	0.0317	9606. ENSP00000344456, 9606. ENSP00000383118, 9606. ENSP00000400175	CTNNB1, CDC42, RHOA
GO:0043488	Regulation of mrna stability	3	183	1.18	0.0329	9606. ENSP00000317985, 9606. ENSP00000379287, 9606. ENSP00000382697	ROCK2, YWHAZ, ROCK1
GO:0045785	Positive regulation of cell adhesion	4	423	0.95	0.0329	9606. ENSP00000348461, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000400175	RAC1, ROCK1, CDC42, RHOA
GO:0001709	Cell fate determination	2	42	1.65	0.0332	9606. ENSP00000344456, 9606. ENSP00000383118	CTNNB1, CDC42
GO:0021795	Cerebral cortex cell migration	2	42	1.65	0.0332	9606. ENSP00000344456, 9606. ENSP00000400175	CTNNB1, RHOA
GO:0045616	Regulation of keratinocyte differentiation	2	42	1.65	0.0332	9606. ENSP00000317985, 9606. ENSP00000382697	ROCK2, ROCK1
GO:0006911	Phagocytosis, engulfment	2	43	1.64	0.0345	9606. ENSP00000348461, 9606. ENSP00000383118	RAC1, CDC42
GO:0071383	Cellular response to steroid hormone stimulus	3	188	1.17	0.0348	9606. ENSP00000344456, 9606. ENSP00000385824, 9606. ENSP00000400175	CTNNB1, FOXO3, RHOA
GO:0008064	Regulation of actin polymerization or depolymerization	3	189	1.17	0.0351	9606. ENSP00000274376, 9606. ENSP00000385720, 9606. ENSP00000400175	RASA1, ARHGAP35, RHOA
GO:0021762	Substantia nigra development	2	45	1.62	0.0368	9606. ENSP00000383118, 9606. ENSP00000400175	CDC42, RHOA
GO:0043123	Positive regulation of i-kappab kinase/nf-kappab signaling	3	194	1.16	0.037	9606. ENSP00000344456, 9606. ENSP00000400175, 9606. ENSP00000439625	CTNNB1, RHOA, PLEKHG5
GO:0016032	Viral process	5	776	0.78	0.0376	9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000348461, 9606. ENSP00000383118, 9606. ENSP00000400175	ROCK2, CTNNB1, RAC1, CDC42, RHOA
GO:0042127	Regulation of cell population proliferation	7	1642	0.6	0.0378	9606. ENSP00000172229, 9606. ENSP00000251849, 9606. ENSP00000344456, 9606. ENSP00000351338, 9606. ENSP00000383118, 9606. ENSP00000385824, 9606. ENSP00000400175	NGFR, RAF1, CTNNB1, PLXNB1, CDC42, FOXO3, RHOA
GO:0048538	Thymus development	2	46	1.61	0.0378	9606. ENSP00000251849, 9606. ENSP00000344456	RAF1, CTNNB1
GO:0051346	Negative regulation of hydrolase activity	4	450	0.92	0.039	9606. ENSP00000172229, 9606. ENSP00000251849, 9606. ENSP00000317985, 9606. ENSP00000382697	NGFR, RAF1, ROCK2, ROCK1
GO:0061383	Trabecula morphogenesis	2	48	1.59	0.0404	9606. ENSP00000351338, 9606. ENSP00000400175	PLXNB1, RHOA
GO:0034446	Substrate adhesion-dependent cell spreading	2	49	1.58	0.042	9606. ENSP00000348461, 9606. ENSP00000400175	RAC1, RHOA
GO:0030100	Regulation of endocytosis	3	205	1.13	0.0421	9606. ENSP00000348461, 9606. ENSP00000382697, 9606. ENSP00000383118	RAC1, ROCK1, CDC42
GO:0008038	Neuron recognition	2	50	1.57	0.0431	9606. ENSP00000379287, 9606. ENSP00000385720	YWHAZ, ARHGAP35

Table S5. the full list of KEGG analysis and GO analysis for RND3

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0031325	Positive regulation of cellular metabolic process	10	3413	0.44	0.0431	9606. ENSP00000172229, 9606. ENSP00000251849, 9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000348461, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000385824, 9606. ENSP00000400175, 9606. ENSP00000409171	NGFR, RAF1, ROCK2, CTNNB1, RAC1, ROCK1, CDC42, FOXO3, RHOA, PLXNB2
GO:0050870	Positive regulation of t cell activation	3	209	1.13	0.0436	9606. ENSP00000348461, 9606. ENSP00000383118, 9606. ENSP00000400175	RAC1, CDC42, RHOA
GO:0009612	Response to mechanical stimulus	3	212	1.12	0.0452	9606. ENSP00000251849, 9606. ENSP00000348461, 9606. ENSP00000400175	RAF1, RAC1, RHOA
GO:1901652	Response to peptide	4	476	0.89	0.0458	9606. ENSP00000172229, 9606. ENSP00000317985, 9606. ENSP00000382697, 9606. ENSP00000385824	NGFR, ROCK2, ROCK1, FOXO3
GO:0006939	Smooth muscle contraction	2	53	1.55	0.0469	9606. ENSP00000317985, 9606. ENSP00000382697	ROCK2, ROCK1
GO:0043281	Regulation of cysteine-type endopeptidase activity involved in apoptotic process	3	216	1.11	0.0469	9606. ENSP00000172229, 9606. ENSP00000251849, 9606. ENSP00000400175	NGFR, RAF1, RHOA
GO:0046580	Negative regulation of ras protein signal transduction	2	53	1.55	0.0469	9606. ENSP00000274376, 9606. ENSP00000385720	RASA1, ARHGAP35
GO:0007186	G protein-coupled receptor signaling pathway	6	1255	0.65	0.0486	9606. ENSP00000317985, 9606. ENSP00000329380, 9606. ENSP00000351338, 9606. ENSP00000382697, 9606. ENSP00000400175, 9606. ENSP00000439625	ROCK2, GP1BA, PLXNB1, ROCK1, RHOA, PLEKHG5
GO:0031295	T cell costimulation	2	55	1.53	0.0496	9606. ENSP00000348461, 9606. ENSP00000383118	RAC1, CDC42
hsa04360	Axon guidance	9	177	1.68	4.63E-11	9606. ENSP00000251849, 9606. ENSP00000274376, 9606. ENSP00000308461, 9606. ENSP00000317985, 9606. ENSP00000351338, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000400175, 9606. ENSP00000409171	RAF1, RASA1, RND1, ROCK2, PLXNB1, ROCK1, CDC42, RHOA, PLXNB2
hsa04510	Focal adhesion	8	198	1.58	3.88E-09	9606. ENSP00000251849, 9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000371897, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000385720, 9606. ENSP00000400175	RAF1, ROCK2, CTNNB1, ARHGAP5, ROCK1, CDC42, ARHGAP35, RHOA
hsa04670	Leukocyte transendothelial migration	7	109	1.78	3.88E-09	9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000371897, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000385720, 9606. ENSP00000400175	ROCK2, CTNNB1, ARHGAP5, ROCK1, CDC42, ARHGAP35, RHOA
hsa04722	Neurotrophin signaling pathway	6	114	1.69	1.97E-07	9606. ENSP00000172229, 9606. ENSP00000251849, 9606. ENSP00000269321, 9606. ENSP00000383118, 9606. ENSP00000385824, 9606. ENSP00000400175	NGFR, RAF1, ARHGDIA, CDC42, FOXO3, RHOA
hsa04062	Chemokine signaling pathway	6	186	1.48	2.65E-06	9606. ENSP00000251849, 9606. ENSP00000317985, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000385824, 9606. ENSP00000400175	RAF1, ROCK2, ROCK1, CDC42, FOXO3, RHOA
hsa05205	Proteoglycans in cancer	6	196	1.46	2.98E-06	9606. ENSP00000251849, 9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000400175	RAF1, ROCK2, CTNNB1, ROCK1, CDC42, RHOA
hsa04810	Regulation of actin cytoskeleton	6	209	1.43	3.70E-06	9606. ENSP00000251849, 9606. ENSP00000317985, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000385720, 9606. ENSP00000400175	RAF1, ROCK2, ROCK1, CDC42, ARHGAP35, RHOA
hsa04611	Platelet activation	5	122	1.58	8.33E-06	9606. ENSP00000317985, 9606. ENSP00000329380, 9606. ENSP00000382697, 9606. ENSP00000385720, 9606. ENSP00000400175	ROCK2, GP1BA, ROCK1, ARHGAP35, RHOA
hsa05200	Pathways in cancer	7	517	1.1	2.95E-05	9606. ENSP00000251849, 9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000400175, 9606. ENSP00000439625	RAF1, ROCK2, CTNNB1, ROCK1, CDC42, RHOA, PLEKHG5
hsa04015	Rap1 signaling pathway	5	202	1.36	7.48E-05	9606. ENSP00000172229, 9606. ENSP00000251849, 9606. ENSP00000344456, 9606. ENSP00000383118, 9606. ENSP00000400175	NGFR, RAF1, CTNNB1, CDC42, RHOA
hsa05132	Salmonella infection	5	209	1.35	8.01E-05	9606. ENSP00000251849, 9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000383118, 9606. ENSP00000400175	RAF1, ROCK2, CTNNB1, CDC42, RHOA
hsa05131	Shigellosis	5	218	1.33	8.98E-05	9606. ENSP00000317985, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000385824, 9606. ENSP00000400175	ROCK2, ROCK1, CDC42, FOXO3, RHOA
hsa05163	Human cytomegalovirus infection	5	218	1.33	8.98E-05	9606. ENSP00000251849, 9606. ENSP00000317985, 9606. ENSP00000344456, 9606. ENSP00000382697, 9606. ENSP00000400175	RAF1, ROCK2, CTNNB1, ROCK1, RHOA
hsa04014	Ras signaling pathway	5	226	1.31	9.15E-05	9606. ENSP00000172229, 9606. ENSP00000251849, 9606. ENSP00000274376, 9606. ENSP00000383118, 9606. ENSP00000400175	NGFR, RAF1, RASA1, CDC42, RHOA
hsa04071	Sphingolipid signaling pathway	4	116	1.51	0.00017	9606. ENSP00000251849, 9606. ENSP00000317985, 9606. ENSP00000382697, 9606. ENSP00000400175	RAF1, ROCK2, ROCK1, RHOA
hsa05135	Yersinia infection	4	125	1.47	0.00021	9606. ENSP00000317985, 9606. ENSP00000382697, 9606. ENSP00000383118, 9606. ENSP00000400175	ROCK2, ROCK1, CDC42, RHOA
hsa04270	Vascular smooth muscle contraction	4	133	1.45	0.00025	9606. ENSP00000251849, 9606. ENSP00000317985, 9606. ENSP00000382697, 9606. ENSP00000400175	RAF1, ROCK2, ROCK1, RHOA
hsa04921	Oxytocin signaling pathway	4	149	1.4	0.00036	9606. ENSP00000251849, 9606. ENSP00000317985, 9606. ENSP00000382697, 9606. ENSP00000400175	RAF1, ROCK2, ROCK1, RHOA

Table S5. the full list of KEGG analysis and GO analysis for RND3

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
hsa04530	Tight junction	4	156	1.38	0.00041	9606.ENSP00000317985, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000400175	ROCK2, ROCK1, CDC42, RHOA
hsa04022	cGMP-PKG signaling pathway	4	162	1.36	0.00045	9606.ENSP00000251849, 9606.ENSP00000317985, 9606.ENSP00000382697, 9606.ENSP00000400175	RAF1, ROCK2, ROCK1, RHOA
hsa05213	Endometrial cancer	3	57	1.69	0.00056	9606.ENSP00000251849, 9606.ENSP00000344456, 9606.ENSP00000385824	RAF1, CTNNB1, FOXO3
hsa05130	Pathogenic Escherichia coli infection	4	187	1.3	0.0007	9606.ENSP00000317985, 9606.ENSP00000382697, 9606.ENSP00000383118, 9606.ENSP00000400175	ROCK2, ROCK1, CDC42, RHOA
hsa04520	Adherens junction	3	67	1.62	0.00081	9606.ENSP00000344456, 9606.ENSP00000383118, 9606.ENSP00000400175	CTNNB1, CDC42, RHOA
hsa05100	Bacterial invasion of epithelial cells	3	70	1.6	0.00088	9606.ENSP00000344456, 9606.ENSP00000383118, 9606.ENSP00000400175	CTNNB1, CDC42, RHOA
hsa04024	cAMP signaling pathway	4	208	1.25	0.00093	9606.ENSP00000251849, 9606.ENSP00000317985, 9606.ENSP00000382697, 9606.ENSP00000400175	RAF1, ROCK2, ROCK1, RHOA
hsa05210	Colorectal cancer	3	82	1.53	0.0013	9606.ENSP00000251849, 9606.ENSP00000344456, 9606.ENSP00000400175	RAF1, CTNNB1, RHOA
hsa04660	T cell receptor signaling pathway	3	101	1.44	0.0022	9606.ENSP00000251849, 9606.ENSP00000383118, 9606.ENSP00000400175	RAF1, CDC42, RHOA
hsa04010	MAPK signaling pathway	4	288	1.11	0.0028	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000274376, 9606.ENSP00000383118	NGFR, RAF1, RASA1, CDC42
hsa04151	PI3K-Akt signaling pathway	4	350	1.03	0.0057	9606.ENSP00000172229, 9606.ENSP00000251849, 9606.ENSP00000379287, 9606.ENSP00000385824	NGFR, RAF1, YWHAZ, FOXO3
hsa04310	Wnt signaling pathway	3	154	1.26	0.0068	9606.ENSP00000317985, 9606.ENSP00000344456, 9606.ENSP00000400175	ROCK2, CTNNB1, RHOA
hsa05160	Hepatitis C	3	156	1.25	0.0068	9606.ENSP00000251849, 9606.ENSP00000344456, 9606.ENSP00000379287	RAF1, CTNNB1, YWHAZ
hsa05206	MicroRNAs in cancer	3	160	1.24	0.0071	9606.ENSP00000251849, 9606.ENSP00000382697, 9606.ENSP00000400175	RAF1, ROCK1, RHOA
hsa05203	Viral carcinogenesis	3	182	1.19	0.0099	9606.ENSP00000379287, 9606.ENSP00000383118, 9606.ENSP00000400175	YWHAZ, CDC42, RHOA
hsa04370	VEGF signaling pathway	2	57	1.51	0.0178	9606.ENSP00000251849, 9606.ENSP00000383118	RAF1, CDC42
hsa05211	Renal cell carcinoma	2	66	1.45	0.0229	9606.ENSP00000251849, 9606.ENSP00000383118	RAF1, CDC42
hsa04917	Prolactin signaling pathway	2	69	1.43	0.0236	9606.ENSP00000251849, 9606.ENSP00000385824	RAF1, FOXO3
hsa05223	Non-small cell lung cancer	2	68	1.44	0.0236	9606.ENSP00000251849, 9606.ENSP00000385824	RAF1, FOXO3
hsa05212	Pancreatic cancer	2	73	1.41	0.0256	9606.ENSP00000251849, 9606.ENSP00000383118	RAF1, CDC42
hsa01521	EGFR tyrosine kinase inhibitor resistance	2	78	1.38	0.0283	9606.ENSP00000251849, 9606.ENSP00000385824	RAF1, FOXO3
hsa04350	TGF-beta signaling pathway	2	91	1.31	0.0356	9606.ENSP00000382697, 9606.ENSP00000400175	ROCK1, RHOA
hsa04666	Fc gamma R-mediated phagocytosis	2	90	1.32	0.0356	9606.ENSP00000251849, 9606.ENSP00000383118	RAF1, CDC42
hsa04912	GnRH signaling pathway	2	89	1.32	0.0356	9606.ENSP00000251849, 9606.ENSP00000383118	RAF1, CDC42
hsa04916	Melanogenesis	2	95	1.29	0.0375	9606.ENSP00000251849, 9606.ENSP00000344456	RAF1, CTNNB1
hsa05165	Human papillomavirus infection	3	325	0.93	0.0375	9606.ENSP00000251849, 9606.ENSP00000344456, 9606.ENSP00000383118	RAF1, CTNNB1, CDC42
hsa05215	Prostate cancer	2	96	1.29	0.0375	9606.ENSP00000251849, 9606.ENSP00000344456	RAF1, CTNNB1
hsa04625	C-type lectin receptor signaling pathway	2	102	1.26	0.0401	9606.ENSP00000251849, 9606.ENSP00000400175	RAF1, RHOA
hsa04928	Parathyroid hormone synthesis, secretion and action	2	103	1.26	0.0401	9606.ENSP00000251849, 9606.ENSP00000400175	RAF1, RHOA

Table S6. the full list of KEGG analysis and GO analysis for TXNIP

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0070646	Protein modification by small protein removal	10	298	1.5	3.11E-09	9606.ENSP00000250495, 9606.ENSP00000258149, 9606.ENSP00000262160, 9606.ENSP00000262238, 9606.ENSP00000263253, 9606.ENSP00000263754, 9606.ENSP00000264389, 9606.ENSP00000337383, 9606.ENSP00000350512, 9606.ENSP00000363377	NEDD8, MDM2, SMAD2, YY1, EP300, KAT2B, COPS4, NLRP3, COPS5, FOXO4
GO:0009719	Response to endogenous stimulus	14	1447	0.95	4.88E-08	9606.ENSP00000212015, 9606.ENSP00000216185, 9606.ENSP00000250003, 9606.ENSP00000258149, 9606.ENSP00000262160, 9606.ENSP00000262238, 9606.ENSP00000262995, 9606.ENSP00000263253, 9606.ENSP00000263754, 9606.ENSP00000307305, 9606.ENSP00000337383, 9606.ENSP00000340944, 9606.ENSP00000363377, 9606.ENSP00000462521	SIRT1, TXN2, MYOD1, MDM2, SMAD2, YY1, GAB1, EP300, KAT2B, DDIT4, NLRP3, PTPN11, FOXO4, TXNIP
GO:0009725	Response to hormone	12	849	1.12	4.88E-08	9606.ENSP00000212015, 9606.ENSP00000216185, 9606.ENSP00000250003, 9606.ENSP00000258149, 9606.ENSP00000262238, 9606.ENSP00000262995, 9606.ENSP00000263253, 9606.ENSP00000263754, 9606.ENSP00000307305, 9606.ENSP00000340944, 9606.ENSP00000363377, 9606.ENSP00000462521	SIRT1, TXN2, MYOD1, MDM2, YY1, GAB1, EP300, KAT2B, DDIT4, PTPN11, FOXO4, TXNIP
GO:0016579	Protein deubiquitination	9	281	1.47	4.88E-08	9606.ENSP00000250495, 9606.ENSP00000258149, 9606.ENSP00000262160, 9606.ENSP00000262238, 9606.ENSP00000263253, 9606.ENSP00000263754, 9606.ENSP00000337383, 9606.ENSP00000350512, 9606.ENSP00000363377	NEDD8, MDM2, SMAD2, YY1, EP300, KAT2B, NLRP3, COPS5, FOXO4
GO:0006950	Response to stress	18	3485	0.68	6.64E-08	9606.ENSP00000212015, 9606.ENSP00000216185, 9606.ENSP00000247470, 9606.ENSP00000250003, 9606.ENSP00000258149, 9606.ENSP00000262160, 9606.ENSP00000262238, 9606.ENSP00000263253, 9606.ENSP00000264389, 9606.ENSP00000307305, 9606.ENSP00000337383, 9606.ENSP00000340944, 9606.ENSP00000350512, 9606.ENSP00000360916, 9606.ENSP00000363377, 9606.ENSP00000363641, 9606.ENSP00000462521, 9606.ENSP00000480499	SIRT1, TXN2, PYCARD, MYOD1, MDM2, SMAD2, YY1, EP300, COPS4, DDIT4, NLRP3, PTPN11, COPS5, VAV2, FOXO4, TXN, TXNIP, ITCH
GO:1901700	Response to oxygen-containing compound	14	1567	0.92	6.84E-08	9606.ENSP00000212015, 9606.ENSP00000216185, 9606.ENSP00000247470, 9606.ENSP00000250003, 9606.ENSP00000258149, 9606.ENSP00000262160, 9606.ENSP00000262238, 9606.ENSP00000262995, 9606.ENSP00000263754, 9606.ENSP00000307305, 9606.ENSP00000337383, 9606.ENSP00000363377, 9606.ENSP00000363641, 9606.ENSP00000462521	SIRT1, TXN2, PYCARD, MYOD1, MDM2, SMAD2, YY1, GAB1, KAT2B, DDIT4, NLRP3, FOXO4, TXN, TXNIP
GO:0006508	Proteolysis	13	1256	0.98	7.65E-08	9606.ENSP00000212015, 9606.ENSP00000247470, 9606.ENSP00000250495, 9606.ENSP00000258149, 9606.ENSP00000262160, 9606.ENSP00000262238, 9606.ENSP00000263253, 9606.ENSP00000263754, 9606.ENSP00000264389, 9606.ENSP00000337383, 9606.ENSP00000350512, 9606.ENSP00000363377, 9606.ENSP00000480499	SIRT1, PYCARD, NEDD8, MDM2, SMAD2, YY1, EP300, KAT2B, COPS4, NLRP3, COPS5, FOXO4, ITCH
GO:0070647	Protein modification by small protein conjugation or removal	12	1021	1.04	1.32E-07	9606.ENSP00000212015, 9606.ENSP00000250495, 9606.ENSP00000258149, 9606.ENSP00000262160, 9606.ENSP00000262238, 9606.ENSP00000263253, 9606.ENSP00000263754, 9606.ENSP00000264389, 9606.ENSP00000337383, 9606.ENSP00000350512, 9606.ENSP00000363377, 9606.ENSP00000480499	SIRT1, NEDD8, MDM2, SMAD2, YY1, EP300, KAT2B, COPS4, NLRP3, COPS5, FOXO4, ITCH
GO:0010033	Response to organic substance	16	3011	0.69	1.36E-06	9606.ENSP00000212015, 9606.ENSP00000216185, 9606.ENSP00000247470, 9606.ENSP00000250003, 9606.ENSP00000250495, 9606.ENSP00000258149, 9606.ENSP00000262160, 9606.ENSP00000262238, 9606.ENSP00000262995, 9606.ENSP00000263253, 9606.ENSP00000263754, 9606.ENSP00000307305, 9606.ENSP00000337383, 9606.ENSP00000340944, 9606.ENSP00000363377, 9606.ENSP00000462521	SIRT1, TXN2, PYCARD, MYOD1, NEDD8, MDM2, SMAD2, YY1, GAB1, EP300, KAT2B, DDIT4, NLRP3, PTPN11, FOXO4, TXNIP
GO:0006974	Cellular response to dna damage stimulus	10	793	1.07	3.81E-06	9606.ENSP00000212015, 9606.ENSP00000247470, 9606.ENSP00000258149, 9606.ENSP00000262238, 9606.ENSP00000263253, 9606.ENSP00000264389, 9606.ENSP00000307305, 9606.ENSP00000340944, 9606.ENSP00000350512, 9606.ENSP00000363377	SIRT1, PYCARD, MDM2, YY1, EP300, COPS4, DDIT4, PTPN11, COPS5, FOXO4
GO:0051716	Cellular response to stimulus	20	6489	0.46	4.44E-06	9606.ENSP00000212015, 9606.ENSP00000216185, 9606.ENSP00000247470, 9606.ENSP00000250003, 9606.ENSP00000258149, 9606.ENSP00000262160, 9606.ENSP00000262238, 9606.ENSP00000262995, 9606.ENSP00000263253, 9606.ENSP00000263754, 9606.ENSP00000264389, 9606.ENSP00000307305, 9606.ENSP00000337383, 9606.ENSP00000340944, 9606.ENSP00000350512, 9606.ENSP00000360916, 9606.ENSP00000363377, 9606.ENSP00000363641, 9606.ENSP00000462521, 9606.ENSP00000480499	SIRT1, TXN2, PYCARD, MYOD1, MDM2, SMAD2, YY1, GAB1, EP300, KAT2B, COPS4, DDIT4, NLRP3, PTPN11, COPS5, VAV2, FOXO4, TXN, TXNIP, ITCH

Table S6. the full list of KEGG analysis and GO analysis for TXNIP

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0050896	Response to stimulus	21	8046	0.39	8.56E-06	9606. ENSP00000212015, 9606. ENSP00000216185, 9606. ENSP00000247470, 9606. ENSP00000250003, 9606. ENSP00000250495, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000262995, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000264389, 9606. ENSP00000307305, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000350512, 9606. ENSP00000360916, 9606. ENSP00000363377, 9606. ENSP00000363641, 9606. ENSP00000462521, 9606. ENSP00000480499	SIRT1, TXN2, PYCARD, MYOD1, NEDD8, MDM2, SMAD2, YY1, GAB1, EP300, KAT2B, COPS4, DDIT4, NLRP3, PTPN11, COPS5, VAV2, FOXO4, TXN, TXNIP, ITCH
GO:0042221	Response to chemical	17	4333	0.56	1.76E-05	9606. ENSP00000212015, 9606. ENSP00000216185, 9606. ENSP00000247470, 9606. ENSP00000250003, 9606. ENSP00000250495, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000262995, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000307305, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000363377, 9606. ENSP00000363641, 9606. ENSP00000462521	SIRT1, TXN2, PYCARD, MYOD1, NEDD8, MDM2, SMAD2, YY1, GAB1, EP300, KAT2B, DDIT4, NLRP3, PTPN11, FOXO4, TXN, TXNIP
GO:0006357	Regulation of transcription by rna polymerase ii	13	2172	0.75	3.15E-05	9606. ENSP00000212015, 9606. ENSP00000250003, 9606. ENSP00000250495, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000337383, 9606. ENSP00000350512, 9606. ENSP00000363377, 9606. ENSP00000363641, 9606. ENSP00000462521	SIRT1, MYOD1, NEDD8, MDM2, SMAD2, YY1, EP300, KAT2B, NLRP3, COPS5, FOXO4, TXN, TXNIP
GO:0042771	Intrinsic apoptotic signaling pathway in response to dna damage by p53 class mediator	4	30	2.09	3.80E-05	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000263253, 9606. ENSP00000307305	SIRT1, PYCARD, EP300, DDIT4
GO:1902531	Regulation of intracellular signal transduction	12	1807	0.79	4.22E-05	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000258149, 9606. ENSP00000262995, 9606. ENSP00000263253, 9606. ENSP00000307305, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000350512, 9606. ENSP00000360916, 9606. ENSP00000363641, 9606. ENSP00000480499	SIRT1, PYCARD, MDM2, GAB1, EP300, DDIT4, NLRP3, PTPN11, COPS5, VAV2, TXN, ITCH
GO:0019219	Regulation of nucleobase-containing compound metabolic process	16	3982	0.57	4.72E-05	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000250003, 9606. ENSP00000250495, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000307305, 9606. ENSP00000337383, 9606. ENSP00000350512, 9606. ENSP00000363377, 9606. ENSP00000363641, 9606. ENSP00000462521, 9606. ENSP00000480499	SIRT1, PYCARD, MYOD1, NEDD8, MDM2, SMAD2, YY1, EP300, KAT2B, DDIT4, NLRP3, COPS5, FOXO4, TXN, TXNIP, ITCH
GO:0006355	Regulation of transcription, dna-templated	15	3388	0.62	5.13E-05	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000250003, 9606. ENSP00000250495, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000337383, 9606. ENSP00000350512, 9606. ENSP00000363377, 9606. ENSP00000363641, 9606. ENSP00000462521, 9606. ENSP00000480499	SIRT1, PYCARD, MYOD1, NEDD8, MDM2, SMAD2, YY1, EP300, KAT2B, NLRP3, COPS5, FOXO4, TXN, TXNIP, ITCH
GO:0009605	Response to external stimulus	13	2310	0.72	5.13E-05	9606. ENSP00000212015, 9606. ENSP00000216185, 9606. ENSP00000247470, 9606. ENSP00000250003, 9606. ENSP00000258149, 9606. ENSP00000262995, 9606. ENSP00000263253, 9606. ENSP00000307305, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000363377, 9606. ENSP00000462521, 9606. ENSP00000480499	SIRT1, TXN2, PYCARD, MYOD1, MDM2, GAB1, EP300, DDIT4, NLRP3, PTPN11, FOXO4, TXNIP, ITCH
GO:0031325	Positive regulation of cellular metabolic process	15	3413	0.61	5.13E-05	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000250003, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000350512, 9606. ENSP00000360916, 9606. ENSP00000363377, 9606. ENSP00000363641, 9606. ENSP00000480499	SIRT1, PYCARD, MYOD1, MDM2, SMAD2, YY1, EP300, KAT2B, NLRP3, PTPN11, COPS5, VAV2, FOXO4, TXN, ITCH
GO:0032870	Cellular response to hormone stimulus	8	569	1.12	5.13E-05	9606. ENSP00000212015, 9606. ENSP00000250003, 9606. ENSP00000258149, 9606. ENSP00000262995, 9606. ENSP00000263754, 9606. ENSP00000307305, 9606. ENSP00000340944, 9606. ENSP00000363377	SIRT1, MYOD1, MDM2, GAB1, KAT2B, DDIT4, PTPN11, FOXO4
GO:0048522	Positive regulation of cellular process	18	5579	0.48	5.13E-05	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000250003, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000262995, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000307305, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000350512, 9606. ENSP00000360916, 9606. ENSP00000363377, 9606. ENSP00000363641, 9606. ENSP00000462521, 9606. ENSP00000480499	SIRT1, PYCARD, MYOD1, MDM2, SMAD2, YY1, GAB1, EP300, KAT2B, DDIT4, NLRP3, PTPN11, COPS5, VAV2, FOXO4, TXN, TXNIP, ITCH

Table S6. the full list of KEGG analysis and GO analysis for TXNIP

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0009628	Response to abiotic stimulus	10	1147	0.91	5.15E-05	9606. ENSP0000212015, 9606. ENSP0000216185, 9606. ENSP0000250003, 9606. ENSP0000258149, 9606. ENSP0000262238, 9606. ENSP0000263253, 9606. ENSP0000307305, 9606. ENSP0000340944, 9606. ENSP0000363641, 9606. ENSP0000462521	SIRT1, TXN2, MYOD1, MDM2, YY1, EP300, DDIT4, PTPN11, TXN, TXNIP
GO:0048583	Regulation of response to stimulus	16	4114	0.56	5.15E-05	9606. ENSP0000212015, 9606. ENSP0000247470, 9606. ENSP0000250003, 9606. ENSP0000258149, 9606. ENSP0000262160, 9606. ENSP0000262238, 9606. ENSP0000262995, 9606. ENSP0000263253, 9606. ENSP0000263754, 9606. ENSP0000307305, 9606. ENSP0000337383, 9606. ENSP0000340944, 9606. ENSP0000350512, 9606. ENSP0000360916, 9606. ENSP0000363641, 9606. ENSP0000480499	SIRT1, PYCARD, MYOD1, MDM2, SMAD2, YY1, GAB1, EP300, KAT2B, DDIT4, NLRP3, PTPN11, COPS5, VAV2, TXN, ITCH
GO:0071310	Cellular response to organic substance	13	2369	0.71	5.15E-05	9606. ENSP0000212015, 9606. ENSP0000247470, 9606. ENSP0000250003, 9606. ENSP0000258149, 9606. ENSP0000262160, 9606. ENSP0000262238, 9606. ENSP0000262995, 9606. ENSP0000263253, 9606. ENSP0000263754, 9606. ENSP0000307305, 9606. ENSP0000337383, 9606. ENSP0000340944, 9606. ENSP0000363377	SIRT1, PYCARD, MYOD1, MDM2, SMAD2, YY1, GAB1, EP300, KAT2B, DDIT4, NLRP3, PTPN11, FOXO4
GO:0070887	Cellular response to chemical stimulus	14	2919	0.65	5.20E-05	9606. ENSP0000212015, 9606. ENSP0000247470, 9606. ENSP0000250003, 9606. ENSP0000258149, 9606. ENSP0000262160, 9606. ENSP0000262238, 9606. ENSP0000262995, 9606. ENSP0000263253, 9606. ENSP0000263754, 9606. ENSP0000307305, 9606. ENSP0000337383, 9606. ENSP0000340944, 9606. ENSP0000363377, 9606. ENSP0000363641	SIRT1, PYCARD, MYOD1, MDM2, SMAD2, YY1, GAB1, EP300, KAT2B, DDIT4, NLRP3, PTPN11, FOXO4, TXN
GO:0071495	Cellular response to endogenous stimulus	10	1181	0.9	5.61E-05	9606. ENSP0000212015, 9606. ENSP0000250003, 9606. ENSP0000258149, 9606. ENSP0000262160, 9606. ENSP0000262995, 9606. ENSP0000263754, 9606. ENSP0000307305, 9606. ENSP0000337383, 9606. ENSP0000340944, 9606. ENSP0000363377	SIRT1, MYOD1, MDM2, SMAD2, GAB1, KAT2B, DDIT4, NLRP3, PTPN11, FOXO4
GO:0010629	Negative regulation of gene expression	12	2014	0.74	7.49E-05	9606. ENSP0000212015, 9606. ENSP0000247470, 9606. ENSP0000258149, 9606. ENSP0000262160, 9606. ENSP0000262238, 9606. ENSP0000263253, 9606. ENSP0000263754, 9606. ENSP0000337383, 9606. ENSP0000363377, 9606. ENSP0000363641, 9606. ENSP0000462521, 9606. ENSP0000480499	SIRT1, PYCARD, MDM2, SMAD2, YY1, EP300, KAT2B, NLRP3, FOXO4, TXN, TXNIP, ITCH
GO:0006464	Cellular protein modification process	14	3063	0.63	8.54E-05	9606. ENSP0000212015, 9606. ENSP0000250003, 9606. ENSP0000250495, 9606. ENSP0000258149, 9606. ENSP0000262160, 9606. ENSP0000262238, 9606. ENSP0000263253, 9606. ENSP0000263754, 9606. ENSP0000264389, 9606. ENSP0000337383, 9606. ENSP0000340944, 9606. ENSP0000350512, 9606. ENSP0000363377, 9606. ENSP0000480499	SIRT1, MYOD1, NEDD8, MDM2, SMAD2, YY1, EP300, KAT2B, COPS4, NLRP3, PTPN11, COPS5, FOXO4, ITCH
GO:0072331	Signal transduction by p53 class mediator	5	123	1.58	8.54E-05	9606. ENSP0000212015, 9606. ENSP0000247470, 9606. ENSP0000258149, 9606. ENSP0000263253, 9606. ENSP0000307305	SIRT1, PYCARD, MDM2, EP300, DDIT4
GO:0009966	Regulation of signal transduction	14	3107	0.62	9.52E-05	9606. ENSP0000212015, 9606. ENSP0000247470, 9606. ENSP0000258149, 9606. ENSP0000262160, 9606. ENSP0000262995, 9606. ENSP0000263253, 9606. ENSP0000263754, 9606. ENSP0000307305, 9606. ENSP0000337383, 9606. ENSP0000340944, 9606. ENSP0000350512, 9606. ENSP0000360916, 9606. ENSP0000363641, 9606. ENSP0000480499	SIRT1, PYCARD, MDM2, SMAD2, GAB1, EP300, KAT2B, DDIT4, NLRP3, PTPN11, COPS5, VAV2, TXN, ITCH
GO:0032479	Regulation of type i interferon production	5	130	1.55	9.71E-05	9606. ENSP0000247470, 9606. ENSP0000262238, 9606. ENSP0000263253, 9606. ENSP0000340944, 9606. ENSP0000480499	PYCARD, YY1, EP300, PTPN11, ITCH
GO:2000026	Regulation of multicellular organismal development	12	2096	0.73	9.71E-05	9606. ENSP0000212015, 9606. ENSP0000250003, 9606. ENSP0000258149, 9606. ENSP0000262160, 9606. ENSP0000262238, 9606. ENSP0000262995, 9606. ENSP0000263253, 9606. ENSP0000263754, 9606. ENSP0000337383, 9606. ENSP0000340944, 9606. ENSP0000363377, 9606. ENSP0000480499	SIRT1, MYOD1, MDM2, SMAD2, YY1, GAB1, EP300, KAT2B, NLRP3, PTPN11, FOXO4, ITCH
GO:0080090	Regulation of primary metabolic process	18	6032	0.44	0.0001	9606. ENSP0000212015, 9606. ENSP0000247470, 9606. ENSP0000250003, 9606. ENSP0000250495, 9606. ENSP0000258149, 9606. ENSP0000262160, 9606. ENSP0000262238, 9606. ENSP0000263253, 9606. ENSP0000263754, 9606. ENSP0000307305, 9606. ENSP0000337383, 9606. ENSP0000340944, 9606. ENSP0000350512, 9606. ENSP0000360916, 9606. ENSP0000363377, 9606. ENSP0000363641, 9606. ENSP0000462521, 9606. ENSP0000480499	SIRT1, PYCARD, MYOD1, NEDD8, MDM2, SMAD2, YY1, EP300, KAT2B, DDIT4, NLRP3, PTPN11, COPS5, VAV2, FOXO4, TXN, TXNIP, ITCH

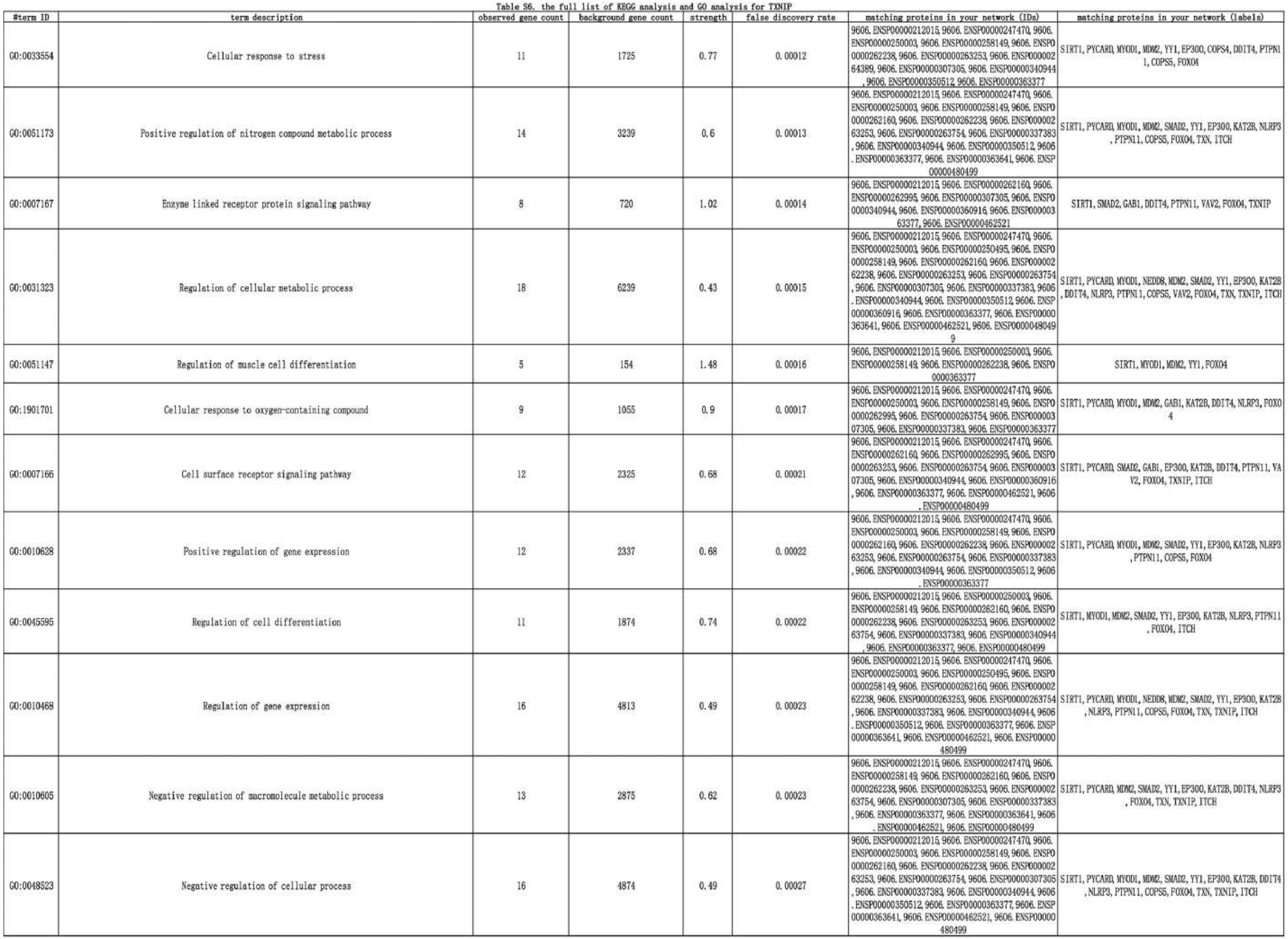


Table S6. the full list of KEGG analysis and GO analysis for TXNIP

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0033554	Cellular response to stress	11	1725	0.77	0.00012	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000250003, 9606. ENSP00000258149, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000264389, 9606. ENSP00000307305, 9606. ENSP00000340944, 9606. ENSP00000350512, 9606. ENSP00000363377	SIRT1, PYCARD, MYOD1, MDM2, YY1, EP300, COPS4, DDIT4, PTPN11, COPS5, FOXO4
GO:0051173	Positive regulation of nitrogen compound metabolic process	14	3239	0.6	0.00013	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000250003, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000350512, 9606. ENSP00000363377, 9606. ENSP00000363641, 9606. ENSP00000480499	SIRT1, PYCARD, MYOD1, MDM2, SMAD2, YY1, EP300, KAT2B, NLRP3, PTPN11, COPS5, FOXO4, TXN, ITCH
GO:0007167	Enzyme linked receptor protein signaling pathway	8	720	1.02	0.00014	9606. ENSP00000212015, 9606. ENSP00000262160, 9606. ENSP00000262995, 9606. ENSP00000307305, 9606. ENSP00000340944, 9606. ENSP00000360916, 9606. ENSP00000363377, 9606. ENSP00000462521	SIRT1, SMAD2, GAB1, DDIT4, PTPN11, VAV2, FOXO4, TXNIP
GO:0031323	Regulation of cellular metabolic process	18	6239	0.43	0.00015	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000250003, 9606. ENSP00000250495, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000307305, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000350512, 9606. ENSP00000360916, 9606. ENSP00000363377, 9606. ENSP00000363641, 9606. ENSP00000462521, 9606. ENSP00000480499	SIRT1, PYCARD, MYOD1, NEDD8, MDM2, SMAD2, YY1, EP300, KAT2B, DDIT4, NLRP3, PTPN11, COPS5, VAV2, FOXO4, TXN, TXNIP, ITCH
GO:0051147	Regulation of muscle cell differentiation	5	154	1.48	0.00016	9606. ENSP00000212015, 9606. ENSP00000250003, 9606. ENSP00000258149, 9606. ENSP00000262238, 9606. ENSP00000363377	SIRT1, MYOD1, MDM2, YY1, FOXO4
GO:1901701	Cellular response to oxygen-containing compound	9	1055	0.9	0.00017	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000250003, 9606. ENSP00000258149, 9606. ENSP00000262995, 9606. ENSP00000263754, 9606. ENSP00000307305, 9606. ENSP00000337383, 9606. ENSP00000363377	SIRT1, PYCARD, MYOD1, MDM2, GAB1, KAT2B, DDIT4, NLRP3, FOXO4
GO:0007166	Cell surface receptor signaling pathway	12	2325	0.68	0.00021	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000262160, 9606. ENSP00000262995, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000307305, 9606. ENSP00000340944, 9606. ENSP00000360916, 9606. ENSP00000363377, 9606. ENSP00000462521, 9606. ENSP00000480499	SIRT1, PYCARD, SMAD2, GAB1, EP300, KAT2B, DDIT4, PTPN11, VAV2, FOXO4, TXNIP, ITCH
GO:0010628	Positive regulation of gene expression	12	2337	0.68	0.00022	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000250003, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000350512, 9606. ENSP00000363377	SIRT1, PYCARD, MYOD1, MDM2, SMAD2, YY1, EP300, KAT2B, NLRP3, PTPN11, COPS5, FOXO4
GO:0045595	Regulation of cell differentiation	11	1874	0.74	0.00022	9606. ENSP00000212015, 9606. ENSP00000250003, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000363377, 9606. ENSP00000480499	SIRT1, MYOD1, MDM2, SMAD2, YY1, EP300, KAT2B, NLRP3, PTPN11, FOXO4, ITCH
GO:0010468	Regulation of gene expression	16	4813	0.49	0.00023	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000250003, 9606. ENSP00000250495, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000350512, 9606. ENSP00000363377, 9606. ENSP00000363641, 9606. ENSP00000462521, 9606. ENSP00000480499	SIRT1, PYCARD, MYOD1, NEDD8, MDM2, SMAD2, YY1, EP300, KAT2B, NLRP3, PTPN11, COPS5, FOXO4, TXN, TXNIP, ITCH
GO:0010605	Negative regulation of macromolecule metabolic process	13	2875	0.62	0.00023	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000307305, 9606. ENSP00000337383, 9606. ENSP00000363377, 9606. ENSP00000363641, 9606. ENSP00000462521, 9606. ENSP00000480499	SIRT1, PYCARD, MDM2, SMAD2, YY1, EP300, KAT2B, DDIT4, NLRP3, FOXO4, TXN, TXNIP, ITCH
GO:0048523	Negative regulation of cellular process	16	4874	0.49	0.00027	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000250003, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000307305, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000350512, 9606. ENSP00000363377, 9606. ENSP00000363641, 9606. ENSP00000462521, 9606. ENSP00000480499	SIRT1, PYCARD, MYOD1, MDM2, SMAD2, YY1, EP300, KAT2B, DDIT4, NLRP3, PTPN11, COPS5, FOXO4, TXN, TXNIP, ITCH

Table S6. the full list of KEGG analysis and GO analysis for TXNIP

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0045934	Negative regulation of nucleobase-containing compound metabolic process	10	1528	0.79	0.00029	9606. ENSP00000212015, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000307305, 9606. ENSP00000363377, 9606. ENSP00000363641, 9606. ENSP00000462521	SIRT1, MDM2, SMAD2, YY1, EP300, KAT2B, DDIT4, FOXO4, TXN, TXNIP
GO:0051172	Negative regulation of nitrogen compound metabolic process	12	2429	0.66	0.00029	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000307305, 9606. ENSP00000363377, 9606. ENSP00000363641, 9606. ENSP00000462521, 9606. ENSP00000480499	SIRT1, PYCARD, MDM2, SMAD2, YY1, EP300, KAT2B, DDIT4, FOXO4, TXN, TXNIP, ITCH
GO:0065009	Regulation of molecular function	16	4913	0.48	0.00029	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000250003, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000350512, 9606. ENSP00000360916, 9606. ENSP00000363377, 9606. ENSP00000363641, 9606. ENSP00000462521, 9606. ENSP00000480499	SIRT1, PYCARD, MYOD1, MDM2, SMAD2, YY1, EP300, KAT2B, NLRP3, PTPN11, COPS5, VAV2, FOXO4, TXN, TXNIP, ITCH
GO:0010604	Positive regulation of macromolecule metabolic process	14	3600	0.56	0.00032	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000250003, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000350512, 9606. ENSP00000363377, 9606. ENSP00000363641, 9606. ENSP00000480499	SIRT1, PYCARD, MYOD1, MDM2, SMAD2, YY1, EP300, KAT2B, NLRP3, PTPN11, COPS5, FOXO4, TXN, ITCH
GO:0019538	Protein metabolic process	15	4251	0.52	0.00032	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000250003, 9606. ENSP00000250495, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000264389, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000350512, 9606. ENSP00000363377, 9606. ENSP00000480499	SIRT1, PYCARD, MYOD1, NEDD8, MDM2, SMAD2, YY1, EP300, KAT2B, COPS4, NLRP3, PTPN11, COPS5, FOXO4, ITCH
GO:0033993	Response to lipid	8	858	0.94	0.00033	9606. ENSP00000247470, 9606. ENSP00000250003, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000307305, 9606. ENSP00000337383, 9606. ENSP00000462521	PYCARD, MYOD1, MDM2, SMAD2, YY1, DDIT4, NLRP3, TXNIP
GO:0051171	Regulation of nitrogen compound metabolic process	17	5836	0.43	0.00036	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000250003, 9606. ENSP00000250495, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000307305, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000350512, 9606. ENSP00000363377, 9606. ENSP00000363641, 9606. ENSP00000462521, 9606. ENSP00000480499	SIRT1, PYCARD, MYOD1, NEDD8, MDM2, SMAD2, YY1, EP300, KAT2B, DDIT4, NLRP3, PTPN11, COPS5, FOXO4, TXN, TXNIP, ITCH
GO:0072359	Circulatory system development	8	872	0.93	0.00036	9606. ENSP00000212015, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262995, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000340944, 9606. ENSP00000360916	SIRT1, MDM2, SMAD2, GAB1, EP300, KAT2B, PTPN11, VAV2
GO:0034644	Cellular response to uv	4	83	1.65	0.00038	9606. ENSP00000212015, 9606. ENSP00000258149, 9606. ENSP00000262238, 9606. ENSP00000263253	SIRT1, MDM2, YY1, EP300
GO:0000122	Negative regulation of transcription by rna polymerase ii	8	895	0.92	0.00041	9606. ENSP00000212015, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000363377, 9606. ENSP00000363641, 9606. ENSP00000462521	SIRT1, MDM2, SMAD2, YY1, EP300, FOXO4, TXN, TXNIP
GO:0032088	Negative regulation of nf-kappab transcription factor activity	4	85	1.64	0.00041	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000337383, 9606. ENSP00000480499	SIRT1, PYCARD, NLRP3, ITCH
GO:0042325	Regulation of phosphorylation	10	1626	0.76	0.00041	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000307305, 9606. ENSP00000340944, 9606. ENSP00000350512, 9606. ENSP00000360916, 9606. ENSP00000363641, 9606. ENSP00000480499	SIRT1, PYCARD, EP300, KAT2B, DDIT4, PTPN11, COPS5, VAV2, TXN, ITCH
GO:0070482	Response to oxygen levels	6	379	1.17	0.00041	9606. ENSP00000212015, 9606. ENSP00000216185, 9606. ENSP00000250003, 9606. ENSP00000258149, 9606. ENSP00000263253, 9606. ENSP00000307305	SIRT1, TXN2, MYOD1, MDM2, EP300, DDIT4
GO:0045944	Positive regulation of transcription by rna polymerase ii	9	1253	0.83	0.00045	9606. ENSP00000212015, 9606. ENSP00000250003, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000337383, 9606. ENSP00000350512, 9606. ENSP00000363377	SIRT1, MYOD1, SMAD2, YY1, EP300, KAT2B, NLRP3, COPS5, FOXO4
GO:0031324	Negative regulation of cellular metabolic process	12	2630	0.63	0.00052	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000307305, 9606. ENSP00000363377, 9606. ENSP00000363641, 9606. ENSP00000462521, 9606. ENSP00000480499	SIRT1, PYCARD, MDM2, SMAD2, YY1, EP300, KAT2B, DDIT4, FOXO4, TXN, TXNIP, ITCH

Table S6. the full list of KEGG analysis and GO analysis for TXNIP

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0010941	Regulation of cell death	10	1696	0.74	0.00055	9606.ENSP00000212015, 9606.ENSP00000247470, 9606.ENSP00000258149, 9606.ENSP00000307305, 9606.ENSP00000337383, 9606.ENSP00000350512, 9606.ENSP00000360916, 9606.ENSP00000363641, 9606.ENSP00000462521, 9606.ENSP00000480499	SIRT1, PYCARD, MDM2, DDIT4, NLRP3, COPS5, VAV2, TXN, TXNIP, ITCH
GO:1901564	Organonitrogen compound metabolic process	16	5244	0.45	0.00055	9606.ENSP00000212015, 9606.ENSP00000216185, 9606.ENSP00000247470, 9606.ENSP00000250003, 9606.ENSP00000250495, 9606.ENSP00000258149, 9606.ENSP00000262160, 9606.ENSP00000262238, 9606.ENSP00000263253, 9606.ENSP00000263754, 9606.ENSP00000264389, 9606.ENSP00000337383, 9606.ENSP00000340944, 9606.ENSP00000350512, 9606.ENSP00000363377, 9606.ENSP00000480499	SIRT1, TXN2, PYCARD, MYOD1, NEDD8, MDM2, SMAD2, YY1, EP300, KAT2B, COPS4, NLRP3, PTPN11, COPS5, FOXO4, ITCH
GO:0051239	Regulation of multicellular organismal process	13	3227	0.57	0.00057	9606.ENSP00000212015, 9606.ENSP00000247470, 9606.ENSP00000250003, 9606.ENSP00000258149, 9606.ENSP00000262160, 9606.ENSP00000262238, 9606.ENSP00000262995, 9606.ENSP00000263253, 9606.ENSP00000263754, 9606.ENSP00000337383, 9606.ENSP00000340944, 9606.ENSP00000363377, 9606.ENSP00000480499	SIRT1, PYCARD, MYOD1, MDM2, SMAD2, YY1, GAB1, EP300, KAT2B, NLRP3, PTPN11, FOXO4, ITCH
GO:0007154	Cell communication	16	5320	0.45	0.00065	9606.ENSP00000212015, 9606.ENSP00000216185, 9606.ENSP00000247470, 9606.ENSP00000250003, 9606.ENSP00000258149, 9606.ENSP00000262160, 9606.ENSP00000262995, 9606.ENSP00000263253, 9606.ENSP00000263754, 9606.ENSP00000307305, 9606.ENSP00000337383, 9606.ENSP00000340944, 9606.ENSP00000360916, 9606.ENSP00000363377, 9606.ENSP00000462521, 9606.ENSP00000480499	SIRT1, TXN2, PYCARD, MYOD1, MDM2, SMAD2, GAB1, EP300, KAT2B, DDIT4, NLRP3, PTPN11, VAV2, FOXO4, TXNIP, ITCH
GO:0051090	Regulation of dna-binding transcription factor activity	6	437	1.11	0.00079	9606.ENSP00000212015, 9606.ENSP00000247470, 9606.ENSP00000263253, 9606.ENSP00000337383, 9606.ENSP00000350512, 9606.ENSP00000480499	SIRT1, PYCARD, EP300, NLRP3, COPS5, ITCH
GO:0006289	Nucleotide-excision repair	4	111	1.53	0.00092	9606.ENSP00000212015, 9606.ENSP00000263253, 9606.ENSP00000264389, 9606.ENSP00000350512	SIRT1, EP300, COPS4, COPS5
GO:0018394	Peptidyl-lysine acetylation	4	113	1.52	0.00096	9606.ENSP00000212015, 9606.ENSP00000250003, 9606.ENSP00000263253, 9606.ENSP00000263754	SIRT1, MYOD1, EP300, KAT2B
GO:0051246	Regulation of protein metabolic process	12	2828	0.6	0.00096	9606.ENSP00000212015, 9606.ENSP00000247470, 9606.ENSP00000250495, 9606.ENSP00000258149, 9606.ENSP00000263253, 9606.ENSP00000263754, 9606.ENSP00000307305, 9606.ENSP00000337383, 9606.ENSP00000340944, 9606.ENSP00000350512, 9606.ENSP00000363641, 9606.ENSP00000480499	SIRT1, PYCARD, NEDD8, MDM2, EP300, KAT2B, DDIT4, NLRP3, PTPN11, COPS5, TXN, ITCH
GO:0051253	Negative regulation of rna metabolic process	9	1422	0.77	0.001	9606.ENSP00000212015, 9606.ENSP00000258149, 9606.ENSP00000262160, 9606.ENSP00000262238, 9606.ENSP00000263253, 9606.ENSP00000263754, 9606.ENSP00000363377, 9606.ENSP00000363641, 9606.ENSP00000462521	SIRT1, MDM2, SMAD2, YY1, EP300, KAT2B, FOXO4, TXN, TXNIP
GO:0060255	Regulation of macromolecule metabolic process	17	6407	0.39	0.0011	9606.ENSP00000212015, 9606.ENSP00000247470, 9606.ENSP00000250003, 9606.ENSP00000250495, 9606.ENSP00000258149, 9606.ENSP00000262160, 9606.ENSP00000262238, 9606.ENSP00000263253, 9606.ENSP00000263754, 9606.ENSP00000307305, 9606.ENSP00000337383, 9606.ENSP00000340944, 9606.ENSP00000350512, 9606.ENSP00000363377, 9606.ENSP00000363641, 9606.ENSP00000462521, 9606.ENSP00000480499	SIRT1, PYCARD, MYOD1, NEDD8, MDM2, SMAD2, YY1, EP300, KAT2B, DDIT4, NLRP3, PTPN11, COPS5, FOXO4, TXN, TXNIP, ITCH
GO:0080134	Regulation of response to stress	9	1437	0.77	0.0011	9606.ENSP00000212015, 9606.ENSP00000247470, 9606.ENSP00000258149, 9606.ENSP00000263253, 9606.ENSP00000337383, 9606.ENSP00000340944, 9606.ENSP00000350512, 9606.ENSP00000363641, 9606.ENSP00000480499	SIRT1, PYCARD, MDM2, EP300, NLRP3, PTPN11, COPS5, TXN, ITCH
GO:0080135	Regulation of cellular response to stress	7	739	0.95	0.0011	9606.ENSP00000212015, 9606.ENSP00000247470, 9606.ENSP00000258149, 9606.ENSP00000263253, 9606.ENSP00000350512, 9606.ENSP00000363641, 9606.ENSP00000480499	SIRT1, PYCARD, MDM2, EP300, COPS5, TXN, ITCH
GO:0018076	N-terminal peptidyl-lysine acetylation	2	3	2.79	0.0014	9606.ENSP00000263253, 9606.ENSP00000263754	EP300, KAT2B
GO:0071363	Cellular response to growth factor stimulus	6	494	1.05	0.0014	9606.ENSP00000212015, 9606.ENSP00000258149, 9606.ENSP00000262160, 9606.ENSP00000262995, 9606.ENSP00000307305, 9606.ENSP00000340944	SIRT1, MDM2, SMAD2, GAB1, DDIT4, PTPN11
GO:1902532	Negative regulation of intracellular signal transduction	6	508	1.04	0.0016	9606.ENSP00000212015, 9606.ENSP00000247470, 9606.ENSP00000258149, 9606.ENSP00000307305, 9606.ENSP00000337383, 9606.ENSP00000480499	SIRT1, PYCARD, MDM2, DDIT4, NLRP3, ITCH
GO:0007169	Transmembrane receptor protein tyrosine kinase signaling pathway	6	518	1.03	0.0017	9606.ENSP00000262995, 9606.ENSP00000307305, 9606.ENSP00000340944, 9606.ENSP00000360916, 9606.ENSP00000363377, 9606.ENSP00000462521	GAB1, DDIT4, PTPN11, VAV2, FOXO4, TXNIP
GO:0018205	Peptidyl-lysine modification	5	299	1.19	0.0018	9606.ENSP00000212015, 9606.ENSP00000250003, 9606.ENSP00000258149, 9606.ENSP00000263253, 9606.ENSP00000263754	SIRT1, MYOD1, MDM2, EP300, KAT2B
GO:0046825	Regulation of protein export from nucleus	3	42	1.82	0.0018	9606.ENSP00000258149, 9606.ENSP00000340944, 9606.ENSP00000363641	MDM2, PTPN11, TXN

Table S6. the full list of KEGG analysis and GO analysis for TXNIP

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0000077	DNA damage checkpoint	4	140	1.43	0.0019	9606. ENSP0000258149, 9606. ENSP0000263253, 9606. ENSP0000340944, 9606. ENSP0000363377	MDM2, EP300, PTPN11, FOXO4
GO:0071496	Cellular response to external stimulus	5	309	1.18	0.002	9606. ENSP0000212015, 9606. ENSP0000216185, 9606. ENSP0000250003, 9606. ENSP0000258149, 9606. ENSP0000340944	SIRT1, TXN2, MYOD1, MDM2, PTPN11
GO:1990785	Response to water-immersion restraint stress	2	4	2.67	0.002	9606. ENSP0000258149, 9606. ENSP0000363377	MDM2, FOXO4
GO:0032480	Negative regulation of type i interferon production	3	45	1.79	0.0021	9606. ENSP0000247470, 9606. ENSP0000262238, 9606. ENSP0000480499	PYCARD, YY1, ITCH
GO:0071214	Cellular response to abiotic stimulus	5	313	1.17	0.0021	9606. ENSP0000212015, 9606. ENSP0000258149, 9606. ENSP0000262238, 9606. ENSP0000263253, 9606. ENSP0000340944	SIRT1, MDM2, YY1, EP300, PTPN11
GO:0006111	Regulation of gluconeogenesis	3	46	1.78	0.0022	9606. ENSP0000212015, 9606. ENSP0000263253, 9606. ENSP0000263754	SIRT1, EP300, KAT2B
GO:0010675	Regulation of cellular carbohydrate metabolic process	4	153	1.39	0.0024	9606. ENSP0000212015, 9606. ENSP0000263253, 9606. ENSP0000263754, 9606. ENSP0000307305	SIRT1, EP300, KAT2B, DDIT4
GO:0048646	Anatomical structure formation involved in morphogenesis	7	883	0.87	0.0028	9606. ENSP0000212015, 9606. ENSP0000250003, 9606. ENSP0000262160, 9606. ENSP0000262995, 9606. ENSP0000263253, 9606. ENSP0000340944, 9606. ENSP0000360916	SIRT1, MYOD1, SMAD2, GAB1, EP300, PTPN11, VAV2
GO:0001666	Response to hypoxia	5	342	1.13	0.0029	9606. ENSP0000212015, 9606. ENSP0000216185, 9606. ENSP0000258149, 9606. ENSP0000263253, 9606. ENSP0000307305	SIRT1, TXN2, MDM2, EP300, DDIT4
GO:0031648	Protein destabilization	3	52	1.73	0.0029	9606. ENSP0000212015, 9606. ENSP0000258149, 9606. ENSP0000263253	SIRT1, MDM2, EP300
GO:0032648	Regulation of interferon-beta production	3	52	1.73	0.0029	9606. ENSP0000247470, 9606. ENSP0000262238, 9606. ENSP0000340944	PYCARD, YY1, PTPN11
GO:0009653	Anatomical structure morphogenesis	10	2165	0.63	0.0032	9606. ENSP0000212015, 9606. ENSP0000250003, 9606. ENSP0000250495, 9606. ENSP0000258149, 9606. ENSP0000262160, 9606. ENSP0000262238, 9606. ENSP0000262995, 9606. ENSP0000263253, 9606. ENSP0000340944, 9606. ENSP0000360916	SIRT1, MYOD1, NEDD8, MDM2, SMAD2, YY1, GAB1, EP300, PTPN11, VAV2
GO:0014070	Response to organic cyclic compound	7	911	0.85	0.0032	9606. ENSP0000216185, 9606. ENSP0000250003, 9606. ENSP0000250495, 9606. ENSP0000258149, 9606. ENSP0000262160, 9606. ENSP0000307305, 9606. ENSP0000462521	TXN2, MYOD1, NEDD8, MDM2, SMAD2, DDIT4, TXNIP
GO:0032268	Regulation of cellular protein metabolic process	11	2693	0.58	0.0032	9606. ENSP0000212015, 9606. ENSP0000247470, 9606. ENSP0000258149, 9606. ENSP0000263253, 9606. ENSP0000263754, 9606. ENSP0000307305, 9606. ENSP0000337383, 9606. ENSP0000340944, 9606. ENSP0000350512, 9606. ENSP0000363641, 9606. ENSP0000480499	SIRT1, PYCARD, MDM2, EP300, KAT2B, DDIT4, NLRP3, PTPN11, COPS5, TXN, ITCH
GO:0016043	Cellular component organization	15	5447	0.41	0.0041	9606. ENSP0000212015, 9606. ENSP0000247470, 9606. ENSP0000250003, 9606. ENSP0000258149, 9606. ENSP0000262160, 9606. ENSP0000262238, 9606. ENSP0000262995, 9606. ENSP0000263253, 9606. ENSP0000263754, 9606. ENSP0000264389, 9606. ENSP0000307305, 9606. ENSP0000337383, 9606. ENSP0000340944, 9606. ENSP0000350512, 9606. ENSP0000360916	SIRT1, PYCARD, MYOD1, MDM2, SMAD2, YY1, GAB1, EP300, KAT2B, COPS4, DDIT4, NLRP3, PTPN11, COPS5, VAV2
GO:0048584	Positive regulation of response to stimulus	10	2257	0.62	0.0042	9606. ENSP0000212015, 9606. ENSP0000247470, 9606. ENSP0000262160, 9606. ENSP0000262995, 9606. ENSP0000263253, 9606. ENSP0000263754, 9606. ENSP0000337383, 9606. ENSP0000340944, 9606. ENSP0000360916, 9606. ENSP0000363641	SIRT1, PYCARD, SMAD2, GAB1, EP300, KAT2B, NLRP3, PTPN11, VAV2, TXN
GO:0006979	Response to oxidative stress	5	393	1.07	0.005	9606. ENSP0000212015, 9606. ENSP0000216185, 9606. ENSP0000258149, 9606. ENSP0000363641, 9606. ENSP0000462521	SIRT1, TXN2, MDM2, TXN, TXNIP
GO:0043434	Response to peptide hormone	5	394	1.07	0.005	9606. ENSP0000212015, 9606. ENSP0000258149, 9606. ENSP0000262995, 9606. ENSP0000263754, 9606. ENSP0000363377	SIRT1, MDM2, GAB1, KAT2B, FOXO4
GO:0000302	Response to reactive oxygen species	4	198	1.27	0.0052	9606. ENSP0000212015, 9606. ENSP0000258149, 9606. ENSP0000363641, 9606. ENSP0000462521	SIRT1, MDM2, TXN, TXNIP
GO:0008152	Metabolic process	18	8298	0.31	0.0052	9606. ENSP0000212015, 9606. ENSP0000216185, 9606. ENSP0000247470, 9606. ENSP0000250003, 9606. ENSP0000250495, 9606. ENSP0000258149, 9606. ENSP0000262160, 9606. ENSP0000262238, 9606. ENSP0000263253, 9606. ENSP0000263754, 9606. ENSP0000264389, 9606. ENSP0000307305, 9606. ENSP0000337383, 9606. ENSP0000340944, 9606. ENSP0000350512, 9606. ENSP0000363377, 9606. ENSP0000363641, 9606. ENSP0000480499	SIRT1, TXN2, PYCARD, MYOD1, NEDD8, MDM2, SMAD2, YY1, EP300, KAT2B, COPS4, DDIT4, NLRP3, PTPN11, COPS5, FOXO4, TXN, ITCH
GO:0010648	Negative regulation of cell communication	8	1382	0.73	0.0052	9606. ENSP0000212015, 9606. ENSP0000247470, 9606. ENSP0000258149, 9606. ENSP0000262160, 9606. ENSP0000307305, 9606. ENSP0000337383, 9606. ENSP0000340944, 9606. ENSP0000480499	SIRT1, PYCARD, MDM2, SMAD2, DDIT4, NLRP3, PTPN11, ITCH

