

Supplementary File 1. ccRCC exhibits transcriptional changes of INI1 target genes

Sub-table 1. INI1 target genes downregulated in ccRCC.

AASS  
ABHD14B  
ABHD5  
ABHD6  
ACAA1  
ACAD10  
ACADM  
ACN9  
ACSF2  
ACSL1  
ACSL4  
ADAL  
AGL  
AGMAT  
AIFM1  
AKIRIN1  
ALDH2  
ALDH3A2  
ALDH7A1  
ALDH9A1  
AMMECR1  
ANKRD9  
ANXA9  
APLP2  
ARHGEF3  
ARL2  
ASAP2  
ASAP3  
ASRGL1  
ASS1  
ATP1A1  
ATP5G3  
ATP5J  
ATP6V0E2  
ATP6V1A  
B4GALT6  
BCAR3  
BEX1  
BEX2  
BEX4  
BHLHB9  
BIN1  
BLCAP  
BMP7  
BNC2  
BPHL  
CA2

CACNA2D2  
CALB1  
CAMTA1  
CCBE1  
CDC14A  
CDC14B  
CDH1  
CDH3  
CDO1  
CDS1  
CENPV  
CGN  
CGNL1  
CHCHD4  
CHN2  
CHPT1  
CKB  
CLASP2  
CLDN7  
CLMN  
CLYBL  
COBL  
COBLL1  
COCH  
COL4A5  
COL4A6  
COL9A2  
COQ10A  
CPS1  
CRABP1  
CRYM  
CTDSPL  
CTGF  
CTNNAL1  
CTSA  
CTSC  
CTSH  
CXADR  
CXCL12  
CYB5D2  
CYR61  
DAB2  
DCBLD2  
DCXR  
DDAH1  
DEPDC1B  
DEPDC7  
DHRS11  
DNMT3L  
DOCK3

DSP  
DUSP9  
DYNLL2  
ECHDC1  
ECHDC2  
EGR1  
EIF1B  
ENPP5  
EPB41L5  
ERBB2  
ERMP1  
ESRRG  
ETFB  
ETNK1  
EYA3  
FAAH  
FAHD1  
FAHD2A  
FAM24B  
FAM46C  
FAM84B  
FAM92A1  
FBLN1  
FBP1  
FBXO21  
FERMT1  
FERMT2  
FHOD3  
FOXA3  
FST  
G3BP2  
GABRB3  
GADD45A  
GALM  
GALNT11  
GATA5  
GATM  
GCH1  
GCHFR  
GGA2  
GGH  
GLS2  
GNG12  
GOLT1A  
GPC3  
GPC4  
GPR160  
GPR89B  
GPC5C  
GPT2

GRB14  
GULP1  
H2AFY2  
HABP4  
HADH  
HIBADH  
HIGD1A  
HINT3  
HMGCR  
HOXD1  
HSD17B12  
HSD17B14  
HSDL2  
HSP90AA1  
HSPA12A  
HSPA4  
HSPD1  
IDH1  
IDH2  
IER3  
IGF2BP2  
IGFBP2  
IGFBP5  
IL11  
INADL  
IRX2  
ITGA2  
ITM2C  
ITPR2  
KCNK5  
KCNN2  
KIAA1522  
KIF13B  
KITLG  
KLF15  
KLHL3  
LAD1  
LAMA2  
LAPTM4B  
LDHD  
LGR4  
LMO3  
LOC729970  
LRP10  
LRRC16A  
LRRC28  
LRRN1  
LSM3  
LYPD6B  
MACROD1

MAL  
MAL2  
MAN1A1  
MAN1C1  
MAOA  
MAP3K9  
MAP4K3  
MBOAT2  
MCCC1  
MCOLN3  
MDH1  
MED20  
MEIS2  
MEST  
METTL7A  
MFAP3L  
MRPL19  
MRPS25  
MRS2  
MT1E  
MT1F  
MT2A  
MUC1  
MYCN  
MYO5C  
MYO6  
N4BP2L2  
NAGLU  
NARS2  
NCOA7  
NDUFA10  
NDUFAF3  
NDUFV1  
NEFH  
NES  
NINL  
NIPSNAP1  
NISCH  
NQO1  
NRK  
NT5C2  
NTN4  
NTNG1  
OAT  
OGG1  
OSBPL6  
OXCT1  
PALM  
PAPLN  
PAPOLA

PAQR5  
PAWR  
PCGF2  
PCK2  
PCYOX1  
PDE3B  
PELI2  
PHF17  
PHKB  
PINK1  
PIP4K2C  
PLEKHB1  
PLEKHB2  
PLEKHG3  
PLEKHH1  
PLS3  
PODXL  
POLR2L  
PPM1H  
PPP1R16B  
PPP1R1A  
PRDX3  
PRICKLE1  
PRKCA  
PRKD1  
PRMT6  
PRSS8  
PSAT1  
PSMA5  
PTPLAD1  
PTPN13  
PTPN4  
QDPR  
RAB25  
RAB3IP  
RAB40B  
RAB7L1  
RABGAP1L  
RAP1GAP  
RASL11B  
RBM47  
RBP5  
RBPMS2  
RDH10  
REEP1  
REEP6  
RENBP  
RHBDD2  
RHOBTB3  
SAT2

SCAMP5  
SCNN1A  
SDHC  
SDHD  
SELENBP1  
SEPP1  
SEPSECS  
SESN2  
SETBP1  
SETMAR  
SFRP1  
SFXN2  
SFXN5  
SH3BP4  
SHISA2  
SHISA3  
SHMT1  
SIK3  
SIX4  
SLAIN1  
SLC16A10  
SLC16A9  
SLC22A17  
SLC25A35  
SLC25A42  
SLC27A2  
SLC29A2  
SLC31A1  
SLC3A2  
SLC4A11  
SMAD6  
SMARCE1  
SMTNL2  
SOBP  
SORD  
SPINT1  
SSTR2  
STK32A  
STRA6  
STX3  
SUCLG2  
SYT1  
TAGLN3  
TCEAL2  
TEX264  
TFDP1  
TGFB3  
THAP4  
THBS1  
THY1

TLCD1  
TM7SF2  
TMEM177  
TNC  
TOB1  
TOX3  
TPD52L1  
TPMT  
TRIM2  
TRMT2B  
TRNP1  
TSPAN12  
TUBB2A  
TUBB2B  
TYRO3  
UBE2E2  
UCHL1  
USP44  
UST  
VAT1L  
VSNL1  
WWC1  
ZDHHC15  
ZDHHC23



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 Sub-table 2.GO term analysis for INI1 target genes downregulated in ccRCC.

Ontology term	Number of genes	Percentage of genes	Corrected P-value	FDR	False Positives	Genes annotated to the term
<a href="#">developmental process</a>	61 of 150 genes	40.7%	3.71e-13	0.00%	0.00	PSMA5, HOXD1, PRMT6, BHLHB9, WWC1, IL11, GPC4, FST, CA2, BIN1, SHISA3, GNG12, POLR2L, IRX2, CACNA2D2, CXADR, CTGF, SMAD6, NEFH, TRNP1, SHISA2, CDO1, TUBB2B, ATP5G3, EPB41L5, RAB7L1, BCAR3, DYNLL2, SOBP, PINK1, LRRN1, EGR1, CYB5D2, PRDX3, PLEKHB1, MAL, N4BP2L2, DSP, SSTR2, NAGLU, BEX1, CXCL12, MYCN, ZDHHC15, TAGLN3, LGR4, DAB2, COL9A2, KLF15, TOB1, NTNG1, PPP1R16B, NTN4, NES, ALDH9A1, QDPR, GATA5, PDE3B, CLASP2, UST, TGFB3
<a href="#">single-organism developmental process</a>	60 of 150 genes	40.0%	8.04e-13	0.00%	0.00	PSMA5, HOXD1, PRMT6, BHLHB9, WWC1, IL11, GPC4, FST, CA2, BIN1, SHISA3, GNG12, POLR2L, IRX2, CACNA2D2, CXADR, CTGF, SMAD6, NEFH, TRNP1, SHISA2, CDO1, TUBB2B, ATP5G3, EPB41L5, RAB7L1, BCAR3, DYNLL2, SOBP, LRRN1, EGR1, CYB5D2, PRDX3, PLEKHB1, MAL, N4BP2L2, DSP, SSTR2, NAGLU, BEX1, CXCL12, MYCN, ZDHHC15, TAGLN3, LGR4, DAB2, COL9A2, KLF15, TOB1, NTNG1, PPP1R16B, NTN4, NES, ALDH9A1, QDPR, GATA5, PDE3B, CLASP2, UST, TGFB3
<a href="#">system development</a>	50 of 150 genes	33.3%	7.30e-12	0.00%	0.00	PSMA5, HOXD1, BHLHB9, IL11, GPC4, FST, CA2, BIN1, GNG12, IRX2, CXADR, CTGF, SMAD6, NEFH, TRNP1, CDO1, TUBB2B, EPB41L5, RAB7L1, BCAR3, DYNLL2, SOBP, LRRN1, CYB5D2, EGR1, PRDX3, MAL, DSP, N4BP2L2, SSTR2, NAGLU, BEX1, CXCL12, MYCN, TAGLN3, LGR4, DAB2, COL9A2, KLF15, NTNG1, PPP1R16B, NTN4, NES, ALDH9A1, QDPR, GATA5, PDE3B, CLASP2, UST, TGFB3
<a href="#">single-multicellular organism process</a>	59 of 150 genes	39.3%	1.71e-11	0.00%	0.00	PSMA5, HOXD1, BHLHB9, WWC1, IL11, GPC4, FST, CA2, BIN1, SHISA3, GNG12, POLR2L, IRX2, CACNA2D2, CXADR, CTGF, SMAD6, NEFH, TRNP1, SHISA2, CDO1, TUBB2B, EPB41L5, RAB7L1, BCAR3, DYNLL2, SOBP, LRRN1, CYB5D2, EGR1, PRDX3, PLEKHB1, MAL, N4BP2L2, DSP, SSTR2, NAGLU, BEX1, CXCL12, MYCN, FERMT1, TAGLN3, LGR4, DAB2, COL9A2, KLF15, TOB1, NTNG1, PPP1R16B, NTN4, NES, ALDH9A1, QDPR, GATA5, PDE3B, CLASP2, GCH1, UST, TGFB3
<a href="#">multicellular organism development</a>	53 of 150 genes	35.3%	2.16e-11	0.00%	0.00	PSMA5, HOXD1, BHLHB9, IL11, GPC4, FST, CA2, BIN1, SHISA3, GNG12, IRX2, CXADR, CTGF, SMAD6, NEFH, TRNP1, SHISA2, CDO1, TUBB2B, EPB41L5, RAB7L1, BCAR3, DYNLL2, SOBP, LRRN1, CYB5D2, EGR1, PRDX3, PLEKHB1, MAL, DSP, N4BP2L2, SSTR2, NAGLU, BEX1, CXCL12, MYCN, TAGLN3, LGR4, DAB2, COL9A2, KLF15, NTN4, PPP1R16B, NTN4, NES, ALDH9A1, QDPR, GATA5, PDE3B, CLASP2, UST, TGFB3
<a href="#">anatomical structure development</a>	55 of 150 genes	36.7%	7.11e-11	0.00%	0.00	PSMA5, HOXD1, BHLHB9, IL11, GPC4, FST, CA2, BIN1, SHISA3, GNG12, IRX2, CACNA2D2, CXADR, CTGF, SMAD6, NEFH, TRNP1, SHISA2, CDO1, TUBB2B, EPB41L5, RAB7L1, BCAR3, DYNLL2, SOBP, PINK1, LRRN1, CYB5D2, EGR1, PRDX3, PLEKHB1, MAL, DSP, N4BP2L2, SSTR2, NAGLU, BEX1, CXCL12, MYCN, TAGLN3, LGR4, DAB2, COL9A2, KLF15, NTNG1, PPP1R16B, NTN4, NES, ALDH9A1, QDPR, GATA5, PDE3B, CLASP2, UST, TGFB3
<a href="#">multicellular organismal process</a>	64 of 150 genes	42.7%	7.53e-11	0.00%	0.00	PSMA5, HOXD1, BHLHB9, WWC1, OAT, IL11, GPC4, FST, CA2, BIN1, SHISA3, GNG12, POLR2L, IRX2, CACNA2D2, CXADR, CTGF, SMAD6, NEFH, TRNP1, SHISA2, KCNK5, CDO1, TUBB2B, EPB41L5, NIPSNAP1, RAB7L1, BCAR3, DYNLL2, SOBP, LRRN1, EGR1, CYB5D2, CRYM, PRDX3, PLEKHB1, MAL, N4BP2L2, DSP, SSTR2, NAGLU, MYCN, BEX1, CXCL12, FERMT1, TAGLN3, LGR4, DAB2, COL9A2, KLF15, TOB1, NTNG1, PPP1R16B, NTN4, NES, ALDH9A1, QDPR, CAMTA1, GATA5, PDE3B, CLASP2, GCH1, UST, TGFB3
<a href="#">single-organism cellular process</a>	89 of 150 genes	59.3%	7.04e-10	0.00%	0.00	HOXD1, PRMT6, DCBLD2, BHLHB9, ANXA9, GPC4, CA2, GULP1, POLR2L, ARL2, NEFH, TRNP1, FAAH, MRPS25, INADL, HABP4, ATP5G3, DYNLL2, CYB5D2, PLEKHB1, DEPDC1B, NAGLU, MYCN, PTPLAD1, DAB2, COL9A2, KLF15, NTNG1, NTN4, NES, GGH, BEX2, ALDH9A1, AGMAT, GATA5, PDE3B, CLASP2, GCH1, PHF17, SH3BP4, TGFB3, PSMA5, AGL, WWC1, IL11, OAT, BIN1, FST, MACROD1, CACNA2D2, CXADR, CTGF, SMAD6, TPD52L1, CDS1, CDO1, KCNK5, TUBB2B, EPB41L5, RAB7L1, EGR1, LRRN1, NINL, PINK1, CRYM, PRDX3, MAL, DSP, N4BP2L2, NDUFA10, SSTR2, SESN2, SLC16A9, CXCL12, BEX1, FERMT1, ZDHHC15, NT5C2, RAB3IP, SLC31A1, LGR4, DUSP9, TOB1, PPP1R16B, TOX3, QDPR, SDHC, PSAT1, UST
<a href="#">single-organism process</a>	107 of 150 genes	71.3%	1.23e-07	0.00%	0.00	HOXD1, PRMT6, DCBLD2, BHLHB9, ANXA9, GPC4, CA2, GULP1, POLR2L, ARL2, NEFH, TRNP1, FAAH, MRPS25, CHCHD4, INADL, HABP4, ATP5G3, BCAR3, DYNLL2, SOBP, CYB5D2, VAT1L, PLEKHB1, MAOA, DEPDC1B, NAGLU, MYCN, PTPLAD1, DAB2, COL9A2, KLF15, NTNG1, NTN4, NES, GGH, BEX2, ALDH9A1, AGMAT, OSBPL6, GATA5, DOCK3, PDE3B, CLASP2, GCH1, PHF17, SH3BP4, TGFB3, PSMA5, AGL, CGN, WWC1, OAT, IL11, BIN1, FST, SHISA3, GNG12, MACROD1, CACNA2D2, IRX2, CXADR, CTGF, SMAD6, TPD52L1, CDS1, SHISA2, CDO1, KCNK5, TUBB2B, SLC25A42, EPB41L5, RAB7L1, PINK1, EGR1, LRRN1, NINL, CRYM, PRDX3, MAL, DSP, N4BP2L2, NDUFA10, SSTR2, SESN2, SLC16A9, CXCL12, BEX1, FERMT1, ZDHHC15, NT5C2, TAGLN3, RAB3IP, SLC31A1, LGR4, DUSP9, HSDL2, TOB1, LDHD, RASL11B, PPP1R16B, TOX3, QDPR, SDHC, ACN9, PSAT1, UST
<a href="#">cellular developmental process</a>	39 of 150 genes	26.0%	7.41e-07	0.00%	0.00	HOXD1, PRMT6, BHLHB9, IL11, FST, CA2, BIN1, CACNA2D2, CXADR, CTGF, SMAD6, NEFH, TUBB2B, EPB41L5, RAB7L1, DYNLL2, CYB5D2, EGR1, PRDX3, PLEKHB1, MAL, DSP, N4BP2L2, NAGLU, BEX1, CXCL12, MYCN, LGR4, DAB2, KLF15, TOB1, NTNG1, NTN4, PPP1R16B, NES, GATA5, CLASP2, UST, TGFB3
<a href="#">animal organ development</a>	34 of 150 genes	22.7%	1.07e-06	0.00%	0.00	PSMA5, IL11, GPC4, FST, CA2, GNG12, IRX2, CXADR, CTGF, SMAD6, NEFH, TRNP1, CDO1, EPB41L5, BCAR3, SOBP, EGR1, PRDX3, DSP, N4BP2L2, SSTR2, NAGLU, CXCL12, MYCN, LGR4, DAB2, KLF15, NTN4, NES, ALDH9A1, QDPR, GATA5, CLASP2, TGFB3
<a href="#">response to endogenous stimulus</a>	23 of 150 genes	15.3%	1.88e-06	0.00%	0.00	AGL, SSTR2, SESN2, CGN, CXCL12, CA2, GNG12, POLR2L, CTGF, SMAD6, DAB2, KLF15, TOB1, CDO1, RASL11B, GGH, EPB41L5, QDPR, GATA5, PDE3B, EGR1, SH3BP4, TGFB3
<a href="#">cell differentiation</a>	37 of 150 genes	24.7%	2.28e-06	0.00%	0.00	HOXD1, BHLHB9, IL11, FST, CA2, BIN1, CACNA2D2, CXADR, CTGF, SMAD6, NEFH, TUBB2B, EPB41L5, RAB7L1, DYNLL2, CYB5D2, EGR1, PRDX3, PLEKHB1, MAL, DSP, N4BP2L2, NAGLU, BEX1, CXCL12, MYCN, LGR4, DAB2, KLF15, TOB1, NTNG1, NTN4, PPP1R16B, GATA5, CLASP2, UST, TGFB3
<a href="#">regulation of developmental process</a>	27 of 150 genes	18.0%	1.21e-05	0.00%	0.00	PSMA5, N4BP2L2, BHLHB9, WWC1, MYCN, CXCL12, GPC4, FST, CA2, BIN1, CACNA2D2, CTGF, LGR4, DAB2, TOB1, PPP1R16B, NTN4, EPB41L5, RAB7L1, PDE3B, CLASP2, PINK1, CYB5D2, EGR1, LRRN1, UST, PLEKHB1
<a href="#">regulation of multicellular organismal process</a>	29 of 150 genes	19.3%	2.06e-05	0.00%	0.00	PSMA5, N4BP2L2, DSP, SSTR2, BHLHB9, WWC1, MYCN, CXCL12, GPC4, FST, CA2, BIN1, POLR2L, CACNA2D2, CXADR, CTGF, LGR4, DAB2, TOB1, PPP1R16B, NTN4, EPB41L5, RAB7L1, PDE3B, CLASP2, CYB5D2, EGR1, LRRN1, UST

