

Figure S1. Identification of DEGs and DECs. (A) PCA of three datasets. (B) Blue bar represents the number of upregulated DEGs or DECs, and orange bar represents the number of downregulated DEGs or DECs. Hierarchical clustering and heatmap analysis of DEGs and DECs are shown in (C) GSE7084, (D) GSE57691 and (E) GSE144431. (F) Venn diagrams present the overlap of up and downregulated DEGs between GSE7084 and GSE57691. DEGs, differentially expressed genes; DECs, differentially expressed circRNAs; PCA, principal component analysis; AAA, abdominal aortic aneurysm.

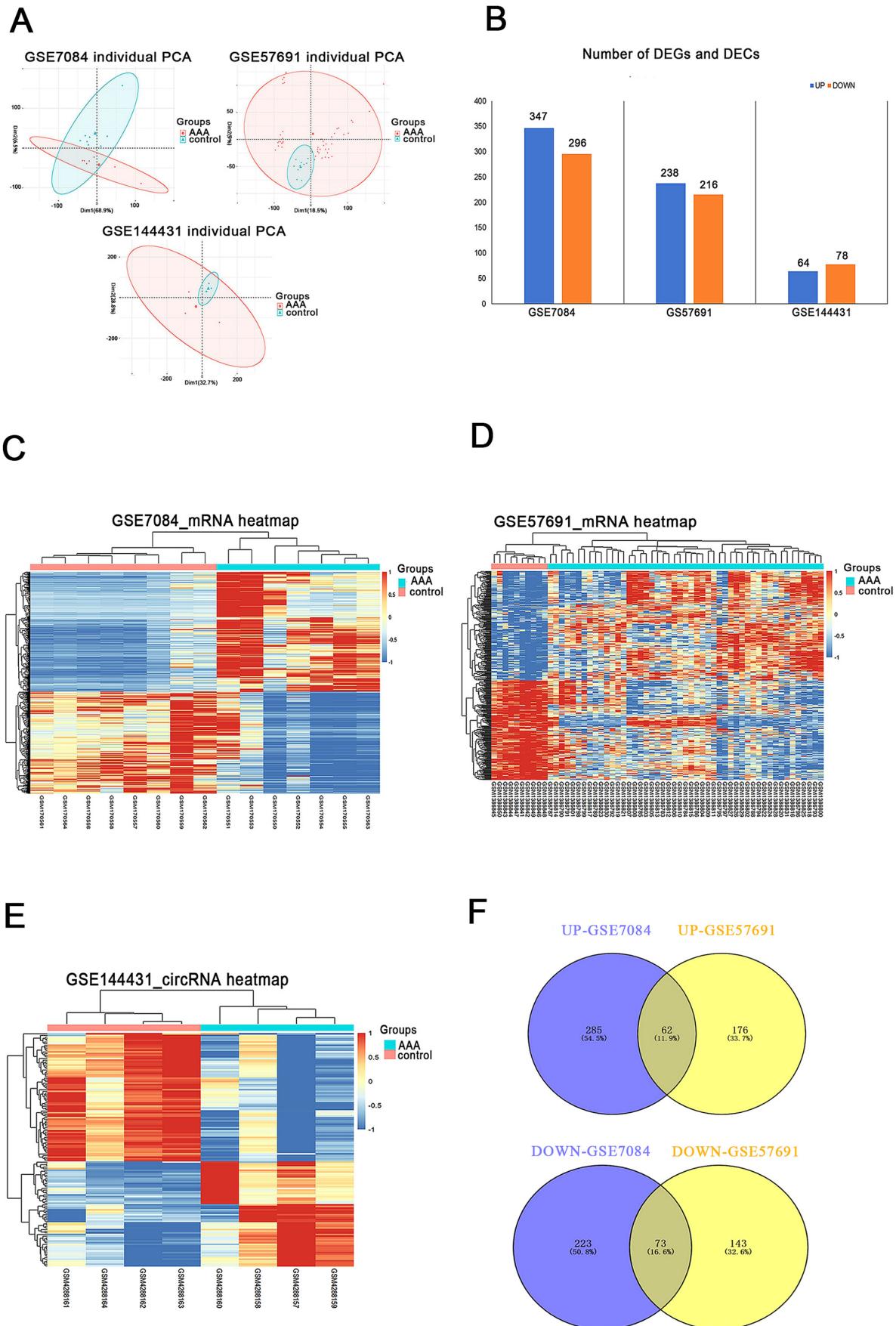


Figure S2. Construction of ceRNA networks. (A) Upregulated circRNAs/mRNAs. (B) The downregulated circRNAs/mRNAs. Red ellipse, upregulated circRNAs; Purple hexagon, upregulated mRNAs; Green ellipse, downregulated circRNAs; Pink hexagon, downregulated mRNAs; light blue diamond, common target miRNAs of circRNAs and mRNAs; miRs, microRNA; IL10RA, interleukin 10 receptor subunit α ; SEMA4A, semaphorin 4A; CEMIP, cell migration inducing hyaluronan-binding protein; ATOH8, atonal bHLH transcription factor 8; PRUNE2, prune homolog 