



Research article

Insight into the potential pathogenesis of human osteoarthritis via single-cell RNA sequencing data on osteoblasts

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Supplementary

Table S1. The marker genes of cluster in normal and osteoarthritis samples.

Samples	gene	p_val	avg_log2FC	pct.1	pct.2	p_val_adj	cluster
Osteoarthritis samples		2.47E-95	0.380587	0.71	0.443	5.02E-91	0
	ALPL	2.66E-06	0.398578	0.551	0.516	0.044635	3
		1.5E-224	0.846915	0.438	0.045	2.8E-220	6
	RUNX2	1.3E-253	1.351444	0.782	0.355	2.7E-249	3
Normal samples	ALPL	0	0.9224447	0.21	0.013	0	8
	RUNX2	0	1.380411	0.403	0.041	0	8

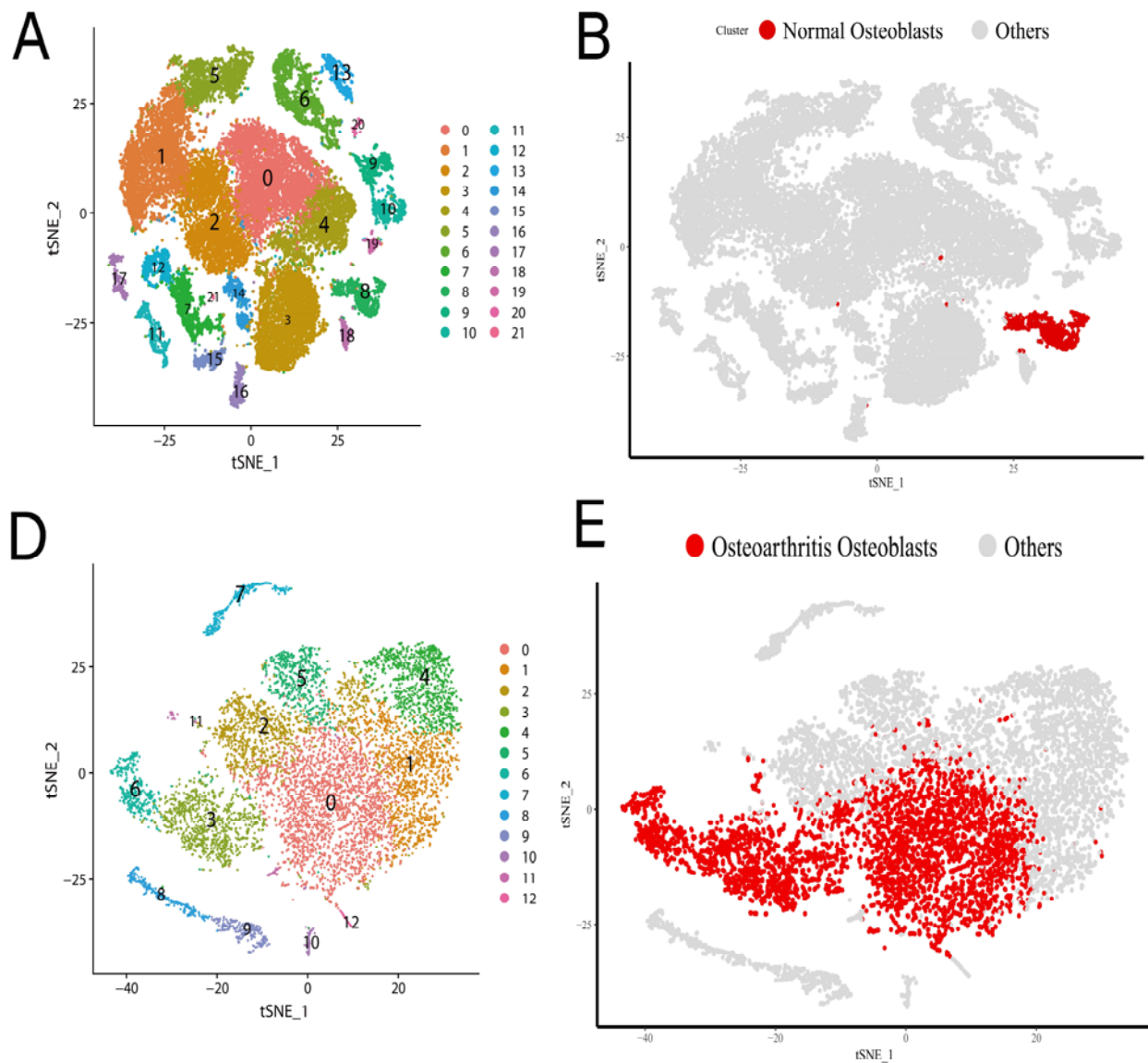


Figure S1. TSNE plot of normal and osteoarthritis sample scRNA-seq data. (A) TSNE plot of normal osteoblasts. (B) clusters 8 annotated as normal osteoblast clusters. (C) TSNE plot of osteoarthritis osteoblasts. (D) cluster 0, 3, 6 annotated as osteoarthritis osteoblasts clusters.