<a href="#">positive regulation of biological process</a>	45 of 150 genes, 30.0%	6026 of 47246 genes, 12.8%	2.72e-05	0.00%	0.00	PSMA5, BHLHB9, WWC1, IL11, FST, CA2, BIN1, POLR2L, CACNA2D2, CTGF, ARL2, TPD52L1, EPB41L5, RAB7L1, BCAR3, DYNLL2, PINK1, NINL, LRRN1, EGR1, CYB5D2, PRDX3, MAL, N4BP2L2, DEPDC1B, BEX1, CXCL12, MYCN, PTPLAD1, LGR4, DAB2, DUSP9, KLF15, TOB1, PPP1R16B, NES, NCOA7, TOX3, CAMTA1, GATA5, CLASP2, GCH1, PHF17, SH3BP4, TGFB3
<a href="#">positive regulation of cellular process</a>	41 of 150 genes, 27.3%	5305 of 47246 genes, 11.2%	5.66e-05	0.00%	0.00	PSMA5, BHLHB9, WWC1, IL11, CA2, BIN1, POLR2L, CTGF, ARL2, TPD52L1, EPB41L5, BCAR3, DYNLL2, PINK1, NINL, LRRN1, CYB5D2, EGR1, PRDX3, MAL, N4BP2L2, DEPDC1B, BEX1, CXCL12, MYCN, PTPLAD1, LGR4, DAB2, DUSP9, KLF15, TOB1, PPP1R16B, NES, NCOA7, TOX3, CAMTA1, GATA5, CLASP2, PHF17, SH3BP4, TGFB3
<a href="#">anatomical structure morphogenesis</a>	27 of 150 genes, 18.0%	2606 of 47246 genes, 5.5%	6.86e-05	0.00%	0.00	PSMA5, DSP, NAGLU, BHLHB9, MYCN, CXCL12, GPC4, CA2, IRX2, CTGF, LGR4, NEFH, DAB2, TRNP1, NTNG1, PPP1R16B, NTN4, NES, EPB41L5, GATA5, PDE3B, CLASP2, BCAR3, SOBP, PINK1, UST, TGFB3
<a href="#">regulation of multicellular organismal development</a>	22 of 150 genes, 14.7%	1802 of 47246 genes, 3.8%	8.61e-05	0.00%	0.00	PSMA5, N4BP2L2, BHLHB9, MYCN, CXCL12, GPC4, FST, CA2, BIN1, CTGF, LGR4, DAB2, PPP1R16B, NTN4, EPB41L5, RAB7L1, PDE3B, CLASP2, CYB5D2, EGR1, LRRN1, UST
<a href="#">response to peptide</a>	11 of 150 genes, 7.3%	461 of 47246 genes, 1.0%	0.00038	0.00%	0.00	SESN2, CXCL12, CA2, GGH, QDPR, GNG12, PDE3B, CTGF, EGR1, KLF15, CDO1
<a href="#">positive regulation of developmental process</a>	17 of 150 genes, 11.3%	1219 of 47246 genes, 2.6%	0.00049	0.00%	0.00	N4BP2L2, BHLHB9, CXCL12, FST, CA2, BIN1, CACNA2D2, CTGF, LGR4, DAB2, PPP1R16B, EPB41L5, CLASP2, CYB5D2, EGR1, LRRN1, PINK1
<a href="#">cellular response to endogenous stimulus</a>	18 of 150 genes, 12.0%	1365 of 47246 genes, 2.9%	0.00049	0.00%	0.00	SSTR2, SESN2, CGN, CA2, GNG12, POLR2L, CTGF, SMAD6, DAB2, KLF15, TOB1, RASL11B, EPB41L5, GATA5, PDE3B, EGR1, SH3BP4, TGFB3
<a href="#">epithelium development</a>	16 of 150 genes, 10.7%	1097 of 47246 genes, 2.3%	0.00062	0.00%	0.00	PSMA5, DSP, MYCN, GPC4, FST, CA2, IRX2, LGR4, SMAD6, DAB2, KLF15, NTN4, PPP1R16B, EPB41L5, GATA5, CLASP2
<a href="#">negative regulation of biological process</a>	39 of 150 genes, 26.0%	5405 of 47246 genes, 11.4%	0.00079	0.00%	0.00	PSMA5, PRMT6, DCBLD2, BHLHB9, WWC1, IL11, FST, BIN1, POLR2L, CTGF, ARL2, SMAD6, EPB41L5, RAB7L1, PINK1, EGR1, CRYM, PRDX3, N4BP2L2, SSTR2, SESN2, CXCL12, MYCN, TAGLN3, LGR4, DAB2, DUSP9, KLF15, TOB1, PPP1R16B, RASL11B, NES, TOX3, LSM3, CLASP2, PDE3B, PHF17, SH3BP4, TGFB3
<a href="#">response to oxygen-containing compound</a>	19 of 150 genes, 12.7%	1573 of 47246 genes, 3.3%	0.00086	0.00%	0.00	SSTR2, SESN2, CXCL12, CA2, GNG12, CTGF, NEFH, KLF15, CDO1, ATP5G3, GGH, QDPR, PDE3B, GCH1, EGR1, PINK1, SH3BP4, TGFB3, PRDX3
<a href="#">nervous system development</a>	24 of 150 genes, 16.0%	2427 of 47246 genes, 5.1%	0.00096	0.00%	0.00	SSTR2, HOXD1, NAGLU, BHLHB9, MYCN, CXCL12, BEX1, BIN1, GNG12, TAGLN3, NEFH, TRNP1, KLF15, NTNG1, NTN4, NES, TUBB2B, RAB7L1, CLASP2, DYNLL2, LRRN1, CYB5D2, UST, MAL
<a href="#">tissue morphogenesis</a>	12 of 150 genes, 8.0%	626 of 47246 genes, 1.3%	0.00111	0.00%	0.00	PSMA5, NTN4, DSP, MYCN, GPC4, CA2, EPB41L5, IRX2, CLASP2, LGR4, DAB2, TGFB3
<a href="#">negative regulation of cell communication</a>	17 of 150 genes, 11.3%	1302 of 47246 genes, 2.8%	0.00122	0.00%	0.00	PSMA5, SESN2, WWC1, CXCL12, IL11, FST, LGR4, SMAD6, DAB2, DUSP9, TOB1, RASL11B, PDE3B, PINK1, EGR1, SH3BP4, TGFB3
<a href="#">negative regulation of signaling</a>	17 of 150 genes, 11.3%	1306 of 47246 genes, 2.8%	0.00127	0.00%	0.00	PSMA5, SESN2, WWC1, CXCL12, IL11, FST, LGR4, SMAD6, DAB2, DUSP9, TOB1, RASL11B, PDE3B, PINK1, EGR1, SH3BP4, TGFB3
<a href="#">animal organ morphogenesis</a>	15 of 150 genes, 10.0%	1025 of 47246 genes, 2.2%	0.00138	0.00%	0.00	PSMA5, NTN4, DSP, NAGLU, MYCN, GPC4, CA2, GATA5, IRX2, BCAR3, CTGF, LGR4, SOBP, DAB2, TGFB3
<a href="#">negative regulation of cellular process</a>	36 of 150 genes, 24.0%	4881 of 47246 genes, 10.3%	0.00147	0.00%	0.00	PSMA5, PRMT6, DCBLD2, BHLHB9, WWC1, IL11, FST, BIN1, CTGF, SMAD6, EPB41L5, RAB7L1, PINK1, EGR1, CRYM, PRDX3, N4BP2L2, SESN2, SSTR2, CXCL12, MYCN, TAGLN3, LGR4, DAB2, DUSP9, KLF15, TOB1, PPP1R16B, RASL11B, NES, TOX3, CLASP2, PDE3B, PHF17, SH3BP4, TGFB3

<a href="#">response to peptide hormone</a>	10 of 150 genes, 6.7%	424 of 47246 genes, 0.9%	0.00151	0.00%	0.00	SESN2, CXCL12, CA2, GGH, QDPR, GNG12, CTGF, PDE3B, EGR1, CDO1
<a href="#">negative regulation of signal transduction</a>	16 of 150 genes, 10.7%	1196 of 47246 genes, 2.5%	0.00191	0.00%	0.00	PSMA5, SESN2, WWC1, CXCL12, FST, LGR4, SMAD6, DAB2, DUSP9, TOB1, RASL11B, PDE3B, PINK1, EGR1, SH3BP4, TGFB3
<a href="#">response to organic substance</a>	28 of 150 genes, 18.7%	3289 of 47246 genes, 7.0%	0.00200	0.00%	0.00	PSMA5, AGL, SSTR2, SESN2, CGN, CXCL12, CA2, GNG12, POLR2L, CTGF, SMAD6, NEFH, DAB2, KLF15, TOB1, CDO1, RASL11B, ATP5G3, GGH, QDPR, EPB41L5, GATA5, PDE3B, GCH1, EGR1, SH3BP4, TGFB3, PRDX3
<a href="#">tissue development</a>	20 of 150 genes, 13.3%	1835 of 47246 genes, 3.9%	0.00208	0.00%	0.00	PSMA5, DSP, MYCN, GPC4, FST, CA2, IRX2, CXADR, CTGF, LGR4, SMAD6, DAB2, KLF15, PPP1R16B, NTN4, EPB41L5, GATA5, CLASP2, EGR1, TGFB3
<a href="#">cellular response to chemical stimulus</a>	27 of 150 genes, 18.0%	3107 of 47246 genes, 6.6%	0.00216	0.00%	0.00	PSMA5, SSTR2, SESN2, CGN, CXCL12, CA2, GNG12, POLR2L, CXADR, CTGF, SLC31A1, SMAD6, NEFH, DAB2, KLF15, TOB1, RASL11B, QDPR, EPB41L5, GATA5, PDE3B, GCH1, EGR1, PINK1, SH3BP4, TGFB3, PRDX3
<a href="#">response to hormone</a>	14 of 150 genes, 9.3%	959 of 47246 genes, 2.0%	0.00331	0.00%	0.00	AGL, SSTR2, SESN2, CXCL12, CA2, GGH, QDPR, GNG12, PDE3B, CTGF, DAB2, EGR1, TGFB3, CDO1
<a href="#">positive regulation of multicellular organismal process</a>	17 of 150 genes, 11.3%	1481 of 47246 genes, 3.1%	0.00684	0.00%	0.00	N4BP2L2, BHLHB9, CXCL12, FST, CA2, BIN1, POLR2L, CACNA2D2, CTGF, LGR4, DAB2, PPP1R16B, EPB41L5, CLASP2, CYB5D2, EGR1, LRRN1
<a href="#">response to chemical</a>	34 of 150 genes, 22.7%	4802 of 47246 genes, 10.2%	0.00776	0.00%	0.00	PSMA5, AGL, CGN, CA2, GNG12, POLR2L, CXADR, CTGF, SMAD6, NEFH, CDO1, ATP5G3, EPB41L5, BCAR3, PINK1, EGR1, PRDX3, NDUFA10, SESN2, SSTR2, CXCL12, SLC31A1, DAB2, KLF15, TOB1, NTN4, RASL11B, GGH, QDPR, GATA5, PDE3B, GCH1, SH3BP4, TGFB3
<a href="#">negative regulation of response to stimulus</a>	17 of 150 genes, 11.3%	1499 of 47246 genes, 3.2%	0.00801	0.00%	0.00	PSMA5, SESN2, WWC1, CXCL12, FST, LGR4, SMAD6, DAB2, DUSP9, TOB1, RASL11B, PDE3B, CLASP2, EGR1, PINK1, SH3BP4, TGFB3
<a href="#">morphogenesis of an epithelium</a>	10 of 150 genes, 6.7%	525 of 47246 genes, 1.1%	0.00995	0.00%	0.00	PSMA5, NTN4, MYCN, GPC4, CA2, EPB41L5, IRX2, CLASP2, LGR4, DAB2

Supplementary File 1. ccRCC exhibits transcriptional changes of INI1 target genes  
Sub-table 3. INI1 target genes upregulated in ccRCC.

ABCA1  
ACTR2  
ADAM9  
ADAMTS2  
AHNAK  
AHR  
AMICA1  
ANO1  
ANO6  
ANTXR1  
ANXA1  
ANXA2  
ANXA2P2  
APOC1  
APOL1  
APOL2  
APOL6  
ARHGAP30  
ARL4A  
ARPC5  
ASF1B  
ASPM  
ATAD2  
ATHL1  
ATL3  
ATP8B3  
AURKA  
AURKB  
AXL  
BHLHE40  
BIRC3  
BIRC5  
BNIP3  
BRCA1  
BRIP1  
BST2  
BTAF1  
BTG3  
BTN2A2  
BTN3A1  
BTN3A2  
BTN3A3  
BUB1  
C1QA  
C1QB  
C1QC  
CALCRL  
CALU  
CARD8  
CASP8

CCDC34  
CCNB1  
CCND1  
CCND3  
CCR5  
CD109  
CD200R1  
CD38  
CD4  
CD58  
CD74  
CD84  
CD86  
CD8A  
CD96  
CD97  
CDC20  
CDC45  
CDC6  
CDCA5  
CDCA7  
CDCP1  
CDK1  
CDKN2A  
CDT1  
CENPE  
CENPK  
CENPM  
CENPQ  
CEP120  
CETP  
CHST14  
CHST7  
CKAP2  
CKAP2L  
CKAP4  
CLEC2D  
CNTLN  
COL23A1  
COL5A2  
COL8A1  
CTHRC1  
CTSS  
CTSZ  
CUL4B  
CXCL10  
CXCL16  
CXCR4  
DARS  
DDB2  
DDX58  
DDX60  
DENND1C

DEPDC1  
DLGAP5  
DLX5  
DNASE2  
DOCK8  
DOK2  
DRAM1  
DSN1  
E2F7  
E2F8  
ECT2  
EDNRB  
EMB  
EMP1  
EMP2  
ENO1  
EOMES  
EPST11  
ERO1L  
ETS1  
FAM114A1  
FAM198B  
FAM46A  
FAM64A  
FANCI  
FBN1  
FBN2  
FBXO5  
FCRL3  
FDXR  
FGFR1  
FKBP10  
FNDC3B  
FOLR2  
FOXF2  
FSTL1  
FYB  
G3BP1  
GALC  
GALNT1  
GALNT12  
GBP1  
GBP4  
GBP5  
GIMAP4  
GIMAP6  
GIMAP7  
GIMAP8  
GJA1  
GM2A  
GNG11  
GNLY  
GPNMB

GPX8  
GRK5  
GSN  
GTSE1  
GXYLT1  
GZMB  
H6PD  
HAPLN1  
HCLS1  
HEY2  
HIST1H1C  
HIST1H2BK  
HJURP  
HK2  
HLA-DQB1  
HLA-DRA  
HMGB2  
HMMR  
HMOX1  
HPSE  
HSPG2  
ID3  
IDO1  
IFI27  
IFI44L  
IFI6  
IFIH1  
IKBIP  
IKZF1  
IL10RA  
IL13RA1  
IL15  
IL2RB  
IL2RG  
IL7R  
INHBB  
INPP5D  
INSIG2  
IQGAP3  
IRF1  
IRF8  
ISG15  
ISG20  
ITGA4  
ITGB1  
ITGB2  
ITK  
ITPRIP  
JAG1  
JRKL  
KAL1  
KCTD9  
KDELC2

KIAA1586  
KIF11  
KIF14  
KIF18B  
KIF20B  
KLF4  
KLHL6  
KRT18  
KRT8  
LAG3  
LAMA4  
LAMC1  
LAMP2  
LAMP3  
LAPTM5  
LCK  
LCP1  
LCP2  
LDHA  
LDLRAD3  
LEPREL4  
LGALS1  
LGALS9  
LILRB4  
LMAN1  
LMNA  
LOX  
LSP1  
LYN  
LYZ  
MAD2L1  
MAP3K8  
MBNL1  
MCL1  
MELK  
MIR210HG  
MIS18BP1  
MKI67  
MPZL2  
MR1  
MS4A4A  
MS4A6A  
MSH2  
MSR1  
MTDH  
MYBL1  
MYEOV  
MYO3A  
MYOF  
MZT1  
N4BP2  
NAB1  
NCAPH



NCOA3  
NEK2  
NFATC2  
NKD2  
NKG7  
NLRC5  
NMI  
NOD2  
NOTCH2  
NOTCH3  
NPM1  
NRP2  
NUP107  
NUSAP1  
OAS2  
OAS3  
OASL  
OSMR  
P4HA1  
PAICS  
PALMD  
PARP14  
PCDHB14  
PDGFD  
PDIA4  
PDIA6  
PELI1  
PHLDA1  
PIK3R3  
PIK3R5  
PLAGL1  
PLEKHG1  
PLIN3  
PLOD1  
PLP2  
PLVAP  
PML  
PON2  
PPAP2C  
PPP1R3B  
PRDM1  
PRDX4  
PRF1  
PRODH  
PRR11  
PRRX1  
PSTPIP1  
PSTPIP2  
PTPRC  
PTRF  
PTTG1  
RAD51AP1  
RBM43

RCN1  
RCSD1  
RECQL  
RFX2  
RGS1  
RHOH  
RNASE6  
RP2  
RPF2  
RPL36  
RPS19  
RPS6KB1  
RRM2  
RSL1D1  
RUNX3  
S100A10  
S100A11  
S100A4  
S1PR1  
SAMD9  
SAMD9L  
SCAF11  
SEC61G  
SEMA6A  
SERPINB1  
SERPING1  
SERPINH1  
SH3PXD2B  
SIGLEC1  
SIX1  
SKA1  
SLAMF7  
SLC16A3  
SLC25A43  
SLC2A1  
SLC7A11  
SLC7A2  
SLFN11  
SLFN12  
SLFN13  
SLFN5  
SMC3  
SMC4  
SMCHD1  
SOAT1  
SOX17  
SP100  
SPARC  
SPRED1  
SRGN  
ST8SIA4  
STAT1  
STK17B

SWAP70  
TACC3  
TAGLN2  
TGFA  
THBD  
THG1L  
TK1  
TLR3  
TLR4  
TLR8  
TMED2  
TMEM123  
TMEM194A  
TMEM45A  
TMTC3  
TMX1  
TMX3  
TNFAIP8  
TNFRSF10A  
TNFRSF10D  
TNIP1  
TOP2A  
TOR1AIP1  
TPBG  
TPX2  
TRAC  
TRAF3IP3  
TRIM21  
TRIM5  
TRIM56  
TTF2  
TTK  
TUBB6  
TYMS  
UBE2C  
UCP2  
UHRF1  
UNC93B1  
VWF  
WASF2  
XAF1  
YME1L1  
ZMAT3  
ZNF217  
ZNF600  
ZNF611  
ZWINT

Supplementary File 1. ccRCC exhibits transcriptional changes of INI1 target genes  
 Sub-table 4. GO term analysis for INI1 target genes upregulated in ccRCC.