2 with BCH domain; CNN1, calponin 1; ZBTB16, zinc finger and BTB domain-containing 16; SOST, sclerostin; TMEM47, transmembrane protein 47; FBXO32, F-box protein 32; NFIA, nuclear factor IA.

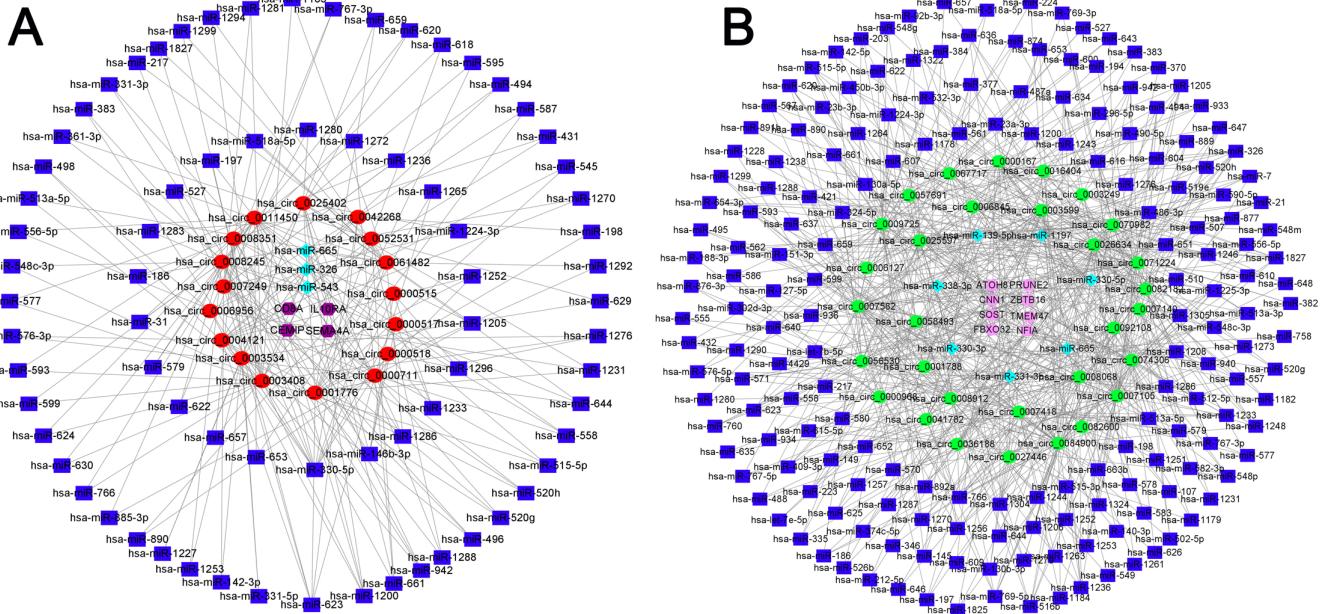


Figure S3. A total of 12 ceRNA networks based on every single DEG. For downregulated DEGs: (A) ATOH8, (B) ZBTB16, (C) TMEM47, (D) SOST, (E) PRUNE2, (F) NFIA, (G) FBXO32 and (H) CNN1. For upregulated DEGs: (I) SEMA4A, (J) CEMIP, (K) IL10RA and (L) CD8A. Green ellipse, downregulated circRNAs; Pink hexagon, downregulated mRNAs; Red ellipses, upregulated circRNAs; Purple hexagon, upregulated mRNAs; Light blue diamond, common target miRNAs of circRNAs and mRNAs; Dark blue rectangle, predicted miRNA of circRNAs or mRNAs. FBXO32, F-box protein 32; TMEM47, transmembrane protein 47; CEMIP, cell migration inducing hyaluronan-binding protein; IL10RA, interleukin 10 receptor subunit α ; SEMA4A, semaphorin 4A; ATOH8, atonal bHLH transcription factor 8; PRUNE2, prune homolog 2 with BCH domain; CNN1, calponin 1; ZBTB16, zinc finger and BTB domain-containing 16; SOST, sclerostin; NFIA, nuclear factor IA.

