LETTER TO THE EDITOR

Comprehensive characterization of human bone marrow microenvironment shows age-related changes

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Supplemental Figures

Table S1. Sample characteristics of JHU and de Jong Cohort

Sample ID	Sex	Age (years)	Clinical History	Sample type	Cells analyzed (number)	Non-hematopoietic cells (%)	Cohort	Samples for JHU vs de Jong comparison
1	F	38	n/a	Bone marrow aspirate	5946	77	JHU	
2	F	36	n/a	Bone marrow aspirate	4444	59.7	JHU	
3	M	30	n/a	Bone marrow aspirate	2344	35.1	JHU	JHU Young 1
4	M	27	n/a	Bone marrow aspirate	4791	89.5	JHU	JHU Young 2
5	M	50	n/a	Bone marrow aspirate	1154	22.4	JHU	
6	F	21	n/a	Bone marrow aspirate	352	25	JHU	
7	M	43	n/a	Bone marrow aspirate	11798	24.2	JHU	
8	M	25	n/a	Bone marrow aspirate	583	21	JHU	JHU Young 3
9	M	27	Atrium septum defect	Bone marrow aspirate	2430	n/a	de Jong	de Jong Young 1
10	M	72	Osteoporosis	Bone marrow aspirate	959	n/a	de Jong	de Jong Old 1
11	M	75	Coronary disease	Bone marrow aspirate	525	n/a	de Jong	de Jong Old 2
12	M	75	Osteoporosis	Bone marrow aspirate	984	n/a	de Jong	de Jong Old 3
13	F	57	Congenital hip dysplasia	Bone marrow aspirate	176	n/a	de Jong	
14	M	53	Coronary disease	Bone marrow aspirate	58	n/a	de Jong	

Figure S1. Cell sorting strategy defines CD45^{-}CD235a^{-}CD71^{-}SLAMF7^{-} cells out of the VD^{+}7-AAD^{-} fraction as human BME.