Gene Ontology term	Number of genes	Percentage of genes	Corrected P-value	FDR	False Positives	Genes annotated to the term
<a href="#">single-organism cellular process</a>	116 of 180 genes,	64.4%	2.85e-17	0.00%	0.00	MESP1, CEP120, TNFAIP8, GCLM, IFI16, AFF4, ANO6, ISG15, CAMSAP1, PELI1, PGK1, GFPT2, ANGPTL4, CERCAM, CXCR7, CHST7, NUP98, EFN A1, HIST1H3H, TMEM214, ID3, NUP153, BTG3, BST2, PRR16, RNF165, UBE2J1, PYCARD, IRX3, ARHGEF6, CDK2AP1, CHST15, COL4A2, DCLRE1B, EDEM2, FAM105B, TNFRSF10B, EFN2, CDCA7, LOX, POLE2, TMEFF2, SCD, RIF1, ID2, SPAST, PXDN, TMEM43, HEYL, FBXO5, RCC2, JAG2, PERP, MORC2, SERPINB9, COL4A1, JMJD6, MBD4, JARID2, PSRC1, ME2, KDEL2, PGAM1, UBASH3B, CCDC109B, TAGLN2, PLXNA3, TTC17, WASF2, SERTAD2, NSMAF, DDIT4, P4HA1, JAK1, CST3, MAFB, TULP3, S100A10, KATNAL1, SIRPA, DUSP1, KIAA0922, FUT11, N4BP2L2, FIGNL1, NID1, CRIP1, SOX11, NPTX2, RFTN1, PREX1, PNMA2, BATF3, NCOA3, ERN1, DIP2A, GXYLT1, JUN, PDK1, VWA1, NCK2, CEBPB, TYMS, VEGFB, EOMES, MCM6, KDM3A, SOX12, FABP6, ADARB1, CD1D, KLF6, STK39, CHST2, ITPR3, CXCL16
<a href="#">negative regulation of biological process</a>	66 of 180 genes,	36.7%	1.73e-15	0.00%	0.00	MESP1, MKI67IP, TNFAIP8, GCLM, IFI16, ISG15, PELI1, ANGPTL4, CXCR7, NUP98, EFNA1, HIST1H3H, ID3, NUP153, BTG3, BST2, UBE2J1, PYCARD, TCERG1, FAM89B, IRX3, S100A11, COL4A2, DCLRE1B, FAM105B, TNFRSF10B, EFN2, TMEFF2, ID2, PXDN, FBXO5, HEYL, RCC2, BHLHE40, SERPINB9, JARID2, HIST1H1C, PSRC1, UBASH3B, PLXNA3, WASF2, DDIT4, SERTAD2, CST3, MAFB, TULP3, DUSP1, KIAA0922, FIGNL1, N4BP2L2, LXN, SOX11, BATF3, ARRDC3, ERN1, DIP2A, JUN, CEBPB, NCK2, VEGFB, EOMES, KDM3A, FABP6, ADARB1, STK39, ITPR3
<a href="#">positive regulation of biological process</a>	68 of 180 genes,	37.8%	2.61e-14	0.00%	0.00	MESP1, CEP120, IFI16, ANO6, ISG15, PELI1, ANGPTL4, CXCR7, EFNA1, HIST1H3H, ID3, BST2, PRR16, RNF165, PYCARD, IRX3, ARHGEF6, CDK2AP1, EDEM2, FAM105B, TNFRSF10B, EFN2, RIF1, ID2, SPAST, FBXO5, HEYL, RCC2, JAG2, PERP, SERPINB9, JARID2, MARCKSL1, PSRC1, RNF125, PLXNA3, WASF2, DDIT4, NSMAF, SERTAD2, JAK1, MAFB, S100A10, DUSP1, N4BP2L2, NID1, SOX11, RFTN1, PNMA2, PREX1, ARRDC3, NCOA3, ERN1, JUN, PDK1, CEBPB, NCK2, VEGFB, EOMES, KDM3A, SOX12, ADARB1, CD1D, KLF6, STK39, ITPR3, CXCL16, PRPF6
<a href="#">negative regulation of cellular process</a>	60 of 180 genes,	33.3%	9.36e-14	0.00%	0.00	SERPINB9, BHLHE40, MESP1, MKI67IP, TNFAIP8, GCLM, JARID2, IFI16, HIST1H1C, PSRC1, ISG15, PELI1, UBASH3B, PLXNA3, ANGPTL4, CXCR7, WASF2, SERTAD2, DDIT4, EFNA1, HIST1H3H, MAFB, ID3, CST3, TULP3, KIAA0922, BTG3, BST2, DUSP1, UBE2J1, PYCARD, TCERG1, N4BP2L2, FIGNL1, FAM89B, IRX3, SOX11, LXN, S100A11, BATF3, DCLRE1B, TNFRSF10B, EFN2, ERN1, JUN, NCK2, CEBPB, VEGFB, TMEFF2, EOMES, ID2, KDM3A, FABP6, ADARB1, PXDN, STK39, FBXO5, HEYL, RCC2, ITPR3
<a href="#">anatomical structure development</a>	66 of 180 genes,	36.7%	2.93e-13	0.00%	0.00	MESP1, CEP120, JMJD6, COL4A1, JARID2, IFI16, AFF4, ANO6, ISG15, CAMSAP1, PGK1, UBASH3B, TAGLN2, PLXNA3, ANGPTL4, CXCR7, WASF2, DDIT4, EFNA1, JAK1, MAFB, ID3, CST3, TULP3, S100A10, KIAA0922, BST2, DUSP1, RNF165, UBE2J1, N4BP2L2, NID1, CRIP1, IRX3, SOX11, PREX1, BATF3, COL4A2, NCOA3, ARRDC3, FAM105B, DONSON, TNFRSF10B, EFN2, JUN, DIP2A, NCK2, LOX, CEBPB, TYMS, VEGFB, TMEFF2, EOMES, ID2, KDM3A, SPAST, SOX12, KLF6, CD1D, CHST2, FBXO5, HEYL, RCC2, MPZL2, JAG2, PERP
<a href="#">single-multicellular organism process</a>	69 of 180 genes,	38.3%	6.45e-13	0.00%	0.00	MESP1, CEP120, IFI16, ANO6, ISG15, CAMSAP1, PELI1, ANGPTL4, CXCR7, EFNA1, HIST1H3H, ID3, BST2, RNF165, UBE2J1, PYCARD, IRX3, COL4A2, FAM105B, TNFRSF10B, EFN2, LOX, RIF1, ID2, SPAST, HEYL, JAG2, PERP, BHLHE40, COL4A1, JMJD6, JARID2, UBASH3B, PLXNA3, WASF2, DDIT4, JAK1, CST3, MAFB, TULP3, DUSP1, KIAA0922, FIGNL1, N4BP2L2, CRIP1, NID1, SOX11, NPTX2, RFTN1, BATF3, PREX1, ARRDC3, NCOA3, DONSON, DIP2A, JUN, VWA1, CEBPB, NCK2, TYMS, VEGFB, EOMES, KDM3A, SOX12, CD1D, KLF6, CHST2, STK39, ITPR3
<a href="#">developmental process</a>	68 of 180 genes,	37.8%	8.84e-13	0.00%	0.00	MESP1, CEP120, JMJD6, COL4A1, JARID2, IFI16, AFF4, ANO6, ISG15, CAMSAP1, PGK1, UBASH3B, TAGLN2, PLXNA3, ANGPTL4, CXCR7, WASF2, DDIT4, EFNA1, JAK1, MAFB, ID3, CST3, TULP3, S100A10, KIAA0922, BST2, DUSP1, RNF165, UBE2J1, N4BP2L2, FIGNL1, NID1, CRIP1, IRX3, SOX11, PREX1, BATF3, COL4A2, NCOA3, ARRDC3, FAM105B, DONSON, TNFRSF10B, EFN2, JUN, DIP2A, NCK2, LOX, CEBPB, TYMS, VEGFB, TMEFF2, RIF1, EOMES, ID2, KDM3A, SPAST, SOX12, KLF6, CD1D, CHST2, FBXO5, HEYL, RCC2, MPZL2, JAG2, PERP
<a href="#">multicellular organismal process</a>	75 of 180 genes,	41.7%	3.33e-12	0.00%	0.00	MESP1, CEP120, GCLM, IFI16, AFF4, ANO6, ISG15, CAMSAP1, PELI1, ANGPTL4, CXCR7, EFNA1, HIST1H3H, ID3, BST2, RNF165, UBE2J1, PYCARD, IRX3, COL4A2, FAM105B, TNFRSF10B, EFN2, LOX, RIF1, ID2, SPAST, FBXO5, HEYL, JAG2, PERP, BHLHE40, COL4A1, JMJD6, JARID2, CCDC50, UBASH3B, PLXNA3, WASF2, DDIT4, JAK1, CST3, MAFB, TULP3, KATNAL1, DUSP1, KIAA0922, FIGNL1, N4BP2L2, CRIP1, NID1, LXN, SOX11, NPTX2, RFTN1, BATF3, PREX1, ARRDC3, NCOA3, DONSON, DIP2A, JUN, VWA1, CEBPB, NCK2, TYMS, VEGFB, EOMES, KDM3A, SOX12, CD1D, KLF6, STK39, CHST2, ITPR3
<a href="#">positive regulation of cellular process</a>	60 of 180 genes,	33.3%	4.38e-12	0.00%	0.00	MESP1, CEP120, JARID2, IFI16, PSRC1, MARCKSL1, RNF125, ANO6, ISG15, PELI1, PLXNA3, CXCR7, WASF2, SERTAD2, NSMAF, DDIT4, EFNA1, MAFB, ID3, S100A10, BST2, DUSP1, PRR16, RNF165, PYCARD, N4BP2L2, IRX3, SOX11, ARHGEF6, CDK2AP1, PREX1, PNMA2, EDEM2, NCOA3, ARRDC3, TNFRSF10B, EFN2, ERN1, JUN, PDK1, NCK2, CEBPB, VEGFB, RIF1, EOMES, ID2, KDM3A, SPAST, SOX12, ADARB1, CD1D, KLF6, FBXO5, HEYL, RCC2, JAG2, PERP, ITPR3, PRPF6, CXCL16

<a href="#">single-organism developmental process</a>	66 of 180 genes, 36.7%	6355 of 47246 genes, 13.5%	6.20e-12	0.00%	0.00	MESP1, CEP120, JMJD6, COL4A1, JARID2, IFI16, AFF4, ANO6, ISG15, CAMSAP1, PGK1, UBASH3B, TAGLN2, PLXNA3, ANGPTL4, CXCR7, WASF2, DDIT4, EFNA1, JAK1, MAFB, ID3, TULP3, S100A10, KIAA0922, BST2, DUSP1, RNF165, UBE2J1, N4BP2L2, FIGNL1, NID1, CRIP1, IRX3, SOX11, PREX1, BATF3, COL4A2, NCOA3, ARRDC3, FAM105B, DONSON, TNFRSF10B, EFN2, JUN, DIP2A, NCK2, LOX, CEBPB, TYMS, VEGFB, TMEFF2, RIF1, EOMES, ID2, KDM3A, SPAST, SOX12, KLF6, CD1D, CHST2, FBXO5, HEYL, RCC2, JAG2, PERP
<a href="#">single-organism process</a>	133 of 180 genes, 73.9%	21413 of 47246 genes, 45.3%	1.01e-11	0.00%	0.00	MESP1, HRASLS, TNFAIP8, IFI16, AFF4, ANO6, SPSB1, ISG15, CAMSAP1, DENND4B, CXCR7, NUP98, EFNA1, HIST1H3H, SRXN1, RNF165, PYCARD, IRX3, ARHGEF6, CHST15, EDEM2, COL4A2, CDCA7, LOX, TMEFF2, SPAST, PXDN, FBXO5, RCC2, JAG2, PERP, SERPINB9, JMJD6, PSRC1, ME2, MARCKSL1, KDELC2, UBASH3B, CCDC109B, TAGLN2, PLXNA3, TTC17, WASF2, NSMAF, DDIT4, JAK1, MAFB, CST3, TULP3, DUSP1, N4BP2L2, FIGNL1, CRIP1, SOX11, NPTX2, RFTN1, WSB1, BATF3, NCOA3, ARRDC3, DONSON, DIP2A, VWA1, NCK2, CEBPB, MCM6, EOMES, SOX12, ADARB1, MPZL2, CXCL16, CEP120, GCLM, PELI1, PGK1, GFPT2, ANGPTL4, CERCAM, CHST7, ID3, TMEM214, LY6E, BTG3, BST2, NUP153, PRR16, UBE2J1, FSTL1, FAM89B, CDK2AP1, DCLRE1B, S100A11, FAM105B, TNFRSF10B, EFN2, POLE2, ID2, RIF1, SCD, HEYL, TMEM43, IL13RA1, MORC2, BHLHE40, COL4A1, MBD4, JARID2, IPO9, PGAM1, SERTAD2, GNG11, P4HA1, KATNAL1, S100A10, KIAA0922, SIRPA, FUT11, NID1, PNMA2, PREX1, ERN1, GXYLT1, JUN, PDK1, TYMS, VEGFB, KDM3A, FABP6, CD1D, KLF6, CHST2, STK39, ITPR3
<a href="#">cell differentiation</a>	50 of 180 genes, 27.8%	3963 of 47246 genes, 8.4%	3.23e-11	0.00%	0.00	MESP1, CEP120, JMJD6, COL4A1, JARID2, IFI16, AFF4, ISG15, CAMSAP1, PGK1, UBASH3B, TAGLN2, PLXNA3, ANGPTL4, CXCR7, WASF2, DDIT4, EFNA1, JAK1, MAFB, ID3, TULP3, S100A10, KIAA0922, RNF165, UBE2J1, N4BP2L2, FIGNL1, IRX3, SOX11, PREX1, BATF3, COL4A2, NCOA3, EFN2, JUN, NCK2, CEBPB, TYMS, EOMES, ID2, KDM3A, SPAST, SOX12, CD1D, KLF6, HEYL, FBXO5, RCC2, JAG2
<a href="#">response to stress</a>	54 of 180 genes, 30.0%	4597 of 47246 genes, 9.7%	3.94e-11	0.00%	0.00	SERPINB9, MBD4, GCLM, IFI16, ANO6, ISG15, PELI1, UBASH3B, ANGPTL4, CXCR7, DDIT4, NUP98, JAK1, HIST1H3H, ID3, CST3, SRXN1, NUP153, BST2, DUSP1, UBE2J1, PYCARD, FIGNL1, FSTL1, CRIP1, LXN, ARHGEF6, RFTN1, PDLIM1, DCLRE1B, EDEM2, FAM105B, TNFRSF10B, ERN1, JUN, PDK1, VWA1, NCK2, CEBPB, LOX, VEGFB, POLE2, TMEFF2, RIF1, ID2, KDM3A, ADARB1, PXDN, CD1D, KLF6, STK39, CHST2, ITPR3, CXCL16
<a href="#">cellular developmental process</a>	50 of 180 genes, 27.8%	4180 of 47246 genes, 8.8%	2.50e-10	0.00%	0.00	MESP1, CEP120, JMJD6, COL4A1, JARID2, IFI16, AFF4, ISG15, CAMSAP1, PGK1, UBASH3B, TAGLN2, PLXNA3, ANGPTL4, CXCR7, WASF2, DDIT4, EFNA1, JAK1, MAFB, ID3, TULP3, S100A10, KIAA0922, RNF165, UBE2J1, N4BP2L2, FIGNL1, IRX3, SOX11, PREX1, BATF3, COL4A2, NCOA3, EFN2, JUN, NCK2, CEBPB, TYMS, EOMES, ID2, KDM3A, SPAST, SOX12, CD1D, KLF6, HEYL, FBXO5, RCC2, JAG2
<a href="#">negative regulation of metabolic process</a>	42 of 180 genes, 23.3%	3015 of 47246 genes, 6.4%	2.67e-10	0.00%	0.00	SERPINB9, BHLHE40, MESP1, MKI67IP, TNFAIP8, JARID2, IFI16, HIST1H1C, ISG15, UBASH3B, DDIT4, NUP98, EFNA1, HIST1H3H, ID3, CST3, NUP153, DUSP1, BST2, UBE2J1, PYCARD, TCERG1, N4BP2L2, SOX11, LXN, BATF3, S100A11, ARRDC3, ERN1, DIP2A, JUN, CEBPB, NCK2, VEGFB, TMEFF2, EOMES, ID2, KDM3A, ADARB1, STK39, HEYL, FBXO5
<a href="#">negative regulation of macromolecule metabolic process</a>	40 of 180 genes, 22.2%	2775 of 47246 genes, 5.9%	3.90e-10	0.00%	0.00	SERPINB9, BHLHE40, MESP1, TNFAIP8, JARID2, IFI16, HIST1H1C, ISG15, UBASH3B, DDIT4, NUP98, EFNA1, HIST1H3H, ID3, CST3, NUP153, DUSP1, BST2, UBE2J1, PYCARD, TCERG1, N4BP2L2, SOX11, LXN, BATF3, S100A11, ERN1, DIP2A, JUN, CEBPB, NCK2, VEGFB, TMEFF2, EOMES, ID2, KDM3A, ADARB1, STK39, HEYL, FBXO5
<a href="#">regulation of cellular process</a>	111 of 180 genes, 61.7%	16557 of 47246 genes, 35.0%	4.95e-10	0.00%	0.00	MESP1, CEP120, MKI67IP, TNFAIP8, GCLM, IFI16, AFF4, ANO6, SPSB1, ISG15, CAMSAP1, PELI1, ANGPTL4, DENND4B, PHTF2, CXCR7, PTRF, NUP98, EFNA1, HIST1H3H, ID3, LY6E, NUP153, BST2, BTG3, PRR16, RNF165, UBE2J1, PYCARD, TCERG1, FSTL1, IRX3, FAM89B, ARHGEF6, CDK2AP1, S100A11, DCLRE1B, EDEM2, FAM105B, TNFRSF10B, EFN2, CDCA7, TMEFF2, RIF1, ID2, SPAST, PXDN, HEYL, FBXO5, RCC2, JAG2, PERP, IL13RA1, SERPINB9, BHLHE40, JMJD6, JARID2, HIST1H1C, PSRC1, MARCKSL1, ME2, RNF125, PGAM1, UBASH3B, PLXNA3, WASF2, SERTAD2, NSMAF, DDIT4, GNG11, JAK1, CST3, MAFB, TULP3, S100A10, DUSP1, KIAA0922, FIGNL1, N4BP2L2, CRIP1, SOX11, LXN, POU5F1B, RFTN1, PDLIM1, WSB1, PREX1, PNMA2, BATF3, NCOA3, ARRDC3, ERN1, DIP2A, JUN, PDK1, NCK2, CEBPB, TYMS, VEGFB, EOMES, KDM3A, SOX12, FABP6, ADARB1, IRF2BP2, CD1D, KLF6, STK39, ITPR3, PRPF6, CXCL16
<a href="#">regulation of biological process</a>	114 of 180 genes, 63.3%	17415 of 47246 genes, 36.9%	8.33e-10	0.00%	0.00	MESP1, CEP120, MKI67IP, TNFAIP8, GCLM, IFI16, AFF4, ANO6, SPSB1, ISG15, CAMSAP1, PELI1, ANGPTL4, DENND4B, PHTF2, CXCR7, PTRF, NUP98, EFNA1, HIST1H3H, ID3, LY6E, NUP153, BST2, BTG3, PRR16, RNF165, UBE2J1, PYCARD, TCERG1, FSTL1, IRX3, FAM89B, ARHGEF6, CDK2AP1, S100A11, COL4A2, DCLRE1B, EDEM2, FAM105B, TNFRSF10B, EFN2, CDCA7, TMEFF2, RIF1, ID2, SPAST, PXDN, HEYL, FBXO5, RCC2, JAG2, PERP, IL13RA1, SERPINB9, BHLHE40, JMJD6, JARID2, HIST1H1C, PSRC1, MARCKSL1, ME2, RNF125, PGAM1, UBASH3B, PLXNA3, WASF2, SERTAD2, NSMAF, DDIT4, GNG11, JAK1, CST3, MAFB, TULP3, S100A10, DUSP1, KIAA0922, N4BP2L2, FIGNL1, NID1, CRIP1, SOX11, LXN, POU5F1B, RFTN1, PDLIM1, EFCAB4A, WSB1, PREX1, PNMA2, BATF3, NCOA3, ARRDC3, ERN1, DIP2A, JUN, PDK1, NCK2, CEBPB, TYMS, VEGFB, EOMES, KDM3A, SOX12, FABP6, ADARB1, IRF2BP2, CD1D, KLF6, STK39, ITPR3, PRPF6, CXCL16