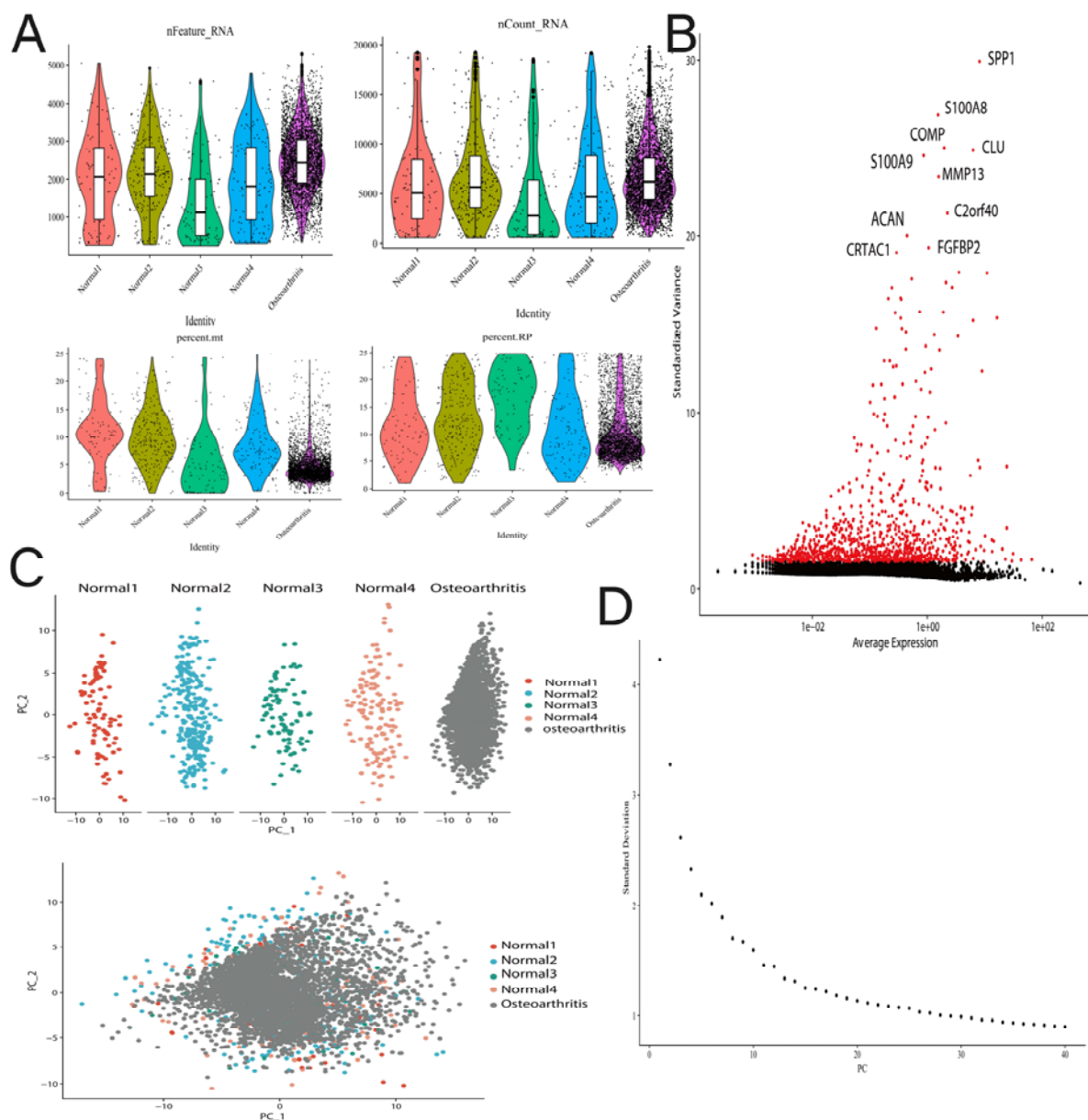


Figure S2. Processing of integration scRNA-seq data. (A) Quality control normal and osteoarthritis osteoblasts. We excluded low-quality cells and total of 4387 osteoblasts were included. (B) The variance diagram. The result shows 19,535 corresponding genes throughout all osteoblasts. The red dots represent highly variable genes, and the black dots represent non-variable genes. The top 10 most variable genes are marked in the plot. (C) PCA identified the significantly available dimensions of scRNA-seq data. The above plot shows that osteoblasts have the same trend of distribution in the same dimension. The lower plot shows that osteoblasts from different samples are highly overlapping in the same dimension. (D) The elbow plot of scRNA-seq data.

Table S2. The marker genes of three types osteoblasts.

Three types osteoblast	Marker genes	References
Pre-osteoblasts	LEPR	A. N. Tikhonova, I. Dolgalev, H. Hu, K. K. Sivaraj, E. Hoxha, Á. Cuesta-Domínguez, et al., The bone marrow microenvironment at single-cell resolution, <i>Nature.</i> , 569 (2019), 222–228. https://doi.org/10.1038/s41586-019-1104-8
	VCAM1	Y. Matsushita, M. Nagata, K. M. Kozloff, J. D. Welch, K. Mizuhashi, N. Tokavanich, et al., A Wnt-mediated transformation of the bone marrow stromal cell identity orchestrates skeletal regeneration, <i>Nat. Commun.</i> , 11 (2020), 332. https://doi.org/10.1038/s41467-019-14029-w