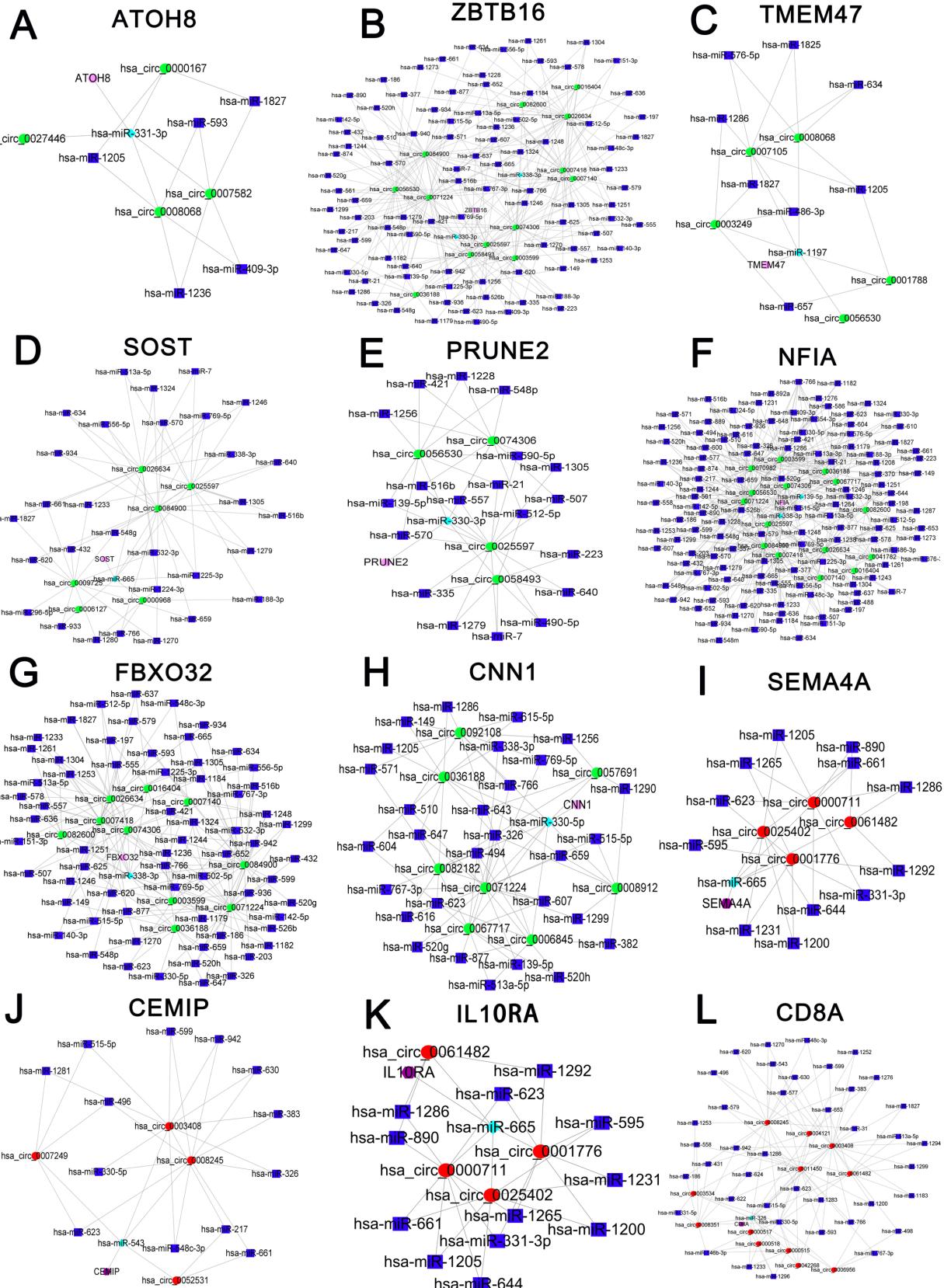


Table SI. Information of the three datasets.

