Supplementary Materials for

Spatial transcriptome and metabolism profiling to identify metabolic heterogeneity in Sjögren syndrome

Yanxiong Shao, Ninging Cao, Fei Qian, Diqing Wu, Yuting Yang, Yichao Xia, Zongze Shen, Lijuan Zhu, Jiajia Li, Yeping Lu, Chaoran Li, Ying Song, Tianyu Xiao, Tianlin Lu, Jingwen Yang, Junqin Lu, Zhenrong Hu, Xudong Wang, Yubo Xu, Jie Zhang

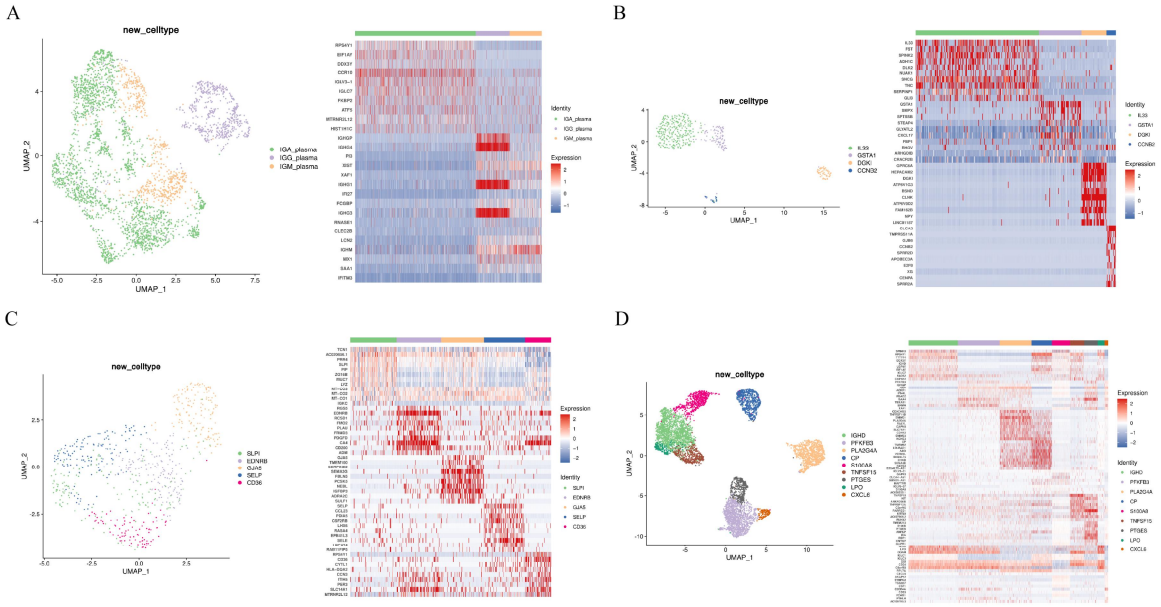

Figure. S1. Subcellular analysis using single-cell sequencing.

A: Dimension reduction of B cells and top markers.
B: Dimension reduction of duct cells and top markers.
C: Dimension reduction of endothelial cells and top markers.
D: Dimension reduction of acinar cells and top markers.