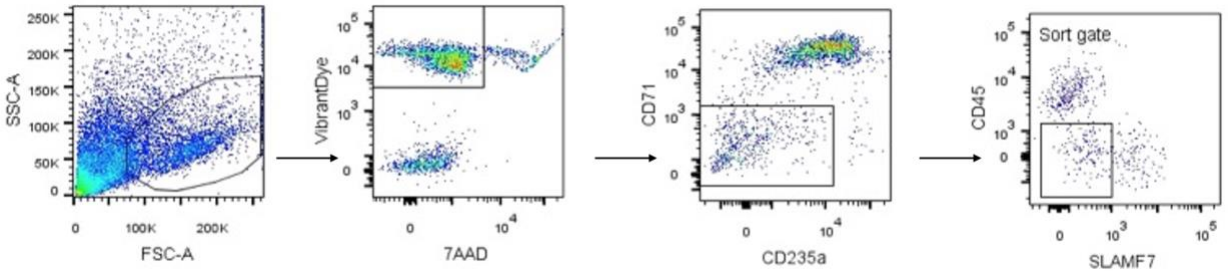
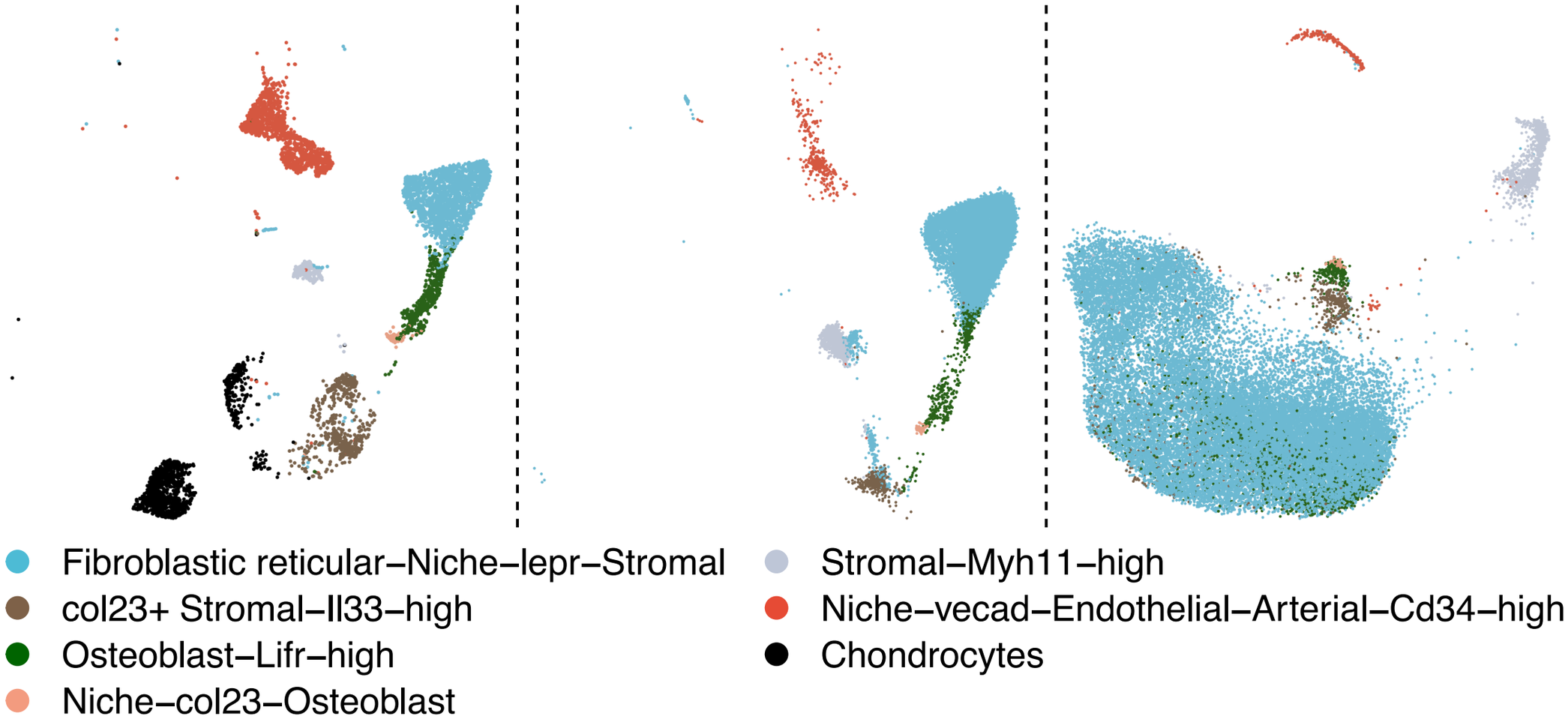