Table S6. the full list of KEGG analysis and GO analysis for TXNIP

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0023057	Negative regulation of signaling	8	1385	0.73	0.0052	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000307305, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000480499	SIRT1, PYCARD, MDM2, SMAD2, DDIT4, NLRP3, PTPN11, ITCH
GO:0001933	Negative regulation of protein phosphorylation	5	411	1.05	0.0058	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000263754, 9606. ENSP00000307305, 9606. ENSP00000480499	SIRT1, PYCARD, KAT2B, DDIT4, ITCH
GO:0007165	Signal transduction	14	4876	0.43	0.0058	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262995, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000307305, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000360916, 9606. ENSP00000363377, 9606. ENSP00000462521, 9606. ENSP00000480499	SIRT1, PYCARD, MDM2, SMAD2, GAB1, EP300, KAT2B, DDIT4, NLRP3, PTPN11, VAV2, FOXO4, TXNIP, ITCH
GO:0031669	Cellular response to nutrient levels	4	204	1.26	0.0058	9606. ENSP00000212015, 9606. ENSP00000216185, 9606. ENSP00000250003, 9606. ENSP00000258149	SIRT1, TXN2, MYOD1, MDM2
GO:0031399	Regulation of protein modification process	9	1870	0.65	0.0059	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000307305, 9606. ENSP00000340944, 9606. ENSP00000350512, 9606. ENSP00000363641, 9606. ENSP00000480499	SIRT1, PYCARD, EP300, KAT2B, DDIT4, PTPN11, COPS5, TXN, ITCH
GO:0000338	Protein deneddylation	2	10	2.27	0.0062	9606. ENSP00000264389, 9606. ENSP00000350512	COPS4, COPS5
GO:0051607	Defense response to virus	4	210	1.25	0.0062	9606. ENSP00000247470, 9606. ENSP00000307305, 9606. ENSP00000337383, 9606. ENSP00000480499	PYCARD, DDIT4, NLRP3, ITCH
GO:0006283	Transcription-coupled nucleotide-excision repair	3	75	1.57	0.0066	9606. ENSP00000263253, 9606. ENSP00000264389, 9606. ENSP00000350512	EP300, COPS4, COPS5
GO:0001932	Regulation of protein phosphorylation	8	1459	0.71	0.0067	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000263754, 9606. ENSP00000307305, 9606. ENSP00000340944, 9606. ENSP00000350512, 9606. ENSP00000363641, 9606. ENSP00000480499	SIRT1, PYCARD, KAT2B, DDIT4, PTPN11, COPS5, TXN, ITCH
GO:0009314	Response to radiation	5	431	1.03	0.0067	9606. ENSP00000212015, 9606. ENSP00000258149, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000363641	SIRT1, MDM2, YY1, EP300, TXN
GO:0043281	Regulation of cysteine-type endopeptidase activity involved in apoptotic process	4	216	1.24	0.0067	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000258149, 9606. ENSP00000337383	SIRT1, PYCARD, MDM2, NLRP3
GO:0071453	Cellular response to oxygen levels	4	216	1.24	0.0067	9606. ENSP00000212015, 9606. ENSP00000250003, 9606. ENSP00000258149, 9606. ENSP00000263253	SIRT1, MYOD1, MDM2, EP300
GO:0010942	Positive regulation of cell death	6	719	0.89	0.0069	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000307305, 9606. ENSP00000337383, 9606. ENSP00000360916, 9606. ENSP00000462521	SIRT1, PYCARD, DDIT4, NLRP3, VAV2, TXNIP
GO:0050794	Regulation of cellular process	20	10932	0.23	0.0069	9606. ENSP00000212015, 9606. ENSP00000216185, 9606. ENSP00000247470, 9606. ENSP00000250003, 9606. ENSP00000250495, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000262995, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000307305, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000350512, 9606. ENSP00000360916, 9606. ENSP00000363377, 9606. ENSP00000363641, 9606. ENSP00000462521, 9606. ENSP00000480499	SIRT1, TXN2, PYCARD, MYOD1, NEDD8, MDM2, SMAD2, YY1, GAB1, EP300, KAT2B, DDIT4, NLRP3, PTPN11, COPS5, VAV2, FOXO4, TXN, TXNIP, ITCH
GO:0051276	Chromosome organization	7	1066	0.79	0.0069	9606. ENSP00000212015, 9606. ENSP00000250003, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000264389, 9606. ENSP00000350512	SIRT1, MYOD1, YY1, EP300, KAT2B, COPS4, COPS5
GO:1901698	Response to nitrogen compound	7	1070	0.78	0.0069	9606. ENSP00000212015, 9606. ENSP00000258149, 9606. ENSP00000262995, 9606. ENSP00000263754, 9606. ENSP00000337383, 9606. ENSP00000363377, 9606. ENSP00000363641	SIRT1, MDM2, GAB1, KAT2B, NLRP3, FOXO4, TXN
GO:0051896	Regulation of protein kinase b signaling	4	226	1.22	0.0074	9606. ENSP00000212015, 9606. ENSP00000262995, 9606. ENSP00000340944, 9606. ENSP00000363641	SIRT1, GAB1, PTPN11, TXN
GO:0031667	Response to nutrient levels	5	449	1.02	0.0076	9606. ENSP00000212015, 9606. ENSP00000216185, 9606. ENSP00000250003, 9606. ENSP00000258149, 9606. ENSP00000363377	SIRT1, TXN2, MYOD1, MDM2, FOXO4
GO:0001817	Regulation of cytokine production	6	742	0.88	0.0078	9606. ENSP00000247470, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000480499	PYCARD, YY1, EP300, NLRP3, PTPN11, ITCH
GO:0032868	Response to insulin	4	231	1.21	0.0079	9606. ENSP00000212015, 9606. ENSP00000262995, 9606. ENSP00000263754, 9606. ENSP00000363377	SIRT1, GAB1, KAT2B, FOXO4
GO:0002682	Regulation of immune system process	8	1514	0.69	0.008	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000360916, 9606. ENSP00000480499	SIRT1, PYCARD, EP300, KAT2B, NLRP3, PTPN11, VAV2, ITCH
GO:0030162	Regulation of proteolysis	6	747	0.87	0.008	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000250495, 9606. ENSP00000258149, 9606. ENSP00000337383, 9606. ENSP00000480499	SIRT1, PYCARD, NEDD8, MDM2, NLRP3, ITCH
GO:0071158	Positive regulation of cell cycle arrest	3	84	1.52	0.008	9606. ENSP00000258149, 9606. ENSP00000263253, 9606. ENSP00000363377	MDM2, EP300, FOXO4

Table S6. the full list of KEGG analysis and GO analysis for TXNIP

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0051149	Positive regulation of muscle cell differentiation	3	88	1.5	0.0089	9606. ENSP00000212015, 9606. ENSP00000250003, 9606. ENSP00000258149	SIRT1, MYOD1, MDM2
GO:0042981	Regulation of apoptotic process	8	1550	0.68	0.0091	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000258149, 9606. ENSP00000337383, 9606. ENSP00000350512, 9606. ENSP00000360916, 9606. ENSP00000462521, 9606. ENSP00000480499	SIRT1, PYCARD, MDM2, NLRP3, COPS5, VAV2, TXNIP, ITCH
GO:0048731	System development	13	4426	0.44	0.0092	9606. ENSP00000212015, 9606. ENSP00000250003, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000262995, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000307305, 9606. ENSP00000340944, 9606. ENSP00000360916, 9606. ENSP00000363377, 9606. ENSP00000462521	SIRT1, MYOD1, MDM2, SMAD2, YY1, GAB1, EP300, KAT2B, DDIT4, PTPN11, VAV2, FOXO4, TXNIP
GO:0032688	Negative regulation of interferon-beta production	2	14	2.12	0.0093	9606. ENSP00000247470, 9606. ENSP00000262238	PYCARD, YY1
GO:0045722	Positive regulation of gluconeogenesis	2	14	2.12	0.0093	9606. ENSP00000212015, 9606. ENSP00000263754	SIRT1, KAT2B
GO:0071704	Organic substance metabolic process	17	7755	0.31	0.0096	9606. ENSP00000212015, 9606. ENSP00000216185, 9606. ENSP00000247470, 9606. ENSP00000250003, 9606. ENSP00000250495, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000264389, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000350512, 9606. ENSP00000363377, 9606. ENSP00000363641, 9606. ENSP00000480499	SIRT1, TXN2, PYCARD, MYOD1, NEDD8, MDM2, SMAD2, YY1, EP300, KAT2B, COPS4, NLRP3, PTPN11, COPS5, FOXO4, TXN, ITCH
GO:0032611	interleukin-1 beta production	2	15	2.09	0.0101	9606. ENSP00000247470, 9606. ENSP00000337383	PYCARD, NLRP3
GO:0043518	Negative regulation of dna damage response, signal transduction by p53 class mediator	2	15	2.09	0.0101	9606. ENSP00000212015, 9606. ENSP00000258149	SIRT1, MDM2
GO:0044092	Negative regulation of molecular function	7	1163	0.75	0.0101	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000258149, 9606. ENSP00000263754, 9606. ENSP00000337383, 9606. ENSP00000462521, 9606. ENSP00000480499	SIRT1, PYCARD, MDM2, KAT2B, NLRP3, TXNIP, ITCH
GO:0048513	Animal organ development	11	3197	0.51	0.0106	9606. ENSP00000212015, 9606. ENSP00000250003, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000307305, 9606. ENSP00000340944, 9606. ENSP00000363377, 9606. ENSP00000462521	SIRT1, MYOD1, MDM2, SMAD2, YY1, EP300, KAT2B, DDIT4, PTPN11, FOXO4, TXNIP
GO:0010225	Response to uv-c	2	16	2.07	0.011	9606. ENSP00000258149, 9606. ENSP00000262238	MDM2, YY1
GO:0044773	Mitotic dna damage checkpoint	3	101	1.44	0.0117	9606. ENSP00000258149, 9606. ENSP00000263253, 9606. ENSP00000363377	MDM2, EP300, FOXO4
GO:0035855	Megakaryocyte development	2	17	2.04	0.0118	9606. ENSP00000263253, 9606. ENSP00000340944	EP300, PTPN11
GO:0048585	Negative regulation of response to stimulus	8	1636	0.66	0.0118	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000307305, 9606. ENSP00000337383, 9606. ENSP00000363641, 9606. ENSP00000480499	SIRT1, PYCARD, MDM2, SMAD2, DDIT4, NLRP3, TXN, ITCH
GO:0071375	Cellular response to peptide hormone stimulus	4	269	1.14	0.0118	9606. ENSP00000258149, 9606. ENSP00000262995, 9606. ENSP00000263754, 9606. ENSP00000363377	MDM2, GAB1, KAT2B, FOXO4
GO:0042127	Regulation of cell population proliferation	8	1642	0.66	0.0119	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000250003, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000263754, 9606. ENSP00000363377, 9606. ENSP00000462521	SIRT1, PYCARD, MYOD1, MDM2, SMAD2, KAT2B, FOXO4, TXNIP
GO:0051091	Positive regulation of dna-binding transcription factor activity	4	271	1.14	0.0119	9606. ENSP00000247470, 9606. ENSP00000263253, 9606. ENSP00000337383, 9606. ENSP00000350512	PYCARD, EP300, NLRP3, COPS5
GO:0006281	DNA repair	5	522	0.95	0.0123	9606. ENSP00000212015, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000264389, 9606. ENSP00000350512	SIRT1, YY1, EP300, COPS4, COPS5
GO:0007507	Heart development	5	522	0.95	0.0123	9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000340944	MDM2, SMAD2, EP300, KAT2B, PTPN11
GO:0009967	Positive regulation of signal transduction	8	1654	0.65	0.0123	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000262160, 9606. ENSP00000262995, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000340944, 9606. ENSP00000363641	SIRT1, PYCARD, SMAD2, GAB1, EP300, KAT2B, PTPN11, TXN
GO:0016573	Histone acetylation	3	105	1.43	0.0123	9606. ENSP00000250003, 9606. ENSP00000263253, 9606. ENSP00000263754	MYOD1, EP300, KAT2B
GO:0030335	Positive regulation of cell migration	5	522	0.95	0.0123	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000258149, 9606. ENSP00000262995, 9606. ENSP00000363377	SIRT1, PYCARD, MDM2, GAB1, FOXO4
GO:0062014	Negative regulation of small molecule metabolic process	3	104	1.43	0.0123	9606. ENSP00000212015, 9606. ENSP00000263253, 9606. ENSP00000307305	SIRT1, EP300, DDIT4
GO:0007221	Positive regulation of transcription of notch receptor target	2	18	2.02	0.0125	9606. ENSP00000263253, 9606. ENSP00000263754	EP300, KAT2B
GO:0002821	Positive regulation of adaptive immune response	3	106	1.42	0.0126	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000337383	SIRT1, PYCARD, NLRP3
GO:0051241	Negative regulation of multicellular organismal process	7	1231	0.72	0.0126	9606. ENSP00000247470, 9606. ENSP00000258149, 9606. ENSP00000262238, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000363377, 9606. ENSP00000480499	PYCARD, MDM2, YY1, NLRP3, PTPN11, FOXO4, ITCH

Table S6. the full list of KEGG analysis and GO analysis for TXNIP

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0051726	Regulation of cell cycle	7	1230	0.72	0.0126	9606. ENSP00000212015, 9606. ENSP00000258149, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000340944, 9606. ENSP00000350512, 9606. ENSP00000363377	SIRT1, MDM2, EP300, KAT2B, PTPN11, COPS5, FOXO4
GO:0001818	Negative regulation of cytokine production	4	280	1.12	0.0127	9606. ENSP00000247470, 9606. ENSP00000262238, 9606. ENSP00000337383, 9606. ENSP00000480499	PYCARD, YY1, NLRP3, ITCH
GO:0048856	Anatomical structure development	14	5402	0.38	0.0131	9606. ENSP00000212015, 9606. ENSP00000250003, 9606. ENSP00000250495, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000262995, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000307305, 9606. ENSP00000340944, 9606. ENSP00000360916, 9606. ENSP00000363377, 9606. ENSP00000462521	SIRT1, MYOD1, NEDD8, MDM2, SMAD2, YY1, GAB1, EP300, KAT2B, DDIT4, PTPN11, VAV2, FOXO4, TXNIP
GO:0030220	Platelet formation	2	19	1.99	0.0133	9606. ENSP00000263253, 9606. ENSP00000340944	EP300, PTPN11
GO:0007517	Muscle organ development	4	291	1.11	0.0141	9606. ENSP00000212015, 9606. ENSP00000250003, 9606. ENSP00000263253, 9606. ENSP00000363377	SIRT1, MYOD1, EP300, FOXO4
GO:0009968	Negative regulation of signal transduction	7	1271	0.71	0.0142	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000307305, 9606. ENSP00000337383, 9606. ENSP00000480499	SIRT1, PYCARD, MDM2, SMAD2, DDIT4, NLRP3, ITCH
GO:0031647	Regulation of protein stability	4	293	1.1	0.0142	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000258149, 9606. ENSP00000263253	SIRT1, PYCARD, MDM2, EP300
GO:0035556	Intracellular signal transduction	8	1712	0.64	0.0142	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000263253, 9606. ENSP00000307305, 9606. ENSP00000360916, 9606. ENSP00000480499	SIRT1, PYCARD, MDM2, SMAD2, EP300, DDIT4, VAV2, ITCH
GO:0048011	Neurotrophin trk receptor signaling pathway	2	20	1.97	0.0142	9606. ENSP00000307305, 9606. ENSP00000340944	DDIT4, PTPN11
GO:0061647	Histone h3-k9 modification	2	20	1.97	0.0142	9606. ENSP00000212015, 9606. ENSP00000263754	SIRT1, KAT2B
GO:0050776	Regulation of immune response	6	896	0.8	0.0151	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000263253, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000360916	SIRT1, PYCARD, EP300, NLRP3, PTPN11, VAV2
GO:0017015	Regulation of transforming growth factor beta receptor signaling pathway	3	119	1.37	0.0153	9606. ENSP00000212015, 9606. ENSP00000262160, 9606. ENSP00000263253	SIRT1, SMAD2, EP300
GO:0042542	Response to hydrogen peroxide	3	119	1.37	0.0153	9606. ENSP00000212015, 9606. ENSP00000258149, 9606. ENSP00000462521	SIRT1, MDM2, TXNIP
GO:0006662	Glycerol ether metabolic process	2	22	1.93	0.0156	9606. ENSP00000216185, 9606. ENSP00000363641	TXN2, TXN
GO:0007219	Notch signaling pathway	3	120	1.37	0.0156	9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000480499	EP300, KAT2B, ITCH
GO:0045786	Negative regulation of cell cycle	5	571	0.91	0.0156	9606. ENSP00000258149, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000340944, 9606. ENSP00000363377	MDM2, EP300, KAT2B, PTPN11, FOXO4
GO:0051240	Positive regulation of multicellular organismal process	8	1770	0.62	0.0162	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000250003, 9606. ENSP00000262160, 9606. ENSP00000262995, 9606. ENSP00000263253, 9606. ENSP00000337383, 9606. ENSP00000340944	SIRT1, PYCARD, MYOD1, SMAD2, GAB1, EP300, NLRP3, PTPN11
GO:0006915	Apoptotic process	6	918	0.78	0.0165	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000263253, 9606. ENSP00000307305, 9606. ENSP00000337383, 9606. ENSP00000480499	SIRT1, PYCARD, EP300, DDIT4, NLRP3, ITCH
GO:0043549	Regulation of kinase activity	6	918	0.78	0.0165	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000263754, 9606. ENSP00000340944, 9606. ENSP00000360916, 9606. ENSP00000363641	SIRT1, PYCARD, KAT2B, PTPN11, VAV2, TXN
GO:0000715	Nucleotide-excision repair, dna damage recognition	2	23	1.91	0.0166	9606. ENSP00000264389, 9606. ENSP00000350512	COPS4, COPS5
GO:0071417	Cellular response to organonitrogen compound	5	590	0.9	0.0176	9606. ENSP00000258149, 9606. ENSP00000262995, 9606. ENSP00000263754, 9606. ENSP00000337383, 9606. ENSP00000363377	MDM2, GAB1, KAT2B, NLRP3, FOXO4
GO:0046628	Positive regulation of insulin receptor signaling pathway	2	24	1.89	0.0178	9606. ENSP00000212015, 9606. ENSP00000340944	SIRT1, PTPN11
GO:1902254	Negative regulation of intrinsic apoptotic signaling pathway by p53 class mediator	2	24	1.89	0.0178	9606. ENSP00000212015, 9606. ENSP00000258149	SIRT1, MDM2
GO:0044238	Primary metabolic process	16	7332	0.31	0.0179	9606. ENSP00000212015, 9606. ENSP00000216185, 9606. ENSP00000247470, 9606. ENSP00000250003, 9606. ENSP00000250495, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000264389, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000350512, 9606. ENSP00000363377, 9606. ENSP00000480499	SIRT1, TXN2, PYCARD, MYOD1, NEDD8, MDM2, SMAD2, YY1, EP300, KAT2B, COPS4, NLRP3, PTPN11, COPS5, FOXO4, ITCH
GO:0002367	Cytokine production involved in immune response	2	25	1.87	0.0189	9606. ENSP00000212015, 9606. ENSP00000337383	SIRT1, NLRP3
GO:0002684	Positive regulation of immune system process	6	949	0.77	0.0189	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000263253, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000360916	SIRT1, PYCARD, EP300, NLRP3, PTPN11, VAV2
GO:0010948	Negative regulation of cell cycle process	4	328	1.06	0.0189	9606. ENSP00000258149, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000363377	MDM2, EP300, KAT2B, FOXO4
GO:0048545	Response to steroid hormone	4	328	1.06	0.0189	9606. ENSP00000250003, 9606. ENSP00000258149, 9606. ENSP00000307305, 9606. ENSP00000462521	MYOD1, MDM2, DDIT4, TXNIP
GO:0060765	Regulation of androgen receptor signaling pathway	2	25	1.87	0.0189	9606. ENSP00000212015, 9606. ENSP00000263253	SIRT1, EP300

Table S6. the full list of KEGG analysis and GO analysis for TXNIP

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0050778	Positive regulation of immune response	5	607	0.89	0.0191	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000263253, 9606. ENSP00000337383, 9606. ENSP00000360916	SIRT1, PYCARD, EP300, NLRP3, VAV2
GO:0044093	Positive regulation of molecular function	8	1842	0.61	0.0197	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000263253, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000350512, 9606. ENSP00000360916, 9606. ENSP00000363641	SIRT1, PYCARD, EP300, NLRP3, PTPN11, COPS5, VAV2, TXN
GO:0043280	Positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	3	136	1.31	0.0202	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000337383	SIRT1, PYCARD, NLRP3
GO:0071901	Negative regulation of protein serine/threonine kinase activity	3	136	1.31	0.0202	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000263754	SIRT1, PYCARD, KAT2B
GO:0009749	Response to glucose	3	138	1.31	0.0207	9606. ENSP00000216185, 9606. ENSP00000262160, 9606. ENSP00000462521	TXN2, SMAD2, TXNIP
GO:0051094	Positive regulation of developmental process	7	1389	0.67	0.0207	9606. ENSP00000212015, 9606. ENSP00000250003, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262995, 9606. ENSP00000263253, 9606. ENSP00000337383	SIRT1, MYOD1, MDM2, SMAD2, GAB1, EP300, NLRP3
GO:0050790	Regulation of catalytic activity	9	2386	0.55	0.0208	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000258149, 9606. ENSP00000263754, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000360916, 9606. ENSP00000363641, 9606. ENSP00000462521	SIRT1, PYCARD, MDM2, KAT2B, NLRP3, PTPN11, VAV2, TXN, TXNIP
GO:0010243	Response to organonitrogen compound	6	987	0.75	0.0217	9606. ENSP00000212015, 9606. ENSP00000258149, 9606. ENSP00000262995, 9606. ENSP00000263754, 9606. ENSP00000337383, 9606. ENSP00000363377	SIRT1, MDM2, GAB1, KAT2B, NLRP3, FOXO4
GO:0051128	Regulation of cellular component organization	9	2402	0.54	0.0217	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000250003, 9606. ENSP00000258149, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000340944, 9606. ENSP00000480499	SIRT1, PYCARD, MYOD1, MDM2, YY1, EP300, KAT2B, PTPN11, ITCH
GO:0045597	Positive regulation of cell differentiation	6	993	0.75	0.0223	9606. ENSP00000212015, 9606. ENSP00000250003, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000263253, 9606. ENSP00000337383	SIRT1, MYOD1, MDM2, SMAD2, EP300, NLRP3
GO:0044237	Cellular metabolic process	16	7513	0.3	0.0224	9606. ENSP00000212015, 9606. ENSP00000216185, 9606. ENSP00000250003, 9606. ENSP00000250495, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000264389, 9606. ENSP00000307305, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000350512, 9606. ENSP00000363377, 9606. ENSP00000480499	SIRT1, TXN2, MYOD1, NEDD8, MDM2, SMAD2, YY1, EP300, KAT2B, COPS4, DDIT4, NLRP3, PTPN11, COPS5, FOXO4, ITCH
GO:0016570	Histone modification	4	351	1.03	0.0225	9606. ENSP00000212015, 9606. ENSP00000250003, 9606. ENSP00000263253, 9606. ENSP00000263754	SIRT1, MYOD1, EP300, KAT2B
GO:0044419	Interspecies interaction between organisms	8	1899	0.59	0.0228	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000258149, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000307305, 9606. ENSP00000337383, 9606. ENSP00000480499	SIRT1, PYCARD, MDM2, EP300, KAT2B, DDIT4, NLRP3, ITCH
GO:0051150	Regulation of smooth muscle cell differentiation	2	30	1.79	0.0238	9606. ENSP00000212015, 9606. ENSP00000363377	SIRT1, FOXO4
GO:0032101	Regulation of response to external stimulus	6	1013	0.74	0.0241	9606. ENSP00000247470, 9606. ENSP00000250003, 9606. ENSP00000263253, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000480499	PYCARD, MYOD1, EP300, NLRP3, PTPN11, ITCH
GO:0060325	Face morphogenesis	2	31	1.78	0.0249	9606. ENSP00000263253, 9606. ENSP00000340944	EP300, PTPN11
GO:0043065	Positive regulation of apoptotic process	5	660	0.85	0.0252	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000337383, 9606. ENSP00000360916, 9606. ENSP00000462521	SIRT1, PYCARD, NLRP3, VAV2, TXNIP
GO:0030154	Cell differentiation	11	3702	0.44	0.0261	9606. ENSP00000212015, 9606. ENSP00000250003, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000262995, 9606. ENSP00000263253, 9606. ENSP00000307305, 9606. ENSP00000340944, 9606. ENSP00000363377, 9606. ENSP00000462521	SIRT1, MYOD1, MDM2, SMAD2, YY1, GAB1, EP300, DDIT4, PTPN11, FOXO4, TXNIP
GO:0009894	Regulation of catabolic process	6	1038	0.73	0.0264	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000258149, 9606. ENSP00000263253, 9606. ENSP00000307305, 9606. ENSP00000480499	SIRT1, PYCARD, MDM2, EP300, DDIT4, ITCH
GO:1902533	Positive regulation of intracellular signal transduction	6	1041	0.73	0.0267	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000262995, 9606. ENSP00000263253, 9606. ENSP00000340944, 9606. ENSP00000363641	SIRT1, PYCARD, GAB1, EP300, PTPN11, TXN
GO:0031347	Regulation of defense response	5	674	0.84	0.0268	9606. ENSP00000247470, 9606. ENSP00000263253, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000480499	PYCARD, EP300, NLRP3, PTPN11, ITCH
GO:0032269	Negative regulation of cellular protein metabolic process	6	1043	0.73	0.0268	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000258149, 9606. ENSP00000263754, 9606. ENSP00000307305, 9606. ENSP00000480499	SIRT1, PYCARD, MDM2, KAT2B, DDIT4, ITCH
GO:0007346	Regulation of mitotic cell cycle	5	676	0.84	0.0271	9606. ENSP00000212015, 9606. ENSP00000258149, 9606. ENSP00000263253, 9606. ENSP00000340944, 9606. ENSP00000363377	SIRT1, MDM2, EP300, PTPN11, FOXO4
GO:0001816	Cytokine production	3	158	1.25	0.0273	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000337383	SIRT1, PYCARD, NLRP3

Table S6. the full list of KEGG analysis and GO analysis for TXNIP

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0045862	Positive regulation of proteolysis	4	377	1	0.0273	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000258149, 9606. ENSP00000337383	SIRT1, PYCARD, MDM2, NLRP3
GO:0045787	Positive regulation of cell cycle	4	388	0.98	0.0297	9606. ENSP00000258149, 9606. ENSP00000263253, 9606. ENSP00000340944, 9606. ENSP00000363377	MDM2, EP300, PTPN11, FOXO4
GO:2001242	Regulation of intrinsic apoptotic signaling pathway	3	164	1.23	0.0297	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000258149	SIRT1, PYCARD, MDM2
GO:0048589	Developmental growth	4	389	0.98	0.0298	9606. ENSP00000250003, 9606. ENSP00000262160, 9606. ENSP00000263253, 9606. ENSP00000340944	MYOD1, SMAD2, EP300, PTPN11
GO:0034504	Protein localization to nucleus	3	165	1.23	0.03	9606. ENSP00000258149, 9606. ENSP00000363641, 9606. ENSP00000462521	MDM2, TXN, TXNIP
GO:0048008	Platelet-derived growth factor receptor signaling pathway	2	36	1.71	0.0305	9606. ENSP00000340944, 9606. ENSP00000462521	PTPN11, TXNIP
GO:0032869	Cellular response to insulin stimulus	3	169	1.22	0.0316	9606. ENSP00000262995, 9606. ENSP00000263754, 9606. ENSP00000363377	GAB1, KAT2B, FOXO4
GO:0051897	Positive regulation of protein kinase b signaling	3	170	1.22	0.032	9606. ENSP00000262995, 9606. ENSP00000340944, 9606. ENSP00000363641	GAB1, PTPN11, TXN
GO:0002831	Regulation of response to biotic stimulus	4	406	0.96	0.0337	9606. ENSP00000247470, 9606. ENSP00000263253, 9606. ENSP00000340944, 9606. ENSP00000480499	PYCARD, EP300, PTPN11, ITCH
GO:0032501	Multicellular organismal process	15	6933	0.3	0.0337	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000250003, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000262995, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000307305, 9606. ENSP00000337383, 9606. ENSP00000340944, 9606. ENSP00000360916, 9606. ENSP00000363377, 9606. ENSP00000462521	SIRT1, PYCARD, MYOD1, MDM2, SMAD2, YY1, GAB1, EP300, KAT2B, DDIT4, NLRP3, PTPN11, VAV2, FOXO4, TXNIP
GO:0010467	Gene expression	8	2056	0.56	0.0339	9606. ENSP00000212015, 9606. ENSP00000247470, 9606. ENSP00000262160, 9606. ENSP00000262238, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000337383, 9606. ENSP00000350512	SIRT1, PYCARD, SMAD2, YY1, EP300, KAT2B, NLRP3, COPS5
GO:0014911	Positive regulation of smooth muscle cell migration	2	39	1.68	0.0342	9606. ENSP00000258149, 9606. ENSP00000363377	MDM2, FOXO4
GO:0045596	Negative regulation of cell differentiation	5	728	0.81	0.0347	9606. ENSP00000212015, 9606. ENSP00000258149, 9606. ENSP00000262238, 9606. ENSP00000340944, 9606. ENSP00000363377	SIRT1, MDM2, YY1, PTPN11, FOXO4
GO:1901796	Regulation of signal transduction by p53 class mediator	3	182	1.19	0.0375	9606. ENSP00000212015, 9606. ENSP00000258149, 9606. ENSP00000263253	SIRT1, MDM2, EP300
GO:0046328	Regulation of jnk cascade	3	183	1.18	0.038	9606. ENSP00000247470, 9606. ENSP00000350512, 9606. ENSP00000480499	PYCARD, COPS5, ITCH
GO:0032007	Negative regulation of tor signaling	2	43	1.64	0.0403	9606. ENSP00000212015, 9606. ENSP00000307305	SIRT1, DDIT4
GO:0042593	Glucose homeostasis	3	188	1.17	0.0407	9606. ENSP00000212015, 9606. ENSP00000340944, 9606. ENSP00000363377	SIRT1, PTPN11, FOXO4
GO:0071456	Cellular response to hypoxia	3	189	1.17	0.0412	9606. ENSP00000212015, 9606. ENSP00000258149, 9606. ENSP00000263253	SIRT1, MDM2, EP300
GO:0043966	Histone h3 acetylation	2	45	1.62	0.0433	9606. ENSP00000250003, 9606. ENSP00000263754	MYOD1, KAT2B
GO:0016032	Viral process	5	776	0.78	0.0447	9606. ENSP00000212015, 9606. ENSP00000258149, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000480499	SIRT1, MDM2, EP300, KAT2B, ITCH
GO:0062012	Regulation of small molecule metabolic process	4	449	0.92	0.0463	9606. ENSP00000212015, 9606. ENSP00000263253, 9606. ENSP00000263754, 9606. ENSP00000307305	SIRT1, EP300, KAT2B, DDIT4
GO:0043124	Negative regulation of i-kappab kinase/nf-kappab signaling	2	47	1.6	0.0464	9606. ENSP00000212015, 9606. ENSP00000247470	SIRT1, PYCARD
GO:1903202	Negative regulation of oxidative stress-induced cell death	2	47	1.6	0.0464	9606. ENSP00000212015, 9606. ENSP00000363641	SIRT1, TXN
GO:0065008	Regulation of biological quality	11	4042	0.4	0.0476	9606. ENSP00000212015, 9606. ENSP00000216185, 9606. ENSP00000247470, 9606. ENSP00000250495, 9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000263253, 9606. ENSP00000340944, 9606. ENSP00000360916, 9606. ENSP00000363377, 9606. ENSP00000363641	SIRT1, TXN2, PYCARD, NEDD8, MDM2, SMAD2, EP300, PTPN11, VAV2, FOXO4, TXN
GO:0040029	Regulation of gene expression, epigenetic	3	202	1.14	0.0477	9606. ENSP00000212015, 9606. ENSP00000263253, 9606. ENSP00000263754	SIRT1, EP300, KAT2B
GO:0072132	Mesenchyme morphogenesis	2	49	1.58	0.0492	9606. ENSP00000258149, 9606. ENSP00000262160	MDM2, SMAD2
GO:0001819	Positive regulation of cytokine production	4	461	0.91	0.0494	9606. ENSP00000247470, 9606. ENSP00000263253, 9606. ENSP00000337383, 9606. ENSP00000340944	PYCARD, EP300, NLRP3, PTPN11
hsa04625	C-type lectin receptor signaling pathway	4	102	1.56	0.00051	9606. ENSP00000247470, 9606. ENSP00000258149, 9606. ENSP00000337383, 9606. ENSP00000340944	PYCARD, MDM2, NLRP3, PTPN11
hsa04330	Notch signaling pathway	2	52	1.55	0.0311	9606. ENSP00000263253, 9606. ENSP00000263754	EP300, KAT2B
hsa04068	FoxO signaling pathway	4	127	1.47	0.00088	9606. ENSP00000212015, 9606. ENSP00000258149, 9606. ENSP00000263253, 9606. ENSP00000363377	SIRT1, MDM2, EP300, FOXO4
hsa04621	NOD-like receptor signaling pathway	5	174	1.43	0.00037	9606. ENSP00000216185, 9606. ENSP00000247470, 9606. ENSP00000337383, 9606. ENSP00000363641, 9606. ENSP00000462521	TXN2, PYCARD, NLRP3, TXN, TXNIP
hsa05133	Pertussis	2	74	1.4	0.05	9606. ENSP00000247470, 9606. ENSP00000337383	PYCARD, NLRP3
hsa04110	Cell cycle	3	120	1.37	0.0108	9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000263253	MDM2, SMAD2, EP300
hsa04919	Thyroid hormone signaling pathway	3	119	1.37	0.0108	9606. ENSP00000258149, 9606. ENSP00000263253, 9606. ENSP00000263754	MDM2, EP300, KAT2B
hsa04218	Cellular senescence	3	150	1.27	0.0157	9606. ENSP00000212015, 9606. ENSP00000258149, 9606. ENSP00000262160	SIRT1, MDM2, SMAD2
hsa05131	Shigellosis	4	218	1.23	0.0035	9606. ENSP00000247470, 9606. ENSP00000258149, 9606. ENSP00000337383, 9606. ENSP00000363377	PYCARD, MDM2, NLRP3, FOXO4
hsa05164	Influenza A	3	165	1.23	0.019	9606. ENSP00000247470, 9606. ENSP00000263253, 9606. ENSP00000337383	PYCARD, EP300, NLRP3
hsa05130	Pathogenic Escherichia coli infection	3	187	1.17	0.0235	9606. ENSP00000247470, 9606. ENSP00000337383, 9606. ENSP00000340944	PYCARD, NLRP3, PTPN11
hsa05166	Human T-cell leukemia virus 1 infection	3	211	1.12	0.0311	9606. ENSP00000262160, 9606. ENSP00000263253, 9606. ENSP00000263754	SMAD2, EP300, KAT2B
hsa04014	Ras signaling pathway	3	226	1.09	0.0335	9606. ENSP00000262995, 9606. ENSP00000340944, 9606. ENSP00000363377	GAB1, PTPN11, FOXO4
hsa04144	Endocytosis	3	241	1.06	0.038	9606. ENSP00000258149, 9606. ENSP00000262160, 9606. ENSP00000480499	MDM2, SMAD2, ITCH

Table S7. the full list of KEGG analysis and GO analysis for VCAM1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0007229	Integrin-mediated signaling pathway	12	94	2.08	1.20E-18	9606.ENSP0000007722, 9606.ENSP0000261023, 9606.ENSP0000264741, 9606.ENSP0000267082, 9606.ENSP00000282588, 9606.ENSP0000293379, 9606.ENSP00000373854, 9606.ENSP0000379350, 9606.ENSP0000380227, 9606.ENSP0000380948, 9606.ENSP0000441691, 9606.ENSP00000454623	ITGA3, ITGAV, ITGA9, ITGB7, ITGA1, ITGA5, ITGAD, ITGB1, ITGA4, ITGB2, ITGAM, ITGAX
GO:0030198	Extracellular matrix organization	15	338	1.62	1.62E-18	9606.ENSP0000007722, 9606.ENSP0000261023, 9606.ENSP0000264741, 9606.ENSP0000264832, 9606.ENSP00000267082, 9606.ENSP0000282588, 9606.ENSP00000293379, 9606.ENSP0000294728, 9606.ENSP0000373854, 9606.ENSP0000379350, 9606.ENSP0000380227, 9606.ENSP00000380948, 9606.ENSP0000398698, 9606.ENSP00000441691, 9606.ENSP0000454623	ITGA3, ITGAV, ITGA9, ICAM1, ITGB7, ITGA1, ITGA5, VCAM1, ITGAD, ITGB1, ITGA4, ITGB2, TNF, ITGAM, ITGAX
GO:0050900	Leukocyte migration	14	316	1.62	3.79E-17	9606.ENSP0000007722, 9606.ENSP0000261023, 9606.ENSP0000264741, 9606.ENSP0000264832, 9606.ENSP00000267082, 9606.ENSP0000282588, 9606.ENSP00000293379, 9606.ENSP0000294728, 9606.ENSP0000379350, 9606.ENSP0000380227, 9606.ENSP0000380948, 9606.ENSP00000398698, 9606.ENSP0000441691, 9606.ENSP00000454623	ITGA3, ITGAV, ITGA9, ICAM1, ITGB7, ITGA1, ITGA5, VCAM1, ITGB1, ITGA4, ITGB2, TNF, ITGAM, ITGAX
GO:0007155	Cell adhesion	17	925	1.23	4.40E-16	9606.ENSP0000007722, 9606.ENSP0000261023, 9606.ENSP0000264741, 9606.ENSP0000264832, 9606.ENSP00000267082, 9606.ENSP0000267257, 9606.ENSP00000282588, 9606.ENSP0000293379, 9606.ENSP0000294728, 9606.ENSP0000356042, 9606.ENSP0000373854, 9606.ENSP00000379350, 9606.ENSP0000380227, 9606.ENSP00000380948, 9606.ENSP0000398698, 9606.ENSP0000441691, 9606.ENSP0000454623	ITGA3, ITGAV, ITGA9, ICAM1, ITGB7, PXN, ITGA1, ITGA5, VCAM1, EZR, ITGAD, ITGB1, ITGA4, ITGB2, TNF, ITGAM, ITGAX
GO:0034113	Heterotypic cell-cell adhesion	9	36	2.37	4.40E-16	9606.ENSP0000261023, 9606.ENSP0000267082, 9606.ENSP0000293379, 9606.ENSP0000294728, 9606.ENSP00000373854, 9606.ENSP0000379350, 9606.ENSP00000380227, 9606.ENSP0000380948, 9606.ENSP0000454623	ITGAV, ITGB7, ITGA5, VCAM1, ITGAD, ITGB1, ITGA4, ITGB2, ITGAX
GO:0007159	Leukocyte cell-cell adhesion	9	56	2.18	1.25E-14	9606.ENSP0000264832, 9606.ENSP0000267082, 9606.ENSP0000293379, 9606.ENSP0000294728, 9606.ENSP00000356042, 9606.ENSP0000379350, 9606.ENSP00000380227, 9606.ENSP0000380948, 9606.ENSP0000398698	ICAM1, ITGB7, ITGA5, VCAM1, EZR, ITGB1, ITGA4, ITGB2, TNF
GO:0045123	Cellular extravasation	8	42	2.25	2.84E-13	9606.ENSP0000264832, 9606.ENSP0000267082, 9606.ENSP0000282588, 9606.ENSP0000294728, 9606.ENSP00000379350, 9606.ENSP0000380227, 9606.ENSP00000380948, 9606.ENSP0000398698	ICAM1, ITGB7, ITGA1, VCAM1, ITGB1, ITGA4, ITGB2, TNF
GO:0016477	Cell migration	15	896	1.19	4.95E-13	9606.ENSP0000007722, 9606.ENSP0000261023, 9606.ENSP0000264741, 9606.ENSP0000264832, 9606.ENSP00000267082, 9606.ENSP0000267257, 9606.ENSP00000282588, 9606.ENSP0000293379, 9606.ENSP0000294728, 9606.ENSP0000379350, 9606.ENSP0000380227, 9606.ENSP00000380948, 9606.ENSP0000398698, 9606.ENSP00000441691, 9606.ENSP0000454623	ITGA3, ITGAV, ITGA9, ICAM1, ITGB7, PXN, ITGA1, ITGA5, VCAM1, ITGB1, ITGA4, ITGB2, TNF, ITGAM, ITGAX
GO:0007166	Cell surface receptor signaling pathway	19	2325	0.88	5.23E-13	9606.ENSP0000007722, 9606.ENSP0000162749, 9606.ENSP0000261023, 9606.ENSP0000262613, 9606.ENSP00000264741, 9606.ENSP0000264832, 9606.ENSP00000267082, 9606.ENSP0000267257, 9606.ENSP0000282588, 9606.ENSP0000293379, 9606.ENSP0000294728, 9606.ENSP00000304915, 9606.ENSP0000373854, 9606.ENSP00000379350, 9606.ENSP0000380227, 9606.ENSP0000380948, 9606.ENSP0000398698, 9606.ENSP0000441691, 9606.ENSP0000454623	ITGA3, TNFRSF1A, ITGAV, SLC9A3R1, ITGA9, ICAM1, ITGB7, PXN, ITGA1, ITGA5, VCAM1, IL13, ITGAD, ITGB1, ITGA4, ITGB2, TNF, ITGAM, ITGAX
GO:0098609	Cell-cell adhesion	13	505	1.38	5.23E-13	9606.ENSP0000261023, 9606.ENSP0000264832, 9606.ENSP0000267082, 9606.ENSP0000293379, 9606.ENSP00000294728, 9606.ENSP0000356042, 9606.ENSP00000373854, 9606.ENSP0000379350, 9606.ENSP0000380227, 9606.ENSP0000380948, 9606.ENSP0000398698, 9606.ENSP00000441691, 9606.ENSP0000454623	ITGAV, ICAM1, ITGB7, ITGA5, VCAM1, EZR, ITGAD, ITGB1, ITGA4, ITGB2, TNF, ITGAM, ITGAX
GO:0006928	Movement of cell or subcellular component	17	1501	1.02	5.29E-13	9606.ENSP0000007722, 9606.ENSP0000261023, 9606.ENSP0000262613, 9606.ENSP0000264741, 9606.ENSP00000264832, 9606.ENSP0000267082, 9606.ENSP00000267257, 9606.ENSP0000282588, 9606.ENSP0000293379, 9606.ENSP0000294728, 9606.ENSP0000356042, 9606.ENSP00000379350, 9606.ENSP0000380227, 9606.ENSP00000380948, 9606.ENSP0000398698, 9606.ENSP0000441691, 9606.ENSP0000454623	ITGA3, ITGAV, SLC9A3R1, ITGA9, ICAM1, ITGB7, PXN, ITGA1, ITGA5, VCAM1, EZR, ITGB1, ITGA4, ITGB2, TNF, ITGAM, ITGAX

Table S7. the full list of KEGG analysis and GO analysis for VCAM1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0033627	Cell adhesion mediated by integrin	7	24	2.43	1.18E-12	9606.ENSP00000261023, 9606.ENSP00000264832, 9606.ENSP00000267082, 9606.ENSP00000293379, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948	ITGAV, ICAM1, ITGB7, ITGA5, ITGB1, ITGA4, ITGB2
GO:0040011	Locomotion	16	1251	1.08	1.18E-12	9606.ENSP00000007722, 9606.ENSP00000261023, 9606.ENSP00000264741, 9606.ENSP00000264832, 9606.ENSP00000267082, 9606.ENSP00000267257, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000294728, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691, 9606.ENSP00000454623	ITGA3, ITGAV, ITGA9, ICAM1, ITGB7, PXN, ITGA1, ITGA5, VCAM1, EZR, ITGB1, ITGA4, ITGB2, TNF, ITGAM, ITGAX
GO:0031589	Cell-substrate adhesion	10	182	1.71	1.67E-12	9606.ENSP00000007722, 9606.ENSP00000261023, 9606.ENSP00000267082, 9606.ENSP00000267257, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000294728, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948	ITGA3, ITGAV, ITGB7, PXN, ITGA1, ITGA5, VCAM1, ITGB1, ITGA4, ITGB2
GO:0007165	Signal transduction	21	4876	0.6	1.49E-10	9606.ENSP00000007722, 9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264741, 9606.ENSP00000264832, 9606.ENSP00000265709, 9606.ENSP00000267082, 9606.ENSP00000267257, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000294728, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000373854, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691, 9606.ENSP00000454623	ITGA3, TNFRSF1A, ITGAV, SLC9A3R1, ITGA9, ICAM1, ANK1, ITGB7, PXN, ITGA1, ITGA5, VCAM1, IL13, EZR, ITGAD, ITGB1, ITGA4, ITGB2, TNF, ITGAM, ITGAX
GO:0007160	Cell-matrix adhesion	8	127	1.77	5.01E-10	9606.ENSP00000007722, 9606.ENSP00000261023, 9606.ENSP00000267082, 9606.ENSP00000282588, 9606.ENSP00000294728, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948	ITGA3, ITGAV, ITGB7, ITGA1, VCAM1, ITGB1, ITGA4, ITGB2
GO:0050901	Leukocyte tethering or rolling	5	19	2.39	1.99E-08	9606.ENSP00000267082, 9606.ENSP00000294728, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000398698	ITGB7, VCAM1, ITGB1, ITGA4, TNF
GO:0002376	Immune system process	16	2481	0.78	2.69E-08	9606.ENSP00000007722, 9606.ENSP00000261023, 9606.ENSP00000264741, 9606.ENSP00000264832, 9606.ENSP00000267082, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000294728, 9606.ENSP00000304915, 9606.ENSP00000373854, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691, 9606.ENSP00000454623	ITGA3, ITGAV, ITGA9, ICAM1, ITGB7, ITGA1, ITGA5, VCAM1, IL13, ITGAD, ITGB1, ITGA4, ITGB2, TNF, ITGAM, ITGAX
GO:0016043	Cellular component organization	20	5447	0.53	5.90E-08	9606.ENSP00000007722, 9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264741, 9606.ENSP00000264832, 9606.ENSP00000265709, 9606.ENSP00000267082, 9606.ENSP00000267257, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000294728, 9606.ENSP00000356042, 9606.ENSP00000373854, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691, 9606.ENSP00000454623	ITGA3, TNFRSF1A, ITGAV, SLC9A3R1, ITGA9, ICAM1, ANK1, ITGB7, PXN, ITGA1, ITGA5, VCAM1, EZR, ITGAD, ITGB1, ITGA4, ITGB2, TNF, ITGAM, ITGAX
GO:0001704	Formation of primary germ layer	6	116	1.68	1.15E-06	9606.ENSP00000007722, 9606.ENSP00000261023, 9606.ENSP00000293379, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948	ITGA3, ITGAV, ITGA5, ITGB1, ITGA4, ITGB2
GO:1905477	Positive regulation of protein localization to membrane	6	129	1.64	2.05E-06	9606.ENSP00000007722, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691	ITGA3, EZR, ITGB1, ITGB2, TNF, ITGAM
GO:0051179	Localization	19	5591	0.5	2.18E-06	9606.ENSP00000007722, 9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264741, 9606.ENSP00000264832, 9606.ENSP00000265709, 9606.ENSP00000267082, 9606.ENSP00000267257, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000294728, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691, 9606.ENSP00000454623	ITGA3, TNFRSF1A, ITGAV, SLC9A3R1, ITGA9, ICAM1, ANK1, ITGB7, PXN, ITGA1, ITGA5, VCAM1, EZR, ITGB1, ITGA4, ITGB2, TNF, ITGAM, ITGAX
GO:0045785	Positive regulation of cell adhesion	8	423	1.25	3.13E-06	9606.ENSP00000007722, 9606.ENSP00000261023, 9606.ENSP00000264832, 9606.ENSP00000293379, 9606.ENSP00000294728, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698	ITGA3, ITGAV, ICAM1, ITGA5, VCAM1, ITGA4, ITGB2, TNF

Table S7. the full list of KEGG analysis and GO analysis for VCAM1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0048583	Regulation of response to stimulus	17	4114	0.59	3.13E-06	9606.ENSP00000007722, 9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000267082, 9606.ENSP00000267257, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000294728, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691	ITGA3, TNFRSF1A, ITGAV, SLC9A3R1, ICAM1, ITGB7, PXN, ITGA1, ITGA5, VCAM1, IL13, EZR, ITGB1, ITGA4, ITGB2, TNF, ITGAM
GO:0070887	Cellular response to chemical stimulus	15	2919	0.68	3.36E-06	9606.ENSP00000162749, 9606.ENSP00000262613, 9606.ENSP00000264741, 9606.ENSP00000264832, 9606.ENSP00000267257, 9606.ENSP00000282588, 9606.ENSP00000294728, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691, 9606.ENSP00000454623	TNFRSF1A, SLC9A3R1, ITGA9, ICAM1, PXN, ITGA1, VCAM1, IL13, EZR, ITGB1, ITGA4, ITGB2, TNF, ITGAM, ITGAX
GO:0050776	Regulation of immune response	10	896	1.02	3.37E-06	9606.ENSP00000264832, 9606.ENSP00000267082, 9606.ENSP00000294728, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691	ICAM1, ITGB7, VCAM1, IL13, EZR, ITGB1, ITGA4, ITGB2, TNF, ITGAM
GO:1904996	Positive regulation of leukocyte adhesion to vascular endothelial cell	4	20	2.27	3.55E-06	9606.ENSP00000264832, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698	ICAM1, ITGA4, ITGB2, TNF
GO:0045321	Leukocyte activation	10	929	1	4.50E-06	9606.ENSP00000261023, 9606.ENSP00000264832, 9606.ENSP00000294728, 9606.ENSP00000304915, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691, 9606.ENSP00000454623	ITGAV, ICAM1, VCAM1, IL13, ITGB1, ITGA4, ITGB2, TNF, ITGAM, ITGAX
GO:0019221	Cytokine-mediated signaling pathway	9	678	1.09	5.06E-06	9606.ENSP00000162749, 9606.ENSP00000264832, 9606.ENSP00000294728, 9606.ENSP00000304915, 9606.ENSP00000379350, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691, 9606.ENSP00000454623	TNFRSF1A, ICAM1, VCAM1, IL13, ITGB1, ITGB2, TNF, ITGAM, ITGAX
GO:0042221	Response to chemical	17	4333	0.56	5.58E-06	9606.ENSP00000007722, 9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264741, 9606.ENSP00000264832, 9606.ENSP00000267257, 9606.ENSP00000282588, 9606.ENSP00000294728, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691, 9606.ENSP00000454623	ITGA3, TNFRSF1A, ITGAV, SLC9A3R1, ITGA9, ICAM1, PXN, ITGA1, VCAM1, IL13, EZR, ITGB1, ITGA4, ITGB2, TNF, ITGAM, ITGAX
GO:0010941	Regulation of cell death	12	1696	0.82	7.94E-06	9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000304915, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691	TNFRSF1A, ITGAV, SLC9A3R1, ICAM1, ITGA1, ITGA5, IL13, ITGB1, ITGA4, ITGB2, TNF, ITGAM
GO:0072657	Protein localization to membrane	8	495	1.18	7.94E-06	9606.ENSP00000162749, 9606.ENSP00000262613, 9606.ENSP00000265709, 9606.ENSP00000267082, 9606.ENSP00000356042, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698	TNFRSF1A, SLC9A3R1, ANK1, ITGB7, EZR, ITGA4, ITGB2, TNF
GO:0071345	Cellular response to cytokine stimulus	10	1013	0.96	8.60E-06	9606.ENSP00000162749, 9606.ENSP00000264832, 9606.ENSP00000294728, 9606.ENSP00000304915, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691, 9606.ENSP00000454623	TNFRSF1A, ICAM1, VCAM1, IL13, ITGB1, ITGA4, ITGB2, TNF, ITGAM, ITGAX
GO:0009653	Anatomical structure morphogenesis	13	2165	0.75	9.21E-06	9606.ENSP00000007722, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000267082, 9606.ENSP00000267257, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000454623	ITGA3, ITGAV, SLC9A3R1, ITGB7, PXN, ITGA1, ITGA5, EZR, ITGB1, ITGA4, ITGB2, TNF, ITGAX
GO:0030335	Positive regulation of cell migration	8	522	1.15	1.11E-05	9606.ENSP00000007722, 9606.ENSP00000261023, 9606.ENSP00000264832, 9606.ENSP00000293379, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000398698, 9606.ENSP00000454623	ITGA3, ITGAV, ICAM1, ITGA5, ITGB1, ITGA4, TNF, ITGAX
GO:0032879	Regulation of localization	14	2740	0.68	1.34E-05	9606.ENSP00000007722, 9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000293379, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691, 9606.ENSP00000454623	ITGA3, TNFRSF1A, ITGAV, SLC9A3R1, ICAM1, ITGA5, IL13, EZR, ITGB1, ITGA4, ITGB2, TNF, ITGAM, ITGAX
GO:0001774	Microglial cell activation	4	32	2.07	1.45E-05	9606.ENSP00000304915, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691	IL13, ITGB2, TNF, ITGAM
GO:0022614	Membrane to membrane docking	3	5	2.75	1.45E-05	9606.ENSP00000264832, 9606.ENSP00000294728, 9606.ENSP00000356042	ICAM1, VCAM1, EZR

Table S7. the full list of KEGG analysis and GO analysis for VCAM1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0048522	Positive regulation of cellular process	18	5579	0.48	1.78E-05	9606.ENSP00000007722, 9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000265709, 9606.ENSP00000267257, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000294728, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691, 9606.ENSP00000454623	ITGA3, TNFRSF1A, ITGAV, SLC9A3R1, ICAM1, ANK1, PXN, ITGA1, ITGA5, VCAM1, IL13, EZR, ITGB1, ITGA4, ITGB2, TNF, ITGAM, ITGAX
GO:0033631	Cell-cell adhesion mediated by integrin	3	6	2.67	1.89E-05	9606.ENSP00000293379, 9606.ENSP00000379350, 9606.ENSP00000380227	ITGA5, ITGB1, ITGA4
GO:0071310	Cellular response to organic substance	13	2369	0.71	2.01E-05	9606.ENSP00000162749, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000267257, 9606.ENSP00000294728, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691, 9606.ENSP00000454623	TNFRSF1A, SLC9A3R1, ICAM1, PXN, VCAM1, IL13, EZR, ITGB1, ITGA4, ITGB2, TNF, ITGAM, ITGAX
GO:0030334	Regulation of cell migration	9	865	0.99	2.45E-05	9606.ENSP00000007722, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000293379, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000398698, 9606.ENSP00000454623	ITGA3, ITGAV, SLC9A3R1, ICAM1, ITGA5, ITGB1, ITGA4, TNF, ITGAX
GO:0042981	Regulation of apoptotic process	11	1550	0.82	2.62E-05	9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000304915, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000398698, 9606.ENSP00000441691	TNFRSF1A, ITGAV, SLC9A3R1, ICAM1, ITGA1, ITGA5, IL13, ITGB1, ITGA4, TNF, ITGAM
GO:0035987	Endodermal cell differentiation	4	41	1.96	2.75E-05	9606.ENSP00000261023, 9606.ENSP00000293379, 9606.ENSP00000380227, 9606.ENSP00000380948	ITGAV, ITGA5, ITGA4, ITGB2
GO:0010033	Response to organic substance	14	3011	0.64	3.10E-05	9606.ENSP00000007722, 9606.ENSP00000162749, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000267257, 9606.ENSP00000294728, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691, 9606.ENSP00000454623	ITGA3, TNFRSF1A, SLC9A3R1, ICAM1, PXN, VCAM1, IL13, EZR, ITGB1, ITGA4, ITGB2, TNF, ITGAM, ITGAX
GO:0030154	Cell differentiation	15	3702	0.58	4.39E-05	9606.ENSP00000007722, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000267082, 9606.ENSP00000267257, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000294728, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691	ITGA3, ITGAV, SLC9A3R1, ICAM1, ITGB7, PXN, ITGA1, ITGA5, VCAM1, EZR, ITGB1, ITGA4, ITGB2, TNF, ITGAM
GO:0098742	Cell-cell adhesion via plasma-membrane adhesion molecules	6	257	1.34	4.46E-05	9606.ENSP00000264832, 9606.ENSP00000293379, 9606.ENSP00000294728, 9606.ENSP00000379350, 9606.ENSP00000380948, 9606.ENSP00000441691	ICAM1, ITGA5, VCAM1, ITGB1, ITGB2, ITGAM
GO:0050730	Regulation of peptidyl-tyrosine phosphorylation	6	258	1.34	4.50E-05	9606.ENSP00000162749, 9606.ENSP00000264832, 9606.ENSP00000293379, 9606.ENSP00000304915, 9606.ENSP00000380948, 9606.ENSP00000398698	TNFRSF1A, ICAM1, ITGA5, IL13, ITGB2, TNF
GO:0034446	Substrate adhesion-dependent cell spreading	4	49	1.88	4.73E-05	9606.ENSP00000261023, 9606.ENSP00000267082, 9606.ENSP00000267257, 9606.ENSP00000380227	ITGAV, ITGB7, PXN, ITGA4
GO:2000351	Regulation of endothelial cell apoptotic process	4	50	1.87	5.04E-05	9606.ENSP00000264832, 9606.ENSP00000304915, 9606.ENSP00000380227, 9606.ENSP00000398698	ICAM1, IL13, ITGA4, TNF
GO:0010243	Response to organonitrogen compound	9	987	0.93	5.95E-05	9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000267257, 9606.ENSP00000294728, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698	SLC9A3R1, ICAM1, PXN, VCAM1, EZR, ITGB1, ITGA4, ITGB2, TNF
GO:0010942	Positive regulation of cell death	8	719	1.02	6.94E-05	9606.ENSP00000162749, 9606.ENSP00000262613, 9606.ENSP00000282588, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691	TNFRSF1A, SLC9A3R1, ITGA1, ITGB1, ITGA4, ITGB2, TNF, ITGAM
GO:0000902	Cell morphogenesis	8	726	1.01	7.38E-05	9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000267082, 9606.ENSP00000267257, 9606.ENSP00000282588, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227	ITGAV, SLC9A3R1, ITGB7, PXN, ITGA1, EZR, ITGB1, ITGA4
GO:0048856	Anatomical structure development	17	5402	0.47	8.38E-05	9606.ENSP00000007722, 9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000267082, 9606.ENSP00000267257, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000294728, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691, 9606.ENSP00000454623	ITGA3, TNFRSF1A, ITGAV, SLC9A3R1, ICAM1, ITGB7, PXN, ITGA1, ITGA5, VCAM1, EZR, ITGB1, ITGA4, ITGB2, TNF, ITGAM, ITGAX
GO:1903078	Positive regulation of protein localization to plasma membrane	4	62	1.78	9.73E-05	9606.ENSP00000007722, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000398698	ITGA3, EZR, ITGB1, TNF

Table S7. the full list of KEGG analysis and GO analysis for VCAM1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0009605	Response to external stimulus	12	2310	0.68	0.00011	9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000264741, 9606.ENSP00000264832, 9606.ENSP00000282588, 9606.ENSP00000294728, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691	TNFRSF1A, ITGAV, ITGA9, ICAM1, ITGA1, VCAM1, IL13, EZR, ITGA4, ITGB2, TNF, ITGAM
GO:0009719	Response to endogenous stimulus	10	1447	0.81	0.00012	9606.ENSP00000007722, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000267257, 9606.ENSP00000294728, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698	ITGA3, SLC9A3R1, ICAM1, PXN, VCAM1, EZR, ITGB1, ITGA4, ITGB2, TNF
GO:0022603	Regulation of anatomical structure morphogenesis	9	1095	0.88	0.00012	9606.ENSP00000162749, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000293379, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000454623	TNFRSF1A, SLC9A3R1, ICAM1, ITGA5, EZR, ITGB1, ITGB2, TNF, ITGAX
GO:0001667	Ameboidal-type cell migration	5	173	1.43	0.00014	9606.ENSP00000267082, 9606.ENSP00000267257, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948	ITGB7, PXN, ITGB1, ITGA4, ITGB2
GO:0000904	Cell morphogenesis involved in differentiation	7	566	1.06	0.00019	9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000267082, 9606.ENSP00000267257, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227	ITGAV, SLC9A3R1, ITGB7, PXN, EZR, ITGB1, ITGA4
GO:0006898	Receptor-mediated endocytosis	5	184	1.4	0.00019	9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000441691	EZR, ITGB1, ITGA4, ITGB2, ITGAM
GO:0048598	Embryonic morphogenesis	7	571	1.06	0.00019	9606.ENSP00000007722, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000293379, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948	ITGA3, ITGAV, SLC9A3R1, ITGA5, ITGB1, ITGA4, ITGB2
GO:0072659	Protein localization to plasma membrane	5	193	1.38	0.00023	9606.ENSP00000162749, 9606.ENSP00000262613, 9606.ENSP00000265709, 9606.ENSP00000356042, 9606.ENSP00000398698	TNFRSF1A, SLC9A3R1, ANK1, EZR, TNF
GO:0050731	Positive regulation of peptidyl-tyrosine phosphorylation	5	196	1.38	0.00024	9606.ENSP00000162749, 9606.ENSP00000264832, 9606.ENSP00000293379, 9606.ENSP00000304915, 9606.ENSP00000398698	TNFRSF1A, ICAM1, ITGA5, IL13, TNF
GO:0071417	Cellular response to organonitrogen compound	7	590	1.04	0.00024	9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000267257, 9606.ENSP00000294728, 9606.ENSP00000356042, 9606.ENSP00000380227, 9606.ENSP00000398698	SLC9A3R1, ICAM1, PXN, VCAM1, EZR, ITGA4, TNF
GO:0048468	Cell development	10	1629	0.76	0.00029	9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000267082, 9606.ENSP00000267257, 9606.ENSP00000282588, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000398698	ITGAV, SLC9A3R1, ICAM1, ITGB7, PXN, ITGA1, EZR, ITGB1, ITGA4, TNF
GO:0048585	Negative regulation of response to stimulus	10	1636	0.76	0.0003	9606.ENSP00000007722, 9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000282588, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000398698	ITGA3, TNFRSF1A, ITGAV, SLC9A3R1, ICAM1, ITGA1, IL13, EZR, ITGB1, TNF
GO:0002703	Regulation of leukocyte mediated immunity	5	209	1.35	0.00031	9606.ENSP00000264832, 9606.ENSP00000304915, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691	ICAM1, IL13, ITGB2, TNF, ITGAM
GO:0050793	Regulation of developmental process	12	2648	0.63	0.00039	9606.ENSP00000007722, 9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000293379, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000454623	ITGA3, TNFRSF1A, ITGAV, SLC9A3R1, ICAM1, ITGA5, IL13, EZR, ITGB1, ITGB2, TNF, ITGAX
GO:0043302	Positive regulation of leukocyte degranulation	3	26	2.03	0.00043	9606.ENSP00000304915, 9606.ENSP00000380948, 9606.ENSP0000441691	IL13, ITGB2, ITGAM
GO:0043065	Positive regulation of apoptotic process	7	660	0.99	0.00044	9606.ENSP00000162749, 9606.ENSP00000262613, 9606.ENSP00000282588, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000398698, 9606.ENSP00000441691	TNFRSF1A, SLC9A3R1, ITGA1, ITGB1, ITGA4, TNF, ITGAM
GO:1901216	Positive regulation of neuron death	4	98	1.58	0.00044	9606.ENSP00000282588, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP0000441691	ITGA1, ITGB2, TNF, ITGAM
GO:1903039	Positive regulation of leukocyte cell-cell adhesion	5	228	1.31	0.00044	9606.ENSP00000264832, 9606.ENSP00000294728, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698	ICAM1, VCAM1, ITGA4, ITGB2, TNF
GO:2000379	Positive regulation of reactive oxygen species metabolic process	4	103	1.56	0.00051	9606.ENSP00000264832, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP0000441691	ICAM1, ITGB2, TNF, ITGAM