<a href="#">regulation of macromolecule metabolic process</a>	75 of 180 genes, 41.7%	8800 of 47246 genes, 18.6%	1.16e-09	0.00%	0.00	MESP1, TNFAIP8, IFI16, AFF4, ISG15, PELI1, PHTF2, CXCR7, PTRF, NUP98, EFNA1, HIST1H3H, ID3, NUP153, BST2, PRR16, RNF165, UBE2J1, PYCARD, TCERG1, FSTL1, IRX3, CDK2AP1, S100A11, EDEM2, FAM105B, TNFRSF10B, CDCA7, TMEFF2, RIF1, ID2, FBXO5, HEYL, PERP, BHLHE40, SERPINB9, JMJD6, JARID2, HIST1H1C, PSRC1, RNF125, PGAM1, UBASH3B, DDIT4, NSMAF, SERTAD2, CST3, MAFB, TULP3, DUSP1, FIGNL1, N4BP2L2, CRIP1, LXN, SOX11, POU5F1B, PDLIM1, BATF3, ARRDC3, NCOA3, ERN1, DIP2A, JUN, CEBPB, NCK2, TYMS, VEGFB, EOMES, KDM3A, SOX12, IRF2BP2, ADARB1, KLF6, STK39, PRPF6
<a href="#">regulation of metabolic process</a>	78 of 180 genes, 43.3%	9416 of 47246 genes, 19.9%	1.31e-09	0.00%	0.00	MESP1, MKI67IP, TNFAIP8, IFI16, AFF4, ISG15, PELI1, PHTF2, CXCR7, PTRF, NUP98, EFNA1, HIST1H3H, ID3, NUP153, BST2, PRR16, RNF165, UBE2J1, PYCARD, TCERG1, FSTL1, IRX3, CDK2AP1, S100A11, EDEM2, FAM105B, TNFRSF10B, CDCA7, TMEFF2, RIF1, ID2, FBXO5, HEYL, PERP, SERPINB9, BHLHE40, JMJD6, JARID2, HIST1H1C, ME2, PSRC1, RNF125, PGAM1, UBASH3B, SERTAD2, DDIT4, NSMAF, CST3, MAFB, TULP3, DUSP1, FIGNL1, N4BP2L2, CRIP1, SOX11, LXN, POU5F1B, PDLIM1, BATF3, ARRDC3, NCOA3, ERN1, DIP2A, JUN, PDK1, CEBPB, NCK2, TYMS, VEGFB, EOMES, KDM3A, SOX12, IRF2BP2, ADARB1, KLF6, STK39, PRPF6
<a href="#">biological regulation</a>	118 of 180 genes, 65.6%	18550 of 47246 genes, 39.3%	1.42e-09	0.00%	0.00	MESP1, CEP120, MKI67IP, TNFAIP8, GCLM, IFI16, AFF4, ANO6, SPSB1, ISG15, CAMSAP1, PELI1, ANGPTL4, DENND4B, PHTF2, CXCR7, PTRF, NUP98, EFNA1, HIST1H3H, ID3, LY6E, NUP153, BST2, BTG3, PRR16, RNF165, UBE2J1, PYCARD, TCERG1, FSTL1, IRX3, FAM89B, DENND5A, ARHGEF6, CDK2AP1, S100A11, COL4A2, DCLRE1B, EDEM2, FAM105B, TNFRSF10B, EFN2, CDCA7, POLE2, TMEFF2, RIF1, ID2, SPAST, PXDN, HEYL, FBXO5, RCC2, JAG2, PERP, IL13RA1, SERPINB9, BHLHE40, JMJD6, JARID2, HIST1H1C, PSRC1, ME2, MARCKSL1, RNF125, PGAM1, UBASH3B, CDC109B, PLXNA3, WASF2, SERTAD2, NSMAF, DDIT4, GNG11, JAK1, CST3, MAFB, TULP3, S100A10, DUSP1, KIAA0922, N4BP2L2, FIGNL1, NID1, CRIP1, SOX11, LXN, POU5F1B, RFTN1, PDLIM1, EFCAB4A, WSB1, PREX1, PNMA2, BATF3, NCOA3, ARRDC3, AHS2, ERN1, DIP2A, JUN, PDK1, NCK2, CEBPB, TYMS, VEGFB, EOMES, KDM3A, SOX12, FABP6, ADARB1, IRF2BP2, CD1D, KLF6, STK39, ITPR3, PRPF6, CXCL16
<a href="#">multicellular organism development</a>	56 of 180 genes, 31.1%	5419 of 47246 genes, 11.5%	2.26e-09	0.00%	0.00	MESP1, CEP120, JMJD6, COL4A1, JARID2, IFI16, ANO6, ISG15, CAMSAP1, UBASH3B, PLXNA3, ANGPTL4, CXCR7, WASF2, DDIT4, EFNA1, JAK1, MAFB, ID3, TULP3, KIAA0922, BST2, DUSP1, RNF165, N4BP2L2, NID1, CRIP1, IRX3, SOX11, PREX1, BATF3, COL4A2, NCOA3, ARRDC3, FAM105B, DONSON, TNFRSF10B, EFN2, JUN, DIP2A, NCK2, LOX, CEBPB, TYMS, VEGFB, EOMES, ID2, KDM3A, SPAST, SOX12, KLF6, CD1D, CHST2, HEYL, JAG2, PERP
<a href="#">cellular process</a>	151 of 180 genes, 83.9%	28346 of 47246 genes, 60.0%	5.11e-09	0.00%	0.00	MESP1, TNFAIP8, IFI16, AFF4, ANO6, SPSB1, ISG15, CAMSAP1, DENND4B, PHTF2, CXCR7, PTRF, NUP98, EFNA1, HIST1H3H, SRXN1, RNF165, PYCARD, PTGFRN, IRX3, ARHGEF6, CHST15, EDEM2, COL4A2, N4BP2, CDCA7, LOX, TMEFF2, SPAST, PXDN, FBXO5, RCC2, JAG2, PERP, SERPINB9, JMJD6, PSRC1, ME2, MARCKSL1, RNF125, KDELC2, UBASH3B, CDC109B, TAGLN2, PLXNA3, TTC17, WASF2, NSMAF, DDIT4, JAK1, MAFB, CST3, TULP3, DUSP1, N4BP2L2, FIGNL1, CRIP1, SOX11, NPTX2, RFTN1, WSB1, BATF3, NCOA3, ARRDC3, DIP2A, VWA1, NCK2, CKAP4, CEBPB, MCM6, EOMES, SOX12, SPCS3, ADARB1, IRF2BP2, CXCL16, CEP120, MKI67IP, GCLM, PELI1, PGK1, GFPT2, ANGPTL4, CERCAM, CHST7, TMEM214, ID3, LY6E, BTG3, BST2, NUP153, PRR16, UBE2J1, TCERG1, FSTL1, RIMKLB, FAM89B, MGEA5, CDK2AP1, DCLRE1B, S100A11, FAM105B, TNFRSF10B, EFN2, POLE2, RNF24, ID2, RIF1, SCD, TMEM43, HEYL, IL13RA1, MORC2, BHLHE40, COL4A1, MBD4, JARID2, HIST1H1C, RPF2, PGAM1, SERTAD2, GNG11, P4HA1, FEM1C, KATNAL1, S100A10, KIAA0922, SIRPA, FUT11, NID1, LXN, POU5F1B, PDLIM1, PNMA2, PREX1, ERN1, GXYLT1, JUN, PDK1, TYMS, VEGFB, KDM3A, SLC25A43, GEMIN5, FABP6, CD1D, KLF6, STK39, CHST2, ITPR3, PRPF6
<a href="#">regulation of primary metabolic process</a>	72 of 180 genes, 40.0%	8676 of 47246 genes, 18.4%	1.70e-08	0.00%	0.00	MESP1, TNFAIP8, IFI16, AFF4, ISG15, PELI1, PHTF2, CXCR7, PTRF, EFNA1, HIST1H3H, ID3, BST2, PRR16, RNF165, UBE2J1, PYCARD, TCERG1, FSTL1, IRX3, CDK2AP1, S100A11, EDEM2, FAM105B, TNFRSF10B, CDCA7, RIF1, ID2, FBXO5, HEYL, PERP, BHLHE40, SERPINB9, JMJD6, JARID2, HIST1H1C, ME2, PSRC1, RNF125, PGAM1, UBASH3B, DDIT4, NSMAF, SERTAD2, CST3, MAFB, TULP3, DUSP1, FIGNL1, N4BP2L2, LXN, SOX11, POU5F1B, PDLIM1, BATF3, ARRDC3, NCOA3, ERN1, JUN, PDK1, CEBPB, NCK2, TYMS, VEGFB, EOMES, KDM3A, SOX12, IRF2BP2, ADARB1, KLF6, STK39, PRPF6
<a href="#">system development</a>	50 of 180 genes, 27.8%	4719 of 47246 genes, 10.0%	2.26e-08	0.00%	0.00	MESP1, CEP120, JMJD6, COL4A1, JARID2, IFI16, ANO6, ISG15, CAMSAP1, UBASH3B, PLXNA3, ANGPTL4, CXCR7, WASF2, DDIT4, EFNA1, JAK1, MAFB, ID3, TULP3, KIAA0922, RNF165, N4BP2L2, NID1, CRIP1, IRX3, SOX11, PREX1, BATF3, COL4A2, NCOA3, ARRDC3, FAM105B, EFN2, JUN, NCK2, CEBPB, LOX, TYMS, VEGFB, EOMES, ID2, KDM3A, SPAST, SOX12, CD1D, KLF6, HEYL, JAG2, PERP
<a href="#">animal organ development</a>	41 of 180 genes, 22.8%	3308 of 47246 genes, 7.0%	2.26e-08	0.00%	0.00	MESP1, CEP120, JMJD6, COL4A1, JARID2, IFI16, ANO6, ISG15, UBASH3B, PLXNA3, WASF2, DDIT4, EFNA1, MAFB, ID3, TULP3, KIAA0922, N4BP2L2, CRIP1, NID1, IRX3, SOX11, PREX1, BATF3, ARRDC3, NCOA3, EFN2, JUN, CEBPB, LOX, TYMS, VEGFB, ID2, EOMES, KDM3A, SOX12, CD1D, KLF6, HEYL, JAG2, PERP
<a href="#">regulation of nitrogen compound metabolic process</a>	71 of 180 genes, 39.4%	8535 of 47246 genes, 18.1%	2.33e-08	0.00%	0.00	MESP1, TNFAIP8, IFI16, AFF4, ISG15, PELI1, PHTF2, CXCR7, PTRF, EFNA1, HIST1H3H, ID3, BST2, PRR16, RNF165, UBE2J1, PYCARD, TCERG1, FSTL1, IRX3, CDK2AP1, S100A11, EDEM2, FAM105B, TNFRSF10B, CDCA7, RIF1, ID2, FBXO5, HEYL, PERP, BHLHE40, SERPINB9, JMJD6, JARID2, HIST1H1C, ME2, PSRC1, RNF125, PGAM1, UBASH3B, DDIT4, NSMAF, SERTAD2, CST3, MAFB, TULP3, DUSP1, FIGNL1, N4BP2L2, LXN, SOX11, POU5F1B, PDLIM1, BATF3, ARRDC3, NCOA3, ERN1, JUN, CEBPB, NCK2, TYMS, VEGFB, EOMES, KDM3A, SOX12, IRF2BP2, ADARB1, KLF6, STK39, PRPF6

<a href="#">anatomical structure morphogenesis</a>	36 of 180 genes, 20.0%	2606 of 47246 genes, 5.5%	2.58e-08	0.00%	0.00	MESP1, JMJD6, COL4A1, CAMSAP1, PLXNA3, ANGPTL4, CXCR7, WASF2, EFNA1, JAK1, MAFB, CST3, ID3, TULP3, S100A10, DUSP1, RNF165, CRIP1, IRX3, SOX11, COL4A2, PREX1, FAM105B, EFN2, JUN, CEBPB, VEGFB, TMEFF2, ID2, EOMES, SPAST, HEYL, JAG2, MPZL2, RCC2, PERP
<a href="#">immune system process</a>	40 of 180 genes, 22.2%	3257 of 47246 genes, 6.9%	5.63e-08	0.00%	0.00	SERPINB9, JMJD6, JARID2, IFI16, RNF125, ANO6, ISG15, PELI1, UBASH3B, CXCR7, WASF2, DDIT4, JAK1, HIST1H3H, MAFB, SIRPA, KIAA0922, BST2, PYCARD, N4BP2L2, CRIP1, SOX11, RFTN1, BATF3, PREX1, FAM105B, TNFRSF10B, EFN2, JUN, CEBPB, NCK2, VEGFB, ID2, EOMES, ADARB1, CD1D, KLF6, PXDN, JAG2, CXCL16
<a href="#">regulation of cellular metabolic process</a>	72 of 180 genes, 40.0%	8943 of 47246 genes, 18.9%	7.32e-08	0.00%	0.00	MESP1, MKI67IP, TNFAIP8, IFI16, AFF4, ISG15, PELI1, PHTF2, CXCR7, PTRF, EFNA1, HIST1H3H, ID3, BST2, PRR16, RNF165, UBE2J1, PYCARD, TCERG1, FSTL1, IRX3, CDK2AP1, S100A11, FAM105B, TNFRSF10B, CDCA7, RIF1, ID2, FBXO5, HEYL, PERP, BHLHE40, SERPINB9, JMJD6, JARID2, HIST1H1C, ME2, PSRC1, RNF125, PGAM1, UBASH3B, DDIT4, NSMAF, SERTAD2, CST3, MAFB, TULP3, DUSP1, FIGNL1, N4BP2L2, LXN, SOX11, POU5F1B, PDLIM1, BATF3, ARRDC3, NCOA3, ERN1, JUN, PDK1, CEBPB, NCK2, TYMS, VEGFB, EOMES, KDM3A, SOX12, IRF2BP2, ADARB1, KLF6, STK39, PRPF6
<a href="#">response to stimulus</a>	88 of 180 genes, 48.9%	12399 of 47246 genes, 26.2%	1.07e-07	0.00%	0.00	MESP1, GCLM, IFI16, ANO6, SPSB1, ISG15, PELI1, ANGPTL4, DENND4B, CXCR7, NUP98, EFNA1, HIST1H3H, ID3, SRXN1, LY6E, NUP153, BST2, RNF165, UBE2J1, PYCARD, FSTL1, DENND5A, FAM89B, ARHGEF6, S100A11, COL4A2, DCLRE1B, EDEM2, FAM105B, TNFRSF10B, EFN2, LOX, POLE2, TMEFF2, RIF1, ID2, PXDN, HEYL, RCC2, JAG2, PERP, IL13RA1, SERPINB9, BHLHE40, COL4A1, JMJD6, MBD4, RNF125, UBASH3B, PLXNA3, WASF2, DDIT4, NSMAF, GNG11, JAK1, CST3, TULP3, DUSP1, KIAA0922, FIGNL1, CRIP1, SOX11, LXN, RFTN1, PDLIM1, WSB1, BATF3, PREX1, ARRDC3, NCOA3, ERN1, JUN, PDK1, VWA1, CEBPB, NCK2, TYMS, VEGFB, EOMES, KDM3A, ADARB1, CD1D, KLF6, STK39, CHST2, ITPR3, CXCL16
<a href="#">cell proliferation</a>	31 of 180 genes, 17.2%	2107 of 47246 genes, 4.5%	1.79e-07	0.00%	0.00	N4BP2L2, FIGNL1, CEP120, CRIP1, SOX11, JARID2, IFI16, MARCKSL1, S100A11, TNFRSF10B, PELI1, EFN2, ERN1, JUN, PDK1, CDCA7, NCK2, CEBPB, TYMS, VEGFB, ID2, DDIT4, JAK1, FABP6, ADARB1, CD1D, KIAA0922, BTG3, BST2, JAG2, PYCARD
<a href="#">negative regulation of nitrogen compound metabolic process</a>	34 of 180 genes, 18.9%	2516 of 47246 genes, 5.3%	1.87e-07	0.00%	0.00	SERPINB9, BHLHE40, MESP1, TNFAIP8, JARID2, IFI16, HIST1H1C, ISG15, UBASH3B, DDIT4, EFNA1, HIST1H3H, CST3, ID3, DUSP1, BST2, UBE2J1, PYCARD, N4BP2L2, TCERG1, LXN, SOX11, BATF3, S100A11, JUN, CEBPB, NCK2, ID2, EOMES, KDM3A, ADARB1, HEYL, FBXO5, STK39
<a href="#">regulation of response to stimulus</a>	46 of 180 genes, 25.6%	4377 of 47246 genes, 9.3%	2.52e-07	0.00%	0.00	SERPINB9, MESP1, GCLM, IFI16, ANO6, PELI1, UBASH3B, PLXNA3, DENND4B, CXCR7, WASF2, DDIT4, NUP98, EFNA1, JAK1, HIST1H3H, TULP3, NUP153, KIAA0922, BST2, DUSP1, RNF165, UBE2J1, PYCARD, FIGNL1, FAM89B, SOX11, ARHGEF6, RFTN1, EDEM2, PREX1, ARRDC3, FAM105B, NCOA3, TNFRSF10B, EFN2, ERN1, JUN, NCK2, VEGFB, RIF1, PXDN, CD1D, STK39, HEYL, JAG2
<a href="#">response to chemical</a>	48 of 180 genes, 26.7%	4802 of 47246 genes, 10.2%	4.88e-07	0.00%	0.00	SERPINB9, COL4A1, MBD4, GCLM, ANO6, ISG15, PELI1, PLXNA3, CXCR7, DDIT4, EFNA1, JAK1, GNG11, ID3, SRXN1, BST2, DUSP1, RNF165, UBE2J1, PYCARD, FSTL1, CRIP1, FAM89B, SOX11, RFTN1, PREX1, COL4A2, EDEM2, NCOA3, FAM105B, TNFRSF10B, EFN2, ERN1, JUN, PDK1, CEBPB, LOX, NCK2, TYMS, VEGFB, ID2, KDM3A, PXDN, KLF6, HEYL, ITPR3, CXCL16, IL13RA1
<a href="#">macromolecule metabolic process</a>	105 of 180 genes, 58.3%	16823 of 47246 genes, 35.6%	7.05e-07	0.00%	0.00	MESP1, MKI67IP, TNFAIP8, IFI16, AFF4, SPSB1, ISG15, PELI1, PHTF2, CXCR7, PTRF, CHST7, NUP98, EFNA1, HIST1H3H, ID3, NUP153, BST2, PRR16, RNF165, UBE2J1, PYCARD, TCERG1, RIMKLB, FSTL1, IRX3, MGEA5, ARHGEF6, CDK2AP1, CHST15, S100A11, COL4A2, DCLRE1B, EDEM2, FAM105B, TNFRSF10B, N4BP2, CDCA7, LOX, RNF24, POLE2, TMEFF2, RIF1, ID2, HEYL, FBXO5, JAG2, PERP, SERPINB9, BHLHE40, COL4A1, JMJD6, MBD4, JARID2, HIST1H1C, PSRC1, RNF125, RPF2, PGAM1, UBASH3B, SERTAD2, DDIT4, NSMAF, P4HA1, JAK1, CST3, MAFB, TULP3, FEM1C, DUSP1, FUT11, FIGNL1, N4BP2L2, CRIP1, SOX11, LXN, POU5F1B, PDLIM1, WSB1, BATF3, ARRDC3, NCOA3, ERN1, DIP2A, GXYLT1, JUN, PDK1, CEBPB, CKAP4, NCK2, TYMS, VEGFB, EOMES, MCM6, SLC25A43, KDM3A, GEMIN5, SOX12, SPCS3, ADARB1, IRF2BP2, KLF6, STK39, CHST2, PRPF6
<a href="#">regulation of multicellular organismal process</a>	35 of 180 genes, 19.4%	2802 of 47246 genes, 5.9%	7.78e-07	0.00%	0.00	MESP1, IFI16, ANO6, ISG15, PELI1, UBASH3B, PLXNA3, ANGPTL4, EFNA1, JAK1, MAFB, CST3, ID3, TULP3, KIAA0922, BST2, UBE2J1, PYCARD, N4BP2L2, IRX3, SOX11, COL4A2, PREX1, ARRDC3, NCOA3, EFN2, JUN, CEBPB, VEGFB, ID2, EOMES, KDM3A, HEYL, STK39, ITPR3