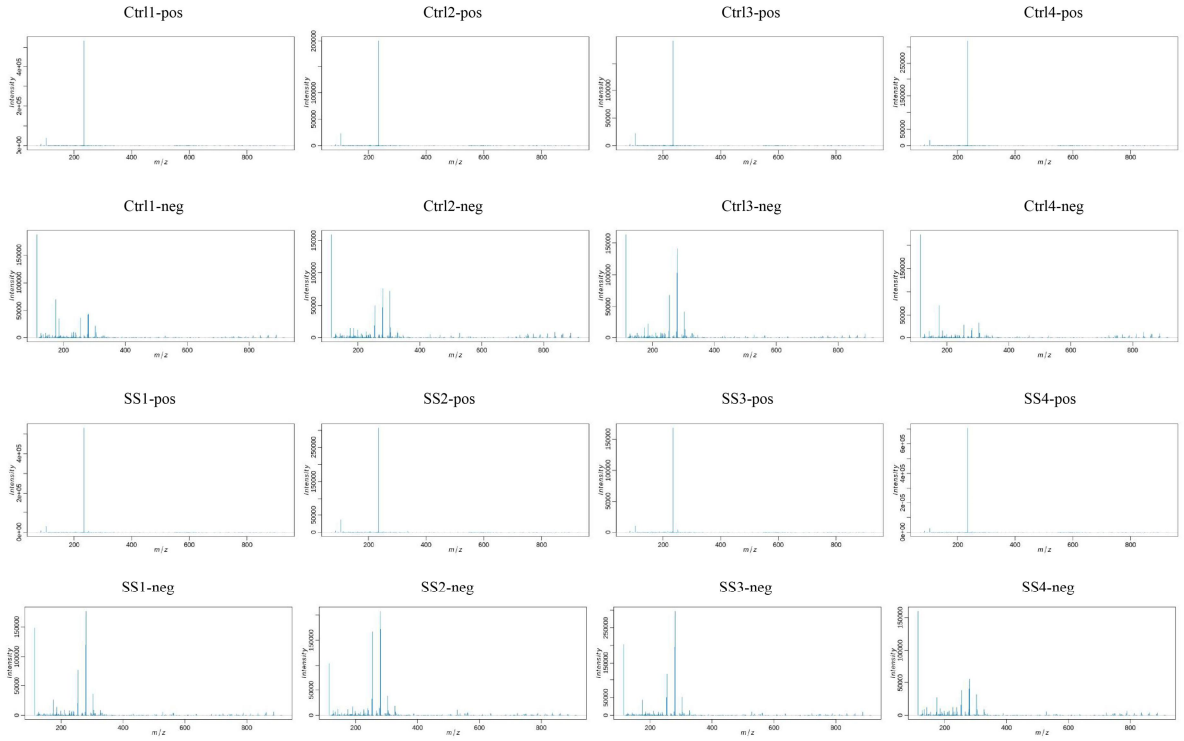

Figure. S2. Mass spectrometry results for spatial metabolism.

Figure. S3. Spatial feature plot of ALOX15 expression.