Table S7. the full list of KEGG analysis and GO analysis for VCAM1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0009888	Tissue development	10	1760	0.72	0.00052	9606.ENSP00000007722, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000293379, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000441691	ITGA3, ITGAV, SLC9A3R1, ICAM1, ITGA5, EZR, ITGB1, ITGA4, ITGB2, ITGAM
GO:0043112	Receptor metabolic process	4	105	1.55	0.00053	9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380948, 9606.ENSP00000398698	EZR, ITGB1, ITGB2, TNF
GO:0051046	Regulation of secretion	7	686	0.98	0.00053	9606.ENSP00000162749, 9606.ENSP00000262613, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691	TNFRSF1A, SLC9A3R1, IL13, EZR, ITGB2, TNF, ITGAM
GO:0009790	Embryo development	8	1002	0.87	0.00055	9606.ENSP00000007722, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000293379, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698	ITGA3, ITGAV, SLC9A3R1, ITGA5, ITGB1, ITGA4, ITGB2, TNF
GO:0051049	Regulation of transport	10	1776	0.72	0.00055	9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691	TNFRSF1A, ITGAV, SLC9A3R1, ICAM1, IL13, EZR, ITGB1, ITGB2, TNF, ITGAM
GO:0051094	Positive regulation of developmental process	9	1389	0.78	0.00063	9606.ENSP00000007722, 9606.ENSP00000162749, 9606.ENSP00000293379, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000454623	ITGA3, TNFRSF1A, ITGA5, IL13, EZR, ITGB1, ITGB2, TNF, ITGAX
GO:0003366	Cell-matrix adhesion involved in ameboidal cell migration	2	2	2.97	0.00066	9606.ENSP00000267082, 9606.ENSP00000380227	ITGB7, ITGA4
GO:0140039	Cell-cell adhesion in response to extracellular stimulus	2	2	2.97	0.00066	9606.ENSP00000294728, 9606.ENSP00000380227	VCAM1, ITGA4
GO:0002888	Positive regulation of myeloid leukocyte mediated immunity	3	35	1.9	0.00086	9606.ENSP00000304915, 9606.ENSP00000380948, 9606.ENSP00000441691	IL13, ITGB2, ITGAM
GO:0001932	Regulation of protein phosphorylation	9	1459	0.76	0.00091	9606.ENSP00000162749, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000380948, 9606.ENSP00000398698	TNFRSF1A, SLC9A3R1, ICAM1, ITGA1, ITGA5, IL13, EZR, ITGB2, TNF
GO:0090322	Regulation of superoxide metabolic process	3	36	1.89	0.00091	9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691	ITGB2, TNF, ITGAM
GO:0044419	Interspecies interaction between organisms	10	1899	0.69	0.00093	9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000264832, 9606.ENSP00000267082, 9606.ENSP00000293379, 9606.ENSP00000294728, 9606.ENSP00000304915, 9606.ENSP00000379350, 9606.ENSP00000398698, 9606.ENSP00000441691	TNFRSF1A, ITGAV, ICAM1, ITGB7, ITGA5, VCAM1, IL13, ITGB1, TNF, ITGAM
GO:0045963	Negative regulation of dopamine metabolic process	2	3	2.79	0.001	9606.ENSP00000380948, 9606.ENSP00000441691	ITGB2, ITGAM
GO:2000363	Positive regulation of prostaglandin-e synthase activity	2	3	2.79	0.001	9606.ENSP00000380948, 9606.ENSP00000441691	ITGB2, ITGAM
GO:0051641	Cellular localization	12	2967	0.58	0.0011	9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000265709, 9606.ENSP00000267082, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691, 9606.ENSP00000454623	TNFRSF1A, ITGAV, SLC9A3R1, ANK1, ITGB7, EZR, ITGB1, ITGA4, ITGB2, TNF, ITGAM, ITGAX
GO:1904646	Cellular response to amyloid-beta	3	39	1.86	0.0011	9606.ENSP00000264832, 9606.ENSP00000294728, 9606.ENSP00000380227	ICAM1, VCAM1, ITGA4
GO:0002705	Positive regulation of leukocyte mediated immunity	4	137	1.43	0.0012	9606.ENSP00000304915, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691	IL13, ITGB2, TNF, ITGAM
GO:0006954	Inflammatory response	6	515	1.04	0.0012	9606.ENSP00000162749, 9606.ENSP00000264832, 9606.ENSP00000304915, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691	TNFRSF1A, ICAM1, IL13, ITGB2, TNF, ITGAM
GO:0007275	Multicellular organism development	15	5023	0.44	0.0013	9606.ENSP00000007722, 9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000294728, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691, 9606.ENSP00000454623	ITGA3, TNFRSF1A, ITGAV, SLC9A3R1, ICAM1, ITGA1, ITGA5, VCAM1, EZR, ITGB1, ITGA4, ITGB2, TNF, ITGAM, ITGAX
GO:0043315	Positive regulation of neutrophil degranulation	2	4	2.67	0.0014	9606.ENSP00000380948, 9606.ENSP00000441691	ITGB2, ITGAM
GO:0045765	Regulation of angiogenesis	5	303	1.19	0.0014	9606.ENSP00000293379, 9606.ENSP00000379350, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000454623	ITGA5, ITGB1, ITGB2, TNF, ITGAX
GO:0045429	Positive regulation of nitric oxide biosynthetic process	3	44	1.8	0.0015	9606.ENSP00000264832, 9606.ENSP00000380948, 9606.ENSP00000398698	ICAM1, ITGB2, TNF
GO:0071496	Cellular response to external stimulus	5	309	1.18	0.0015	9606.ENSP00000162749, 9606.ENSP00000264832, 9606.ENSP00000294728, 9606.ENSP00000304915, 9606.ENSP00000380227	TNFRSF1A, ICAM1, VCAM1, IL13, ITGA4
GO:1903532	Positive regulation of secretion by cell	5	312	1.17	0.0015	9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691	IL13, EZR, ITGB2, TNF, ITGAM

Table S7. the full list of KEGG analysis and GO analysis for VCAM1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0006955	Immune response	9	1588	0.72	0.0016	9606.ENSP00000261023, 9606.ENSP00000264832, 9606.ENSP00000294728, 9606.ENSP00000304915, 9606.ENSP00000373854, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691, 9606.ENSP00000454623	ITGAV, ICAM1, VCAM1, IL13, ITGAD, ITGB2, TNF, ITGAM, ITGAX
GO:0009966	Regulation of signal transduction	12	3107	0.56	0.0016	9606.ENSP00000007722, 9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000267257, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000398698	ITGA3, TNFRSF1A, ITGAV, SLC9A3R1, ICAM1, PXN, ITGA1, ITGA5, IL13, EZR, ITGB1, TNF
GO:0060627	Regulation of vesicle-mediated transport	6	550	1.01	0.0016	9606.ENSP00000261023, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691	ITGAV, IL13, EZR, ITGB2, TNF, ITGAM
GO:1901214	Regulation of neuron death	5	317	1.17	0.0016	9606.ENSP00000282588, 9606.ENSP00000304915, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691	ITGA1, IL13, ITGB2, TNF, ITGAM
GO:0008360	Regulation of cell shape	4	153	1.39	0.0017	9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000356042, 9606.ENSP00000380948	SLC9A3R1, ICAM1, EZR, ITGB2
GO:0043113	Receptor clustering	3	48	1.77	0.0017	9606.ENSP00000267082, 9606.ENSP00000380227, 9606.ENSP00000380948	ITGB7, ITGA4, ITGB2
GO:0048731	System development	14	4426	0.47	0.0017	9606.ENSP00000007722, 9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000294728, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000398698, 9606.ENSP00000441691, 9606.ENSP00000454623	ITGA3, TNFRSF1A, ITGAV, SLC9A3R1, ICAM1, ITGA1, ITGA5, VCAM1, EZR, ITGB1, ITGA4, TNF, ITGAM, ITGAX
GO:0007157	Heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules	3	49	1.76	0.0018	9606.ENSP00000264832, 9606.ENSP00000293379, 9606.ENSP00000294728	ICAM1, ITGA5, VCAM1
GO:0035088	Establishment or maintenance of apical/basal cell polarity	3	50	1.75	0.0018	9606.ENSP00000262613, 9606.ENSP00000265709, 9606.ENSP00000356042	SLC9A3R1, ANK1, EZR
GO:0042127	Regulation of cell population proliferation	9	1642	0.71	0.0018	9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000282588, 9606.ENSP00000294728, 9606.ENSP00000304915, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000398698, 9606.ENSP00000454623	ITGAV, SLC9A3R1, ITGA1, VCAM1, IL13, ITGB1, ITGA4, TNF, ITGAX
GO:0002274	Myeloid leukocyte activation	6	585	0.98	0.002	9606.ENSP00000261023, 9606.ENSP00000304915, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691, 9606.ENSP00000454623	ITGAV, IL13, ITGB2, TNF, ITGAM, ITGAX
GO:0051239	Regulation of multicellular organismal process	12	3227	0.54	0.002	9606.ENSP00000007722, 9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000293379, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000454623	ITGA3, TNFRSF1A, ITGAV, SLC9A3R1, ICAM1, ITGA5, IL13, EZR, ITGB1, ITGB2, TNF, ITGAX
GO:0009968	Negative regulation of signal transduction	8	1271	0.77	0.0023	9606.ENSP00000007722, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000282588, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000398698	ITGA3, ITGAV, SLC9A3R1, ICAM1, ITGA1, EZR, ITGB1, TNF
GO:0045766	Positive regulation of angiogenesis	4	169	1.34	0.0023	9606.ENSP00000293379, 9606.ENSP00000379350, 9606.ENSP00000380948, 9606.ENSP00000454623	ITGA5, ITGB1, ITGB2, ITGAX
GO:0008284	Positive regulation of cell population proliferation	7	919	0.85	0.0024	9606.ENSP00000261023, 9606.ENSP00000294728, 9606.ENSP00000304915, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000398698, 9606.ENSP00000454623	ITGAV, VCAM1, IL13, ITGB1, ITGA4, TNF, ITGAX
GO:0006952	Defense response	8	1296	0.76	0.0025	9606.ENSP00000162749, 9606.ENSP00000264832, 9606.ENSP00000294728, 9606.ENSP00000304915, 9606.ENSP00000379350, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691	TNFRSF1A, ICAM1, VCAM1, IL13, ITGB1, ITGB2, TNF, ITGAM
GO:0051050	Positive regulation of transport	7	923	0.85	0.0025	9606.ENSP00000262613, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691	SLC9A3R1, IL13, EZR, ITGB1, ITGB2, TNF, ITGAM
GO:0043525	Positive regulation of neuron apoptotic process	3	58	1.68	0.0026	9606.ENSP00000282588, 9606.ENSP00000398698, 9606.ENSP00000441691	ITGA1, TNF, ITGAM
GO:0002684	Positive regulation of immune system process	7	949	0.84	0.0029	9606.ENSP00000264832, 9606.ENSP00000294728, 9606.ENSP00000304915, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691	ICAM1, VCAM1, IL13, ITGA4, ITGB2, TNF, ITGAM
GO:1903530	Regulation of secretion by cell	6	630	0.95	0.0029	9606.ENSP00000162749, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691	TNFRSF1A, IL13, EZR, ITGB2, TNF, ITGAM
GO:0051240	Positive regulation of multicellular organismal process	9	1770	0.68	0.003	9606.ENSP00000007722, 9606.ENSP00000264832, 9606.ENSP00000293379, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000454623	ITGA3, ICAM1, ITGA5, IL13, EZR, ITGB1, ITGB2, TNF, ITGAX

Table S7. the full list of KEGG analysis and GO analysis for VCAM1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0048584	Positive regulation of response to stimulus	10	2257	0.62	0.0031	9606.ENSP00000162749, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000304915, 9606.ENSP00000379350, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691	TNFRSF1A, SLC9A3R1, ICAM1, ITGA1, ITGA5, IL13, ITGB1, ITGB2, TNF, ITGAM
GO:0031623	Receptor internalization	3	64	1.64	0.0033	9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380948	EZR, ITGB1, ITGB2
GO:0071550	Death-inducing signaling complex assembly	2	8	2.37	0.0033	9606.ENSP00000162749, 9606.ENSP00000398698	TNFRSF1A, TNF
GO:0046649	Lymphocyte activation	5	390	1.08	0.0034	9606.ENSP00000264832, 9606.ENSP00000294728, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948	ICAM1, VCAM1, ITGB1, ITGA4, ITGB2
GO:0007163	Establishment or maintenance of cell polarity	4	197	1.28	0.0036	9606.ENSP00000262613, 9606.ENSP00000265709, 9606.ENSP00000356042, 9606.ENSP00000379350	SLC9A3R1, ANK1, EZR, ITGB1
GO:0043542	Endothelial cell migration	3	67	1.62	0.0036	9606.ENSP00000267257, 9606.ENSP00000379350, 9606.ENSP00000380948	PXN, ITGB1, ITGB2
GO:0042531	Positive regulation of tyrosine phosphorylation of stat protein	3	68	1.61	0.0037	9606.ENSP00000162749, 9606.ENSP00000304915, 9606.ENSP00000398698	TNFRSF1A, IL13, TNF
GO:0023035	CD40 signaling pathway	2	9	2.32	0.0038	9606.ENSP00000293379, 9606.ENSP00000379350	ITGA5, ITGB1
GO:0060341	Regulation of cellular localization	7	1027	0.8	0.0042	9606.ENSP00000007722, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691	ITGA3, IL13, EZR, ITGB1, ITGB2, TNF, ITGAM
GO:0006909	Phagocytosis	4	210	1.25	0.0044	9606.ENSP00000261023, 9606.ENSP00000379350, 9606.ENSP00000380948, 9606.ENSP00000441691	ITGAV, ITGB1, ITGB2, ITGAM
GO:0030593	Neutrophil chemotaxis	3	74	1.58	0.0045	9606.ENSP00000264741, 9606.ENSP00000282588, 9606.ENSP00000380948	ITGA9, ITGA1, ITGB2
GO:1901701	Cellular response to oxygen-containing compound	7	1055	0.79	0.0048	9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000267257, 9606.ENSP00000294728, 9606.ENSP00000356042, 9606.ENSP00000380227, 9606.ENSP00000398698	SLC9A3R1, ICAM1, PXN, VCAM1, EZR, ITGA4, TNF
GO:0045199	Maintenance of epithelial cell apical/basal polarity	2	11	2.23	0.0051	9606.ENSP00000262613, 9606.ENSP00000265709	SLC9A3R1, ANK1
GO:0003008	System process	9	1942	0.64	0.0054	9606.ENSP00000007722, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000267257, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000398698	ITGA3, SLC9A3R1, ICAM1, PXN, ITGA1, ITGA5, EZR, ITGB1, TNF
GO:0051051	Negative regulation of transport	5	443	1.02	0.0054	9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000398698	TNFRSF1A, ITGAV, SLC9A3R1, ICAM1, TNF
GO:0030033	Microvillus assembly	2	12	2.19	0.0057	9606.ENSP00000262613, 9606.ENSP00000356042	SLC9A3R1, EZR
GO:2000304	Positive regulation of ceramide biosynthetic process	2	12	2.19	0.0057	9606.ENSP00000162749, 9606.ENSP00000398698	TNFRSF1A, TNF
GO:0016032	Viral process	6	776	0.86	0.0071	9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000264832, 9606.ENSP00000267082, 9606.ENSP00000293379, 9606.ENSP00000379350	TNFRSF1A, ITGAV, ICAM1, ITGB7, ITGA5, ITGB1
GO:0097242	Amyloid-beta clearance	2	14	2.12	0.0072	9606.ENSP00000380948, 9606.ENSP00000441691	ITGB2, ITGAM
GO:0031341	Regulation of cell killing	3	91	1.49	0.0073	9606.ENSP00000264832, 9606.ENSP00000304915, 9606.ENSP00000441691	ICAM1, IL13, ITGAM
GO:1901700	Response to oxygen-containing compound	8	1567	0.68	0.0073	9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000267257, 9606.ENSP00000294728, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000380227, 9606.ENSP00000398698	SLC9A3R1, ICAM1, PXN, VCAM1, IL13, EZR, ITGA4, TNF
GO:1903140	Regulation of establishment of endothelial barrier	2	15	2.09	0.0079	9606.ENSP00000162749, 9606.ENSP00000398698	TNFRSF1A, TNF
GO:0032501	Multicellular organismal process	16	6933	0.33	0.0088	9606.ENSP00000007722, 9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000267257, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000294728, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691, 9606.ENSP00000454623	ITGA3, TNFRSF1A, ITGAV, SLC9A3R1, ICAM1, PXN, ITGA1, ITGA5, VCAM1, EZR, ITGB1, ITGA4, ITGB2, TNF, ITGAM, ITGAX
GO:0097191	Extrinsic apoptotic signaling pathway	3	100	1.45	0.0091	9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000398698	TNFRSF1A, ITGAV, TNF
GO:0009967	Positive regulation of signal transduction	8	1654	0.65	0.0102	9606.ENSP00000162749, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000304915, 9606.ENSP00000379350, 9606.ENSP00000398698	TNFRSF1A, SLC9A3R1, ICAM1, ITGA1, ITGA5, IL13, ITGB1, TNF
GO:2000811	Negative regulation of anoikis	2	18	2.02	0.0106	9606.ENSP00000293379, 9606.ENSP00000379350	ITGA5, ITGB1
GO:2001237	Negative regulation of extrinsic apoptotic signaling pathway	3	106	1.42	0.0106	9606.ENSP00000261023, 9606.ENSP00000264832, 9606.ENSP00000398698	ITGAV, ICAM1, TNF
GO:0030183	B cell differentiation	3	110	1.41	0.0116	9606.ENSP00000294728, 9606.ENSP00000379350, 9606.ENSP00000380227	VCAM1, ITGB1, ITGA4
GO:0071404	Cellular response to low-density lipoprotein particle stimulus	2	19	1.99	0.0116	9606.ENSP00000379350, 9606.ENSP00000380948	ITGB1, ITGB2
GO:0097190	Apoptotic signaling pathway	4	286	1.11	0.0116	9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000398698, 9606.ENSP00000441691	TNFRSF1A, ITGAV, TNF, ITGAM
GO:0006935	Chemotaxis	5	545	0.93	0.0118	9606.ENSP00000261023, 9606.ENSP00000264741, 9606.ENSP00000282588, 9606.ENSP00000356042, 9606.ENSP00000380948	ITGAV, ITGA9, ITGA1, EZR, ITGB2

Table S7. the full list of KEGG analysis and GO analysis for VCAM1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0032930	Positive regulation of superoxide anion generation	2	20	1.97	0.0122	9606.ENSP00000380948, 9606.ENSP00000441691	ITGB2, ITGAM
GO:0034142	Toll-like receptor 4 signaling pathway	2	20	1.97	0.0122	9606.ENSP00000380948, 9606.ENSP00000441691	ITGB2, ITGAM
GO:0070372	Regulation of erk1 and erk2 cascade	4	292	1.11	0.0122	9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000356042, 9606.ENSP00000398698	SLC9A3R1, ICAM1, EZR, TNF
GO:0002693	Positive regulation of cellular extravasation	2	21	1.95	0.0131	9606.ENSP00000264832, 9606.ENSP00000380227	ICAM1, ITGA4
GO:0010888	Negative regulation of lipid storage	2	21	1.95	0.0131	9606.ENSP00000261023, 9606.ENSP00000398698	ITGAV, TNF
GO:0043066	Negative regulation of apoptotic process	6	893	0.8	0.0132	9606.ENSP00000261023, 9606.ENSP00000264832, 9606.ENSP00000293379, 9606.ENSP00000304915, 9606.ENSP00000379350, 9606.ENSP00000398698	ITGAV, ICAM1, ITGA5, IL13, ITGB1, TNF
GO:0050890	Cognition	4	302	1.09	0.0135	9606.ENSP00000007722, 9606.ENSP00000293379, 9606.ENSP00000379350, 9606.ENSP00000398698	ITGA3, ITGA5, ITGB1, TNF
GO:0010155	Regulation of proton transport	2	22	1.93	0.0141	9606.ENSP00000262613, 9606.ENSP00000304915	SLC9A3R1, IL13
GO:0051246	Regulation of protein metabolic process	10	2828	0.52	0.0143	9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000380948, 9606.ENSP00000398698	TNFRSF1A, ITGAV, SLC9A3R1, ICAM1, ITGA1, ITGA5, IL13, EZR, ITGB2, TNF
GO:0035024	Negative regulation of rho protein signal transduction	2	23	1.91	0.0151	9606.ENSP00000007722, 9606.ENSP00000379350	ITGA3, ITGB1
GO:0006950	Response to stress	11	3485	0.47	0.0161	9606.ENSP00000162749, 9606.ENSP00000264741, 9606.ENSP00000264832, 9606.ENSP00000267257, 9606.ENSP00000293379, 9606.ENSP00000294728, 9606.ENSP00000304915, 9606.ENSP00000379350, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691	TNFRSF1A, ITGA9, ICAM1, PXN, ITGA5, VCAM1, IL13, ITGB1, ITGB2, TNF, ITGAM
GO:0016192	Vesicle-mediated transport	8	1805	0.62	0.0165	9606.ENSP00000261023, 9606.ENSP00000265709, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000441691, 9606.ENSP00000454623	ITGAV, ANK1, EZR, ITGB1, ITGA4, ITGB2, ITGAM, ITGAX
GO:0048523	Negative regulation of cellular process	13	4874	0.4	0.0166	9606.ENSP00000007722, 9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691	ITGA3, TNFRSF1A, ITGAV, SLC9A3R1, ICAM1, ITGA1, ITGA5, IL13, EZR, ITGB1, ITGB2, TNF, ITGAM
GO:1902531	Regulation of intracellular signal transduction	8	1807	0.62	0.0166	9606.ENSP00000007722, 9606.ENSP00000162749, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000282588, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000398698	ITGA3, TNFRSF1A, SLC9A3R1, ICAM1, ITGA1, EZR, ITGB1, TNF
GO:1901653	Cellular response to peptide	4	331	1.05	0.018	9606.ENSP00000264832, 9606.ENSP00000267257, 9606.ENSP00000294728, 9606.ENSP00000380227	ICAM1, PXN, VCAM1, ITGA4
GO:0002696	Positive regulation of leukocyte activation	4	332	1.05	0.0181	9606.ENSP00000294728, 9606.ENSP00000304915, 9606.ENSP00000380948, 9606.ENSP00000441691	VCAM1, IL13, ITGB2, ITGAM
GO:0048333	Mesodermal cell differentiation	2	26	1.86	0.0182	9606.ENSP00000007722, 9606.ENSP00000379350	ITGA3, ITGB1
GO:0002521	Leukocyte differentiation	4	338	1.04	0.0191	9606.ENSP00000294728, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000398698	VCAM1, ITGB1, ITGA4, TNF
GO:0051649	Establishment of localization in cell	9	2375	0.55	0.0191	9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000265709, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000441691, 9606.ENSP00000454623	ITGAV, SLC9A3R1, ANK1, EZR, ITGB1, ITGA4, ITGB2, ITGAM, ITGAX
GO:0034698	Response to gonadotropin	2	27	1.84	0.0192	9606.ENSP00000007722, 9606.ENSP00000264832	ITGA3, ICAM1
GO:0002366	Leukocyte activation involved in immune response	5	626	0.87	0.0198	9606.ENSP00000261023, 9606.ENSP00000264832, 9606.ENSP00000380948, 9606.ENSP00000441691, 9606.ENSP00000454623	ITGAV, ICAM1, ITGB2, ITGAM, ITGAX
GO:0002443	Leukocyte mediated immunity	5	641	0.86	0.0215	9606.ENSP00000261023, 9606.ENSP00000264832, 9606.ENSP00000380948, 9606.ENSP00000441691, 9606.ENSP00000454623	ITGAV, ICAM1, ITGB2, ITGAM, ITGAX
GO:0002687	Positive regulation of leukocyte migration	3	144	1.29	0.0215	9606.ENSP00000264832, 9606.ENSP00000380227, 9606.ENSP00000398698	ICAM1, ITGA4, TNF
GO:0051222	Positive regulation of protein transport	4	352	1.02	0.0215	9606.ENSP00000356042, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691	EZR, ITGB2, TNF, ITGAM
GO:2000352	Negative regulation of endothelial cell apoptotic process	2	29	1.81	0.0215	9606.ENSP00000264832, 9606.ENSP00000304915	ICAM1, IL13
GO:0090314	Positive regulation of protein targeting to membrane	2	30	1.79	0.0226	9606.ENSP00000380948, 9606.ENSP00000441691	ITGB2, ITGAM
GO:0001934	Positive regulation of protein phosphorylation	6	1019	0.74	0.0235	9606.ENSP00000162749, 9606.ENSP00000264832, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000304915, 9606.ENSP00000398698	TNFRSF1A, ICAM1, ITGA1, ITGA5, IL13, TNF
GO:0030856	Regulation of epithelial cell differentiation	3	151	1.27	0.024	9606.ENSP00000162749, 9606.ENSP00000304915, 9606.ENSP00000398698	TNFRSF1A, IL13, TNF
GO:0061028	Establishment of endothelial barrier	2	32	1.77	0.0251	9606.ENSP00000264832, 9606.ENSP00000356042	ICAM1, EZR
GO:0072678	T cell migration	2	32	1.77	0.0251	9606.ENSP00000264832, 9606.ENSP00000267082	ICAM1, ITGB7
GO:1902533	Positive regulation of intracellular signal transduction	6	1041	0.73	0.0258	9606.ENSP00000162749, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000282588, 9606.ENSP00000379350, 9606.ENSP00000398698	TNFRSF1A, SLC9A3R1, ICAM1, ITGA1, ITGB1, TNF
GO:0051092	Positive regulation of nf-kappab transcription factor activity	3	158	1.25	0.0268	9606.ENSP00000264832, 9606.ENSP00000380948, 9606.ENSP00000398698	ICAM1, ITGB2, TNF

Table S7. the full list of KEGG analysis and GO analysis for VCAM1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0031175	Neuron projection development	5	680	0.84	0.027	9606.ENSP00000262613, 9606.ENSP00000282588, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227	SLC9A3R1, ITGA1, EZR, ITGB1, ITGA4
GO:0034767	Positive regulation of ion transmembrane transport	3	160	1.24	0.0276	9606.ENSP00000262613, 9606.ENSP00000304915, 9606.ENSP00000379350	SLC9A3R1, IL13, ITGB1
GO:0051656	Establishment of organelle localization	4	385	0.99	0.0283	9606.ENSP00000262613, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227	SLC9A3R1, EZR, ITGB1, ITGA4
GO:0008625	Extrinsic apoptotic signaling pathway via death domain receptors	2	35	1.73	0.0286	9606.ENSP00000162749, 9606.ENSP00000398698	TNFRSF1A, TNF
GO:0010959	Regulation of metal ion transport	4	391	0.98	0.0297	9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000304915, 9606.ENSP00000379350	SLC9A3R1, ICAM1, IL13, ITGB1
GO:0002437	Inflammatory response to antigenic stimulus	2	37	1.7	0.0315	9606.ENSP00000264832, 9606.ENSP00000398698	ICAM1, TNF
GO:0046903	Secretion	6	1097	0.71	0.0325	9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000265709, 9606.ENSP00000380948, 9606.ENSP00000441691, 9606.ENSP00000454623	ITGAV, SLC9A3R1, ANK1, ITGB2, ITGAM, ITGAX
GO:0048513	Animal organ development	10	3197	0.46	0.033	9606.ENSP00000007722, 9606.ENSP00000162749, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000294728, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000398698, 9606.ENSP00000441691, 9606.ENSP00000454623	ITGA3, TNFRSF1A, SLC9A3R1, ICAM1, VCAM1, ITGB1, ITGA4, TNF, ITGAM, ITGAX
GO:0048699	Generation of neurons	7	1551	0.62	0.0335	9606.ENSP00000007722, 9606.ENSP00000262613, 9606.ENSP00000282588, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000398698	ITGA3, SLC9A3R1, ITGA1, EZR, ITGB1, ITGA4, TNF
GO:0019222	Regulation of metabolic process	15	6948	0.3	0.0343	9606.ENSP00000007722, 9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000267257, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691, 9606.ENSP00000454623	ITGA3, TNFRSF1A, ITGAV, SLC9A3R1, ICAM1, PXN, ITGA1, ITGA5, IL13, EZR, ITGB1, ITGB2, TNF, ITGAM, ITGAX
GO:0030866	Cortical actin cytoskeleton organization	2	39	1.68	0.0343	9606.ENSP00000356042, 9606.ENSP00000398698	EZR, TNF
GO:0043408	Regulation of mapk cascade	5	725	0.81	0.0343	9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000282588, 9606.ENSP00000356042, 9606.ENSP00000398698	SLC9A3R1, ICAM1, ITGA1, EZR, TNF
GO:0071634	Regulation of transforming growth factor beta production	2	39	1.68	0.0343	9606.ENSP00000261023, 9606.ENSP00000304915	ITGAV, IL13
GO:2001233	Regulation of apoptotic signaling pathway	4	409	0.96	0.0343	9606.ENSP00000261023, 9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000398698	ITGAV, SLC9A3R1, ICAM1, TNF
GO:0120036	Plasma membrane bounded cell projection organization	6	1122	0.7	0.0356	9606.ENSP00000007722, 9606.ENSP00000262613, 9606.ENSP00000282588, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227	ITGA3, SLC9A3R1, ITGA1, EZR, ITGB1, ITGA4
GO:0009893	Positive regulation of metabolic process	11	3893	0.42	0.0358	9606.ENSP00000007722, 9606.ENSP00000162749, 9606.ENSP00000264832, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691, 9606.ENSP00000454623	ITGA3, TNFRSF1A, ICAM1, ITGA1, ITGA5, IL13, EZR, ITGB2, TNF, ITGAM, ITGAX
GO:2000026	Regulation of multicellular organismal development	8	2096	0.55	0.0376	9606.ENSP00000007722, 9606.ENSP00000162749, 9606.ENSP00000293379, 9606.ENSP00000304915, 9606.ENSP00000379350, 9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000454623	ITGA3, TNFRSF1A, ITGA5, IL13, ITGB1, ITGB2, TNF, ITGAX
GO:0006911	Phagocytosis, engulfment	2	43	1.64	0.04	9606.ENSP00000380948, 9606.ENSP00000441691	ITGB2, ITGAM
GO:0032270	Positive regulation of cellular protein metabolic process	7	1635	0.6	0.0433	9606.ENSP00000162749, 9606.ENSP00000264832, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000304915, 9606.ENSP00000356042, 9606.ENSP00000398698	TNFRSF1A, ICAM1, ITGA1, ITGA5, IL13, EZR, TNF
GO:0002064	Epithelial cell development	3	195	1.16	0.0438	9606.ENSP00000262613, 9606.ENSP00000264832, 9606.ENSP00000356042	SLC9A3R1, ICAM1, EZR
GO:0048667	Cell morphogenesis involved in neuron differentiation	4	445	0.92	0.0442	9606.ENSP00000262613, 9606.ENSP00000356042, 9606.ENSP00000379350, 9606.ENSP00000380227	SLC9A3R1, EZR, ITGB1, ITGA4
GO:0006887	Exocytosis	5	789	0.77	0.0468	9606.ENSP00000261023, 9606.ENSP00000265709, 9606.ENSP00000380948, 9606.ENSP00000441691, 9606.ENSP00000454623	ITGAV, ANK1, ITGB2, ITGAM, ITGAX
hsa04810	Regulation of actin cytoskeleton	13	209	1.76	2.26E-18	9606.ENSP00000007722, 9606.ENSP00000261023, 9606.ENSP00000264741, 9606.ENSP00000267082, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000356042, 9606.ENSP00000373854, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000380948, 9606.ENSP00000441691, 9606.ENSP00000454623	ITGA3, ITGAV, ITGA9, ITGB7, ITGA1, ITGA5, EZR, ITGAD, ITGB1, ITGA4, ITGB2, ITGAM, ITGAX
hsa05410	Hypertrophic cardiomyopathy	9	89	1.97	6.34E-14	9606.ENSP00000007722, 9606.ENSP00000261023, 9606.ENSP00000264741, 9606.ENSP00000267082, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000398698	ITGA3, ITGAV, ITGA9, ITGB7, ITGA1, ITGA5, ITGB1, ITGA4, TNF
hsa05414	Dilated cardiomyopathy	9	95	1.95	7.35E-14	9606.ENSP00000007722, 9606.ENSP00000261023, 9606.ENSP00000264741, 9606.ENSP00000267082, 9606.ENSP00000282588, 9606.ENSP00000293379, 9606.ENSP00000379350, 9606.ENSP00000380227, 9606.ENSP00000398698	ITGA3, ITGAV, ITGA9, ITGB7, ITGA1, ITGA5, ITGB1, ITGA4, TNF

Table S7. the full list of KEGG analysis and GO analysis for VCAM1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
hsa05165	Human papillomavirus infection	11	325	1.5	8.18E-13	9606. ENSP0000007722, 9606. ENSP00000162749, 9606. ENSP00000261023, 9606. ENSP00000262613, 9606. ENSP00000264741, 9606. ENSP00000267082, 9606. ENSP00000282588, 9606. ENSP00000293379, 9606. ENSP00000379350, 9606. ENSP00000380227, 9606. ENSP00000398698	ITGA3, TNFRSF1A, ITGAV, SLC9A3R1, ITGA9, ITGB7, ITGA1, ITGA5, ITGB1, ITGA4, TNF
hsa04514	Cell adhesion molecules	9	137	1.79	1.01E-12	9606. ENSP00000261023, 9606. ENSP00000264741, 9606. ENSP00000264832, 9606. ENSP00000267082, 9606. ENSP00000294728, 9606. ENSP00000379350, 9606. ENSP00000380227, 9606. ENSP00000380948, 9606. ENSP00000441691	ITGAV, ITGA9, ICAM1, ITGB7, VCAM1, ITGB1, ITGA4, ITGB2, ITGAM
hsa05412	Arrhythmogenic right ventricular cardiomyopathy	8	76	1.99	1.01E-12	9606. ENSP0000007722, 9606. ENSP00000261023, 9606. ENSP00000264741, 9606. ENSP00000267082, 9606. ENSP00000282588, 9606. ENSP00000293379, 9606. ENSP00000379350, 9606. ENSP00000380227	ITGA3, ITGAV, ITGA9, ITGB7, ITGA1, ITGA5, ITGB1, ITGA4
hsa04512	ECM-receptor interaction	8	88	1.93	2.29E-12	9606. ENSP0000007722, 9606. ENSP00000261023, 9606. ENSP00000264741, 9606. ENSP00000267082, 9606. ENSP00000282588, 9606. ENSP00000293379, 9606. ENSP00000379350, 9606. ENSP00000380227	ITGA3, ITGAV, ITGA9, ITGB7, ITGA1, ITGA5, ITGB1, ITGA4
hsa04510	Focal adhesion	8	198	1.58	9.70E-10	9606. ENSP0000007722, 9606. ENSP00000261023, 9606. ENSP00000264741, 9606. ENSP00000267082, 9606. ENSP00000282588, 9606. ENSP00000293379, 9606. ENSP00000379350, 9606. ENSP00000380227	ITGA3, ITGAV, ITGA9, ITGB7, ITGA1, ITGA5, ITGB1, ITGA4
hsa04670	Leukocyte transendothelial migration	7	109	1.78	9.70E-10	9606. ENSP00000264832, 9606. ENSP00000294728, 9606. ENSP00000356042, 9606. ENSP00000379350, 9606. ENSP00000380227, 9606. ENSP00000380948, 9606. ENSP00000441691	ICAM1, VCAM1, EZR, ITGB1, ITGA4, ITGB2, ITGAM
hsa04640	Hematopoietic cell lineage	6	91	1.79	2.17E-08	9606. ENSP0000007722, 9606. ENSP00000282588, 9606. ENSP00000293379, 9606. ENSP00000380227, 9606. ENSP00000398698, 9606. ENSP00000441691	ITGA3, ITGA1, ITGA5, ITGA4, TNF, ITGAM
hsa04151	PI3K-Akt signaling pathway	8	350	1.33	5.82E-08	9606. ENSP0000007722, 9606. ENSP00000261023, 9606. ENSP00000264741, 9606. ENSP00000267082, 9606. ENSP00000282588, 9606. ENSP00000293379, 9606. ENSP00000379350, 9606. ENSP00000380227	ITGA3, ITGAV, ITGA9, ITGB7, ITGA1, ITGA5, ITGB1, ITGA4
hsa05140	Leishmaniasis	5	70	1.82	3.90E-07	9606. ENSP00000379350, 9606. ENSP00000380227, 9606. ENSP00000380948, 9606. ENSP00000398698, 9606. ENSP00000441691	ITGB1, ITGA4, ITGB2, TNF, ITGAM
hsa05133	Pertussis	5	74	1.8	4.69E-07	9606. ENSP00000293379, 9606. ENSP00000379350, 9606. ENSP00000380948, 9606. ENSP00000398698, 9606. ENSP00000441691	ITGA5, ITGB1, ITGB2, TNF, ITGAM
hsa05205	Proteoglycans in cancer	6	196	1.46	1.28E-06	9606. ENSP00000261023, 9606. ENSP00000265709, 9606. ENSP00000293379, 9606. ENSP00000356042, 9606. ENSP00000379350, 9606. ENSP00000398698	ITGAV, ANK1, ITGA5, EZR, ITGB1, TNF
hsa05144	Malaria	4	46	1.91	4.88E-06	9606. ENSP00000264832, 9606. ENSP00000294728, 9606. ENSP00000380948, 9606. ENSP00000398698	ICAM1, VCAM1, ITGB2, TNF
hsa05418	Fluid shear stress and atherosclerosis	5	130	1.55	5.65E-06	9606. ENSP00000162749, 9606. ENSP00000261023, 9606. ENSP00000264832, 9606. ENSP00000294728, 9606. ENSP00000398698	TNFRSF1A, ITGAV, ICAM1, VCAM1, TNF
hsa04145	Phagosome	5	142	1.52	8.12E-06	9606. ENSP00000261023, 9606. ENSP00000293379, 9606. ENSP00000379350, 9606. ENSP00000380948, 9606. ENSP00000441691	ITGAV, ITGA5, ITGB1, ITGB2, ITGAM
hsa05152	Tuberculosis	5	168	1.44	1.72E-05	9606. ENSP00000162749, 9606. ENSP00000380948, 9606. ENSP00000398698, 9606. ENSP00000441691, 9606. ENSP00000454623	TNFRSF1A, ITGB2, TNF, ITGAM, ITGAX
hsa05130	Pathogenic Escherichia coli infection	5	187	1.4	2.72E-05	9606. ENSP00000162749, 9606. ENSP00000262613, 9606. ENSP00000356042, 9606. ENSP00000379350, 9606. ENSP00000398698	TNFRSF1A, SLC9A3R1, EZR, ITGB1, TNF
hsa04064	NF-kappa B signaling pathway	4	101	1.57	7.31E-05	9606. ENSP00000162749, 9606. ENSP00000264832, 9606. ENSP00000294728, 9606. ENSP00000398698	TNFRSF1A, ICAM1, VCAM1, TNF
hsa04668	TNF signaling pathway	4	112	1.52	0.0001	9606. ENSP00000162749, 9606. ENSP00000264832, 9606. ENSP00000294728, 9606. ENSP00000398698	TNFRSF1A, ICAM1, VCAM1, TNF
hsa05135	Yersinia infection	4	125	1.47	0.00014	9606. ENSP00000293379, 9606. ENSP00000379350, 9606. ENSP00000380227, 9606. ENSP00000398698	ITGA5, ITGB1, ITGA4, TNF
hsa05143	African trypanosomiasis	3	36	1.89	0.00014	9606. ENSP00000264832, 9606. ENSP00000294728, 9606. ENSP00000398698	ICAM1, VCAM1, TNF
hsa05134	Legionellosis	3	55	1.71	0.00044	9606. ENSP00000380948, 9606. ENSP00000398698, 9606. ENSP00000441691	ITGB2, TNF, ITGAM
hsa05166	Human T-cell leukemia virus 1 infection	4	211	1.25	0.00098	9606. ENSP00000162749, 9606. ENSP00000264832, 9606. ENSP00000380948, 9606. ENSP00000398698	TNFRSF1A, ICAM1, ITGB2, TNF
hsa05131	Shigellosis	4	218	1.23	0.0011	9606. ENSP00000162749, 9606. ENSP00000293379, 9606. ENSP00000379350, 9606. ENSP00000398698	TNFRSF1A, ITGA5, ITGB1, TNF
hsa04610	Complement and coagulation cascades	3	82	1.53	0.0012	9606. ENSP00000380948, 9606. ENSP00000441691, 9606. ENSP00000454623	ITGB2, ITGAM, ITGAX
hsa05150	Staphylococcus aureus infection	3	86	1.51	0.0013	9606. ENSP00000264832, 9606. ENSP00000380948, 9606. ENSP00000441691	ICAM1, ITGB2, ITGAM
hsa05323	Rheumatoid arthritis	3	85	1.52	0.0013	9606. ENSP00000264832, 9606. ENSP00000380948, 9606. ENSP00000398698	ICAM1, ITGB2, TNF

Table S7. the full list of KEGG analysis and GO analysis for VCAM1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
hsa05222	Small cell lung cancer	3	92	1.48	0.0015	9606.ENSP00000007722, 9606.ENSP00000261023, 9606.ENSP00000379350	ITGA3, ITGAV, ITGB1
hsa04933	AGE-RAGE signaling pathway in diabetic complications	3	98	1.46	0.0018	9606.ENSP00000264832, 9606.ENSP00000294728, 9606.ENSP00000398698	ICAM1, VCAM1, TNF
hsa05146	Amoebiasis	3	100	1.45	0.0018	9606.ENSP00000380948, 9606.ENSP00000398698, 9606.ENSP00000441691	ITGB2, TNF, ITGAM
hsa05145	Toxoplasmosis	3	105	1.43	0.0021	9606.ENSP00000162749, 9606.ENSP00000379350, 9606.ENSP00000398698	TNFRSF1A, ITGB1, TNF
hsa04650	Natural killer cell mediated cytotoxicity	3	121	1.36	0.003	9606.ENSP00000264832, 9606.ENSP00000380948, 9606.ENSP00000398698	ICAM1, ITGB2, TNF
hsa05310	Asthma	2	27	1.84	0.0042	9606.ENSP00000304915, 9606.ENSP00000398698	IL13, TNF
hsa04530	Tight junction	3	156	1.25	0.0059	9606.ENSP00000262613, 9606.ENSP00000356042, 9606.ENSP00000379350	SLC9A3R1, EZR, ITGB1
hsa05164	Influenza A	3	165	1.23	0.0067	9606.ENSP00000162749, 9606.ENSP00000264832, 9606.ENSP00000398698	TNFRSF1A, ICAM1, TNF
hsa04672	Intestinal immune network for IgA production	2	43	1.64	0.0093	9606.ENSP00000267082, 9606.ENSP00000380227	ITGB7, ITGA4
hsa04015	Rap1 signaling pathway	3	202	1.14	0.0113	9606.ENSP00000379350, 9606.ENSP00000380948, 9606.ENSP00000441691	ITGB1, ITGB2, ITGAM
hsa05163	Human cytomegalovirus infection	3	218	1.11	0.0136	9606.ENSP00000162749, 9606.ENSP00000261023, 9606.ENSP00000398698	TNFRSF1A, ITGAV, TNF
hsa05416	Viral myocarditis	2	55	1.53	0.0138	9606.ENSP00000264832, 9606.ENSP00000380948	ICAM1, ITGB2
hsa05321	Inflammatory bowel disease	2	60	1.49	0.0159	9606.ENSP00000304915, 9606.ENSP00000398698	IL13, TNF
hsa05200	Pathways in cancer	4	517	0.86	0.0161	9606.ENSP00000007722, 9606.ENSP00000261023, 9606.ENSP00000304915, 9606.ENSP00000379350	ITGA3, ITGAV, IL13, ITGB1
hsa04664	Fc epsilon RI signaling pathway	2	66	1.45	0.0182	9606.ENSP00000304915, 9606.ENSP00000398698	IL13, TNF
hsa04920	Adipocytokine signaling pathway	2	69	1.43	0.0194	9606.ENSP00000162749, 9606.ENSP00000398698	TNFRSF1A, TNF
hsa05100	Bacterial invasion of epithelial cells	2	70	1.43	0.0195	9606.ENSP00000293379, 9606.ENSP00000379350	ITGA5, ITGB1
hsa04060	Cytokine-cytokine receptor interaction	3	282	1	0.0239	9606.ENSP00000162749, 9606.ENSP00000304915, 9606.ENSP00000398698	TNFRSF1A, IL13, TNF
hsa04657	IL-17 signaling pathway	2	92	1.31	0.0316	9606.ENSP00000304915, 9606.ENSP00000398698	IL13, TNF
hsa04061	Viral protein interaction with cytokine and cytokine receptor	2	96	1.29	0.0335	9606.ENSP00000162749, 9606.ENSP00000398698	TNFRSF1A, TNF
hsa05142	Chagas disease	2	99	1.27	0.0349	9606.ENSP00000162749, 9606.ENSP00000398698	TNFRSF1A, TNF
hsa04931	Insulin resistance	2	107	1.24	0.0396	9606.ENSP00000162749, 9606.ENSP00000398698	TNFRSF1A, TNF
hsa04071	Sphingolipid signaling pathway	2	116	1.21	0.0453	9606.ENSP00000162749, 9606.ENSP00000398698	TNFRSF1A, TNF
hsa04380	Osteoclast differentiation	2	122	1.18	0.0489	9606.ENSP00000162749, 9606.ENSP00000398698	TNFRSF1A, TNF

Table S8. the full list of KEGG analysis and GO analysis for BHLHE40

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0006974	Cellular response to dna damage stimulus	15	793	1.25	8.31E-13	9606.ENSP00000008527,9606.ENSP00000212015,9606.ENSP00000229769,9606.ENSP00000267430,9606.ENSP00000287647,9606.ENSP00000289081,9606.ENSP00000308583,9606.ENSP00000308741,9606.ENSP00000310356,9606.ENSP00000317039,9606.ENSP00000330875,9606.ENSP00000333283,9606.ENSP00000338283,9606.ENSP00000347232,9606.ENSP00000466121	CRY1, SIRT1, FANCE, FANCM, FANCD2, FANCC, APITD1, CLOCK, RMI2, RMI1, FANCF, C17orf70, NPAS2, BLM, C19orf40
GO:0036297	Interstrand cross-link repair	8	56	2.12	1.04E-11	9606.ENSP00000229769,9606.ENSP00000267430,9606.ENSP00000287647,9606.ENSP00000289081,9606.ENSP00000308583,9606.ENSP00000330875,9606.ENSP00000333283,9606.ENSP00000466121	FANCE, FANCM, FANCD2, FANCC, APITD1, FANCF, C17orf70, C19orf40
GO:0006281	DNA repair	12	522	1.33	1.50E-10	9606.ENSP00000212015,9606.ENSP00000229769,9606.ENSP00000267430,9606.ENSP00000287647,9606.ENSP00000289081,9606.ENSP00000308583,9606.ENSP00000310356,9606.ENSP00000317039,9606.ENSP00000330875,9606.ENSP00000333283,9606.ENSP00000347232,9606.ENSP00000466121	SIRT1, FANCE, FANCM, FANCD2, FANCC, APITD1, RMI2, RMI1, FANCF, C17orf70, BLM, C19orf40
GO:0006259	DNA metabolic process	13	750	1.21	2.11E-10	9606.ENSP00000212015,9606.ENSP00000229769,9606.ENSP00000267430,9606.ENSP00000287647,9606.ENSP00000289081,9606.ENSP00000308583,9606.ENSP00000310356,9606.ENSP00000317039,9606.ENSP00000330875,9606.ENSP00000333283,9606.ENSP00000347232,9606.ENSP00000442336,9606.ENSP00000466121	SIRT1, FANCE, FANCM, FANCD2, FANCC, APITD1, RMI2, RMI1, FANCF, C17orf70, BLM, TOP3A, C19orf40
GO:0033554	Cellular response to stress	16	1725	0.94	4.84E-10	9606.ENSP00000008527,9606.ENSP00000212015,9606.ENSP00000229769,9606.ENSP00000267430,9606.ENSP00000287647,9606.ENSP00000289081,9606.ENSP00000308583,9606.ENSP00000308741,9606.ENSP00000310356,9606.ENSP00000317039,9606.ENSP00000330875,9606.ENSP00000333283,9606.ENSP00000338283,9606.ENSP00000347232,9606.ENSP00000384517,9606.ENSP00000466121	CRY1, SIRT1, FANCE, FANCM, FANCD2, FANCC, APITD1, CLOCK, RMI2, RMI1, FANCF, C17orf70, NPAS2, BLM, ARNTL, C19orf40
GO:0032922	Circadian regulation of gene expression	7	65	2	1.61E-09	9606.ENSP00000008527,9606.ENSP00000212015,9606.ENSP00000242728,9606.ENSP00000256495,9606.ENSP00000308741,9606.ENSP00000338283,9606.ENSP00000384517	CRY1, SIRT1, BHLHE41, BHLHE40, CLOCK, NPAS2, ARNTL
GO:0051304	Chromosome separation	4	30	2.09	5.18E-05	9606.ENSP00000267430,9606.ENSP00000308583,9606.ENSP00000317039,9606.ENSP00000442336	FANCM, APITD1, RMI1, TOP3A
GO:0006260	DNA replication	6	205	1.44	7.39E-05	9606.ENSP00000267430,9606.ENSP00000308583,9606.ENSP00000310356,9606.ENSP00000317039,9606.ENSP00000347232,9606.ENSP00000442336	FANCM, APITD1, RMI2, RMI1, BLM, TOP3A
GO:0033144	ulation of intracellular steroid hormone receptor signa	4	36	2.02	8.60E-05	9606.ENSP00000008527,9606.ENSP00000212015,9606.ENSP00000308741,9606.ENSP00000384517	CRY1, SIRT1, CLOCK, ARNTL
GO:2000323	tive regulation of glucocorticoid receptor signaling pat	3	6	2.67	8.60E-05	9606.ENSP00000008527,9606.ENSP00000308741,9606.ENSP00000384517	CRY1, CLOCK, ARNTL
GO:0007131	Reciprocal meiotic recombination	4	53	1.85	0.0003	9606.ENSP00000267430,9606.ENSP00000287647,9606.ENSP00000308583,9606.ENSP00000317039	FANCM, FANCD2, APITD1, RMI1
GO:0022414	Reproductive process	10	1400	0.82	0.00041	9606.ENSP00000212015,9606.ENSP00000232424,9606.ENSP00000267430,9606.ENSP00000287647,9606.ENSP00000289081,9606.ENSP00000308583,9606.ENSP00000308741,9606.ENSP00000317039,9606.ENSP00000384517,9606.ENSP00000442336	SIRT1, HES1, FANCM, FANCD2, FANCC, APITD1, CLOCK, RMI1, ARNTL, TOP3A
GO:0051775	Response to redox state	3	14	2.3	0.00044	9606.ENSP00000308741,9606.ENSP00000338283,9606.ENSP00000384517	CLOCK, NPAS2, ARNTL
GO:0000712	Resolution of meiotic recombination intermediates	3	17	2.22	0.00064	9606.ENSP00000267430,9606.ENSP00000308583,9606.ENSP00000317039	FANCM, APITD1, RMI1
GO:1901796	Regulation of signal transduction by p53 class mediator	5	182	1.41	0.00069	9606.ENSP00000212015,9606.ENSP00000310356,9606.ENSP00000317039,9606.ENSP00000347232,9606.ENSP00000442336	SIRT1, RMI2, RMI1, BLM, TOP3A
GO:0044260	Cellular macromolecule metabolic process	16	4976	0.48	0.00077	9606.ENSP00000008527,9606.ENSP00000212015,9606.ENSP00000229769,9606.ENSP00000267430,9606.ENSP00000287647,9606.ENSP00000289081,9606.ENSP00000308583,9606.ENSP00000308741,9606.ENSP00000310356,9606.ENSP00000317039,9606.ENSP00000330875,9606.ENSP00000333283,9606.ENSP00000347232,9606.ENSP00000384517,9606.ENSP00000442336,9606.ENSP00000466121	CRY1, SIRT1, FANCE, FANCM, FANCD2, FANCC, APITD1, CLOCK, RMI2, RMI1, FANCF, C17orf70, BLM, ARNTL, TOP3A, C19orf40

Table S8. the full list of KEGG analysis and GO analysis for BHLHE40

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0045132	Meiotic chromosome segregation	4	87	1.63	0.0011	9606.ENSP00000267430, 9606.ENSP00000287647, 9606.ENSP00000308583, 9606.ENSP00000317039	FANCM, FANCD2, APITD1, RMI1
GO:0097150	Neuronal stem cell population maintenance	3	23	2.08	0.0011	9606.ENSP00000232424, 9606.ENSP00000287647, 9606.ENSP00000289081	HES1, FANCD2, FANCC
GO:0006310	DNA recombination	5	219	1.33	0.0013	9606.ENSP00000267430, 9606.ENSP00000287647, 9606.ENSP00000308583, 9606.ENSP00000317039, 9606.ENSP00000347232	FANCM, FANCD2, APITD1, RMI1, BLM
GO:0051321	Meiotic cell cycle	5	220	1.33	0.0013	9606.ENSP00000267430, 9606.ENSP00000287647, 9606.ENSP00000308583, 9606.ENSP00000317039, 9606.ENSP00000442336	FANCM, FANCD2, APITD1, RMI1, TOP3A
GO:0009648	Photoperiodism	3	27	2.02	0.0016	9606.ENSP00000008527, 9606.ENSP00000256495, 9606.ENSP00000308741	CRY1, BHLHE40, CLOCK
GO:0009314	Response to radiation	6	431	1.11	0.0017	9606.ENSP00000008527, 9606.ENSP00000212015, 9606.ENSP00000256495, 9606.ENSP00000287647, 9606.ENSP00000308741, 9606.ENSP00000347232	CRY1, SIRT1, BHLHE40, FANCD2, CLOCK, BLM
GO:0031297	Replication fork processing	3	32	1.94	0.0023	9606.ENSP00000267430, 9606.ENSP00000308583, 9606.ENSP00000347232	FANCM, APITD1, BLM
GO:0042752	Regulation of circadian rhythm	4	117	1.5	0.0025	9606.ENSP00000008527, 9606.ENSP00000256495, 9606.ENSP00000308741, 9606.ENSP00000384517	CRY1, BHLHE40, CLOCK, ARNTL
GO:0007059	Chromosome segregation	5	268	1.24	0.0027	9606.ENSP00000267430, 9606.ENSP00000287647, 9606.ENSP00000308583, 9606.ENSP00000317039, 9606.ENSP00000442336	FANCM, FANCD2, APITD1, RMI1, TOP3A
GO:0051276	Chromosome organization	8	1066	0.84	0.0027	9606.ENSP00000212015, 9606.ENSP00000267430, 9606.ENSP00000287647, 9606.ENSP00000308583, 9606.ENSP00000308741, 9606.ENSP00000310356, 9606.ENSP00000347232, 9606.ENSP00000442336	SIRT1, FANCM, FANCD2, APITD1, CLOCK, RMI2, BLM, TOP3A
GO:0051716	Cellular response to stimulus	17	6489	0.39	0.0029	9606.ENSP00000008527, 9606.ENSP00000212015, 9606.ENSP00000229769, 9606.ENSP00000232424, 9606.ENSP00000267430, 9606.ENSP00000287647, 9606.ENSP00000289081, 9606.ENSP00000308583, 9606.ENSP00000308741, 9606.ENSP00000310356, 9606.ENSP00000317039, 9606.ENSP00000330875, 9606.ENSP00000333283, 9606.ENSP00000338283, 9606.ENSP00000347232, 9606.ENSP00000384517, 9606.ENSP00000466121	CRY1, SIRT1, FANCE, HES1, FANCM, FANCD2, FANCC, APITD1, CLOCK, RMI2, RMI1, FANCF, C17orf70, NPAS2, BLM, ARNTL, C19orf40
GO:0045934	regulation of nucleobase-containing compound metabolic	9	1528	0.74	0.004	9606.ENSP00000008527, 9606.ENSP00000212015, 9606.ENSP00000232424, 9606.ENSP00000242728, 9606.ENSP00000256495, 9606.ENSP00000308741, 9606.ENSP00000310356, 9606.ENSP00000347232, 9606.ENSP00000384517	CRY1, SIRT1, HES1, BHLHE41, BHLHE40, CLOCK, RMI2, BLM, ARNTL
GO:0010212	Response to ionizing radiation	4	145	1.41	0.0049	9606.ENSP00000212015, 9606.ENSP00000287647, 9606.ENSP00000308741, 9606.ENSP00000347232	SIRT1, FANCD2, CLOCK, BLM
GO:0071103	DNA conformation change	5	328	1.15	0.006	9606.ENSP00000212015, 9606.ENSP00000267430, 9606.ENSP00000308583, 9606.ENSP00000347232, 9606.ENSP00000442336	SIRT1, FANCM, APITD1, BLM, TOP3A
GO:0051726	Regulation of cell cycle	8	1230	0.78	0.0063	9606.ENSP00000008527, 9606.ENSP00000212015, 9606.ENSP00000232424, 9606.ENSP00000287647, 9606.ENSP00000308741, 9606.ENSP00000310356, 9606.ENSP00000347232, 9606.ENSP00000384517	CRY1, SIRT1, HES1, FANCD2, CLOCK, RMI2, BLM, ARNTL
GO:0071478	Cellular response to radiation	4	170	1.34	0.008	9606.ENSP00000008527, 9606.ENSP00000212015, 9606.ENSP00000308741, 9606.ENSP00000347232	CRY1, SIRT1, CLOCK, BLM
GO:0050896	Response to stimulus	18	8046	0.32	0.0084	9606.ENSP00000008527, 9606.ENSP00000212015, 9606.ENSP00000229769, 9606.ENSP00000232424, 9606.ENSP00000256495, 9606.ENSP00000267430, 9606.ENSP00000287647, 9606.ENSP00000289081, 9606.ENSP00000308583, 9606.ENSP00000308741, 9606.ENSP00000310356, 9606.ENSP00000317039, 9606.ENSP00000330875, 9606.ENSP00000333283, 9606.ENSP00000338283, 9606.ENSP00000347232, 9606.ENSP00000384517, 9606.ENSP00000466121	CRY1, SIRT1, FANCE, HES1, BHLHE40, FANCM, FANCD2, FANCC, APITD1, CLOCK, RMI2, RMI1, FANCF, C17orf70, NPAS2, BLM, ARNTL, C19orf40
GO:0090400	Stress-induced premature senescence	2	8	2.37	0.0117	9606.ENSP00000212015, 9606.ENSP00000384517	SIRT1, ARNTL
GO:2000074	Regulation of type b pancreatic cell development	2	8	2.37	0.0117	9606.ENSP00000308741, 9606.ENSP00000384517	CLOCK, ARNTL
GO:0071479	Cellular response to ionizing radiation	3	67	1.62	0.0127	9606.ENSP00000212015, 9606.ENSP00000308741, 9606.ENSP00000347232	SIRT1, CLOCK, BLM
GO:0006302	Double-strand break repair	4	204	1.26	0.0145	9606.ENSP00000267430, 9606.ENSP00000287647, 9606.ENSP00000317039, 9606.ENSP00000347232	FANCM, FANCD2, RMI1, BLM

Table S8. the full list of KEGG analysis and GO analysis for BHLHE40

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:2000113	ive regulation of cellular macromolecule biosynthetic pr	8	1470	0.71	0.0187	9606.ENSP00000008527,9606.ENSP00000212015,9606.ENSP00000232424,9606.ENSP00000242728,9606.ENSP00000256495,9606.ENSP00000308741,9606.ENSP00000347232,9606.ENSP00000384517	CRY1,SIRT1,HES1,BHLHE41,BHLHE40,CLOCK,BLM,ARNTL
GO:2001020	Regulation of response to dna damage stimulus	4	225	1.22	0.02	9606.ENSP00000008527,9606.ENSP00000212015,9606.ENSP00000310356,9606.ENSP00000338283	CRY1,SIRT1,RMI2,NPAS2
GO:0034599	Cellular response to oxidative stress	4	244	1.18	0.0263	9606.ENSP00000212015,9606.ENSP00000287647,9606.ENSP00000289081,9606.ENSP00000384517	SIRT1,FANCD2,FANCC,ARNTL
GO:0006807	Nitrogen compound metabolic process	16	6852	0.34	0.0293	9606.ENSP00000008527,9606.ENSP00000212015,9606.ENSP00000229769,9606.ENSP00000267430,9606.ENSP00000287647,9606.ENSP00000289081,9606.ENSP00000308583,9606.ENSP00000308741,9606.ENSP00000310356,9606.ENSP00000317039,9606.ENSP00000330875,9606.ENSP00000333283,9606.ENSP00000347232,9606.ENSP00000384517,9606.ENSP00000442336,9606.ENSP00000466121	CRY1,SIRT1,FANCE,FANCM,FANCD2,FANCC,APITD1,CLOCK,RMI2,RMI1,FANCF,C17orf70,BLM,ARNTL,TOP3A,C19orf40
GO:0000724	Double-strand break repair via homologous recombination	3	102	1.44	0.0361	9606.ENSP00000267430,9606.ENSP00000317039,9606.ENSP00000347232	FANCM,RMI1,BLM
GO:0045892	Negative regulation of transcription, dna-templated	7	1273	0.71	0.0474	9606.ENSP00000008527,9606.ENSP00000212015,9606.ENSP00000232424,9606.ENSP00000242728,9606.ENSP00000256495,9606.ENSP00000308741,9606.ENSP00000384517	CRY1,SIRT1,HES1,BHLHE41,BHLHE40,CLOCK,ARNTL
hsa03460	Fanconi anemia pathway	13	51	2.38	8.82E-26	9606.ENSP00000229769,9606.ENSP00000232424,9606.ENSP00000267430,9606.ENSP00000287647,9606.ENSP00000289081,9606.ENSP00000308583,9606.ENSP00000310356,9606.ENSP00000317039,9606.ENSP00000330875,9606.ENSP00000333283,9606.ENSP00000347232,9606.ENSP00000442336,9606.ENSP00000466121	FANCE,HES1,FANCM,FANCD2,FANCC,APITD1,RMI2,RMI1,FANCF,C17orf70,BLM,TOP3A,C19orf40
hsa04710	Circadian rhythm	6	30	2.27	2.22E-10	9606.ENSP00000008527,9606.ENSP00000242728,9606.ENSP00000256495,9606.ENSP00000308741,9606.ENSP00000338283,9606.ENSP00000384517	CRY1,BHLHE41,BHLHE40,CLOCK,NPAS2,ARNTL