<a href="#">negative regulation of cellular metabolic process</a>	34 of 180 genes, 18.9%	2662 of 47246 genes, 5.6%	8.14e-07	0.00%	0.00	SERPINB9, BHLHE40, MESP1, MKI67IP, TNFAIP8, JARID2, IFI16, HIST1H1C, ISG15, UBASH3B, DDIT4, EFNA1, HIST1H3H, CST3, ID3, DUSP1, BST2, PYCARD, N4BP2L2, TCERG1, LXN, SOX11, BATF3, S100A11, JUN, CEBPB, NCK2, ID2, EOMES, KDM3A, ADARB1, HEYL, FBXO5, STK39
<a href="#">cellular response to chemical stimulus</a>	37 of 180 genes, 20.6%	3107 of 47246 genes, 6.6%	8.43e-07	0.00%	0.00	SERPINB9, COL4A1, ANO6, ISG15, CXCR7, DDIT4, JAK1, GNG11, ID3, BST2, DUSP1, RNF165, PYCARD, FSTL1, CRIP1, FAM89B, SOX11, COL4A2, EDEM2, PREX1, FAM105B, NCOA3, TNFRSF10B, ERN1, JUN, PDK1, CEBPB, NCK2, VEGFB, ID2, KDM3A, KLF6, PXDN, HEYL, ITPR3, CXCL16, IL13RA1
<a href="#">response to external stimulus</a>	32 of 180 genes, 17.8%	2398 of 47246 genes, 5.1%	9.84e-07	0.00%	0.00	SERPINB9, BHLHE40, IFI16, ANO6, ISG15, PELI1, UBASH3B, PLXNA3, CXCR7, DDIT4, EFNA1, HIST1H3H, BST2, RNF165, PYCARD, FSTL1, DENND5A, LXN, BATF3, PREX1, FAM105B, TNFRSF10B, EFN2, JUN, CEBPB, TYMS, VEGFB, ID2, ADARB1, CD1D, STK39, CXCL16
<a href="#">response to organic substance</a>	38 of 180 genes, 21.1%	3289 of 47246 genes, 7.0%	1.09e-06	0.00%	0.00	COL4A1, MBD4, ISG15, PELI1, CXCR7, DDIT4, JAK1, GNG11, ID3, DUSP1, BST2, RNF165, UBE2J1, PYCARD, FSTL1, CRIP1, FAM89B, SOX11, RFTN1, COL4A2, EDEM2, FAM105B, NCOA3, TNFRSF10B, ERN1, JUN, CEBPB, LOX, NCK2, TYMS, VEGFB, KDM3A, KLF6, PXDN, HEYL, ITPR3, CXCL16, IL13RA1
<a href="#">cellular macromolecule metabolic process</a>	97 of 180 genes, 53.9%	15022 of 47246 genes, 31.8%	1.15e-06	0.00%	0.00	MESP1, MKI67IP, TNFAIP8, IFI16, AFF4, SPSB1, ISG15, PELI1, PHTF2, CXCR7, PTRF, CHST7, NUP98, EFNA1, HIST1H3H, ID3, NUP153, BST2, PRR16, RNF165, UBE2J1, PYCARD, TCERG1, RIMKLB, FSTL1, IRX3, MGEA5, ARHGEF6, CDK2AP1, CHST15, S100A11, COL4A2, DCLRE1B, EDEM2, FAM105B, TNFRSF10B, CDCA7, LOX, RNF24, POLE2, RIF1, ID2, FBXO5, HEYL, JAG2, PERP, SERPINB9, BHLHE40, JMJD6, MBD4, JARID2, HIST1H1C, PSRC1, RNF125, RPF2, UBASH3B, SERTAD2, DDIT4, JAK1, P4HA1, CST3, MAFB, TULP3, FEM1C, DUSP1, FUT11, FIGNL1, N4BP2L2, SOX11, LXN, POU5F1B, PDLIM1, WSB1, BATF3, ARRDC3, NCOA3, ERN1, GXYLT1, JUN, PDK1, CEBPB, CKAP4, NCK2, TYMS, VEGFB, EOMES, MCM6, SLC25A43, KDM3A, GEMIN5, SOX12, SPCS3, ADARB1, IRF2BP2, KLF6, STK39, PRPF6
<a href="#">negative regulation of molecular function</a>	23 of 180 genes, 12.8%	1277 of 47246 genes, 2.7%	1.37e-06	0.00%	0.00	SERPINB9, BHLHE40, MKI67IP, TNFAIP8, SOX11, LXN, IFI16, FAM105B, PELI1, UBASH3B, JUN, ANGPTL4, ID2, CST3, ID3, ADARB1, STK39, FBXO5, DUSP1, BST2, HEYL, RCC2, PYCARD
<a href="#">intrinsic apoptotic signaling pathway</a>	12 of 180 genes, 6.7%	282 of 47246 genes, 0.6%	1.83e-06	0.00%	0.00	PDK1, FIGNL1, NCK2, CEBPB, CRIP1, CXCR7, IFI16, DDIT4, TNFRSF10B, PERP, ERN1, PYCARD
<a href="#">cellular metabolic process</a>	111 of 180 genes, 61.7%	18601 of 47246 genes, 39.4%	2.00e-06	0.00%	0.00	MESP1, MKI67IP, TNFAIP8, GCLM, IFI16, AFF4, SPSB1, ISG15, PELI1, PGK1, GFPT2, PHTF2, CXCR7, PTRF, CHST7, NUP98, EFNA1, HIST1H3H, ID3, NUP153, BST2, PRR16, RNF165, UBE2J1, PYCARD, TCERG1, RIMKLB, FSTL1, IRX3, MGEA5, ARHGEF6, CDK2AP1, CHST15, S100A11, COL4A2, DCLRE1B, EDEM2, FAM105B, TNFRSF10B, N4BP2, CDCA7, LOX, RNF24, POLE2, SCD, RIF1, ID2, PXDN, HEYL, FBXO5, JAG2, PERP, MORC2, SERPINB9, BHLHE40, JMJD6, MBD4, JARID2, HIST1H1C, PSRC1, ME2, RNF125, KDEL2, RPF2, PGAM1, UBASH3B, SERTAD2, NSMAF, DDIT4, P4HA1, JAK1, CST3, MAFB, TULP3, FEM1C, DUSP1, FUT11, FIGNL1, N4BP2L2, SOX11, LXN, POU5F1B, PDLIM1, WSB1, PREX1, BATF3, NCOA3, ARRDC3, ERN1, GXYLT1, JUN, PDK1, NCK2, CEBPB, CKAP4, TYMS, VEGFB, EOMES, MCM6, SLC25A43, KDM3A, GEMIN5, SOX12, FABP6, SPCS3, ADARB1, IRF2BP2, KLF6, STK39, CHST2, PRPF6
<a href="#">cell activation</a>	20 of 180 genes, 11.1%	985 of 47246 genes, 2.1%	2.52e-06	0.00%	0.00	JMJD6, SOX11, PREX1, BATF3, PELI1, EFN2, UBASH3B, JUN, CEBPB, NCK2, EOMES, ID2, MAFB, CD1D, KLF6, BST2, KIAA0922, JAG2, ITPR3, PYCARD
<a href="#">hematopoietic or lymphoid organ development</a>	18 of 180 genes, 10.0%	785 of 47246 genes, 1.7%	2.66e-06	0.00%	0.00	N4BP2L2, JMJD6, JARID2, IFI16, PREX1, BATF3, ISG15, UBASH3B, JUN, CEBPB, WASF2, EOMES, ID2, MAFB, CD1D, KLF6, KIAA0922, JAG2
<a href="#">positive regulation of macromolecule metabolic process</a>	35 of 180 genes, 19.4%	2952 of 47246 genes, 6.2%	3.04e-06	0.00%	0.00	SERPINB9, MESP1, JARID2, IFI16, PSRC1, RNF125, PELI1, CXCR7, SERTAD2, EFNA1, HIST1H3H, MAFB, PRR16, PYCARD, SOX11, CDK2AP1, EDEM2, ARRDC3, NCOA3, TNFRSF10B, ERN1, JUN, CEBPB, NCK2, VEGFB, ID2, EOMES, RIF1, KDM3A, SOX12, KLF6, HEYL, FBXO5, PERP, PRPF6
<a href="#">regulation of molecular function</a>	40 of 180 genes, 22.2%	3737 of 47246 genes, 7.9%	3.21e-06	0.00%	0.00	SERPINB9, BHLHE40, MKI67IP, TNFAIP8, GCLM, IFI16, PSRC1, PELI1, UBASH3B, ANGPTL4, DENND4B, NSMAF, EFNA1, JAK1, ID3, CST3, S100A10, BST2, DUSP1, PYCARD, DENND5A, SOX11, ARHGEF6, LXN, PREX1, ARRDC3, FAM105B, NCOA3, TNFRSF10B, AHS2, ERN1, JUN, NCK2, ID2, ADARB1, STK39, FBXO5, HEYL, RCC2, PERP
<a href="#">leukocyte activation</a>	18 of 180 genes, 10.0%	798 of 47246 genes, 1.7%	3.44e-06	0.00%	0.00	JMJD6, SOX11, PREX1, BATF3, PELI1, EFN2, JUN, CEBPB, NCK2, EOMES, ID2, MAFB, CD1D, KLF6, BST2, KIAA0922, JAG2, PYCARD
<a href="#">positive regulation of metabolic process</a>	37 of 180 genes, 20.6%	3305 of 47246 genes, 7.0%	4.52e-06	0.00%	0.00	SERPINB9, MESP1, JARID2, IFI16, PSRC1, RNF125, PELI1, CXCR7, SERTAD2, NSMAF, EFNA1, HIST1H3H, MAFB, PRR16, PYCARD, SOX11, CDK2AP1, EDEM2, ARRDC3, NCOA3, TNFRSF10B, ERN1, JUN, PDK1, CEBPB, NCK2, VEGFB, ID2, EOMES, RIF1, KDM3A, SOX12, KLF6, HEYL, FBXO5, PERP, PRPF6



<a href="#">circulatory system development</a>	20 of 180 genes, 11.1%	1040 of 47246 genes, 2.2%	6.31e-06	0.00%	0.00	MESP1, CRIP1, JMJD6, COL4A1, SOX11, COL4A2, FAM105B, EFN2, JUN, LOX, ANGPTL4, VEGFB, CXCR7, WASF2, EOMES, ID2, EFNA1, JAK1, ID3, HEYL
<a href="#">immune system development</a>	18 of 180 genes, 10.0%	832 of 47246 genes, 1.8%	6.57e-06	0.00%	0.00	N4BP2L2, JMJD6, JARID2, IFI16, PREX1, BATF3, ISG15, UBASH3B, JUN, CEBPB, WASF2, EOMES, ID2, MAFB, CD1D, KLF6, KIAA0922, JAG2
<a href="#">hemopoiesis</a>	17 of 180 genes, 9.4%	741 of 47246 genes, 1.6%	7.68e-06	0.00%	0.00	N4BP2L2, JMJD6, IFI16, PREX1, BATF3, ISG15, UBASH3B, JUN, CEBPB, EOMES, ID2, WASF2, MAFB, CD1D, KLF6, KIAA0922, JAG2
<a href="#">anatomical structure formation involved in morphogenesis</a>	20 of 180 genes, 11.1%	1053 of 47246 genes, 2.2%	7.77e-06	0.00%	0.00	MESP1, JMJD6, IRX3, COL4A1, SOX11, COL4A2, FAM105B, EFN2, JUN, ANGPTL4, VEGFB, CXCR7, WASF2, EOMES, EFNA1, JAK1, TULP3, HEYL, DUSP1, PERP
<a href="#">positive regulation of nitrogen compound metabolic process</a>	34 of 180 genes, 18.9%	2910 of 47246 genes, 6.2%	7.83e-06	0.00%	0.00	MESP1, JARID2, IFI16, PSRC1, RNF125, PELI1, CXCR7, SERTAD2, NSMAF, EFNA1, MAFB, PRR16, PYCARD, SOX11, CDK2AP1, EDEM2, ARRDC3, NCOA3, TNFRSF10B, ERN1, JUN, CEBPB, NCK2, VEGFB, ID2, EOMES, RIF1, KDM3A, SOX12, KLF6, HEYL, FBXO5, PERP, PRPF6
<a href="#">leukocyte differentiation</a>	14 of 180 genes, 7.8%	483 of 47246 genes, 1.0%	1.02e-05	0.00%	0.00	CEBPB, JMJD6, IFI16, ID2, EOMES, PREX1, BATF3, MAFB, KLF6, CD1D, KIAA0922, JAG2, UBASH3B, JUN
<a href="#">lymphocyte activation</a>	16 of 180 genes, 8.9%	672 of 47246 genes, 1.4%	1.32e-05	0.00%	0.00	NCK2, CEBPB, JMJD6, SOX11, ID2, EOMES, PREX1, MAFB, KLF6, CD1D, PELI1, KIAA0922, BST2, EFN2, JAG2, PYCARD
<a href="#">regulation of immune system process</a>	25 of 180 genes, 13.9%	1702 of 47246 genes, 3.6%	1.45e-05	0.00%	0.00	SERPINB9, N4BP2L2, SOX11, IFI16, RFTN1, ANO6, FAM105B, ISG15, PELI1, EFN2, UBASH3B, JUN, CEBPB, NCK2, VEGFB, CXCR7, WASF2, ID2, HIST1H3H, JAK1, MAFB, CD1D, BST2, KIAA0922, PYCARD
<a href="#">regulation of developmental process</a>	30 of 180 genes, 16.7%	2396 of 47246 genes, 5.1%	1.56e-05	0.00%	0.00	N4BP2L2, MESP1, IRX3, SOX11, PREX1, ANO6, COL4A2, NCOA3, ISG15, CAMSAP1, EFN2, UBASH3B, JUN, PLXNA3, CEBPB, ANGPTL4, VEGFB, EOMES, ID2, KDM3A, EFNA1, JAK1, MAFB, CST3, ID3, TULP3, S100A10, HEYL, KIAA0922, RCC2
<a href="#">organic substance metabolic process</a>	114 of 180 genes, 63.3%	19974 of 47246 genes, 42.3%	1.63e-05	0.00%	0.00	MESP1, HRASLS, MKI67IP, TNFAIP8, GCLM, IFI16, AFF4, SPSB1, ISG15, PELI1, PGK1, GFPT2, PHTF2, CXCR7, PTRF, CHST7, NUP98, EFNA1, HIST1H3H, ID3, NUP153, BST2, PRR16, RNF165, UBE2J1, PYCARD, TCERG1, RIMKLB, FSTL1, IRX3, MGEA5, ARHGEF6, CDK2AP1, CHST15, S100A11, COL4A2, DCLRE1B, EDEM2, FAM105B, TNFRSF10B, N4BP2, CDCA7, LOX, RNF24, POLE2, TMEFF2, SCD, RIF1, ID2, HEYL, FBXO5, JAG2, PERP, MORC2, SERPINB9, BHLHE40, COL4A1, JMJD6, MBD4, JARID2, HIST1H1C, PSRC1, ME2, RNF125, KDELC2, RPF2, PGAM1, UBASH3B, SERTAD2, NSMAF, DDIT4, P4HA1, JAK1, CST3, MAFB, TULP3, FEM1C, DUSP1, FUT11, N4BP2L2, FIGNL1, CRIP1, SOX11, LXN, POU5F1B, PDLIM1, WSB1, BATF3, NCOA3, ARRDC3, ERN1, DIP2A, GXYLT1, JUN, PDK1, NCK2, CEBPB, CKAP4, TYMS, VEGFB, EOMES, MCM6, SLC25A43, KDM3A, GEMIN5, SOX12, FABP6, SPCS3, ADARB1, IRF2BP2, KLF6, STK39, CHST2, PRPF6
<a href="#">apoptotic process</a>	28 of 180 genes, 15.6%	2123 of 47246 genes, 4.5%	1.73e-05	0.00%	0.00	SERPINB9, FIGNL1, CRIP1, TNFAIP8, GCLM, ARHGEF6, IFI16, PNMA2, ANO6, TNFRSF10B, ERN1, JUN, DIP2A, PDK1, CDCA7, NCK2, CEBPB, ANGPTL4, VEGFB, CXCR7, NSMAF, DDIT4, TMEM214, ID3, DUSP1, JAG2, PERP, PYCARD
<a href="#">cell death</a>	29 of 180 genes, 16.1%	2273 of 47246 genes, 4.8%	1.90e-05	0.00%	0.00	SERPINB9, FIGNL1, CRIP1, TNFAIP8, SOX11, GCLM, ARHGEF6, IFI16, PNMA2, ANO6, TNFRSF10B, ERN1, JUN, DIP2A, PDK1, CDCA7, NCK2, CEBPB, ANGPTL4, VEGFB, CXCR7, NSMAF, DDIT4, TMEM214, ID3, DUSP1, JAG2, PERP, PYCARD
<a href="#">cellular response to organic substance</a>	31 of 180 genes, 17.2%	2572 of 47246 genes, 5.4%	2.06e-05	0.00%	0.00	FSTL1, FAM89B, COL4A1, SOX11, EDEM2, COL4A2, NCOA3, FAM105B, ISG15, TNFRSF10B, ERN1, JUN, NCK2, CEBPB, VEGFB, CXCR7, KDM3A, DDIT4, JAK1, GNG11, ID3, PXDN, KLF6, DUSP1, BST2, HEYL, RNF165, ITPR3, PYCARD, IL13RA1, CXCL16
<a href="#">cellular component organization</a>	61 of 180 genes, 33.9%	7860 of 47246 genes, 16.6%	2.12e-05	0.00%	0.00	CEP120, MKI67IP, JMJD6, COL4A1, GCLM, JARID2, HIST1H1C, PSRC1, ANO6, RPF2, CAMSAP1, PLXNA3, ANGPTL4, TTC17, WASF2, SERTAD2, DDIT4, NUP98, EFNA1, P4HA1, HIST1H3H, CST3, S100A10, KATNAL1, NUP153, BST2, DUSP1, PRR16, RNF165, PYCARD, FIGNL1, PTGFRN, NID1, ARHGEF6, RFTN1, PREX1, COL4A2, DCLRE1B, NCOA3, EFN2, JUN, PDK1, VWA1, LOX, NCK2, POLE2, TMEFF2, ID2, MCM6, KDM3A, SPAST, GEMIN5, SOX12, PXDN, TMEM43, FBXO5, RCC2, PERP, ITPR3, PRPF6, CXCL16
<a href="#">programmed cell death</a>	28 of 180 genes, 15.6%	2148 of 47246 genes, 4.5%	2.23e-05	0.00%	0.00	SERPINB9, FIGNL1, CRIP1, TNFAIP8, GCLM, ARHGEF6, IFI16, PNMA2, ANO6, TNFRSF10B, ERN1, JUN, DIP2A, PDK1, CDCA7, NCK2, CEBPB, ANGPTL4, VEGFB, CXCR7, NSMAF, DDIT4, TMEM214, ID3, DUSP1, JAG2, PERP, PYCARD
<a href="#">regulation of protein metabolic process</a>	33 of 180 genes, 18.3%	2894 of 47246 genes, 6.1%	2.47e-05	0.00%	0.00	SERPINB9, TNFAIP8, JARID2, IFI16, PSRC1, RNF125, ISG15, PELI1, UBASH3B, CXCR7, DDIT4, EFNA1, CST3, DUSP1, BST2, PRR16, UBE2J1, PYCARD, LXN, CDK2AP1, EDEM2, ARRDC3, TNFRSF10B, ERN1, JUN, CEBPB, NCK2, VEGFB, KDM3A, ADARB1, FBXO5, STK39, PERP

