Supplementary Materials

Endothelial cell heterogeneity and immune-metabolic crosstalk in scleroderma: insights from single-cell RNA sequencing

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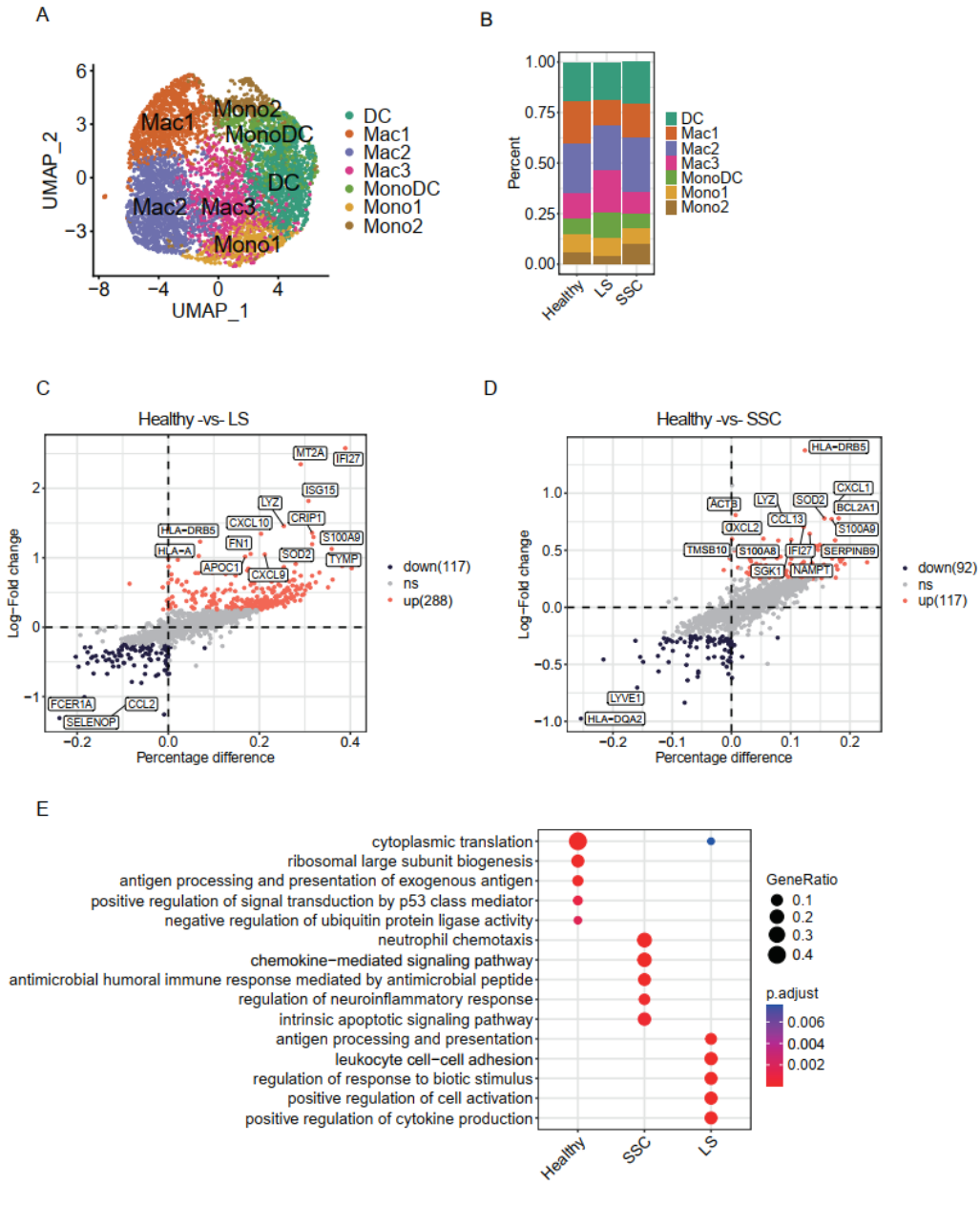
Myeloid Cell Subcluster Analysis

Subclustering of myeloid cells identified several groups, including monocytes (Mono1, Mono2), macrophages (Mac1, Mac2, Mac3), dendritic cells (DC), and MonoDC cells (Figure S1A). The proportions of these cell types across samples are shown in Figure S1B.

Differential expression analysis between groups revealed commonly upregulated genes in both LS and SSC compared to healthy controls, such as HLA-DRB5 and IFI27. Functional enrichment analysis of these differential genes showed that the SSC group was enriched for pathways related to chemokine-mediated signaling and intrinsic apoptotic signaling, while the LS group was enriched for cytokine production pathways (positive regulation of cytokine production).



Supplementary Figure 1. We present Myeloid Cell Atlas and Differential Analysis Between Groups in editable images I supplementary Figure 1A-E. A: UMAP plot showing the annotation of myeloid cell subpopulations. B: Bar chart depicting the proportions of each myeloid subpopulation across groups. C: Cross volcano plot comparing differences between the healthy group and LS group. The x-axis shows the difference in cell proportions, and the y-axis shows the log fold change (logFC). Genes with the highest fold changes are labeled. D: Cross volcano plot comparing differences between the healthy group and SSC group. E: Functional enrichment analysis of differentially expressed genes between groups.