Table S1. Clinical and demographic characteristics of the patients

	Patient 1	Patient 2
Gender	Female	Female
Age (years)	74	72
BMI	26.89	29.14
TKA	Right	Left
KSS score	54	58
Chronic conditions	Hypertension (grade II)	Type 2 diabetes, hypertension (gradeI)

Table S2. Markers of each cell type

Cell type	Markers
B cell	CD79A, BANK1, MS4A1
NK cell	GZMB, NKG7
NKT cell	NKG7, CD3D
T cell	CD3D, CD3G
DC	LILRA4, PTCRA
Monocyte	CSTA, FCN1
Macrophage	CD14, CD68, CSF1R, C1QC, F13A1
EC	PECAM1, CLDN5
MSC	MCAM
OB	RUNX2, CDH11
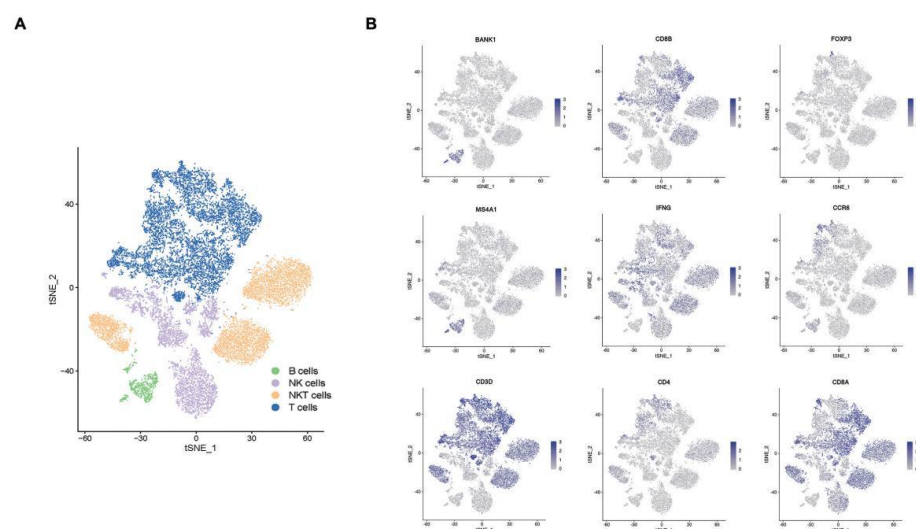
supplementary figure S1