Table S9. the full list of KEGG analysis and GO analysis for DUSP1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0031098	Stress-activated protein kinase signaling cascade	10	144	1.81	2.83E-12	9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000241014, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000333685, 9606.ENSP00000356070, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK1, TAB1, MAPK14, MAPK8IP1, MAP2K2, MAPK3, MAPK11, MAPKAPK2, MAPK8, ZFP36
GO:0000165	MAPK cascade	12	370	1.48	4.11E-12	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000241014, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000333685, 9606.ENSP00000356070, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK12, MAPK1, TAB1, MAPK14, MAPK8IP1, MAP2K2, MAPK3, DUSP6, MAPK11, MAPKAPK2, MAPK8, ZFP36
GO:0051403	Stress-activated mapk cascade	9	107	1.89	5.87E-12	9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000241014, 9606.ENSP00000263025, 9606.ENSP00000333685, 9606.ENSP00000356070, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK1, TAB1, MAPK14, MAPK8IP1, MAPK3, MAPK11, MAPKAPK2, MAPK8, ZFP36
GO:0051173	Positive regulation of nitrogen compound metabolic process	19	3239	0.74	5.80E-10	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239938, 9606.ENSP00000241014, 9606.ENSP00000252818, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK12, MAPK1, TAB1, MAPK14, NR3C1, EGR1, MAPK8IP1, JUND, MAP2K2, MAPK3, DUSP6, JUNB, FOS, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A, MAPK8, ZFP36
GO:0034097	Response to cytokine	14	1101	1.07	5.93E-10	9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000252818, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK1, TAB1, MAPK14, DUSP1, EGR1, JUND, MAPK3, JUNB, FOS, MAPK11, HSP90AA1, MAPKAPK2, MAPK8, ZFP36
GO:0043405	Regulation of map kinase activity	10	342	1.44	1.68E-09	9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000239223, 9606.ENSP00000241014, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000333685, 9606.ENSP00000356070	MAPK1, TAB1, MAPK14, DUSP1, MAPK8IP1, MAP2K2, MAPK3, DUSP6, MAPK11, MAPKAPK2
GO:0071310	Cellular response to organic substance	17	2369	0.83	1.68E-09	9606.ENSP00000001008, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000252818, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000378974, 9606.ENSP00000469647	FKBP4, MAPK1, TAB1, MAPK14, NR3C1, DUSP1, EGR1, JUND, MAPK3, JUNB, FOS, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A, MAPK8, ZFP36
GO:0010604	Positive regulation of macromolecule metabolic process	19	3600	0.69	2.29E-09	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239938, 9606.ENSP00000241014, 9606.ENSP00000252818, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK12, MAPK1, TAB1, MAPK14, NR3C1, EGR1, MAPK8IP1, JUND, MAP2K2, MAPK3, DUSP6, JUNB, FOS, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A, MAPK8, ZFP36
GO:0010033	Response to organic substance	18	3011	0.75	2.61E-09	9606.ENSP00000001008, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000252818, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000378974, 9606.ENSP00000469647	FKBP4, MAPK1, TAB1, MAPK14, NR3C1, DUSP1, EGR1, JUND, MAPK3, DUSP6, JUNB, FOS, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A, MAPK8, ZFP36
GO:0000187	Activation of mapk activity	8	157	1.68	4.41E-09	9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000333685, 9606.ENSP00000356070	MAPK1, TAB1, MAPK14, MAP2K2, MAPK3, DUSP6, MAPK11, MAPKAPK2

Table S9. the full list of KEGG analysis and GO analysis for DUSP1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0051338	Regulation of transferase activity	13	1036	1.07	4.41E-09	9606.ENSP00000215832,9606.ENSP00000216160,9606.ENSP00000229795,9606.ENSP00000239223,9606.ENSP00000239938,9606.ENSP00000241014,9606.ENSP00000262948,9606.ENSP00000263025,9606.ENSP00000279488,9606.ENSP00000333685,9606.ENSP00000335153,9606.ENSP00000356070,9606.ENSP00000469647	MAPK1, TAB1, MAPK14, DUSP1, EGR1, MAPK8IP1, MAP2K2, MAPK3, DUSP6, MAPK11, HSP90AA1, MAPKAPK2, ZFP36
GO:0033554	Cellular response to stress	15	1725	0.91	5.12E-09	9606.ENSP00000215659,9606.ENSP00000215832,9606.ENSP00000216160,9606.ENSP00000229795,9606.ENSP00000239938,9606.ENSP00000241014,9606.ENSP00000262948,9606.ENSP00000263025,9606.ENSP00000306245,9606.ENSP00000333685,9606.ENSP00000335153,9606.ENSP00000356070,9606.ENSP00000364802,9606.ENSP00000378974,9606.ENSP00000469647	MAPK12, MAPK1, TAB1, MAPK14, EGR1, MAPK8IP1, MAP2K2, MAPK3, FOS, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A, MAPK8, ZFP36
GO:0045859	Regulation of protein kinase activity	12	812	1.14	5.40E-09	9606.ENSP00000215832,9606.ENSP00000216160,9606.ENSP00000229795,9606.ENSP00000239223,9606.ENSP00000239938,9606.ENSP00000241014,9606.ENSP00000262948,9606.ENSP00000263025,9606.ENSP00000279488,9606.ENSP00000333685,9606.ENSP00000335153,9606.ENSP00000356070	MAPK1, TAB1, MAPK14, DUSP1, EGR1, MAPK8IP1, MAP2K2, MAPK3, DUSP6, MAPK11, HSP90AA1, MAPKAPK2
GO:0033993	Response to lipid	12	858	1.11	8.93E-09	9606.ENSP00000001008,9606.ENSP00000215832,9606.ENSP00000229795,9606.ENSP00000231509,9606.ENSP00000239223,9606.ENSP00000252818,9606.ENSP00000263025,9606.ENSP00000303315,9606.ENSP00000306245,9606.ENSP00000356070,9606.ENSP00000378974,9606.ENSP00000469647	FKBP4, MAPK1, MAPK14, NR3C1, DUSP1, JUND, MAPK3, JUNB, FOS, MAPKAPK2, MAPK8, ZFP36
GO:0065009	Regulation of molecular function	20	4913	0.58	1.24E-08	9606.ENSP00000215659,9606.ENSP00000215832,9606.ENSP00000216160,9606.ENSP00000229795,9606.ENSP00000231509,9606.ENSP00000239223,9606.ENSP00000239938,9606.ENSP00000241014,9606.ENSP00000252818,9606.ENSP00000262948,9606.ENSP00000263025,9606.ENSP00000279488,9606.ENSP00000303315,9606.ENSP00000306245,9606.ENSP00000333685,9606.ENSP00000335153,9606.ENSP00000356070,9606.ENSP00000364802,9606.ENSP00000378974,9606.ENSP00000469647	MAPK12, MAPK1, TAB1, MAPK14, NR3C1, DUSP1, EGR1, MAPK8IP1, JUND, MAP2K2, MAPK3, DUSP6, JUNB, FOS, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A, MAPK8, ZFP36
GO:0031325	Positive regulation of cellular metabolic process	18	3413	0.69	1.28E-08	9606.ENSP00000215659,9606.ENSP00000215832,9606.ENSP00000216160,9606.ENSP00000229795,9606.ENSP00000231509,9606.ENSP00000239938,9606.ENSP00000241014,9606.ENSP00000252818,9606.ENSP00000262948,9606.ENSP00000263025,9606.ENSP00000279488,9606.ENSP00000303315,9606.ENSP00000306245,9606.ENSP00000333685,9606.ENSP00000335153,9606.ENSP00000356070,9606.ENSP00000364802,9606.ENSP00000469647	MAPK12, MAPK1, TAB1, MAPK14, NR3C1, EGR1, MAPK8IP1, JUND, MAP2K2, MAPK3, DUSP6, JUNB, FOS, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A, ZFP36
GO:0032496	Response to lipopolysaccharide	9	313	1.43	1.31E-08	9606.ENSP00000215832,9606.ENSP00000229795,9606.ENSP00000252818,9606.ENSP00000263025,9606.ENSP00000303315,9606.ENSP00000306245,9606.ENSP00000356070,9606.ENSP00000378974,9606.ENSP00000469647	MAPK1, MAPK14, JUND, MAPK3, JUNB, FOS, MAPKAPK2, MAPK8, ZFP36
GO:0050790	Regulation of catalytic activity	16	2386	0.8	1.70E-08	9606.ENSP00000215659,9606.ENSP00000215832,9606.ENSP00000216160,9606.ENSP00000229795,9606.ENSP00000239223,9606.ENSP00000239938,9606.ENSP00000241014,9606.ENSP00000262948,9606.ENSP00000263025,9606.ENSP00000279488,9606.ENSP00000333685,9606.ENSP00000335153,9606.ENSP00000356070,9606.ENSP00000364802,9606.ENSP00000378974,9606.ENSP00000469647	MAPK12, MAPK1, TAB1, MAPK14, DUSP1, EGR1, MAPK8IP1, MAP2K2, MAPK3, DUSP6, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A, MAPK8, ZFP36
GO:0070848	Response to growth factor	10	524	1.25	2.78E-08	9606.ENSP00000215832,9606.ENSP00000216160,9606.ENSP00000229795,9606.ENSP00000231509,9606.ENSP00000239938,9606.ENSP00000263025,9606.ENSP00000279488,9606.ENSP00000306245,9606.ENSP00000356070,9606.ENSP00000469647	MAPK1, TAB1, MAPK14, NR3C1, EGR1, MAPK3, DUSP6, FOS, MAPKAPK2, ZFP36
GO:0071345	Cellular response to cytokine stimulus	12	1013	1.04	3.57E-08	9606.ENSP00000215832,9606.ENSP00000216160,9606.ENSP00000229795,9606.ENSP00000239223,9606.ENSP00000239938,9606.ENSP00000263025,9606.ENSP00000303315,9606.ENSP00000306245,9606.ENSP00000333685,9606.ENSP00000335153,9606.ENSP00000378974,9606.ENSP00000469647	MAPK1, TAB1, MAPK14, DUSP1, EGR1, MAPK3, JUNB, FOS, MAPK11, HSP90AA1, MAPK8, ZFP36
GO:0045860	Positive regulation of protein kinase activity	10	550	1.23	4.04E-08	9606.ENSP00000215832,9606.ENSP00000216160,9606.ENSP00000229795,9606.ENSP00000239938,9606.ENSP00000262948,9606.ENSP00000263025,9606.ENSP00000279488,9606.ENSP00000333685,9606.ENSP00000335153,9606.ENSP00000356070	MAPK1, TAB1, MAPK14, EGR1, MAP2K2, MAPK3, DUSP6, MAPK11, HSP90AA1, MAPKAPK2

Table S9. the full list of KEGG analysis and GO analysis for DUSP1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0051716	Cellular response to stimulus	21	6489	0.48	4.04E-08	9606.ENSP00000001008, 9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000241014, 9606.ENSP00000252818, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000378974, 9606.ENSP00000469647	FKBP4, MAPK12, MAPK1, TAB1, MAPK14, NR3C1, DUSP1, EGR1, MAPK8IP1, JUND, MAP2K2, MAPK3, DUSP6, JUNB, FOS, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A, MAPK8, ZFP36
GO:0051247	Positive regulation of protein metabolic process	14	1715	0.88	4.56E-08	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000241014, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000378974	MAPK12, MAPK1, TAB1, MAPK14, EGR1, MAPK8IP1, MAP2K2, MAPK3, DUSP6, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A, MAPK8
GO:0032268	Regulation of cellular protein metabolic process	16	2693	0.74	7.28E-08	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000241014, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK12, MAPK1, TAB1, MAPK14, DUSP1, EGR1, MAPK8IP1, MAP2K2, MAPK3, DUSP6, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A, MAPK8, ZFP36
GO:0048522	Positive regulation of cellular process	20	5579	0.52	7.96E-08	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000241014, 9606.ENSP00000252818, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK12, MAPK1, TAB1, MAPK14, NR3C1, DUSP1, EGR1, MAPK8IP1, JUND, MAP2K2, MAPK3, DUSP6, JUNB, FOS, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A, MAPK8, ZFP36
GO:0019219	Regulation of nucleobase-containing compound metabolic process	18	3982	0.62	9.79E-08	9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000241014, 9606.ENSP00000252818, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK1, TAB1, MAPK14, NR3C1, DUSP1, EGR1, MAPK8IP1, JUND, MAP2K2, MAPK3, JUNB, FOS, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A, MAPK8, ZFP36
GO:1900034	Regulation of cellular response to heat	6	79	1.85	1.06E-07	9606.ENSP00000001008, 9606.ENSP00000215832, 9606.ENSP00000263025, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000364802	FKBP4, MAPK1, MAPK3, HSP90AA1, MAPKAPK2, HSPA1A
GO:0031399	Regulation of protein modification process	14	1870	0.84	1.17E-07	9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000241014, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000378974	MAPK1, TAB1, MAPK14, DUSP1, EGR1, MAPK8IP1, MAP2K2, MAPK3, DUSP6, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A, MAPK8
GO:0043085	Positive regulation of catalytic activity	13	1489	0.91	1.17E-07	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000378974	MAPK12, MAPK1, TAB1, MAPK14, EGR1, MAP2K2, MAPK3, DUSP6, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A, MAPK8
GO:0007165	Signal transduction	19	4876	0.56	1.38E-07	9606.ENSP00000001008, 9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000241014, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000378974, 9606.ENSP00000469647	FKBP4, MAPK12, MAPK1, TAB1, MAPK14, NR3C1, DUSP1, EGR1, MAPK8IP1, MAP2K2, MAPK3, DUSP6, JUNB, FOS, MAPK11, HSP90AA1, MAPKAPK2, MAPK8, ZFP36

Table S9. the full list of KEGG analysis and GO analysis for DUSP1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0051171	Regulation of nitrogen compound metabolic process	20	5836	0.5	1.50E-07	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000241014, 9606.ENSP00000252818, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK12, MAPK1, TAB1, MAPK14, NR3C1, DUSP1, EGR1, MAPK8IP1, JUND, MAP2K2, MAPK3, DUSP6, JUNB, FOS, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A, MAPK8, ZFP36
GO:0006950	Response to stress	17	3485	0.66	1.66E-07	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000241014, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK12, MAPK1, TAB1, MAPK14, DUSP1, EGR1, MAPK8IP1, MAP2K2, MAPK3, DUSP6, FOS, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A, MAPK8, ZFP36
GO:0014070	Response to organic cyclic compound	11	911	1.05	1.66E-07	9606.ENSP00000001008, 9606.ENSP00000215832, 9606.ENSP00000231509, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000252818, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000469647	FKBP4, MAPK1, NR3C1, DUSP1, EGR1, JUND, MAPK3, DUSP6, JUNB, FOS, ZFP36
GO:0018105	Peptidyl-serine phosphorylation	7	177	1.57	1.75E-07	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000356070, 9606.ENSP00000378974	MAPK12, MAPK1, MAPK14, MAP2K2, MAPK3, MAPKAPK2, MAPK8
GO:0044260	Cellular macromolecule metabolic process	19	4976	0.55	1.78E-07	9606.ENSP00000001008, 9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239223, 9606.ENSP00000241014, 9606.ENSP00000252818, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000378974, 9606.ENSP00000469647	FKBP4, MAPK12, MAPK1, TAB1, MAPK14, NR3C1, DUSP1, MAPK8IP1, JUND, MAP2K2, MAPK3, DUSP6, FOS, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A, MAPK8, ZFP36
GO:0080090	Regulation of primary metabolic process	20	6032	0.49	2.55E-07	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000241014, 9606.ENSP00000252818, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK12, MAPK1, TAB1, MAPK14, NR3C1, DUSP1, EGR1, MAPK8IP1, JUND, MAP2K2, MAPK3, DUSP6, JUNB, FOS, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A, MAPK8, ZFP36
GO:0071363	Cellular response to growth factor stimulus	9	494	1.23	2.71E-07	9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239938, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000356070, 9606.ENSP00000469647	MAPK1, TAB1, MAPK14, NR3C1, EGR1, MAPK3, FOS, MAPKAPK2, ZFP36
GO:0032270	Positive regulation of cellular protein metabolic process	13	1635	0.87	2.78E-07	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000241014, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000364802	MAPK12, MAPK1, TAB1, MAPK14, EGR1, MAPK8IP1, MAP2K2, MAPK3, DUSP6, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A
GO:0001934	Positive regulation of protein phosphorylation	11	1019	1	4.01E-07	9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000241014, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070	MAPK1, TAB1, MAPK14, EGR1, MAPK8IP1, MAP2K2, MAPK3, DUSP6, MAPK11, HSP90AA1, MAPKAPK2
GO:0031323	Regulation of cellular metabolic process	20	6239	0.48	4.01E-07	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000241014, 9606.ENSP00000252818, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK12, MAPK1, TAB1, MAPK14, NR3C1, DUSP1, EGR1, MAPK8IP1, JUND, MAP2K2, MAPK3, DUSP6, JUNB, FOS, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A, MAPK8, ZFP36

Table S9. the full list of KEGG analysis and GO analysis for DUSP1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0035556	Intracellular signal transduction	13	1712	0.85	4.14E-07	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000239223, 9606.ENSP00000241014, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000333685, 9606.ENSP00000356070, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK12, MAPK1, TAB1, MAPK14, DUSP1, MAPK8IP1, MAP2K2, MAPK3, DUSP6, MAPK11, MAPKAPK2, MAPK8, ZFP36
GO:1902533	Positive regulation of intracellular signal transduction	11	1041	0.99	4.60E-07	9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000241014, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000364802	MAPK1, TAB1, MAPK14, MAPK8IP1, MAP2K2, MAPK3, DUSP6, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A
GO:0043410	Positive regulation of mapk cascade	9	543	1.19	4.73E-07	9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000241014, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000333685, 9606.ENSP00000356070	MAPK1, TAB1, MAPK14, MAPK8IP1, MAP2K2, MAPK3, DUSP6, MAPK11, MAPKAPK2
GO:0060255	Regulation of macromolecule metabolic process	20	6407	0.46	6.05E-07	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000241014, 9606.ENSP00000252818, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK12, MAPK1, TAB1, MAPK14, NR3C1, DUSP1, EGR1, MAPK8IP1, JUND, MAP2K2, MAPK3, DUSP6, JUNB, FOS, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A, MAPK8, ZFP36
GO:2000112	Regulation of cellular macromolecule biosynthetic process	17	3878	0.61	6.07E-07	9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000241014, 9606.ENSP00000252818, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000364802, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK1, TAB1, MAPK14, NR3C1, DUSP1, EGR1, MAPK8IP1, JUND, MAP2K2, MAPK3, JUNB, FOS, MAPK11, HSP90AA1, HSPA1A, MAPK8, ZFP36
GO:0010628	Positive regulation of gene expression	14	2337	0.75	1.16E-06	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239938, 9606.ENSP00000252818, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK1, MAPK14, NR3C1, EGR1, JUND, MAP2K2, MAPK3, JUNB, FOS, MAPK11, MAPKAPK2, HSPA1A, MAPK8, ZFP36
GO:0044419	Interspecies interaction between organisms	13	1899	0.8	1.22E-06	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000252818, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK1, MAPK14, EGR1, JUND, MAPK3, JUNB, FOS, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A, MAPK8, ZFP36
GO:0071495	Cellular response to endogenous stimulus	11	1181	0.94	1.39E-06	9606.ENSP00000001008, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000231509, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000252818, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000469647	FKBP4, MAPK1, TAB1, NR3C1, DUSP1, EGR1, JUND, MAPK3, JUNB, FOS, ZFP36
GO:0051090	Regulation of dna-binding transcription factor activity	8	437	1.23	1.72E-06	9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000364802, 9606.ENSP00000378974	MAPK1, TAB1, MAPK14, MAPK3, FOS, MAPK11, HSPA1A, MAPK8
GO:1901700	Response to oxygen-containing compound	12	1567	0.85	1.74E-06	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000252818, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000356070, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK1, MAPK14, NR3C1, DUSP1, EGR1, JUND, MAPK3, JUNB, FOS, MAPKAPK2, MAPK8, ZFP36
GO:0051707	Response to other organism	11	1256	0.91	2.38E-06	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000252818, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000356070, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK1, MAPK14, EGR1, JUND, MAPK3, JUNB, FOS, MAPK11, MAPKAPK2, MAPK8, ZFP36
GO:0009967	Positive regulation of signal transduction	12	1654	0.83	2.93E-06	9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000241014, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000378974	MAPK1, TAB1, MAPK14, MAPK8IP1, MAP2K2, MAPK3, DUSP6, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A, MAPK8

Table S9. the full list of KEGG analysis and GO analysis for DUSP1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0051252	Regulation of rna metabolic process	16	3722	0.6	3.35E-06	9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239938, 9606.ENSP00000241014, 9606.ENSP00000252818, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK1, TAB1, MAPK14, NR3C1, EGR1, MAPK8IP1, JUND, MAP2K2, MAPK3, JUNB, FOS, MAPK11, MAPKAPK2, HSPA1A, MAPK8, ZFP36
GO:0006796	Phosphate-containing compound metabolic process	13	2107	0.76	3.43E-06	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000239223, 9606.ENSP00000241014, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000333685, 9606.ENSP00000356070, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK12, MAPK1, TAB1, MAPK14, DUSP1, MAPK8IP1, MAP2K2, MAPK3, DUSP6, MAPK11, MAPKAPK2, MAPK8, ZFP36
GO:0007167	Enzyme linked receptor protein signaling pathway	9	720	1.07	3.66E-06	9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070	MAPK1, TAB1, MAPK14, EGR1, MAPK3, FOS, MAPK11, HSP90AA1, MAPKAPK2
GO:0038093	Fc receptor signaling pathway	6	177	1.5	4.09E-06	9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000335153, 9606.ENSP00000378974	MAPK1, TAB1, MAPK3, FOS, HSP90AA1, MAPK8
GO:0080135	Regulation of cellular response to stress	9	739	1.05	4.38E-06	9606.ENSP00000001008, 9606.ENSP00000215832, 9606.ENSP00000239223, 9606.ENSP00000241014, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000364802	FKBP4, MAPK1, DUSP1, MAPK8IP1, MAP2K2, MAPK3, HSP90AA1, MAPKAPK2, HSPA1A
GO:0090170	Regulation of golgi inheritance	3	4	2.84	5.01E-06	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025	MAPK1, MAP2K2, MAPK3
GO:0043412	Macromolecule modification	15	3277	0.63	6.14E-06	9606.ENSP00000001008, 9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000239223, 9606.ENSP00000241014, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000356070, 9606.ENSP00000378974, 9606.ENSP00000469647	FKBP4, MAPK12, MAPK1, TAB1, MAPK14, DUSP1, MAPK8IP1, MAP2K2, MAPK3, DUSP6, FOS, MAPK11, MAPKAPK2, MAPK8, ZFP36
GO:0071248	Cellular response to metal ion	6	193	1.46	6.46E-06	9606.ENSP00000215832, 9606.ENSP00000252818, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000378974	MAPK1, JUND, MAPK3, JUNB, FOS, MAPK8
GO:1902531	Regulation of intracellular signal transduction	12	1807	0.79	6.90E-06	9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000239223, 9606.ENSP00000241014, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000364802	MAPK1, TAB1, MAPK14, DUSP1, MAPK8IP1, MAP2K2, MAPK3, DUSP6, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A
GO:0080134	Regulation of response to stress	11	1437	0.85	7.67E-06	9606.ENSP00000001008, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000239223, 9606.ENSP00000241014, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000364802	FKBP4, MAPK1, TAB1, MAPK14, DUSP1, MAPK8IP1, MAP2K2, MAPK3, HSP90AA1, MAPKAPK2, HSPA1A
GO:0006355	Regulation of transcription, dna-templated	15	3388	0.62	8.89E-06	9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239938, 9606.ENSP00000241014, 9606.ENSP00000252818, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000364802, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK1, TAB1, MAPK14, NR3C1, EGR1, MAPK8IP1, JUND, MAP2K2, MAPK3, JUNB, FOS, MAPK11, HSPA1A, MAPK8, ZFP36
GO:0010038	Response to metal ion	7	367	1.25	9.79E-06	9606.ENSP00000215832, 9606.ENSP00000239223, 9606.ENSP00000252818, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000378974	MAPK1, DUSP1, JUND, MAPK3, JUNB, FOS, MAPK8
GO:0009612	Response to mechanical stimulus	6	212	1.42	1.01E-05	9606.ENSP00000229795, 9606.ENSP00000252818, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000378974	MAPK14, JUND, MAPK3, JUNB, FOS, MAPK8
GO:0010468	Regulation of gene expression	17	4813	0.52	1.11E-05	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239938, 9606.ENSP00000241014, 9606.ENSP00000252818, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK12, MAPK1, TAB1, MAPK14, NR3C1, EGR1, MAPK8IP1, JUND, MAP2K2, MAPK3, JUNB, FOS, MAPK11, MAPKAPK2, HSPA1A, MAPK8, ZFP36

Table S9. the full list of KEGG analysis and GO analysis for DUSP1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0009628	Response to abiotic stimulus	10	1147	0.91	1.12E-05	9606.ENSP00000229795,9606.ENSP00000239223,9606.ENSP00000239938,9606.ENSP00000252818,9606.ENSP00000263025,9606.ENSP00000303315,9606.ENSP00000306245,9606.ENSP00000335153,9606.ENSP00000364802,9606.ENSP00000378974	MAPK14,DUSP1,EGR1,JUND,MAPK3,JUNB,FOS,HSP90AA1,HSPA1A,MAPK8
GO:0071276	Cellular response to cadmium ion	4	37	2	1.12E-05	9606.ENSP00000215832,9606.ENSP00000263025,9606.ENSP00000306245,9606.ENSP00000378974	MAPK1,MAPK3,FOS,MAPK8
GO:0048583	Regulation of response to stimulus	16	4114	0.56	1.15E-05	9606.ENSP00000001008,9606.ENSP00000215832,9606.ENSP00000216160,9606.ENSP00000229795,9606.ENSP00000239223,9606.ENSP00000239938,9606.ENSP00000241014,9606.ENSP00000262948,9606.ENSP00000263025,9606.ENSP00000279488,9606.ENSP00000306245,9606.ENSP00000333685,9606.ENSP00000335153,9606.ENSP00000356070,9606.ENSP00000364802,9606.ENSP00000378974	FKBP4,MAPK1,TAB1,MAPK14,DUSP1,EGR1,MAPK8IP1,MAP2K2,MAPK3,DUSP6,FOS,MAPK11,HSP90AA1,MAPKAPK2,HSPA1A,MAPK8
GO:0002682	Regulation of immune system process	11	1514	0.83	1.17E-05	9606.ENSP00000215832,9606.ENSP00000216160,9606.ENSP00000229795,9606.ENSP00000239223,9606.ENSP00000241014,9606.ENSP00000263025,9606.ENSP00000306245,9606.ENSP00000335153,9606.ENSP00000364802,9606.ENSP00000378974,9606.ENSP00000469647	MAPK1,TAB1,MAPK14,DUSP1,MAPK8IP1,MAPK3,FOS,HSP90AA1,HSPA1A,MAPK8,ZFP36
GO:0009725	Response to hormone	9	849	0.99	1.17E-05	9606.ENSP00000001008,9606.ENSP00000215832,9606.ENSP00000231509,9606.ENSP00000239223,9606.ENSP00000239938,9606.ENSP00000252818,9606.ENSP00000303315,9606.ENSP00000306245,9606.ENSP00000469647	FKBP4,MAPK1,NR3C1,DUSP1,EGR1,JUND,JUNB,FOS,ZFP36
GO:0045935	Positive regulation of nucleobase-containing compound metabolic process	12	1927	0.76	1.19E-05	9606.ENSP00000215832,9606.ENSP00000229795,9606.ENSP00000231509,9606.ENSP00000239938,9606.ENSP00000252818,9606.ENSP00000262948,9606.ENSP00000263025,9606.ENSP00000303315,9606.ENSP00000306245,9606.ENSP00000335153,9606.ENSP00000364802,9606.ENSP00000469647	MAPK1,MAPK14,NR3C1,EGR1,JUND,MAP2K2,MAPK3,JUNB,FOS,HSP90AA1,HSPA1A,ZFP36
GO:0038066	p38MAPK cascade	3	7	2.6	1.38E-05	9606.ENSP00000229795,9606.ENSP00000356070,9606.ENSP00000469647	MAPK14,MAPKAPK2,ZFP36
GO:0038095	Fc-epsilon receptor signaling pathway	5	115	1.61	1.61E-05	9606.ENSP00000215832,9606.ENSP00000216160,9606.ENSP00000263025,9606.ENSP00000306245,9606.ENSP00000378974	MAPK1,TAB1,MAPK3,FOS,MAPK8
GO:0006464	Cellular protein modification process	14	3063	0.63	2.24E-05	9606.ENSP00000001008,9606.ENSP00000215659,9606.ENSP00000215832,9606.ENSP00000216160,9606.ENSP00000229795,9606.ENSP00000239223,9606.ENSP00000241014,9606.ENSP00000262948,9606.ENSP00000263025,9606.ENSP00000279488,9606.ENSP00000333685,9606.ENSP00000356070,9606.ENSP00000378974,9606.ENSP00000469647	FKBP4,MAPK12,MAPK1,TAB1,MAPK14,DUSP1,MAPK8IP1,MAP2K2,MAPK3,DUSP6,MAPK11,MAPKAPK2,MAPK8,ZFP36
GO:0006807	Nitrogen compound metabolic process	19	6852	0.41	2.24E-05	9606.ENSP00000001008,9606.ENSP00000215659,9606.ENSP00000215832,9606.ENSP00000216160,9606.ENSP00000229795,9606.ENSP00000231509,9606.ENSP00000239223,9606.ENSP00000241014,9606.ENSP00000252818,9606.ENSP00000262948,9606.ENSP00000263025,9606.ENSP00000279488,9606.ENSP00000306245,9606.ENSP00000333685,9606.ENSP00000335153,9606.ENSP00000356070,9606.ENSP00000364802,9606.ENSP00000378974,9606.ENSP00000469647	FKBP4,MAPK12,MAPK1,TAB1,MAPK14,NR3C1,DUSP1,MAPK8IP1,JUND,MAP2K2,MAPK3,DUSP6,FOS,MAPK11,HSP90AA1,MAPKAPK2,HSPA1A,MAPK8,ZFP36
GO:0009314	Response to radiation	7	431	1.18	2.47E-05	9606.ENSP00000229795,9606.ENSP00000239223,9606.ENSP00000239938,9606.ENSP00000252818,9606.ENSP00000303315,9606.ENSP00000306245,9606.ENSP00000378974	MAPK14,DUSP1,EGR1,JUND,JUNB,FOS,MAPK8
GO:0042127	Regulation of cell population proliferation	11	1642	0.8	2.47E-05	9606.ENSP00000215832,9606.ENSP00000229795,9606.ENSP00000239223,9606.ENSP00000239938,9606.ENSP00000241014,9606.ENSP00000252818,9606.ENSP00000263025,9606.ENSP00000303315,9606.ENSP00000333685,9606.ENSP00000364802,9606.ENSP00000469647	MAPK1,MAPK14,DUSP1,EGR1,MAPK8IP1,JUND,MAPK3,JUNB,MAPK11,HSPA1A,ZFP36
GO:0009966	Regulation of signal transduction	14	3107	0.62	2.59E-05	9606.ENSP00000215832,9606.ENSP00000216160,9606.ENSP00000229795,9606.ENSP00000239223,9606.ENSP00000239938,9606.ENSP00000241014,9606.ENSP00000262948,9606.ENSP00000263025,9606.ENSP00000279488,9606.ENSP00000333685,9606.ENSP00000335153,9606.ENSP00000356070,9606.ENSP00000364802,9606.ENSP00000378974	MAPK1,TAB1,MAPK14,DUSP1,EGR1,MAPK8IP1,MAP2K2,MAPK3,DUSP6,MAPK11,HSP90AA1,MAPKAPK2,HSPA1A,MAPK8
GO:0071675	Regulation of mononuclear cell migration	4	53	1.85	3.79E-05	9606.ENSP00000215832,9606.ENSP00000229795,9606.ENSP00000239223,9606.ENSP00000263025	MAPK1,MAPK14,DUSP1,MAPK3

Table S9. the full list of KEGG analysis and GO analysis for DUSP1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0051254	Positive regulation of rna metabolic process	11	1759	0.77	4.83E-05	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239938, 9606.ENSP00000252818, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000364802, 9606.ENSP00000469647	MAPK1, MAPK14, NR3C1, EGR1, JUND, MAP2K2, MAPK3, JUNB, FOS, HSPA1A, ZFP36
GO:0048519	Negative regulation of biological process	17	5389	0.47	5.55E-05	9606.ENSP00000001008, 9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000241014, 9606.ENSP00000252818, 9606.ENSP00000262948, 9606.ENSP00000279488, 9606.ENSP00000303315, 9606.ENSP00000333685, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000378974, 9606.ENSP00000469647	FKBP4, MAPK12, MAPK1, MAPK14, NR3C1, DUSP1, EGR1, MAPK8IP1, JUND, MAP2K2, DUSP6, JUNB, MAPK11, MAPKAPK2, HSPA1A, MAPK8, ZFP36
GO:0051094	Positive regulation of developmental process	10	1389	0.83	5.67E-05	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000252818, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000364802, 9606.ENSP00000469647	MAPK12, MAPK1, MAPK14, EGR1, JUND, JUNB, FOS, MAPK11, HSPA1A, ZFP36
GO:0044238	Primary metabolic process	19	7332	0.38	6.90E-05	9606.ENSP00000001008, 9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239223, 9606.ENSP00000241014, 9606.ENSP00000252818, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000378974, 9606.ENSP00000469647	FKBP4, MAPK12, MAPK1, TAB1, MAPK14, NR3C1, DUSP1, MAPK8IP1, JUND, MAP2K2, MAPK3, DUSP6, FOS, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A, MAPK8, ZFP36
GO:0060420	Regulation of heart growth	4	67	1.75	8.75E-05	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000279488, 9606.ENSP00000333685	MAPK1, MAPK14, DUSP6, MAPK11
GO:0071396	Cellular response to lipid	7	528	1.09	8.75E-05	9606.ENSP00000001008, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000263025, 9606.ENSP00000378974, 9606.ENSP00000469647	FKBP4, MAPK1, MAPK14, NR3C1, MAPK3, MAPK8, ZFP36
GO:0048010	Vascular endothelial growth factor receptor signaling pathway	4	69	1.73	9.64E-05	9606.ENSP00000229795, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070	MAPK14, MAPK11, HSP90AA1, MAPKAPK2
GO:0048523	Negative regulation of cellular process	16	4874	0.49	0.00011	9606.ENSP00000001008, 9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000241014, 9606.ENSP00000252818, 9606.ENSP00000279488, 9606.ENSP00000303315, 9606.ENSP00000333685, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000378974, 9606.ENSP00000469647	FKBP4, MAPK12, MAPK1, MAPK14, NR3C1, DUSP1, EGR1, MAPK8IP1, JUND, DUSP6, JUNB, MAPK11, MAPKAPK2, HSPA1A, MAPK8, ZFP36
GO:0070935	3-UTR-mediated mRNA stabilization	3	17	2.22	0.00011	9606.ENSP00000229795, 9606.ENSP00000356070, 9606.ENSP00000469647	MAPK14, MAPKAPK2, ZFP36
GO:0007565	Female pregnancy	5	183	1.41	0.00012	9606.ENSP00000001008, 9606.ENSP00000215832, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245	FKBP4, MAPK1, MAPK3, JUNB, FOS
GO:0032870	Cellular response to hormone stimulus	7	569	1.06	0.00013	9606.ENSP00000001008, 9606.ENSP00000231509, 9606.ENSP00000239223, 9606.ENSP00000252818, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000469647	FKBP4, NR3C1, DUSP1, JUND, JUNB, FOS, ZFP36
GO:0071222	Cellular response to lipopolysaccharide	5	185	1.4	0.00013	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK1, MAPK14, MAPK3, MAPK8, ZFP36
GO:0010759	Positive regulation of macrophage chemotaxis	3	19	2.17	0.00014	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000263025	MAPK1, MAPK14, MAPK3
GO:0019538	Protein metabolic process	15	4251	0.52	0.00014	9606.ENSP00000001008, 9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000239223, 9606.ENSP00000241014, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000378974, 9606.ENSP00000469647	FKBP4, MAPK12, MAPK1, TAB1, MAPK14, DUSP1, MAPK8IP1, MAP2K2, MAPK3, DUSP6, MAPK11, HSP90AA1, MAPKAPK2, MAPK8, ZFP36
GO:2000641	Regulation of early endosome to late endosome transport	3	19	2.17	0.00014	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025	MAPK1, MAP2K2, MAPK3
GO:0007178	Transmembrane receptor protein serine/threonine kinase signaling pathway	5	195	1.38	0.00016	9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000263025, 9606.ENSP00000306245	TAB1, MAPK14, EGR1, MAPK3, FOS

Table S9. the full list of KEGG analysis and GO analysis for DUSP1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0018193	Peptidyl-amino acid modification	8	867	0.93	0.00016	9606.ENSP00000001008, 9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000356070, 9606.ENSP00000378974	FKBP4, MAPK12, MAPK1, MAPK14, MAP2K2, MAPK3, MAPKAPK2, MAPK8
GO:0000302	Response to reactive oxygen species	5	198	1.37	0.00017	9606.ENSP00000215832, 9606.ENSP00000239223, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000378974	MAPK1, DUSP1, MAPK3, FOS, MAPK8
GO:0031281	Positive regulation of cyclase activity	3	23	2.08	0.00022	9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000378974	MAPK14, MAPK3, MAPK8
GO:0006979	Response to oxidative stress	6	393	1.15	0.00023	9606.ENSP00000215832, 9606.ENSP00000239223, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000364802, 9606.ENSP00000378974	MAPK1, DUSP1, MAPK3, FOS, HSPA1A, MAPK8
GO:0046697	Decidualization	3	25	2.05	0.00027	9606.ENSP00000215832, 9606.ENSP00000263025, 9606.ENSP00000303315	MAPK1, MAPK3, JUNB
GO:0050793	Regulation of developmental process	12	2648	0.63	0.00027	9606.ENSP00000001008, 9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000252818, 9606.ENSP00000279488, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000364802, 9606.ENSP00000469647	FKBP4, MAPK12, MAPK1, MAPK14, EGR1, JUND, DUSP6, JUNB, FOS, MAPK11, HSPA1A, ZFP36
GO:0051591	Response to camp	4	98	1.58	0.0003	9606.ENSP00000239223, 9606.ENSP00000252818, 9606.ENSP00000303315, 9606.ENSP00000306245	DUSP1, JUND, JUNB, FOS
GO:0032872	Regulation of stress-activated mapk cascade	5	228	1.31	0.00031	9606.ENSP00000215832, 9606.ENSP00000239223, 9606.ENSP00000241014, 9606.ENSP00000262948, 9606.ENSP00000263025	MAPK1, DUSP1, MAPK8IP1, MAP2K2, MAPK3
GO:0010243	Response to organonitrogen compound	8	987	0.88	0.00037	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000252818, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245	MAPK1, MAPK14, DUSP1, EGR1, JUND, MAPK3, JUNB, FOS
GO:0050794	Regulation of cellular process	21	10932	0.25	0.00037	9606.ENSP00000001008, 9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000241014, 9606.ENSP00000252818, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000378974, 9606.ENSP00000469647	FKBP4, MAPK12, MAPK1, TAB1, MAPK14, NR3C1, DUSP1, EGR1, MAPK8IP1, JUND, MAP2K2, MAPK3, DUSP6, JUNB, FOS, MAPK11, HSP90AA1, MAPKAPK2, HSPA1A, MAPK8, ZFP36
GO:0045597	Positive regulation of cell differentiation	8	993	0.88	0.00038	9606.ENSP00000215659, 9606.ENSP00000229795, 9606.ENSP00000252818, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000364802, 9606.ENSP00000469647	MAPK12, MAPK14, JUND, JUNB, FOS, MAPK11, HSPA1A, ZFP36
GO:0070371	ERK1 and ERK2 cascade	3	29	1.98	0.00039	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025	MAPK1, MAP2K2, MAPK3
GO:0034599	Cellular response to oxidative stress	5	244	1.28	0.00041	9606.ENSP00000215832, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000364802, 9606.ENSP00000378974	MAPK1, MAPK3, FOS, HSPA1A, MAPK8
GO:2000278	Regulation of dna biosynthetic process	4	114	1.51	0.00051	9606.ENSP00000215832, 9606.ENSP00000239223, 9606.ENSP00000263025, 9606.ENSP00000335153	MAPK1, DUSP1, MAPK3, HSP90AA1
GO:0001819	Positive regulation of cytokine production	6	461	1.08	0.00052	9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000263025, 9606.ENSP00000333685, 9606.ENSP00000356070, 9606.ENSP00000364802	MAPK14, EGR1, MAPK3, MAPK11, MAPKAPK2, HSPA1A
GO:0007166	Cell surface receptor signaling pathway	11	2325	0.64	0.00055	9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070, 9606.ENSP00000378974	MAPK1, TAB1, MAPK14, EGR1, MAPK3, JUNB, FOS, MAPK11, HSP90AA1, MAPKAPK2, MAPK8
GO:1901701	Cellular response to oxygen-containing compound	8	1055	0.85	0.00056	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239938, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK1, MAPK14, NR3C1, EGR1, MAPK3, FOS, MAPK8, ZFP36
GO:0031663	Lipopolysaccharide-mediated signaling pathway	3	34	1.91	0.00057	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000263025	MAPK1, MAPK14, MAPK3
GO:0010605	Negative regulation of macromolecule metabolic process	12	2875	0.59	0.00058	9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000241014, 9606.ENSP00000252818, 9606.ENSP00000262948, 9606.ENSP00000279488, 9606.ENSP00000303315, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000469647	MAPK14, NR3C1, DUSP1, EGR1, MAPK8IP1, JUND, MAP2K2, DUSP6, JUNB, MAPKAPK2, HSPA1A, ZFP36

Table S9. the full list of KEGG analysis and GO analysis for DUSP1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0001817	Regulation of cytokine production	7	742	0.94	0.00059	9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000263025, 9606.ENSP00000333685, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000469647	MAPK14, EGR1, MAPK3, MAPK11, MAPKAPK2, HSPA1A, ZFP36
GO:0045595	Regulation of cell differentiation	10	1874	0.7	0.0006	9606.ENSP00000001008, 9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000252818, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000364802, 9606.ENSP00000469647	FKBP4, MAPK12, MAPK1, MAPK14, JUND, JUNB, FOS, MAPK11, HSPA1A, ZFP36
GO:0002688	Regulation of leukocyte chemotaxis	4	124	1.48	0.00065	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000239223, 9606.ENSP00000263025	MAPK1, MAPK14, DUSP1, MAPK3
GO:0007568	Aging	5	274	1.23	0.00065	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000252818, 9606.ENSP00000263025, 9606.ENSP00000306245	MAPK1, MAPK14, JUND, MAPK3, FOS
GO:0051973	Positive regulation of telomerase activity	3	36	1.89	0.00065	9606.ENSP00000215832, 9606.ENSP00000263025, 9606.ENSP00000335153	MAPK1, MAPK3, HSP90AA1
GO:0010557	Positive regulation of macromolecule biosynthetic process	10	1906	0.69	0.00068	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239938, 9606.ENSP00000252818, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000335153	MAPK1, MAPK14, NR3C1, EGR1, JUND, MAP2K2, MAPK3, JUNB, FOS, HSP90AA1
GO:0051172	Negative regulation of nitrogen compound metabolic process	11	2429	0.63	0.00078	9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000241014, 9606.ENSP00000252818, 9606.ENSP00000279488, 9606.ENSP00000303315, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000469647	MAPK14, NR3C1, DUSP1, EGR1, MAPK8IP1, JUND, DUSP6, JUNB, MAPKAPK2, HSPA1A, ZFP36
GO:0034614	Cellular response to reactive oxygen species	4	133	1.45	0.00084	9606.ENSP00000215832, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000378974	MAPK1, MAPK3, FOS, MAPK8
GO:1902895	Positive regulation of pri-mirna transcription by rna polymerase ii	3	40	1.84	0.00085	9606.ENSP00000231509, 9606.ENSP00000239938, 9606.ENSP00000306245	NR3C1, EGR1, FOS
GO:0007169	Transmembrane receptor protein tyrosine kinase signaling pathway	6	518	1.03	0.0009	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000356070	MAPK1, MAPK14, MAPK3, MAPK11, HSP90AA1, MAPKAPK2
GO:0045934	Negative regulation of nucleobase-containing compound metabolic process	9	1528	0.74	0.0009	9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000252818, 9606.ENSP00000303315, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000469647	MAPK14, NR3C1, DUSP1, EGR1, JUND, JUNB, MAPKAPK2, HSPA1A, ZFP36
GO:0007258	JUN phosphorylation	2	4	2.67	0.001	9606.ENSP00000241014, 9606.ENSP00000378974	MAPK8IP1, MAPK8
GO:0031328	Positive regulation of cellular biosynthetic process	10	2005	0.67	0.001	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239938, 9606.ENSP00000252818, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000335153	MAPK1, MAPK14, NR3C1, EGR1, JUND, MAP2K2, MAPK3, JUNB, FOS, HSP90AA1
GO:0060043	Regulation of cardiac muscle cell proliferation	3	43	1.81	0.001	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000333685	MAPK1, MAPK14, MAPK11
GO:0034198	Cellular response to amino acid starvation	3	45	1.79	0.0011	9606.ENSP00000215832, 9606.ENSP00000263025, 9606.ENSP00000378974	MAPK1, MAPK3, MAPK8
GO:0045893	Positive regulation of transcription, dna-templated	9	1587	0.72	0.0011	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239938, 9606.ENSP00000252818, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245	MAPK1, MAPK14, NR3C1, EGR1, JUND, MAP2K2, MAPK3, JUNB, FOS
GO:0051384	Response to glucocorticoid	4	147	1.4	0.0011	9606.ENSP00000231509, 9606.ENSP00000239223, 9606.ENSP00000306245, 9606.ENSP00000469647	NR3C1, DUSP1, FOS, ZFP36
GO:0071407	Cellular response to organic cyclic compound	6	537	1.02	0.0011	9606.ENSP00000001008, 9606.ENSP00000215832, 9606.ENSP00000231509, 9606.ENSP00000239938, 9606.ENSP00000263025, 9606.ENSP00000469647	FKBP4, MAPK1, NR3C1, EGR1, MAPK3, ZFP36
GO:0051592	Response to calcium ion	4	150	1.4	0.0012	9606.ENSP00000239223, 9606.ENSP00000252818, 9606.ENSP00000303315, 9606.ENSP00000306245	DUSP1, JUND, JUNB, FOS
GO:0070849	Response to epidermal growth factor	3	47	1.77	0.0012	9606.ENSP00000215832, 9606.ENSP00000263025, 9606.ENSP00000469647	MAPK1, MAPK3, ZFP36
GO:0001890	Placenta development	4	154	1.38	0.0013	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000303315	MAPK1, MAPK14, MAPK3, JUNB
GO:0048545	Response to steroid hormone	5	328	1.15	0.0013	9606.ENSP00000001008, 9606.ENSP00000231509, 9606.ENSP00000239223, 9606.ENSP00000306245, 9606.ENSP00000469647	FKBP4, NR3C1, DUSP1, FOS, ZFP36
GO:0010608	Posttranscriptional regulation of gene expression	6	574	0.99	0.0014	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000356070, 9606.ENSP00000364802, 9606.ENSP00000469647	MAPK1, MAPK14, MAPK3, MAPKAPK2, HSPA1A, ZFP36

Table S9. the full list of KEGG analysis and GO analysis for DUSP1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0031324	Negative regulation of cellular metabolic process	11	2630	0.59	0.0014	9606.ENSP00000229795,9606.ENSP00000231509,9606.ENSP00000239223,9606.ENSP00000239938,9606.ENSP00000241014,9606.ENSP00000252818,9606.ENSP00000279488,9606.ENSP00000303315,9606.ENSP00000356070,9606.ENSP00000364802,9606.ENSP00000469647	MAPK14, NR3C1, DUSP1, EGR1, MAPK8IP1, JUND, DUSP6, JUNB, MAPKAPK2, HSPA1A, ZFP36
GO:0031329	Regulation of cellular catabolic process	7	875	0.87	0.0014	9606.ENSP00000229795,9606.ENSP00000263025,9606.ENSP00000335153,9606.ENSP00000356070,9606.ENSP00000364802,9606.ENSP00000378974,9606.ENSP00000469647	MAPK14, MAPK3, HSP90AA1, MAPKAPK2, HSPA1A, MAPK8, ZFP36
GO:0045646	Regulation of erythrocyte differentiation	3	49	1.76	0.0014	9606.ENSP00000229795,9606.ENSP00000364802,9606.ENSP00000469647	MAPK14, HSPA1A, ZFP36
GO:0051726	Regulation of cell cycle	8	1230	0.78	0.0014	9606.ENSP00000215659,9606.ENSP00000229795,9606.ENSP00000239223,9606.ENSP00000252818,9606.ENSP00000262948,9606.ENSP00000303315,9606.ENSP00000335153,9606.ENSP00000364802	MAPK12, MAPK14, DUSP1, JUND, MAP2K2, JUNB, HSP90AA1, HSPA1A
GO:0072584	Caveolin-mediated endocytosis	2	5	2.57	0.0014	9606.ENSP00000215832,9606.ENSP00000263025	MAPK1, MAPK3
GO:0120041	Positive regulation of macrophage proliferation	2	5	2.57	0.0014	9606.ENSP00000215832,9606.ENSP00000263025	MAPK1, MAPK3
GO:0051239	Regulation of multicellular organismal process	12	3227	0.54	0.0015	9606.ENSP00000001008,9606.ENSP00000215832,9606.ENSP00000229795,9606.ENSP00000239938,9606.ENSP00000252818,9606.ENSP00000263025,9606.ENSP00000279488,9606.ENSP00000306245,9606.ENSP00000333685,9606.ENSP00000356070,9606.ENSP00000364802,9606.ENSP00000469647	FKBP4, MAPK1, MAPK14, EGR1, JUND, MAPK3, DUSP6, FOS, MAPK11, MAPKAPK2, HSPA1A, ZFP36
GO:0050776	Regulation of immune response	7	896	0.86	0.0016	9606.ENSP00000215832,9606.ENSP00000216160,9606.ENSP00000229795,9606.ENSP00000263025,9606.ENSP00000306245,9606.ENSP00000335153,9606.ENSP00000378974	MAPK1, TAB1, MAPK14, MAPK3, FOS, HSP90AA1, MAPK8
GO:0060440	Trachea formation	2	6	2.49	0.0017	9606.ENSP00000215832,9606.ENSP00000263025	MAPK1, MAPK3
GO:0032386	Regulation of intracellular transport	5	360	1.11	0.0019	9606.ENSP00000215832,9606.ENSP00000229795,9606.ENSP00000262948,9606.ENSP00000263025,9606.ENSP00000378974	MAPK1, MAPK14, MAP2K2, MAPK3, MAPK8
GO:0071347	Cellular response to interleukin-1	4	174	1.33	0.0019	9606.ENSP00000216160,9606.ENSP00000239938,9606.ENSP00000263025,9606.ENSP00000333685	TAB1, EGR1, MAPK3, MAPK11
GO:1902949	Positive regulation of tau-protein kinase activity	2	7	2.43	0.0021	9606.ENSP00000239938,9606.ENSP00000335153	EGR1, HSP90AA1
GO:0002684	Positive regulation of immune system process	7	949	0.84	0.0022	9606.ENSP00000215832,9606.ENSP00000216160,9606.ENSP00000229795,9606.ENSP00000263025,9606.ENSP00000306245,9606.ENSP00000335153,9606.ENSP00000364802	MAPK1, TAB1, MAPK14, MAPK3, FOS, HSP90AA1, HSPA1A
GO:0043488	Regulation of mrna stability	4	183	1.31	0.0023	9606.ENSP00000229795,9606.ENSP00000356070,9606.ENSP00000364802,9606.ENSP00000469647	MAPK14, MAPKAPK2, HSPA1A, ZFP36
GO:0051240	Positive regulation of multicellular organismal process	9	1770	0.68	0.0023	9606.ENSP00000215832,9606.ENSP00000229795,9606.ENSP00000239938,9606.ENSP00000252818,9606.ENSP00000263025,9606.ENSP00000306245,9606.ENSP00000333685,9606.ENSP00000356070,9606.ENSP00000364802	MAPK1, MAPK14, EGR1, JUND, MAPK3, FOS, MAPK11, MAPKAPK2, HSPA1A
GO:0006975	DNA damage induced protein phosphorylation	2	8	2.37	0.0026	9606.ENSP00000215659,9606.ENSP00000263025	MAPK12, MAPK3
GO:0060020	Bergmann glial cell differentiation	2	8	2.37	0.0026	9606.ENSP00000215832,9606.ENSP00000263025	MAPK1, MAPK3
GO:0061308	Cardiac neural crest cell development involved in heart development	2	8	2.37	0.0026	9606.ENSP00000215832,9606.ENSP00000263025	MAPK1, MAPK3
GO:0030278	Regulation of ossification	4	197	1.28	0.0029	9606.ENSP00000215832,9606.ENSP00000229795,9606.ENSP00000252818,9606.ENSP00000263025	MAPK1, MAPK14, JUND, MAPK3
GO:0042594	Response to starvation	4	198	1.27	0.0029	9606.ENSP00000215832,9606.ENSP00000263025,9606.ENSP00000378974,9606.ENSP00000469647	MAPK1, MAPK3, MAPK8, ZFP36
GO:0042473	Outer ear morphogenesis	2	9	2.32	0.003	9606.ENSP00000215832,9606.ENSP00000263025	MAPK1, MAPK3
GO:1905050	Positive regulation of metallopeptidase activity	2	9	2.32	0.003	9606.ENSP00000229795,9606.ENSP00000263025	MAPK14, MAPK3
GO:0019221	Cytokine-mediated signaling pathway	6	678	0.92	0.0031	9606.ENSP00000216160,9606.ENSP00000239938,9606.ENSP00000263025,9606.ENSP00000303315,9606.ENSP00000306245,9606.ENSP00000335153	TAB1, EGR1, MAPK3, JUNB, FOS, HSP90AA1
GO:0051253	Negative regulation of rna metabolic process	8	1422	0.72	0.0033	9606.ENSP00000229795,9606.ENSP00000231509,9606.ENSP00000239938,9606.ENSP00000252818,9606.ENSP00000303315,9606.ENSP00000356070,9606.ENSP00000364802,9606.ENSP00000469647	MAPK14, NR3C1, EGR1, JUND, JUNB, MAPKAPK2, HSPA1A, ZFP36
GO:0060341	Regulation of cellular localization	7	1027	0.8	0.0033	9606.ENSP00000215832,9606.ENSP00000229795,9606.ENSP00000262948,9606.ENSP00000263025,9606.ENSP00000335153,9606.ENSP00000378974,9606.ENSP00000469647	MAPK1, MAPK14, MAP2K2, MAPK3, HSP90AA1, MAPK8, ZFP36
GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis	3	73	1.58	0.0035	9606.ENSP00000215832,9606.ENSP00000263025,9606.ENSP00000335153	MAPK1, MAPK3, HSP90AA1
GO:0048608	Reproductive structure development	5	420	1.05	0.0035	9606.ENSP00000001008,9606.ENSP00000215832,9606.ENSP00000229795,9606.ENSP00000263025,9606.ENSP00000303315	FKBP4, MAPK1, MAPK14, MAPK3, JUNB

Table S9. the full list of KEGG analysis and GO analysis for DUSP1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0051128	Regulation of cellular component organization	10	2402	0.59	0.0037	9606.ENSP00000001008, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000239223, 9606.ENSP00000241014, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000335153, 9606.ENSP00000364802, 9606.ENSP00000378974	FKBP4, MAPK1, MAPK14, DUSP1, MAPK8IP1, MAP2K2, MAPK3, HSP90AA1, HSPA1A, MAPK8
GO:0043407	Negative regulation of map kinase activity	3	76	1.57	0.0038	9606.ENSP00000239223, 9606.ENSP00000241014, 9606.ENSP00000279488	DUSP1, MAPK8IP1, DUSP6
GO:0006897	Endocytosis	5	433	1.03	0.0039	9606.ENSP00000215832, 9606.ENSP00000241014, 9606.ENSP00000263025, 9606.ENSP00000335153, 9606.ENSP00000356070	MAPK1, MAPK8IP1, MAPK3, HSP90AA1, MAPKAPK2
GO:0097011	Cellular response to granulocyte macrophage colony-stimulating factor stimulus	2	11	2.23	0.004	9606.ENSP00000215832, 9606.ENSP00000469647	MAPK1, ZFP36
GO:0007254	JNK cascade	3	85	1.52	0.0051	9606.ENSP00000216160, 9606.ENSP00000241014, 9606.ENSP00000378974	TAB1, MAPK8IP1, MAPK8
GO:0031668	Cellular response to extracellular stimulus	4	236	1.2	0.0051	9606.ENSP00000215832, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000378974	MAPK1, MAPK3, FOS, MAPK8
GO:0071277	Cellular response to calcium ion	3	85	1.52	0.0051	9606.ENSP00000252818, 9606.ENSP00000303315, 9606.ENSP00000306245	JUND, JUNB, FOS
GO:0051149	Positive regulation of muscle cell differentiation	3	88	1.5	0.0055	9606.ENSP00000215659, 9606.ENSP00000229795, 9606.ENSP00000333685	MAPK12, MAPK14, MAPK11
GO:0071356	Cellular response to tumor necrosis factor	4	245	1.18	0.0058	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000469647	MAPK1, MAPK14, MAPK3, ZFP36
GO:0009991	Response to extracellular stimulus	5	483	0.98	0.0062	9606.ENSP00000215832, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK1, MAPK3, FOS, MAPK8, ZFP36
GO:0070498	interleukin-1-mediated signaling pathway	3	96	1.46	0.007	9606.ENSP00000216160, 9606.ENSP00000239938, 9606.ENSP00000263025	TAB1, EGR1, MAPK3
GO:0001568	Blood vessel development	5	500	0.97	0.0072	9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000303315	MAPK1, TAB1, MAPK14, EGR1, JUNB
GO:0045637	Regulation of myeloid cell differentiation	4	260	1.16	0.0072	9606.ENSP00000229795, 9606.ENSP00000306245, 9606.ENSP00000364802, 9606.ENSP00000469647	MAPK14, FOS, HSPA1A, ZFP36
GO:2000026	Regulation of multicellular organismal development	9	2096	0.6	0.0074	9606.ENSP00000001008, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000279488, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000364802, 9606.ENSP00000469647	FKBP4, MAPK1, MAPK14, EGR1, DUSP6, FOS, MAPK11, HSPA1A, ZFP36
GO:0045639	Positive regulation of myeloid cell differentiation	3	99	1.45	0.0075	9606.ENSP00000229795, 9606.ENSP00000306245, 9606.ENSP00000364802	MAPK14, FOS, HSPA1A
GO:1902532	Negative regulation of intracellular signal transduction	5	508	0.96	0.0076	9606.ENSP00000229795, 9606.ENSP00000239223, 9606.ENSP00000241014, 9606.ENSP00000279488, 9606.ENSP00000364802	MAPK14, DUSP1, MAPK8IP1, DUSP6, HSPA1A
GO:0051130	Positive regulation of cellular component organization	7	1209	0.73	0.0081	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000241014, 9606.ENSP00000263025, 9606.ENSP00000335153, 9606.ENSP00000364802, 9606.ENSP00000378974	MAPK1, MAPK14, MAPK8IP1, MAPK3, HSP90AA1, HSPA1A, MAPK8
GO:1904355	Positive regulation of telomere capping	2	17	2.04	0.0081	9606.ENSP00000215832, 9606.ENSP00000263025	MAPK1, MAPK3
GO:0035994	Response to muscle stretch	2	18	2.02	0.0089	9606.ENSP00000229795, 9606.ENSP00000306245	MAPK14, FOS
GO:0042026	Protein refolding	2	18	2.02	0.0089	9606.ENSP00000335153, 9606.ENSP00000364802	HSP90AA1, HSPA1A
GO:0006357	Regulation of transcription by rna polymerase ii	9	2172	0.59	0.0093	9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239938, 9606.ENSP00000252818, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000364802, 9606.ENSP00000469647	MAPK14, NR3C1, EGR1, JUND, MAPK3, JUNB, FOS, HSPA1A, ZFP36
GO:0044344	Cellular response to fibroblast growth factor stimulus	3	108	1.41	0.0093	9606.ENSP00000215832, 9606.ENSP00000263025, 9606.ENSP00000469647	MAPK1, MAPK3, ZFP36
GO:0010941	Regulation of cell death	8	1696	0.64	0.0099	9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000241014, 9606.ENSP00000279488, 9606.ENSP00000306245, 9606.ENSP00000364802, 9606.ENSP00000378974, 9606.ENSP00000469647	DUSP1, EGR1, MAPK8IP1, DUSP6, FOS, HSPA1A, MAPK8, ZFP36
GO:0032879	Regulation of localization	10	2740	0.53	0.0099	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000239223, 9606.ENSP00000241014, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000335153, 9606.ENSP00000364802, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK1, MAPK14, DUSP1, MAPK8IP1, MAP2K2, MAPK3, HSP90AA1, HSPA1A, MAPK8, ZFP36
GO:0045944	Positive regulation of transcription by rna polymerase ii	7	1253	0.72	0.0099	9606.ENSP00000229795, 9606.ENSP00000231509, 9606.ENSP00000239938, 9606.ENSP00000252818, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245	MAPK14, NR3C1, EGR1, JUND, MAPK3, JUNB, FOS
GO:0072359	Circulatory system development	6	872	0.81	0.0102	9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000263025, 9606.ENSP00000303315	MAPK1, TAB1, MAPK14, EGR1, MAPK3, JUNB
GO:0007517	Muscle organ development	4	291	1.11	0.0103	9606.ENSP00000215659, 9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000306245	MAPK12, MAPK14, EGR1, FOS