<a href="#">cellular component organization or biogenesis</a>	62 of 180 genes, 34.4%	8125 of 47246 genes, 17.2%	2.90e-05	0.00%	0.00	CEP120, MKI67IP, JMJD6, COL4A1, GCLM, JARID2, HIST1H1C, PSRC1, ANO6, RPF2, CAMSAP1, PLXNA3, ANGPTL4, TTC17, WASF2, SERTAD2, NSMAF, DDIT4, NUP98, EFNA1, P4HA1, HIST1H3H, CST3, S100A10, KATNAL1, NUP153, BST2, DUSP1, PRR16, RNF165, PYCARD, FIGNL1, PTGFRN, NID1, ARHGEF6, RFTN1, PREX1, COL4A2, DCLRE1B, NCOA3, EFN2, JUN, PDK1, VWA1, LOX, NCK2, POLE2, TMEFF2, ID2, MCM6, KDM3A, SPAST, GEMIN5, SOX12, PXDN, TMEM43, FBXO5, RCC2, PERP, ITPR3, PRPF6, CXCL16
<a href="#">negative regulation of multicellular organismal process</a>	19 of 180 genes, 10.6%	1030 of 47246 genes, 2.2%	3.07e-05	0.00%	0.00	N4BP2L2, MESP1, IRX3, SOX11, COL4A2, ARRDC3, ISG15, UBASH3B, PLXNA3, ID2, EFNA1, ID3, CST3, MAFB, TULP3, KIAA0922, BST2, STK39, PYCARD
<a href="#">macromolecule biosynthetic process</a>	65 of 180 genes, 36.1%	8775 of 47246 genes, 18.6%	3.49e-05	0.00%	0.00	MESP1, MKI67IP, IFI16, AFF4, ISG15, PELI1, PHTF2, PTRF, CHST7, NUP98, EFNA1, HIST1H3H, ID3, NUP153, PRR16, RNF165, UBE2J1, PYCARD, TCERG1, FSTL1, IRX3, CDK2AP1, CHST15, S100A11, COL4A2, FAM105B, CDCA7, POLE2, TMEFF2, ID2, FBXO5, HEYL, BHLHE40, JMJD6, JARID2, HIST1H1C, PSRC1, NSMAF, SERTAD2, MAFB, TULP3, DUSP1, FUT11, N4BP2L2, SOX11, POU5F1B, PDLIM1, BATF3, NCOA3, ERN1, JUN, GXYLT1, CEBPB, NCK2, TYMS, VEGFB, EOMES, MCM6, KDM3A, SLC25A43, SOX12, IRF2BP2, KLF6, CHST2, PRPF6
<a href="#">positive regulation of cellular metabolic process</a>	34 of 180 genes, 18.9%	3118 of 47246 genes, 6.6%	4.29e-05	0.00%	0.00	MESP1, JARID2, IFI16, PSRC1, RNF125, PELI1, CXCR7, SERTAD2, NSMAF, EFNA1, MAFB, PRR16, PYCARD, SOX11, CDK2AP1, ARRDC3, NCOA3, TNFRSF10B, ERN1, JUN, PDK1, CEBPB, NCK2, VEGFB, ID2, EOMES, RIF1, KDM3A, SOX12, KLF6, HEYL, FBXO5, PERP, PRPF6
<a href="#">primary metabolic process</a>	110 of 180 genes, 61.1%	19269 of 47246 genes, 40.8%	4.86e-05	0.00%	0.00	MESP1, HRASLS, MKI67IP, TNFAIP8, GCLM, IFI16, AFF4, SPSB1, ISG15, PELI1, PGK1, GFPT2, PHTF2, CXCR7, PTRF, CHST7, NUP98, EFNA1, HIST1H3H, ID3, NUP153, BST2, PRR16, RNF165, UBE2J1, PYCARD, TCERG1, RIMKLB, FSTL1, IRX3, MGEA5, ARHGEF6, CDK2AP1, CHST15, S100A11, COL4A2, DCLRE1B, EDEM2, FAM105B, TNFRSF10B, N4BP2, CDCA7, LOX, RNF24, POLE2, SCD, RIF1, ID2, HEYL, FBXO5, JAG2, PERP, MORC2, SERPINB9, BHLHE40, JMJD6, MBD4, JARID2, HIST1H1C, PSRC1, ME2, RNF125, KDELC2, RPF2, PGAM1, UBASH3B, SERTAD2, NSMAF, DDIT4, P4HA1, JAK1, CST3, MAFB, TULP3, FEM1C, DUSP1, FUT11, FIGNL1, N4BP2L2, SOX11, LXN, POU5F1B, PDLIM1, WSB1, BATF3, NCOA3, ARRDC3, ERN1, GXYLT1, JUN, PDK1, NCK2, CEBPB, CKAP4, TYMS, VEGFB, EOMES, MCM6, SLC25A43, KDM3A, GEMIN5, SOX12, FABP6, SPCS3, ADARB1, IRF2BP2, KLF6, STK39, CHST2, PRPF6
<a href="#">regulation of response to stress</a>	22 of 180 genes, 12.2%	1438 of 47246 genes, 3.0%	6.06e-05	0.00%	0.00	SERPINB9, FIGNL1, IFI16, RFTN1, ANO6, EDEM2, FAM105B, PELI1, UBASH3B, ERN1, NCK2, VEGFB, CXCR7, RIF1, NUP98, HIST1H3H, JAK1, CD1D, STK39, NUP153, UBE2J1, PYCARD
<a href="#">nitrogen compound metabolic process</a>	105 of 180 genes, 58.3%	18216 of 47246 genes, 38.6%	9.90e-05	0.00%	0.00	MESP1, MKI67IP, TNFAIP8, GCLM, IFI16, AFF4, SPSB1, ISG15, PELI1, PGK1, GFPT2, PHTF2, CXCR7, PTRF, CHST7, NUP98, EFNA1, HIST1H3H, ID3, NUP153, BST2, PRR16, RNF165, UBE2J1, PYCARD, TCERG1, RIMKLB, FSTL1, IRX3, MGEA5, ARHGEF6, CDK2AP1, CHST15, S100A11, COL4A2, DCLRE1B, EDEM2, FAM105B, TNFRSF10B, N4BP2, CDCA7, LOX, RNF24, POLE2, RIF1, ID2, HEYL, FBXO5, JAG2, PERP, SERPINB9, BHLHE40, JMJD6, MBD4, JARID2, HIST1H1C, PSRC1, ME2, RNF125, RPF2, PGAM1, UBASH3B, SERTAD2, DDIT4, NSMAF, P4HA1, JAK1, CST3, MAFB, TULP3, FEM1C, DUSP1, FUT11, FIGNL1, N4BP2L2, SOX11, LXN, POU5F1B, PDLIM1, WSB1, BATF3, ARRDC3, NCOA3, ERN1, GXYLT1, JUN, PDK1, CEBPB, CKAP4, NCK2, TYMS, VEGFB, EOMES, MCM6, SLC25A43, KDM3A, GEMIN5, SOX12, SPCS3, ADARB1, IRF2BP2, KLF6, STK39, CHST2, PRPF6
<a href="#">organic substance biosynthetic process</a>	71 of 180 genes, 39.4%	10334 of 47246 genes, 21.9%	0.00012	0.00%	0.00	MESP1, MKI67IP, GCLM, IFI16, AFF4, ISG15, PELI1, PGK1, GFPT2, PHTF2, PTRF, CHST7, NUP98, EFNA1, HIST1H3H, ID3, NUP153, PRR16, RNF165, UBE2J1, PYCARD, TCERG1, FSTL1, IRX3, CDK2AP1, CHST15, S100A11, COL4A2, FAM105B, CDCA7, POLE2, TMEFF2, SCD, ID2, FBXO5, HEYL, BHLHE40, JMJD6, JARID2, HIST1H1C, PSRC1, PGAM1, NSMAF, SERTAD2, MAFB, TULP3, DUSP1, FUT11, N4BP2L2, SOX11, POU5F1B, PDLIM1, BATF3, NCOA3, ERN1, GXYLT1, JUN, PDK1, CEBPB, NCK2, TYMS, VEGFB, EOMES, MCM6, KDM3A, SLC25A43, SOX12, IRF2BP2, KLF6, CHST2, PRPF6
<a href="#">apoptotic signaling pathway</a>	14 of 180 genes, 7.8%	595 of 47246 genes, 1.3%	0.00013	0.00%	0.00	PDK1, FIGNL1, NCK2, CEBPB, CRIP1, GCLM, CXCR7, IFI16, DDIT4, TNFRSF10B, PERP, ERN1, PYCARD, JUN
<a href="#">locomotion</a>	24 of 180 genes, 13.3%	1779 of 47246 genes, 3.8%	0.00014	0.00%	0.00	MESP1, PREX1, ANO6, ARRDC3, EFN2, JUN, NCK2, PLXNA3, VEGFB, CXCR7, WASF2, TMEFF2, ID2, DDIT4, EFNA1, JAK1, ADARB1, SIRPA, BST2, RCC2, JAG2, RNF165, PYCARD, CXCL16

<a href="#">regulation of multicellular organismal development</a>	24 of 180 genes, 13.3%	1802 of 47246 genes, 3.8%	0.00018	0.00%	0.00	N4BP2L2, MESP1, IRX3, SOX11, PREX1, ANO6, COL4A2, NCOA3, ISG15, EFNB2, UBASH3B, JUN, PLXNA3, CEBPB, ANGPTL4, VEGFB, EOMES, ID2, EFNA1, JAK1, MAFB, TULP3, HEYL, KIAA0922
<a href="#">regulation of cellular protein metabolic process</a>	30 of 180 genes, 16.7%	2705 of 47246 genes, 5.7%	0.00022	0.00%	0.00	SERPINB9, TNFAIP8, LXN, JARID2, IFI16, CDK2AP1, PSRC1, RNF125, ARDC3, ISG15, TNFRSF10B, PELI1, UBASH3B, ERN1, JUN, NCK2, VEGFB, CXCR7, DDIT4, KDM3A, EFNA1, CST3, ADARB1, STK39, DUSP1, BST2, FBXO5, PRR16, PERP, PYCARD
<a href="#">tissue development</a>	24 of 180 genes, 13.3%	1835 of 47246 genes, 3.9%	0.00025	0.00%	0.00	MESP1, CRIP1, IRX3, COL4A1, SOX11, ANO6, COL4A2, NCOA3, ARRDC3, EFNB2, PGK1, JUN, TAGLN2, CEBPB, TYMS, TMEFF2, EOMES, ID2, EFNA1, ID3, TULP3, DUSP1, HEYL, JAG2
<a href="#">biosynthetic process</a>	71 of 180 genes, 39.4%	10524 of 47246 genes, 22.3%	0.00026	0.00%	0.00	MESP1, MKI67IP, GCLM, IFI16, AFF4, ISG15, PELI1, PGK1, GFPT2, PHTF2, PTRF, CHST7, NUP98, EFNA1, HIST1H3H, ID3, NUP153, PRR16, RNF165, UBE2J1, PYCARD, TCERG1, FSTL1, IRX3, CDK2AP1, CHST15, S100A11, COL4A2, FAM105B, CDCA7, POLE2, TMEFF2, SCD, ID2, FBXO5, HEYL, BHLHE40, JMJD6, JARID2, HIST1H1C, PSRC1, PGAM1, NSMAF, SERTAD2, MAFB, TULP3, DUSP1, FUT11, N4BP2L2, SOX11, POU5F1B, PDLIM1, BATF3, NCOA3, ERN1, GXYLT1, JUN, PDK1, CEBPB, NCK2, TYMS, VEGFB, EOMES, MCM6, KDM3A, SLC25A43, SOX12, IRF2BP2, KLF6, CHST2, PRPF6
<a href="#">supramolecular fiber organization</a>	16 of 180 genes, 8.9%	836 of 47246 genes, 1.8%	0.00026	0.00%	0.00	FIGNL1, CEP120, PSRC1, PREX1, LOX, NCK2, TTC17, TMEFF2, WASF2, SPAST, P4HA1, CST3, KATNAL1, S100A10, FBXO5, PYCARD
<a href="#">heart development</a>	13 of 180 genes, 7.2%	533 of 47246 genes, 1.1%	0.00026	0.00%	0.00	MESP1, LOX, CRIP1, JMJD6, VEGFB, SOX11, ID2, EOMES, EFNA1, ID3, EFNB2, HEYL, JUN
<a href="#">response to abiotic stimulus</a>	19 of 180 genes, 10.6%	1191 of 47246 genes, 2.5%	0.00029	0.00%	0.00	FIGNL1, BHLHE40, CRIP1, DENND5A, MBD4, LXN, IFI16, PDLIM1, TNFRSF10B, JUN, PDK1, ANGPTL4, ID2, DDIT4, KDM3A, NUP98, STK39, DUSP1, NUP153
<a href="#">single organism cell adhesion</a>	15 of 180 genes, 8.3%	743 of 47246 genes, 1.6%	0.00033	0.00%	0.00	NCK2, CEBPB, CERCAM, EFNA1, PREX1, S100A10, CD1D, PELI1, EFNB2, KIAA0922, RCC2, MPZL2, UBASH3B, PERP, PYCARD
<a href="#">cellular response to stimulus</a>	70 of 180 genes, 38.9%	10381 of 47246 genes, 22.0%	0.00034	0.00%	0.00	MESP1, GCLM, IFI16, ANO6, SPSB1, ISG15, PELI1, DENND4B, CXCR7, NUP98, EFNA1, ID3, LY6E, NUP153, BST2, RNF165, UBE2J1, PYCARD, FSTL1, FAM89B, ARHGEF6, S100A11, COL4A2, DCLRE1B, EDEM2, FAM105B, TNFRSF10B, EFNB2, POLE2, RIF1, ID2, PXDN, HEYL, RCC2, JAG2, PERP, IL13RA1, SERPINB9, COL4A1, JMJD6, MBD4, UBASH3B, PLXNA3, WASF2, DDIT4, NSMAF, GNG11, JAK1, TULP3, DUSP1, KIAA0922, FIGNL1, CRIP1, SOX11, RFTN1, WSB1, PREX1, ARRDC3, NCOA3, ERN1, JUN, PDK1, CEBPB, NCK2, VEGFB, KDM3A, KLF6, STK39, ITPR3, CXCL16
<a href="#">metabolic process</a>	118 of 180 genes, 65.6%	22013 of 47246 genes, 46.6%	0.00036	0.00%	0.00	MESP1, HRASLS, MKI67IP, TNFAIP8, GCLM, IFI16, AFF4, SPSB1, ISG15, PELI1, PGK1, GFPT2, PHTF2, CXCR7, PTRF, CHST7, NUP98, EFNA1, HIST1H3H, ID3, SRXN1, NUP153, BST2, PRR16, RNF165, UBE2J1, PYCARD, TCERG1, RIMKLB, FSTL1, IRX3, MGEA5, ARHGEF6, CDK2AP1, CHST15, S100A11, COL4A2, DCLRE1B, EDEM2, FAM105B, TNFRSF10B, N4BP2, CDCA7, LOX, RNF24, POLE2, TMEFF2, SCD, RIF1, ID2, SPAST, PXDN, HEYL, FBXO5, JAG2, PERP, MORC2, SERPINB9, BHLHE40, COL4A1, JMJD6, MBD4, JARID2, HIST1H1C, PSRC1, ME2, RNF125, KDELC2, RPF2, PGAM1, UBASH3B, SERTAD2, NSMAF, DDIT4, P4HA1, JAK1, CST3, MAFB, TULP3, FEM1C, DUSP1, FUT11, N4BP2L2, FIGNL1, CRIP1, SOX11, LXN, POU5F1B, PDLIM1, WSB1, PREX1, BATF3, NCOA3, ARRDC3, ERN1, DIP2A, GXYLT1, JUN, PDK1, NCK2, CEBPB, CKAP4, TYMS, VEGFB, EOMES, MCM6, SLC25A43, KDM3A, GEMIN5, SOX12, FABP6, SPCS3, ADARB1, IRF2BP2, KLF6, STK39, CHST2, PRPF6
<a href="#">negative regulation of nucleobase-containing compound metabolic process</a>	21 of 180 genes, 11.7%	1472 of 47246 genes, 3.1%	0.00040	0.00%	0.00	TCERG1, N4BP2L2, BHLHE40, MESP1, SOX11, JARID2, IFI16, HIST1H1C, S100A11, BATF3, JUN, NCK2, CEBPB, EOMES, ID2, DDIT4, EFNA1, HIST1H3H, ID3, HEYL, DUSP1
<a href="#">T cell activation</a>	12 of 180 genes, 6.7%	465 of 47246 genes, 1.0%	0.00044	0.00%	0.00	NCK2, CEBPB, JMJD6, EOMES, PREX1, MAFB, CD1D, PELI1, EFNB2, KIAA0922, JAG2, PYCARD
<a href="#">cell migration</a>	20 of 180 genes, 11.1%	1354 of 47246 genes, 2.9%	0.00046	0.00%	0.00	MESP1, PREX1, ANO6, EFNB2, JUN, NCK2, PLXNA3, VEGFB, WASF2, TMEFF2, DDIT4, EFNA1, JAK1, ADARB1, SIRPA, BST2, JAG2, RCC2, CXCL16, PYCARD
<a href="#">cellular protein metabolic process</a>	58 of 180 genes, 32.2%	7926 of 47246 genes, 16.8%	0.00046	0.00%	0.00	SERPINB9, JMJD6, TNFAIP8, JARID2, IFI16, HIST1H1C, PSRC1, RNF125, SPSB1, ISG15, PELI1, UBASH3B, CXCR7, DDIT4, NUP98, EFNA1, P4HA1, JAK1, HIST1H3H, CST3, FEM1C, NUP153, BST2, DUSP1, PRR16, RNF165, FUT11, UBE2J1, PYCARD, RIMKLB, SOX11, ARHGEF6, LXN, MGEA5, CDK2AP1, WSB1, EDEM2, NCOA3, ARRDC3, FAM105B, TNFRSF10B, ERN1, GXYLT1, JUN, PDK1, CKAP4, LOX, NCK2, VEGFB, RNF24, SLC25A43, KDM3A, SPCS3, ADARB1, STK39, FBXO5, JAG2, PERP
<a href="#">blood vessel development</a>	14 of 180 genes, 7.8%	659 of 47246 genes, 1.4%	0.00047	0.00%	0.00	MESP1, LOX, ANGPTL4, JMJD6, COL4A1, VEGFB, CXCR7, WASF2, EFNA1, COL4A2, JAK1, FAM105B, EFNB2, JUN
<a href="#">cellular macromolecule biosynthetic process</a>	61 of 180 genes, 33.9%	8547 of 47246 genes, 18.1%	0.00047	0.00%	0.00	BHLHE40, MESP1, MKI67IP, JMJD6, JARID2, IFI16, AFF4, HIST1H1C, PSRC1, ISG15, PELI1, PHTF2, SERTAD2, PTRF, CHST7, NUP98, EFNA1, HIST1H3H, MAFB, ID3, TULP3, DUSP1, PRR16, RNF165, FUT11, UBE2J1, PYCARD, TCERG1, N4BP2L2, FSTL1, IRX3, SOX11, POU5F1B, CDK2AP1, PDLIM1, CHST15, S100A11, COL4A2, BATF3, NCOA3, FAM105B, ERN1, GXYLT1, JUN, CDCA7, NCK2, CEBPB, TYMS, VEGFB, POLE2, MCM6, EOMES, ID2, SLC25A43, KDM3A, SOX12, IRF2BP2, KLF6, FBXO5, HEYL, PRPF6