Single-cell profiling of human OA subchondral bone immune cells

(A)t-SNE plots of Immune cells colored by cluster

(B)Dot plots showing the expression of indicated markers for each cell types on the t-SNE map.
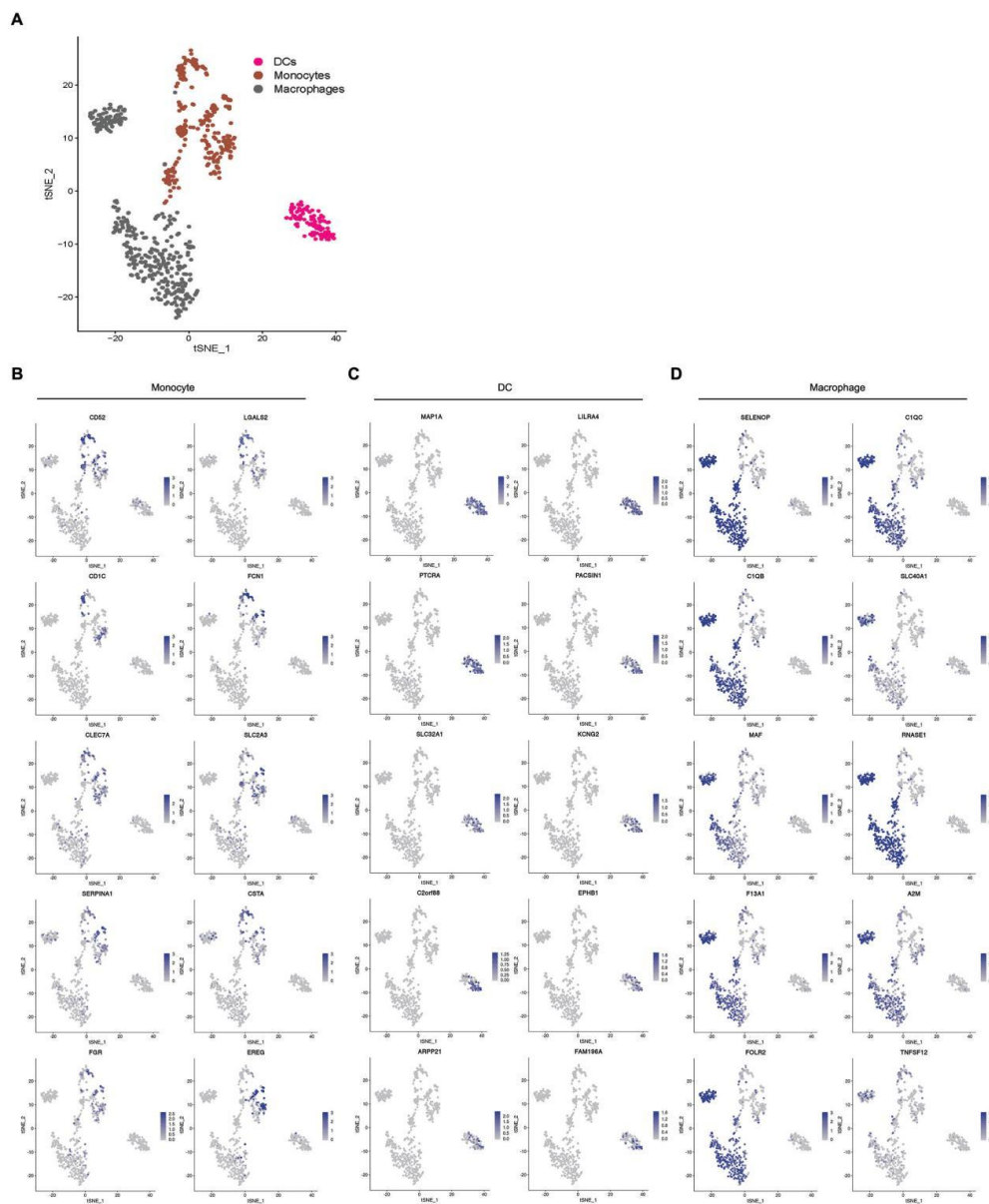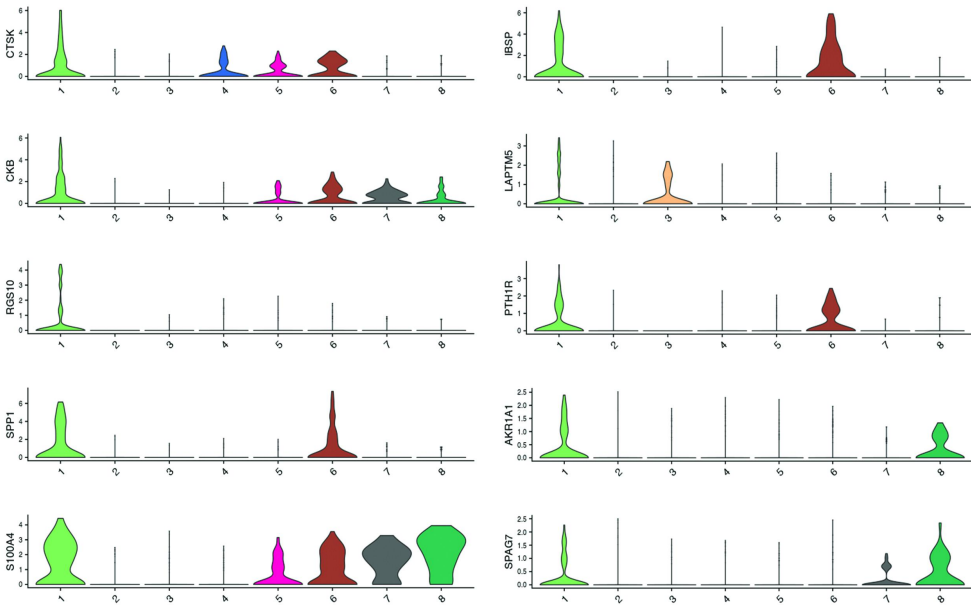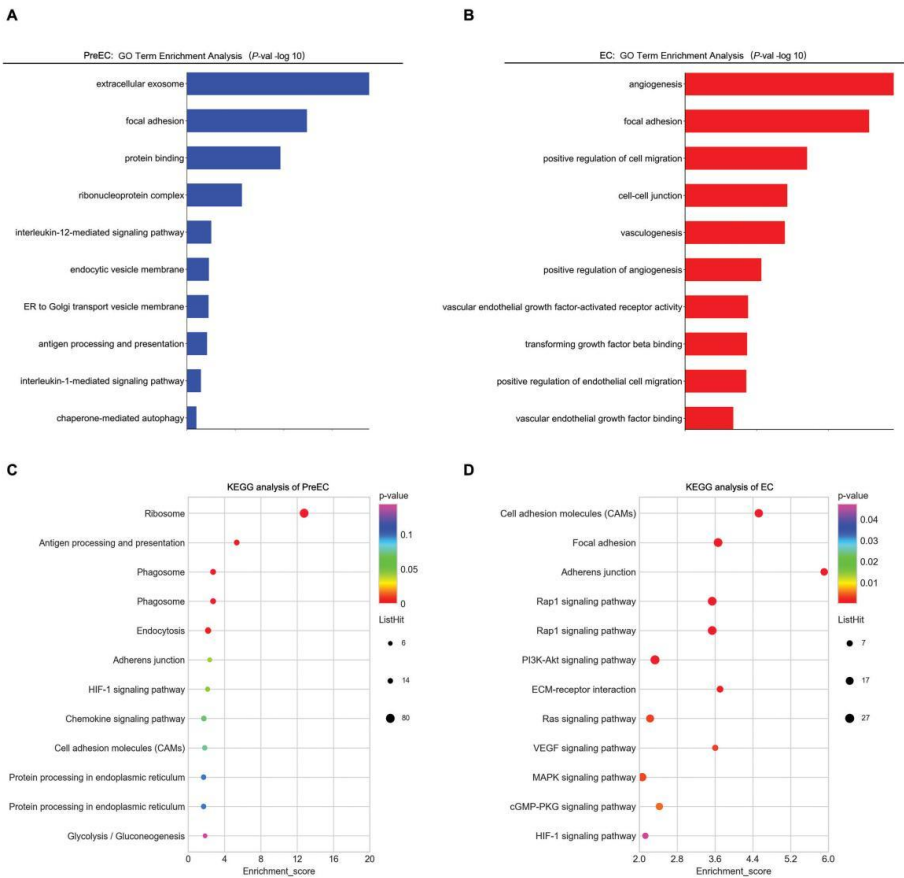
supplementary figure S2