Mature osteoblasts	COL1A1	Y. Matsushita, M. Nagata, K. M. Kozloff, J. D. Welch, K. Mizuhashi, N. Tokavanich, et al., A Wnt-mediated transformation of the bone marrow stromal cell identity orchestrates skeletal regeneration, <i>Nat. Commun.</i> , 11 (2020), 332. https://doi.org/10.1038/s41467-019-14029-w
	BGLAP	
	SPP1	
	IBSP	
Undetermined osteoblasts	IFITM5	Y. Gong, J. Yang, X. Li, C. Zhou, Y. Chen, Z. Wang, et al., A systematic dissection of human primary osteoblasts in vivo at single-cell resolution, <i>Aging (Albany NY)</i> , 13 (2021), 20629–20650. https://doi.org/10.18632/aging.203452
	NR4A1	
	NR4A2	

Table S3. Subpopulations marker gene in clusters.

p_val	avg_log2FC	pct.1	pct.2	p_val_adj	cluster	gene
3.9E-104	0.723159	0.977	0.725	7.7E-100	0	LEPR
9.66E-21	0.283456	0.912	0.755	1.89E-16	1	LEPR
3.44E-29	0.511964	0.941	0.759	6.72E-25	2	LEPR
1.2E-145	0.945964	0.97	0.722	2.4E-141	0	VCAM1
1.52E-26	0.320779	0.92	0.747	2.97E-22	1	VCAM1
3E-32	3.004142	0.964	0.852	5.87E-28	5	COL1A1
5.7E-288	6.407156	0.969	0.11	1.1E-283	5	SPP1
2.1E-242	2.864353	0.819	0.074	4.1E-238	5	IFITM5
3.19E-87	0.735645	0.448	0.119	6.23E-83	3	BGLAP
1.12E-31	0.566216	0.383	0.145	2.19E-27	4	BGLAP
2.1E-184	3.402838	0.87	0.134	4E-180	5	BGLAP
1.7E-192	1.375491	0.773	0.203	3.2E-188	3	IBSP
6.76E-70	1.293849	0.659	0.249	1.32E-65	4	IBSP
1.9E-123	2.273024	0.979	0.253	3.8E-119	5	IBSP