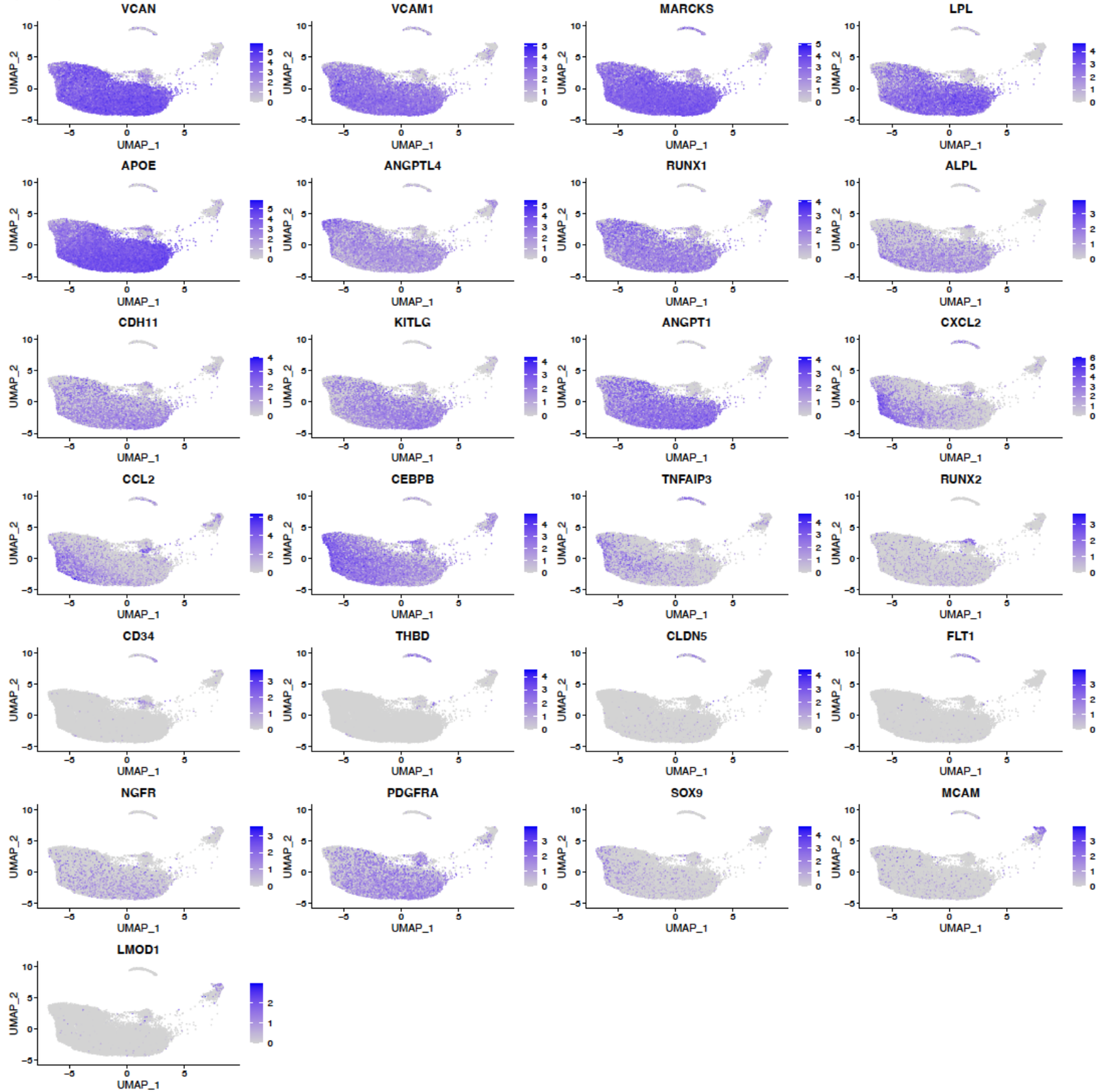