Single-cell profiling of human OA subchondral bone myeloid cells

(A)t-SNE plots of myeloid cells colored by cluster

(B-D)Dot plots showing the expression of indicated markers for each cell types on the t-SNE map.

supplementary figure S3

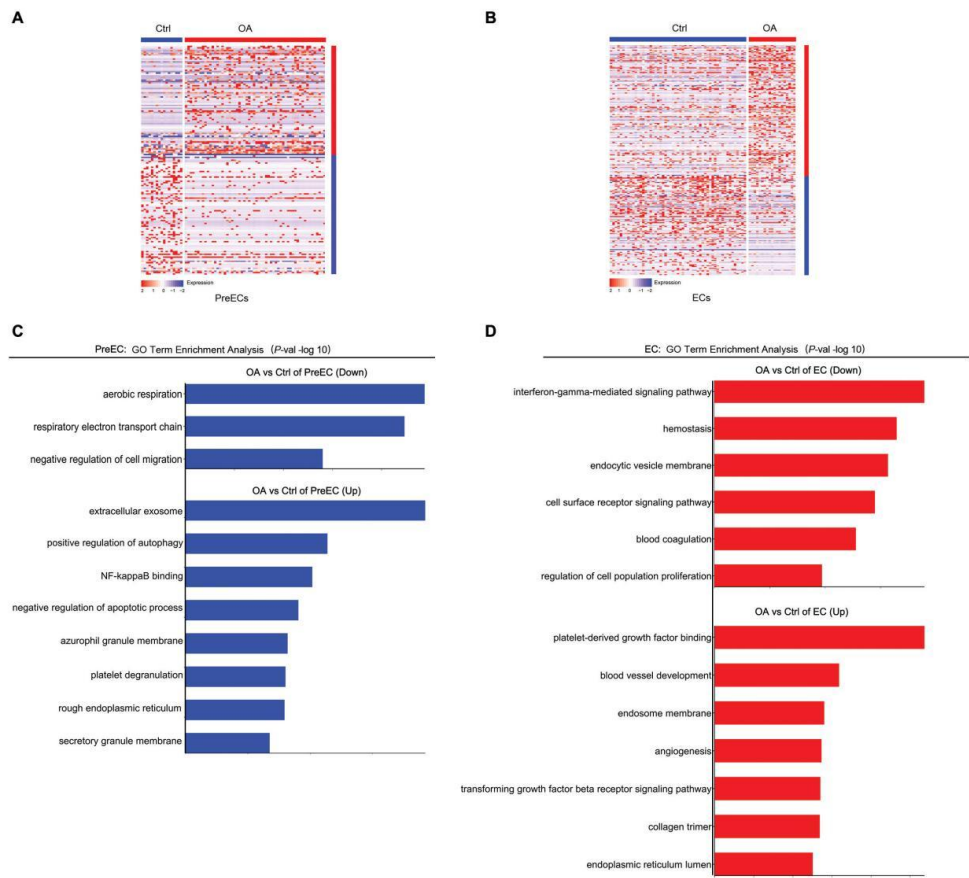**supplementary figure S4**

Identification of Pre-ECs and ECs

(A) Enriched GO functions of upregulated genes in Pre-ECs.

(B) Enriched GO functions of upregulated genes in ECs.

(C) Enrichment plot from KEGG pathway analysis for Pre-ECs.

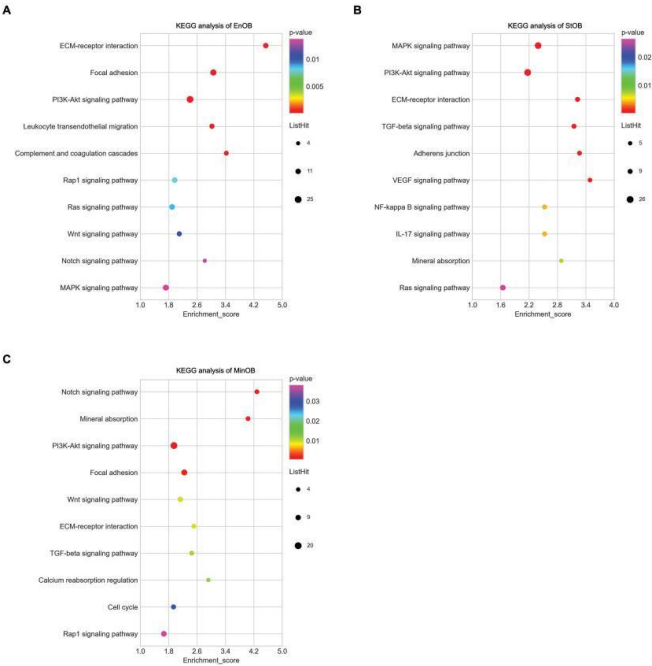(D) Enrichment plot from KEGG pathway analysis for ECs.
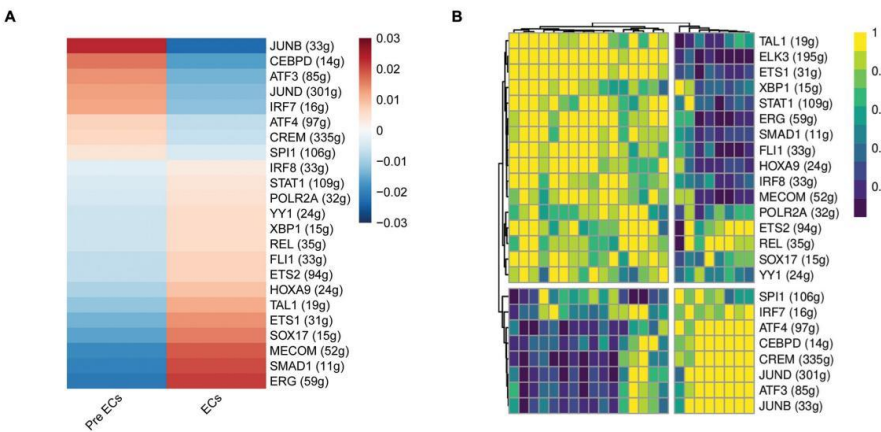
supplementary figure S5

