

Table S1 DEGs identified in the three integrated datasets

Gene symbol	Up/down regulation	logFC	P value
<i>FRZB</i>	Up	1.165105482	1.74E-07
<i>PHLDA1</i>	Up	0.597089286	3.28E-07
<i>ASPN</i>	Up	1.044125975	3.39E-07
<i>CFH</i>	Up	0.957198888	2.76E-06
<i>ODC1</i>	Up	0.50478927	8.72E-06
<i>ATP10D</i>	Up	0.53649503	3.26E-05
<i>OMD</i>	Up	0.847559371	4.01E-05
<i>TSC22D3</i>	Up	0.6614161	0.000136
<i>LRRC17</i>	Up	0.72475092	0.000164
<i>DPT</i>	Up	0.623966442	0.0002
<i>COL1A2</i>	Up	0.637546144	0.000321
<i>SFRP4</i>	Up	1.053731958	0.000385
<i>OGN</i>	Up	0.868700631	0.000455
<i>CXCR4</i>	Up	0.985731242	0.000484
<i>COL3A1</i>	Up	0.64436839	0.000673
<i>PIK3IP1</i>	Up	0.583009267	0.000883
<i>ACE2</i>	Up	0.632017279	0.000985
<i>NPPB</i>	Up	2.002072319	0.001148
<i>CTGF</i>	Up	0.734968945	0.001377
<i>MXRA5</i>	Up	0.6393268	0.001456
<i>NPPA</i>	Up	0.89706059	0.001795
<i>SCRG1</i>	Up	0.617794477	0.002428
<i>IGFBP2</i>	Up	0.540245111	0.002716
<i>POSTN</i>	Up	0.853311859	0.003052
<i>RASL11B</i>	Up	0.628420997	0.003557
<i>LUM</i>	Up	0.603016401	0.004928
<i>COL1A1</i>	Up	0.51368708	0.006032
<i>FMOD</i>	Up	0.632510749	0.007007
<i>NAP1L3</i>	Up	0.820553842	0.007808
<i>ITK</i>	Up	0.779948693	0.008944
<i>STYK1</i>	Up	0.584066585	0.018427
<i>NPR3</i>	Up	0.526544295	0.018467
<i>LTBP2</i>	Up	0.640958469	0.020436
<i>LAX1</i>	Up	0.539479733	0.049019
<i>PPP1R1A</i>	Down	-0.65868	5.94E-07
<i>C1orf105</i>	Down	-1.17338	1.14E-06
<i>IDH2</i>	Down	-0.59402	1.94E-06
<i>ENDOG</i>	Down	-0.58604	2.62E-06
<i>CCDC69</i>	Down	-0.53694	3.02E-06
<i>PYGM</i>	Down	-0.65979	1.42E-05
<i>MID1IP1</i>	Down	-0.72805	5.55E-05
<i>PTDSS1</i>	Down	-0.56072	6.19E-05
<i>ATP2A2</i>	Down	-0.54897	8.81E-05
<i>MYH6</i>	Down	-0.88604	0.000123
<i>FCN3</i>	Down	-0.75035	0.000146
<i>MOG</i>	Down	-0.61171	0.000152
<i>PTP4A3</i>	Down	-0.57048	0.000302
<i>RARRES1</i>	Down	-1.04067	0.002039
<i>RRAD</i>	Down	-0.78475	0.006446
<i>LYVE1</i>	Down	-0.61581	0.00991
<i>CORIN</i>	Down	-0.69927	0.019628
<i>SERPINA3</i>	Down	-0.64048	0.023801
<i>MYL7</i>	Down	-0.60221	0.029289

DEG, differentially expressed gene.

**Table S2** Top 4 significantly enriched GO terms and KEGG pathways of CGs

Category	Term	Description	Count	P value
BP term	GO:0030199	Collagen fibril organization	6	2.14E-08
BP term	GO:0008217	Regulation of blood pressure	6	2.94E-07
BP term	GO:0042340	Keratan sulfate catabolic process	4	2.14E-06
BP term	GO:0001501	Skeletal system development	6	1.19E-05
CC term	GO:0005615	Extracellular space	21	1.91E-13
CC term	GO:0005578	Proteinaceous extracellular matrix	10	3.16E-09
CC term	GO:0031012	Extracellular matrix	10	7.52E-09
CC term	GO:0005576	Extracellular region	17	4.34E-08
MF term	GO:0008201	Heparin binding	6	1.85E-05
MF term	GO:0048407	Platelet-derived growth factor binding	3	2.27E-04
MF term	GO:0005201	Extracellular matrix structural constituent	4	3.57E-04
MF term	GO:0001618	Virus receptor activity	3	0.009
KEGG pathway	hsa04974	Protein digestion and absorption	4	0.001
KEGG pathway	hsa04512	ECM-receptor interaction	3	0.019
KEGG pathway	hsa05146	Amoebiasis	3	0.028
KEGG pathway	hsa04611	Platelet activation	3	0.040

GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; CGs, common genes; BP, biological process; CC, cellular component; MF, molecular function.

**Table S3** Top 10 hub genes with higher degree of connectivity

Gene symbol	Gene description	Score
<i>COL3A1</i>	Collagen type III alpha 1 chain	13
<i>POSTN</i>	Periostin	13
<i>COL1A1</i>	Collagen type I alpha 1 chain	12
<i>ASPN</i>	Asporin	10
<i>LUM</i>	Lumican	10
<i>FMOD</i>	Fibromodulin	10
<i>CTGF</i>	Connective tissue growth factor	9
<i>OGN</i>	Osteoglycin	9
<i>COL1A2</i>	Collagen type I alpha 2 chain	9
<i>DPT</i>	Dermatopontin	7