Table S4. The result of different analysis between 7-cluster and pre-osteoblasts cluster.

gene	p_val	avg_log2FC	pct.1	pct.2	p_val_adj
MALAT1	1.92E-71	-2.823348041	0.623	0.993	3.75E-67
NEAT1	6.89E-66	-2.37224894	0.137	0.968	1.35E-61
RSRP1	3.78E-53	-1.709344608	0.123	0.878	7.39E-49
PNISR	8.05E-52	-1.462357744	0.137	0.932	1.57E-47
N4BP2L2	1.29E-50	-1.450133847	0.116	0.882	2.53E-46
DDX17	1.03E-49	-1.456646557	0.151	0.933	2.00E-45
WSB1	5.18E-48	-1.382470617	0.178	0.924	1.01E-43
VCAM1	1.61E-43	-1.673350073	0.349	0.947	3.14E-39
VCAN	3.51E-43	-1.721825741	0.459	0.956	6.85E-39
PLPP3	1.01E-41	-1.630387501	0.26	0.897	1.97E-37
ZFP36L1	1.22E-41	-1.206989493	0.363	0.972	2.39E-37
FOXC1	1.25E-41	-1.298750912	0.185	0.884	2.44E-37
JUN	1.32E-39	-2.133556141	0.178	0.817	2.59E-35
ODF2L	4.90E-39	-1.165024251	0.096	0.744	9.57E-35
AKAP9	5.43E-37	-1.167921996	0.137	0.8	1.06E-32
PLEKHH2	7.28E-37	-1.328473801	0.062	0.679	1.42E-32
RPS18	1.43E-36	1.157859733	0.979	0.993	2.79E-32
RPL21	3.23E-36	1.26277441	0.932	0.983	6.32E-32
ARGLU1	3.74E-36	-1.064217663	0.137	0.801	7.31E-32
RPL12	6.09E-35	1.159830754	0.945	0.985	1.19E-30
CHL1	7.34E-35	-1.248928889	0.295	0.93	1.43E-30
ANGPT1	1.34E-34	-1.231618591	0.164	0.812	2.63E-30
TNFAIP6	3.94E-34	-1.693110626	0.151	0.747	7.69E-30
RPLP1	5.51E-34	1.06007762	0.993	0.998	1.08E-29
SLC5A3	8.88E-34	-1.658331824	0.116	0.726	1.73E-29
RPL37	1.31E-33	1.181056491	0.959	0.992	2.55E-29
PDGFRA	2.38E-33	-1.029737062	0.24	0.888	4.64E-29
ABCA8	2.55E-33	-1.199932284	0.199	0.832	4.97E-29
RPL35	1.25E-32	1.294606511	0.904	0.975	2.43E-28
DUSP1	2.54E-32	-1.289971764	0.171	0.78	4.96E-28
KCNQ1OT1	3.06E-32	-1.413831288	0.068	0.652	5.98E-28
RPL7A	9.73E-32	1.074552863	0.952	0.993	1.90E-27
ARL4C	9.91E-32	-1.053703308	0.185	0.807	1.94E-27
RPS19	1.32E-31	1.23097188	0.89	0.988	2.59E-27
RPS16	1.51E-31	1.340480245	0.87	0.954	2.94E-27
RPS3A	1.68E-31	1.143038464	0.938	0.988	3.28E-27
LEPR	1.92E-31	-1.211419035	0.418	0.946	3.75E-27
RPS12	2.77E-31	1.096447753	0.959	0.995	5.41E-27
RPS6	6.75E-31	1.358268256	0.89	0.967	1.32E-26
FOS	9.56E-31	-1.61469463	0.247	0.802	1.87E-26
SPRY1	1.23E-30	-1.209086391	0.171	0.773	2.39E-26

