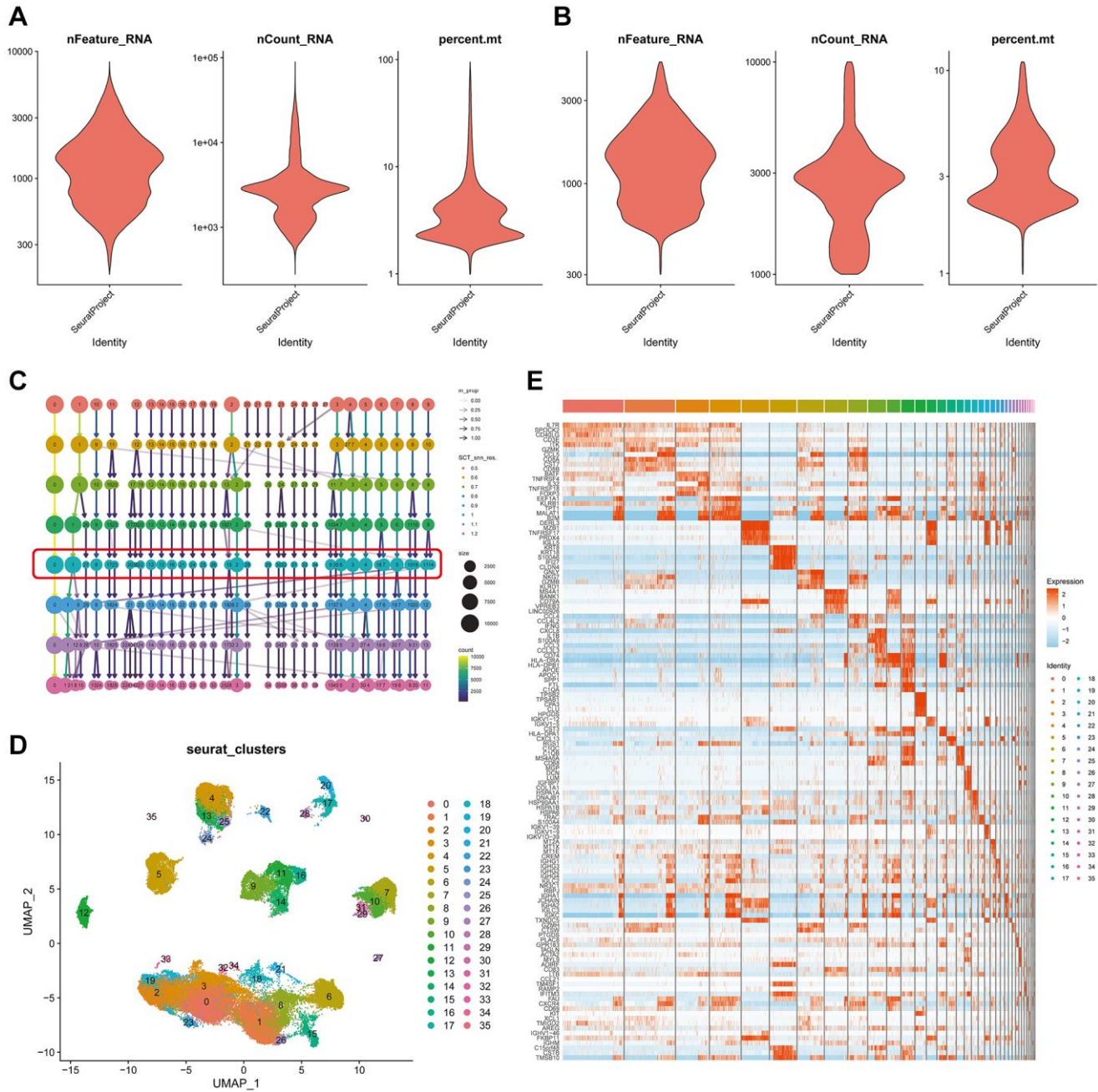