Dataset	Platform	Groups
GSE7084	Sentrix Human-6 Expression BeadChip (GPL2507)	Seven AAA and eight healthy
GSE57691	Illumina HumanHT-12 V4.0 expression beadchip (GPL10558)	49 AAA and 10 healthy
GSE144431	074301 Arraystar Human CircRNA microarray V2 (GPL21825)	Four AAA and four healthy

AAA, abdominal aortic aneurysm.

Table SII. Characteristics of AAA and control subjects used for RT-qPCR.

Group	Sex	Age (years)	BMI (kg/m ²)	Smoking	SBP (mmHg)	DBP (mmHg)	Hypertension	Diabetes	Hyperlipidemia	Maximum aortic diameter (cm)
AAA	Male	64	24.34	Yes	152	95	Yes	No	Yes	7.25
AAA	Male	78	25.76	No	130	75	No	No	No	6.74
AAA	Male	70	22.68	Yes	167	95	Yes	No	No	6.60
AAA	Male	60	25.35	No	153	100	Yes	No	Yes	5.30
Control	Male	58	24.72	Yes	128	87	No	No	Yes	2.00
Control	Male	62	24.61	No	145	91	Yes	No	No	2.20
Control	Female	53	22.60	No	115	76	No	No	No	1.70
Control	Male	60	23.81	No	121	80	No	No	No	1.90

AAA, abdominal aortic tumor; RT-qPCR, reverse transcription-quantitative polymerase chain reaction; BMI, body mass index; SBP, systolic blood pressure; DBP, diastolic blood pressure.

Table SIII. Primer sequences of CNN1 and CD8A.

Gene ID	Gene	Forward Primer (5'-3')	Reverse Primer (5'-3')
1264	CNN1	TGAAGAACGATCAATGAGTCAACCC	CGTTCACCTGTTCCCTTCG
925	CD8A	CAGGGAACCGAAGACGTGTT	TAGACGTATCTGCCGAAAGG
60	β -actin	ATGTGGCCGAGGACTTGATT	AGTGGGGTGGCTTTAGGATG

CNN1, calponin 1.

Table SVIII. GO term enrichment analysis for differentially expressed genes (P<0.05).

ID	Term	P-value	Genes	Z-score
GO:0006955	Immune response	1.18x10 ⁻⁷	SBSPON, CXCL8, SEMA4D, OSM, WAS, CXCL13, CXCL2, JCHAIN, VPREB3, CD8A, IL1B, GPR183, CCL3, CCR7, LTB, HLA-DQA1, HLA-DQB1	3.64
GO:0005615	Extracellular space	6.65x10 ⁻⁵	SEMA4A, CXCL8, SEMA4D, CCL3L1, IGFBP2, OSM, PDGFA, CXCL13, CXCL2, LIME1, MMP9, GLDN, JCHAIN, VPREB3, ACTC1, FRZB, IL1B, CCL3, LTB, SOST, IL13RA2, SCRG1, RAMP1, TIMP4	0.82
GO:0005576	Extracellular region	1.41x10 ⁻⁴	FCN1, CEMIP, FCMR, CXCL8, CCL3L1, PDGFA, CXCL13, CXCL2, JCHAIN, FRZB, CCL3, FDCSP, SOST, IL13RA2, NPTX2, IGFBP2, OSM, MMP9, CD2, MMP12, NOV, CD8A, IL1B, MZB1, FIBIN, FGF13	1.57
GO:0006954	Inflammatory response	1.44x10 ⁻⁴	AOC3, GBP5, MMP25, CXCL8, CCL3L1, IL1B, NFKBIZ, CCL3, CXCR4, CCR7, CXCL13, CXCL2	2.89
GO:0070098	Chemokine-mediated signaling	2.00x10 ⁻⁴	CXCL8, CCL3L1, CCL3, CXCR4, CXCL13,	2.45