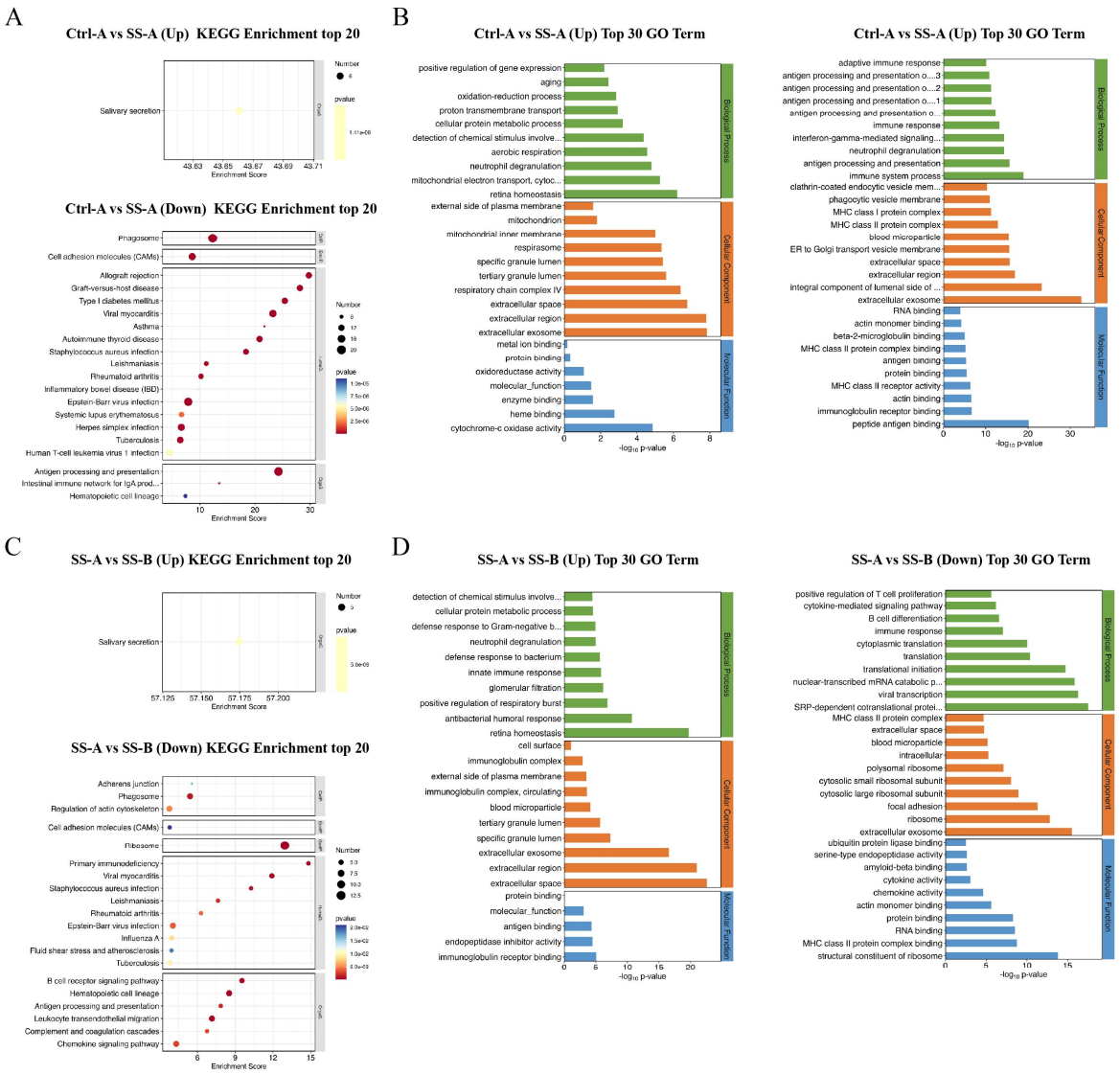

Figure. S4. Enrichment analysis of differentially expressed genes in the CD4$^+$ T cells in each section.

A: KEGG analysis of differentially expressed genes between the Ctrl-A and SS-A groups.
B: Gene Ontology analysis of differentially expressed genes between the Ctrl-A and SS-A groups.
C: KEGG analysis of differentially expressed genes between the SS-A and SS-B groups.
D: Gene Ontology analysis of differentially expressed genes between the SS-A and SS-B groups.

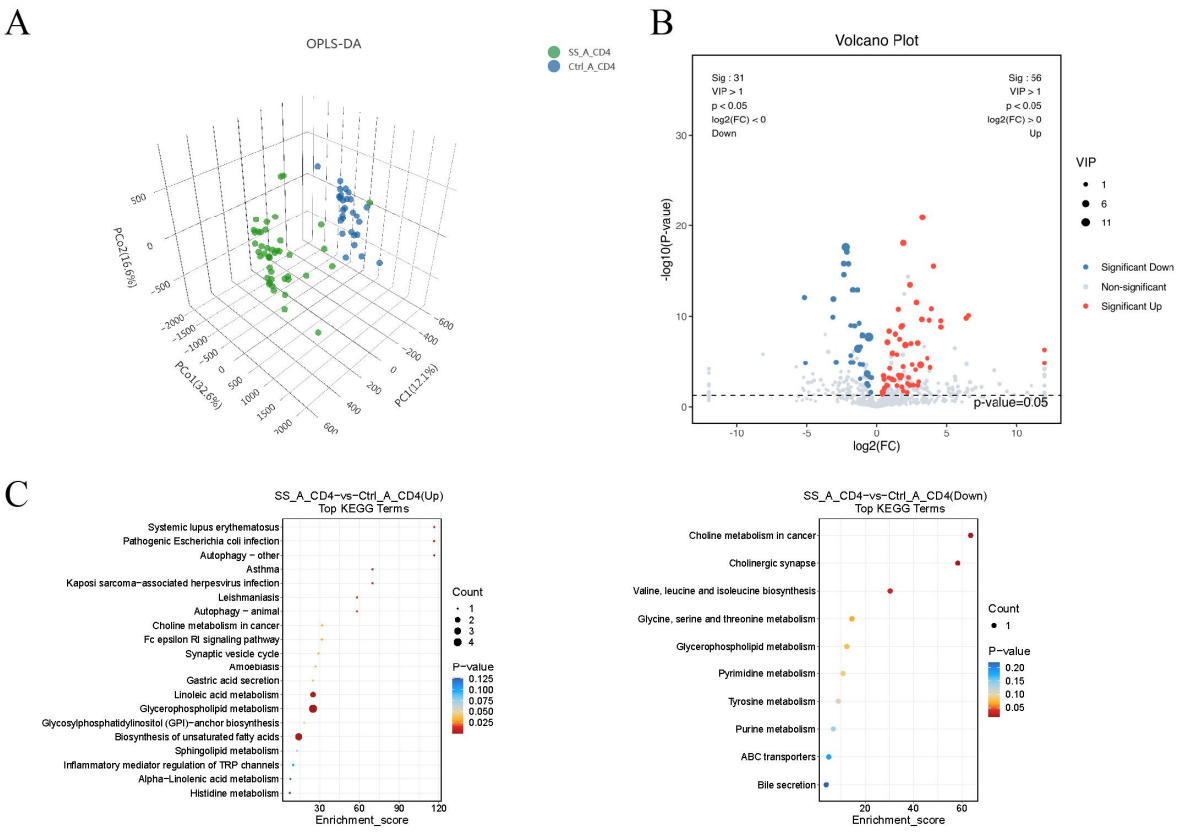

Figure. S5. Analysis of differentially expressed metabolites in the CD4$^+$ T cells in each section.

A: OPLS-DA of differentially expressed metabolites between the SS-A and Ctrl-A groups.
B: Volcano plot of differentially expressed metabolites between the SS-A and Ctrl-A groups.
C: KEGG analysis of differentially expressed metabolites between the SS-A and Ctrl-A groups.