Table S9. the full list of KEGG analysis and GO analysis for DUSP1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0051348	Negative regulation of transferase activity	4	294	1.1	0.0107	9606.ENSP00000239223, 9606.ENSP00000241014, 9606.ENSP00000279488, 9606.ENSP00000469647	DUSP1, MAPK8IP1, DUSP6, ZFP36
GO:0030878	Thyroid gland development	2	21	1.95	0.0113	9606.ENSP00000215832, 9606.ENSP00000263025	MAPK1, MAPK3
GO:0051131	Chaperone-mediated protein complex assembly	2	21	1.95	0.0113	9606.ENSP00000335153, 9606.ENSP00000364802	HSP90AA1, HSPA1A
GO:0060716	Labyrinthine layer blood vessel development	2	21	1.95	0.0113	9606.ENSP00000215832, 9606.ENSP00000303315	MAPK1, JUNB
GO:0000122	Negative regulation of transcription by rna polymerase ii	6	895	0.8	0.0114	9606.ENSP00000231509, 9606.ENSP00000239938, 9606.ENSP00000252818, 9606.ENSP00000303315, 9606.ENSP00000364802, 9606.ENSP00000469647	NR3C1, EGR1, JUND, JUNB, HSPA1A, ZFP36
GO:0009416	Response to light stimulus	4	302	1.09	0.0116	9606.ENSP00000239223, 9606.ENSP00000252818, 9606.ENSP00000306245, 9606.ENSP00000378974	DUSP1, JUND, FOS, MAPK8
GO:0033043	Regulation of organelle organization	7	1306	0.7	0.0123	9606.ENSP00000001008, 9606.ENSP00000215832, 9606.ENSP00000239223, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000364802, 9606.ENSP00000378974	FKBP4, MAPK1, DUSP1, MAP2K2, MAPK3, HSPA1A, MAPK8
GO:0002429	Immune response-activating cell surface receptor signaling pathway	4	311	1.08	0.0128	9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000263025, 9606.ENSP00000335153	MAPK1, TAB1, MAPK3, HSP90AA1
GO:0007519	Skeletal muscle tissue development	3	124	1.35	0.0131	9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000306245	MAPK14, EGR1, FOS
GO:0071214	Cellular response to abiotic stimulus	4	313	1.08	0.0131	9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000263025, 9606.ENSP00000378974	MAPK14, EGR1, MAPK3, MAPK8
GO:2000637	Positive regulation of gene silencing by mirna	2	24	1.89	0.014	9606.ENSP00000262948, 9606.ENSP00000469647	MAP2K2, ZFP36
GO:0050778	Positive regulation of immune response	5	607	0.89	0.0156	9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000335153	MAPK1, TAB1, MAPK14, MAPK3, HSP90AA1
GO:0060045	Positive regulation of cardiac muscle cell proliferation	2	26	1.86	0.016	9606.ENSP00000215832, 9606.ENSP00000229795	MAPK1, MAPK14
GO:0048534	Hematopoietic or lymphoid organ development	5	619	0.88	0.0166	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000263025, 9606.ENSP00000303315	MAPK1, MAPK14, EGR1, MAPK3, JUNB
GO:0007006	Mitochondrial membrane organization	3	137	1.31	0.0167	9606.ENSP00000335153, 9606.ENSP00000364802, 9606.ENSP00000378974	HSP90AA1, HSPA1A, MAPK8
GO:0022414	Reproductive process	7	1400	0.67	0.0176	9606.ENSP00000001008, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245	FKBP4, MAPK1, MAPK14, EGR1, MAPK3, JUNB, FOS
GO:0034654	Nucleobase-containing compound biosynthetic process	6	995	0.75	0.0186	9606.ENSP00000215832, 9606.ENSP00000231509, 9606.ENSP00000252818, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000335153	MAPK1, NR3C1, JUND, MAPK3, FOS, HSP90AA1
GO:0032502	Developmental process	14	5841	0.35	0.0203	9606.ENSP00000001008, 9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000252818, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000335153, 9606.ENSP00000356070	FKBP4, MAPK12, MAPK1, TAB1, MAPK14, DUSP1, EGR1, JUND, MAPK3, DUSP6, JUNB, FOS, HSP90AA1, MAPKAPK2
GO:0033044	Regulation of chromosome organization	4	359	1.02	0.0203	9606.ENSP00000215832, 9606.ENSP00000239223, 9606.ENSP00000263025, 9606.ENSP00000378974	MAPK1, DUSP1, MAPK3, MAPK8
GO:0071560	Cellular response to transforming growth factor beta stimulus	3	149	1.27	0.0204	9606.ENSP00000216160, 9606.ENSP00000231509, 9606.ENSP00000306245	TAB1, NR3C1, FOS
GO:0030154	Cell differentiation	11	3702	0.44	0.0222	9606.ENSP00000001008, 9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000252818, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000335153	FKBP4, MAPK12, MAPK1, MAPK14, EGR1, JUND, MAPK3, DUSP6, JUNB, FOS, HSP90AA1
GO:0045648	Positive regulation of erythrocyte differentiation	2	32	1.77	0.0222	9606.ENSP00000229795, 9606.ENSP00000364802	MAPK14, HSPA1A
GO:0098586	Cellular response to virus	2	32	1.77	0.0222	9606.ENSP00000229795, 9606.ENSP00000333685	MAPK14, MAPK11
GO:2000113	Negative regulation of cellular macromolecule biosynthetic process	7	1470	0.65	0.0226	9606.ENSP00000231509, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000252818, 9606.ENSP00000303315, 9606.ENSP00000364802, 9606.ENSP00000469647	NR3C1, DUSP1, EGR1, JUND, JUNB, HSPA1A, ZFP36
GO:0040008	Regulation of growth	5	676	0.84	0.0232	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000279488, 9606.ENSP00000333685, 9606.ENSP00000364802	MAPK1, MAPK14, DUSP6, MAPK11, HSPA1A
GO:0045862	Positive regulation of proteolysis	4	377	1	0.0234	9606.ENSP00000215659, 9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000364802	MAPK12, MAPK14, MAPK3, HSPA1A
GO:0032212	Positive regulation of telomere maintenance via telomerase	2	34	1.74	0.0243	9606.ENSP00000215832, 9606.ENSP00000263025	MAPK1, MAPK3
GO:0001775	Cell activation	6	1075	0.72	0.0261	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000263025, 9606.ENSP00000335153, 9606.ENSP00000364802	MAPK1, MAPK14, EGR1, MAPK3, HSP90AA1, HSPA1A
GO:0030522	Intracellular receptor signaling pathway	3	166	1.23	0.0264	9606.ENSP00000001008, 9606.ENSP00000216160, 9606.ENSP00000231509	FKBP4, TAB1, NR3C1

Table S9. the full list of KEGG analysis and GO analysis for DUSP1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0031331	Positive regulation of cellular catabolic process	4	397	0.97	0.0275	9606.ENSP00000263025, 9606.ENSP00000335153, 9606.ENSP00000364802, 9606.ENSP00000469647	MAPK3, HSP90AA1, HSPA1A, ZFP36
GO:0009266	Response to temperature stimulus	3	170	1.22	0.0278	9606.ENSP00000306245, 9606.ENSP00000335153, 9606.ENSP00000364802	FOS, HSP90AA1, HSPA1A
GO:0030324	Lung development	3	170	1.22	0.0278	9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000263025	MAPK1, TAB1, MAPK3
GO:0048513	Animal organ development	10	3197	0.46	0.0288	9606.ENSP00000001008, 9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000356070	FKBP4, MAPK12, MAPK1, TAB1, MAPK14, EGR1, MAPK3, JUNB, FOS, MAPKAPK2
GO:0010942	Positive regulation of cell death	5	719	0.81	0.029	9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000279488, 9606.ENSP00000306245, 9606.ENSP00000378974	DUSP1, EGR1, DUSP6, FOS, MAPK8
GO:0042981	Regulation of apoptotic process	7	1550	0.62	0.0291	9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000241014, 9606.ENSP00000279488, 9606.ENSP00000364802, 9606.ENSP00000378974, 9606.ENSP00000469647	DUSP1, EGR1, MAPK8IP1, DUSP6, HSPA1A, MAPK8, ZFP36
GO:0032735	Positive regulation of interleukin-12 production	2	40	1.67	0.0312	9606.ENSP00000229795, 9606.ENSP00000333685	MAPK14, MAPK11
GO:0035924	Cellular response to vascular endothelial growth factor stimulus	2	40	1.67	0.0312	9606.ENSP00000229795, 9606.ENSP00000356070	MAPK14, MAPKAPK2
GO:0042307	Positive regulation of protein import into nucleus	2	41	1.66	0.0326	9606.ENSP00000215832, 9606.ENSP00000229795	MAPK1, MAPK14
GO:0090090	Negative regulation of canonical wnt signaling pathway	3	183	1.18	0.0333	9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000241014	MAPK14, EGR1, MAPK8IP1
GO:0030316	Osteoclast differentiation	2	42	1.65	0.0337	9606.ENSP00000229795, 9606.ENSP00000303315	MAPK14, JUNB
GO:0090316	Positive regulation of intracellular protein transport	3	184	1.18	0.0337	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000378974	MAPK1, MAPK14, MAPK8
GO:0048856	Anatomical structure development	13	5402	0.35	0.0353	9606.ENSP00000001008, 9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000239223, 9606.ENSP00000239938, 9606.ENSP00000252818, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000335153, 9606.ENSP00000356070	FKBP4, MAPK12, MAPK1, TAB1, MAPK14, DUSP1, EGR1, JUND, MAPK3, JUNB, FOS, HSP90AA1, MAPKAPK2
GO:0071383	Cellular response to steroid hormone stimulus	3	188	1.17	0.0355	9606.ENSP00000001008, 9606.ENSP00000231509, 9606.ENSP00000469647	FKBP4, NR3C1, ZFP36
GO:0060425	Lung morphogenesis	2	44	1.63	0.0366	9606.ENSP00000215832, 9606.ENSP00000263025	MAPK1, MAPK3
GO:0044092	Negative regulation of molecular function	6	1163	0.68	0.0367	9606.ENSP00000239223, 9606.ENSP00000241014, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000378974, 9606.ENSP00000469647	DUSP1, MAPK8IP1, MAPK3, DUSP6, MAPK8, ZFP36
GO:0046777	Protein autophosphorylation	3	192	1.16	0.0371	9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000356070	MAP2K2, MAPK3, MAPKAPK2
GO:0051345	Positive regulation of hydrolase activity	5	772	0.78	0.038	9606.ENSP00000215659, 9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000364802, 9606.ENSP00000378974	MAPK12, MAPK14, MAPK3, HSPA1A, MAPK8
GO:0016032	Viral process	5	776	0.78	0.0388	9606.ENSP00000215832, 9606.ENSP00000263025, 9606.ENSP00000335153, 9606.ENSP00000364802, 9606.ENSP00000469647	MAPK1, MAPK3, HSP90AA1, HSPA1A, ZFP36
GO:0032873	Negative regulation of stress-activated mapk cascade	2	46	1.61	0.039	9606.ENSP00000239223, 9606.ENSP00000241014	DUSP1, MAPK8IP1
GO:0043330	Response to exogenous dsrna	2	46	1.61	0.039	9606.ENSP00000215832, 9606.ENSP00000263025	MAPK1, MAPK3
GO:0048538	Thymus development	2	46	1.61	0.039	9606.ENSP00000215832, 9606.ENSP00000263025	MAPK1, MAPK3
GO:0010952	Positive regulation of peptidase activity	3	198	1.15	0.0397	9606.ENSP00000215659, 9606.ENSP00000229795, 9606.ENSP00000263025	MAPK12, MAPK14, MAPK3
GO:1901028	of mitochondrial outer membrane permeabilization involved in apoptotic signali	2	47	1.6	0.0399	9606.ENSP00000364802, 9606.ENSP00000378974	HSPA1A, MAPK8
GO:1901654	Response to ketone	3	199	1.15	0.04	9606.ENSP00000231509, 9606.ENSP00000239223, 9606.ENSP00000306245	NR3C1, DUSP1, FOS
GO:0009409	Response to cold	2	48	1.59	0.0411	9606.ENSP00000306245, 9606.ENSP00000335153	FOS, HSP90AA1
GO:0060324	Face development	2	48	1.59	0.0411	9606.ENSP00000215832, 9606.ENSP00000263025	MAPK1, MAPK3
GO:0006974	Cellular response to dna damage stimulus	5	793	0.77	0.0412	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000356070	MAPK12, MAPK1, MAPK14, MAPK3, MAPKAPK2
GO:0006470	Protein dephosphorylation	3	204	1.14	0.0422	9606.ENSP00000216160, 9606.ENSP00000239223, 9606.ENSP00000279488	TAB1, DUSP1, DUSP6
GO:0035914	Skeletal muscle cell differentiation	2	51	1.56	0.0452	9606.ENSP00000239938, 9606.ENSP00000306245	EGR1, FOS
GO:0006457	Protein folding	3	213	1.12	0.0467	9606.ENSP00000001008, 9606.ENSP00000335153, 9606.ENSP00000364802	FKBP4, HSP90AA1, HSPA1A
GO:0000186	Activation of mapkk activity	2	53	1.55	0.0481	9606.ENSP00000215832, 9606.ENSP00000263025	MAPK1, MAPK3
GO:0031113	Regulation of microtubule polymerization	2	53	1.55	0.0481	9606.ENSP00000001008, 9606.ENSP00000364802	FKBP4, HSPA1A
GO:0043312	Neutrophil degranulation	4	484	0.89	0.0493	9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000335153, 9606.ENSP00000364802	MAPK1, MAPK14, HSP90AA1, HSPA1A

Table S9. the full list of KEGG analysis and GO analysis for DUSP1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
hsa04010	MAPK signaling pathway	14	288	1.66	1.13E-18	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000239223, 9606.ENSP00000241014, 9606.ENSP00000252818, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000356070, 9606.ENSP00000378974	MAPK12, MAPK1, TAB1, MAPK14, DUSP1, MAPK8IP1, JUND, MAP2K2, MAPK3, DUSP6, FOS, MAPK11, MAPKAPK2, MAPK8
hsa04380	Osteoclast differentiation	10	122	1.88	7.60E-15	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000252818, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK1, TAB1, MAPK14, JUND, MAPK3, JUNB, FOS, MAPK11, MAPK8
hsa04657	IL-17 signaling pathway	9	92	1.96	5.60E-14	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000252818, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000378974	MAPK12, MAPK1, MAPK14, JUND, MAPK3, FOS, MAPK11, HSP90AA1, MAPK8
hsa04620	Toll-like receptor signaling pathway	9	101	1.92	9.29E-14	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK1, TAB1, MAPK14, MAP2K2, MAPK3, FOS, MAPK11, MAPK8
hsa04668	TNF signaling pathway	9	112	1.87	1.80E-13	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK1, TAB1, MAPK14, MAPK3, JUNB, FOS, MAPK11, MAPK8
hsa05167	Kaposi sarcoma-associated herpesvirus infection	10	187	1.7	1.80E-13	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000356070, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK12, MAPK1, MAPK14, MAP2K2, MAPK3, FOS, MAPK11, MAPKAPK2, MAPK8, ZFP36
hsa04935	Growth hormone synthesis, secretion and action	9	118	1.85	2.01E-13	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000303315, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK1, MAPK14, MAP2K2, MAPK3, JUNB, FOS, MAPK11, MAPK8
hsa04917	Prolactin signaling pathway	8	69	2.03	2.88E-13	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK1, MAPK14, MAP2K2, MAPK3, FOS, MAPK11, MAPK8
hsa05132	Salmonella infection	10	209	1.65	2.88E-13	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000378974	MAPK12, MAPK1, TAB1, MAPK14, MAP2K2, MAPK3, FOS, MAPK11, HSP90AA1, MAPK8
hsa05135	Yersinia infection	9	125	1.83	2.88E-13	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK1, TAB1, MAPK14, MAP2K2, MAPK3, FOS, MAPK11, MAPK8
hsa04912	GnRH signaling pathway	8	89	1.92	1.59E-12	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK1, MAPK14, EGR1, MAP2K2, MAPK3, MAPK11, MAPK8
hsa05161	Hepatitis B	9	159	1.72	1.59E-12	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK1, TAB1, MAPK14, MAP2K2, MAPK3, FOS, MAPK11, MAPK8
hsa01522	Endocrine resistance	8	95	1.89	2.20E-12	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK1, MAPK14, MAP2K2, MAPK3, FOS, MAPK11, MAPK8
hsa04659	Th17 cell differentiation	8	101	1.87	3.26E-12	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000378974	MAPK12, MAPK1, MAPK14, MAPK3, FOS, MAPK11, HSP90AA1, MAPK8
hsa04660	T cell receptor signaling pathway	8	101	1.87	3.26E-12	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK1, MAPK14, MAP2K2, MAPK3, FOS, MAPK11, MAPK8
hsa04370	VEGF signaling pathway	7	57	2.06	6.68E-12	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000333685, 9606.ENSP00000356070	MAPK12, MAPK1, MAPK14, MAP2K2, MAPK3, MAPK11, MAPKAPK2

Table S9. the full list of KEGG analysis and GO analysis for DUSP1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
hsa04722	Neurotrophin signaling pathway	8	114	1.82	6.75E-12	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000333685, 9606.ENSP00000356070, 9606.ENSP00000378974	MAPK12, MAPK1, MAPK14, MAP2K2, MAPK3, MAPK11, MAPKAPK2, MAPK8
hsa05170	Human immunodeficiency virus 1 infection	9	204	1.61	8.80E-12	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK1, TAB1, MAPK14, MAP2K2, MAPK3, FOS, MAPK11, MAPK8
hsa04664	Fc epsilon RI signaling pathway	7	66	1.99	1.46E-11	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK1, MAPK14, MAP2K2, MAPK3, MAPK11, MAPK8
hsa04926	Relaxin signaling pathway	8	128	1.77	1.46E-11	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK1, MAPK14, MAP2K2, MAPK3, FOS, MAPK11, MAPK8
hsa05140	Leishmaniasis	7	70	1.97	1.95E-11	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000333685	MAPK12, MAPK1, TAB1, MAPK14, MAPK3, FOS, MAPK11
hsa05133	Pertussis	7	74	1.95	2.69E-11	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK1, MAPK14, MAPK3, FOS, MAPK11, MAPK8
hsa04658	Th1 and Th2 cell differentiation	7	87	1.87	7.51E-11	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK1, MAPK14, MAPK3, FOS, MAPK11, MAPK8
hsa05235	PD-L1 expression and PD-1 checkpoint pathway in cancer	7	88	1.87	7.77E-11	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000333685	MAPK12, MAPK1, MAPK14, MAP2K2, MAPK3, FOS, MAPK11
hsa04621	NOD-like receptor signaling pathway	8	174	1.63	1.16E-10	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000378974	MAPK12, MAPK1, TAB1, MAPK14, MAPK3, MAPK11, HSP90AA1, MAPK8
hsa04914	Progesterone-mediated oocyte maturation	7	94	1.84	1.16E-10	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000378974	MAPK12, MAPK1, MAPK14, MAPK3, MAPK11, HSP90AA1, MAPK8
hsa04933	AGE-RAGE signaling pathway in diabetic complications	7	98	1.82	1.41E-10	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000263025, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK1, MAPK14, EGR1, MAPK3, MAPK11, MAPK8
hsa05142	Chagas disease	7	99	1.82	1.46E-10	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK1, MAPK14, MAPK3, FOS, MAPK11, MAPK8
hsa04625	C-type lectin receptor signaling pathway	7	102	1.81	1.72E-10	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000333685, 9606.ENSP00000356070, 9606.ENSP00000378974	MAPK12, MAPK1, MAPK14, MAPK3, MAPK11, MAPKAPK2, MAPK8
hsa05130	Pathogenic Escherichia coli infection	8	187	1.6	1.72E-10	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK1, TAB1, MAPK14, MAPK3, FOS, MAPK11, MAPK8
hsa05145	Toxoplasmosis	7	105	1.79	1.95E-10	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK1, TAB1, MAPK14, MAPK3, MAPK11, MAPK8
hsa04071	Sphingolipid signaling pathway	7	116	1.75	3.68E-10	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK1, MAPK14, MAP2K2, MAPK3, MAPK11, MAPK8
hsa04068	FoxO signaling pathway	7	127	1.71	6.55E-10	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK1, MAPK14, MAP2K2, MAPK3, MAPK11, MAPK8

Table S9. the full list of KEGG analysis and GO analysis for DUSP1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
hsa05418	Fluid shear stress and atherosclerosis	7	130	1.7	7.43E-10	9606.ENSP00000215659, 9606.ENSP00000229795, 9606.ENSP00000239223, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000335153, 9606.ENSP00000378974	MAPK12, MAPK14, DUSP1, FOS, MAPK11, HSP90AA1, MAPK8
hsa04218	Cellular senescence	7	150	1.64	1.89E-09	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000333685, 9606.ENSP00000356070	MAPK12, MAPK1, MAPK14, MAP2K2, MAPK3, MAPK11, MAPKAPK2
hsa05166	Human T-cell leukemia virus 1 infection	7	211	1.49	1.83E-08	9606.ENSP00000215832, 9606.ENSP00000239938, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000378974, 9606.ENSP00000469647	MAPK1, EGR1, MAP2K2, MAPK3, FOS, MAPK8, ZFP36
hsa05131	Shigellosis	7	218	1.48	2.21E-08	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK1, TAB1, MAPK14, MAPK3, MAPK11, MAPK8
hsa04915	Estrogen signaling pathway	6	133	1.62	5.04E-08	9606.ENSP00000001008, 9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000335153	FKBP4, MAPK1, MAP2K2, MAPK3, FOS, HSP90AA1
hsa04550	Signaling pathways regulating pluripotency of stem cells	6	140	1.6	6.60E-08	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000333685	MAPK12, MAPK1, MAPK14, MAP2K2, MAPK3, MAPK11
hsa05020	Prion disease	7	265	1.39	7.63E-08	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000239938, 9606.ENSP00000263025, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK1, MAPK14, EGR1, MAPK3, MAPK11, MAPK8
hsa04723	Retrograde endocannabinoid signaling	6	145	1.59	7.68E-08	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK1, MAPK14, MAPK3, MAPK11, MAPK8
hsa05152	Tuberculosis	6	168	1.52	1.75E-07	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK1, MAPK14, MAPK3, MAPK11, MAPK8
hsa05210	Colorectal cancer	5	82	1.75	2.31E-07	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000378974	MAPK1, MAP2K2, MAPK3, FOS, MAPK8
hsa05205	Proteoglycans in cancer	6	196	1.46	4.07E-07	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000333685	MAPK12, MAPK1, MAPK14, MAP2K2, MAPK3, MAPK11
hsa04015	Rap1 signaling pathway	6	202	1.44	4.69E-07	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000333685	MAPK12, MAPK1, MAPK14, MAP2K2, MAPK3, MAPK11
hsa05231	Choline metabolism in cancer	5	96	1.69	4.69E-07	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000378974	MAPK1, MAP2K2, MAPK3, FOS, MAPK8
hsa04928	Parathyroid hormone synthesis, secretion and action	5	103	1.66	6.30E-07	9606.ENSP00000215832, 9606.ENSP00000239938, 9606.ENSP00000252818, 9606.ENSP00000263025, 9606.ENSP00000306245	MAPK1, EGR1, JUND, MAPK3, FOS
hsa05163	Human cytomegalovirus infection	6	218	1.41	6.89E-07	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000333685	MAPK12, MAPK1, MAPK14, MAP2K2, MAPK3, MAPK11
hsa04114	Oocyte meiosis	5	120	1.59	1.26E-06	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000333685	MAPK12, MAPK1, MAPK14, MAPK3, MAPK11
hsa04611	Platelet activation	5	122	1.58	1.33E-06	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000333685	MAPK12, MAPK1, MAPK14, MAPK3, MAPK11
hsa04728	Dopaminergic synapse	5	128	1.56	1.64E-06	9606.ENSP00000215659, 9606.ENSP00000229795, 9606.ENSP00000306245, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK14, FOS, MAPK11, MAPK8
hsa04210	Apoptosis	5	132	1.55	1.87E-06	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000378974	MAPK1, MAP2K2, MAPK3, FOS, MAPK8
hsa04261	Adrenergic signaling in cardiomyocytes	5	147	1.5	3.07E-06	9606.ENSP00000215659, 9606.ENSP00000215832, 9606.ENSP00000229795, 9606.ENSP00000263025, 9606.ENSP00000333685	MAPK12, MAPK1, MAPK14, MAPK3, MAPK11
hsa05221	Acute myeloid leukemia	4	66	1.75	5.32E-06	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000279488	MAPK1, MAP2K2, MAPK3, DUSP6
hsa05120	Epithelial cell signaling in Helicobacter pylori infection	4	67	1.75	5.53E-06	9606.ENSP00000215659, 9606.ENSP00000229795, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK14, MAPK11, MAPK8
hsa04622	RIG-I-like receptor signaling pathway	4	70	1.73	6.42E-06	9606.ENSP00000215659, 9606.ENSP00000229795, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK14, MAPK11, MAPK8

Table S9. the full list of KEGG analysis and GO analysis for DUSP1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
hsa04662	B cell receptor signaling pathway	4	78	1.68	9.53E-06	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000306245	MAPK1, MAP2K2, MAPK3, FOS
hsa05169	Epstein-Barr virus infection	5	193	1.38	1.04E-05	9606.ENSP00000215659, 9606.ENSP00000216160, 9606.ENSP00000229795, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, TAB1, MAPK14, MAPK11, MAPK8
hsa04012	ErbB signaling pathway	4	83	1.65	1.17E-05	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000378974	MAPK1, MAP2K2, MAPK3, MAPK8
hsa04024	cAMP signaling pathway	5	208	1.35	1.43E-05	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000378974	MAPK1, MAP2K2, MAPK3, FOS, MAPK8
hsa04750	Inflammatory mediator regulation of TRP channels	4	94	1.6	1.82E-05	9606.ENSP00000215659, 9606.ENSP00000229795, 9606.ENSP00000333685, 9606.ENSP00000378974	MAPK12, MAPK14, MAPK11, MAPK8
hsa05215	Prostate cancer	4	96	1.59	1.94E-05	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000335153	MAPK1, MAP2K2, MAPK3, HSP90AA1
hsa05216	Thyroid cancer	3	36	1.89	5.05E-05	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025	MAPK1, MAP2K2, MAPK3
hsa04140	Autophagy - animal	4	130	1.46	6.01E-05	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000378974	MAPK1, MAP2K2, MAPK3, MAPK8
hsa04371	Apelin signaling pathway	4	131	1.45	6.10E-05	9606.ENSP00000215832, 9606.ENSP00000239938, 9606.ENSP00000262948, 9606.ENSP00000263025	MAPK1, EGR1, MAP2K2, MAPK3
hsa04910	Insulin signaling pathway	4	133	1.45	6.36E-05	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000378974	MAPK1, MAP2K2, MAPK3, MAPK8
hsa05200	Pathways in cancer	6	517	1.03	6.81E-05	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000306245, 9606.ENSP00000335153, 9606.ENSP00000378974	MAPK1, MAP2K2, MAPK3, FOS, HSP90AA1, MAPK8
hsa05219	Bladder cancer	3	41	1.83	6.81E-05	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025	MAPK1, MAP2K2, MAPK3
hsa05224	Breast cancer	4	145	1.41	8.48E-05	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000306245	MAPK1, MAP2K2, MAPK3, FOS
hsa04930	Type II diabetes mellitus	3	46	1.78	9.10E-05	9606.ENSP00000215832, 9606.ENSP00000263025, 9606.ENSP00000378974	MAPK1, MAPK3, MAPK8
hsa04921	Oxytocin signaling pathway	4	149	1.4	9.14E-05	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000306245	MAPK1, MAP2K2, MAPK3, FOS
hsa05213	Endometrial cancer	3	57	1.69	0.00016	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025	MAPK1, MAP2K2, MAPK3
hsa04730	Long-term depression	3	59	1.68	0.00018	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025	MAPK1, MAP2K2, MAPK3
hsa04929	GnRH secretion	3	63	1.65	0.00021	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025	MAPK1, MAP2K2, MAPK3
hsa04720	Long-term potentiation	3	64	1.64	0.00022	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025	MAPK1, MAP2K2, MAPK3
hsa05211	Renal cell carcinoma	3	66	1.63	0.00024	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025	MAPK1, MAP2K2, MAPK3
hsa05223	Non-small cell lung cancer	3	68	1.61	0.00025	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025	MAPK1, MAP2K2, MAPK3
hsa05230	Central carbon metabolism in cancer	3	69	1.61	0.00026	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025	MAPK1, MAP2K2, MAPK3
hsa05212	Pancreatic cancer	3	73	1.58	0.00029	9606.ENSP00000215832, 9606.ENSP00000263025, 9606.ENSP00000378974	MAPK1, MAPK3, MAPK8
hsa05214	Glioma	3	72	1.59	0.00029	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025	MAPK1, MAP2K2, MAPK3
hsa05218	Melanoma	3	72	1.59	0.00029	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025	MAPK1, MAP2K2, MAPK3
hsa05220	Chronic myeloid leukemia	3	75	1.57	0.00031	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025	MAPK1, MAP2K2, MAPK3
hsa01521	EGFR tyrosine kinase inhibitor resistance	3	78	1.55	0.00035	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025	MAPK1, MAP2K2, MAPK3
hsa04014	Ras signaling pathway	4	226	1.22	0.00038	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025, 9606.ENSP00000378974	MAPK1, MAP2K2, MAPK3, MAPK8
hsa04540	Gap junction	3	87	1.51	0.00046	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025	MAPK1, MAP2K2, MAPK3
hsa04713	Circadian entrainment	3	92	1.48	0.00054	9606.ENSP00000215832, 9606.ENSP00000263025, 9606.ENSP00000306245	MAPK1, MAPK3, FOS
hsa04916	Melanogenesis	3	95	1.47	0.00058	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025	MAPK1, MAP2K2, MAPK3
hsa04066	HIF-1 signaling pathway	3	106	1.42	0.00079	9606.ENSP00000215832, 9606.ENSP00000262948, 9606.ENSP00000263025	MAPK1, MAP2K2, MAPK3
hsa04726	Serotonergic synapse	3	108	1.41	0.00083	9606.ENSP00000215832, 9606.ENSP00000239223, 9606.ENSP00000263025	MAPK1, DUSP1, MAPK3
hsa04670	Leukocyte transendothelial migration	3	109	1.41	0.00084	9606.ENSP00000215659, 9606.ENSP00000229795, 9606.ENSP00000333685	MAPK12, MAPK14, MAPK11

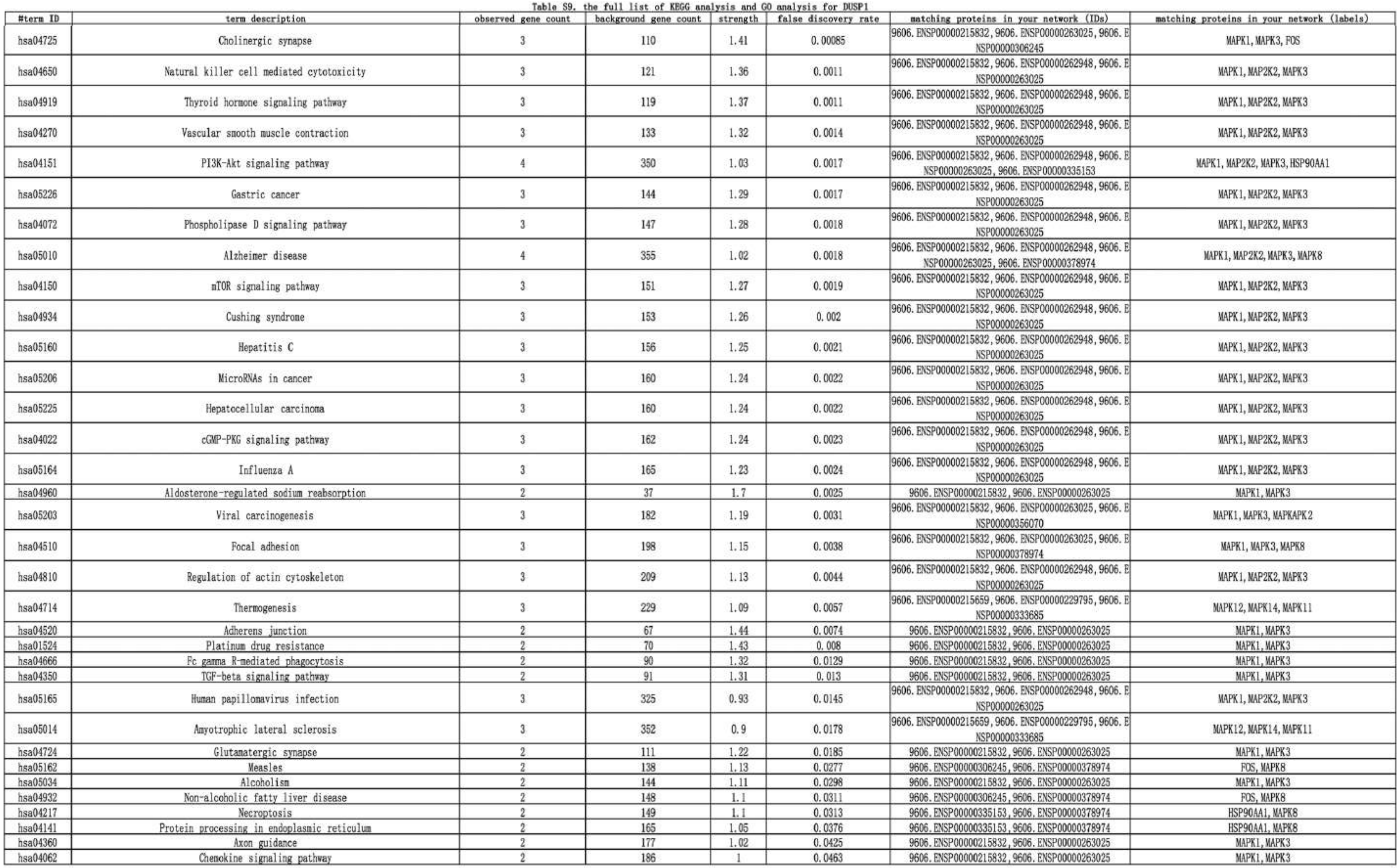


Table S9. the full list of KEGG analysis and GO analysis for DUSP1

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
hsa04725	Cholinergic synapse	3	110	1.41	0.00085	9606.ENSP00000215832,9606.ENSP00000263025,9606.ENSP00000306245	MAPK1,MAPK3,FOS
hsa04650	Natural killer cell mediated cytotoxicity	3	121	1.36	0.0011	9606.ENSP00000215832,9606.ENSP00000262948,9606.ENSP00000263025	MAPK1,MAP2K2,MAPK3
hsa04919	Thyroid hormone signaling pathway	3	119	1.37	0.0011	9606.ENSP00000215832,9606.ENSP00000262948,9606.ENSP00000263025	MAPK1,MAP2K2,MAPK3
hsa04270	Vascular smooth muscle contraction	3	133	1.32	0.0014	9606.ENSP00000215832,9606.ENSP00000262948,9606.ENSP00000263025	MAPK1,MAP2K2,MAPK3
hsa04151	PI3K-Akt signaling pathway	4	350	1.03	0.0017	9606.ENSP00000215832,9606.ENSP00000262948,9606.ENSP00000263025,9606.ENSP00000335153	MAPK1,MAP2K2,MAPK3,HSP90AA1
hsa05226	Gastric cancer	3	144	1.29	0.0017	9606.ENSP00000215832,9606.ENSP00000262948,9606.ENSP00000263025	MAPK1,MAP2K2,MAPK3
hsa04072	Phospholipase D signaling pathway	3	147	1.28	0.0018	9606.ENSP00000215832,9606.ENSP00000262948,9606.ENSP00000263025	MAPK1,MAP2K2,MAPK3
hsa05010	Alzheimer disease	4	355	1.02	0.0018	9606.ENSP00000215832,9606.ENSP00000262948,9606.ENSP00000263025,9606.ENSP00000378974	MAPK1,MAP2K2,MAPK3,MAPK8
hsa04150	mTOR signaling pathway	3	151	1.27	0.0019	9606.ENSP00000215832,9606.ENSP00000262948,9606.ENSP00000263025	MAPK1,MAP2K2,MAPK3
hsa04934	Cushing syndrome	3	153	1.26	0.002	9606.ENSP00000215832,9606.ENSP00000262948,9606.ENSP00000263025	MAPK1,MAP2K2,MAPK3
hsa05160	Hepatitis C	3	156	1.25	0.0021	9606.ENSP00000215832,9606.ENSP00000262948,9606.ENSP00000263025	MAPK1,MAP2K2,MAPK3
hsa05206	MicroRNAs in cancer	3	160	1.24	0.0022	9606.ENSP00000215832,9606.ENSP00000262948,9606.ENSP00000263025	MAPK1,MAP2K2,MAPK3
hsa05225	Hepatocellular carcinoma	3	160	1.24	0.0022	9606.ENSP00000215832,9606.ENSP00000262948,9606.ENSP00000263025	MAPK1,MAP2K2,MAPK3
hsa04022	cGMP-PKG signaling pathway	3	162	1.24	0.0023	9606.ENSP00000215832,9606.ENSP00000262948,9606.ENSP00000263025	MAPK1,MAP2K2,MAPK3
hsa05164	Influenza A	3	165	1.23	0.0024	9606.ENSP00000215832,9606.ENSP00000262948,9606.ENSP00000263025	MAPK1,MAP2K2,MAPK3
hsa04960	Aldosterone-regulated sodium reabsorption	2	37	1.7	0.0025	9606.ENSP00000215832,9606.ENSP00000263025	MAPK1,MAPK3
hsa05203	Viral carcinogenesis	3	182	1.19	0.0031	9606.ENSP00000215832,9606.ENSP00000263025,9606.ENSP00000356070	MAPK1,MAPK3,MAPKAPK2
hsa04510	Focal adhesion	3	198	1.15	0.0038	9606.ENSP00000215832,9606.ENSP00000263025,9606.ENSP00000378974	MAPK1,MAPK3,MAPK8
hsa04810	Regulation of actin cytoskeleton	3	209	1.13	0.0044	9606.ENSP00000215832,9606.ENSP00000262948,9606.ENSP00000263025	MAPK1,MAP2K2,MAPK3
hsa04714	Thermogenesis	3	229	1.09	0.0057	9606.ENSP00000215659,9606.ENSP00000229795,9606.ENSP00000333685	MAPK12,MAPK14,MAPK11
hsa04520	Adherens junction	2	67	1.44	0.0074	9606.ENSP00000215832,9606.ENSP00000263025	MAPK1,MAPK3
hsa01524	Platinum drug resistance	2	70	1.43	0.008	9606.ENSP00000215832,9606.ENSP00000263025	MAPK1,MAPK3
hsa04666	Fc gamma R-mediated phagocytosis	2	90	1.32	0.0129	9606.ENSP00000215832,9606.ENSP00000263025	MAPK1,MAPK3
hsa04350	TGF-beta signaling pathway	2	91	1.31	0.013	9606.ENSP00000215832,9606.ENSP00000263025	MAPK1,MAPK3
hsa05165	Human papillomavirus infection	3	325	0.93	0.0145	9606.ENSP00000215832,9606.ENSP00000262948,9606.ENSP00000263025	MAPK1,MAP2K2,MAPK3
hsa05014	Amyotrophic lateral sclerosis	3	352	0.9	0.0178	9606.ENSP00000215659,9606.ENSP00000229795,9606.ENSP00000333685	MAPK12,MAPK14,MAPK11
hsa04724	Glutamatergic synapse	2	111	1.22	0.0185	9606.ENSP00000215832,9606.ENSP00000263025	MAPK1,MAPK3
hsa05162	Measles	2	138	1.13	0.0277	9606.ENSP00000306245,9606.ENSP00000378974	FOS,MAPK8
hsa05034	Alcoholism	2	144	1.11	0.0298	9606.ENSP00000215832,9606.ENSP00000263025	MAPK1,MAPK3
hsa04932	Non-alcoholic fatty liver disease	2	148	1.1	0.0311	9606.ENSP00000306245,9606.ENSP00000378974	FOS,MAPK8
hsa04217	Necroptosis	2	149	1.1	0.0313	9606.ENSP00000335153,9606.ENSP00000378974	HSP90AA1,MAPK8
hsa04141	Protein processing in endoplasmic reticulum	2	165	1.05	0.0376	9606.ENSP00000335153,9606.ENSP00000378974	HSP90AA1,MAPK8
hsa04360	Axon guidance	2	177	1.02	0.0425	9606.ENSP00000215832,9606.ENSP00000263025	MAPK1,MAPK3
hsa04062	Chemokine signaling pathway	2	186	1	0.0463	9606.ENSP00000215832,9606.ENSP00000263025	MAPK1,MAPK3

Table S10. the full list of KEGG analysis and GO analysis for INHBA

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO0090092	Regulation of transmembrane receptor protein serinethreonine kinase signaling pathway	20	244	1.88	5.04E-33	9606. ENSP00000166139, 9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000262435, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	FSTL3, TGFB1, TGFB3, ACVR2A, INHBA, FST, GDF11, MSTN, SMAD2, CREBBP, SMURF2, EP300, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0007178	Transmembrane receptor protein serinethreonine kinase signaling pathway	18	195	1.93	1.81E-29	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000262435, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000287727, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	TGFB1, TGFB3, ACVR2A, INHBA, FST, GDF11, MSTN, SMAD2, SMURF2, ACVR1, BMP6, ZFYVE9, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0090100	ositive regulation of transmembrane receptor protein serinethreonine kinase signaling pathwa	16	110	2.13	2.72E-28	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	TGFB1, TGFB3, ACVR2A, INHBA, GDF11, MSTN, SMAD2, CREBBP, EP300, ACVR1, BMP6, BMP10, ACVR2B, ENG, ACVRL1, ACVR1B
GO0010862	Positive regulation of pathway-restricted smad protein phosphorylation	12	49	2.36	2.43E-22	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	TGFB1, TGFB3, ACVR2A, INHBA, GDF11, MSTN, ACVR1, BMP6, BMP10, ENG, ACVRL1, ACVR1B
GO0071363	Cellular response to growth factor stimulus	16	494	1.48	1.17E-18	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000256759, 9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000262435, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000287727, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	TGFB1, TGFB3, ACVR2A, FST, MSTN, SMAD2, SMURF2, ACVR1, BMP6, ZFYVE9, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0030509	BMP signaling pathway	11	90	2.06	1.86E-17	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000256759, 9606. ENSP00000262435, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574	TGFB1, TGFB3, ACVR2A, FST, SMURF2, ACVR1, BMP6, BMP10, ACVR2B, ENG, ACVRL1
GO0032924	Activin receptor signaling pathway	9	25	2.53	1.86E-17	9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000262160, 9606. ENSP00000263640, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000373574, 9606. ENSP00000442656	ACVR2A, INHBA, SMAD2, ACVR1, BMP10, SMAD3, ACVR2B, ACVRL1, ACVR1B
GO2000026	Regulation of multicellular organismal development	20	2096	0.95	8.06E-16	9606. ENSP00000166139, 9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000262435, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	FSTL3, TGFB1, TGFB3, ACVR2A, INHBA, FST, GDF11, MSTN, SMAD2, CREBBP, SMURF2, EP300, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0007166	Cell surface receptor signaling pathway	20	2325	0.9	5.82E-15	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000262435, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000287727, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	TGFB1, TGFB3, ACVR2A, INHBA, FST, GDF11, MSTN, SMAD2, CREBBP, SMURF2, EP300, ACVR1, BMP6, ZFYVE9, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B

Table S10. the full list of KEGG analysis and GO analysis for INHBA

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO0045595	Regulation of cell differentiation	19	1874	0.98	7.16E-15	9606. ENSP00000166139, 9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	FSTL3, TGFB1, TGFB3, ACVR2A, INHBA, FST, GDF11, MSTN, SMAD2, CREBBP, EP300, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0060395	SMAD protein signal transduction	9	59	2.15	9.65E-15	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000242208, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000332973	TGFB1, TGFB3, INHBA, GDF11, MSTN, SMAD2, BMP6, BMP10, SMAD3
GO0009967	Positive regulation of signal transduction	18	1654	1.01	4.17E-14	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000262435, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	TGFB1, TGFB3, ACVR2A, INHBA, GDF11, MSTN, SMAD2, CREBBP, SMURF2, EP300, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0009719	Response to endogenous stimulus	17	1447	1.04	1.97E-13	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000262435, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000287727, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574	TGFB1, TGFB3, ACVR2A, INHBA, FST, MSTN, SMAD2, SMURF2, EP300, ACVR1, BMP6, ZFYVE9, BMP10, SMAD3, ACVR2B, ENG, ACVRL1
GO0071495	Cellular response to endogenous stimulus	16	1181	1.1	3.06E-13	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000262435, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000287727, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574	TGFB1, TGFB3, ACVR2A, INHBA, FST, MSTN, SMAD2, SMURF2, ACVR1, BMP6, ZFYVE9, BMP10, SMAD3, ACVR2B, ENG, ACVRL1
GO0070887	Cellular response to chemical stimulus	20	2919	0.81	3.19E-13	9606. ENSP00000166139, 9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000262435, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000287727, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	FSTL3, TGFB1, TGFB3, ACVR2A, INHBA, FST, MSTN, SMAD2, CREBBP, SMURF2, EP300, ACVR1, BMP6, ZFYVE9, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0007179	Transforming growth factor beta receptor signaling pathway	9	98	1.93	4.58E-13	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000263640, 9606. ENSP00000287727, 9606. ENSP00000332973, 9606. ENSP00000362299, 9606. ENSP00000373574	TGFB1, TGFB3, MSTN, SMAD2, ACVR1, ZFYVE9, SMAD3, ENG, ACVRL1
GO0032925	Regulation of activin receptor signaling pathway	7	24	2.43	7.06E-13	9606. ENSP00000166139, 9606. ENSP00000241416, 9606. ENSP00000256759, 9606. ENSP00000262160, 9606. ENSP00000263640, 9606. ENSP00000340361, 9606. ENSP00000442656	FSTL3, ACVR2A, FST, SMAD2, ACVR1, ACVR2B, ACVR1B
GO0090287	Regulation of cellular response to growth factor stimulus	11	280	1.56	9.68E-13	9606. ENSP00000166139, 9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000256759, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000262435, 9606. ENSP00000263253, 9606. ENSP00000332973, 9606. ENSP00000362299, 9606. ENSP00000373574	FSTL3, TGFB1, TGFB3, FST, SMAD2, CREBBP, SMURF2, EP300, SMAD3, ENG, ACVRL1
GO0051094	Positive regulation of developmental process	16	1389	1.03	2.83E-12	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000262160, 9606. ENSP00000262435, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	TGFB1, TGFB3, ACVR2A, INHBA, FST, SMAD2, SMURF2, EP300, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B

Table S10. the full list of KEGG analysis and GO analysis for INHBA

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
G00090101	egative regulation of transmembrane receptor protein serinethreonine kinase signaling pathwa	9	124	1.83	2.83E-12	9606. ENSP00000166139, 9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000256759, 9606. ENSP00000262160, 9606. ENSP00000262435, 9606. ENSP00000263640, 9606. ENSP00000332973, 9606. ENSP00000362299	FSTL3, TGFB1, TGFB3, FST, SMAD2, SMURF2, ACVR1, SMAD3, ENG
G00051240	Positive regulation of multicellular organismal process	17	1770	0.95	3.40E-12	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000262435, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	TGFB1, TGFB3, ACVR2A, INHBA, FST, SMAD2, CREBBP, SMURF2, EP300, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
G00030501	Positive regulation of bone mineralization	7	40	2.21	1.13E-11	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000332973, 9606. ENSP00000340361	TGFB1, TGFB3, ACVR2A, ACVR1, BMP6, SMAD3, ACVR2B
G00071310	Cellular response to organic substance	18	2369	0.85	1.13E-11	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000262435, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000287727, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	TGFB1, TGFB3, ACVR2A, INHBA, FST, MSTN, SMAD2, SMURF2, EP300, ACVR1, BMP6, ZFYVE9, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
G00009887	Animal organ morphogenesis	14	967	1.13	1.57E-11	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000257868, 9606. ENSP00000262160, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574	TGFB1, TGFB3, INHBA, FST, GDF11, SMAD2, EP300, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1
G00045893	Positive regulation of transcription, dna-templated	16	1587	0.97	1.66E-11	9606. ENSP00000166139, 9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	FSTL3, TGFB1, TGFB3, ACVR2A, INHBA, MSTN, SMAD2, CREBBP, EP300, ACVR1, BMP6, BMP10, SMAD3, ENG, ACVRL1, ACVR1B
G00045597	Positive regulation of cell differentiation	14	993	1.12	2.15E-11	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000262160, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	TGFB1, TGFB3, ACVR2A, INHBA, SMAD2, EP300, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
G00051173	Positive regulation of nitrogen compound metabolic process	19	3239	0.74	6.30E-11	9606. ENSP00000166139, 9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000262435, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	FSTL3, TGFB1, TGFB3, ACVR2A, INHBA, GDF11, MSTN, SMAD2, CREBBP, SMURF2, EP300, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
G00006357	Regulation of transcription by rna polymerase ii	17	2172	0.86	6.58E-11	9606. ENSP00000166139, 9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000262435, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	FSTL3, TGFB1, TGFB3, ACVR2A, INHBA, FST, SMAD2, CREBBP, SMURF2, EP300, ACVR1, BMP6, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B

Table S10. the full list of KEGG analysis and GO analysis for INHBA

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO0009888	Tissue development	16	1760	0.93	6.81E-11	9606. ENSP00000221930, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	TGFB1, ACVR2A, INHBA, FST, GDF11, MSTN, SMAD2, EP300, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0017015	Regulation of transforming growth factor beta receptor signaling pathway	8	119	1.8	1.22E-10	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000262435, 9606. ENSP00000263253, 9606. ENSP00000332973, 9606. ENSP00000362299	TGFB1, TGFB3, SMAD2, CREBBP, SMURF2, EP300, SMAD3, ENG
GO0006355	Regulation of transcription, dna-templated	19	3388	0.72	1.28E-10	9606. ENSP00000166139, 9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000262435, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	FSTL3, TGFB1, TGFB3, ACVR2A, INHBA, FST, MSTN, SMAD2, CREBBP, SMURF2, EP300, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0045937	Positive regulation of phosphate metabolic process	14	1164	1.05	1.40E-10	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	TGFB1, TGFB3, ACVR2A, INHBA, GDF11, MSTN, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0001501	Skeletal system development	11	499	1.31	2.03E-10	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000256759, 9606. ENSP00000257868, 9606. ENSP00000262160, 9606. ENSP00000263253, 9606. ENSP00000283147, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299	TGFB1, TGFB3, ACVR2A, FST, GDF11, SMAD2, EP300, BMP6, SMAD3, ACVR2B, ENG
GO0010604	Positive regulation of macromolecule metabolic process	19	3600	0.69	3.29E-10	9606. ENSP00000166139, 9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000262435, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	FSTL3, TGFB1, TGFB3, ACVR2A, INHBA, GDF11, MSTN, SMAD2, CREBBP, SMURF2, EP300, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0045944	Positive regulation of transcription by rna polymerase ii	14	1253	1.02	3.29E-10	9606. ENSP00000166139, 9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000332973, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	FSTL3, TGFB1, TGFB3, ACVR2A, INHBA, SMAD2, CREBBP, EP300, ACVR1, BMP6, SMAD3, ENG, ACVRL1, ACVR1B
GO0009790	Embryo development	13	1002	1.08	4.77E-10	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	TGFB1, TGFB3, ACVR2A, INHBA, SMAD2, CREBBP, EP300, ACVR1, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0001934	Positive regulation of protein phosphorylation	13	1019	1.08	5.64E-10	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	TGFB1, TGFB3, ACVR2A, INHBA, GDF11, MSTN, ACVR1, BMP6, BMP10, ACVR2B, ENG, ACVRL1, ACVR1B
GO0051247	Positive regulation of protein metabolic process	15	1715	0.91	8.63E-10	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000262435, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	TGFB1, TGFB3, ACVR2A, INHBA, GDF11, MSTN, SMURF2, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B

Table S10. the full list of KEGG analysis and GO analysis for INHBA

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO0048513	Animal organ development	18	3197	0.72	1.02E-09	9606. ENSP00000166139, 9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	FSTL3, TGFB1, TGFB3, ACVR2A, INHBA, FST, GDF11, MSTN, SMAD2, EP300, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0009653	Anatomical structure morphogenesis	16	2165	0.84	1.08E-09	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000257868, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574	TGFB1, TGFB3, ACVR2A, INHBA, FST, GDF11, SMAD2, CREBBP, EP300, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1
GO0060429	Epithelium development	13	1109	1.04	1.42E-09	9606. ENSP00000221930, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000257868, 9606. ENSP00000262160, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	TGFB1, INHBA, FST, GDF11, SMAD2, EP300, ACVR1, BMP6, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0019220	Regulation of phosphate metabolic process	15	1816	0.89	1.68E-09	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	TGFB1, TGFB3, ACVR2A, INHBA, GDF11, MSTN, EP300, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0010718	Positive regulation of epithelial to mesenchymal transition	6	47	2.08	2.30E-09	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000262160, 9606. ENSP00000263640, 9606. ENSP00000332973, 9606. ENSP00000362299	TGFB1, TGFB3, SMAD2, ACVR1, SMAD3, ENG
GO0031325	Positive regulation of cellular metabolic process	18	3413	0.69	2.66E-09	9606. ENSP00000166139, 9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	FSTL3, TGFB1, TGFB3, ACVR2A, INHBA, GDF11, MSTN, SMAD2, CREBBP, EP300, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0007498	Mesoderm development	7	117	1.75	5.24E-09	9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000257868, 9606. ENSP00000262160, 9606. ENSP00000263640, 9606. ENSP00000332973, 9606. ENSP00000340361	ACVR2A, INHBA, GDF11, SMAD2, ACVR1, SMAD3, ACVR2B
GO0042325	Regulation of phosphorylation	14	1626	0.9	7.23E-09	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	TGFB1, TGFB3, ACVR2A, INHBA, GDF11, MSTN, EP300, ACVR1, BMP6, BMP10, ACVR2B, ENG, ACVRL1, ACVR1B
GO0032270	Positive regulation of cellular protein metabolic process	14	1635	0.9	7.70E-09	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	TGFB1, TGFB3, ACVR2A, INHBA, GDF11, MSTN, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0051716	Cellular response to stimulus	21	6489	0.48	1.17E-08	9606. ENSP00000166139, 9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000262435, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000287727, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	FSTL3, TGFB1, TGFB3, ACVR2A, INHBA, FST, GDF11, MSTN, SMAD2, CREBBP, SMURF2, EP300, ACVR1, BMP6, ZFYVE9, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B

Table S10. the full list of KEGG analysis and GO analysis for INHBA

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO0048598	Embryonic morphogenesis	10	571	1.21	1.68E-08	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000263640, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299	TGFB1, TGFB3, ACVR2A, INHBA, SMAD2, CREBBP, ACVR1, SMAD3, ACVR2B, ENG
GO0035295	Tube development	11	851	1.08	3.44E-08	9606. ENSP00000166139, 9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000257868, 9606. ENSP00000262160, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574	FSTL3, TGFB1, TGFB3, GDF11, SMAD2, EP300, ACVR1, SMAD3, ACVR2B, ENG, ACVRL1
GO0090288	Negative regulation of cellular response to growth factor stimulus	7	158	1.62	3.55E-08	9606. ENSP00000166139, 9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000262160, 9606. ENSP00000262435, 9606. ENSP00000332973, 9606. ENSP00000362299	FSTL3, TGFB1, TGFB3, SMAD2, SMURF2, SMAD3, ENG
GO0007389	Pattern specification process	9	432	1.29	3.99E-08	9606. ENSP00000241416, 9606. ENSP00000256759, 9606. ENSP00000257868, 9606. ENSP00000262160, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299	ACVR2A, FST, GDF11, SMAD2, EP300, ACVR1, SMAD3, ACVR2B, ENG
GO0030512	Negative regulation of transforming growth factor beta receptor signaling pathway	6	81	1.84	4.14E-08	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000262160, 9606. ENSP00000262435, 9606. ENSP00000332973, 9606. ENSP00000362299	TGFB1, TGFB3, SMAD2, SMURF2, SMAD3, ENG
GO0031399	Regulation of protein modification process	14	1870	0.84	4.15E-08	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	TGFB1, TGFB3, ACVR2A, INHBA, GDF11, MSTN, EP300, ACVR1, BMP6, BMP10, ACVR2B, ENG, ACVRL1, ACVR1B
GO0051246	Regulation of protein metabolic process	16	2828	0.72	4.47E-08	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000262435, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	TGFB1, TGFB3, ACVR2A, INHBA, GDF11, MSTN, SMURF2, EP300, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0048523	Negative regulation of cellular process	19	4874	0.56	5.09E-08	9606. ENSP00000166139, 9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000262435, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	FSTL3, TGFB1, TGFB3, INHBA, FST, GDF11, MSTN, SMAD2, CREBBP, SMURF2, EP300, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0032927	Positive regulation of activin receptor signaling pathway	4	8	2.67	5.64E-08	9606. ENSP00000241416, 9606. ENSP00000262160, 9606. ENSP00000340361, 9606. ENSP00000442656	ACVR2A, SMAD2, ACVR2B, ACVR1B
GO0051171	Regulation of nitrogen compound metabolic process	20	5836	0.5	5.64E-08	9606. ENSP00000166139, 9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000262435, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	FSTL3, TGFB1, TGFB3, ACVR2A, INHBA, FST, GDF11, MSTN, SMAD2, CREBBP, SMURF2, EP300, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0030510	Regulation of bmp signaling pathway	6	90	1.79	7.00E-08	9606. ENSP00000166139, 9606. ENSP00000256759, 9606. ENSP00000262160, 9606. ENSP00000262435, 9606. ENSP00000362299, 9606. ENSP00000373574	FSTL3, FST, SMAD2, SMURF2, ENG, ACVRL1
GO0007275	Multicellular organism development	19	5023	0.55	8.44E-08	9606. ENSP00000166139, 9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	FSTL3, TGFB1, TGFB3, ACVR2A, INHBA, FST, GDF11, MSTN, SMAD2, CREBBP, EP300, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B

Table S10. the full list of KEGG analysis and GO analysis for INHBA

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO0010629	Negative regulation of gene expression	14	2014	0.81	1.01E-07	9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000242208, 9606.ENSP00000256759, 9606.ENSP00000262160, 9606.ENSP00000262367, 9606.ENSP00000262435, 9606.ENSP00000263253, 9606.ENSP00000283147, 9606.ENSP00000332973, 9606.ENSP00000340361, 9606.ENSP00000362299, 9606.ENSP00000373574, 9606.ENSP00000442656	TGFB1, TGFB3, INHBA, FST, SMAD2, CREBBP, SMURF2, EP300, BMP6, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0080090	Regulation of primary metabolic process	20	6032	0.49	1.02E-07	9606.ENSP00000166139, 9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000241416, 9606.ENSP00000242208, 9606.ENSP00000256759, 9606.ENSP00000257868, 9606.ENSP00000260950, 9606.ENSP00000262160, 9606.ENSP00000262367, 9606.ENSP00000262435, 9606.ENSP00000263253, 9606.ENSP00000263640, 9606.ENSP00000283147, 9606.ENSP00000295379, 9606.ENSP00000332973, 9606.ENSP00000340361, 9606.ENSP00000362299, 9606.ENSP00000373574, 9606.ENSP00000442656	FSTL3, TGFB1, TGFB3, ACVR2A, INHBA, FST, GDF11, MSTN, SMAD2, CREBBP, SMURF2, EP300, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0048518	Positive regulation of biological process	20	6112	0.48	1.31E-07	9606.ENSP00000166139, 9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000241416, 9606.ENSP00000242208, 9606.ENSP00000256759, 9606.ENSP00000257868, 9606.ENSP00000260950, 9606.ENSP00000262160, 9606.ENSP00000262367, 9606.ENSP00000262435, 9606.ENSP00000263253, 9606.ENSP00000263640, 9606.ENSP00000283147, 9606.ENSP00000295379, 9606.ENSP00000332973, 9606.ENSP00000340361, 9606.ENSP00000362299, 9606.ENSP00000373574, 9606.ENSP00000442656	FSTL3, TGFB1, TGFB3, ACVR2A, INHBA, FST, GDF11, MSTN, SMAD2, CREBBP, SMURF2, EP300, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0007507	Heart development	9	522	1.21	1.76E-07	9606.ENSP00000221930, 9606.ENSP00000262160, 9606.ENSP00000263253, 9606.ENSP00000263640, 9606.ENSP00000295379, 9606.ENSP00000332973, 9606.ENSP00000340361, 9606.ENSP00000362299, 9606.ENSP00000373574	TGFB1, SMAD2, EP300, ACVR1, BMP10, SMAD3, ACVR2B, ENG, ACVRL1
GO0031323	Regulation of cellular metabolic process	20	6239	0.48	1.89E-07	9606.ENSP00000166139, 9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000241416, 9606.ENSP00000242208, 9606.ENSP00000256759, 9606.ENSP00000257868, 9606.ENSP00000260950, 9606.ENSP00000262160, 9606.ENSP00000262367, 9606.ENSP00000262435, 9606.ENSP00000263253, 9606.ENSP00000263640, 9606.ENSP00000283147, 9606.ENSP00000295379, 9606.ENSP00000332973, 9606.ENSP00000340361, 9606.ENSP00000362299, 9606.ENSP00000373574, 9606.ENSP00000442656	FSTL3, TGFB1, TGFB3, ACVR2A, INHBA, FST, GDF11, MSTN, SMAD2, CREBBP, SMURF2, EP300, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0072132	Mesenchyme morphogenesis	5	49	1.98	2.75E-07	9606.ENSP00000262160, 9606.ENSP00000263640, 9606.ENSP00000332973, 9606.ENSP00000362299, 9606.ENSP00000373574	SMAD2, ACVR1, SMAD3, ENG, ACVRL1
GO0032268	Regulation of cellular protein metabolic process	15	2693	0.72	3.06E-07	9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000241416, 9606.ENSP00000242208, 9606.ENSP00000257868, 9606.ENSP00000260950, 9606.ENSP00000263253, 9606.ENSP00000263640, 9606.ENSP00000283147, 9606.ENSP00000295379, 9606.ENSP00000332973, 9606.ENSP00000340361, 9606.ENSP00000362299, 9606.ENSP00000373574, 9606.ENSP00000442656	TGFB1, TGFB3, ACVR2A, INHBA, GDF11, MSTN, EP300, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0060255	Regulation of macromolecule metabolic process	20	6407	0.46	3.06E-07	9606.ENSP00000166139, 9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000241416, 9606.ENSP00000242208, 9606.ENSP00000256759, 9606.ENSP00000257868, 9606.ENSP00000260950, 9606.ENSP00000262160, 9606.ENSP00000262367, 9606.ENSP00000262435, 9606.ENSP00000263253, 9606.ENSP00000263640, 9606.ENSP00000283147, 9606.ENSP00000295379, 9606.ENSP00000332973, 9606.ENSP00000340361, 9606.ENSP00000362299, 9606.ENSP00000373574, 9606.ENSP00000442656	FSTL3, TGFB1, TGFB3, ACVR2A, INHBA, FST, GDF11, MSTN, SMAD2, CREBBP, SMURF2, EP300, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0048729	Tissue morphogenesis	9	561	1.17	3.08E-07	9606.ENSP00000221930, 9606.ENSP00000242208, 9606.ENSP00000256759, 9606.ENSP00000262160, 9606.ENSP00000263640, 9606.ENSP00000295379, 9606.ENSP00000332973, 9606.ENSP00000362299, 9606.ENSP00000373574	TGFB1, INHBA, FST, SMAD2, ACVR1, BMP10, SMAD3, ENG, ACVRL1