	pathway		CXCL2	
GO:0008009	Chemokine activity	4.02x10 ⁻⁴	CXCL8, CCL3L1, CCL3, CXCL13, CXCL2	2.24
GO:0005578	Proteinaceous extracellular matrix	6.49x10 ⁻⁴	MMP12, SBSPON, MMP25, NOV, SPOCK2, SOST, MMP9, GLDN, TIMP4	-0.33
GO:0006936	Muscle contraction	1.31x10 ⁻³	CKMT2, FXYD1, LMOD1, SORBS1, CRYAB, MYL9	-2.45
GO:0030018	Z disc	1.52x10 ⁻³	SYNPO2, NEXN, KCNA5, FBXO32, CRYAB, MYL9	-2.45
GO:0008285	Negative regulation of cell proliferation	3.17x10 ⁻³	CXCL8, CCL3L1, FRZB, TGFB1I1, IL1B, ZBTB16, OSM, SPEG, LDOC1, PIM2	0.00
GO:0003779	Actin binding	3.73x10 ⁻³	CNN1, SYNPO2, LMOD1, WAS, STK38L, CXCR4, SORBS1, CORO1A	-0.71
GO:0009897	External side of plasma membrane	4.11x10 ⁻³	CD2, CD79A, CD83, SELL, CD8A, CD19, CCR7	2.65
GO:0050852	T cell receptor signaling pathway	5.35x10 ⁻³	ITK, WAS, CD3D, LIME1, HLA-DQA1, HLA-DQB1	2.45
GO:0002250	Adaptive immune response	5.35x10 ⁻³	ITK, CD79A, GPR183, PRDM1, LIME1, JCHAIN	2.45
GO:0042110	T cell activation	5.38x10 ⁻³	CD2, ITK, CD8A, WAS	2.00
GO:0019722	Calcium-mediated signaling	6.75x10 ⁻³	CXCL8, RCAN2, CCL3, CXCR4	1.00
GO:0002407	Dendritic cell chemotaxis	7.17x10 ⁻³	GPR183, CXCR4, CCR7	1.73

GO:0043066	Negative regulation of apoptotic process	7.72x10 ⁻³	BLK, PLAC8, FCMR, ACTC1, SEMA4D, UCP2, PIM2, CRYAB, MMP9, IER3	1.90
GO:0050853	B cell receptor signaling pathway	7.91x10 ⁻³	BLK, CD79A, CD19, LIME1	2.00
GO:0009612	Response to mechanical stimulus	1.01x10 ⁻²	IGFBP2, FOSB, KCNA5, SOST	-1.00
GO:0090023	Positive regulation of neutrophil chemotaxis	1.19x10 ⁻²	CXCL8, CCR7, CXCL2	1.73
GO:0007267	Cell-cell signaling	1.28x10 ⁻²	NOV, IL1B, CCL3, PDGFA, LTB, FGF13, CXCL13	0.38
GO:0030335	Positive regulation of cell migration	1.30x10 ⁻²	SEMA4A, CEMIP, SEMA4D, CCL3, PDGFA, CORO1A	1.63
GO:0005102	Receptor binding	1.31x10 ⁻²	BLK, CD2, ITK, SEMA4D, IGFBP2, ICAM3, KCNA5, LTB	1.41
GO:0030593	Neutrophil chemotaxis	1.37x10 ⁻²	CXCL8, CCL3L1, IL1B, CCL3	2.00
GO:0006935	Chemotaxis	1.38x10 ⁻²	CXCL8, CCL3, CXCR4, CCR7, CXCL2	2.24
GO:0007015	Actin filament organization	1.73x10 ⁻²	LMOD1, WAS, SORBS1, CORO1A	0.00
GO:0015026	Coreceptor activity	1.91x10 ⁻²	CD8A, CXCR4, RAMP1	0.58
GO:0006816	Calcium ion transport	1.99x10 ⁻²	PLN, CCL3, RAMP1, CORO1A	0.00
GO:0005925	Focal adhesion	2.13x10 ⁻²	CNN1, ACTC1, CSRP2, TGFB1I1, SYNPO2, ITGA8, NEXN, SORBS1	-2.83
GO:0008360	Regulation of cell shape	2.18x10 ⁻²	SEMA4A, SEMA4D, CCL3, SHROOM3, CORO1A	1.34