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gene	p_val	avg_log2FC	pct.1	pct.2	p_val_adj
EBF1	5.42E-30	-1.005653715	0.171	0.776	1.06E-25
CCNL1	9.57E-30	-1.043583721	0.075	0.625	1.87E-25
JUND	2.11E-29	-1.213677712	0.384	0.92	4.12E-25
THBS1	3.83E-29	-1.154522671	0.219	0.801	7.49E-25
ID4	4.87E-29	-1.028760933	0.26	0.84	9.52E-25
RPLP2	6.64E-29	1.141130787	0.884	0.984	1.30E-24
SLC1A3	1.11E-28	-1.040170824	0.13	0.688	2.16E-24
RPL36	1.28E-28	1.262948283	0.863	0.965	2.49E-24
RPS4X	1.52E-28	1.119281908	0.904	0.981	2.97E-24
POLR2J3.1	2.28E-28	-1.116019374	0.055	0.564	4.45E-24
IGKC	2.34E-28	2.750579981	0.315	0.071	4.57E-24
MAPK10	2.82E-28	-1.033557763	0.062	0.59	5.51E-24
RPL28	5.43E-28	1.029476922	0.918	0.998	1.06E-23
RPL6	7.24E-28	1.208045626	0.87	0.963	1.41E-23
RPS2	8.67E-28	1.47618126	0.863	0.974	1.69E-23
RPL26	1.20E-26	1.020916568	0.904	0.992	2.35E-22
RETREG1	1.35E-26	-1.047456271	0.096	0.632	2.64E-22
RPL9	1.74E-26	1.093318255	0.884	0.985	3.40E-22
HBB	7.32E-26	1.911278762	0.842	0.952	1.43E-21
RPL13A	3.76E-25	1.473186214	0.822	0.944	7.34E-21
RPL37A	5.89E-25	1.328507908	0.842	0.975	1.15E-20
RPL3	2.30E-24	1.052517802	0.89	0.986	4.50E-20
C11orf96	5.45E-23	-1.220783627	0.274	0.788	1.06E-18
CTGF	1.25E-22	-1.341350291	0.13	0.621	2.43E-18
RPS3	3.92E-22	1.036560315	0.863	0.985	7.65E-18
TRAM1	4.81E-22	-1.061503427	0.288	0.823	9.40E-18
FOSB	4.57E-21	-1.320280967	0.116	0.579	8.92E-17
RPL10A	3.05E-20	1.062970231	0.836	0.955	5.97E-16
RPL18A	8.64E-20	1.05788879	0.836	0.983	1.69E-15
ZFP36	8.68E-19	-1.017484488	0.164	0.631	1.70E-14
S100A8	6.76E-18	2.174260483	0.205	0.046	1.32E-13
DEFA3	1.71E-17	1.686323173	0.199	0.044	3.35E-13
UBA52	1.04E-15	1.065020166	0.781	0.958	2.04E-11
RPL27A	2.61E-15	1.260898726	0.774	0.933	5.09E-11
S100A9	2.92E-15	2.493087805	0.185	0.043	5.70E-11
IGLC2	3.82E-15	2.858528662	0.205	0.054	7.46E-11
RPLP0	7.22E-15	1.124983182	0.781	0.948	1.41E-10
RPL7	8.76E-15	1.338562571	0.753	0.894	1.71E-10
RPS29	1.30E-14	1.058494857	0.801	0.976	2.54E-10
RPS11	5.83E-14	1.158986701	0.76	0.947	1.14E-09
RPS5	3.30E-13	1.12182576	0.747	0.906	6.45E-09
IGHA1	6.42E-13	1.34738994	0.151	0.035	1.25E-08

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gene	p_val	avg_log2FC	pct.1	pct.2	p_val_adj
RACK1	8.85E-12	1.119644002	0.747	0.939	1.73E-07
RPL27	1.13E-10	1.068268813	0.74	0.941	2.20E-06
RPL23	2.01E-10	1.253832114	0.705	0.9	3.93E-06
HP	5.01E-10	-1.296910806	0.233	0.525	9.80E-06
RPS20	6.73E-10	1.330529375	0.664	0.808	1.32E-05
GAPDH	4.50E-09	1.616993711	0.671	0.847	8.80E-05
HBA2	5.92E-09	2.164224919	0.63	0.75	0.000116
LGALS1	5.26E-08	1.180224175	0.795	0.964	0.001027
IGHG4	7.93E-07	1.344073343	0.13	0.045	0.015485
RPSA	9.29E-07	1.032971499	0.658	0.89	0.018141

Table S5. The number of subpopulations osteoblasts cells in different sample.

