Supplementary

Table S1 Top and down 20 regulated genes list

DEGs	Gene symbol
Upregulated	ABCA1,ADAMTS7,ADRB3,AMMECR1L,ANGPTL2,AQP2,ARID1B,ARMCX2,ATF5,DMAC2L,ATXN10,B2M,BASP1,BMPR2,BSDC1,AAMDC,KXD1,C3orf33,CAMTA2,CCDC112,CCDC141,CCDC89,CCND2,CCNL1,NOCT,CD320,CD37,CDK17,CEP350,CNN3,CNNM3,CPXM2,CTPS2,CUX1,CXCR5,DAAM2,DAXX,DCAF11,DCTN1,DECR2,DENND1A,DENND2A,DNAJA1,DNAJB14,DUSP14,DUSP2,EDC3,EFNA3,EGR3,EIF4G3,ELK3,EOMES,RETREG2,FCRL1,FOXG1,FOXJ2,FCSK,GADD45G,GBP6,PAXBP1,GDNF,GLCCI1,GPM6B,GPR34,GPR39,GRAMD1A,GYG1,GZF1,HLA-DOA,HOXD10,HPS4,HSD17B11,HSF4,IFFO2,IFI35,IFIT1,IFIT1B,IGF2R,IL27RA,IMMP1L,INO80,IQSEC1,IRF7,IRF8,ISG15,ITM2A,KCNE1,KCNN4,KDM5B,BLTP2,KANSL3,ATOSA,KIF26B,KIRREL3,KRT85,LCLAT1,C3orf80,LYPD6B,MAPK8IP3,CGAS,MESD
Downregulated	METTL2B,MLPH,MOCS3,MSL1,MTF2,MUC4,MXD4,NARF,NCF4,NDFIP2,NDRG1,NEK7,NICN1,NR4A1,NR4A2,NRIP1,PABPC1,PACSIN1,PAM,PANK4,PARP11,PARP6,PCGF5,PEX6,JADE2,PHLDA1,PIK3R3,PITPNM1,PLCB2,PLD2,PLD3,PLEKHA1,PLEKHA8,PLOD1,PLXDC2,PML,PNISR,PNMA2,PPIP5K1,PRDM15,HELZ2,PRKCH,PRKRA,PTPRS,PURA,RAMP1,RAMP2,RAPGEF6,RASGRF2,RC3H2,RCOR3,REEP5,RELB,RFX5,RGL2,RNF2,RPS27,RTP4,RYBP,SELENOP,SESN3,SKP1,SLAMF1,SLC45A3,SLC6A5,SMURF2,SON,SPAG17,SPEN,SPINT2,SPTBN1,SSH1,SSH2,TDRD7,THRSP,TIMM17B,TMIE,TMX2,TNFRSF18,TOR3A,TOX,TRIM21,TRIM72,TRRAP,TSC22D4,TSPAN32,UBIAD1,VWA3A,XPR1,ZBTB20,ZBTB4,TUT4,ZCCHC12,ZCCHC13,ZKSCAN3,ZNF436,ZNF579,ZNF711

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Table S2 DAVID result

GO Terms	ID	Group	Adjusted P value	FDR
GOTERM_MF_DIRECT	GO:1990837	sequence-specific double-stranded DNA binding	4.52E-04	0.098094537
GOTERM_CC_DIRECT	GO:0000785	chromatin	4.94E-04	0.083071971
GOTERM_BP_DIRECT	GO:0045944	positive regulation of transcription from RNA polymerase II promoter	0.001146745	0.076977994
GOTERM_MF_DIRECT	GO:0043565	sequence-specific DNA binding	0.00156977	0.017032007
GOTERM_BP_DIRECT	GO:0002376	immune system process	0.002435691	0.076977994
GOTERM_BP_DIRECT	GO:0071360	cellular response to exogenous dsRNA	0.003303777	0.076977994
GOTERM_BP_DIRECT	GO:0071357	cellular response to type I interferon	0.009045309	0.1
GOTERM_MF_DIRECT	GO:0005515	protein binding	0.014115691	0.1
GOTERM_BP_DIRECT	GO:0030501	positive regulation of bone mineralization	0.016986516	0.1
GOTERM_BP_DIRECT	GO:0051607	defense response to virus	0.021832459	0.1
GOTERM_BP_DIRECT	GO:0008344	adult locomotory behavior	0.02326153	0.1
GOTERM_BP_DIRECT	GO:0045597	positive regulation of cell differentiation	0.028496889	0.1
GOTERM_BP_DIRECT	GO:0046605	regulation of centrosome cycle	0.031306223	0.1
GOTERM_BP_DIRECT	GO:0021516	dorsal spinal cord development	0.035698713	0.1
GOTERM_BP_DIRECT	GO:0050688	regulation of defense response to virus	0.035698713	0.1
GOTERM_BP_DIRECT	GO:0009791	post-embryonic development	0.040211445	0.1
GOTERM_CC_DIRECT	GO:0005887	integral component of plasma membrane	0.042481901	0.1
GOTERM_BP_DIRECT	GO:0021517	ventral spinal cord development	0.044424703	0.1
GOTERM_BP_DIRECT	GO:0045893	positive regulation of transcription, DNA-templated	0.046028333	0.1
GOTERM_BP_DIRECT	GO:0006357	regulation of transcription from RNA polymerase II promoter	0.048022927	0.1
GOTERM_BP_DIRECT	GO:0070585	protein localization to mitochondrion	0.048758378	0.1
GOTERM_BP_DIRECT	GO:0032729	positive regulation of interferon-gamma production	0.049985927	0.1