Table S10. the full list of KEGG analysis and GO analysis for INHBA

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO0048522	Positive regulation of cellular process	19	5579	0.5	5.11E-07	9606.ENSP00000166139, 9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000241416, 9606.ENSP00000242208, 9606.ENSP00000257868, 9606.ENSP00000260950, 9606.ENSP00000262160, 9606.ENSP00000262367, 9606.ENSP00000262435, 9606.ENSP00000263253, 9606.ENSP00000263640, 9606.ENSP00000283147, 9606.ENSP00000295379, 9606.ENSP00000332973, 9606.ENSP00000340361, 9606.ENSP00000362299, 9606.ENSP00000373574, 9606.ENSP00000442656	FSTL3, TGFB1, TGFB3, ACVR2A, INHBA, GDF11, MSTN, SMAD2, CREBBP, SMURF2, EP300, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0045926	Negative regulation of growth	7	247	1.42	5.68E-07	9606.ENSP00000221930, 9606.ENSP00000242208, 9606.ENSP00000260950, 9606.ENSP00000295379, 9606.ENSP00000332973, 9606.ENSP00000373574, 9606.ENSP00000442656	TGFB1, INHBA, MSTN, BMP10, SMAD3, ACVRL1, ACVR1B
GO0045637	Regulation of myeloid cell differentiation	7	260	1.4	7.95E-07	9606.ENSP00000166139, 9606.ENSP00000221930, 9606.ENSP00000241416, 9606.ENSP00000242208, 9606.ENSP00000262367, 9606.ENSP00000263253, 9606.ENSP00000442656	FSTL3, TGFB1, ACVR2A, INHBA, CREBBP, EP300, ACVR1B
GO0048646	Anatomical structure formation involved in morphogenesis	10	883	1.02	8.08E-07	9606.ENSP00000221930, 9606.ENSP00000242208, 9606.ENSP00000262160, 9606.ENSP00000263253, 9606.ENSP00000263640, 9606.ENSP00000295379, 9606.ENSP00000332973, 9606.ENSP00000340361, 9606.ENSP00000362299, 9606.ENSP00000373574	TGFB1, INHBA, SMAD2, EP300, ACVR1, BMP10, SMAD3, ACVR2B, ENG, ACVRL1
GO0000122	Negative regulation of transcription by rna polymerase ii	10	895	1.02	9.11E-07	9606.ENSP00000221930, 9606.ENSP00000256759, 9606.ENSP00000262160, 9606.ENSP00000262367, 9606.ENSP00000262435, 9606.ENSP00000263253, 9606.ENSP00000283147, 9606.ENSP00000332973, 9606.ENSP00000340361, 9606.ENSP00000362299	TGFB1, FST, SMAD2, CREBBP, SMURF2, EP300, BMP6, SMAD3, ACVR2B, ENG
GO0043009	Chordate embryonic development	9	640	1.12	9.11E-07	9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000241416, 9606.ENSP00000262160, 9606.ENSP00000263253, 9606.ENSP00000263640, 9606.ENSP00000332973, 9606.ENSP00000373574, 9606.ENSP00000442656	TGFB1, TGFB3, ACVR2A, SMAD2, EP300, ACVR1, SMAD3, ACVRL1, ACVR1B
GO0007369	Gastrulation	6	159	1.55	1.50E-06	9606.ENSP00000241416, 9606.ENSP00000242208, 9606.ENSP00000262160, 9606.ENSP00000263640, 9606.ENSP00000332973, 9606.ENSP00000340361	ACVR2A, INHBA, SMAD2, ACVR1, SMAD3, ACVR2B
GO0008285	Negative regulation of cell population proliferation	9	696	1.08	1.79E-06	9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000242208, 9606.ENSP00000257868, 9606.ENSP00000260950, 9606.ENSP00000262160, 9606.ENSP00000332973, 9606.ENSP00000362299, 9606.ENSP00000373574	TGFB1, TGFB3, INHBA, GDF11, MSTN, SMAD2, SMAD3, ENG, ACVRL1
GO0009892	Negative regulation of metabolic process	15	3124	0.65	2.18E-06	9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000242208, 9606.ENSP00000256759, 9606.ENSP00000260950, 9606.ENSP00000262160, 9606.ENSP00000262367, 9606.ENSP00000262435, 9606.ENSP00000263253, 9606.ENSP00000283147, 9606.ENSP00000332973, 9606.ENSP00000340361, 9606.ENSP00000362299, 9606.ENSP00000373574, 9606.ENSP00000442656	TGFB1, TGFB3, INHBA, FST, MSTN, SMAD2, CREBBP, SMURF2, EP300, BMP6, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0030308	Negative regulation of cell growth	6	187	1.48	3.73E-06	9606.ENSP00000221930, 9606.ENSP00000242208, 9606.ENSP00000295379, 9606.ENSP00000332973, 9606.ENSP00000373574, 9606.ENSP00000442656	TGFB1, INHBA, BMP10, SMAD3, ACVRL1, ACVR1B
GO0010648	Negative regulation of cell communication	11	1382	0.87	3.74E-06	9606.ENSP00000166139, 9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000242208, 9606.ENSP00000256759, 9606.ENSP00000260950, 9606.ENSP00000262160, 9606.ENSP00000262435, 9606.ENSP00000263640, 9606.ENSP00000332973, 9606.ENSP00000362299	FSTL3, TGFB1, TGFB3, INHBA, FST, MSTN, SMAD2, SMURF2, ACVR1, SMAD3, ENG
GO0023057	Negative regulation of signaling	11	1385	0.87	3.80E-06	9606.ENSP00000166139, 9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000242208, 9606.ENSP00000256759, 9606.ENSP00000260950, 9606.ENSP00000262160, 9606.ENSP00000262435, 9606.ENSP00000263640, 9606.ENSP00000332973, 9606.ENSP00000362299	FSTL3, TGFB1, TGFB3, INHBA, FST, MSTN, SMAD2, SMURF2, ACVR1, SMAD3, ENG
GO0060021	Roof of mouth development	5	91	1.71	4.37E-06	9606.ENSP00000238682, 9606.ENSP00000242208, 9606.ENSP00000257868, 9606.ENSP00000262160, 9606.ENSP00000340361	TGFB3, INHBA, GDF11, SMAD2, ACVR2B
GO0061036	Positive regulation of cartilage development	4	32	2.07	5.02E-06	9606.ENSP00000283147, 9606.ENSP00000295379, 9606.ENSP00000332973, 9606.ENSP00000373574	BMP6, BMP10, SMAD3, ACVRL1
GO2000113	Negative regulation of cellular macromolecule biosynthetic process	11	1470	0.84	6.85E-06	9606.ENSP00000221930, 9606.ENSP00000256759, 9606.ENSP00000262160, 9606.ENSP00000262367, 9606.ENSP00000262435, 9606.ENSP00000263253, 9606.ENSP00000283147, 9606.ENSP00000332973, 9606.ENSP00000340361, 9606.ENSP00000362299, 9606.ENSP00000373574	TGFB1, FST, SMAD2, CREBBP, SMURF2, EP300, BMP6, SMAD3, ACVR2B, ENG, ACVRL1
GO0060485	Mesenchyme development	6	212	1.42	7.37E-06	9606.ENSP00000221930, 9606.ENSP00000262160, 9606.ENSP00000263640, 9606.ENSP00000332973, 9606.ENSP00000362299, 9606.ENSP00000373574	TGFB1, SMAD2, ACVR1, SMAD3, ENG, ACVRL1

Table S10. the full list of KEGG analysis and GO analysis for INHBA

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO0009952	Anteriorposterior pattern specification	6	214	1.42	7.73E-06	9606.ENSP00000241416, 9606.ENSP00000257868, 9606.ENSP00000262160, 9606.ENSP00000263253, 9606.ENSP00000332973, 9606.ENSP00000340361	ACVR2A, GDF11, SMAD2, EP300, SMAD3, ACVR2B
GO0045934	Negative regulation of nucleobase-containing compound metabolic process	11	1528	0.83	9.89E-06	9606.ENSP00000221930, 9606.ENSP00000256759, 9606.ENSP00000262160, 9606.ENSP00000262367, 9606.ENSP00000262435, 9606.ENSP00000263253, 9606.ENSP00000283147, 9606.ENSP00000332973, 9606.ENSP00000340361, 9606.ENSP00000362299, 9606.ENSP00000373574	TGFB1, FST, SMAD2, CREBBP, SMURF2, EP300, BMP6, SMAD3, ACVR2B, ENG, ACVRL1
GO0030334	Regulation of cell migration	9	865	0.99	1.04E-05	9606.ENSP00000221930, 9606.ENSP00000260950, 9606.ENSP00000262435, 9606.ENSP00000263640, 9606.ENSP00000295379, 9606.ENSP00000332973, 9606.ENSP00000362299, 9606.ENSP00000373574, 9606.ENSP00000442656	TGFB1, MSTN, SMURF2, ACVR1, BMP10, SMAD3, ENG, ACVRL1, ACVR1B
GO0007183	SMAD protein complex assembly	3	7	2.6	1.07E-05	9606.ENSP00000221930, 9606.ENSP00000262160, 9606.ENSP00000332973	TGFB1, SMAD2, SMAD3
GO0045667	Regulation of osteoblast differentiation	5	117	1.6	1.35E-05	9606.ENSP00000241416, 9606.ENSP00000263640, 9606.ENSP00000283147, 9606.ENSP00000332973, 9606.ENSP00000340361	ACVR2A, ACVR1, BMP6, SMAD3, ACVR2B
GO0007368	Determination of leftright symmetry	5	120	1.59	1.51E-05	9606.ENSP00000241416, 9606.ENSP00000263640, 9606.ENSP00000332973, 9606.ENSP00000340361, 9606.ENSP00000362299	ACVR2A, ACVR1, SMAD3, ACVR2B, ENG
GO0051241	Negative regulation of multicellular organismal process	10	1231	0.88	1.52E-05	9606.ENSP00000166139, 9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000242208, 9606.ENSP00000257868, 9606.ENSP00000260950, 9606.ENSP00000295379, 9606.ENSP00000332973, 9606.ENSP00000340361, 9606.ENSP00000373574	FSTL3, TGFB1, TGFB3, INHBA, GDF11, MSTN, BMP10, SMAD3, ACVR2B, ACVRL1
GO0006464	Cellular protein modification process	14	3063	0.63	1.71E-05	9606.ENSP00000166139, 9606.ENSP00000221930, 9606.ENSP00000241416, 9606.ENSP00000262160, 9606.ENSP00000262367, 9606.ENSP00000262435, 9606.ENSP00000263253, 9606.ENSP00000263640, 9606.ENSP00000295379, 9606.ENSP00000332973, 9606.ENSP00000340361, 9606.ENSP00000362299, 9606.ENSP00000373574, 9606.ENSP00000442656	FSTL3, TGFB1, ACVR2A, SMAD2, CREBBP, SMURF2, EP300, ACVR1, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0003007	Heart morphogenesis	6	251	1.35	1.77E-05	9606.ENSP00000221930, 9606.ENSP00000263640, 9606.ENSP00000295379, 9606.ENSP00000332973, 9606.ENSP00000362299, 9606.ENSP00000373574	TGFB1, ACVR1, BMP10, SMAD3, ENG, ACVRL1
GO0048617	Embryonic foregut morphogenesis	3	9	2.49	1.82E-05	9606.ENSP00000262160, 9606.ENSP00000332973, 9606.ENSP00000340361	SMAD2, SMAD3, ACVR2B
GO0042127	Regulation of cell population proliferation	11	1642	0.8	1.86E-05	9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000242208, 9606.ENSP00000257868, 9606.ENSP00000260950, 9606.ENSP00000262160, 9606.ENSP00000283147, 9606.ENSP00000295379, 9606.ENSP00000332973, 9606.ENSP00000362299, 9606.ENSP00000373574	TGFB1, TGFB3, INHBA, GDF11, MSTN, SMAD2, BMP6, BMP10, SMAD3, ENG, ACVRL1
GO0009968	Negative regulation of signal transduction	10	1271	0.87	1.93E-05	9606.ENSP00000166139, 9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000256759, 9606.ENSP00000260950, 9606.ENSP00000262160, 9606.ENSP00000262435, 9606.ENSP00000263640, 9606.ENSP00000332973, 9606.ENSP00000362299	FSTL3, TGFB1, TGFB3, FST, MSTN, SMAD2, SMURF2, ACVR1, SMAD3, ENG
GO0007548	Sex differentiation	6	259	1.33	2.00E-05	9606.ENSP00000166139, 9606.ENSP00000241416, 9606.ENSP00000242208, 9606.ENSP00000256759, 9606.ENSP00000283147, 9606.ENSP00000442656	FSTL3, ACVR2A, INHBA, FST, BMP6, ACVR1B
GO0006468	Protein phosphorylation	9	952	0.94	2.05E-05	9606.ENSP00000221930, 9606.ENSP00000241416, 9606.ENSP00000262160, 9606.ENSP00000263640, 9606.ENSP00000295379, 9606.ENSP00000340361, 9606.ENSP00000362299, 9606.ENSP00000373574, 9606.ENSP00000442656	TGFB1, ACVR2A, SMAD2, ACVR1, BMP10, ACVR2B, ENG, ACVRL1, ACVR1B
GO0032926	Negative regulation of activin receptor signaling pathway	3	10	2.45	2.25E-05	9606.ENSP00000166139, 9606.ENSP00000256759, 9606.ENSP00000263640	FSTL3, FST, ACVR1
GO0031324	Negative regulation of cellular metabolic process	13	2630	0.66	2.47E-05	9606.ENSP00000221930, 9606.ENSP00000242208, 9606.ENSP00000256759, 9606.ENSP00000260950, 9606.ENSP00000262160, 9606.ENSP00000262367, 9606.ENSP00000262435, 9606.ENSP00000263253, 9606.ENSP00000283147, 9606.ENSP00000332973, 9606.ENSP00000340361, 9606.ENSP00000362299, 9606.ENSP00000373574	TGFB1, INHBA, FST, MSTN, SMAD2, CREBBP, SMURF2, EP300, BMP6, SMAD3, ACVR2B, ENG, ACVRL1
GO0001822	Kidney development	6	271	1.31	2.51E-05	9606.ENSP00000166139, 9606.ENSP00000257868, 9606.ENSP00000262160, 9606.ENSP00000283147, 9606.ENSP00000332973, 9606.ENSP00000340361	FSTL3, GDF11, SMAD2, BMP6, SMAD3, ACVR2B
GO0038092	Nodal signaling pathway	3	11	2.41	2.75E-05	9606.ENSP00000262160, 9606.ENSP00000332973, 9606.ENSP00000442656	SMAD2, SMAD3, ACVR1B

Table S10. the full list of KEGG analysis and GO analysis for INHBA

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO0045596	Negative regulation of cell differentiation	8	728	1.01	3.54E-05	9606. ENSP00000166139, 9606. ENSP00000221930, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000332973, 9606. ENSP00000373574	FSTL3, TGFB1, INHBA, FST, GDF11, MSTN, SMAD3, ACVRL1
GO0060389	Pathway-restricted smad protein phosphorylation	3	13	2.33	4.09E-05	9606. ENSP00000221930, 9606. ENSP00000263640, 9606. ENSP00000295379	TGFB1, ACVR1, BMP10
GO0045669	Positive regulation of osteoblast differentiation	4	60	1.79	4.11E-05	9606. ENSP00000241416, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000340361	ACVR2A, ACVR1, BMP6, ACVR2B
GO0060841	Venous blood vessel development	3	15	2.27	5.83E-05	9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574	ACVR2B, ENG, ACVRL1
GO0001707	Mesoderm formation	4	67	1.75	6.12E-05	9606. ENSP00000242208, 9606. ENSP00000262160, 9606. ENSP00000263640, 9606. ENSP00000332973	INHBA, SMAD2, ACVR1, SMAD3
GO0030324	Lung development	5	170	1.44	6.55E-05	9606. ENSP00000166139, 9606. ENSP00000238682, 9606. ENSP00000262160, 9606. ENSP00000263253, 9606. ENSP00000340361	FSTL3, TGFB3, SMAD2, EP300, ACVR2B
GO0060391	Positive regulation of smad protein signal transduction	3	16	2.24	6.78E-05	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000283147	TGFB1, TGFB3, BMP6
GO0002682	Regulation of immune system process	10	1514	0.79	8.18E-05	9606. ENSP00000166139, 9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000260950, 9606. ENSP00000262367, 9606. ENSP00000263253, 9606. ENSP00000332973, 9606. ENSP00000442656	FSTL3, TGFB1, TGFB3, ACVR2A, INHBA, MSTN, CREBBP, EP300, SMAD3, ACVR1B
GO0031016	Pancreas development	4	73	1.71	8.18E-05	9606. ENSP00000257868, 9606. ENSP00000262160, 9606. ENSP00000283147, 9606. ENSP00000340361	GDF11, SMAD2, BMP6, ACVR2B
GO0001666	Response to hypoxia	6	342	1.21	8.43E-05	9606. ENSP00000238682, 9606. ENSP00000262367, 9606. ENSP00000263253, 9606. ENSP00000332973, 9606. ENSP00000362299, 9606. ENSP00000373574	TGFB3, CREBBP, EP300, SMAD3, ENG, ACVRL1
GO0007423	Sensory organ development	7	563	1.06	8.92E-05	9606. ENSP00000238682, 9606. ENSP00000242208, 9606. ENSP00000257868, 9606. ENSP00000283147, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000373574	TGFB3, INHBA, GDF11, BMP6, SMAD3, ACVR2B, ACVRL1
GO0045446	Endothelial cell differentiation	4	76	1.69	9.36E-05	9606. ENSP00000263640, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574	ACVR1, ACVR2B, ENG, ACVRL1
GO0019538	Protein metabolic process	15	4251	0.52	0.0001	9606. ENSP00000166139, 9606. ENSP00000221930, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000262435, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	FSTL3, TGFB1, ACVR2A, INHBA, SMAD2, CREBBP, SMURF2, EP300, ACVR1, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0001654	Eye development	6	365	1.19	0.00012	9606. ENSP00000242208, 9606. ENSP00000257868, 9606. ENSP00000283147, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000373574	INHBA, GDF11, BMP6, SMAD3, ACVR2B, ACVRL1
GO0032332	Positive regulation of chondrocyte differentiation	3	20	2.15	0.00012	9606. ENSP00000283147, 9606. ENSP00000332973, 9606. ENSP00000373574	BMP6, SMAD3, ACVRL1
GO0030154	Cell differentiation	14	3702	0.55	0.00014	9606. ENSP00000166139, 9606. ENSP00000221930, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000257868, 9606. ENSP00000262160, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574	FSTL3, TGFB1, INHBA, FST, GDF11, SMAD2, EP300, ACVR1, BMP6, BMP10, SMAD3, ACVR2B, ENG, ACVRL1
GO0001701	In utero embryonic development	6	382	1.17	0.00015	9606. ENSP00000238682, 9606. ENSP00000262160, 9606. ENSP00000263640, 9606. ENSP00000332973, 9606. ENSP00000373574, 9606. ENSP00000442656	TGFB3, SMAD2, ACVR1, SMAD3, ACVRL1, ACVR1B
GO0002244	Hematopoietic progenitor cell differentiation	4	90	1.62	0.00016	9606. ENSP00000166139, 9606. ENSP00000221930, 9606. ENSP00000242208, 9606. ENSP00000256759	FSTL3, TGFB1, INHBA, FST
GO0045137	Development of primary sexual characteristics	5	211	1.34	0.00016	9606. ENSP00000166139, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000442656	FSTL3, ACVR2A, INHBA, FST, ACVR1B
GO0048589	Developmental growth	6	389	1.16	0.00016	9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000263253, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361	MSTN, SMAD2, EP300, BMP10, SMAD3, ACVR2B
GO0030325	Adrenal gland development	3	24	2.07	0.00018	9606. ENSP00000166139, 9606. ENSP00000262160, 9606. ENSP00000332973	FSTL3, SMAD2, SMAD3
GO0048771	Tissue remodeling	4	96	1.59	0.00021	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000340361, 9606. ENSP00000373574	TGFB1, TGFB3, ACVR2B, ACVRL1
GO0001702	Gastrulation with mouth forming second	3	26	2.03	0.00022	9606. ENSP00000241416, 9606. ENSP00000263640, 9606. ENSP00000340361	ACVR2A, ACVR1, ACVR2B
GO0032967	Positive regulation of collagen biosynthetic process	3	26	2.03	0.00022	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000362299	TGFB1, TGFB3, ENG

Table S10. the full list of KEGG analysis and GO analysis for INHBA

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO0035239	Tube morphogenesis	7	656	1	0.00022	9606.ENSP00000221930, 9606.ENSP00000262160, 9606.ENSP00000263640, 9606.ENSP00000332973, 9606.ENSP00000340361, 9606.ENSP00000362299, 9606.ENSP00000373574	TGFB1, SMAD2, ACVR1, SMAD3, ACVR2B, ENG, ACVRL1
GO0045639	Positive regulation of myeloid cell differentiation	4	99	1.58	0.00023	9606.ENSP00000221930, 9606.ENSP00000241416, 9606.ENSP00000242208, 9606.ENSP00000442656	TGFB1, ACVR2A, INHBA, ACVR1B
GO0070723	Response to cholesterol	3	27	2.02	0.00024	9606.ENSP00000221930, 9606.ENSP00000242208, 9606.ENSP00000262160	TGFB1, INHBA, SMAD2
GO0097191	Extrinsic apoptotic signaling pathway	4	100	1.57	0.00024	9606.ENSP00000221930, 9606.ENSP00000242208, 9606.ENSP00000332973, 9606.ENSP00000442656	TGFB1, INHBA, SMAD3, ACVR1B
GO0014741	Negative regulation of muscle hypertrophy	3	28	2	0.00026	9606.ENSP00000260950, 9606.ENSP00000295379, 9606.ENSP00000332973	MSTN, BMP10, SMAD3
GO0032879	Regulation of localization	12	2740	0.61	0.00027	9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000242208, 9606.ENSP00000260950, 9606.ENSP00000262435, 9606.ENSP00000263640, 9606.ENSP00000283147, 9606.ENSP00000295379, 9606.ENSP00000332973, 9606.ENSP00000362299, 9606.ENSP00000373574, 9606.ENSP00000442656	TGFB1, TGFB3, INHBA, MSTN, SMURF2, ACVR1, BMP6, BMP10, SMAD3, ENG, ACVRL1, ACVR1B
GO0050794	Regulation of cellular process	21	10932	0.25	0.00027	9606.ENSP00000166139, 9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000241416, 9606.ENSP00000242208, 9606.ENSP00000256759, 9606.ENSP00000257868, 9606.ENSP00000260950, 9606.ENSP00000262160, 9606.ENSP00000262367, 9606.ENSP00000262435, 9606.ENSP00000263253, 9606.ENSP00000263640, 9606.ENSP00000283147, 9606.ENSP00000287727, 9606.ENSP00000295379, 9606.ENSP00000332973, 9606.ENSP00000340361, 9606.ENSP00000362299, 9606.ENSP00000373574, 9606.ENSP00000442656	FSTL3, TGFB1, TGFB3, ACVR2A, INHBA, FST, GDF11, MSTN, SMAD2, CREBBP, SMURF2, EP300, ACVR1, BMP6, ZFYVE9, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0002009	Morphogenesis of an epithelium	6	435	1.11	0.00028	9606.ENSP00000221930, 9606.ENSP00000256759, 9606.ENSP00000263640, 9606.ENSP00000332973, 9606.ENSP00000362299, 9606.ENSP00000373574	TGFB1, FST, ACVR1, SMAD3, ENG, ACVRL1
GO0048705	Skeletal system morphogenesis	5	240	1.29	0.00028	9606.ENSP00000238682, 9606.ENSP00000262160, 9606.ENSP00000283147, 9606.ENSP00000332973, 9606.ENSP00000340361	TGFB3, SMAD2, BMP6, SMAD3, ACVR2B
GO0042060	Wound healing	6	439	1.1	0.00029	9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000262160, 9606.ENSP00000332973, 9606.ENSP00000362299, 9606.ENSP00000373574	TGFB1, TGFB3, SMAD2, SMAD3, ENG, ACVRL1
GO0003209	Cardiac atrium morphogenesis	3	30	1.97	0.0003	9606.ENSP00000263640, 9606.ENSP00000295379, 9606.ENSP00000362299	ACVR1, BMP10, ENG
GO0048568	Embryonic organ development	6	448	1.1	0.00032	9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000262160, 9606.ENSP00000263640, 9606.ENSP00000332973, 9606.ENSP00000362299	TGFB1, TGFB3, SMAD2, ACVR1, SMAD3, ENG
GO0022414	Reproductive process	9	1400	0.78	0.00035	9606.ENSP00000166139, 9606.ENSP00000238682, 9606.ENSP00000241416, 9606.ENSP00000242208, 9606.ENSP00000256759, 9606.ENSP00000260950, 9606.ENSP00000263640, 9606.ENSP00000283147, 9606.ENSP00000442656	FSTL3, TGFB3, ACVR2A, INHBA, FST, MSTN, ACVR1, BMP6, ACVR1B
GO0070483	Detection of hypoxia	2	2	2.97	0.00035	9606.ENSP00000238682, 9606.ENSP00000362299	TGFB3, ENG
GO0045648	Positive regulation of erythrocyte differentiation	3	32	1.94	0.00036	9606.ENSP00000241416, 9606.ENSP00000242208, 9606.ENSP00000442656	ACVR2A, INHBA, ACVR1B
GO0001503	Ossification	5	265	1.25	0.00042	9606.ENSP00000166139, 9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000283147, 9606.ENSP00000332973	FSTL3, TGFB1, TGFB3, BMP6, SMAD3
GO0003203	Endocardial cushion morphogenesis	3	34	1.91	0.00042	9606.ENSP00000263640, 9606.ENSP00000362299, 9606.ENSP00000373574	ACVR1, ENG, ACVRL1
GO0030513	Positive regulation of bmp signaling pathway	3	34	1.91	0.00042	9606.ENSP00000262160, 9606.ENSP00000362299, 9606.ENSP00000373574	SMAD2, ENG, ACVRL1
GO0035270	Endocrine system development	4	120	1.49	0.00043	9606.ENSP00000166139, 9606.ENSP00000262160, 9606.ENSP00000283147, 9606.ENSP00000332973	FSTL3, SMAD2, BMP6, SMAD3
GO0042476	Odontogenesis	4	120	1.49	0.00043	9606.ENSP00000238682, 9606.ENSP00000242208, 9606.ENSP00000256759, 9606.ENSP00000340361	TGFB3, INHBA, FST, ACVR2B
GO0061061	Muscle structure development	6	479	1.07	0.00045	9606.ENSP00000221930, 9606.ENSP00000260950, 9606.ENSP00000263253, 9606.ENSP00000263640, 9606.ENSP00000295379, 9606.ENSP00000362299	TGFB1, MSTN, EP300, ACVR1, BMP10, ENG
GO0048511	Rhythmic process	5	271	1.24	0.00046	9606.ENSP00000238682, 9606.ENSP00000242208, 9606.ENSP00000260950, 9606.ENSP00000262367, 9606.ENSP00000263253	TGFB3, INHBA, MSTN, CREBBP, EP300
GO0014706	Striated muscle tissue development	5	280	1.22	0.00053	9606.ENSP00000221930, 9606.ENSP00000263253, 9606.ENSP00000263640, 9606.ENSP00000295379, 9606.ENSP00000362299	TGFB1, EP300, ACVR1, BMP10, ENG
GO0003206	Cardiac chamber morphogenesis	4	128	1.46	0.00054	9606.ENSP00000221930, 9606.ENSP00000263640, 9606.ENSP00000295379, 9606.ENSP00000362299	TGFB1, ACVR1, BMP10, ENG
GO0018076	N-terminal peptidyl-lysine acetylation	2	3	2.79	0.00054	9606.ENSP00000262367, 9606.ENSP00000263253	CREBBP, EP300
GO0048565	Digestive tract development	4	128	1.46	0.00054	9606.ENSP00000238682, 9606.ENSP00000262160, 9606.ENSP00000332973, 9606.ENSP00000340361	TGFB3, SMAD2, SMAD3, ACVR2B

Table S10. the full list of KEGG analysis and GO analysis for INHBA

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO0065009	Regulation of molecular function	15	4913	0.45	0.00054	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000263253, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299	TGFB1, TGFB3, ACVR2A, INHBA, FST, GDF11, MSTN, SMAD2, CREBBP, EP300, BMP6, BMP10, SMAD3, ACVR2B, ENG
GO0003231	Cardiac ventricle development	4	129	1.46	0.00055	9606. ENSP00000221930, 9606. ENSP00000263640, 9606. ENSP00000295379, 9606. ENSP00000362299	TGFB1, ACVR1, BMP10, ENG
GO0048706	Embryonic skeletal system development	4	130	1.46	0.00056	9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000262160, 9606. ENSP00000332973	TGFB3, ACVR2A, SMAD2, SMAD3
GO0043902	Positive regulation of multi-organism process	3	39	1.86	0.00057	9606. ENSP00000242208, 9606. ENSP00000262435, 9606. ENSP00000442656	INHBA, SMURF2, ACVR1B
GO0097190	Apoptotic signaling pathway	5	286	1.21	0.00057	9606. ENSP00000221930, 9606. ENSP00000242208, 9606. ENSP00000263253, 9606. ENSP00000332973, 9606. ENSP00000442656	TGFB1, INHBA, EP300, SMAD3, ACVR1B
GO0016202	Regulation of striated muscle tissue development	4	133	1.45	0.0006	9606. ENSP00000221930, 9606. ENSP00000260950, 9606. ENSP00000295379, 9606. ENSP00000332973	TGFB1, MSTN, BMP10, SMAD3
GO0007517	Muscle organ development	5	291	1.2	0.00061	9606. ENSP00000221930, 9606. ENSP00000260950, 9606. ENSP00000263253, 9606. ENSP00000295379, 9606. ENSP00000362299	TGFB1, MSTN, EP300, BMP10, ENG
GO0032103	Positive regulation of response to external stimulus	6	511	1.04	0.00061	9606. ENSP00000221930, 9606. ENSP00000260950, 9606. ENSP00000262367, 9606. ENSP00000263253, 9606. ENSP00000283147, 9606. ENSP00000332973	TGFB1, MSTN, CREBBP, EP300, BMP6, SMAD3
GO0044260	Cellular macromolecule metabolic process	15	4976	0.45	0.00062	9606. ENSP00000166139, 9606. ENSP00000221930, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000262435, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000295379, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000362299, 9606. ENSP00000373574, 9606. ENSP00000442656	FSTL3, TGFB1, ACVR2A, INHBA, SMAD2, CREBBP, SMURF2, EP300, ACVR1, BMP10, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0030335	Positive regulation of cell migration	6	522	1.03	0.00067	9606. ENSP00000221930, 9606. ENSP00000260950, 9606. ENSP00000262435, 9606. ENSP00000263640, 9606. ENSP00000332973, 9606. ENSP00000442656	TGFB1, MSTN, SMURF2, ACVR1, SMAD3, ACVR1B
GO0009628	Response to abiotic stimulus	8	1147	0.81	0.00068	9606. ENSP00000238682, 9606. ENSP00000260950, 9606. ENSP00000262367, 9606. ENSP00000263253, 9606. ENSP00000283147, 9606. ENSP00000332973, 9606. ENSP00000362299, 9606. ENSP00000373574	TGFB3, MSTN, CREBBP, EP300, BMP6, SMAD3, ENG, ACVRL1
GO0048562	Embryonic organ morphogenesis	5	301	1.19	0.00068	9606. ENSP00000238682, 9606. ENSP00000262160, 9606. ENSP00000263640, 9606. ENSP00000332973, 9606. ENSP00000362299	TGFB3, SMAD2, ACVR1, SMAD3, ENG
GO0048609	Multicellular organismal reproductive process	7	807	0.91	0.00068	9606. ENSP00000166139, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000260950, 9606. ENSP00000263640	FSTL3, TGFB3, ACVR2A, INHBA, FST, MSTN, ACVR1
GO2000826	Regulation of heart morphogenesis	3	42	1.82	0.00068	9606. ENSP00000263640, 9606. ENSP00000295379, 9606. ENSP00000362299	ACVR1, BMP10, ENG
GO0060562	Epithelial tube morphogenesis	5	307	1.18	0.00074	9606. ENSP00000221930, 9606. ENSP00000263640, 9606. ENSP00000332973, 9606. ENSP00000362299, 9606. ENSP00000373574	TGFB1, ACVR1, SMAD3, ENG, ACVRL1
GO0022602	Ovulation cycle process	3	44	1.8	0.00075	9606. ENSP00000238682, 9606. ENSP00000242208, 9606. ENSP00000260950	TGFB3, INHBA, MSTN
GO0043010	Camera-type eye development	5	318	1.17	0.00086	9606. ENSP00000242208, 9606. ENSP00000257868, 9606. ENSP00000332973, 9606. ENSP00000340361, 9606. ENSP00000373574	INHBA, GDF11, SMAD3, ACVR2B, ACVRL1
GO0009725	Response to hormone	7	849	0.89	0.00089	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000242208, 9606. ENSP00000260950, 9606. ENSP00000263253, 9606. ENSP00000283147, 9606. ENSP00000362299	TGFB1, TGFB3, INHBA, MSTN, EP300, BMP6, ENG
GO0033993	Response to lipid	7	858	0.88	0.00094	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000242208, 9606. ENSP00000260950, 9606. ENSP00000262160, 9606. ENSP00000283147, 9606. ENSP00000362299	TGFB1, TGFB3, INHBA, MSTN, SMAD2, BMP6, ENG
GO0048701	Embryonic cranial skeleton morphogenesis	3	48	1.77	0.00094	9606. ENSP00000238682, 9606. ENSP00000262160, 9606. ENSP00000332973	TGFB3, SMAD2, SMAD3
GO0055010	Ventricular cardiac muscle tissue morphogenesis	3	48	1.77	0.00094	9606. ENSP00000221930, 9606. ENSP00000295379, 9606. ENSP00000362299	TGFB1, BMP10, ENG
GO0048545	Response to steroid hormone	5	328	1.15	0.00097	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000260950, 9606. ENSP00000283147, 9606. ENSP00000362299	TGFB1, TGFB3, MSTN, BMP6, ENG
GO0010936	Negative regulation of macrophage cytokine production	2	5	2.57	0.00098	9606. ENSP00000221930, 9606. ENSP00000238682	TGFB1, TGFB3
GO0043932	Ossification involved in bone remodeling	2	5	2.57	0.00098	9606. ENSP00000221930, 9606. ENSP00000238682	TGFB1, TGFB3

Table S10. the full list of KEGG analysis and GO analysis for INHBA

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO0046661	Male sex differentiation	4	156	1.38	0.00098	9606.ENSP00000166139, 9606.ENSP00000241416, 9606.ENSP00000242208, 9606.ENSP00000283147	FSTL3, ACVR2A, INHBA, BMP6
GO1905007	tive regulation of epithelial to mesenchymal transition involved in endocardial cushion forma	2	5	2.57	0.00098	9606.ENSP00000263640, 9606.ENSP00000362299	ACVR1, ENG
GO0010596	Negative regulation of endothelial cell migration	3	52	1.73	0.0011	9606.ENSP00000221930, 9606.ENSP00000295379, 9606.ENSP00000373574	TGFB1, BMP10, ACVRL1
GO0048738	Cardiac muscle tissue development	4	160	1.37	0.0011	9606.ENSP00000221930, 9606.ENSP00000263640, 9606.ENSP00000295379, 9606.ENSP00000362299	TGFB1, ACVR1, BMP10, ENG
GO0050678	Regulation of epithelial cell proliferation	5	339	1.14	0.0011	9606.ENSP00000221930, 9606.ENSP00000283147, 9606.ENSP00000332973, 9606.ENSP00000362299, 9606.ENSP00000373574	TGFB1, BMP6, SMAD3, ENG, ACVRL1
GO0007182	Common-partner smad protein phosphorylation	2	6	2.49	0.0013	9606.ENSP00000221930, 9606.ENSP00000262160	TGFB1, SMAD2
GO0014070	Response to organic cyclic compound	7	911	0.85	0.0013	9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000242208, 9606.ENSP00000260950, 9606.ENSP00000262160, 9606.ENSP00000283147, 9606.ENSP00000362299	TGFB1, TGFB3, INHBA, MSTN, SMAD2, BMP6, ENG
GO0055009	Atrial cardiac muscle tissue morphogenesis	2	6	2.49	0.0013	9606.ENSP00000295379, 9606.ENSP00000362299	BMP10, ENG
GO0002684	Positive regulation of immune system process	7	949	0.84	0.0016	9606.ENSP00000221930, 9606.ENSP00000241416, 9606.ENSP00000242208, 9606.ENSP00000260950, 9606.ENSP00000262367, 9606.ENSP00000263253, 9606.ENSP00000442656	TGFB1, ACVR2A, INHBA, MSTN, CREBBP, EP300, ACVR1B
GO0003006	Developmental process involved in reproduction	7	945	0.84	0.0016	9606.ENSP00000166139, 9606.ENSP00000241416, 9606.ENSP00000242208, 9606.ENSP00000256759, 9606.ENSP00000263640, 9606.ENSP00000283147, 9606.ENSP00000442656	FSTL3, ACVR2A, INHBA, FST, ACVR1, BMP6, ACVR1B
GO0010742	Macrophage derived foam cell differentiation	2	7	2.43	0.0016	9606.ENSP00000221930, 9606.ENSP00000263253	TGFB1, EP300
GO0060836	Lymphatic endothelial cell differentiation	2	7	2.43	0.0016	9606.ENSP00000340361, 9606.ENSP00000373574	ACVR2B, ACVRL1
GO1901165	Positive regulation of trophoblast cell migration	2	7	2.43	0.0016	9606.ENSP00000262435, 9606.ENSP00000442656	SMURF2, ACVR1B
GO0002520	Immune system development	6	652	0.93	0.0019	9606.ENSP00000166139, 9606.ENSP00000221930, 9606.ENSP00000242208, 9606.ENSP00000256759, 9606.ENSP00000263253, 9606.ENSP00000332973	FSTL3, TGFB1, INHBA, FST, EP300, SMAD3
GO0035912	Dorsal aorta morphogenesis	2	8	2.37	0.0019	9606.ENSP00000362299, 9606.ENSP00000373574	ENG, ACVRL1
GO0044087	Regulation of cellular component biogenesis	7	971	0.83	0.0019	9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000260950, 9606.ENSP00000263253, 9606.ENSP00000295379, 9606.ENSP00000332973, 9606.ENSP00000373574	TGFB1, TGFB3, MSTN, EP300, BMP10, SMAD3, ACVRL1
GO0065008	Regulation of biological quality	13	4042	0.48	0.0019	9606.ENSP00000221930, 9606.ENSP00000241416, 9606.ENSP00000242208, 9606.ENSP00000260950, 9606.ENSP00000262160, 9606.ENSP00000262367, 9606.ENSP00000263253, 9606.ENSP00000283147, 9606.ENSP00000332973, 9606.ENSP00000340361, 9606.ENSP00000362299, 9606.ENSP00000373574, 9606.ENSP00000442656	TGFB1, ACVR2A, INHBA, MSTN, SMAD2, CREBBP, EP300, BMP6, SMAD3, ACVR2B, ENG, ACVRL1, ACVR1B
GO0008015	Blood circulation	5	394	1.07	0.0021	9606.ENSP00000221930, 9606.ENSP00000283147, 9606.ENSP00000332973, 9606.ENSP00000362299, 9606.ENSP00000373574	TGFB1, BMP6, SMAD3, ENG, ACVRL1
GO0006950	Response to stress	12	3485	0.51	0.0023	9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000242208, 9606.ENSP00000260950, 9606.ENSP00000262160, 9606.ENSP00000262367, 9606.ENSP00000263253, 9606.ENSP00000263640, 9606.ENSP00000283147, 9606.ENSP00000332973, 9606.ENSP00000362299, 9606.ENSP00000373574	TGFB1, TGFB3, INHBA, MSTN, SMAD2, CREBBP, EP300, ACVR1, BMP6, SMAD3, ENG, ACVRL1
GO0030855	Epithelial cell differentiation	6	673	0.92	0.0023	9606.ENSP00000263640, 9606.ENSP00000283147, 9606.ENSP00000332973, 9606.ENSP00000340361, 9606.ENSP00000362299, 9606.ENSP00000373574	ACVR1, BMP6, SMAD3, ACVR2B, ENG, ACVRL1
GO0060348	Bone development	4	199	1.27	0.0023	9606.ENSP00000238682, 9606.ENSP00000263253, 9606.ENSP00000283147, 9606.ENSP00000362299	TGFB3, EP300, BMP6, ENG
GO1903242	Regulation of cardiac muscle hypertrophy in response to stress	2	9	2.32	0.0023	9606.ENSP00000295379, 9606.ENSP00000332973	BMP10, SMAD3
GO0003143	Embryonic heart tube morphogenesis	3	70	1.6	0.0024	9606.ENSP00000263640, 9606.ENSP00000332973, 9606.ENSP00000362299	ACVR1, SMAD3, ENG
GO0048732	Gland development	5	410	1.06	0.0024	9606.ENSP00000166139, 9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000262160, 9606.ENSP00000332973	FSTL3, TGFB1, TGFB3, SMAD2, SMAD3
GO0008406	Gonad development	4	205	1.26	0.0025	9606.ENSP00000166139, 9606.ENSP00000241416, 9606.ENSP00000242208, 9606.ENSP00000256759	FSTL3, ACVR2A, INHBA, FST
GO0001942	Hair follicle development	3	74	1.58	0.0027	9606.ENSP00000242208, 9606.ENSP00000256759, 9606.ENSP00000442656	INHBA, FST, ACVR1B
GO0031053	Primary mirna processing	2	10	2.27	0.0027	9606.ENSP00000262160, 9606.ENSP00000332973	SMAD2, SMAD3
GO0043627	Response to estrogen	3	74	1.58	0.0027	9606.ENSP00000238682, 9606.ENSP00000260950, 9606.ENSP00000263253	TGFB3, MSTN, EP300
GO0048340	Paraxial mesoderm morphogenesis	2	10	2.27	0.0027	9606.ENSP00000262160, 9606.ENSP00000332973	SMAD2, SMAD3
GO0048608	Reproductive structure development	5	420	1.05	0.0027	9606.ENSP00000166139, 9606.ENSP00000241416, 9606.ENSP00000242208, 9606.ENSP00000256759, 9606.ENSP00000283147	FSTL3, ACVR2A, INHBA, FST, BMP6
GO1901203	Positive regulation of extracellular matrix assembly	2	10	2.27	0.0027	9606.ENSP00000221930, 9606.ENSP00000332973	TGFB1, SMAD3

Table S10. the full list of KEGG analysis and GO analysis for INHBA

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO0051128	Regulation of cellular component organization	10	2402	0.59	0.0028	9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000242208, 9606.ENSP00000260950, 9606.ENSP00000263253, 9606.ENSP00000283147, 9606.ENSP00000295379, 9606.ENSP00000332973, 9606.ENSP00000373574, 9606.ENSP00000442656	TGFB1, TGFB3, INHBA, MSTN, EP300, BMP6, BMP10, SMAD3, ACVRL1, ACVR1B
GO0007492	Endoderm development	3	76	1.57	0.0029	9606.ENSP00000242208, 9606.ENSP00000262160, 9606.ENSP00000332973	INHBA, SMAD2, SMAD3
GO0030155	Regulation of cell adhesion	6	712	0.89	0.0029	9606.ENSP00000166139, 9606.ENSP00000221930, 9606.ENSP00000283147, 9606.ENSP00000332973, 9606.ENSP00000362299, 9606.ENSP00000373574	FSTL3, TGFB1, BMP6, SMAD3, ENG, ACVRL1
GO0001946	Lymphangiogenesis	2	11	2.23	0.003	9606.ENSP00000340361, 9606.ENSP00000373574	ACVR2B, ACVRL1
GO0046879	Hormone secretion	3	77	1.56	0.003	9606.ENSP00000242208, 9606.ENSP00000262160, 9606.ENSP00000340361	INHBA, SMAD2, ACVR2B
GO0048642	Negative regulation of skeletal muscle tissue development	2	11	2.23	0.003	9606.ENSP00000221930, 9606.ENSP00000260950	TGFB1, MSTN
GO0001817	Regulation of cytokine production	6	742	0.88	0.0035	9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000242208, 9606.ENSP00000262367, 9606.ENSP00000263253, 9606.ENSP00000332973	TGFB1, TGFB3, INHBA, CREBBP, EP300, SMAD3
GO2000243	Positive regulation of reproductive process	3	82	1.53	0.0035	9606.ENSP00000242208, 9606.ENSP00000262435, 9606.ENSP00000442656	INHBA, SMURF2, ACVR1B
GO0097305	Response to alcohol	4	233	1.2	0.0037	9606.ENSP00000221930, 9606.ENSP00000242208, 9606.ENSP00000260950, 9606.ENSP00000262160	TGFB1, INHBA, MSTN, SMAD2
GO0001657	Ureteric bud development	3	86	1.51	0.0039	9606.ENSP00000257868, 9606.ENSP00000262160, 9606.ENSP00000332973	GDF11, SMAD2, SMAD3
GO0050673	Epithelial cell proliferation	3	88	1.5	0.0042	9606.ENSP00000241416, 9606.ENSP00000256759, 9606.ENSP00000373574	ACVR2A, FST, ACVRL1
GO0051149	Positive regulation of muscle cell differentiation	3	88	1.5	0.0042	9606.ENSP00000221930, 9606.ENSP00000295379, 9606.ENSP00000362299	TGFB1, BMP10, ENG
GO0060840	Artery development	3	88	1.5	0.0042	9606.ENSP00000340361, 9606.ENSP00000362299, 9606.ENSP00000373574	ACVR2B, ENG, ACVRL1
GO0110110	Positive regulation of animal organ morphogenesis	3	89	1.5	0.0043	9606.ENSP00000263640, 9606.ENSP00000295379, 9606.ENSP00000362299	ACVR1, BMP10, ENG
GO0035265	Organ growth	3	96	1.46	0.0052	9606.ENSP00000262160, 9606.ENSP00000295379, 9606.ENSP00000340361	SMAD2, BMP10, ACVR2B
GO0046545	Development of primary female sexual characteristics	3	96	1.46	0.0052	9606.ENSP00000242208, 9606.ENSP00000256759, 9606.ENSP00000442656	INHBA, FST, ACVR1B
GO2000027	Regulation of animal organ morphogenesis	4	257	1.16	0.0052	9606.ENSP00000262435, 9606.ENSP00000263640, 9606.ENSP00000295379, 9606.ENSP00000362299	SMURF2, ACVR1, BMP10, ENG
GO0001568	Blood vessel development	5	500	0.97	0.0053	9606.ENSP00000221930, 9606.ENSP00000263640, 9606.ENSP00000340361, 9606.ENSP00000362299, 9606.ENSP00000373574	TGFB1, ACVR1, ACVR2B, ENG, ACVRL1
GO0030336	Negative regulation of cell migration	4	262	1.15	0.0055	9606.ENSP00000221930, 9606.ENSP00000295379, 9606.ENSP00000362299, 9606.ENSP00000373574	TGFB1, BMP10, ENG, ACVRL1
GO0043117	Positive regulation of vascular permeability	2	16	2.07	0.0055	9606.ENSP00000221930, 9606.ENSP00000283147	TGFB1, BMP6
GO0110020	Regulation of actomyosin structure organization	3	98	1.46	0.0055	9606.ENSP00000238682, 9606.ENSP00000295379, 9606.ENSP00000332973	TGFB3, BMP10, SMAD3
GO0045603	Positive regulation of endothelial cell differentiation	2	17	2.04	0.006	9606.ENSP00000283147, 9606.ENSP00000373574	BMP6, ACVRL1
GO0007221	Positive regulation of transcription of notch receptor target	2	18	2.02	0.0066	9606.ENSP00000262367, 9606.ENSP00000263253	CREBBP, EP300
GO0061298	Retina vasculature development in camera-type eye	2	18	2.02	0.0066	9606.ENSP00000340361, 9606.ENSP00000373574	ACVR2B, ACVRL1
GO0016579	Protein deubiquitination	4	281	1.12	0.0069	9606.ENSP00000262160, 9606.ENSP00000262435, 9606.ENSP00000263253, 9606.ENSP00000332973	SMAD2, SMURF2, EP300, SMAD3
GO0044089	Positive regulation of cellular component biogenesis	5	542	0.93	0.0074	9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000260950, 9606.ENSP00000295379, 9606.ENSP00000332973	TGFB1, TGFB3, MSTN, BMP10, SMAD3
GO0023019	Signal transduction involved in regulation of gene expression	2	20	1.97	0.0079	9606.ENSP00000262160, 9606.ENSP00000332973	SMAD2, SMAD3
GO0060039	Pericardium development	2	20	1.97	0.0079	9606.ENSP00000262160, 9606.ENSP00000332973	SMAD2, SMAD3
GO0030097	Hemopoiesis	5	570	0.91	0.0093	9606.ENSP00000166139, 9606.ENSP00000221930, 9606.ENSP00000242208, 9606.ENSP00000256759, 9606.ENSP00000263253	FSTL3, TGFB1, INHBA, FST, EP300
GO0045649	Regulation of macrophage differentiation	2	22	1.93	0.0093	9606.ENSP00000221930, 9606.ENSP00000242208	TGFB1, INHBA
GO0002761	Regulation of myeloid leukocyte differentiation	3	121	1.36	0.0095	9606.ENSP00000166139, 9606.ENSP00000221930, 9606.ENSP00000242208	FSTL3, TGFB1, INHBA
GO1903532	Positive regulation of secretion by cell	4	312	1.08	0.0099	9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000242208, 9606.ENSP00000283147	TGFB1, TGFB3, INHBA, BMP6
GO0071214	Cellular response to abiotic stimulus	4	313	1.08	0.01	9606.ENSP00000262367, 9606.ENSP00000263253, 9606.ENSP00000283147, 9606.ENSP00000362299	CREBBP, EP300, BMP6, ENG
GO0044057	Regulation of system process	5	592	0.9	0.0108	9606.ENSP00000242208, 9606.ENSP00000260950, 9606.ENSP00000283147, 9606.ENSP00000295379, 9606.ENSP00000332973	INHBA, MSTN, BMP6, BMP10, SMAD3
GO0061311	Cell surface receptor signaling pathway involved in heart development	2	24	1.89	0.0108	9606.ENSP00000221930, 9606.ENSP00000263640	TGFB1, ACVR1
GO0062009	Secondary palate development	2	24	1.89	0.0108	9606.ENSP00000238682, 9606.ENSP00000262160	TGFB3, SMAD2
GO0000082	G1S transition of mitotic cell cycle	3	128	1.34	0.0109	9606.ENSP00000242208, 9606.ENSP00000263640, 9606.ENSP00000442656	INHBA, ACVR1, ACVR1B
GO0050680	Negative regulation of epithelial cell proliferation	3	131	1.33	0.0115	9606.ENSP00000221930, 9606.ENSP00000362299, 9606.ENSP00000373574	TGFB1, ENG, ACVRL1

Table S10. the full list of KEGG analysis and GO analysis for INHBA

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO0008584	Male gonad development	3	133	1.32	0.012	9606.ENSP00000166139, 9606.ENSP00000241416, 9606.ENSP00000242208	FSTL3, ACVR2A, INHBA
GO0001936	Regulation of endothelial cell proliferation	3	134	1.32	0.0122	9606.ENSP00000283147, 9606.ENSP00000362299, 9606.ENSP00000373574	BMP6, ENG, ACVRL1
GO0010614	Negative regulation of cardiac muscle hypertrophy	2	26	1.86	0.0122	9606.ENSP00000295379, 9606.ENSP00000332973	BMP10, SMAD3
GO1903047	Mitotic cell cycle process	5	616	0.88	0.0126	9606.ENSP00000221930, 9606.ENSP00000242208, 9606.ENSP00000263253, 9606.ENSP00000263640, 9606.ENSP00000442656	TGFB1, INHBA, EP300, ACVR1, ACVR1B
GO0045662	Negative regulation of myoblast differentiation	2	27	1.84	0.013	9606.ENSP00000221930, 9606.ENSP00000260950	TGFB1, MSTN
GO2000679	Positive regulation of transcription regulatory region dna binding	2	27	1.84	0.013	9606.ENSP00000221930, 9606.ENSP00000263253	TGFB1, EP300
GO0022402	Cell cycle process	6	976	0.76	0.0131	9606.ENSP00000221930, 9606.ENSP00000242208, 9606.ENSP00000263253, 9606.ENSP00000263640, 9606.ENSP00000332973, 9606.ENSP00000442656	TGFB1, INHBA, EP300, ACVR1, SMAD3, ACVR1B
GO0032940	Secretion by cell	6	979	0.76	0.0132	9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000242208, 9606.ENSP00000262160, 9606.ENSP00000340361, 9606.ENSP00000362299	TGFB1, TGFB3, INHBA, SMAD2, ACVR2B, ENG
GO0007050	Cell cycle arrest	3	141	1.3	0.0137	9606.ENSP00000221930, 9606.ENSP00000242208, 9606.ENSP00000332973	TGFB1, INHBA, SMAD3
GO0001569	Branching involved in blood vessel morphogenesis	2	29	1.81	0.0146	9606.ENSP00000263640, 9606.ENSP00000362299	ACVR1, ENG
GO0030511	Positive regulation of transforming growth factor beta receptor signaling pathway	2	29	1.81	0.0146	9606.ENSP00000262367, 9606.ENSP00000263253	CREBBP, EP300
GO0051222	Positive regulation of protein transport	4	352	1.02	0.0146	9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000283147, 9606.ENSP00000332973	TGFB1, TGFB3, BMP6, SMAD3
GO1904837	beta-catenin-TCF complex assembly	2	29	1.81	0.0146	9606.ENSP00000262367, 9606.ENSP00000263253	CREBBP, EP300
GO0050921	Positive regulation of chemotaxis	3	147	1.28	0.0152	9606.ENSP00000221930, 9606.ENSP00000260950, 9606.ENSP00000332973	TGFB1, MSTN, SMAD3
GO0007435	Salivary gland morphogenesis	2	30	1.79	0.0153	9606.ENSP00000221930, 9606.ENSP00000238682	TGFB1, TGFB3
GO0090263	Positive regulation of canonical wnt signaling pathway	3	148	1.28	0.0155	9606.ENSP00000221930, 9606.ENSP00000262435, 9606.ENSP00000332973	TGFB1, SMURF2, SMAD3
GO0060325	Face morphogenesis	2	31	1.78	0.0162	9606.ENSP00000238682, 9606.ENSP00000263253	TGFB3, EP300
GO0048762	Mesenchymal cell differentiation	3	152	1.26	0.0166	9606.ENSP00000221930, 9606.ENSP00000263640, 9606.ENSP00000362299	TGFB1, ACVR1, ENG
GO0003008	System process	8	1942	0.58	0.0167	9606.ENSP00000221930, 9606.ENSP00000242208, 9606.ENSP00000260950, 9606.ENSP00000263253, 9606.ENSP00000283147, 9606.ENSP00000332973, 9606.ENSP00000362299, 9606.ENSP00000373574	TGFB1, INHBA, MSTN, EP300, BMP6, SMAD3, ENG, ACVRL1
GO0001974	Blood vessel remodeling	2	32	1.77	0.017	9606.ENSP00000340361, 9606.ENSP00000373574	ACVR2B, ACVRL1
GO0051145	Smooth muscle cell differentiation	2	32	1.77	0.017	9606.ENSP00000263640, 9606.ENSP00000362299	ACVR1, ENG
GO0051098	Regulation of binding	4	373	1	0.0175	9606.ENSP00000221930, 9606.ENSP00000262160, 9606.ENSP00000263253, 9606.ENSP00000332973	TGFB1, SMAD2, EP300, SMAD3
GO0043537	Negative regulation of blood vessel endothelial cell migration	2	35	1.73	0.0198	9606.ENSP00000221930, 9606.ENSP00000373574	TGFB1, ACVRL1
GO0061384	Heart trabecula morphogenesis	2	35	1.73	0.0198	9606.ENSP00000295379, 9606.ENSP00000362299	BMP10, ENG
GO0031960	Response to corticosteroid	3	164	1.23	0.02	9606.ENSP00000260950, 9606.ENSP00000283147, 9606.ENSP00000362299	MSTN, BMP6, ENG
GO0050714	Positive regulation of protein secretion	3	167	1.22	0.0208	9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000283147	TGFB1, TGFB3, BMP6
GO0022603	Regulation of anatomical structure morphogenesis	6	1095	0.71	0.0221	9606.ENSP00000221930, 9606.ENSP00000262435, 9606.ENSP00000263640, 9606.ENSP00000295379, 9606.ENSP00000362299, 9606.ENSP00000373574	TGFB1, SMURF2, ACVR1, BMP10, ENG, ACVRL1
GO0048514	Blood vessel morphogenesis	4	410	0.96	0.0239	9606.ENSP00000221930, 9606.ENSP00000263640, 9606.ENSP00000362299, 9606.ENSP00000373574	TGFB1, ACVR1, ENG, ACVRL1
GO1901700	Response to oxygen-containing compound	7	1567	0.62	0.0245	9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000242208, 9606.ENSP00000260950, 9606.ENSP00000262160, 9606.ENSP00000283147, 9606.ENSP00000340361	TGFB1, TGFB3, INHBA, MSTN, SMAD2, BMP6, ACVR2B
GO0030073	Insulin secretion	2	40	1.67	0.0247	9606.ENSP00000262160, 9606.ENSP00000340361	SMAD2, ACVR2B
GO1902895	Positive regulation of pri-mirna transcription by rna polymerase ii	2	40	1.67	0.0247	9606.ENSP00000221930, 9606.ENSP00000332973	TGFB1, SMAD3
GO0045216	Cell-cell junction organization	3	180	1.19	0.0253	9606.ENSP00000221930, 9606.ENSP00000238682, 9606.ENSP00000332973	TGFB1, TGFB3, SMAD3
GO0042307	Positive regulation of protein import into nucleus	2	41	1.66	0.0258	9606.ENSP00000221930, 9606.ENSP00000332973	TGFB1, SMAD3
GO0008217	Regulation of blood pressure	3	182	1.19	0.0259	9606.ENSP00000332973, 9606.ENSP00000362299, 9606.ENSP00000373574	SMAD3, ENG, ACVRL1
GO0001937	Negative regulation of endothelial cell proliferation	2	43	1.64	0.028	9606.ENSP00000362299, 9606.ENSP00000373574	ENG, ACVRL1
GO0055025	Positive regulation of cardiac muscle tissue development	2	44	1.63	0.0291	9606.ENSP00000221930, 9606.ENSP00000295379	TGFB1, BMP10
GO0048468	Cell development	7	1629	0.6	0.03	9606.ENSP00000257868, 9606.ENSP00000263253, 9606.ENSP00000263640, 9606.ENSP00000283147, 9606.ENSP00000295379, 9606.ENSP00000332973, 9606.ENSP00000362299	GDF11, EP300, ACVR1, BMP6, BMP10, SMAD3, ENG
GO0032570	Response to progesterone	2	45	1.62	0.0301	9606.ENSP00000221930, 9606.ENSP00000238682	TGFB1, TGFB3
GO0044060	Regulation of endocrine process	2	45	1.62	0.0301	9606.ENSP00000242208, 9606.ENSP00000283147	INHBA, BMP6
GO0050731	Positive regulation of peptidyl-tyrosine phosphorylation	3	196	1.15	0.0312	9606.ENSP00000221930, 9606.ENSP00000263640, 9606.ENSP00000283147	TGFB1, ACVR1, BMP6
GO0050999	Regulation of nitric-oxide synthase activity	2	46	1.61	0.0312	9606.ENSP00000241416, 9606.ENSP00000362299	ACVR2A, ENG
GO0042326	Negative regulation of phosphorylation	4	449	0.92	0.0319	9606.ENSP00000221930, 9606.ENSP00000242208, 9606.ENSP00000260950, 9606.ENSP00000362299	TGFB1, INHBA, MSTN, ENG

Table S10. the full list of KEGG analysis and GO analysis for INHBA

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO1902905	Positive regulation of supramolecular fiber organization	3	198	1.15	0.0319	9606. ENSP00000238682, 9606. ENSP00000295379, 9606. ENSP00000332973	TGFB3, BMP10, SMAD3
GO0002683	Negative regulation of immune system process	4	450	0.92	0.032	9606. ENSP00000166139, 9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000242208	FSTL3, TGFB1, TGFB3, INHBA
GO1901654	Response to ketone	3	199	1.15	0.0321	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000260950	TGFB1, TGFB3, MSTN
GO0045599	Negative regulation of fat cell differentiation	2	48	1.59	0.0332	9606. ENSP00000221930, 9606. ENSP00000332973	TGFB1, SMAD3
GO0001819	Positive regulation of cytokine production	4	461	0.91	0.0345	9606. ENSP00000221930, 9606. ENSP00000262367, 9606. ENSP00000263253, 9606. ENSP00000332973	TGFB1, CREBBP, EP300, SMAD3
GO0051130	Positive regulation of cellular component organization	6	1209	0.67	0.0345	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000260950, 9606. ENSP00000263253, 9606. ENSP00000295379, 9606. ENSP00000332973	TGFB1, TGFB3, MSTN, EP300, BMP10, SMAD3
GO0030514	Negative regulation of bmp signaling pathway	2	50	1.57	0.0355	9606. ENSP00000166139, 9606. ENSP00000262435	FSTL3, SMURF2
GO0045747	Positive regulation of notch signaling pathway	2	50	1.57	0.0355	9606. ENSP00000262367, 9606. ENSP00000263253	CREBBP, EP300
GO0001706	Endoderm formation	2	52	1.55	0.0379	9606. ENSP00000242208, 9606. ENSP00000262160	INHBA, SMAD2
GO0002762	Negative regulation of myeloid leukocyte differentiation	2	52	1.55	0.0379	9606. ENSP00000166139, 9606. ENSP00000242208	FSTL3, INHBA
GO0003179	Heart valve morphogenesis	2	52	1.55	0.0379	9606. ENSP00000221930, 9606. ENSP00000263640	TGFB1, ACVR1
GO0031648	Protein destabilization	2	52	1.55	0.0379	9606. ENSP00000262367, 9606. ENSP00000263253	CREBBP, EP300
GO0051496	Positive regulation of stress fiber assembly	2	53	1.55	0.039	9606. ENSP00000238682, 9606. ENSP00000332973	TGFB3, SMAD3
GO0040011	Locomotion	6	1251	0.65	0.04	9606. ENSP00000221930, 9606. ENSP00000260950, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000362299, 9606. ENSP00000373574	TGFB1, MSTN, EP300, ACVR1, ENG, ACVRL1
GO0051495	Positive regulation of cytoskeleton organization	3	220	1.1	0.0409	9606. ENSP00000238682, 9606. ENSP00000295379, 9606. ENSP00000332973	TGFB3, BMP10, SMAD3
GO0008283	Cell population proliferation	4	493	0.88	0.0424	9606. ENSP00000241416, 9606. ENSP00000256759, 9606. ENSP00000295379, 9606. ENSP00000373574	ACVR2A, FST, BMP10, ACVRL1
GO0051896	Regulation of protein kinase b signaling	3	226	1.09	0.0436	9606. ENSP00000221930, 9606. ENSP00000260950, 9606. ENSP00000362299	TGFB1, MSTN, ENG
GO0035306	Positive regulation of dephosphorylation	2	58	1.51	0.045	9606. ENSP00000221930, 9606. ENSP00000332973	TGFB1, SMAD3
GO0051155	Positive regulation of striated muscle cell differentiation	2	59	1.5	0.0463	9606. ENSP00000221930, 9606. ENSP00000295379	TGFB1, BMP10
GO0045912	Negative regulation of carbohydrate metabolic process	2	60	1.49	0.0476	9606. ENSP00000221930, 9606. ENSP00000263253	TGFB1, EP300
hsa04350	TGF-beta signaling pathway	14	91	2.16	2.49E-25	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000256759, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000262435, 9606. ENSP00000263253, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000287727, 9606. ENSP00000332973, 9606. ENSP00000340361	TGFB1, TGFB3, ACVR2A, INHBA, FST, SMAD2, CREBBP, SMURF2, EP300, ACVR1, BMP6, ZFYVE9, SMAD3, ACVR2B
hsa04060	Cytokine-cytokine receptor interaction	11	282	1.56	3.61E-13	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000257868, 9606. ENSP00000260950, 9606. ENSP00000263640, 9606. ENSP00000283147, 9606. ENSP00000295379, 9606. ENSP00000340361, 9606. ENSP00000373574	TGFB1, TGFB3, ACVR2A, INHBA, GDF11, MSTN, ACVR1, BMP6, BMP10, ACVR2B, ACVRL1
hsa04110	Cell cycle	6	120	1.67	3.53E-07	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000263253, 9606. ENSP00000332973	TGFB1, TGFB3, SMAD2, CREBBP, EP300, SMAD3
hsa04550	Signaling pathways regulating pluripotency of stem cells	6	140	1.6	6.43E-07	9606. ENSP00000241416, 9606. ENSP00000242208, 9606. ENSP00000262160, 9606. ENSP00000263640, 9606. ENSP00000332973, 9606. ENSP00000340361	ACVR2A, INHBA, SMAD2, ACVR1, SMAD3, ACVR2B
hsa05166	Human T-cell leukemia virus 1 infection	6	211	1.42	5.48E-06	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000263253, 9606. ENSP00000332973	TGFB1, TGFB3, SMAD2, CREBBP, EP300, SMAD3
hsa04068	FoxO signaling pathway	5	127	1.56	1.35E-05	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000262367, 9606. ENSP00000263253, 9606. ENSP00000332973	TGFB1, TGFB3, CREBBP, EP300, SMAD3
hsa04390	Hippo signaling pathway	5	153	1.48	2.82E-05	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000262160, 9606. ENSP00000283147, 9606. ENSP00000332973	TGFB1, TGFB3, SMAD2, BMP6, SMAD3
hsa05161	Hepatitis B	5	159	1.47	2.82E-05	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000262367, 9606. ENSP00000263253, 9606. ENSP00000332973	TGFB1, TGFB3, CREBBP, EP300, SMAD3
hsa05321	Inflammatory bowel disease	4	60	1.79	2.82E-05	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000262160, 9606. ENSP00000332973	TGFB1, TGFB3, SMAD2, SMAD3
hsa05211	Renal cell carcinoma	4	66	1.75	2.87E-05	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000262367, 9606. ENSP00000263253	TGFB1, TGFB3, CREBBP, EP300
hsa05212	Pancreatic cancer	4	73	1.71	3.84E-05	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000262160, 9606. ENSP00000332973	TGFB1, TGFB3, SMAD2, SMAD3
hsa05210	Colorectal cancer	4	82	1.66	5.48E-05	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000262160, 9606. ENSP00000332973	TGFB1, TGFB3, SMAD2, SMAD3
hsa04933	AGE-RAGE signaling pathway in diabetic complications	4	98	1.58	0.0001	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000262160, 9606. ENSP00000332973	TGFB1, TGFB3, SMAD2, SMAD3