Sample	Cluster	Cells(n)	Percentage (%)
Normal1	Mature osteoblasts	44	50.6
Normal2	Mature osteoblasts	106	38.7
Normal3	Mature osteoblasts	20	23.3
Normal4	Mature osteoblasts	43	33.1
Osteoarthritis	Mature osteoblasts	995	26.1
Normal1	Pre-osteoblasts	30	34.5
Normal2	Pre-osteoblasts	115	42
Normal3	Pre-osteoblasts	42	48.8
Normal4	Pre-osteoblasts	61	46.9
Osteoarthritis	Pre-osteoblasts	2761	72.5
Normal1	undetermined osteoblasts	13	14.9
Normal2	undetermined osteoblasts	53	19.3
Normal3	undetermined osteoblasts	24	27.9
Normal4	undetermined osteoblasts	26	20
Osteoarthritis	undetermined osteoblasts	54	1.4

Table S6. Identification of marker genes.

p_value	avg_log2FC	pct.1	pct.2	p_value_adj	genes
4.13E-51	2.715193973	0.42	0.097	8.07E-47	HP
1.25E-126	2.545016258	0.816	0.426	2.44E-122	IGFBP4
4.36E-183	2.384592999	0.897	0.388	8.51E-179	MDK
1.83E-197	2.128149914	0.99	0.671	3.57E-193	APOE
1.34E-80	2.101851293	0.58	0.144	2.62E-76	IGFBP2
8.47E-88	1.986037768	0.523	0.059	1.65E-83	LBP
1.19E-174	1.959082479	0.983	0.714	2.33E-170	CFD
2.00E-117	1.891477554	0.859	0.482	3.92E-113	VCAN
7.91E-104	1.832268262	0.772	0.307	1.54E-99	SLPI
9.81E-147	1.831091254	0.84	0.338	1.92E-142	TMEM176B
1.80E-101	1.828337821	0.802	0.35	3.52E-97	PTGDS

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p_value	avg_log2FC	pct.1	pct.2	p_value_adj	genes
2.02E-101	1.759748063	0.698	0.218	3.94E-97	SFRP1
8.40E-129	1.740631793	0.782	0.265	1.64E-124	TMEM176A
5.93E-70	1.626445046	0.585	0.196	1.16E-65	SLC5A3
1.51E-88	1.610051148	0.668	0.26	2.94E-84	MRPS6
4.77E-136	1.533671192	0.92	0.549	9.32E-132	GAS6
4.08E-71	1.475048215	0.533	0.114	7.97E-67	C7
2.33E-109	1.412273263	0.932	0.712	4.56E-105	MARCKS
7.10E-56	1.39974103	0.443	0.09	1.39E-51	VMO1
2.80E-103	1.36800174	0.96	0.745	5.48E-99	MGP
3.80E-104	1.323698444	0.851	0.458	7.42E-100	LHFPL6
8.27E-138	1.279109914	0.942	0.643	1.61E-133	FCGRT
3.02E-95	1.277928684	0.887	0.575	5.90E-91	FBN1
1.96E-110	1.266802	0.93	0.522	3.83E-106	CXCL12
2.31E-105	1.255572871	0.894	0.537	4.51E-101	OLFML3
1.03E-97	1.240295982	0.861	0.432	2.01E-93	GGT5
1.74E-51	1.211411256	0.41	0.076	3.41E-47	STMN2
1.69E-96	1.208629679	0.813	0.354	3.31E-92	CHL1
3.69E-108	1.203376121	0.905	0.542	7.21E-104	RARRES2
1.20E-91	1.199073124	0.655	0.177	2.34E-87	PPP1R14A
6.80E-93	1.180185251	0.767	0.392	1.33E-88	C1orf122
3.35E-24	1.16679826	0.31	0.106	6.54E-20	AGT
3.79E-76	1.151314741	0.712	0.321	7.41E-72	EFEMP1
2.97E-128	1.150076189	0.965	0.683	5.80E-124	MXRA8
5.13E-70	1.137104397	0.753	0.449	1.00E-65	TRAM1
2.02E-69	1.131021782	0.642	0.227	3.95E-65	ANGPT1
1.83E-74	1.116379601	0.83	0.497	3.58E-70	VCAM1
4.36E-125	1.061787862	0.975	0.792	8.52E-121	CD81
8.62E-121	1.058355233	0.963	0.728	1.68E-116	CD99
2.51E-89	1.056727601	0.914	0.711	4.90E-85	HSP90B1
4.28E-89	1.049581616	0.878	0.532	8.36E-85	EPHX1
6.08E-72	1.036574491	0.622	0.179	1.19E-67	CHRD1
2.68E-70	1.03199552	0.623	0.225	5.23E-66	PLTP
4.42E-95	1.02990458	0.867	0.494	8.64E-91	CDKN1C
3.80E-60	1.026850658	0.578	0.199	7.42E-56	SLC1A3
4.66E-20	-1.002606926	0.093	0.213	9.11E-16	ADAMTS1
6.24E-12	-1.002799166	0.47	0.527	1.22E-07	NFKBIZ
8.23E-07	-1.002965121	0.828	0.801	0.016082289	GAPDH
3.85E-76	-1.021001323	0.002	0.104	7.52E-72	DEFA4
2.27E-13	-1.025739311	0.559	0.608	4.44E-09	SOC3
4.57E-43	-1.043184563	0.476	0.679	8.92E-39	PABPC1
1.01E-08	-1.053168057	0.318	0.397	0.00019768	SOD3
1.92E-73	-1.059896161	0.791	0.837	3.75E-69	RPS20
3.16E-33	-1.085752708	0.016	0.102	6.16E-29	MIA
2.47E-20	-1.092550801	0.118	0.248	4.83E-16	TGFBI
5.33E-31	-1.093642036	0.943	0.948	1.04E-26	HBB
9.94E-42	-1.107097226	0.402	0.641	1.94E-37	IER2
2.57E-35	-1.110456186	0.252	0.48	5.03E-31	CD9