<a href="#">negative regulation of immune system process</a>	11 of 180 genes, 6.1%	386 of 47246 genes, 0.8%	0.00053	0.00%	0.00	SERPINB9, N4BP2L2, CEBPB, SOX11, IFI16, ID2, MAFB, BST2, KIAA0922, PELI1, UBASH3B
<a href="#">negative regulation of response to stimulus</a>	21 of 180 genes, 11.7%	1499 of 47246 genes, 3.2%	0.00054	0.00%	0.00	SERPINB9, FIGNL1, MESP1, FAM89B, GCLM, IFI16, FAM105B, TNFRSF10B, UBASH3B, NCK2, PLXNA3, CXCR7, DDIT4, TULP3, PXDN, DUSP1, BST2, HEYL, KIAA0922, UBE2J1, PYCARD
<a href="#">negative regulation of protein metabolic process</a>	19 of 180 genes, 10.6%	1241 of 47246 genes, 2.6%	0.00054	0.00%	0.00	SERPINB9, TNFAIP8, LXN, JARID2, IFI16, ISG15, UBASH3B, JUN, NCK2, DDIT4, KDM3A, CST3, ADARB1, FBXO5, DUSP1, BST2, STK39, UBE2J1, PYCARD
<a href="#">regulation of nucleobase-containing compound metabolic process</a>	51 of 180 genes, 28.3%	6580 of 47246 genes, 13.9%	0.00058	0.00%	0.00	BHLHE40, MESP1, JMJD6, JARID2, IFI16, AFF4, HIST1H1C, PSRC1, ME2, PGAM1, PELI1, PHTF2, SERTAD2, PTRF, DDIT4, EFNA1, HIST1H3H, MAFB, ID3, TULP3, DUSP1, RNF165, PYCARD, TCERG1, FIGNL1, FSTL1, N4BP2L2, IRX3, SOX11, POU5F1B, PDLIM1, S100A11, BATF3, NCOA3, FAM105B, ERN1, JUN, CDCA7, CEBPB, NCK2, TYMS, RIF1, EOMES, ID2, KDM3A, SOX12, IRF2BP2, KLF6, HEYL, FBXO5, PRPF6
<a href="#">regulation of cell proliferation</a>	22 of 180 genes, 12.2%	1655 of 47246 genes, 3.5%	0.00067	0.00%	0.00	N4BP2L2, SOX11, JARID2, MARCKSL1, S100A11, TNFRSF10B, PELI1, EFN2, JUN, CDCA7, CEBPB, NCK2, VEGFB, ID2, JAK1, FABP6, ADARB1, CD1D, BTG3, KIAA0922, JAG2, PYCARD
<a href="#">vasculature development</a>	14 of 180 genes, 7.8%	681 of 47246 genes, 1.4%	0.00069	0.00%	0.00	MESP1, LOX, ANGPTL4, JMJD6, COL4A1, VEGFB, CXCR7, WASF2, EFNA1, COL4A2, JAK1, FAM105B, EFN2, JUN
<a href="#">angiogenesis</a>	12 of 180 genes, 6.7%	488 of 47246 genes, 1.0%	0.00074	0.00%	0.00	ANGPTL4, JMJD6, COL4A1, VEGFB, CXCR7, WASF2, EFNA1, COL4A2, JAK1, FAM105B, EFN2, JUN
<a href="#">regulation of transcription from RNA polymerase II promoter</a>	25 of 180 genes, 13.9%	2099 of 47246 genes, 4.4%	0.00078	0.00%	0.00	TCERG1, N4BP2L2, FSTL1, BHLHE40, MESP1, SOX11, JARID2, IFI16, HIST1H1C, BATF3, NCOA3, JUN, NCK2, CEBPB, EOMES, ID2, KDM3A, EFNA1, SOX12, ID3, MAFB, KLF6, HEYL, RNF165, PRPF6
<a href="#">cardiovascular system development</a>	14 of 180 genes, 7.8%	688 of 47246 genes, 1.5%	0.00078	0.00%	0.00	MESP1, LOX, ANGPTL4, JMJD6, COL4A1, VEGFB, CXCR7, WASF2, EFNA1, COL4A2, JAK1, FAM105B, EFN2, JUN
<a href="#">negative regulation of gene expression</a>	23 of 180 genes, 12.8%	1826 of 47246 genes, 3.9%	0.00091	0.00%	0.00	TCERG1, N4BP2L2, BHLHE40, MESP1, SOX11, JARID2, IFI16, HIST1H1C, BATF3, ERN1, JUN, DIP2A, NCK2, CEBPB, VEGFB, EOMES, ID2, NUP98, EFNA1, HIST1H3H, ID3, NUP153, HEYL
<a href="#">regulation of cell adhesion</a>	14 of 180 genes, 7.8%	697 of 47246 genes, 1.5%	0.00091	0.00%	0.00	NCK2, CEBPB, NID1, EFNA1, PREX1, S100A10, CD1D, EFN2, KIAA0922, PELI1, RCC2, JAG2, UBASH3B, PYCARD
<a href="#">cellular biosynthetic process</a>	68 of 180 genes, 37.8%	10201 of 47246 genes, 21.6%	0.00091	0.00%	0.00	MESP1, MKI67IP, GCLM, IFI16, AFF4, ISG15, PELI1, GFPT2, PHTF2, PTRF, CHST7, NUP98, EFNA1, HIST1H3H, ID3, NUP153, PRR16, RNF165, UBE2J1, PYCARD, TCERG1, FSTL1, IRX3, CDK2AP1, CHST15, S100A11, COL4A2, FAM105B, CDCA7, POLE2, SCD, ID2, FBXO5, HEYL, BHLHE40, JMJD6, JARID2, HIST1H1C, PSRC1, NSMAF, SERTAD2, MAFB, TULP3, DUSP1, FUT11, N4BP2L2, SOX11, POU5F1B, PDLIM1, BATF3, NCOA3, ERN1, GXYLT1, JUN, PDK1, CEBPB, NCK2, TYMS, VEGFB, EOMES, MCM6, KDM3A, SLC25A43, SOX12, IRF2BP2, KLF6, CHST2, PRPF6
<a href="#">nucleobase-containing compound metabolic process</a>	67 of 180 genes, 37.2%	9990 of 47246 genes, 21.1%	0.00093	0.00%	0.00	MESP1, MKI67IP, IFI16, AFF4, ISG15, PELI1, PGK1, GFPT2, PHTF2, PTRF, NUP98, EFNA1, HIST1H3H, ID3, NUP153, RNF165, PYCARD, TCERG1, FSTL1, IRX3, CDK2AP1, S100A11, COL4A2, DCLRE1B, FAM105B, N4BP2, CDCA7, POLE2, RIF1, ID2, FBXO5, HEYL, BHLHE40, JMJD6, MBD4, JARID2, HIST1H1C, ME2, PSRC1, RPF2, PGAM1, DDIT4, SERTAD2, MAFB, TULP3, DUSP1, FIGNL1, N4BP2L2, SOX11, POU5F1B, PDLIM1, BATF3, NCOA3, ERN1, JUN, CEBPB, NCK2, TYMS, EOMES, MCM6, KDM3A, GEMIN5, SOX12, IRF2BP2, ADARB1, KLF6, PRPF6
<a href="#">urogenital system development</a>	10 of 180 genes, 5.6%	326 of 47246 genes, 0.7%	0.00096	0.00%	0.00	NID1, CRIP1, JMJD6, IRX3, COL4A1, SOX11, ID2, ID3, EFN2, HEYL
<a href="#">nucleic acid metabolic process</a>	62 of 180 genes, 34.4%	8932 of 47246 genes, 18.9%	0.00096	0.00%	0.00	BHLHE40, MESP1, MKI67IP, JMJD6, MBD4, JARID2, IFI16, AFF4, HIST1H1C, PSRC1, RPF2, ISG15, PELI1, PHTF2, SERTAD2, PTRF, NUP98, EFNA1, HIST1H3H, MAFB, ID3, TULP3, NUP153, DUSP1, RNF165, PYCARD, TCERG1, N4BP2L2, FIGNL1, FSTL1, IRX3, SOX11, POU5F1B, CDK2AP1, PDLIM1, S100A11, COL4A2, BATF3, DCLRE1B, NCOA3, FAM105B, N4BP2, ERN1, JUN, CDCA7, NCK2, CEBPB, TYMS, POLE2, RIF1, MCM6, EOMES, ID2, KDM3A, GEMIN5, SOX12, ADARB1, IRF2BP2, KLF6, FBXO5, HEYL, PRPF6
<a href="#">cell surface receptor signaling pathway</a>	34 of 180 genes, 18.9%	3572 of 47246 genes, 7.6%	0.00104	0.00%	0.00	MESP1, JMJD6, GCLM, ANO6, ISG15, PELI1, PLXNA3, CXCR7, WASF2, DDIT4, EFNA1, JAK1, TULP3, LY6E, KIAA0922, BST2, RNF165, PYCARD, FSTL1, FAM89B, SOX11, RFTN1, FAM105B, TNFRSF10B, EFN2, JUN, NCK2, VEGFB, PXDN, HEYL, JAG2, RCC2, PERP, IL13RA1
<a href="#">negative regulation of cellular protein metabolic process</a>	18 of 180 genes, 10.0%	1176 of 47246 genes, 2.5%	0.00113	0.00%	0.00	SERPINB9, TNFAIP8, LXN, JARID2, IFI16, ISG15, UBASH3B, JUN, NCK2, DDIT4, KDM3A, CST3, ADARB1, FBXO5, DUSP1, BST2, STK39, PYCARD
<a href="#">regulation of cell death</a>	22 of 180 genes, 12.2%	1711 of 47246 genes, 3.6%	0.00116	0.00%	0.00	SERPINB9, FIGNL1, TNFAIP8, SOX11, GCLM, ARHGEF6, PNMA2, ANO6, TNFRSF10B, JUN, DIP2A, CEBPB, NCK2, ANGPTL4, VEGFB, CXCR7, DDIT4, NSMAF, ID3, DUSP1, PERP, PYCARD
<a href="#">myeloid cell differentiation</a>	10 of 180 genes, 5.6%	339 of 47246 genes, 0.7%	0.00137	0.00%	0.00	CEBPB, JMJD6, WASF2, IFI16, ID2, BATF3, MAFB, ISG15, UBASH3B, JUN

<a href="#">negative regulation of macromolecule biosynthetic process</a>	21 of 180 genes, 11.7%	1593 of 47246 genes, 3.4%	0.00143	0.00%	0.00	TCERG1, N4BP2L2, BHLHE40, MESP1, SOX11, JARID2, IFI16, HIST1H1C, S100A11, BATF3, JUN, NCK2, CEBPB, TMEFF2, EOMES, ID2, EFNA1, HIST1H3H, ID3, HEYL, DUSP1
<a href="#">regulation of signal transduction</a>	31 of 180 genes, 17.2%	3118 of 47246 genes, 6.6%	0.00144	0.00%	0.00	FIGNL1, MESP1, FAM89B, SOX11, GCLM, ARHGEF6, PREX1, NCOA3, FAM105B, ARRDC3, TNFRSF10B, PELI1, UBASH3B, ERN1, JUN, NCK2, DENND4B, VEGFB, CXCR7, DDIT4, EFNA1, JAK1, TULP3, PXDN, DUSP1, BST2, HEYL, KIAA0922, JAG2, RNF165, PYCARD
<a href="#">regulation of cell differentiation</a>	21 of 180 genes, 11.7%	1596 of 47246 genes, 3.4%	0.00148	0.00%	0.00	N4BP2L2, MESP1, IRX3, SOX11, PREX1, NCOA3, ISG15, EFN2, UBASH3B, JUN, CEBPB, PLXNA3, EOMES, ID2, EFNA1, ID3, MAFB, S100A10, HEYL, KIAA0922, RCC2
<a href="#">negative regulation of transcription, DNA-templated</a>	18 of 180 genes, 10.0%	1212 of 47246 genes, 2.6%	0.00174	0.00%	0.00	TCERG1, N4BP2L2, BHLHE40, MESP1, SOX11, JARID2, IFI16, HIST1H1C, BATF3, JUN, CEBPB, NCK2, EOMES, ID2, EFNA1, HIST1H3H, ID3, HEYL
<a href="#">transcription from RNA polymerase II promoter</a>	26 of 180 genes, 14.4%	2351 of 47246 genes, 5.0%	0.00181	0.00%	0.00	TCERG1, N4BP2L2, FSTL1, BHLHE40, MESP1, SOX11, JARID2, IFI16, AFF4, HIST1H1C, BATF3, NCOA3, JUN, NCK2, CEBPB, EOMES, ID2, KDM3A, EFNA1, SOX12, ID3, MAFB, KLF6, HEYL, RNF165, PRPF6
<a href="#">positive regulation of developmental process</a>	18 of 180 genes, 10.0%	1219 of 47246 genes, 2.6%	0.00189	0.00%	0.00	N4BP2L2, MESP1, IRX3, SOX11, PREX1, ANO6, NCOA3, ISG15, EFN2, JUN, CEBPB, ANGPTL4, VEGFB, EOMES, ID2, JAK1, S100A10, HEYL
<a href="#">cell motility</a>	20 of 180 genes, 11.1%	1484 of 47246 genes, 3.1%	0.00190	0.00%	0.00	MESP1, PREX1, ANO6, EFN2, JUN, NCK2, PLXNA3, VEGFB, WASF2, TMEFF2, DDIT4, EFNA1, JAK1, ADARB1, SIRPA, BST2, JAG2, RCC2, CXCL16, PYCARD
<a href="#">localization of cell</a>	20 of 180 genes, 11.1%	1484 of 47246 genes, 3.1%	0.00190	0.00%	0.00	MESP1, PREX1, ANO6, EFN2, JUN, NCK2, PLXNA3, VEGFB, WASF2, TMEFF2, DDIT4, EFNA1, JAK1, ADARB1, SIRPA, BST2, JAG2, RCC2, CXCL16, PYCARD
<a href="#">negative regulation of developmental process</a>	15 of 180 genes, 8.3%	856 of 47246 genes, 1.8%	0.00195	0.00%	0.00	N4BP2L2, PLXNA3, MESP1, IRX3, SOX11, ID2, EFNA1, COL4A2, CST3, ID3, MAFB, TULP3, KIAA0922, RCC2, UBASH3B
<a href="#">defense response</a>	22 of 180 genes, 12.2%	1767 of 47246 genes, 3.7%	0.00198	0.00%	0.00	SERPINB9, LXN, IFI16, RFTN1, ANO6, FAM105B, ISG15, TNFRSF10B, PELI1, CEBPB, CXCR7, DDIT4, HIST1H3H, JAK1, CST3, ADARB1, CD1D, STK39, CHST2, BST2, PYCARD, CXCL16
<a href="#">epithelium development</a>	17 of 180 genes, 9.4%	1097 of 47246 genes, 2.3%	0.00199	0.00%	0.00	MESP1, IRX3, COL4A1, SOX11, NCOA3, EFN2, PGK1, JUN, CEBPB, TAGLN2, TYMS, ID2, TMEFF2, ID3, TULP3, HEYL, JAG2
<a href="#">neurogenesis</a>	21 of 180 genes, 11.7%	1630 of 47246 genes, 3.5%	0.00206	0.00%	0.00	MESP1, CEP120, IRX3, SOX11, PREX1, CAMSAP1, EFN2, JUN, CEBPB, NCK2, PLXNA3, EOMES, ID2, DDIT4, SPAST, EFNA1, ID3, TULP3, HEYL, JAG2, RNF165
<a href="#">negative regulation of cellular macromolecule biosynthetic process</a>	20 of 180 genes, 11.1%	1494 of 47246 genes, 3.2%	0.00211	0.00%	0.00	TCERG1, N4BP2L2, BHLHE40, MESP1, SOX11, JARID2, IFI16, HIST1H1C, S100A11, BATF3, JUN, NCK2, CEBPB, EOMES, ID2, EFNA1, HIST1H3H, ID3, HEYL, DUSP1
<a href="#">regulation of catalytic activity</a>	31 of 180 genes, 17.2%	3183 of 47246 genes, 6.7%	0.00222	0.00%	0.00	SERPINB9, MKI67IP, DENND5A, TNFAIP8, LXN, GCLM, ARHGEF6, IFI16, PSRC1, PREX1, ARRDC3, TNFRSF10B, AHS2, UBASH3B, ERN1, JUN, NCK2, ANGPTL4, DENND4B, NSMAF, EFNA1, JAK1, CST3, S100A10, ADARB1, BST2, DUSP1, FBXO5, RCC2, PERP, PYCARD
<a href="#">negative regulation of sequence-specific DNA binding transcription factor activity</a>	7 of 180 genes, 3.9%	143 of 47246 genes, 0.3%	0.00233	0.00%	0.00	BHLHE40, ID3, FAM105B, PELI1, HEYL, ID2, PYCARD
<a href="#">regulation of macromolecule biosynthetic process</a>	50 of 180 genes, 27.8%	6691 of 47246 genes, 14.2%	0.00236	0.00%	0.00	BHLHE40, MESP1, JMJD6, JARID2, IFI16, AFF4, HIST1H1C, PSRC1, PELI1, PHTF2, SERTAD2, PTRF, NSMAF, EFNA1, HIST1H3H, MAFB, ID3, TULP3, DUSP1, PRR16, RNF165, UBE2J1, PYCARD, TCERG1, FSTL1, N4BP2L2, IRX3, SOX11, POU5F1B, PDLIM1, S100A11, BATF3, FAM105B, NCOA3, ERN1, JUN, CDCA7, CEBPB, NCK2, TYMS, TMEFF2, ID2, EOMES, KDM3A, SOX12, IRF2BP2, KLF6, HEYL, FBXO5, PRPF6
<a href="#">heterocycle metabolic process</a>	67 of 180 genes, 37.2%	10263 of 47246 genes, 21.7%	0.00256	0.00%	0.00	MESP1, MKI67IP, IFI16, AFF4, ISG15, PELI1, PGK1, GFPT2, PHTF2, PTRF, NUP98, EFNA1, HIST1H3H, ID3, NUP153, RNF165, PYCARD, TCERG1, FSTL1, IRX3, CDK2AP1, S100A11, COL4A2, DCLRE1B, FAM105B, N4BP2, CDCA7, POLE2, RIF1, ID2, FBXO5, HEYL, BHLHE40, JMJD6, MBD4, JARID2, HIST1H1C, ME2, PSRC1, RPF2, PGAM1, DDIT4, SERTAD2, MAFB, TULP3, DUSP1, FIGNL1, N4BP2L2, SOX11, POU5F1B, PDLIM1, BATF3, NCOA3, ERN1, JUN, CEBPB, NCK2, TYMS, EOMES, MCM6, KDM3A, GEMIN5, SOX12, IRF2BP2, ADARB1, KLF6, PRPF6
<a href="#">response to external biotic stimulus</a>	16 of 180 genes, 8.9%	995 of 47246 genes, 2.1%	0.00259	0.00%	0.00	SERPINB9, IFI16, BATF3, ISG15, TNFRSF10B, PELI1, JUN, CEBPB, CXCR7, DDIT4, HIST1H3H, ADARB1, CD1D, BST2, CXCL16, PYCARD
<a href="#">response to other organism</a>	16 of 180 genes, 8.9%	995 of 47246 genes, 2.1%	0.00259	0.00%	0.00	SERPINB9, IFI16, BATF3, ISG15, TNFRSF10B, PELI1, JUN, CEBPB, CXCR7, DDIT4, HIST1H3H, ADARB1, CD1D, BST2, CXCL16, PYCARD
<a href="#">regulation of biosynthetic process</a>	51 of 180 genes, 28.3%	6939 of 47246 genes, 14.7%	0.00292	0.00%	0.00	BHLHE40, MESP1, JMJD6, JARID2, IFI16, AFF4, HIST1H1C, PSRC1, PELI1, PHTF2, SERTAD2, PTRF, NSMAF, EFNA1, HIST1H3H, MAFB, ID3, TULP3, DUSP1, PRR16, RNF165, UBE2J1, PYCARD, TCERG1, FSTL1, N4BP2L2, IRX3, SOX11, POU5F1B, PDLIM1, S100A11, BATF3, FAM105B, NCOA3, ERN1, JUN, CDCA7, PDK1, CEBPB, NCK2, TYMS, TMEFF2, ID2, EOMES, KDM3A, SOX12, IRF2BP2, KLF6, HEYL, FBXO5, PRPF6