Table S10. the full list of KEGG analysis and GO analysis for INHBA

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
hsa05200	Pathways in cancer	6	517	1.03	0.00033	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000262160, 9606. ENSP00000262367, 9606. ENSP00000263253, 9606. ENSP00000332973	TGFB1, TGFB3, SMAD2, CREBBP, EP300, SMAD3
hsa05226	Gastric cancer	4	144	1.41	0.00038	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000262160, 9606. ENSP00000332973	TGFB1, TGFB3, SMAD2, SMAD3
hsa04218	Cellular senescence	4	150	1.4	0.00042	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000262160, 9606. ENSP00000332973	TGFB1, TGFB3, SMAD2, SMAD3
hsa05225	Hepatocellular carcinoma	4	160	1.37	0.0005	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000262160, 9606. ENSP00000332973	TGFB1, TGFB3, SMAD2, SMAD3
hsa05152	Tuberculosis	4	168	1.35	0.00057	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000262367, 9606. ENSP00000263253	TGFB1, TGFB3, CREBBP, EP300
hsa04520	Adherens junction	3	67	1.62	0.00098	9606. ENSP00000262367, 9606. ENSP00000263253, 9606. ENSP00000332973	CREBBP, EP300, SMAD3
hsa05220	Chronic myeloid leukemia	3	75	1.57	0.0013	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000332973	TGFB1, TGFB3, SMAD3
hsa04144	Endocytosis	4	241	1.19	0.0019	9606. ENSP00000262160, 9606. ENSP00000262435, 9606. ENSP00000287727, 9606. ENSP00000332973	SMAD2, SMURF2, ZFYVE9, SMAD3
hsa04659	Th17 cell differentiation	3	101	1.44	0.0026	9606. ENSP00000221930, 9606. ENSP00000262160, 9606. ENSP00000332973	TGFB1, SMAD2, SMAD3
hsa05142	Chagas disease	3	99	1.45	0.0026	9606. ENSP00000221930, 9606. ENSP00000238682, 9606. ENSP00000262160	TGFB1, TGFB3, SMAD2
hsa05418	Fluid shear stress and atherosclerosis	3	130	1.33	0.0052	9606. ENSP00000241416, 9606. ENSP00000263640, 9606. ENSP00000340361	ACVR2A, ACVR1, ACVR2B
hsa04310	Wnt signaling pathway	3	154	1.26	0.0081	9606. ENSP00000262367, 9606. ENSP00000263253, 9606. ENSP00000332973	CREBBP, EP300, SMAD3
hsa05144	Malaria	2	46	1.61	0.0155	9606. ENSP00000221930, 9606. ENSP00000238682	TGFB1, TGFB3
hsa04330	Notch signaling pathway	2	52	1.55	0.0189	9606. ENSP00000262367, 9606. ENSP00000263253	CREBBP, EP300
hsa04720	Long-term potentiation	2	64	1.46	0.027	9606. ENSP00000262367, 9606. ENSP00000263253	CREBBP, EP300
hsa05140	Leishmaniasis	2	70	1.43	0.031	9606. ENSP00000221930, 9606. ENSP00000238682	TGFB1, TGFB3
hsa05323	Rheumatoid arthritis	2	85	1.34	0.0434	9606. ENSP00000221930, 9606. ENSP00000238682	TGFB1, TGFB3
hsa05410	Hypertrophic cardiomyopathy	2	89	1.32	0.0459	9606. ENSP00000221930, 9606. ENSP00000238682	TGFB1, TGFB3

Table S11. the full list of KEGG analysis and GO analysis for NOX4

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0006801	Superoxide metabolic process	9	37	2.19	2.34E-13	9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000289473, 9606.ENSP00000342848, 9606.ENSP00000356505, 9606.ENSP00000362057, 9606.ENSP00000367851, 9606.ENSP00000380334, 9606.ENSP00000380450	CYBA, NOX4, NCF1, NOXA1, NCF2, NOX1, CYBB, NCF4, NOXO1
GO:0072593	Reactive oxygen species metabolic process	11	112	1.79	2.34E-13	9606.ENSP00000241052, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000342848, 9606.ENSP00000356505, 9606.ENSP00000362057, 9606.ENSP00000367851, 9606.ENSP00000380334, 9606.ENSP00000380450	CAT, CYBA, NOX4, EGFR, NCF1, NOXA1, NCF2, NOX1, CYBB, NCF4, NOXO1
GO:0070887	Cellular response to chemical stimulus	25	2919	0.73	3.00E-12	9606.ENSP00000222139, 9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000306275, 9606.ENSP00000327801, 9606.ENSP00000341208, 9606.ENSP00000356505, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851, 9606.ENSP00000380334	EPOR, CAT, TICAM1, CYBA, NOX4, KDR, NRP1, EGFR, LY96, NCF1, S100B, STAT5B, FIGF, INSR, CD14, KCNK3, P4HB, STAT5A, NCF2, PTPN1, NOX1, TLR4, AGER, CYBB, NCF4
GO:0042554	Superoxide anion generation	7	16	2.44	9.25E-12	9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000289473, 9606.ENSP00000342848, 9606.ENSP00000356505, 9606.ENSP00000362057, 9606.ENSP00000367851	CYBA, NOX4, NCF1, NOXA1, NCF2, NOX1, CYBB
GO:0006950	Response to stress	25	3485	0.66	1.22E-10	9606.ENSP00000200453, 9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000304236, 9606.ENSP00000306275, 9606.ENSP00000327801, 9606.ENSP00000341208, 9606.ENSP00000356505, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851, 9606.ENSP00000380334, 9606.ENSP00000475924	PPP1R15A, CAT, TICAM1, CYBA, NOX4, KDR, NRP1, EGFR, LY96, NCF1, S100B, STAT5B, FIGF, CD14, KCNK3, P4HB, STAT5A, NCF2, PTPN1, NOX1, TLR4, AGER, CYBB, NCF4, POLDIP2
GO:0048010	Vascular endothelial growth factor receptor signaling pathway	8	69	1.86	6.14E-10	9606.ENSP00000261623, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000289473, 9606.ENSP00000297904, 9606.ENSP00000356505, 9606.ENSP00000367851, 9606.ENSP00000380334	CYBA, KDR, NRP1, NCF1, FIGF, NCF2, CYBB, NCF4
GO:0048584	Positive regulation of response to stimulus	21	2257	0.77	6.14E-10	9606.ENSP00000200453, 9606.ENSP00000222139, 9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210	PPP1R15A, EPOR, CAT, TICAM1, RAC2, CYBA, NOX4, KDR, NRP1, EGFR, LY96, NCF1, S100B, STAT5B, FIGF, INSR, CD14, PTPN1, NOX1, TLR4, AGER
GO:0007169	Transmembrane receptor protein tyrosine kinase signaling pathway	13	518	1.2	7.78E-10	9606.ENSP00000261623, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000341208, 9606.ENSP00000356505, 9606.ENSP00000360683, 9606.ENSP00000367851, 9606.ENSP00000380334	CYBA, KDR, NRP1, EGFR, NCF1, STAT5B, FIGF, INSR, STAT5A, NCF2, PTPN1, CYBB, NCF4

Table S11. the full list of KEGG analysis and GO analysis for NOX4

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0042221	Response to chemical	26	4333	0.58	7.78E-10	9606.ENSP00000222139, 9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000306275, 9606.ENSP00000327801, 9606.ENSP00000341208, 9606.ENSP00000356505, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851, 9606.ENSP00000380334	EPOR, CAT, TICAM1, RAC2, CYBA, NOX4, KDR, NRP1, EGFR, LY96, NCF1, S100B, STAT5B, FIGF, INSR, CD14, KCNK3, P4HB, STAT5A, NCF2, PTPN1, NOX1, TLR4, AGER, CYBB, NCF4
GO:1902533	Positive regulation of intracellular signal transduction	16	1041	0.99	8.24E-10	9606.ENSP00000222139, 9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000291700, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210	EPOR, CAT, TICAM1, RAC2, NOX4, KDR, NRP1, EGFR, NCF1, S100B, INSR, CD14, PTPN1, NOX1, TLR4, AGER
GO:0045730	Respiratory burst	6	18	2.32	1.44E-09	9606.ENSP00000261623, 9606.ENSP00000289473, 9606.ENSP00000356505, 9606.ENSP00000362057, 9606.ENSP00000367851, 9606.ENSP00000380334	CYBA, NCF1, NCF2, NOX1, CYBB, NCF4
GO:0009967	Positive regulation of signal transduction	18	1654	0.84	3.95E-09	9606.ENSP00000222139, 9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000291700, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210	EPOR, CAT, TICAM1, RAC2, CYBA, NOX4, KDR, NRP1, EGFR, LY96, NCF1, S100B, INSR, CD14, PTPN1, NOX1, TLR4, AGER
GO:0007166	Cell surface receptor signaling pathway	20	2325	0.73	7.55E-09	9606.ENSP00000222139, 9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000327801, 9606.ENSP00000341208, 9606.ENSP00000356505, 9606.ENSP00000360683, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851, 9606.ENSP00000380334	EPOR, TICAM1, CYBA, KDR, NRP1, EGFR, LY96, NCF1, STAT5B, FIGF, INSR, CD14, P4HB, STAT5A, NCF2, PTPN1, TLR4, AGER, CYBB, NCF4
GO:0045454	Cell redox homeostasis	7	60	1.87	8.94E-09	9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000289473, 9606.ENSP00000327801, 9606.ENSP00000356505, 9606.ENSP00000367851, 9606.ENSP00000380334	RAC2, CYBA, NCF1, P4HB, NCF2, CYBB, NCF4
GO:2000377	Regulation of reactive oxygen species metabolic process	9	188	1.48	1.25E-08	9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000275493, 9606.ENSP00000303830, 9606.ENSP00000342848, 9606.ENSP00000363089, 9606.ENSP00000380450	TICAM1, RAC2, CYBA, NOX4, EGFR, INSR, NOXA1, TLR4, NOXO1
GO:0008284	Positive regulation of cell population proliferation	14	919	0.98	2.35E-08	9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000341208, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210	TICAM1, RAC2, CYBA, KDR, NRP1, EGFR, S100B, STAT5B, FIGF, INSR, STAT5A, NOX1, TLR4, AGER

Table S11. the full list of KEGG analysis and GO analysis for NOX4

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0051716	Cellular response to stimulus	28	6489	0.44	3.58E-08	9606.ENSP00000200453, 9606.ENSP00000222139, 9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000306275, 9606.ENSP00000327801, 9606.ENSP00000341208, 9606.ENSP00000356505, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851, 9606.ENSP00000380334, 9606.ENSP00000475924	PPP1R15A, EPOR, CAT, TICAM1, RAC2, CYBA, NOX4, KDR, NRP1, EGFR, LY96, NCF1, S100B, STAT5B, FIGF, INSR, CD14, KCNK3, P4HB, STAT5A, NCF2, PTPN1, NOX1, TLR4, AGER, CYBB, NCF4, POLDIP2
GO:0032760	Positive regulation of tumor necrosis factor production	7	88	1.7	7.35E-08	9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000284818, 9606.ENSP00000304236, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	TICAM1, CYBA, LY96, CD14, TLR4, AGER, CYBB
GO:0071310	Cellular response to organic substance	19	2369	0.7	7.66E-08	9606.ENSP00000222139, 9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000327801, 9606.ENSP00000341208, 9606.ENSP00000360683, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	EPOR, CAT, TICAM1, CYBA, NOX4, KDR, NRP1, EGFR, LY96, STAT5B, FIGF, INSR, CD14, P4HB, STAT5A, PTPN1, TLR4, AGER, CYBB
GO:1901701	Cellular response to oxygen-containing compound	14	1055	0.92	1.10E-07	9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000341208, 9606.ENSP00000360683, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	TICAM1, CYBA, NOX4, EGFR, LY96, NCF1, STAT5B, INSR, CD14, STAT5A, PTPN1, TLR4, AGER, CYBB
GO:1902531	Regulation of intracellular signal transduction	17	1807	0.77	1.10E-07	9606.ENSP00000222139, 9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000291700, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000327801, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210	EPOR, CAT, TICAM1, RAC2, NOX4, KDR, NRP1, EGFR, NCF1, S100B, INSR, CD14, P4HB, PTPN1, NOX1, TLR4, AGER
GO:0032103	Positive regulation of response to external stimulus	11	511	1.13	1.11E-07	9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000363089, 9606.ENSP00000364210	TICAM1, RAC2, CYBA, KDR, NRP1, EGFR, LY96, STAT5B, FIGF, TLR4, AGER
GO:0006952	Defense response	15	1296	0.86	1.15E-07	9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000304236, 9606.ENSP00000341208, 9606.ENSP00000356505, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	TICAM1, CYBA, NOX4, EGFR, LY96, NCF1, S100B, STAT5B, CD14, STAT5A, NCF2, NOX1, TLR4, AGER, CYBB
GO:0070482	Response to oxygen levels	10	379	1.22	1.19E-07	9606.ENSP00000241052, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000291700, 9606.ENSP00000297904, 9606.ENSP00000306275, 9606.ENSP00000327801, 9606.ENSP00000362057, 9606.ENSP00000364210, 9606.ENSP00000367851	CAT, CYBA, NOX4, S100B, FIGF, KCNK3, P4HB, NOX1, AGER, CYBB
GO:0044093	Positive regulation of molecular function	17	1842	0.77	1.22E-07	9606.ENSP00000200453, 9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000303830, 9606.ENSP00000342848, 9606.ENSP00000356505, 9606.ENSP00000360683, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000380334, 9606.ENSP00000380450	PPP1R15A, CAT, TICAM1, CYBA, NOX4, KDR, NRP1, EGFR, NCF1, INSR, NOXA1, NCF2, PTPN1, TLR4, AGER, NCF4, NOXO1

Table S11. the full list of KEGG analysis and GO analysis for NOX4

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0062197	Cellular response to chemical stress	9	293	1.29	2.79E-07	9606.ENSP00000241052, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000356505, 9606.ENSP00000362057, 9606.ENSP00000367851, 9606.ENSP00000380334	CAT, CYBA, NOX4, EGFR, NCF1, NCF2, NOX1, CYBB, NCF4
GO:0042592	Homeostatic process	16	1676	0.78	3.17E-07	9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000303830, 9606.ENSP00000306275, 9606.ENSP00000327801, 9606.ENSP00000356505, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851, 9606.ENSP00000380334	RAC2, CYBA, NOX4, KDR, EGFR, NCF1, STAT5B, INSR, KCNK3, P4HB, NCF2, NOX1, TLR4, AGER, CYBB, NCF4
GO:0010033	Response to organic substance	20	3011	0.62	3.48E-07	9606.ENSP00000222139, 9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000327801, 9606.ENSP00000341208, 9606.ENSP00000360683, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	EPOR, CAT, TICAM1, CYBA, NOX4, KDR, NRP1, EGFR, LY96, S100B, STAT5B, FIGF, INSR, CD14, P4HB, STAT5A, PTPN1, TLR4, AGER, CYBB
GO:0009966	Regulation of signal transduction	20	3107	0.61	5.93E-07	9606.ENSP00000200453, 9606.ENSP00000222139, 9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000291700, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000327801, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210	PPP1R15A, EPOR, CAT, TICAM1, RAC2, CYBA, NOX4, KDR, NRP1, EGFR, LY96, NCF1, S100B, INSR, CD14, P4HB, PTPN1, NOX1, TLR4, AGER
GO:0034128	Negative regulation of myd88-independent toll-like receptor signaling pathway	4	7	2.56	6.17E-07	9606.ENSP00000248244, 9606.ENSP00000284818, 9606.ENSP00000304236, 9606.ENSP00000363089	TICAM1, LY96, CD14, TLR4
GO:0043085	Positive regulation of catalytic activity	15	1489	0.8	6.17E-07	9606.ENSP00000200453, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000303830, 9606.ENSP00000342848, 9606.ENSP00000356505, 9606.ENSP00000360683, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000380334, 9606.ENSP00000380450	PPP1R15A, CYBA, NOX4, KDR, NRP1, EGFR, NCF1, INSR, NOXA1, NCF2, PTPN1, TLR4, AGER, NCF4, NOXO1
GO:0001666	Response to hypoxia	9	342	1.22	8.71E-07	9606.ENSP00000241052, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000291700, 9606.ENSP00000297904, 9606.ENSP00000306275, 9606.ENSP00000327801, 9606.ENSP00000364210, 9606.ENSP00000367851	CAT, CYBA, NOX4, S100B, FIGF, KCNK3, P4HB, AGER, CYBB
GO:1901700	Response to oxygen-containing compound	15	1567	0.78	1.11E-06	9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000341208, 9606.ENSP00000360683, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	CAT, TICAM1, CYBA, NOX4, EGFR, LY96, NCF1, STAT5B, INSR, CD14, STAT5A, PTPN1, TLR4, AGER, CYBB
GO:0048583	Regulation of response to stimulus	22	4114	0.53	1.13E-06	9606.ENSP00000200453, 9606.ENSP00000222139, 9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000327801, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210	PPP1R15A, EPOR, CAT, TICAM1, RAC2, CYBA, NOX4, KDR, NRP1, EGFR, LY96, NCF1, S100B, STAT5B, FIGF, INSR, CD14, P4HB, PTPN1, NOX1, TLR4, AGER
GO:0034599	Cellular response to oxidative stress	8	244	1.32	1.28E-06	9606.ENSP00000241052, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000356505, 9606.ENSP00000367851, 9606.ENSP00000380334	CAT, CYBA, NOX4, EGFR, NCF1, NCF2, CYBB, NCF4

Table S11. the full list of KEGG analysis and GO analysis for NOX4

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0006954	Inflammatory response	10	515	1.09	1.40E-06	9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000304236, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	TICAM1, CYBA, NOX4, EGFR, LY96, CD14, NOX1, TLR4, AGER, CYBB
GO:0023052	Signaling	24	5239	0.46	1.77E-06	9606.ENSP00000200453, 9606.ENSP00000222139, 9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000306275, 9606.ENSP00000327801, 9606.ENSP00000341208, 9606.ENSP00000356505, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851, 9606.ENSP00000380334	PPP1R15A, EPOR, TICAM1, RAC2, CYBA, KDR, NRP1, EGFR, LY96, NCF1, STAT5B, FIGF, INSR, CD14, KCNK3, P4HB, STAT5A, NCF2, PTPN1, NOX1, TLR4, AGER, CYBB, NCF4
GO:0042127	Regulation of cell population proliferation	15	1642	0.76	1.77E-06	9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000341208, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210	TICAM1, RAC2, CYBA, NOX4, KDR, NRP1, EGFR, S100B, STAT5B, FIGF, INSR, STAT5A, NOX1, TLR4, AGER
GO:0042743	Hydrogen peroxide metabolic process	5	39	1.91	2.01E-06	9606.ENSP00000241052, 9606.ENSP00000261623, 9606.ENSP00000275493, 9606.ENSP00000362057, 9606.ENSP0000367851	CAT, CYBA, EGFR, NOX1, CYBB
GO:0009628	Response to abiotic stimulus	13	1147	0.85	2.06E-06	9606.ENSP00000241052, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000275493, 9606.ENSP00000291700, 9606.ENSP00000297904, 9606.ENSP00000304236, 9606.ENSP00000306275, 9606.ENSP00000327801, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	CAT, CYBA, NOX4, EGFR, S100B, FIGF, CD14, KCNK3, P4HB, NOX1, TLR4, AGER, CYBB
GO:0043410	Positive regulation of mapk cascade	10	543	1.07	2.06E-06	9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000303830, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210	NOX4, KDR, NRP1, EGFR, NCF1, INSR, PTPN1, NOX1, TLR4, AGER
GO:0007154	Cell communication	24	5320	0.45	2.25E-06	9606.ENSP00000200453, 9606.ENSP00000222139, 9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000306275, 9606.ENSP00000327801, 9606.ENSP00000341208, 9606.ENSP00000356505, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851, 9606.ENSP00000380334	PPP1R15A, EPOR, TICAM1, RAC2, CYBA, KDR, NRP1, EGFR, LY96, NCF1, STAT5B, FIGF, INSR, CD14, KCNK3, P4HB, STAT5A, NCF2, PTPN1, NOX1, TLR4, AGER, CYBB, NCF4
GO:0007165	Signal transduction	23	4876	0.47	3.04E-06	9606.ENSP00000200453, 9606.ENSP00000222139, 9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000327801, 9606.ENSP00000341208, 9606.ENSP00000356505, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851, 9606.ENSP00000380334	PPP1R15A, EPOR, TICAM1, RAC2, CYBA, KDR, NRP1, EGFR, LY96, NCF1, STAT5B, FIGF, INSR, CD14, P4HB, STAT5A, NCF2, PTPN1, NOX1, TLR4, AGER, CYBB, NCF4
GO:0033554	Cellular response to stress	15	1725	0.74	3.04E-06	9606.ENSP00000200453, 9606.ENSP00000241052, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000291700, 9606.ENSP00000306275, 9606.ENSP00000327801, 9606.ENSP00000356505, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000367851, 9606.ENSP00000380334, 9606.ENSP00000475924	PPP1R15A, CAT, CYBA, NOX4, EGFR, NCF1, S100B, KCNK3, P4HB, NCF2, PTPN1, NOX1, CYBB, NCF4, POLDIP2

Table S11. the full list of KEGG analysis and GO analysis for NOX4

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0010243	Response to organonitrogen compound	12	987	0.89	3.86E-06	9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000275493, 9606.ENSP00000293328, 9606.ENSP00000303830, 9606.ENSP00000341208, 9606.ENSP00000360683, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	CAT, TICAM1, CYBA, NOX4, EGFR, STAT5B, INSR, STAT5A, PTPN1, TLR4, AGER, CYBB
GO:0051240	Positive regulation of multicellular organismal process	15	1770	0.73	3.86E-06	9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000304236, 9606.ENSP00000341208, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	TICAM1, CYBA, KDR, NRP1, EGFR, LY96, S100B, STAT5B, FIGF, CD14, STAT5A, NOX1, TLR4, AGER, CYBB
GO:0071417	Cellular response to organonitrogen compound	10	590	1.03	3.86E-06	9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000275493, 9606.ENSP00000293328, 9606.ENSP00000303830, 9606.ENSP00000341208, 9606.ENSP00000360683, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	CYBA, NOX4, EGFR, STAT5B, INSR, STAT5A, PTPN1, TLR4, AGER, CYBB
GO:2000379	Positive regulation of reactive oxygen species metabolic process	6	103	1.57	3.86E-06	9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000275493, 9606.ENSP00000303830, 9606.ENSP00000363089	TICAM1, CYBA, NOX4, EGFR, INSR, TLR4
GO:0060263	Regulation of respiratory burst	4	15	2.23	4.18E-06	9606.ENSP00000249071, 9606.ENSP00000303830, 9606.ENSP00000342848, 9606.ENSP00000380450	RAC2, INSR, NOXA1, NOXO1
GO:0048518	Positive regulation of biological process	25	6112	0.41	4.38E-06	9606.ENSP00000200453, 9606.ENSP00000222139, 9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000327801, 9606.ENSP00000341208, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851, 9606.ENSP00000475924	PPP1R15A, EPOR, CAT, TICAM1, RAC2, CYBA, NOX4, KDR, NRP1, EGFR, LY96, NCF1, S100B, STAT5B, FIGF, INSR, CD14, P4HB, STAT5A, PTPN1, NOX1, TLR4, AGER, CYBB, POLDIP2
GO:0050679	Positive regulation of epithelial cell proliferation	7	192	1.36	4.44E-06	9606.ENSP00000261623, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000297904, 9606.ENSP00000341208, 9606.ENSP00000363089	CYBA, KDR, NRP1, EGFR, FIGF, STAT5A, TLR4
GO:0031401	Positive regulation of protein modification process	13	1252	0.82	4.47E-06	9606.ENSP00000200453, 9606.ENSP00000248244, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210	PPP1R15A, TICAM1, NOX4, KDR, NRP1, EGFR, NCF1, FIGF, INSR, PTPN1, NOX1, TLR4, AGER
GO:0032101	Regulation of response to external stimulus	12	1013	0.87	4.47E-06	9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000360683, 9606.ENSP00000363089, 9606.ENSP00000364210	TICAM1, RAC2, CYBA, KDR, NRP1, EGFR, LY96, STAT5B, FIGF, PTPN1, TLR4, AGER
GO:0048522	Positive regulation of cellular process	24	5579	0.43	4.79E-06	9606.ENSP00000200453, 9606.ENSP00000222139, 9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000327801, 9606.ENSP00000341208, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000475924	PPP1R15A, EPOR, CAT, TICAM1, RAC2, CYBA, NOX4, KDR, NRP1, EGFR, LY96, NCF1, S100B, STAT5B, FIGF, INSR, CD14, P4HB, STAT5A, PTPN1, NOX1, TLR4, AGER, POLDIP2
GO:0001819	Positive regulation of cytokine production	9	461	1.09	5.97E-06	9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000284818, 9606.ENSP00000293328, 9606.ENSP00000304236, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	TICAM1, CYBA, LY96, STAT5B, CD14, NOX1, TLR4, AGER, CYBB

Table S11. the full list of KEGG analysis and GO analysis for NOX4

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:1901652	Response to peptide	9	476	1.08	7.58E-06	9606.ENSP00000241052, 9606.ENSP00000261623, 9606.ENSP00000293328, 9606.ENSP00000303830, 9606.ENSP00000341208, 9606.ENSP00000360683, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	CAT, CYBA, STAT5B, INSR, STAT5A, PTPN1, TLR4, AGER, CYBB
GO:0014066	Regulation of phosphatidylinositol 3-kinase signaling	6	123	1.49	8.55E-06	9606.ENSP00000222139, 9606.ENSP00000241052, 9606.ENSP00000263923, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000303830	EPOR, CAT, KDR, EGFR, NCF1, INSR
GO:0050789	Regulation of biological process	31	11475	0.23	1.21E-05	9606.ENSP00000200453, 9606.ENSP00000222139, 9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000306275, 9606.ENSP00000323148, 9606.ENSP00000327801, 9606.ENSP00000341208, 9606.ENSP00000342848, 9606.ENSP00000356505, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851, 9606.ENSP00000380334, 9606.ENSP00000380450, 9606.ENSP0000475924	PPP1R15A, EPOR, CAT, TICAM1, RAC2, CYBA, NOX4, KDR, NRP1, EGFR, LY96, NCF1, S100B, STAT5B, FIGF, INSR, CD14, KCNK3, ZKSCAN1, P4HB, STAT5A, NOXA1, NCF2, PTPN1, NOX1, TLR4, AGER, CYBB, NCF4, NOXO1, POLDIP2
GO:0019725	Cellular homeostasis	11	895	0.89	1.25E-05	9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000289473, 9606.ENSP00000306275, 9606.ENSP00000327801, 9606.ENSP00000356505, 9606.ENSP00000362057, 9606.ENSP00000364210, 9606.ENSP00000367851, 9606.ENSP00000380334	RAC2, CYBA, NOX4, NCF1, KCNK3, P4HB, NCF2, NOX1, AGER, CYBB, NCF4
GO:0045087	Innate immune response	10	703	0.95	1.49E-05	9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000291700, 9606.ENSP00000304236, 9606.ENSP00000356505, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	TICAM1, CYBA, LY96, NCF1, S100B, CD14, NCF2, TLR4, AGER, CYBB
GO:0030335	Positive regulation of cell migration	9	522	1.04	1.51E-05	9606.ENSP00000249071, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000341208, 9606.ENSP00000364210	RAC2, NOX4, KDR, NRP1, EGFR, FIGF, INSR, STAT5A, AGER
GO:0070266	Necroptotic process	4	23	2.04	1.51E-05	9606.ENSP00000248244, 9606.ENSP00000284818, 9606.ENSP00000304236, 9606.ENSP00000363089	TICAM1, LY96, CD14, TLR4
GO:0045937	Positive regulation of phosphate metabolic process	12	1164	0.81	1.69E-05	9606.ENSP00000200453, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210	PPP1R15A, NOX4, KDR, NRP1, EGFR, NCF1, FIGF, INSR, PTPN1, NOX1, TLR4, AGER
GO:0034121	Regulation of toll-like receptor signaling pathway	5	69	1.66	1.74E-05	9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000284818, 9606.ENSP00000304236, 9606.ENSP00000363089	TICAM1, CYBA, LY96, CD14, TLR4
GO:0065009	Regulation of molecular function	22	4913	0.45	1.80E-05	9606.ENSP00000200453, 9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000323148, 9606.ENSP00000341208, 9606.ENSP00000342848, 9606.ENSP00000356505, 9606.ENSP00000360683, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000380334, 9606.ENSP00000380450	PPP1R15A, CAT, TICAM1, RAC2, CYBA, NOX4, KDR, NRP1, EGFR, NCF1, STAT5B, FIGF, INSR, ZKSCAN1, STAT5A, NOXA1, NCF2, PTPN1, TLR4, AGER, NCF4, NOXO1
GO:0009719	Response to endogenous stimulus	13	1447	0.75	1.89E-05	9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000275493, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000303830, 9606.ENSP00000341208, 9606.ENSP00000360683, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	CAT, TICAM1, CYBA, NOX4, EGFR, S100B, STAT5B, INSR, STAT5A, PTPN1, TLR4, AGER, CYBB

Table S11. the full list of KEGG analysis and GO analysis for NOX4

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0050790	Regulation of catalytic activity	16	2386	0.63	1.89E-05	9606.ENSP00000200453, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000303830, 9606.ENSP00000342848, 9606.ENSP00000356505, 9606.ENSP00000360683, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000380334, 9606.ENSP00000380450	PPP1R15A, RAC2, CYBA, NOX4, KDR, NRP1, EGFR, NCF1, INSR, NOXA1, NCF2, PTPN1, TLR4, AGER, NCF4, NOXO1
GO:0002479	n processing and presentation of exogenous peptide antigen via mhc class i, tap-dep	5	75	1.62	2.36E-05	9606.ENSP00000261623, 9606.ENSP00000289473, 9606.ENSP00000356505, 9606.ENSP00000367851, 9606.ENSP00000380334	CYBA, NCF1, NCF2, CYBB, NCF4
GO:0010604	Positive regulation of macromolecule metabolic process	19	3600	0.52	2.36E-05	9606.ENSP00000200453, 9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000341208, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	PPP1R15A, TICAM1, CYBA, NOX4, KDR, NRP1, EGFR, LY96, NCF1, STAT5B, FIGF, INSR, CD14, STAT5A, PTPN1, NOX1, TLR4, AGER, CYBB
GO:0065008	Regulation of biological quality	20	4042	0.49	2.36E-05	9606.ENSP00000200453, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000303830, 9606.ENSP00000306275, 9606.ENSP00000327801, 9606.ENSP00000341208, 9606.ENSP00000356505, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851, 9606.ENSP00000380334	PPP1R15A, RAC2, CYBA, NOX4, KDR, NRP1, EGFR, NCF1, S100B, STAT5B, INSR, KCNK3, P4HB, STAT5A, NCF2, NOX1, TLR4, AGER, CYBB, NCF4
GO:0035666	TRIF-dependent toll-like receptor signaling pathway	4	30	1.93	3.21E-05	9606.ENSP00000248244, 9606.ENSP00000284818, 9606.ENSP00000304236, 9606.ENSP00000363089	TICAM1, LY96, CD14, TLR4
GO:0001934	Positive regulation of protein phosphorylation	11	1019	0.83	3.51E-05	9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210	NOX4, KDR, NRP1, EGFR, NCF1, FIGF, INSR, PTPN1, NOX1, TLR4, AGER
GO:0031399	Regulation of protein modification process	14	1870	0.67	4.07E-05	9606.ENSP00000200453, 9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210	PPP1R15A, TICAM1, RAC2, NOX4, KDR, NRP1, EGFR, NCF1, FIGF, INSR, PTPN1, NOX1, TLR4, AGER
GO:0014068	Positive regulation of phosphatidylinositol 3-kinase signaling	5	87	1.56	4.22E-05	9606.ENSP00000222139, 9606.ENSP00000241052, 9606.ENSP00000263923, 9606.ENSP00000289473, 9606.ENSP00000303830	EPOR, CAT, KDR, NCF1, INSR
GO:0070372	Regulation of erk1 and erk2 cascade	7	292	1.18	4.52E-05	9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000360683, 9606.ENSP00000363089, 9606.ENSP00000364210	NOX4, KDR, NRP1, EGFR, PTPN1, TLR4, AGER
GO:0019222	Regulation of metabolic process	25	6948	0.36	4.61E-05	9606.ENSP00000200453, 9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000323148, 9606.ENSP00000341208, 9606.ENSP00000342848, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851, 9606.ENSP00000380450, 9606.ENSP00000475924	PPP1R15A, CAT, TICAM1, RAC2, CYBA, NOX4, KDR, NRP1, EGFR, LY96, NCF1, STAT5B, FIGF, INSR, CD14, ZKSCAN1, STAT5A, NOXA1, PTPN1, NOX1, TLR4, AGER, CYBB, NOXO1, POLDIP2
GO:0031663	Lipopolysaccharide-mediated signaling pathway	4	34	1.87	4.67E-05	9606.ENSP00000248244, 9606.ENSP00000284818, 9606.ENSP00000304236, 9606.ENSP00000363089	TICAM1, LY96, CD14, TLR4

Table S11. the full list of KEGG analysis and GO analysis for NOX4

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0044419	Interspecies interaction between organisms	14	1899	0.67	4.67E-05	9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000263923, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000291700, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000356505, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	TICAM1, CYBA, KDR, EGFR, LY96, NCF1, S100B, FIGF, INSR, CD14, NCF2, TLR4, AGER, CYBB
GO:0050794	Regulation of cellular process	30	10932	0.24	4.76E-05	9606.ENSP00000200453, 9606.ENSP00000222139, 9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000323148, 9606.ENSP00000327801, 9606.ENSP00000341208, 9606.ENSP00000342848, 9606.ENSP00000356505, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851, 9606.ENSP00000380334, 9606.ENSP00000380450, 9606.ENSP00000475924	PPP1R15A, EPOR, CAT, TICAM1, RAC2, CYBA, NOX4, KDR, NRP1, EGFR, LY96, NCF1, S100B, STAT5B, FIGF, INSR, CD14, ZKSCAN1, P4HB, STAT5A, NOXA1, NCF2, PTPN1, NOX1, TLR4, AGER, CYBB, NCF4, NOXO1, POLDIP2
GO:0046328	Regulation of jnk cascade	6	183	1.32	5.53E-05	9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210	EGFR, NCF1, PTPN1, NOX1, TLR4, AGER
GO:0001938	Positive regulation of endothelial cell proliferation	5	94	1.53	5.57E-05	9606.ENSP00000261623, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000297904, 9606.ENSP00000341208	CYBA, KDR, NRP1, FIGF, STAT5A
GO:0033993	Response to lipid	10	858	0.87	6.12E-05	9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000304236, 9606.ENSP00000363089, 9606.ENSP00000367851	CAT, TICAM1, CYBA, EGFR, LY96, S100B, STAT5B, CD14, TLR4, CYBB
GO:0009605	Response to external stimulus	15	2310	0.61	6.64E-05	9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000291700, 9606.ENSP00000297904, 9606.ENSP00000304236, 9606.ENSP00000356505, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	CAT, TICAM1, RAC2, CYBA, NRP1, EGFR, LY96, NCF1, S100B, FIGF, CD14, NCF2, TLR4, AGER, CYBB
GO:1901653	Cellular response to peptide	7	331	1.13	8.86E-05	9606.ENSP00000261623, 9606.ENSP00000293328, 9606.ENSP00000303830, 9606.ENSP00000341208, 9606.ENSP00000360683, 9606.ENSP00000363089, 9606.ENSP00000364210	CYBA, STAT5B, INSR, STAT5A, PTPN1, TLR4, AGER
GO:0071363	Cellular response to growth factor stimulus	8	494	1.01	9.12E-05	9606.ENSP00000241052, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830	CAT, NOX4, KDR, NRP1, EGFR, STAT5B, FIGF, INSR
GO:0070374	Positive regulation of erk1 and erk2 cascade	6	209	1.26	0.0001	9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000363089, 9606.ENSP00000364210	NOX4, KDR, NRP1, EGFR, TLR4, AGER
GO:0001932	Regulation of protein phosphorylation	12	1459	0.72	0.00012	9606.ENSP00000249071, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210	RAC2, NOX4, KDR, NRP1, EGFR, NCF1, FIGF, INSR, PTPN1, NOX1, TLR4, AGER
GO:0051239	Regulation of multicellular organismal process	17	3227	0.52	0.00014	9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000306275, 9606.ENSP00000341208, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	TICAM1, CYBA, KDR, NRP1, EGFR, LY96, S100B, STAT5B, FIGF, INSR, CD14, KCNK3, STAT5A, NOX1, TLR4, AGER, CYBB
GO:0019220	Regulation of phosphate metabolic process	13	1816	0.65	0.00017	9606.ENSP00000200453, 9606.ENSP00000249071, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210	PPP1R15A, RAC2, NOX4, KDR, NRP1, EGFR, NCF1, FIGF, INSR, PTPN1, NOX1, TLR4, AGER

Table S11. the full list of KEGG analysis and GO analysis for NOX4

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0051707	Response to other organism	11	1256	0.74	0.0002	9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000291700, 9606.ENSP00000297904, 9606.ENSP00000304236, 9606.ENSP00000356505, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	TICAM1, CYBA, LY96, NCF1, S100B, FIGF, CD14, NCF2, TLR4, AGER, CYBB
GO:0048708	Astrocyte differentiation	4	55	1.66	0.00022	9606.ENSP00000275493, 9606.ENSP00000291700, 9606.ENSP00000363089, 9606.ENSP00000364210	EGFR, S100B, TLR4, AGER
GO:0060397	Growth hormone receptor signaling pathway via jak-stat	3	14	2.13	0.00023	9606.ENSP00000293328, 9606.ENSP00000341208, 9606.ENSP00000360683	STAT5B, STAT5A, PTPN1
GO:1903428	Positive regulation of reactive oxygen species biosynthetic process	4	56	1.65	0.00023	9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000303830, 9606.ENSP00000363089	TICAM1, CYBA, INSR, TLR4
GO:0043434	Response to peptide hormone	7	394	1.05	0.00024	9606.ENSP00000241052, 9606.ENSP00000261623, 9606.ENSP00000293328, 9606.ENSP00000303830, 9606.ENSP00000341208, 9606.ENSP00000360683, 9606.ENSP00000367851	CAT, CYBA, STAT5B, INSR, STAT5A, PTPN1, CYBB
GO:0046330	Positive regulation of jnk cascade	5	137	1.36	0.00026	9606.ENSP00000289473, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210	NCF1, PTPN1, NOX1, TLR4, AGER
GO:0043406	Positive regulation of map kinase activity	6	265	1.16	0.00034	9606.ENSP00000263317, 9606.ENSP00000275493, 9606.ENSP00000303830, 9606.ENSP00000360683, 9606.ENSP00000363089, 9606.ENSP00000364210	NOX4, EGFR, INSR, PTPN1, TLR4, AGER
GO:0046686	Response to cadmium ion	4	63	1.6	0.00034	9606.ENSP00000241052, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000367851	CAT, EGFR, NCF1, CYBB
GO:0050921	Positive regulation of chemotaxis	5	147	1.33	0.00035	9606.ENSP00000249071, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000297904, 9606.ENSP00000364210	RAC2, KDR, NRP1, FIGF, AGER
GO:0010628	Positive regulation of gene expression	14	2337	0.58	0.00041	9606.ENSP00000200453, 9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000341208, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	PPP1R15A, TICAM1, CYBA, EGFR, LY96, NCF1, STAT5B, INSR, CD14, STAT5A, NOX1, TLR4, AGER, CYBB
GO:0033674	Positive regulation of kinase activity	8	624	0.91	0.00041	9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000303830, 9606.ENSP00000360683, 9606.ENSP00000363089, 9606.ENSP00000364210	NOX4, KDR, EGFR, NCF1, INSR, PTPN1, TLR4, AGER
GO:0009725	Response to hormone	9	849	0.83	0.00043	9606.ENSP00000241052, 9606.ENSP00000261623, 9606.ENSP00000275493, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000303830, 9606.ENSP00000341208, 9606.ENSP00000360683, 9606.ENSP00000367851	CAT, CYBA, EGFR, S100B, STAT5B, INSR, STAT5A, PTPN1, CYBB
GO:0032879	Regulation of localization	15	2740	0.54	0.00046	9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000341208, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	RAC2, CYBA, NOX4, KDR, NRP1, EGFR, FIGF, INSR, CD14, STAT5A, PTPN1, NOX1, TLR4, AGER, CYBB
GO:0010310	Regulation of hydrogen peroxide metabolic process	3	20	1.98	0.00055	9606.ENSP00000249071, 9606.ENSP00000342848, 9606.ENSP00000380450	RAC2, NOXA1, NOXO1
GO:0034142	Toll-like receptor 4 signaling pathway	3	20	1.98	0.00055	9606.ENSP00000284818, 9606.ENSP00000304236, 9606.ENSP00000363089	LY96, CD14, TLR4
GO:0038084	Vascular endothelial growth factor signaling pathway	3	20	1.98	0.00055	9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000297904	KDR, NRP1, FIGF
GO:0007249	I-kappaB kinase/NF-kappaB signaling	4	74	1.53	0.00057	9606.ENSP00000248244, 9606.ENSP00000284818, 9606.ENSP00000304236, 9606.ENSP00000363089	TICAM1, LY96, CD14, TLR4
GO:0080134	Regulation of response to stress	11	1437	0.68	0.00061	9606.ENSP00000200453, 9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000327801, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210	PPP1R15A, TICAM1, CYBA, EGFR, NCF1, STAT5B, P4HB, PTPN1, NOX1, TLR4, AGER
GO:0022900	Electron transport chain	5	174	1.26	0.0007	9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000289473, 9606.ENSP00000356505, 9606.ENSP00000367851	CYBA, NOX4, NCF1, NCF2, CYBB

Table S11. the full list of KEGG analysis and GO analysis for NOX4

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0002376	Immune system process	14	2481	0.55	0.00073	9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000263923, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000304236, 9606.ENSP00000356505, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851, 9606.ENSP00000380334	CAT, TICAM1, CYBA, KDR, LY96, NCF1, S100B, STAT5B, CD14, NCF2, TLR4, AGER, CYBB, NCF4
GO:0043549	Regulation of kinase activity	9	918	0.79	0.00073	9606.ENSP00000249071, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000303830, 9606.ENSP00000360683, 9606.ENSP00000363089, 9606.ENSP00000364210	RAC2, NOX4, KDR, EGFR, NCF1, INSR, PTPN1, TLR4, AGER
GO:0031323	Regulation of cellular metabolic process	22	6239	0.35	0.00076	9606.ENSP00000200453, 9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000323148, 9606.ENSP00000341208, 9606.ENSP00000342848, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000380450, 9606.ENSP00000475924	PPP1R15A, CAT, TICAM1, RAC2, CYBA, NOX4, KDR, NRP1, EGFR, NCF1, STAT5B, FIGF, INSR, ZKSCAN1, STAT5A, NOXA1, PTPN1, NOX1, TLR4, AGER, NOXO1, POLDIP2
GO:1901224	Positive regulation of nik/nf-kappab signaling	4	82	1.49	0.00079	9606.ENSP00000275493, 9606.ENSP00000304236, 9606.ENSP00000363089, 9606.ENSP00000364210	EGFR, CD14, TLR4, AGER
GO:1903409	Reactive oxygen species biosynthetic process	3	25	1.88	0.00088	9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000367851	CYBA, NOX4, CYBB
GO:0050927	Positive regulation of positive chemotaxis	3	26	1.86	0.00098	9606.ENSP00000263923, 9606.ENSP00000297904, 9606.ENSP00000364210	KDR, FIGF, AGER
GO:0060255	Regulation of macromolecule metabolic process	22	6407	0.34	0.0011	9606.ENSP00000200453, 9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000323148, 9606.ENSP00000341208, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	PPP1R15A, CAT, TICAM1, RAC2, CYBA, NOX4, KDR, NRP1, EGFR, LY96, NCF1, STAT5B, FIGF, INSR, CD14, ZKSCAN1, STAT5A, PTPN1, NOX1, TLR4, AGER, CYBB
GO:0031325	Positive regulation of cellular metabolic process	16	3413	0.47	0.0012	9606.ENSP00000200453, 9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000341208, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210	PPP1R15A, TICAM1, CYBA, NOX4, KDR, NRP1, EGFR, NCF1, STAT5B, FIGF, INSR, STAT5A, PTPN1, NOX1, TLR4, AGER
GO:0032755	Positive regulation of interleukin-6 production	4	94	1.43	0.0012	9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000363089, 9606.ENSP00000364210	TICAM1, CYBA, TLR4, AGER
GO:0080135	Regulation of cellular response to stress	8	739	0.83	0.0012	9606.ENSP00000200453, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000327801, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210	PPP1R15A, EGFR, NCF1, P4HB, PTPN1, NOX1, TLR4, AGER
GO:0010035	Response to inorganic substance	7	538	0.91	0.0013	9606.ENSP00000241052, 9606.ENSP00000263923, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000304236, 9606.ENSP00000306275, 9606.ENSP00000367851	CAT, KDR, EGFR, NCF1, CD14, KCNK3, CYBB
GO:0002703	Regulation of leukocyte mediated immunity	5	209	1.18	0.0014	9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000293328, 9606.ENSP00000363089, 9606.ENSP00000364210	TICAM1, RAC2, STAT5B, TLR4, AGER
GO:0006909	Phagocytosis	5	210	1.18	0.0014	9606.ENSP00000249071, 9606.ENSP00000304236, 9606.ENSP00000356505, 9606.ENSP00000363089, 9606.ENSP00000380334	RAC2, CD14, NCF2, TLR4, NCF4
GO:0006955	Immune response	11	1588	0.64	0.0014	9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000291700, 9606.ENSP00000304236, 9606.ENSP00000356505, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	CAT, TICAM1, CYBA, LY96, NCF1, S100B, CD14, NCF2, TLR4, AGER, CYBB

Table S11. the full list of KEGG analysis and GO analysis for NOX4

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0045860	Positive regulation of protein kinase activity	7	550	0.9	0.0015	9606.ENSP00000263317, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000303830, 9606.ENSP00000360683, 9606.ENSP00000363089, 9606.ENSP00000364210	NOX4, EGFR, NCF1, INSR, PTPN1, TLR4, AGER
GO:0002755	MyD88-dependent toll-like receptor signaling pathway	3	33	1.76	0.0016	9606.ENSP00000284818, 9606.ENSP00000304236, 9606.ENSP00000363089	LY96, CD14, TLR4
GO:0010038	Response to metal ion	6	367	1.01	0.0016	9606.ENSP00000241052, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000304236, 9606.ENSP00000306275, 9606.ENSP00000367851	CAT, EGFR, NCF1, CD14, KCNK3, CYBB
GO:0038083	Peptidyl-tyrosine autophosphorylation	3	32	1.77	0.0016	9606.ENSP00000263923, 9606.ENSP00000275493, 9606.ENSP00000303830	KDR, EGFR, INSR
GO:0050670	Regulation of lymphocyte proliferation	5	218	1.16	0.0016	9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000293328, 9606.ENSP00000363089, 9606.ENSP00000364210	TICAM1, RAC2, STAT5B, TLR4, AGER
GO:0071453	Cellular response to oxygen levels	5	216	1.16	0.0016	9606.ENSP00000291700, 9606.ENSP00000306275, 9606.ENSP00000327801, 9606.ENSP00000362057, 9606.ENSP00000367851	S100B, KCNK3, P4HB, NOX1, CYBB
GO:1904845	Cellular response to l-glutamine	2	3	2.62	0.0016	9606.ENSP00000261623, 9606.ENSP00000367851	CYBA, CYBB
GO:0051234	Establishment of localization	18	4479	0.4	0.0017	9606.ENSP00000241052, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000306275, 9606.ENSP00000341208, 9606.ENSP00000356505, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851, 9606.ENSP00000380334	CAT, RAC2, CYBA, NRP1, EGFR, NCF1, STAT5B, FIGF, INSR, CD14, KCNK3, STAT5A, NCF2, NOX1, TLR4, AGER, CYBB, NCF4
GO:0001775	Cell activation	9	1075	0.72	0.002	9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000275493, 9606.ENSP00000293328, 9606.ENSP00000304236, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	CAT, TICAM1, CYBA, EGFR, STAT5B, CD14, TLR4, AGER, CYBB
GO:0002274	Myeloid leukocyte activation	7	585	0.88	0.002	9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000304236, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	CAT, TICAM1, CYBA, CD14, TLR4, AGER, CYBB
GO:0045859	Regulation of protein kinase activity	8	812	0.79	0.002	9606.ENSP00000249071, 9606.ENSP00000263317, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000303830, 9606.ENSP00000360683, 9606.ENSP00000363089, 9606.ENSP00000364210	RAC2, NOX4, EGFR, NCF1, INSR, PTPN1, TLR4, AGER
GO:0009891	Positive regulation of biosynthetic process	12	2040	0.57	0.0022	9606.ENSP00000200453, 9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000303830, 9606.ENSP00000341208, 9606.ENSP00000362057, 9606.ENSP00000363089	PPP1R15A, TICAM1, CYBA, NOX4, KDR, EGFR, NCF1, STAT5B, INSR, STAT5A, NOX1, TLR4
GO:0010941	Regulation of cell death	11	1696	0.61	0.0022	9606.ENSP00000241052, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000327801, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089	CAT, NOX4, KDR, NRP1, EGFR, S100B, STAT5B, P4HB, PTPN1, NOX1, TLR4
GO:0014002	Astrocyte development	3	37	1.71	0.0022	9606.ENSP00000275493, 9606.ENSP00000363089, 9606.ENSP00000364210	EGFR, TLR4, AGER
GO:0032497	Detection of lipopolysaccharide	2	4	2.5	0.0022	9606.ENSP00000284818, 9606.ENSP00000363089	LY96, TLR4
GO:0051128	Regulation of cellular component organization	13	2402	0.53	0.0022	9606.ENSP00000200453, 9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089	PPP1R15A, TICAM1, RAC2, CYBA, NOX4, KDR, NRP1, EGFR, INSR, CD14, PTPN1, NOX1, TLR4

Table S11. the full list of KEGG analysis and GO analysis for NOX4

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0051179	Localization	20	5591	0.35	0.0022	9606.ENSP00000200453, 9606.ENSP00000241052, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000306275, 9606.ENSP00000341208, 9606.ENSP00000356505, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851, 9606.ENSP00000380334	PPP1R15A, CAT, RAC2, CYBA, KDR, NRP1, EGFR, NCF1, STAT5B, FIGF, INSR, CD14, KCNK3, STAT5A, NCF2, NOX1, TLR4, AGER, CYBB, NCF4
GO:0071276	Cellular response to cadmium ion	3	37	1.71	0.0022	9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000367851	EGFR, NCF1, CYBB
GO:0006091	Generation of precursor metabolites and energy	6	405	0.97	0.0024	9606.ENSP00000241052, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000289473, 9606.ENSP00000356505, 9606.ENSP00000367851	CAT, CYBA, NOX4, NCF1, NCF2, CYBB
GO:0051173	Positive regulation of nitrogen compound metabolic process	15	3239	0.47	0.0024	9606.ENSP00000200453, 9606.ENSP00000248244, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000341208, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210	PPP1R15A, TICAM1, NOX4, KDR, NRP1, EGFR, NCF1, STAT5B, FIGF, INSR, STAT5A, PTPN1, NOX1, TLR4, AGER
GO:0098761	Cellular response to interleukin-7	3	42	1.65	0.0029	9606.ENSP00000293328, 9606.ENSP00000327801, 9606.ENSP00000341208	STAT5B, P4HB, STAT5A
GO:0080184	Response to phenylpropanoid	2	5	2.4	0.003	9606.ENSP00000241052, 9606.ENSP00000275493	CAT, EGFR
GO:1903898	Negative regulation of perk-mediated unfolded protein response	2	5	2.4	0.003	9606.ENSP00000200453, 9606.ENSP00000360683	PPP1R15A, PTPN1
GO:1904044	Response to aldosterone	2	5	2.4	0.003	9606.ENSP00000261623, 9606.ENSP00000367851	CYBA, CYBB
GO:0050730	Regulation of peptidyl-tyrosine phosphorylation	5	258	1.09	0.0031	9606.ENSP00000263317, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000360683	NOX4, NRP1, EGFR, NCF1, PTPN1
GO:0045429	Positive regulation of nitric oxide biosynthetic process	3	44	1.63	0.0032	9606.ENSP00000248244, 9606.ENSP00000303830, 9606.ENSP00000363089	TICAM1, INSR, TLR4
GO:0016192	Vesicle-mediated transport	11	1805	0.59	0.0035	9606.ENSP00000241052, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000356505, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851, 9606.ENSP00000380334	CAT, RAC2, CYBA, FIGF, INSR, CD14, NCF2, TLR4, AGER, CYBB, NCF4
GO:0035272	Exocrine system development	3	46	1.61	0.0036	9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000303830	NRP1, EGFR, INSR
GO:0045927	Positive regulation of growth	5	267	1.07	0.0036	9606.ENSP00000261623, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000293328, 9606.ENSP00000303830	CYBA, NRP1, EGFR, STAT5B, INSR
GO:0050671	Positive regulation of lymphocyte proliferation	4	134	1.28	0.0036	9606.ENSP00000248244, 9606.ENSP00000293328, 9606.ENSP00000363089, 9606.ENSP00000364210	TICAM1, STAT5B, TLR4, AGER
GO:0071375	Cellular response to peptide hormone stimulus	5	269	1.07	0.0037	9606.ENSP00000261623, 9606.ENSP00000293328, 9606.ENSP00000303830, 9606.ENSP00000341208, 9606.ENSP00000360683	CYBA, STAT5B, INSR, STAT5A, PTPN1
GO:0014070	Response to organic cyclic compound	8	911	0.74	0.0038	9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000275493, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000367851	CAT, TICAM1, CYBA, NOX4, EGFR, S100B, STAT5B, CYBB
GO:0031347	Regulation of defense response	7	674	0.82	0.0042	9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000275493, 9606.ENSP00000293328, 9606.ENSP00000360683, 9606.ENSP00000363089, 9606.ENSP00000364210	TICAM1, CYBA, EGFR, STAT5B, PTPN1, TLR4, AGER
GO:0045321	Leukocyte activation	8	929	0.74	0.0043	9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000293328, 9606.ENSP00000304236, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	CAT, TICAM1, CYBA, STAT5B, CD14, TLR4, AGER, CYBB
GO:0051130	Positive regulation of cellular component organization	9	1209	0.67	0.0043	9606.ENSP00000200453, 9606.ENSP00000249071, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000362057, 9606.ENSP00000363089	PPP1R15A, RAC2, NOX4, KDR, NRP1, INSR, CD14, NOX1, TLR4

Table S11. the full list of KEGG analysis and GO analysis for NOX4

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0006810	Transport	17	4353	0.39	0.0044	9606.ENSP00000241052, 9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000265371, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000306275, 9606.ENSP00000341208, 9606.ENSP00000356505, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851, 9606.ENSP00000380334	CAT, RAC2, CYBA, NRP1, NCF1, STAT5B, FIGF, INSR, CD14, KCNK3, STAT5A, NCF2, NOX1, TLR4, AGER, CYBB, NCF4
GO:0050729	Positive regulation of inflammatory response	4	144	1.24	0.0046	9606.ENSP00000248244, 9606.ENSP00000275493, 9606.ENSP00000293328, 9606.ENSP00000363089	TICAM1, EGFR, STAT5B, TLR4
GO:0019530	Taurine metabolic process	2	7	2.26	0.0047	9606.ENSP00000293328, 9606.ENSP00000341208	STAT5B, STAT5A
GO:0060753	Regulation of mast cell chemotaxis	2	7	2.26	0.0047	9606.ENSP00000249071, 9606.ENSP00000297904	RAC2, FIGF
GO:0097190	Apoptotic signaling pathway	5	286	1.04	0.0047	9606.ENSP00000200453, 9606.ENSP00000248244, 9606.ENSP00000284818, 9606.ENSP00000304236, 9606.ENSP00000363089	PPP1R15A, TICAM1, LY96, CD14, TLR4
GO:0034284	Response to monosaccharide	4	148	1.23	0.0049	9606.ENSP00000241052, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000364210	CAT, CYBA, NOX4, AGER
GO:0042116	Macrophage activation	3	53	1.55	0.0049	9606.ENSP00000248244, 9606.ENSP00000363089, 9606.ENSP00000364210	TICAM1, TLR4, AGER
GO:0042981	Regulation of apoptotic process	10	1550	0.61	0.0049	9606.ENSP00000241052, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000327801, 9606.ENSP00000360683, 9606.ENSP00000362057	CAT, NOX4, KDR, NRP1, EGFR, S100B, STAT5B, P4HB, PTPN1, NOX1
GO:0050793	Regulation of developmental process	13	2648	0.49	0.0051	9606.ENSP00000249071, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000327801, 9606.ENSP00000341208, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	RAC2, KDR, NRP1, EGFR, S100B, STAT5B, FIGF, INSR, P4HB, STAT5A, TLR4, AGER, CYBB
GO:0006968	Cellular defense response	3	54	1.54	0.0052	9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000356505	LY96, NCF1, NCF2
GO:0050665	Hydrogen peroxide biosynthetic process	2	8	2.2	0.0056	9606.ENSP00000261623, 9606.ENSP00000367851	CYBA, CYBB
GO:0043536	Positive regulation of blood vessel endothelial cell migration	3	56	1.53	0.0057	9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000341208	KDR, NRP1, STAT5A
GO:0045931	Positive regulation of mitotic cell cycle	4	156	1.21	0.0058	9606.ENSP00000275493, 9606.ENSP00000293328, 9606.ENSP00000303830, 9606.ENSP00000475924	EGFR, STAT5B, INSR, POLDIP2
GO:0051092	Positive regulation of nf-kappab transcription factor activity	4	158	1.2	0.0061	9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000363089, 9606.ENSP00000364210	CAT, TICAM1, TLR4, AGER
GO:0002040	Sprouting angiogenesis	3	59	1.51	0.0064	9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000297904	KDR, NRP1, FIGF
GO:0038113	interleukin-9-mediated signaling pathway	2	9	2.15	0.0066	9606.ENSP00000293328, 9606.ENSP00000341208	STAT5B, STAT5A
GO:0071214	Cellular response to abiotic stimulus	5	313	1	0.0066	9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000275493, 9606.ENSP00000362057, 9606.ENSP00000363089	CYBA, NOX4, EGFR, NOX1, TLR4
GO:0031960	Response to corticosteroid	4	164	1.19	0.0068	9606.ENSP00000261623, 9606.ENSP00000275493, 9606.ENSP00000291700, 9606.ENSP00000367851	CYBA, EGFR, S100B, CYBB
GO:0032722	Positive regulation of chemokine production	3	61	1.49	0.0069	9606.ENSP00000248244, 9606.ENSP00000363089, 9606.ENSP00000364210	TICAM1, TLR4, AGER
GO:0045766	Positive regulation of angiogenesis	4	169	1.17	0.0075	9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000297904, 9606.ENSP00000367851	KDR, NRP1, FIGF, CYBB
GO:0051897	Positive regulation of protein kinase b signaling	4	170	1.17	0.0076	9606.ENSP00000249071, 9606.ENSP00000263317, 9606.ENSP00000275493, 9606.ENSP00000303830	RAC2, NOX4, EGFR, INSR
GO:0140052	Cellular response to oxidised low-density lipoprotein particle stimulus	2	10	2.1	0.0077	9606.ENSP00000248244, 9606.ENSP00000363089	TICAM1, TLR4
GO:0061098	Positive regulation of protein tyrosine kinase activity	3	66	1.46	0.0084	9606.ENSP00000263317, 9606.ENSP00000289473, 9606.ENSP00000360683	NOX4, NCF1, PTPN1
GO:1903201	Regulation of oxidative stress-induced cell death	3	67	1.45	0.0087	9606.ENSP00000327801, 9606.ENSP00000362057, 9606.ENSP00000363089	P4HB, NOX1, TLR4
GO:0038110	interleukin-2-mediated signaling pathway	2	11	2.06	0.0088	9606.ENSP00000293328, 9606.ENSP00000341208	STAT5B, STAT5A
GO:0071223	Cellular response to lipoteichoic acid	2	11	2.06	0.0088	9606.ENSP00000304236, 9606.ENSP00000363089	CD14, TLR4
GO:0071230	Cellular response to amino acid stimulus	3	69	1.44	0.0092	9606.ENSP00000261623, 9606.ENSP00000275493, 9606.ENSP00000367851	CYBA, EGFR, CYBB
GO:0060627	Regulation of vesicle-mediated transport	6	550	0.84	0.0095	9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000265371, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000360683	RAC2, CYBA, NRP1, INSR, CD14, PTPN1
GO:0071333	Cellular response to glucose stimulus	3	71	1.43	0.0099	9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000364210	CYBA, NOX4, AGER
GO:0002730	Regulation of dendritic cell cytokine production	2	12	2.02	0.01	9606.ENSP00000248244, 9606.ENSP00000363089	TICAM1, TLR4

Table S11. the full list of KEGG analysis and GO analysis for NOX4

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0050727	Regulation of inflammatory response	5	351	0.95	0.0101	9606.ENSP00000248244, 9606.ENSP00000275493, 9606.ENSP00000293328, 9606.ENSP00000363089, 9606.ENSP00000364210	TICAM1, EGFR, STAT5B, TLR4, AGER
GO:0051094	Positive regulation of developmental process	9	1389	0.61	0.0101	9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000327801, 9606.ENSP00000364210, 9606.ENSP00000367851	KDR, NRP1, S100B, STAT5B, FIGF, INSR, P4HB, AGER, CYBB
GO:0042593	Glucose homeostasis	4	188	1.13	0.0103	9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000303830, 9606.ENSP00000364210	CYBA, NOX4, INSR, AGER
GO:0071456	Cellular response to hypoxia	4	189	1.13	0.0105	9606.ENSP00000291700, 9606.ENSP00000306275, 9606.ENSP00000327801, 9606.ENSP00000367851	S100B, KCNK3, P4HB, CYBB
GO:0032870	Cellular response to hormone stimulus	6	569	0.82	0.0108	9606.ENSP00000261623, 9606.ENSP00000275493, 9606.ENSP00000293328, 9606.ENSP00000303830, 9606.ENSP00000341208, 9606.ENSP00000360683	CYBA, EGFR, STAT5B, INSR, STAT5A, PTPN1
GO:0035723	interleukin-15-mediated signaling pathway	2	13	1.99	0.0111	9606.ENSP00000293328, 9606.ENSP00000341208	STAT5B, STAT5A
GO:0071248	Cellular response to metal ion	4	193	1.12	0.0111	9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000306275, 9606.ENSP00000367851	EGFR, NCF1, KCNK3, CYBB
GO:0050731	Positive regulation of peptidyl-tyrosine phosphorylation	4	196	1.11	0.0115	9606.ENSP00000263317, 9606.ENSP00000265371, 9606.ENSP00000289473, 9606.ENSP00000360683	NOX4, NRP1, NCF1, PTPN1
GO:0031349	Positive regulation of defense response	5	367	0.93	0.0117	9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000275493, 9606.ENSP00000293328, 9606.ENSP00000363089	TICAM1, CYBA, EGFR, STAT5B, TLR4
GO:0051049	Regulation of transport	10	1776	0.55	0.0122	9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000367851	RAC2, CYBA, NRP1, EGFR, INSR, CD14, PTPN1, NOX1, TLR4, CYBB
GO:0048878	Chemical homeostasis	8	1124	0.65	0.0123	9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000275493, 9606.ENSP00000303830, 9606.ENSP00000306275, 9606.ENSP00000362057, 9606.ENSP00000364210	CYBA, NOX4, KDR, EGFR, INSR, KCNK3, NOX1, AGER
GO:0071260	Cellular response to mechanical stimulus	3	79	1.38	0.0123	9606.ENSP00000261623, 9606.ENSP00000275493, 9606.ENSP00000363089	CYBA, EGFR, TLR4
GO:0010468	Regulation of gene expression	17	4813	0.35	0.0127	9606.ENSP00000200453, 9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000263923, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000303830, 9606.ENSP00000304236, 9606.ENSP00000323148, 9606.ENSP00000341208, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	PPP1R15A, CAT, TICAM1, CYBA, KDR, EGFR, LY96, NCF1, STAT5B, INSR, CD14, ZKSCAN1, STAT5A, NOX1, TLR4, AGER, CYBB
GO:0032481	Positive regulation of type i interferon production	3	80	1.37	0.0127	9606.ENSP00000248244, 9606.ENSP00000304236, 9606.ENSP00000363089	TICAM1, CD14, TLR4
GO:0050930	Induction of positive chemotaxis	2	15	1.93	0.0135	9606.ENSP00000297904, 9606.ENSP00000364210	FIGF, AGER
GO:0010810	Regulation of cell-substrate adhesion	4	212	1.08	0.0148	9606.ENSP00000249071, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000327801	RAC2, KDR, NRP1, P4HB
GO:0050871	Positive regulation of b cell activation	3	85	1.35	0.0148	9606.ENSP00000248244, 9606.ENSP00000293328, 9606.ENSP00000363089	TICAM1, STAT5B, TLR4
GO:0051770	Positive regulation of nitric-oxide synthase biosynthetic process	2	16	1.9	0.015	9606.ENSP00000263923, 9606.ENSP00000363089	KDR, TLR4
GO:0072359	Circulatory system development	7	872	0.7	0.015	9606.ENSP00000222139, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000362057	EPOR, NOX4, KDR, NRP1, FIGF, INSR, NOX1
GO:0048661	Positive regulation of smooth muscle cell proliferation	3	88	1.33	0.0162	9606.ENSP00000261623, 9606.ENSP00000275493, 9606.ENSP00000362057	CYBA, EGFR, NOX1
GO:0002366	Leukocyte activation involved in immune response	6	626	0.78	0.0165	9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000304236, 9606.ENSP00000363089, 9606.ENSP00000367851	CAT, TICAM1, CYBA, CD14, TLR4, CYBB
GO:0048731	System development	16	4426	0.36	0.0165	9606.ENSP00000222139, 9606.ENSP00000241052, 9606.ENSP00000249071, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000306275, 9606.ENSP00000341208, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210	EPOR, CAT, RAC2, NOX4, KDR, NRP1, EGFR, S100B, STAT5B, FIGF, INSR, KCNK3, STAT5A, NOX1, TLR4, AGER
GO:1903209	Positive regulation of oxidative stress-induced cell death	2	17	1.87	0.0165	9606.ENSP00000362057, 9606.ENSP00000363089	NOX1, TLR4
GO:0002831	Regulation of response to biotic stimulus	5	406	0.89	0.017	9606.ENSP00000261623, 9606.ENSP00000284818, 9606.ENSP00000293328, 9606.ENSP00000360683, 9606.ENSP00000363089	CYBA, LY96, STAT5B, PTPN1, TLR4