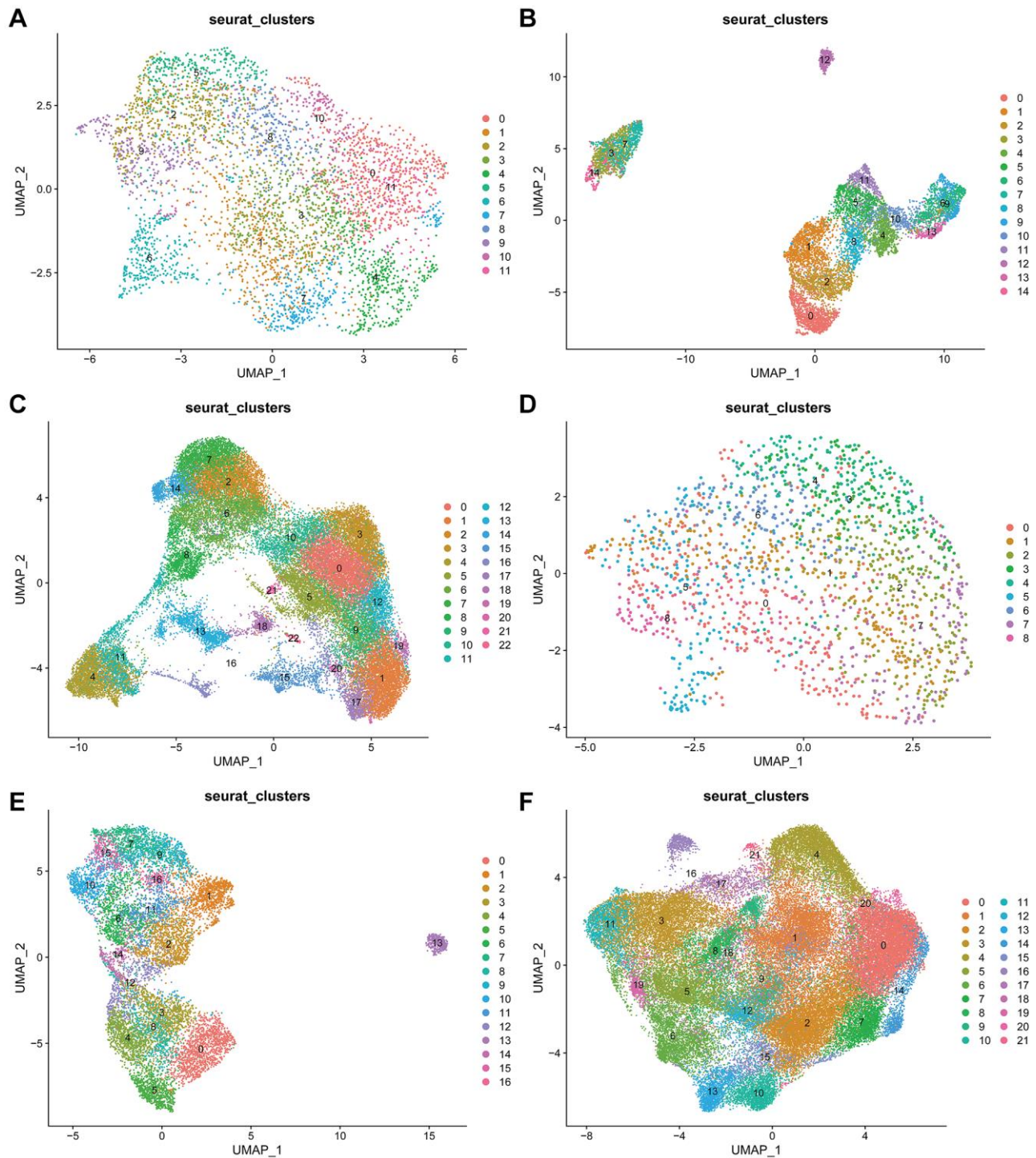