<a href="#">cellular aromatic compound metabolic process</a>	67 of 180 genes, 37.2%	10308 of 47246 genes, 21.8%	0.00301	0.00%	0.00	MESP1, MKI67IP, IFI16, AFF4, ISG15, PELI1, PGK1, GFPT2, PHTF2, PTRF, NUP98, EFNA1, HIST1H3H, ID3, NUP153, RNF165, PYCARD, TCERG1, FSTL1, IRX3, CDK2AP1, S100A11, COL4A2, DCLRE1B, FAM105B, N4BP2, CDCA7, POLE2, RIF1, ID2, FBXO5, HEYL, BHLHE40, JMJD6, MBD4, JARID2, HIST1H1C, ME2, PSRC1, RPF2, PGAM1, DDIT4, SERTAD2, MAFB, TULP3, DUSP1, FIGNL1, N4BP2L2, SOX11, POU5F1B, PDLIM1, BATF3, NCOA3, ERN1, JUN, CEBPB, NCK2, TYMS, EOMES, MCM6, KDM3A, GEMIN5, SOX12, IRF2BP2, ADARB1, KLF6, PRPF6
<a href="#">renal system development</a>	9 of 180 genes, 5.0%	288 of 47246 genes, 0.6%	0.00307	0.00%	0.00	NID1, JMJD6, IRX3, COL4A1, SOX11, ID2, ID3, EFNB2, HEYL
<a href="#">negative regulation of nucleic acid-templated transcription</a>	18 of 180 genes, 10.0%	1262 of 47246 genes, 2.7%	0.00308	0.00%	0.00	TCERG1, N4BP2L2, BHLHE40, MESP1, SOX11, JARID2, IFI16, HIST1H1C, BATF3, JUN, CEBPB, NCK2, EOMES, ID2, EFNA1, HIST1H3H, ID3, HEYL
<a href="#">cellular nitrogen compound metabolic process</a>	72 of 180 genes, 40.0%	11434 of 47246 genes, 24.2%	0.00320	0.00%	0.00	MESP1, MKI67IP, GCLM, IFI16, AFF4, ISG15, PELI1, PGK1, GFPT2, PHTF2, PTRF, NUP98, EFNA1, HIST1H3H, ID3, NUP153, PRR16, RNF165, PYCARD, TCERG1, FSTL1, IRX3, CDK2AP1, S100A11, COL4A2, DCLRE1B, FAM105B, N4BP2, CDCA7, POLE2, RIF1, ID2, FBXO5, HEYL, BHLHE40, JMJD6, MBD4, JARID2, HIST1H1C, ME2, PSRC1, RPF2, PGAM1, SERTAD2, DDIT4, NSMAF, MAFB, TULP3, DUSP1, FIGNL1, N4BP2L2, SOX11, POU5F1B, PDLIM1, BATF3, NCOA3, ERN1, JUN, CEBPB, NCK2, TYMS, EOMES, MCM6, SLC25A43, KDM3A, GEMIN5, SOX12, SPCS3, IRF2BP2, ADARB1, KLF6, PRPF6
<a href="#">neuron differentiation</a>	19 of 180 genes, 10.6%	1405 of 47246 genes, 3.0%	0.00341	0.00%	0.00	IRX3, SOX11, PREX1, CAMSAP1, EFNB2, JUN, CEBPB, NCK2, PLXNA3, EOMES, ID2, DDIT4, EFNA1, SPAST, ID3, TULP3, HEYL, JAG2, RNF165
<a href="#">organic cyclic compound metabolic process</a>	68 of 180 genes, 37.8%	10573 of 47246 genes, 22.4%	0.00353	0.00%	0.00	MESP1, MKI67IP, IFI16, AFF4, ISG15, PELI1, PGK1, GFPT2, PHTF2, PTRF, NUP98, EFNA1, HIST1H3H, ID3, NUP153, RNF165, PYCARD, TCERG1, FSTL1, IRX3, CDK2AP1, S100A11, COL4A2, DCLRE1B, FAM105B, N4BP2, CDCA7, POLE2, RIF1, ID2, FBXO5, HEYL, BHLHE40, JMJD6, MBD4, JARID2, HIST1H1C, ME2, PSRC1, RPF2, PGAM1, DDIT4, SERTAD2, MAFB, TULP3, DUSP1, FIGNL1, N4BP2L2, SOX11, POU5F1B, PDLIM1, BATF3, NCOA3, ERN1, JUN, CEBPB, NCK2, TYMS, EOMES, MCM6, KDM3A, GEMIN5, FBAP6, SOX12, IRF2BP2, ADARB1, KLF6, PRPF6
<a href="#">negative regulation of biosynthetic process</a>	21 of 180 genes, 11.7%	1688 of 47246 genes, 3.6%	0.00357	0.00%	0.00	TCERG1, N4BP2L2, BHLHE40, MESP1, SOX11, JARID2, IFI16, HIST1H1C, S100A11, BATF3, JUN, NCK2, CEBPB, TMEFF2, EOMES, ID2, EFNA1, HIST1H3H, ID3, HEYL, DUSP1
<a href="#">blood vessel morphogenesis</a>	12 of 180 genes, 6.7%	568 of 47246 genes, 1.2%	0.00361	0.00%	0.00	ANGPTL4, JMJD6, COL4A1, VEGFB, CXCR7, WASF2, EFNA1, COL4A2, JAK1, FAM105B, EFNB2, JUN
<a href="#">negative regulation of RNA biosynthetic process</a>	18 of 180 genes, 10.0%	1278 of 47246 genes, 2.7%	0.00367	0.00%	0.00	TCERG1, N4BP2L2, BHLHE40, MESP1, SOX11, JARID2, IFI16, HIST1H1C, BATF3, JUN, CEBPB, NCK2, EOMES, ID2, EFNA1, HIST1H3H, ID3, HEYL
<a href="#">organonitrogen compound metabolic process</a>	71 of 180 genes, 39.4%	11256 of 47246 genes, 23.8%	0.00374	0.00%	0.00	TNFAIP8, GCLM, IFI16, SPSB1, ISG15, PELI1, PGK1, GFPT2, CXCR7, CHST7, NUP98, EFNA1, HIST1H3H, NUP153, BST2, PRR16, RNF165, UBE2J1, PYCARD, RIMKLB, MGEA5, ARHGEF6, CDK2AP1, CHST15, EDEM2, FAM105B, TNFRSF10B, LOX, RNF24, FBXO5, JAG2, PERP, SERPINB9, JMJD6, MBD4, JARID2, HIST1H1C, ME2, PSRC1, RNF125, PGAM1, UBASH3B, DDIT4, NSMAF, JAK1, P4HA1, CST3, FEM1C, DUSP1, FUT11, FIGNL1, LXN, SOX11, WSB1, ARRDC3, NCOA3, ERN1, GXYLT1, JUN, PDK1, CEBPB, CKAP4, NCK2, TYMS, VEGFB, KDM3A, SLC25A43, ADARB1, SPCS3, CHST2, STK39
<a href="#">negative regulation of transcription from RNA polymerase II promoter</a>	14 of 180 genes, 7.8%	793 of 47246 genes, 1.7%	0.00413	0.00%	0.00	TCERG1, N4BP2L2, BHLHE40, NCK2, SOX11, JARID2, IFI16, ID2, EOMES, HIST1H1C, EFNA1, BATF3, ID3, JUN
<a href="#">multi-organism process</a>	27 of 180 genes, 15.0%	2626 of 47246 genes, 5.6%	0.00435	0.00%	0.00	SERPINB9, IFI16, AFF4, BATF3, ISG15, TNFRSF10B, PELI1, EFNB2, JUN, CEBPB, TYMS, CXCR7, WASF2, KDM3A, DDIT4, NUP98, HIST1H3H, KATNAL1, ADARB1, CD1D, NUP153, BST2, FBXO5, JAG2, UBE2J1, PYCARD, CXCL16
<a href="#">epithelial cell differentiation</a>	12 of 180 genes, 6.7%	580 of 47246 genes, 1.2%	0.00447	0.00%	0.00	TAGLN2, MESP1, CEBPB, TYMS, COL4A1, SOX11, ID2, ID3, NCOA3, PGK1, JAG2, JUN
<a href="#">nucleobase-containing compound biosynthetic process</a>	52 of 180 genes, 28.9%	7244 of 47246 genes, 15.3%	0.00451	0.00%	0.00	BHLHE40, MESP1, MKI67IP, JMJD6, JARID2, IFI16, AFF4, HIST1H1C, PSRC1, ISG15, PELI1, GFPT2, PHTF2, SERTAD2, PTRF, NUP98, EFNA1, HIST1H3H, MAFB, ID3, TULP3, NUP153, DUSP1, RNF165, PYCARD, TCERG1, FSTL1, N4BP2L2, IRX3, SOX11, POU5F1B, PDLIM1, COL4A2, BATF3, NCOA3, FAM105B, ERN1, JUN, CDCA7, NCK2, CEBPB, TYMS, POLE2, EOMES, ID2, KDM3A, SOX12, IRF2BP2, KLF6, HEYL, FBXO5, PRPF6
<a href="#">regulation of gene expression</a>	51 of 180 genes, 28.3%	7045 of 47246 genes, 14.9%	0.00457	0.00%	0.00	SERPINB9, BHLHE40, MESP1, JMJD6, JARID2, IFI16, AFF4, HIST1H1C, PSRC1, PELI1, PHTF2, SERTAD2, PTRF, NUP98, EFNA1, HIST1H3H, MAFB, ID3, TULP3, NUP153, PRR16, RNF165, PYCARD, TCERG1, FSTL1, N4BP2L2, CRIP1, IRX3, SOX11, POU5F1B, PDLIM1, BATF3, FAM105B, NCOA3, ERN1, DIP2A, JUN, CDCA7, CEBPB, NCK2, TYMS, VEGFB, EOMES, ID2, KDM3A, SOX12, IRF2BP2, KLF6, HEYL, FBXO5, PRPF6
<a href="#">regulation of cell communication</a>	32 of 180 genes, 17.8%	3470 of 47246 genes, 7.3%	0.00465	0.00%	0.00	MESP1, GCLM, PELI1, UBASH3B, DENND4B, CXCR7, DDIT4, EFNA1, JAK1, TULP3, DUSP1, BST2, KIAA0922, RNF165, PYCARD, FIGNL1, FAM89B, ARHGEF6, SOX11, PREX1, ARRDC3, FAM105B, NCOA3, TNFRSF10B, ERN1, JUN, NCK2, VEGFB, PXDN, HEYL, JAG2, ITPR3
<a href="#">response to biotic stimulus</a>	16 of 180 genes, 8.9%	1044 of 47246 genes, 2.2%	0.00479	0.00%	0.00	SERPINB9, IFI16, BATF3, ISG15, TNFRSF10B, PELI1, JUN, CEBPB, CXCR7, DDIT4, HIST1H3H, ADARB1, CD1D, BST2, CXCL16, PYCARD

<a href="#">positive regulation of gene expression</a>	21 of 180 genes, 11.7%	1727 of 47246 genes, 3.7%	0.00509	0.00%	0.00	SERPINB9, MESP1, SOX11, IFI16, PSRC1, NCOA3, ERN1, JUN, CEBPB, NCK2, EOMES, ID2, KDM3A, SERTAD2, HIST1H3H, SOX12, MAFB, KLF6, HEYL, PRR16, PRPF6
<a href="#">regulation of cellular biosynthetic process</a>	50 of 180 genes, 27.8%	6887 of 47246 genes, 14.6%	0.00549	0.00%	0.00	BHLHE40, MESP1, JMJD6, JARID2, IFI16, AFF4, HIST1H1C, PSRC1, PELI1, PHTF2, SERTAD2, PTRF, NSMAF, EFNA1, HIST1H3H, MAFB, ID3, TULP3, DUSP1, PRR16, RNF165, UBE2J1, PYCARD, TCERG1, FSTL1, N4BP2L2, IRX3, SOX11, POU5F1B, PDLIM1, S100A11, BATF3, FAM105B, NCOA3, ERN1, JUN, CDCA7, PDK1, CEBPB, NCK2, TYMS, ID2, EOMES, KDM3A, SOX12, IRF2BP2, KLF6, HEYL, FBXO5, PRPF6
<a href="#">negative regulation of cell proliferation</a>	13 of 180 genes, 7.2%	700 of 47246 genes, 1.5%	0.00554	0.00%	0.00	NCK2, CEBPB, SOX11, JARID2, ID2, S100A11, FABP6, ADARB1, PELI1, BTG3, EFN2, KIAA0922, JUN
<a href="#">negative regulation of RNA metabolic process</a>	18 of 180 genes, 10.0%	1322 of 47246 genes, 2.8%	0.00586	0.00%	0.00	TCERG1, N4BP2L2, BHLHE40, MESP1, SOX11, JARID2, IFI16, HIST1H1C, BATF3, JUN, CEBPB, NCK2, EOMES, ID2, EFNA1, HIST1H3H, ID3, HEYL
<a href="#">regulation of apoptotic process</a>	20 of 180 genes, 11.1%	1606 of 47246 genes, 3.4%	0.00626	0.00%	0.00	SERPINB9, FIGNL1, TNFAIP8, GCLM, ARHGEF6, PNMA2, ANO6, TNFRSF10B, JUN, DIP2A, CEBPB, NCK2, ANGPTL4, VEGFB, CXCR7, NSMAF, ID3, DUSP1, PERP, PYCARD
<a href="#">symbiosis, encompassing mutualism through parasitism</a>	17 of 180 genes, 9.4%	1200 of 47246 genes, 2.5%	0.00660	0.00%	0.00	SERPINB9, IFI16, BATF3, ISG15, EFN2, JUN, TYMS, CXCR7, WASF2, DDIT4, NUP98, HIST1H3H, ADARB1, CD1D, BST2, NUP153, PYCARD
<a href="#">interspecies interaction between organisms</a>	17 of 180 genes, 9.4%	1203 of 47246 genes, 2.5%	0.00682	0.00%	0.00	SERPINB9, IFI16, BATF3, ISG15, EFN2, JUN, TYMS, CXCR7, WASF2, DDIT4, NUP98, HIST1H3H, ADARB1, CD1D, BST2, NUP153, PYCARD
<a href="#">negative regulation of protein modification process</a>	12 of 180 genes, 6.7%	605 of 47246 genes, 1.3%	0.00687	0.00%	0.00	NCK2, JARID2, KDM3A, DDIT4, ADARB1, ISG15, STK39, DUSP1, FBXO5, UBASH3B, PYCARD, JUN
<a href="#">lymphocyte differentiation</a>	9 of 180 genes, 5.0%	318 of 47246 genes, 0.7%	0.00688	0.00%	0.00	PREX1, MAFB, KLF6, JMJD6, CD1D, KIAA0922, JAG2, ID2, EOMES
<a href="#">RNA biosynthetic process</a>	48 of 180 genes, 26.7%	6542 of 47246 genes, 13.8%	0.00695	0.00%	0.00	BHLHE40, MESP1, MKI67IP, JMJD6, JARID2, IFI16, AFF4, HIST1H1C, PSRC1, PELI1, PHTF2, SERTAD2, PTRF, NUP98, EFNA1, HIST1H3H, MAFB, ID3, TULP3, NUP153, RNF165, PYCARD, TCERG1, FSTL1, N4BP2L2, IRX3, SOX11, POU5F1B, PDLIM1, COL4A2, BATF3, FAM105B, NCOA3, ERN1, JUN, CDCA7, CEBPB, NCK2, TYMS, ID2, EOMES, KDM3A, SOX12, IRF2BP2, KLF6, HEYL, FBXO5, PRPF6
<a href="#">regulation of programmed cell death</a>	20 of 180 genes, 11.1%	1619 of 47246 genes, 3.4%	0.00705	0.00%	0.00	SERPINB9, FIGNL1, TNFAIP8, GCLM, ARHGEF6, PNMA2, ANO6, TNFRSF10B, JUN, DIP2A, CEBPB, NCK2, ANGPTL4, VEGFB, CXCR7, NSMAF, ID3, DUSP1, PERP, PYCARD
<a href="#">regulation of hydrolase activity</a>	22 of 180 genes, 12.2%	1913 of 47246 genes, 4.0%	0.00711	0.00%	0.00	SERPINB9, MKI67IP, DENND5A, TNFAIP8, LXN, ARHGEF6, IFI16, PREX1, TNFRSF10B, AHS2, ERN1, JUN, NCK2, ANGPTL4, DENND4B, JAK1, CST3, S100A10, BST2, RCC2, PERP, PYCARD
<a href="#">regulation of signaling</a>	32 of 180 genes, 17.8%	3543 of 47246 genes, 7.5%	0.00718	0.00%	0.00	MESP1, GCLM, PELI1, UBASH3B, DENND4B, CXCR7, DDIT4, EFNA1, JAK1, TULP3, DUSP1, BST2, KIAA0922, RNF165, PYCARD, FIGNL1, FAM89B, ARHGEF6, SOX11, PREX1, ARRDC3, FAM105B, NCOA3, TNFRSF10B, ERN1, JUN, NCK2, VEGFB, PDXN, HEYL, JAG2, ITPR3
<a href="#">regulation of locomotion</a>	14 of 180 genes, 7.8%	836 of 47246 genes, 1.8%	0.00756	0.00%	0.00	PLXNA3, VEGFB, TMEFF2, EFNA1, ANO6, ARRDC3, ADARB1, BST2, EFN2, RCC2, JAG2, PYCARD, CXCL16, JUN
<a href="#">aromatic compound biosynthetic process</a>	52 of 180 genes, 28.9%	7375 of 47246 genes, 15.6%	0.00766	0.00%	0.00	BHLHE40, MESP1, MKI67IP, JMJD6, JARID2, IFI16, AFF4, HIST1H1C, PSRC1, ISG15, PELI1, GFPT2, PHTF2, SERTAD2, PTRF, NUP98, EFNA1, HIST1H3H, MAFB, ID3, TULP3, NUP153, DUSP1, RNF165, PYCARD, TCERG1, FSTL1, N4BP2L2, IRX3, SOX11, POU5F1B, PDLIM1, COL4A2, BATF3, NCOA3, FAM105B, ERN1, JUN, CDCA7, NCK2, CEBPB, TYMS, POLE2, EOMES, ID2, KDM3A, SOX12, IRF2BP2, KLF6, HEYL, FBXO5, PRPF6
<a href="#">heterocycle biosynthetic process</a>	52 of 180 genes, 28.9%	7401 of 47246 genes, 15.7%	0.00849	0.00%	0.00	BHLHE40, MESP1, MKI67IP, JMJD6, JARID2, IFI16, AFF4, HIST1H1C, PSRC1, ISG15, PELI1, GFPT2, PHTF2, SERTAD2, PTRF, NUP98, EFNA1, HIST1H3H, MAFB, ID3, TULP3, NUP153, DUSP1, RNF165, PYCARD, TCERG1, FSTL1, N4BP2L2, IRX3, SOX11, POU5F1B, PDLIM1, COL4A2, BATF3, NCOA3, FAM105B, ERN1, JUN, CDCA7, NCK2, CEBPB, TYMS, POLE2, EOMES, ID2, KDM3A, SOX12, IRF2BP2, KLF6, HEYL, FBXO5, PRPF6
<a href="#">cell development</a>	23 of 180 genes, 12.8%	2088 of 47246 genes, 4.4%	0.00858	0.00%	0.00	JMJD6, IRX3, SOX11, AFF4, PREX1, CAMSAP1, EFN2, JUN, NCK2, PLXNA3, TYMS, WASF2, EOMES, ID2, KDM3A, EFNA1, SPAST, S100A10, HEYL, FBXO5, RCC2, RNF165, UBE2J1
<a href="#">cellular response to stress</a>	25 of 180 genes, 13.9%	2402 of 47246 genes, 5.1%	0.00864	0.00%	0.00	FIGNL1, CRIP1, MBD4, ARHGEF6, IFI16, DCLRE1B, EDEM2, ISG15, TNFRSF10B, ERN1, JUN, PDK1, CEBPB, NCK2, POLE2, CXCR7, RIF1, ID2, DDIT4, NUP98, KLF6, STK39, NUP153, UBE2J1, PYCARD