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p_value	avg_log2FC	pct.1	pct.2	p_value_adj	genes
8.30E-07	-1.131077582	0.772	0.69	0.016209653	JUN
6.04E-93	-1.148452381	0.996	0.941	1.18E-88	MT-ND1
3.46E-64	-1.153044436	0.12	0.378	6.77E-60	KLF4
5.55E-52	-1.166111224	0.1	0.321	1.08E-47	NR4A1
1.67E-296	-1.169955838	0.002	0.352	3.25E-292	IGLC3
7.29E-76	-1.179148986	0.019	0.179	1.42E-71	RGCC
8.94E-37	-1.191421136	0.709	0.813	1.75E-32	JUNB
1.62E-114	-1.195302271	0.996	0.965	3.16E-110	MT-CO1
6.24E-21	-1.196549005	0.934	0.827	1.22E-16	NEAT1
3.32E-26	-1.197435343	0.549	0.648	6.49E-22	DDX3X
6.00E-89	-1.204504046	0	0.106	1.17E-84	RETN
6.84E-35	-1.213707694	0.216	0.414	1.34E-30	BTG2
3.94E-18	-1.226115985	0.255	0.399	7.70E-14	SFRP4
2.08E-42	-1.226450811	0.156	0.373	4.06E-38	AC020916.1
1.97E-24	-1.239095953	0.254	0.412	3.85E-20	SLC2A3
1.53E-15	-1.240670445	0.622	0.652	2.99E-11	ZFP36
3.38E-79	-1.255362092	0.002	0.104	6.61E-75	LCN2
4.57E-124	-1.261675971	0.997	0.953	8.94E-120	MT-ATP6
1.03E-140	-1.2649958	0.001	0.168	2.00E-136	MPO
9.51E-121	-1.266640594	0.937	0.931	1.86E-116	RPL13A
4.55E-20	-1.288747168	0.723	0.78	8.89E-16	HBA2
3.47E-39	-1.298711937	0.026	0.14	6.78E-35	HAPLN1
1.59E-68	-1.308792342	0.084	0.324	3.11E-64	ATF3
2.18E-35	-1.318093562	0.041	0.168	4.25E-31	OGN
9.61E-25	-1.321190076	0.422	0.182	1.88E-20	CHI3L2
2.44E-44	-1.328268921	0.16	0.38	4.77E-40	NAMPT
4.90E-183	-1.364350405	0.001	0.217	9.58E-179	IGHG2
8.77E-62	-1.413335168	0.007	0.114	1.71E-57	SERPINA1
2.71E-11	-1.41452253	0.409	0.482	5.30E-07	IRF1
5.56E-22	-1.435070006	0.242	0.392	1.09E-17	IER3
8.32E-153	-1.450576655	0.996	0.964	1.63E-148	MT-CO3
1.10E-181	-1.498653031	0.003	0.234	2.15E-177	LYZ
6.49E-43	-1.526833344	0.032	0.161	1.27E-38	NDUFA4L2
2.49E-48	-1.529569881	0.012	0.113	4.87E-44	ACAN
5.55E-31	-1.550191347	0.154	0.343	1.08E-26	SERPINE2
5.91E-29	-1.579905312	0.298	0.477	1.16E-24	SOD2
1.55E-67	-1.693073924	0.014	0.147	3.03E-63	CRTAC1
0.00E+00	-1.695209407	0.003	0.452	0.00E+00	IGHG1
0.00E+00	-1.762331807	0.006	0.536	0.00E+00	IGHG4
2.45E-41	-1.776771776	0.508	0.652	4.79E-37	EGR1
2.83E-95	-1.785730359	0.002	0.125	5.52E-91	LTF
3.16E-10	-1.803135837	0.28	0.367	6.17E-06	MT1X
2.07E-44	-1.875583799	0.577	0.693	4.05E-40	FOSB
1.73E-28	-1.925447301	0.821	0.785	3.37E-24	FN1
3.82E-31	-1.936091811	0.03	0.135	7.45E-27	FGFBP2
7.17E-256	-1.9592022	0.001	0.305	1.40E-251	CXCL8
1.04E-140	-1.979819628	0.001	0.168	2.02E-136	CAMP