GO:0005887	Integral component of plasma membrane	2.19×10^{-2}	CD83, SEMA4D, PCDH7, ICAM3, KCNA5, P2RY8, CD2, CD79A, SELL, CD8A, CD19, GPR183, FXYD1, CD37, SLC25A4, GPRC5C, RAMP1, HLA-DQA1	1.41
GO:0008016	Regulation of heart contraction	2.29×10^{-2}	PLN, FXYD1, HSPB7	-1.73
GO:0005886	Plasma membrane	2.72×10^{-2}	CEMIP, CD83, CXCR4, ICAM3, KCNA5, CORO1A, CD3D, GLDN, P2RY8, TMEM47, CD79A, RGS5, MMP25, KCNMB1, CD19, TBC1D10C, CCR7, HLA-DQA1, AOC3, SEMA4A, SEMA4D, IL10RA, ZBTB16, PCDH7, KCNAB1, SORBS1, LIME1, CD2, SELL, CD8A, GPR183, MAP1B, FXYD1, ITGA8, LTB, PTPRCAP, FGF13, RAMP1, MRAP2, HLA-DQB1	1.26
GO:0050919	Negative chemotaxis	2.72×10^{-2}	SEMA4A, SEMA4D, PDGFA	0.58
GO:0030017	Sarcomere	3.11×10^{-2}	ACTC1, LMOD1, TIMP4	-1.73
GO:0005911	Cell-cell junction	3.40×10^{-2}	CD2, TMEM47, ITK, WAS, CORO1A	1.34
GO:0032496	Response to lipopolysaccharide	3.60×10^{-2}	IL10RA, CCR7, CXCL13, CXCL2, TIMP4	1.34
GO:0032387	Negative regulation of intracellular transport	3.73×10^{-2}	MAP1B, CRYAB	-1.41
GO:0034705	Potassium channel complex	4.17×10^{-2}	KCNAB1, KCNA5	-1.41

GO:0008131	Primary amine oxidase activity	4.19×10^{-2}	AOC3, MAOA	-1.41
GO:0070374	Positive regulation of ERK1 and ERK2 cascade	4.39×10^{-2}	CCL3L1, GPR183, CCL3, PDGFA, CCR7	1.34
GO:0050776	Regulation of immune response	4.63×10^{-2}	SELL, CD8A, CD19, ICAM3, CD3D	2.24
GO:0045600	Positive regulation of fat cell differentiation	4.92×10^{-2}	FRZB, ZBTB16, LMO3	-1.73
GO:0051781	Positive regulation of cell division	4.92×10^{-2}	IL1B, OSM, PDGFA	0.58

GO, Gene Ontology

Table SIX. KEGG pathway enrichment analysis for differentially expressed genes (P<0.05).

ID	Term	P-value	Genes	Z-score
hsa04060	Cytokine-cytokine receptor interaction	4.64x10 ⁻⁵	CXCL8, CCL3L1, IL1B, IL10RA, OSM, CCL3, CXCR4, CCR7, LTB, CXCL13, CXCL2	3.32
hsa05323	Rheumatoid arthritis	1.17x10 ⁻⁴	CXCL8, CCL3L1, IL1B, CCL3, LTB, HLA-DQA1, HLA-DQB1	2.65
hsa04062	Chemokine signaling pathway	2.12x10 ⁻⁴	ITK, CXCL8, CCL3L1, CCL3, WAS, CXCR4, CCR7, CXCL13, CXCL2	3.00
hsa05132	Salmonella infection	7.93x10 ⁻⁴	CXCL8, CCL3L1, IL1B, CCL3, WAS, CXCL2	2.45
hsa04640	Hematopoietic cell lineage	9.83x10 ⁻⁴	CD2, CD8A, IL1B, CD19, CD37, CD3D	2.45
hsa04514	Cell adhesion molecules (CAMs)	1.52x10 ⁻³	CD2, SELL, CD8A, ITGA8, ICAM3, HLA-DQA1, HLA-DQB1	1.89
hsa05340	Primary immunodeficiency	3.27x10 ⁻³	CD79A, CD8A, CD19, CD3D	2.00
hsa05142	Chagas disease (American trypanosomiasis)	1.33x10 ⁻²	CXCL8, CCL3L1, IL1B, CCL3, CD3D	2.24
hsa04270	Vascular smooth muscle contraction	1.97x10 ⁻²	PPP1R14A, KCNMB1, MRVI1, RAMP1, MYL9	-2.24
hsa05332	Graft-versus-host disease	3.42x10 ⁻²	IL1B, HLA-DQA1, HLA-DQB1	1.73
hsa00350	Tyrosine metabolism	3.82x10 ⁻²	AOC3, MAOA, ADH1B	-1.73

KEGG, Kyoto Encyclopedia of Genes and Genomes.