SUPPLEMENTARY FIGURES

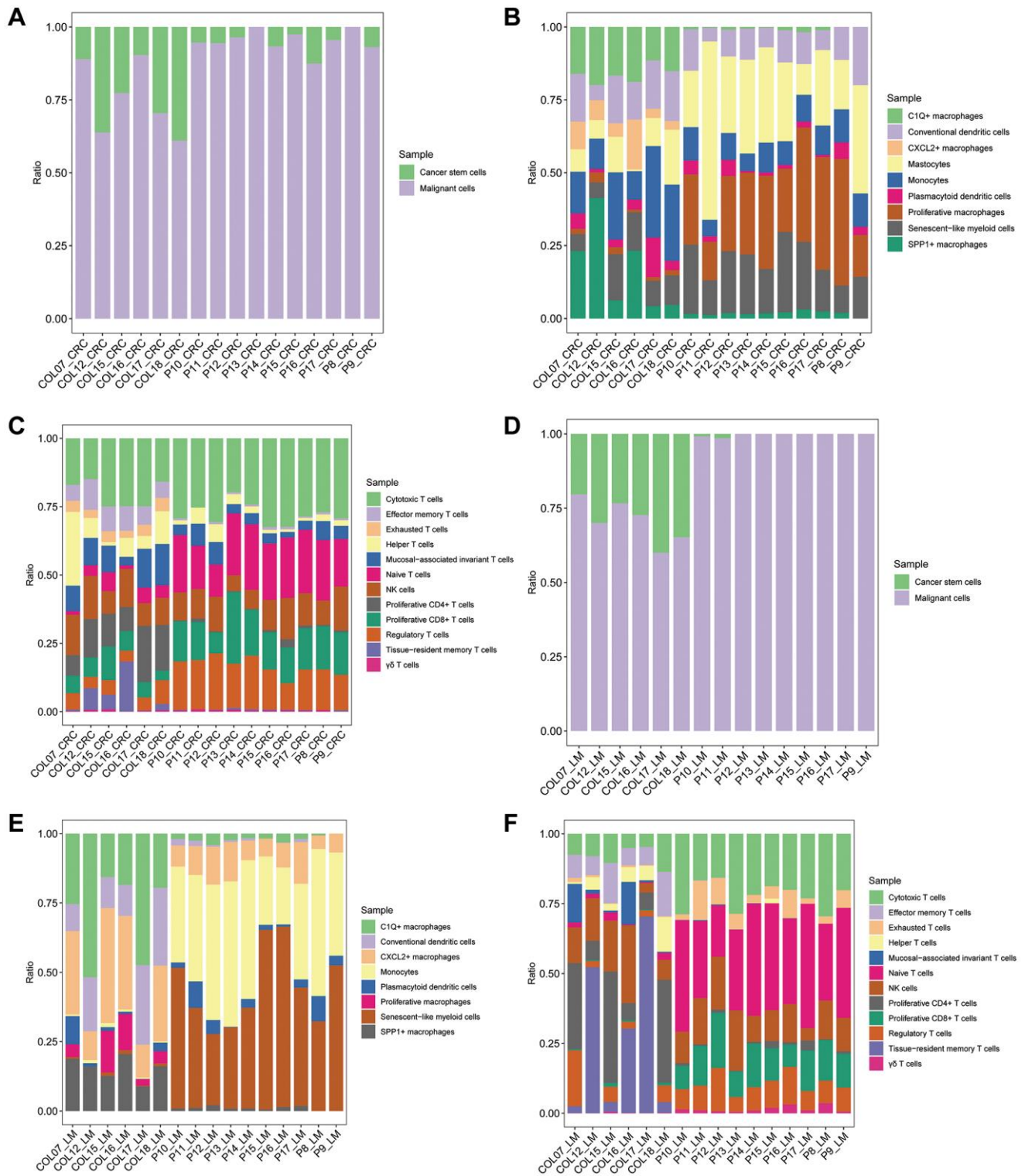


**Supplementary Figure 1. Quality control and dimensionality reduction clustering of primary colorectal cancer scRNA-Seq data.** (A, B) Data features before (A) and after (B) quality control of scRNA-Seq data. (C) Clustree dendrogram demonstrating dimensionality reduction clustering at varying resolutions (0.5–1.2). (D) Dimensionality reduction clustering of all cells utilizing the UMAP plot at the appropriate resolution. (E) Heatmap presenting the gene expression levels of the top 5 differentially expressed genes across distinct clusters.





**Supplementary Figure 3. Dimensionality reduction clustering results of main cell types.** (A–C) UMAP plots for dimensionality reduction clustering of epithelial cells (A), myeloid cells (B), and NK/T cells (C) in primary colorectal cancer tissues. (D–F) UMAP plots for dimensionality reduction clustering of epithelial cells (D), myeloid cells (E), and NK/T cells (F) in liver metastasis tissues.



**Supplementary Figure 4. Proportion plots of main cell types and their subtypes.** (A–C) Proportion plots representing the distribution of cell subtypes within epithelial cells (A), myeloid cells (B), and NK/T cells (C) in primary colorectal cancer tissues. (D–F) Proportion plots illustrating the distribution of cell subtypes within epithelial cells (D), myeloid cells (E), and NK/T cells (F) in liver metastasis tissues.