Continued on next page

p_value	avg_log2FC	pct.1	pct.2	p_value_adj	genes
0.00E+00	-2.065265607	0.002	0.466	0.00E+00	IGHA1
1.21E-87	-2.213662682	0.176	0.508	2.37E-83	S100A4
6.31E-292	-2.428571487	0.019	0.447	1.23E-287	DEFA3
8.24E-09	-2.571046693	0.317	0.399	1.61E-04	C2orf40
1.67E-122	-2.583869097	0.001	0.149	3.27E-118	S100A12
0.00E+00	-2.597988804	0.012	0.626	0.00E+00	IGLC2
0.00E+00	-2.726156454	0.001	0.525	0.00E+00	XIST
2.06E-60	-3.328133411	0.033	0.196	4.03E-56	COMP
0.00E+00	-4.454887634	0.009	0.536	0.00E+00	S100A9
0.00E+00	-4.654498694	0.009	0.879	0.00E+00	IGKC
0.00E+00	-5.057995763	0.015	0.584	0.00E+00	S100A8

Table S7. The result of KEGG enrichment of hub genes.

ID	Term	Term PValue	Term PValue Corrected with Bonferroni step down	Group p PValue	Group PValue Corrected with Bonferroni step down	% Associated Genes	Associated Genes
KEG G:04 657	IL-17 signaling pathway	3.50 E-7	2.10E-6	3.50E-7	1.05E-6	5.32	[CXCL8, FOSB, JUN, LCN2, S100A8]
KEG G:04 380	Osteoclast differentiation	5.29 E-5	2.11E-4	1.39E-5	2.79E-5	3.13	[FOSB, JUN, JUNB, SOCS3]
KEG G:04 668	TNF signaling pathway	3.13 E-5	1.56E-4	1.39E-5	2.79E-5	3.57	[IRF1, JUN, JUNB, SOCS3]
KEG G:04 933	AGE-RAGE signaling pathway in diabetic complications	6.04 E-4	6.04E-4	3.07E-5	3.07E-5	3.00	[CXCL8, EGR1, JUN]
KEG G:05 133	Pertussis	2.69 E-4	8.07E-4	3.07E-5	3.07E-5	3.95	[CXCL8, IRF1, JUN]
KEG G:05 323	Rheumatoid arthritis	4.88 E-4	9.76E-4	3.07E-5	3.07E-5	3.23	[CXCL12, CXCL8, JUN]



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