The difference between Pre-ECs and ECs in transcriptional regulation

Single-cell regulatory network inference and clustering (SCENIC) analysis showing distinct regulons between ECs and Pre-ECs.The heatmap listing only the regulons with significant differences

supplementary figure S6

Identification of OA group and Ctrl group in endothelial cells

(A) Heatmap of DEGs between OA group and Ctrl group in Pre-ECs and ECs

(B) GO functions enrichment analysis of OA versus ctrl upregulated genes in Pre-ECs and ECs

Supplemental material

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supplementary figure S7

KEGG showing enrichment of pathways among EnOBs, StOBs and MinOBs

(A) Enrichment plot from KEGG pathway analysis for EnOBs

(B) Enrichment plot from KEGG pathway analysis for StOBs

(C) Enrichment plot from KEGG pathway analysis for MinOBs

supplementary figure S8

Identification of EnOB, StOB and MinOB

(A) Pseudotemporal expression dynamics of marker gene in EnOBs,StOBs and MinOBs. All single cells in the EnOBs,StOBs and MinOBs cell lineage are ordered based on pseudotime.
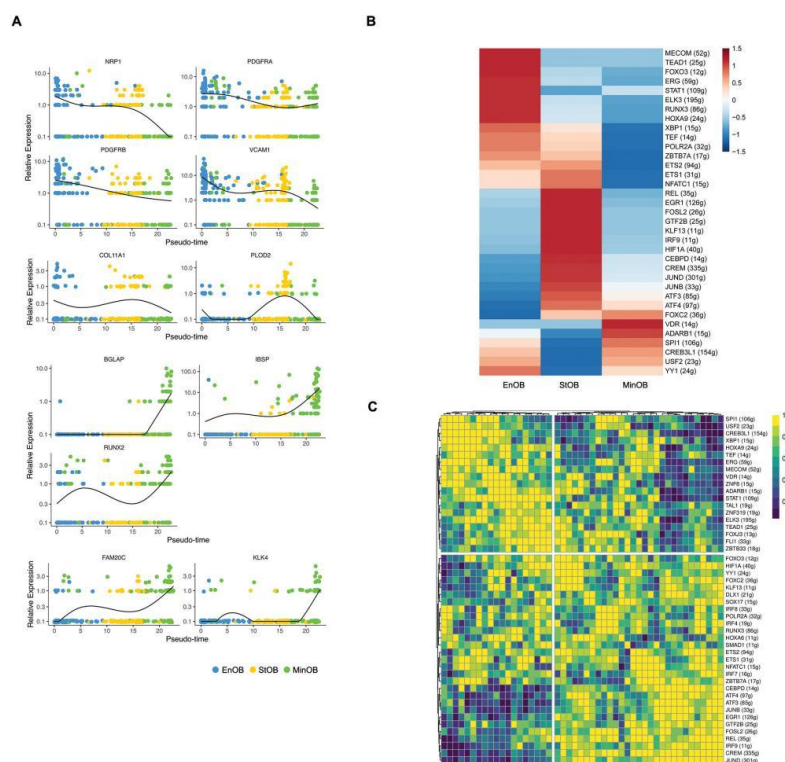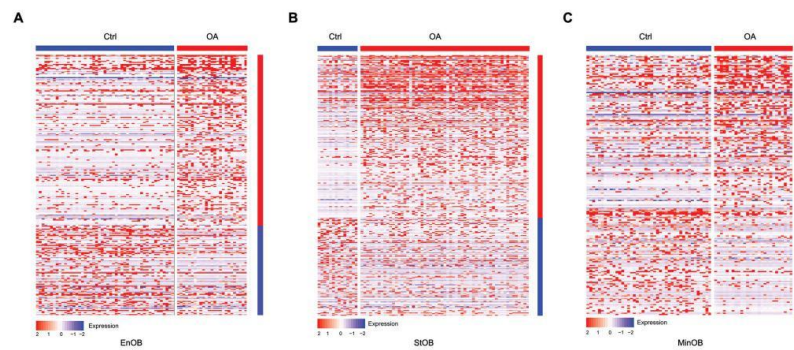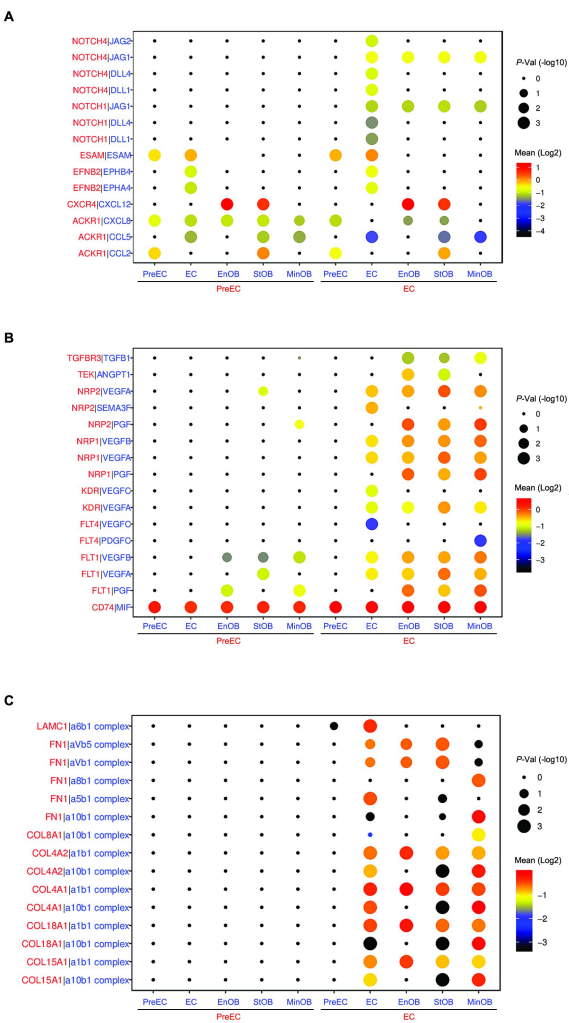
(B-C) Single-cell regulatory network inference and clustering (SCENIC) analysis showing distinct regulons among EnOBs,StOBs and MinOBs.The heatmap listing only the regulons with significant differences.

supplementary figure S9

Identification of OA group and Ctrl group in osteoblasts

(A) Heatmap of DEGs between OA group and Ctrl group in EnOBs

(B) Heatmap of DEGs between OA group and Ctrl group in StOBs

(C) Heatmap of DEGs between OA group and Ctrl group in MinOBs

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supplementary figure S10

Vascular endothelial cell and osteoblast subtype interaction

CellPhoneDB analysis showing the number of ligand-receptor interactions between endothelial cell subpopulation and osteoblast subpopulation.

Bubble plots show ligand-receptor pairs of cytokines (A) , growth factors (B) and integrin (C) between endothelial cells subpopulation.