Table S11. the full list of KEGG analysis and GO analysis for NOX4

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0002699	Positive regulation of immune effector process	4	223	1.05	0.0171	9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000293328, 9606.ENSP00000363089	TICAM1, RAC2, STAT5B, TLR4
GO:0048732	Gland development	5	410	0.89	0.0177	9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000293328, 9606.ENSP00000303830, 9606.ENSP00000341208	NRP1, EGFR, STAT5B, INSR, STAT5A
GO:0010557	Positive regulation of macromolecule biosynthetic process	10	1906	0.52	0.0196	9606.ENSP00000200453, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000303830, 9606.ENSP00000341208, 9606.ENSP00000362057, 9606.ENSP00000363089	PPP1R15A, NOX4, KDR, EGFR, NCF1, STAT5B, INSR, STAT5A, NOX1, TLR4
GO:0097305	Response to alcohol	4	233	1.03	0.0196	9606.ENSP00000241052, 9606.ENSP00000261623, 9606.ENSP00000304236, 9606.ENSP00000367851	CAT, CYBA, CD14, CYBB
GO:0045785	Positive regulation of cell adhesion	5	423	0.87	0.0199	9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000293328, 9606.ENSP00000327801, 9606.ENSP00000364210	KDR, NRP1, STAT5B, P4HB, AGER
GO:0032930	Positive regulation of superoxide anion generation	2	20	1.8	0.021	9606.ENSP00000261623, 9606.ENSP00000275493	CYBA, EGFR
GO:0048143	Astrocyte activation	2	20	1.8	0.021	9606.ENSP00000275493, 9606.ENSP00000364210	EGFR, AGER
GO:0061081	itive regulation of myeloid leukocyte cytokine production involved in immune respo	2	20	1.8	0.021	9606.ENSP00000248244, 9606.ENSP00000363089	TICAM1, TLR4
GO:0002042	Cell migration involved in sprouting angiogenesis	2	21	1.78	0.0227	9606.ENSP00000263923, 9606.ENSP00000265371	KDR, NRP1
GO:0032816	Positive regulation of natural killer cell activation	2	21	1.78	0.0227	9606.ENSP00000248244, 9606.ENSP00000293328	TICAM1, STAT5B
GO:0040008	Regulation of growth	6	676	0.75	0.0227	9606.ENSP00000261623, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000293328, 9606.ENSP00000303830, 9606.ENSP00000341208	CYBA, NRP1, EGFR, STAT5B, INSR, STAT5A
GO:0090050	Positive regulation of cell migration involved in sprouting angiogenesis	2	21	1.78	0.0227	9606.ENSP00000263923, 9606.ENSP00000265371	KDR, NRP1
GO:1900017	Positive regulation of cytokine production involved in inflammatory response	2	21	1.78	0.0227	9606.ENSP00000248244, 9606.ENSP00000363089	TICAM1, TLR4
GO:0002833	Positive regulation of response to biotic stimulus	4	247	1.01	0.0234	9606.ENSP00000261623, 9606.ENSP00000284818, 9606.ENSP00000293328, 9606.ENSP00000363089	CYBA, LY96, STAT5B, TLR4
GO:0003081	Regulation of systemic arterial blood pressure by renin-angiotensin	2	22	1.76	0.0241	9606.ENSP00000261623, 9606.ENSP00000362057	CYBA, NOX1
GO:0009968	Negative regulation of signal transduction	8	1271	0.6	0.0241	9606.ENSP00000200453, 9606.ENSP00000248244, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000304236, 9606.ENSP00000360683, 9606.ENSP00000363089	PPP1R15A, TICAM1, NRP1, EGFR, LY96, CD14, PTPN1, TLR4
GO:0055093	Response to hyperoxia	2	22	1.76	0.0241	9606.ENSP00000241052, 9606.ENSP00000362057	CAT, NOX1
GO:0045453	Bone resorption	2	23	1.74	0.026	9606.ENSP00000249071, 9606.ENSP00000263317	RAC2, NOX4
GO:0048585	Negative regulation of response to stimulus	9	1636	0.54	0.0269	9606.ENSP00000200453, 9606.ENSP00000248244, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000304236, 9606.ENSP00000360683, 9606.ENSP00000363089, 9606.ENSP00000364210	PPP1R15A, TICAM1, NRP1, EGFR, LY96, CD14, PTPN1, TLR4, AGER
GO:0007611	Learning or memory	4	259	0.99	0.0271	9606.ENSP00000275493, 9606.ENSP00000291700, 9606.ENSP00000303830, 9606.ENSP00000364210	EGFR, S100B, INSR, AGER
GO:0007417	Central nervous system development	7	988	0.65	0.0276	9606.ENSP00000222139, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000291700, 9606.ENSP00000306275, 9606.ENSP00000363089, 9606.ENSP00000364210	EPOR, NRP1, EGFR, S100B, KCNK3, TLR4, AGER
GO:0042104	Positive regulation of activated t cell proliferation	2	24	1.72	0.0276	9606.ENSP00000293328, 9606.ENSP00000364210	STAT5B, AGER
GO:0030155	Regulation of cell adhesion	6	712	0.73	0.0284	9606.ENSP00000249071, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000293328, 9606.ENSP00000327801, 9606.ENSP00000364210	RAC2, KDR, NRP1, STAT5B, P4HB, AGER
GO:0051894	Positive regulation of focal adhesion assembly	2	25	1.7	0.0294	9606.ENSP00000263923, 9606.ENSP00000265371	KDR, NRP1
GO:0009889	Regulation of biosynthetic process	15	4210	0.35	0.0296	9606.ENSP00000200453, 9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000303830, 9606.ENSP00000323148, 9606.ENSP00000341208, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210	PPP1R15A, CAT, TICAM1, CYBA, NOX4, KDR, EGFR, NCF1, STAT5B, INSR, ZKSCAN1, STAT5A, NOX1, TLR4, AGER
GO:0051781	Positive regulation of cell division	3	117	1.21	0.0312	9606.ENSP00000241052, 9606.ENSP00000297904, 9606.ENSP00000303830	CAT, FIGF, INSR
GO:1900745	Positive regulation of p38mapk cascade	2	26	1.69	0.0312	9606.ENSP00000289473, 9606.ENSP00000364210	NCF1, AGER
GO:0044237	Cellular metabolic process	21	7513	0.25	0.0314	9606.ENSP00000200453, 9606.ENSP00000241052, 9606.ENSP00000261623, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000303830, 9606.ENSP00000327801, 9606.ENSP00000341208, 9606.ENSP00000342848, 9606.ENSP00000356505, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000367851, 9606.ENSP00000380334, 9606.ENSP00000380450, 9606.ENSP00000475924	PPP1R15A, CAT, CYBA, NOX4, KDR, NRP1, EGFR, NCF1, STAT5B, INSR, P4HB, STAT5A, NOXA1, NCF2, PTPN1, NOX1, TLR4, CYBB, NCF4, NOXO1, POLDIP2
GO:1902175	Regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	2	27	1.67	0.0333	9606.ENSP00000327801, 9606.ENSP00000362057	P4HB, NOX1

Table S11. the full list of KEGG analysis and GO analysis for NOX4

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:1990776	Response to angiotensin	2	27	1.67	0.0333	9606.ENSP00000261623, 9606.ENSP00000367851	CYBA, CYBB
GO:0051171	Regulation of nitrogen compound metabolic process	18	5836	0.29	0.0349	9606.ENSP00000200453, 9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000323148, 9606.ENSP00000341208, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210	PPP1R15A, CAT, TICAM1, RAC2, NOX4, KDR, NRP1, EGFR, NCF1, STAT5B, FIGF, INSR, ZKSCAN1, STAT5A, PTPN1, NOX1, TLR4, AGER
GO:0035556	Intracellular signal transduction	9	1712	0.52	0.0353	9606.ENSP00000200453, 9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000263923, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000304236, 9606.ENSP00000360683, 9606.ENSP00000363089	PPP1R15A, TICAM1, RAC2, KDR, EGFR, LY96, CD14, PTPN1, TLR4
GO:0045471	Response to ethanol	3	123	1.19	0.0353	9606.ENSP00000241052, 9606.ENSP00000304236, 9606.ENSP00000367851	CAT, CD14, CYBB
GO:0010811	Positive regulation of cell-substrate adhesion	3	124	1.18	0.0358	9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000327801	KDR, NRP1, P4HB
GO:0022604	Regulation of cell morphogenesis	5	498	0.8	0.0363	9606.ENSP00000249071, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000291700, 9606.ENSP00000327801	RAC2, KDR, NRP1, S100B, P4HB
GO:2000026	Regulation of multicellular organismal development	10	2096	0.48	0.0363	9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000367851	KDR, NRP1, EGFR, S100B, STAT5B, FIGF, INSR, TLR4, AGER, CYBB
GO:0001569	Branching involved in blood vessel morphogenesis	2	29	1.64	0.037	9606.ENSP00000263923, 9606.ENSP00000265371	KDR, NRP1
GO:0007435	Salivary gland morphogenesis	2	30	1.62	0.0389	9606.ENSP00000265371, 9606.ENSP00000275493	NRP1, EGFR
GO:0038111	interleukin-7-mediated signaling pathway	2	30	1.62	0.0389	9606.ENSP00000293328, 9606.ENSP00000341208	STAT5B, STAT5A
GO:0071480	Cellular response to gamma radiation	2	31	1.61	0.0409	9606.ENSP00000261623, 9606.ENSP00000263317	CYBA, NOX4
GO:0048856	Anatomical structure development	17	5402	0.3	0.0419	9606.ENSP00000222139, 9606.ENSP00000241052, 9606.ENSP00000249071, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000291700, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000306275, 9606.ENSP00000341208, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210, 9606.ENSP00000475924	EPOR, CAT, RAC2, NOX4, KDR, NRP1, EGFR, S100B, STAT5B, FIGF, INSR, KCNK3, STAT5A, NOX1, TLR4, AGER, POLDIP2
GO:0002275	Myeloid cell activation involved in immune response	5	522	0.78	0.043	9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000304236, 9606.ENSP00000367851	CAT, TICAM1, CYBA, CD14, CYBB
GO:0032990	Cell part morphogenesis	5	525	0.78	0.0436	9606.ENSP00000249071, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000291700, 9606.ENSP00000475924	RAC2, NRP1, EGFR, S100B, POLDIP2
GO:0009653	Anatomical structure morphogenesis	10	2165	0.46	0.044	9606.ENSP00000249071, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000291700, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000362057, 9606.ENSP00000475924	RAC2, NOX4, KDR, NRP1, EGFR, S100B, FIGF, INSR, NOX1, POLDIP2
GO:0071396	Cellular response to lipid	5	528	0.78	0.0444	9606.ENSP00000248244, 9606.ENSP00000275493, 9606.ENSP00000284818, 9606.ENSP00000304236, 9606.ENSP00000363089	TICAM1, EGFR, LY96, CD14, TLR4
GO:0022603	Regulation of anatomical structure morphogenesis	7	1095	0.61	0.0447	9606.ENSP00000249071, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000291700, 9606.ENSP00000297904, 9606.ENSP00000327801, 9606.ENSP00000367851	RAC2, KDR, NRP1, S100B, FIGF, P4HB, CYBB
GO:0046903	Secretion	7	1097	0.61	0.0449	9606.ENSP00000241052, 9606.ENSP00000261623, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000304236, 9606.ENSP00000341208, 9606.ENSP00000367851	CAT, CYBA, STAT5B, FIGF, CD14, STAT5A, CYBB
GO:0034097	Response to cytokine	7	1101	0.6	0.0457	9606.ENSP00000222139, 9606.ENSP00000261623, 9606.ENSP00000293328, 9606.ENSP00000304236, 9606.ENSP00000327801, 9606.ENSP00000341208, 9606.ENSP00000363089	EPOR, CYBA, STAT5B, CD14, P4HB, STAT5A, TLR4
GO:0008045	Motor neuron axon guidance	2	34	1.57	0.0467	9606.ENSP00000249071, 9606.ENSP00000265371	RAC2, NRP1
GO:0032728	Positive regulation of interferon-beta production	2	34	1.57	0.0467	9606.ENSP00000248244, 9606.ENSP00000363089	TICAM1, TLR4
GO:0001525	Angiogenesis	4	315	0.9	0.048	9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000297904, 9606.ENSP00000362057	KDR, NRP1, FIGF, NOX1
GO:0032355	Response to estradiol	3	142	1.12	0.048	9606.ENSP00000241052, 9606.ENSP00000275493, 9606.ENSP00000293328	CAT, EGFR, STAT5B

Table S11. the full list of KEGG analysis and GO analysis for NOX4

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0080090	Regulation of primary metabolic process	18	6032	0.27	0.0481	9606.ENSP00000200453, 9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000323148, 9606.ENSP00000341208, 9606.ENSP00000360683, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210	PPP1R15A, CAT, TICAM1, RAC2, NOX4, KDR, NRP1, EGFR, NCF1, STAT5B, FIGF, INSR, ZKSCAN1, STAT5A, PTPN1, NOX1, TLR4, AGER
GO:0044089	Positive regulation of cellular component biogenesis	5	542	0.77	0.0482	9606.ENSP00000249071, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000265371, 9606.ENSP00000363089	RAC2, NOX4, KDR, NRP1, TLR4
GO:0002687	Positive regulation of leukocyte migration	3	144	1.12	0.0492	9606.ENSP00000249071, 9606.ENSP00000297904, 9606.ENSP00000364210	RAC2, FIGF, AGER
GO:0010556	Regulation of macromolecule biosynthetic process	14	3976	0.35	0.0492	9606.ENSP00000200453, 9606.ENSP00000241052, 9606.ENSP00000248244, 9606.ENSP00000263317, 9606.ENSP00000263923, 9606.ENSP00000275493, 9606.ENSP00000289473, 9606.ENSP00000293328, 9606.ENSP00000303830, 9606.ENSP00000323148, 9606.ENSP00000341208, 9606.ENSP00000362057, 9606.ENSP00000363089, 9606.ENSP00000364210	PPP1R15A, CAT, TICAM1, NOX4, KDR, EGFR, NCF1, STAT5B, INSR, ZKSCAN1, STAT5A, NOX1, TLR4, AGER
hsa04933	AGE-RAGE signaling pathway in diabetic complications	7	98	1.65	8.23E-08	9606.ENSP00000263317, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000341208, 9606.ENSP00000362057, 9606.ENSP00000364210, 9606.ENSP00000367851	NOX4, STAT5B, FIGF, STAT5A, NOX1, AGER, CYBB
hsa05140	Leishmaniasis	6	70	1.73	3.19E-07	9606.ENSP00000261623, 9606.ENSP00000289473, 9606.ENSP00000356505, 9606.ENSP00000363089, 9606.ENSP00000367851, 9606.ENSP00000380334	CYBA, NCF1, NCF2, TLR4, CYBB, NCF4
hsa04145	Phagosome	7	142	1.49	3.22E-07	9606.ENSP00000261623, 9606.ENSP00000289473, 9606.ENSP00000304236, 9606.ENSP00000356505, 9606.ENSP00000363089, 9606.ENSP00000367851, 9606.ENSP00000380334	CYBA, NCF1, CD14, NCF2, TLR4, CYBB, NCF4
hsa04670	Leukocyte transendothelial migration	6	109	1.54	1.96E-06	9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000289473, 9606.ENSP00000356505, 9606.ENSP00000367851, 9606.ENSP00000380334	RAC2, CYBA, NCF1, NCF2, CYBB, NCF4
hsa05418	Fluid shear stress and atherosclerosis	6	130	1.46	4.29E-06	9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000263923, 9606.ENSP00000289473, 9606.ENSP00000356505, 9606.ENSP00000362057	RAC2, CYBA, KDR, NCF1, NCF2, NOX1
hsa04380	Osteoclast differentiation	5	122	1.41	8.78E-05	9606.ENSP00000261623, 9606.ENSP00000289473, 9606.ENSP00000356505, 9606.ENSP00000362057, 9606.ENSP00000380334	CYBA, NCF1, NCF2, NOX1, NCF4
hsa04217	Necroptosis	5	149	1.33	0.00017	9606.ENSP00000248244, 9606.ENSP00000293328, 9606.ENSP00000341208, 9606.ENSP00000363089, 9606.ENSP00000367851	TICAM1, STAT5B, STAT5A, TLR4, CYBB
hsa04520	Adherens junction	4	67	1.58	0.00017	9606.ENSP00000249071, 9606.ENSP00000275493, 9606.ENSP00000303830, 9606.ENSP00000360683	RAC2, EGFR, INSR, PTPN1
hsa05020	Prion disease	6	265	1.16	0.00017	9606.ENSP00000249071, 9606.ENSP00000261623, 9606.ENSP00000289473, 9606.ENSP00000356505, 9606.ENSP00000367851, 9606.ENSP00000380334	RAC2, CYBA, NCF1, NCF2, CYBB, NCF4
hsa04010	MAPK signaling pathway	6	288	1.12	0.0002	9606.ENSP00000249071, 9606.ENSP00000263923, 9606.ENSP00000275493, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000304236	RAC2, KDR, EGFR, FIGF, INSR, CD14
hsa05133	Pertussis	4	74	1.53	0.00021	9606.ENSP00000248244, 9606.ENSP00000284818, 9606.ENSP00000304236, 9606.ENSP00000363089	TICAM1, LY96, CD14, TLR4
hsa04015	Rap1 signaling pathway	5	202	1.19	0.00048	9606.ENSP00000249071, 9606.ENSP00000263923, 9606.ENSP00000275493, 9606.ENSP00000297904, 9606.ENSP00000303830	RAC2, KDR, EGFR, FIGF, INSR
hsa04151	PI3K-Akt signaling pathway	6	350	1.03	0.00048	9606.ENSP00000222139, 9606.ENSP00000263923, 9606.ENSP00000275493, 9606.ENSP00000297904, 9606.ENSP00000303830, 9606.ENSP00000363089	EPOR, KDR, EGFR, FIGF, INSR, TLR4
hsa04064	NF-kappa B signaling pathway	4	101	1.4	0.00053	9606.ENSP00000248244, 9606.ENSP00000284818, 9606.ENSP00000304236, 9606.ENSP00000363089	TICAM1, LY96, CD14, TLR4
hsa04620	Toll-like receptor signaling pathway	4	101	1.4	0.00053	9606.ENSP00000248244, 9606.ENSP00000284818, 9606.ENSP00000304236, 9606.ENSP00000363089	TICAM1, LY96, CD14, TLR4
hsa04066	HIF-1 signaling pathway	4	106	1.38	0.00055	9606.ENSP00000275493, 9606.ENSP00000303830, 9606.ENSP00000363089, 9606.ENSP00000367851	EGFR, INSR, TLR4, CYBB
hsa04014	Ras signaling pathway	5	226	1.15	0.00057	9606.ENSP00000249071, 9606.ENSP00000263923, 9606.ENSP00000275493, 9606.ENSP00000297904, 9606.ENSP00000303830	RAC2, KDR, EGFR, FIGF, INSR
hsa04630	JAK-STAT signaling pathway	4	160	1.2	0.0023	9606.ENSP00000222139, 9606.ENSP00000275493, 9606.ENSP00000293328, 9606.ENSP00000341208	EPOR, EGFR, STAT5B, STAT5A

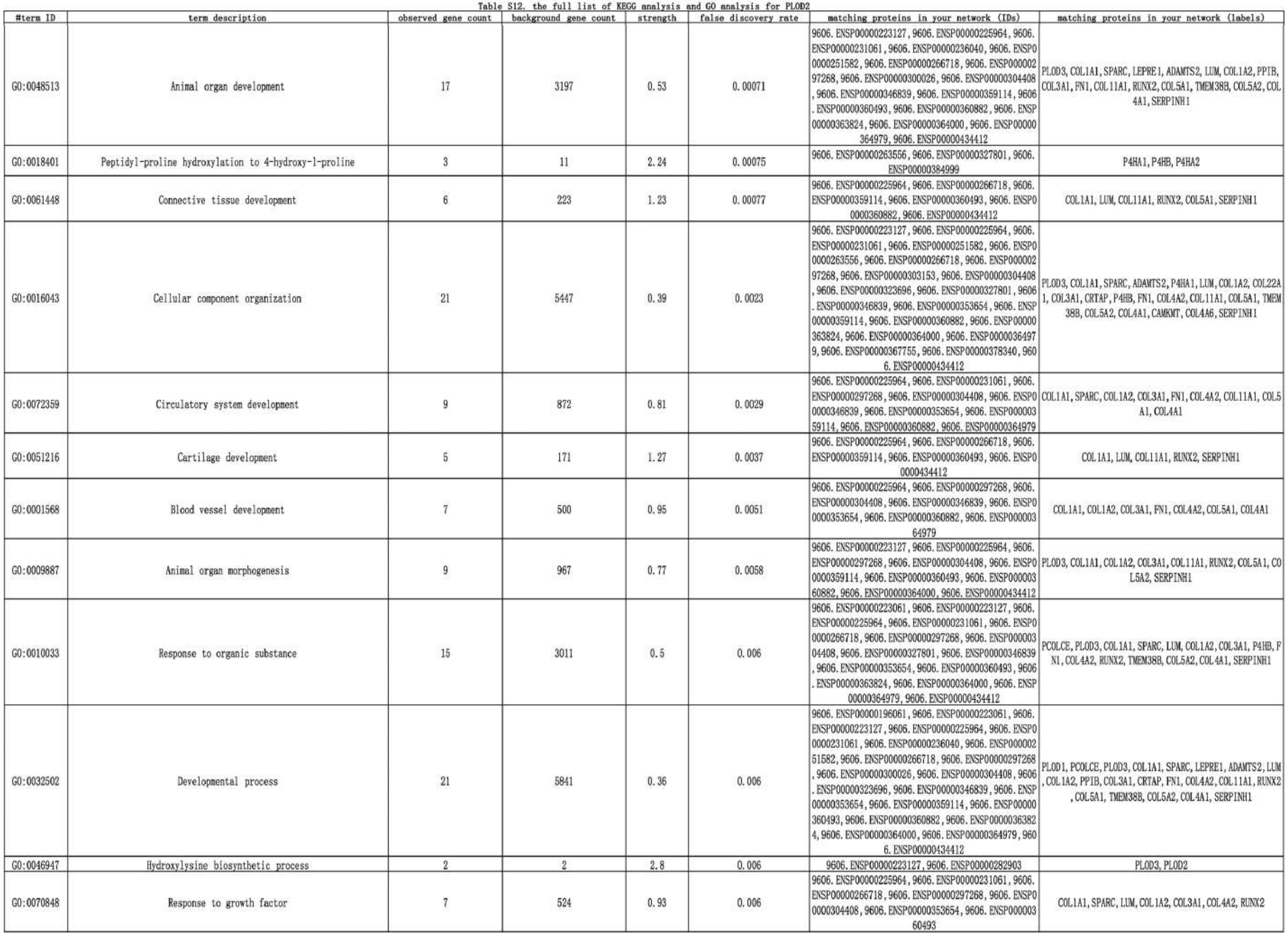
Table S11. the full list of KEGG analysis and GO analysis for NOX4

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
hsa05161	Hepatitis B	4	159	1.2	0.0023	9606.ENSP00000248244, 9606.ENSP00000293328, 9606.ENSP00000341208, 9606.ENSP00000363089	TICAM1, STAT5B, STAT5A, TLR4
hsa05200	Pathways in cancer	6	517	0.86	0.0025	9606.ENSP00000222139, 9606.ENSP00000249071, 9606.ENSP00000275493, 9606.ENSP00000293328, 9606.ENSP00000297904, 9606.ENSP00000341208	EPOR, RAC2, EGFR, STAT5B, FIGF, STAT5A
hsa04621	NOD-like receptor signaling pathway	4	174	1.16	0.0027	9606.ENSP00000248244, 9606.ENSP00000261623, 9606.ENSP00000363089, 9606.ENSP00000367851	TICAM1, CYBA, TLR4, CYBB
hsa05221	Acute myeloid leukemia	3	66	1.46	0.0027	9606.ENSP00000293328, 9606.ENSP00000304236, 9606.ENSP00000341208	STAT5B, CD14, STAT5A
hsa05223	Non-small cell lung cancer	3	68	1.44	0.0028	9606.ENSP00000275493, 9606.ENSP00000293328, 9606.ENSP00000341208	EGFR, STAT5B, STAT5A
hsa05010	Alzheimer disease	5	355	0.95	0.0033	9606.ENSP00000263317, 9606.ENSP00000303830, 9606.ENSP00000362057, 9606.ENSP00000364210, 9606.ENSP00000367851	NOX4, INSR, NOX1, AGER, CYBB
hsa04510	Focal adhesion	4	198	1.11	0.0037	9606.ENSP00000249071, 9606.ENSP00000263923, 9606.ENSP00000275493, 9606.ENSP00000297904	RAC2, KDR, EGFR, FIGF
hsa04012	ErbB signaling pathway	3	83	1.36	0.0043	9606.ENSP00000275493, 9606.ENSP00000293328, 9606.ENSP00000341208	EGFR, STAT5B, STAT5A
hsa05235	PD-L1 expression and PD-1 checkpoint pathway in cancer	3	88	1.33	0.0049	9606.ENSP00000248244, 9606.ENSP00000275493, 9606.ENSP00000363089	TICAM1, EGFR, TLR4
hsa05135	Yersinia infection	3	125	1.18	0.0128	9606.ENSP00000248244, 9606.ENSP00000249071, 9606.ENSP00000363089	TICAM1, RAC2, TLR4
hsa04068	FoxO signaling pathway	3	127	1.17	0.013	9606.ENSP00000241052, 9606.ENSP00000275493, 9606.ENSP00000303830	CAT, EGFR, INSR
hsa05162	Measles	3	138	1.14	0.0158	9606.ENSP00000293328, 9606.ENSP00000341208, 9606.ENSP00000363089	STAT5B, STAT5A, TLR4
hsa04062	Chemokine signaling pathway	3	186	1.01	0.0353	9606.ENSP00000249071, 9606.ENSP00000289473, 9606.ENSP00000293328	RAC2, NCF1, STAT5B
hsa05134	Legionellosis	2	55	1.36	0.0384	9606.ENSP00000304236, 9606.ENSP00000363089	CD14, TLR4
hsa05205	Proteoglycans in cancer	3	196	0.99	0.0384	9606.ENSP00000263923, 9606.ENSP00000275493, 9606.ENSP00000363089	KDR, EGFR, TLR4
hsa04370	VEGF signaling pathway	2	57	1.35	0.0387	9606.ENSP00000249071, 9606.ENSP00000263923	RAC2, KDR
hsa04213	Longevity regulating pathway - multiple species	2	61	1.32	0.0428	9606.ENSP00000241052, 9606.ENSP00000303830	CAT, INSR
hsa05132	Salmonella infection	3	209	0.96	0.0428	9606.ENSP00000284818, 9606.ENSP00000304236, 9606.ENSP00000363089	LY96, CD14, TLR4
hsa05166	Human T-cell leukemia virus 1 infection	3	211	0.95	0.0428	9606.ENSP00000265371, 9606.ENSP00000293328, 9606.ENSP00000341208	NRP1, STAT5B, STAT5A
hsa05131	Shigellosis	3	218	0.94	0.0446	9606.ENSP00000275493, 9606.ENSP00000304236, 9606.ENSP00000363089	EGFR, CD14, TLR4
hsa04917	Prolactin signaling pathway	2	69	1.26	0.0484	9606.ENSP00000293328, 9606.ENSP00000341208	STAT5B, STAT5A

Table S12. the full list of KEGG analysis and GO analysis for PLOD2

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0030198	Extracellular matrix organization	19	338	1.55	8.19E-22	9606.ENSP00000223127, 9606.ENSP00000225964, 9606.ENSP00000231061, 9606.ENSP00000251582, 9606.ENSP00000263556, 9606.ENSP00000266718, 9606.ENSP00000297268, 9606.ENSP00000303153, 9606.ENSP00000304408, 9606.ENSP00000323696, 9606.ENSP00000346839, 9606.ENSP00000353654, 9606.ENSP00000359114, 9606.ENSP00000360882, 9606.ENSP00000363824, 9606.ENSP00000364000, 9606.ENSP00000364979, 9606.ENSP00000378340, 9606.ENSP00000434412	PLOD3, COL1A1, SPARC, ADAMTS2, P4HA1, LUM, COL1A2, COL22A1, COL3A1, CRTAP, FN1, COL4A2, COL11A1, COL5A1, TMEM38B, COL5A2, COL4A1, COL4A6, SERPINH1
GO:0030199	Collagen fibril organization	12	46	2.22	7.75E-20	9606.ENSP00000223127, 9606.ENSP00000225964, 9606.ENSP00000251582, 9606.ENSP00000263556, 9606.ENSP00000266718, 9606.ENSP00000297268, 9606.ENSP00000304408, 9606.ENSP00000323696, 9606.ENSP00000359114, 9606.ENSP00000360882, 9606.ENSP00000364000, 9606.ENSP00000434412	PLOD3, COL1A1, ADAMTS2, P4HA1, LUM, COL1A2, COL3A1, CRTAP, COL11A1, COL5A1, COL5A2, SERPINH1
GO:0018126	Protein hydroxylation	8	27	2.27	1.08E-12	9606.ENSP00000196061, 9606.ENSP00000223127, 9606.ENSP00000236040, 9606.ENSP00000263556, 9606.ENSP00000282903, 9606.ENSP00000323696, 9606.ENSP00000327801, 9606.ENSP00000384999	PLOD1, PLOD3, LEPRE1, P4HA1, PLOD2, CRTAP, P4HB, P4HA2
GO:0001501	Skeletal system development	12	499	1.18	1.67E-08	9606.ENSP00000225964, 9606.ENSP00000231061, 9606.ENSP00000236040, 9606.ENSP00000266718, 9606.ENSP00000297268, 9606.ENSP00000300026, 9606.ENSP00000304408, 9606.ENSP00000359114, 9606.ENSP00000360493, 9606.ENSP00000363824, 9606.ENSP00000364000, 9606.ENSP00000434412	COL1A1, SPARC, LEPRE1, LUM, COL1A2, PPIB, COL3A1, COL11A1, RUNX2, TMEM38B, COL5A2, SERPINH1
GO:0018208	Peptidyl-proline modification	7	60	1.87	1.79E-08	9606.ENSP00000236040, 9606.ENSP00000263556, 9606.ENSP00000300026, 9606.ENSP00000317232, 9606.ENSP00000323696, 9606.ENSP00000327801, 9606.ENSP00000384999	LEPRE1, P4HA1, PPIB, FKBP10, CRTAP, P4HB, P4HA2
GO:0032963	Collagen metabolic process	7	63	1.85	2.15E-08	9606.ENSP00000223127, 9606.ENSP00000225964, 9606.ENSP00000236040, 9606.ENSP00000251582, 9606.ENSP00000297268, 9606.ENSP00000360882, 9606.ENSP00000434412	PLOD3, COL1A1, LEPRE1, ADAMTS2, COL1A2, COL5A1, SERPINH1
GO:0019511	Peptidyl-proline hydroxylation	5	16	2.29	2.01E-07	9606.ENSP00000236040, 9606.ENSP00000263556, 9606.ENSP00000323696, 9606.ENSP00000327801, 9606.ENSP00000384999	LEPRE1, P4HA1, CRTAP, P4HB, P4HA2
GO:0038063	Collagen-activated tyrosine kinase receptor signaling pathway	4	11	2.36	8.87E-06	9606.ENSP00000225964, 9606.ENSP00000353654, 9606.ENSP00000364979, 9606.ENSP00000378340	COL1A1, COL4A2, COL4A1, COL4A6
GO:0060348	Bone development	7	199	1.35	2.91E-05	9606.ENSP00000225964, 9606.ENSP00000231061, 9606.ENSP00000236040, 9606.ENSP00000300026, 9606.ENSP00000360493, 9606.ENSP00000363824, 9606.ENSP00000434412	COL1A1, SPARC, LEPRE1, PPIB, RUNX2, TMEM38B, SERPINH1
GO:0018193	Peptidyl-amino acid modification	11	867	0.9	5.04E-05	9606.ENSP00000196061, 9606.ENSP00000223127, 9606.ENSP00000236040, 9606.ENSP00000263556, 9606.ENSP00000282903, 9606.ENSP00000300026, 9606.ENSP00000317232, 9606.ENSP00000323696, 9606.ENSP00000327801, 9606.ENSP00000367755, 9606.ENSP00000384999	PLOD1, PLOD3, LEPRE1, P4HA1, PLOD2, PPIB, FKBP10, CRTAP, P4HB, CAMKMT, P4HA2
GO:0071230	Cellular response to amino acid stimulus	5	69	1.66	9.67E-05	9606.ENSP00000225964, 9606.ENSP00000297268, 9606.ENSP00000304408, 9606.ENSP00000364000, 9606.ENSP00000364979	COL1A1, COL1A2, COL3A1, COL5A2, COL4A1
GO:0009888	Tissue development	14	1760	0.7	0.00012	9606.ENSP00000196061, 9606.ENSP00000223127, 9606.ENSP00000225964, 9606.ENSP00000266718, 9606.ENSP00000297268, 9606.ENSP00000304408, 9606.ENSP00000346839, 9606.ENSP00000353654, 9606.ENSP00000359114, 9606.ENSP00000360493, 9606.ENSP00000360882, 9606.ENSP00000363824, 9606.ENSP00000364979, 9606.ENSP00000434412	PLOD1, PLOD3, COL1A1, LUM, COL1A2, COL3A1, FN1, COL4A2, COL11A1, RUNX2, COL5A1, TMEM38B, COL4A1, SERPINH1
GO:0001503	Ossification	7	265	1.22	0.00014	9606.ENSP00000225964, 9606.ENSP00000231061, 9606.ENSP00000297268, 9606.ENSP00000359114, 9606.ENSP00000360493, 9606.ENSP00000363824, 9606.ENSP00000364000	COL1A1, SPARC, COL1A2, COL11A1, RUNX2, TMEM38B, COL5A2
GO:0017185	Peptidyl-lysine hydroxylation	3	8	2.37	0.00042	9606.ENSP00000196061, 9606.ENSP00000223127, 9606.ENSP00000282903	PLOD1, PLOD3, PLOD2
GO:0032964	Collagen biosynthetic process	3	9	2.32	0.00053	9606.ENSP00000225964, 9606.ENSP00000360882, 9606.ENSP00000434412	COL1A1, COL5A1, SERPINH1

Table S12. the full list of KEGG analysis and GO analysis for PLOD2



#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0048513	Animal organ development	17	3197	0.53	0.00071	9606.ENSP00000223127, 9606.ENSP00000225964, 9606.ENSP00000231061, 9606.ENSP00000236040, 9606.ENSP00000251582, 9606.ENSP00000266718, 9606.ENSP00000297268, 9606.ENSP00000300026, 9606.ENSP00000304408, 9606.ENSP00000346839, 9606.ENSP00000359114, 9606.ENSP00000360493, 9606.ENSP00000360882, 9606.ENSP00000363824, 9606.ENSP00000364000, 9606.ENSP00000364979, 9606.ENSP00000434412	PLOD3, COL1A1, SPARC, LEPRE1, ADAMTS2, LUM, COL1A2, PPIB, COL3A1, FN1, COL11A1, RUNX2, COL5A1, TMEM38B, COL5A2, COL4A1, SERPINH1
GO:0018401	Peptidyl-proline hydroxylation to 4-hydroxy-l-proline	3	11	2.24	0.00075	9606.ENSP00000263556, 9606.ENSP00000327801, 9606.ENSP00000384999	P4HA1, P4HB, P4HA2
GO:0061448	Connective tissue development	6	223	1.23	0.00077	9606.ENSP00000225964, 9606.ENSP00000266718, 9606.ENSP00000359114, 9606.ENSP00000360493, 9606.ENSP00000360882, 9606.ENSP00000434412	COL1A1, LUM, COL11A1, RUNX2, COL5A1, SERPINH1
GO:0016043	Cellular component organization	21	5447	0.39	0.0023	9606.ENSP00000223127, 9606.ENSP00000225964, 9606.ENSP00000231061, 9606.ENSP00000251582, 9606.ENSP00000263556, 9606.ENSP00000266718, 9606.ENSP00000297268, 9606.ENSP00000303153, 9606.ENSP00000304408, 9606.ENSP00000323696, 9606.ENSP00000327801, 9606.ENSP00000346839, 9606.ENSP00000353654, 9606.ENSP00000359114, 9606.ENSP00000360882, 9606.ENSP00000363824, 9606.ENSP00000364000, 9606.ENSP00000364979, 9606.ENSP00000367755, 9606.ENSP00000378340, 9606.ENSP00000434412	PLOD3, COL1A1, SPARC, ADAMTS2, P4HA1, LUM, COL1A2, COL22A1, COL3A1, CRTAP, P4HB, FN1, COL4A2, COL11A1, COL5A1, TMEM38B, COL5A2, COL4A1, CAMKMT, COL4A6, SERPINH1
GO:0072359	Circulatory system development	9	872	0.81	0.0029	9606.ENSP00000225964, 9606.ENSP00000231061, 9606.ENSP00000297268, 9606.ENSP00000304408, 9606.ENSP00000346839, 9606.ENSP00000353654, 9606.ENSP00000359114, 9606.ENSP00000360882, 9606.ENSP00000364979	COL1A1, SPARC, COL1A2, COL3A1, FN1, COL4A2, COL11A1, COL5A1, COL4A1
GO:0051216	Cartilage development	5	171	1.27	0.0037	9606.ENSP00000225964, 9606.ENSP00000266718, 9606.ENSP00000359114, 9606.ENSP00000360493, 9606.ENSP00000434412	COL1A1, LUM, COL11A1, RUNX2, SERPINH1
GO:0001568	Blood vessel development	7	500	0.95	0.0051	9606.ENSP00000225964, 9606.ENSP00000297268, 9606.ENSP00000304408, 9606.ENSP00000346839, 9606.ENSP00000353654, 9606.ENSP00000360882, 9606.ENSP00000364979	COL1A1, COL1A2, COL3A1, FN1, COL4A2, COL5A1, COL4A1
GO:0009887	Animal organ morphogenesis	9	967	0.77	0.0058	9606.ENSP00000223127, 9606.ENSP00000225964, 9606.ENSP00000297268, 9606.ENSP00000304408, 9606.ENSP00000359114, 9606.ENSP00000360493, 9606.ENSP00000360882, 9606.ENSP00000364000, 9606.ENSP00000434412	PLOD3, COL1A1, COL1A2, COL3A1, COL11A1, RUNX2, COL5A1, COL5A2, SERPINH1
GO:0010033	Response to organic substance	15	3011	0.5	0.006	9606.ENSP00000223061, 9606.ENSP00000223127, 9606.ENSP00000225964, 9606.ENSP00000231061, 9606.ENSP00000266718, 9606.ENSP00000297268, 9606.ENSP00000304408, 9606.ENSP00000327801, 9606.ENSP00000346839, 9606.ENSP00000353654, 9606.ENSP00000360493, 9606.ENSP00000363824, 9606.ENSP00000364000, 9606.ENSP00000364979, 9606.ENSP00000434412	PCOLCE, PLOD3, COL1A1, SPARC, LUM, COL1A2, COL3A1, P4HB, FN1, COL4A2, RUNX2, TMEM38B, COL5A2, COL4A1, SERPINH1
GO:0032502	Developmental process	21	5841	0.36	0.006	9606.ENSP00000196061, 9606.ENSP00000223061, 9606.ENSP00000223127, 9606.ENSP00000225964, 9606.ENSP00000231061, 9606.ENSP00000236040, 9606.ENSP00000251582, 9606.ENSP00000266718, 9606.ENSP00000297268, 9606.ENSP00000300026, 9606.ENSP00000304408, 9606.ENSP00000323696, 9606.ENSP00000346839, 9606.ENSP00000353654, 9606.ENSP00000359114, 9606.ENSP00000360493, 9606.ENSP00000360882, 9606.ENSP00000363824, 9606.ENSP00000364000, 9606.ENSP00000364979, 9606.ENSP00000434412	PLOD1, PCOLCE, PLOD3, COL1A1, SPARC, LEPRE1, ADAMTS2, LUM, COL1A2, PPIB, COL3A1, CRTAP, FN1, COL4A2, COL11A1, RUNX2, COL5A1, TMEM38B, COL5A2, COL4A1, SERPINH1
GO:0046947	Hydroxylysine biosynthetic process	2	2	2.8	0.006	9606.ENSP00000223127, 9606.ENSP00000282903	PLOD3, PLOD2
GO:0070848	Response to growth factor	7	524	0.93	0.006	9606.ENSP00000225964, 9606.ENSP00000231061, 9606.ENSP00000266718, 9606.ENSP00000297268, 9606.ENSP00000304408, 9606.ENSP00000353654, 9606.ENSP00000360493	COL1A1, SPARC, LUM, COL1A2, COL3A1, COL4A2, RUNX2

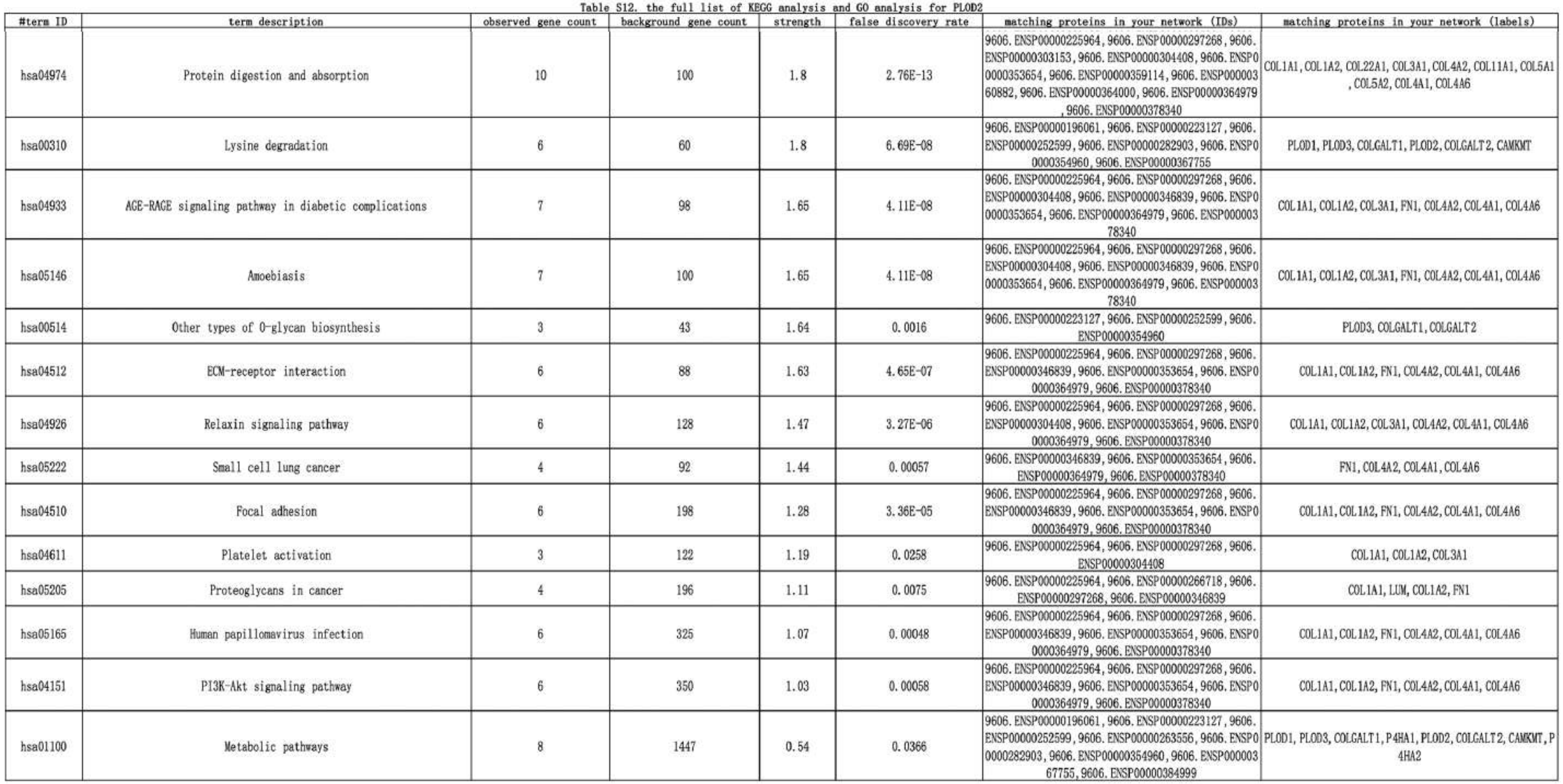
Table S12. the full list of KEGG analysis and GO analysis for PLOD2

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0048856	Anatomical structure development	20	5402	0.37	0.007	9606.ENSP00000196061, 9606.ENSP00000223061, 9606.ENSP00000223127, 9606.ENSP00000225964, 9606.ENSP00000231061, 9606.ENSP00000236040, 9606.ENSP00000251582, 9606.ENSP00000266718, 9606.ENSP00000297268, 9606.ENSP00000300026, 9606.ENSP00000304408, 9606.ENSP00000346839, 9606.ENSP00000353654, 9606.ENSP00000359114, 9606.ENSP00000360493, 9606.ENSP00000360882, 9606.ENSP00000363824, 9606.ENSP00000364000, 9606.ENSP00000364979, 9606.ENSP00000434412	PLOD1, PCOLCE, PLOD3, COL1A1, SPARC, LEPRE1, ADAMTS2, LUM, COL1A2, PPIB, COL3A1, FN1, COL4A2, COL11A1, RUNX2, COL5A1, TMEM38B, COL5A2, COL4A1, SERPINH1
GO:0048731	System development	18	4426	0.41	0.0076	9606.ENSP00000223127, 9606.ENSP00000225964, 9606.ENSP00000231061, 9606.ENSP00000236040, 9606.ENSP00000251582, 9606.ENSP00000266718, 9606.ENSP00000297268, 9606.ENSP00000300026, 9606.ENSP00000304408, 9606.ENSP00000346839, 9606.ENSP00000353654, 9606.ENSP00000359114, 9606.ENSP00000360493, 9606.ENSP00000360882, 9606.ENSP00000363824, 9606.ENSP00000364000, 9606.ENSP00000364979, 9606.ENSP00000434412	PLOD3, COL1A1, SPARC, LEPRE1, ADAMTS2, LUM, COL1A2, PPIB, COL3A1, FN1, COL4A2, COL11A1, RUNX2, COL5A1, TMEM38B, COL5A2, COL4A1, SERPINH1
GO:1901874	Negative regulation of post-translational protein modification	2	3	2.62	0.008	9606.ENSP00000236040, 9606.ENSP00000323696	LEPRE1, CRTAP
GO:1903225	Negative regulation of endodermal cell differentiation	2	3	2.62	0.008	9606.ENSP00000360882, 9606.ENSP00000364000	COL5A1, COL5A2
GO:0043588	Skin development	6	382	1	0.0088	9606.ENSP00000225964, 9606.ENSP00000251582, 9606.ENSP00000297268, 9606.ENSP00000304408, 9606.ENSP00000360882, 9606.ENSP00000364000	COL1A1, ADAMTS2, COL1A2, COL3A1, COL5A1, COL5A2
GO:0007275	Multicellular organism development	19	5023	0.38	0.0092	9606.ENSP00000223061, 9606.ENSP00000223127, 9606.ENSP00000225964, 9606.ENSP00000231061, 9606.ENSP00000236040, 9606.ENSP00000251582, 9606.ENSP00000266718, 9606.ENSP00000297268, 9606.ENSP00000300026, 9606.ENSP00000304408, 9606.ENSP00000346839, 9606.ENSP00000353654, 9606.ENSP00000359114, 9606.ENSP00000360493, 9606.ENSP00000360882, 9606.ENSP00000363824, 9606.ENSP00000364000, 9606.ENSP00000364979, 9606.ENSP00000434412	PCOLCE, PLOD3, COL1A1, SPARC, LEPRE1, ADAMTS2, LUM, COL1A2, PPIB, COL3A1, FN1, COL4A2, COL11A1, RUNX2, COL5A1, TMEM38B, COL5A2, COL4A1, SERPINH1
GO:0071310	Cellular response to organic substance	13	2369	0.54	0.0092	9606.ENSP00000223061, 9606.ENSP00000223127, 9606.ENSP00000225964, 9606.ENSP00000231061, 9606.ENSP00000297268, 9606.ENSP00000304408, 9606.ENSP00000327801, 9606.ENSP00000346839, 9606.ENSP00000353654, 9606.ENSP00000360493, 9606.ENSP00000363824, 9606.ENSP00000364000, 9606.ENSP00000364979	PCOLCE, PLOD3, COL1A1, SPARC, COL1A2, COL3A1, P4HB, FN1, COL4A2, RUNX2, TMEM38B, COL5A2, COL4A1
GO:0043170	Macromolecule metabolic process	21	6137	0.33	0.0102	9606.ENSP00000196061, 9606.ENSP00000223061, 9606.ENSP00000223127, 9606.ENSP00000236040, 9606.ENSP00000251582, 9606.ENSP00000263556, 9606.ENSP00000266718, 9606.ENSP00000282903, 9606.ENSP00000300026, 9606.ENSP00000304408, 9606.ENSP00000317232, 9606.ENSP00000323696, 9606.ENSP00000327801, 9606.ENSP00000346839, 9606.ENSP00000353654, 9606.ENSP00000359114, 9606.ENSP00000360493, 9606.ENSP00000360882, 9606.ENSP00000367755, 9606.ENSP00000384999, 9606.ENSP00000434412	PLOD1, PCOLCE, PLOD3, LEPRE1, ADAMTS2, P4HA1, LUM, PLOD2, PPIB, COL3A1, FKBP10, CRTAP, P4HB, FN1, COL4A2, COL11A1, RUNX2, COL5A1, CAMKMT, P4HA2, SERPINH1
GO:0035295	Tube development	8	851	0.77	0.0118	9606.ENSP00000223127, 9606.ENSP00000231061, 9606.ENSP00000251582, 9606.ENSP00000304408, 9606.ENSP00000346839, 9606.ENSP00000353654, 9606.ENSP00000363824, 9606.ENSP00000364979	PLOD3, SPARC, ADAMTS2, COL3A1, FN1, COL4A2, TMEM38B, COL4A1
GO:0035987	Endodermal cell differentiation	3	41	1.66	0.0124	9606.ENSP00000346839, 9606.ENSP00000353654, 9606.ENSP00000359114	FN1, COL4A2, COL11A1
GO:0002063	Chondrocyte development	3	42	1.65	0.013	9606.ENSP00000359114, 9606.ENSP00000360493, 9606.ENSP00000434412	COL11A1, RUNX2, SERPINH1
GO:0009719	Response to endogenous stimulus	10	1447	0.64	0.0134	9606.ENSP00000223127, 9606.ENSP00000225964, 9606.ENSP00000231061, 9606.ENSP00000297268, 9606.ENSP00000304408, 9606.ENSP00000353654, 9606.ENSP00000360493, 9606.ENSP00000363824, 9606.ENSP00000364000, 9606.ENSP00000364979	PLOD3, COL1A1, SPARC, COL1A2, COL3A1, COL4A2, RUNX2, TMEM38B, COL5A2, COL4A1

Table S12. the full list of KEGG analysis and GO analysis for PLOD2

#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
GO:0019538	Protein metabolic process	17	4251	0.4	0.0149	9606.ENSP00000196061, 9606.ENSP00000223061, 9606.ENSP00000223127, 9606.ENSP00000236040, 9606.ENSP00000251582, 9606.ENSP00000263556, 9606.ENSP00000282903, 9606.ENSP00000300026, 9606.ENSP00000304408, 9606.ENSP00000317232, 9606.ENSP00000323696, 9606.ENSP00000327801, 9606.ENSP00000346839, 9606.ENSP00000359114, 9606.ENSP00000367755, 9606.ENSP00000384999, 9606.ENSP00000434412	PLOD1, PCOLCE, PLOD3, LEPRE1, ADAMTS2, P4HA1, PLOD2, PPIB, COL3A1, FKBP10, CRTAP, P4HB, FN1, COL11A1, CAMKMT, P4HA2, SERPINH1
GO:0042060	Wound healing	6	439	0.94	0.0149	9606.ENSP00000225964, 9606.ENSP00000231061, 9606.ENSP00000297268, 9606.ENSP00000304408, 9606.ENSP00000346839, 9606.ENSP00000360882	COL1A1, SPARC, COL1A2, COL3A1, FN1, COL5A1
GO:0009653	Anatomical structure morphogenesis	12	2165	0.54	0.0154	9606.ENSP00000223127, 9606.ENSP00000225964, 9606.ENSP00000297268, 9606.ENSP00000304408, 9606.ENSP00000346839, 9606.ENSP00000353654, 9606.ENSP00000359114, 9606.ENSP00000360493, 9606.ENSP00000360882, 9606.ENSP00000364000, 9606.ENSP00000364979, 9606.ENSP00000434412	PLOD3, COL1A1, COL1A2, COL3A1, FN1, COL4A2, COL11A1, RUNX2, COL5A1, COL5A2, COL4A1, SERPINH1
GO:0071495	Cellular response to endogenous stimulus	9	1181	0.68	0.0155	9606.ENSP00000223127, 9606.ENSP00000225964, 9606.ENSP00000297268, 9606.ENSP00000304408, 9606.ENSP00000353654, 9606.ENSP00000360493, 9606.ENSP00000363824, 9606.ENSP00000364000, 9606.ENSP00000364979	PLOD3, COL1A1, COL1A2, COL3A1, COL4A2, RUNX2, TMEM38B, COL5A2, COL4A1
GO:0035989	Tendon development	2	6	2.32	0.0157	9606.ENSP00000359114, 9606.ENSP00000360882	COL11A1, COL5A1
GO:0008152	Metabolic process	24	8298	0.26	0.018	9606.ENSP00000196061, 9606.ENSP00000223061, 9606.ENSP00000223127, 9606.ENSP00000225964, 9606.ENSP00000236040, 9606.ENSP00000251582, 9606.ENSP00000263556, 9606.ENSP00000266718, 9606.ENSP00000282903, 9606.ENSP00000297268, 9606.ENSP00000300026, 9606.ENSP00000304408, 9606.ENSP00000317232, 9606.ENSP00000323696, 9606.ENSP00000327801, 9606.ENSP00000346839, 9606.ENSP00000353654, 9606.ENSP00000359114, 9606.ENSP00000360493, 9606.ENSP00000360882, 9606.ENSP00000363824, 9606.ENSP00000367755, 9606.ENSP00000384999, 9606.ENSP00000434412	PLOD1, PCOLCE, PLOD3, COL1A1, LEPRE1, ADAMTS2, P4HA1, LUM, PLOD2, COL1A2, PPIB, COL3A1, FKBP10, CRTAP, P4HB, FN1, COL4A2, COL11A1, RUNX2, COL5A1, TMEM38B, CAMKMT, P4HA2, SERPINH1
GO:0071560	Cellular response to transforming growth factor beta stimulus	4	149	1.23	0.0208	9606.ENSP00000225964, 9606.ENSP00000297268, 9606.ENSP00000304408, 9606.ENSP00000353654	COL1A1, COL1A2, COL3A1, COL4A2
GO:0061077	Chaperone-mediated protein folding	3	55	1.54	0.0223	9606.ENSP00000236040, 9606.ENSP00000300026, 9606.ENSP00000323696	LEPRE1, PPIB, CRTAP
GO:0007167	Enzyme linked receptor protein signaling pathway	7	720	0.79	0.0239	9606.ENSP00000225964, 9606.ENSP00000297268, 9606.ENSP00000304408, 9606.ENSP00000353654, 9606.ENSP00000360493, 9606.ENSP00000364979, 9606.ENSP00000378340	COL1A1, COL1A2, COL3A1, COL4A2, RUNX2, COL4A1, COL4A6
GO:0071363	Cellular response to growth factor stimulus	6	494	0.88	0.0239	9606.ENSP00000225964, 9606.ENSP00000231061, 9606.ENSP00000297268, 9606.ENSP00000304408, 9606.ENSP00000353654, 9606.ENSP00000360493	COL1A1, SPARC, COL1A2, COL3A1, COL4A2, RUNX2
GO:0030324	Lung development	4	170	1.17	0.0314	9606.ENSP00000223127, 9606.ENSP00000231061, 9606.ENSP00000251582, 9606.ENSP00000363824	PLOD3, SPARC, ADAMTS2, TMEM38B
GO:0043589	Skin morphogenesis	2	11	2.06	0.0358	9606.ENSP00000225964, 9606.ENSP00000297268	COL1A1, COL1A2
GO:0060350	Endochondral bone morphogenesis	3	70	1.43	0.0391	9606.ENSP00000225964, 9606.ENSP00000360493, 9606.ENSP00000434412	COL1A1, RUNX2, SERPINH1
GO:1901564	Organonitrogen compound metabolic process	18	5244	0.34	0.0453	9606.ENSP00000196061, 9606.ENSP00000223061, 9606.ENSP00000223127, 9606.ENSP00000236040, 9606.ENSP00000251582, 9606.ENSP00000263556, 9606.ENSP00000266718, 9606.ENSP00000282903, 9606.ENSP00000300026, 9606.ENSP00000304408, 9606.ENSP00000317232, 9606.ENSP00000323696, 9606.ENSP00000327801, 9606.ENSP00000346839, 9606.ENSP00000359114, 9606.ENSP00000367755, 9606.ENSP00000384999, 9606.ENSP00000434412	PLOD1, PCOLCE, PLOD3, LEPRE1, ADAMTS2, P4HA1, LUM, PLOD2, PPIB, COL3A1, FKBP10, CRTAP, P4HB, FN1, COL11A1, CAMKMT, P4HA2, SERPINH1
GO:0032501	Multicellular organismal process	21	6933	0.28	0.0471	9606.ENSP00000223061, 9606.ENSP00000223127, 9606.ENSP00000225964, 9606.ENSP00000231061, 9606.ENSP00000236040, 9606.ENSP00000251582, 9606.ENSP00000266718, 9606.ENSP00000297268, 9606.ENSP00000300026, 9606.ENSP00000304408, 9606.ENSP00000323696, 9606.ENSP00000327801, 9606.ENSP00000346839, 9606.ENSP00000353654, 9606.ENSP00000359114, 9606.ENSP00000360493, 9606.ENSP00000360882, 9606.ENSP00000363824, 9606.ENSP00000364000, 9606.ENSP00000364979, 9606.ENSP00000434412	PCOLCE, PLOD3, COL1A1, SPARC, LEPRE1, ADAMTS2, LUM, COL1A2, PPIB, COL3A1, CRTAP, P4HB, FN1, COL4A2, COL11A1, RUNX2, COL5A1, TMEM38B, COL5A2, COL4A1, SERPINH1

Table S12. the full list of KEGG analysis and GO analysis for PLOD2



#term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (IDs)	matching proteins in your network (labels)
hsa04974	Protein digestion and absorption	10	100	1.8	2.76E-13	9606.ENSP00000225964, 9606.ENSP00000297268, 9606.ENSP00000303153, 9606.ENSP00000304408, 9606.ENSP00000353654, 9606.ENSP00000359114, 9606.ENSP00000360882, 9606.ENSP00000364000, 9606.ENSP00000364979, 9606.ENSP00000378340	COL1A1, COL1A2, COL22A1, COL3A1, COL4A2, COL11A1, COL5A1, COL5A2, COL4A1, COL4A6
hsa00310	Lysine degradation	6	60	1.8	6.69E-08	9606.ENSP00000196061, 9606.ENSP00000223127, 9606.ENSP00000252599, 9606.ENSP00000282903, 9606.ENSP00000354960, 9606.ENSP00000367755	PLOD1, PLOD3, COLGALT1, PLOD2, COLGALT2, CAMKMT
hsa04933	AGE-RAGE signaling pathway in diabetic complications	7	98	1.65	4.11E-08	9606.ENSP00000225964, 9606.ENSP00000297268, 9606.ENSP00000304408, 9606.ENSP00000346839, 9606.ENSP00000353654, 9606.ENSP00000364979, 9606.ENSP00000378340	COL1A1, COL1A2, COL3A1, FN1, COL4A2, COL4A1, COL4A6
hsa05146	Amoebiasis	7	100	1.65	4.11E-08	9606.ENSP00000225964, 9606.ENSP00000297268, 9606.ENSP00000304408, 9606.ENSP00000346839, 9606.ENSP00000353654, 9606.ENSP00000364979, 9606.ENSP00000378340	COL1A1, COL1A2, COL3A1, FN1, COL4A2, COL4A1, COL4A6
hsa00514	Other types of O-glycan biosynthesis	3	43	1.64	0.0016	9606.ENSP00000223127, 9606.ENSP00000252599, 9606.ENSP00000354960	PLOD3, COLGALT1, COLGALT2
hsa04512	ECM-receptor interaction	6	88	1.63	4.65E-07	9606.ENSP00000225964, 9606.ENSP00000297268, 9606.ENSP00000346839, 9606.ENSP00000353654, 9606.ENSP00000364979, 9606.ENSP00000378340	COL1A1, COL1A2, FN1, COL4A2, COL4A1, COL4A6
hsa04926	Relaxin signaling pathway	6	128	1.47	3.27E-06	9606.ENSP00000225964, 9606.ENSP00000297268, 9606.ENSP00000304408, 9606.ENSP00000353654, 9606.ENSP00000364979, 9606.ENSP00000378340	COL1A1, COL1A2, COL3A1, COL4A2, COL4A1, COL4A6
hsa05222	Small cell lung cancer	4	92	1.44	0.00057	9606.ENSP00000346839, 9606.ENSP00000353654, 9606.ENSP00000364979, 9606.ENSP00000378340	FN1, COL4A2, COL4A1, COL4A6
hsa04510	Focal adhesion	6	198	1.28	3.36E-05	9606.ENSP00000225964, 9606.ENSP00000297268, 9606.ENSP00000346839, 9606.ENSP00000353654, 9606.ENSP00000364979, 9606.ENSP00000378340	COL1A1, COL1A2, FN1, COL4A2, COL4A1, COL4A6
hsa04611	Platelet activation	3	122	1.19	0.0258	9606.ENSP00000225964, 9606.ENSP00000297268, 9606.ENSP00000304408	COL1A1, COL1A2, COL3A1
hsa05205	Proteoglycans in cancer	4	196	1.11	0.0075	9606.ENSP00000225964, 9606.ENSP00000266718, 9606.ENSP00000297268, 9606.ENSP00000346839	COL1A1, LUM, COL1A2, FN1
hsa05165	Human papillomavirus infection	6	325	1.07	0.00048	9606.ENSP00000225964, 9606.ENSP00000297268, 9606.ENSP00000346839, 9606.ENSP00000353654, 9606.ENSP00000364979, 9606.ENSP00000378340	COL1A1, COL1A2, FN1, COL4A2, COL4A1, COL4A6
hsa04151	PI3K-Akt signaling pathway	6	350	1.03	0.00058	9606.ENSP00000225964, 9606.ENSP00000297268, 9606.ENSP00000346839, 9606.ENSP00000353654, 9606.ENSP00000364979, 9606.ENSP00000378340	COL1A1, COL1A2, FN1, COL4A2, COL4A1, COL4A6
hsa01100	Metabolic pathways	8	1447	0.54	0.0366	9606.ENSP00000196061, 9606.ENSP00000223127, 9606.ENSP00000252599, 9606.ENSP00000263556, 9606.ENSP00000282903, 9606.ENSP00000354960, 9606.ENSP00000367755, 9606.ENSP00000384999	PLOD1, PLOD3, COLGALT1, P4HA1, PLOD2, COLGALT2, CAMKMT, P4HA2