

Supplementary figures

Fig S1. Enrichment analysis of the common DEGs. A: GO enrichment analysis bubble plot. The color intensity of nodes represents the adjusted p-value, and the node size indicates the number of genes. B: Kyoto Encyclopedia of Genes and Genomes enrichment bubble plot of DEGs.

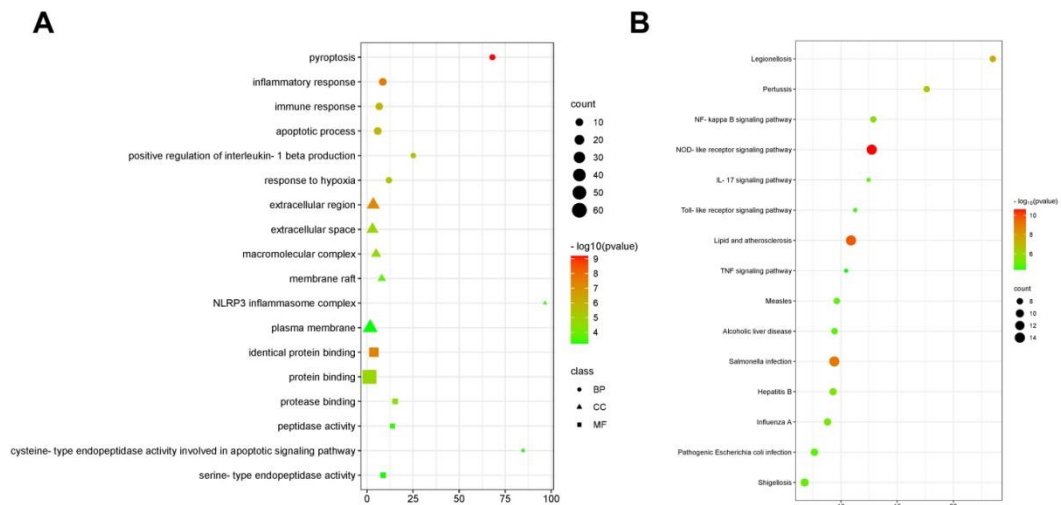


Fig S2. Protein–protein interaction network of DEGs.