Figure S2. A) Translation of murine to human BME single-cell RNA-sequencing map with representation of previously published murine bone marrow microenvironment (BME) data (GSE128423) (6) with genes converted to their human orthologs (panel 1), mapping of human data on the murine stroma matrix (panel 2) and representation of these labels on the unbiased clustering of the human data (panel 3). **B)** Expression of selected genes in different BME clusters. **C)** Heat map showing receptor-ligand interactions between cells of the bone marrow microenvironment (BME). x-axis represents the clusters with first cluster producing the receptor and the second cluster producing the ligand. y-axis represents the individual receptor-ligand pair. **D)** Percentage of murine equivalent cells that overlap with their respective human stroma population from “de Jong” samples. Only murine clusters representing more than 15% of their equivalent human population were depicted. **E)** Heat map depicting differences in gene expression within the MSC1 population between old and young donors. The arrow points towards expression of CXCL12, arrow heads point towards expression of genes involved in AP1 complex.

A) Murine to human BME single-cell RNA-sequencing map

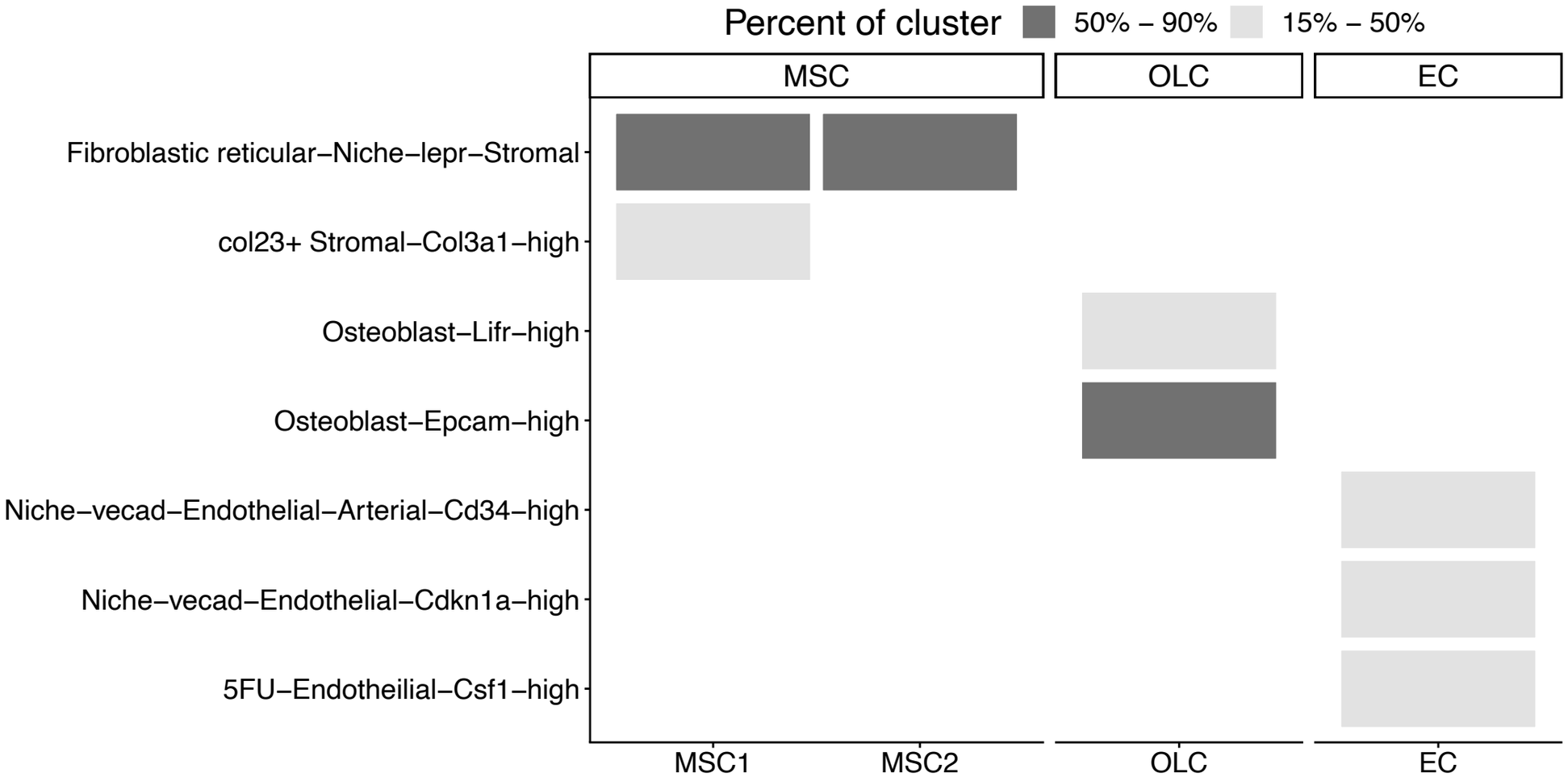


B) Expression of selected BME cluster genes



C) Receptor-ligand interaction of human BME

D) De Jong cohort clusters with murine equivalent clusters



E) Heatmap of DEG between old and young donors in MSC1 cluster