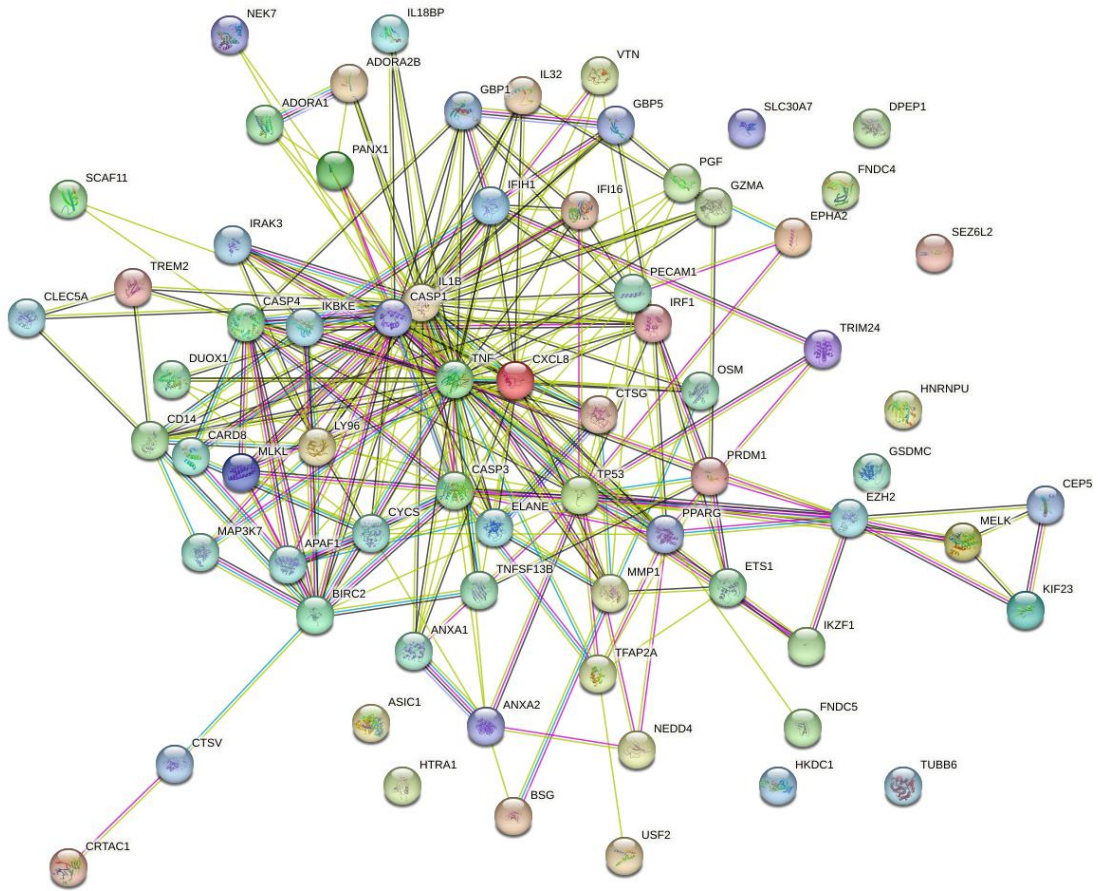


Table S1 Primer sequence

Primers	Sequence (5'-3')
GAPDH-F	AACTTTGGCATTGTGGAAGG
GAPDH-R	ACACATTGGGGGTAGGAACA
BIRC2-F	GGGGACAGTCCTGTTGAAAA
BIRC2-R	GGCTAGAGCACAGGTTGGAG
CXCL8-F	GGCAAGATGAGAGTGCACAA
CXCL8-R	AGATGTCCTGGATGGCAAAG
APAF1-F	GTTCAAAGCCGAGACAGGAG
APAF1-R	ATTGACTTGCTCCGAGTGCT
PPARG-F	TTTTCAAGGGTGCCAGTTTC
PPARG-R	AATCCTTGGCCCTCTGAGAT
CYCS-F	CCAAATCTCCACGGTCTGTT
CYCS-R	GTCTGCCCTTTCTCCCTTCT
TP53-F	TACAAGCAAGCACAGGCATC
TP53-R	CGCTCCACCAAGTTTTTCATT

Table S2 The top 25 differentially expressed genes in the GSE60436 dataset

Name	Description	log2FoldChange	pval	up/down
MMP9	matrix metalloproteinase 9	6.79	1.72E-39	up
COL6A3	collagen type VI alpha 3 chain	5.90	1.85E-35	up
PRND	prion protein 2 (dublet)	5.36	6.68E-24	up
ANGPT2	angiopoietin 2	5.22	8.03E-32	up
POSTN	periostin	5.17	3.80E-32	up
COL1A1	collagen type I alpha 1 chain	5.12	2.28E-35	up
APLN	apelin	5.11	4.41E-30	up
COL5A2	collagen type V alpha 2 chain	5.08	2.30E-34	up
SERPINE1	serpin family E member 1	5.02	4.59E-34	up
THBS2	thrombospondin 2	4.92	3.66E-33	up
TNC	tenascin C	4.80	1.46E-31	up
MMP11	matrix metalloproteinase 11	4.61	6.18E-25	up
COL4A1	collagen type IV alpha 1 chain	4.55	6.44E-33	up
C5orf46	chromosome 5 open reading frame 46	4.52	1.59E-28	up
CST1	cystatin SN	4.22	1.10E-20	up
ITGA1	integrin subunit alpha 1	4.20	2.22E-31	up
COL4A2	collagen type IV alpha 2 chain	4.14	5.54E-29	up

LOX	lysyl oxidase	4.13	3.02E-30	up
ESM1	endothelial cell specific molecule 1	4.10	1.35E-29	up
TNFAIP 6	TNF alpha induced protein 6	4.07	3.03E-30	up
CTHRC1	collagen triple helix repeat containing 1	4.07	7.33E-31	up
COL5A1	collagen type V alpha 1 chain	4.07	3.00E-27	up
FAP	fibroblast activation protein alpha	4.06	7.53E-31	up
CDH13	cadherin 13	4.03	2.73E-27	up
LUM	lumican	4.00	2.03E-25	up
SLC45A 2	solute carrier family 45 member 2	-5.06	1.70E-34	down
OPTC	opticin	-5.11	3.94E-33	down
CHRNA 3	cholinergic receptor nicotinic alpha 3 subunit	-5.13	2.73E-31	down
CLIC6	chloride intracellular channel 6	-5.14	5.23E-30	down
ALDH1A 2	aldehyde dehydrogenase 1 family member A2	-5.16	7.09E-35	down
TRPM3	transient receptor potential cation channel subfamily M member 3	-5.17	5.14E-36	down
SCARA5	scavenger receptor class A member 5	-5.17	5.46E-36	down
SLC16A 8	solute carrier family 16 member 8	-5.19	3.95E-34	down

TYR	tyrosinase	-5.46	3.74E-37	down
PTGDS	prostaglandin D2 synthase	-5.50	1.19E-26	down
BCO1	beta-carotene oxygenase 1	-5.58	1.19E-36	down
TSPAN1 0	tetraspanin 10	-5.75	1.88E-36	down
MLANA	melan-A	-5.82	4.97E-38	down
PCP4	Purkinje cell protein 4	-5.84	6.02E-27	down
HMGCS 2	3-hydroxy-3-methylglutaryl-CoA synthase 2	-5.91	1.76E-37	down
PITX1	paired like homeodomain 1	-5.95	1.70E-38	down
FAM150 B	family with sequence similarity 150 member B	-5.97	5.41E-39	down
PI16	peptidase inhibitor 16	-6.01	2.79E-35	down
RLBP1	retinaldehyde binding protein 1	-6.25	1.72E-33	down
RPE65	RPE65, retinoid isomerohydrolase	-6.47	4.43E-40	down
BEST1	bestrophin 1	-6.65	1.65E-40	down
TYRP1	tyrosinase related protein 1	-7.02	1.97E-42	down
RGR	retinal G protein coupled receptor	-7.07	3.98E-38	down
PMEL	premelanosome protein	-7.63	4.23E-43	down
TTR	transthyretin	-8.00	3.25E-44	down
