

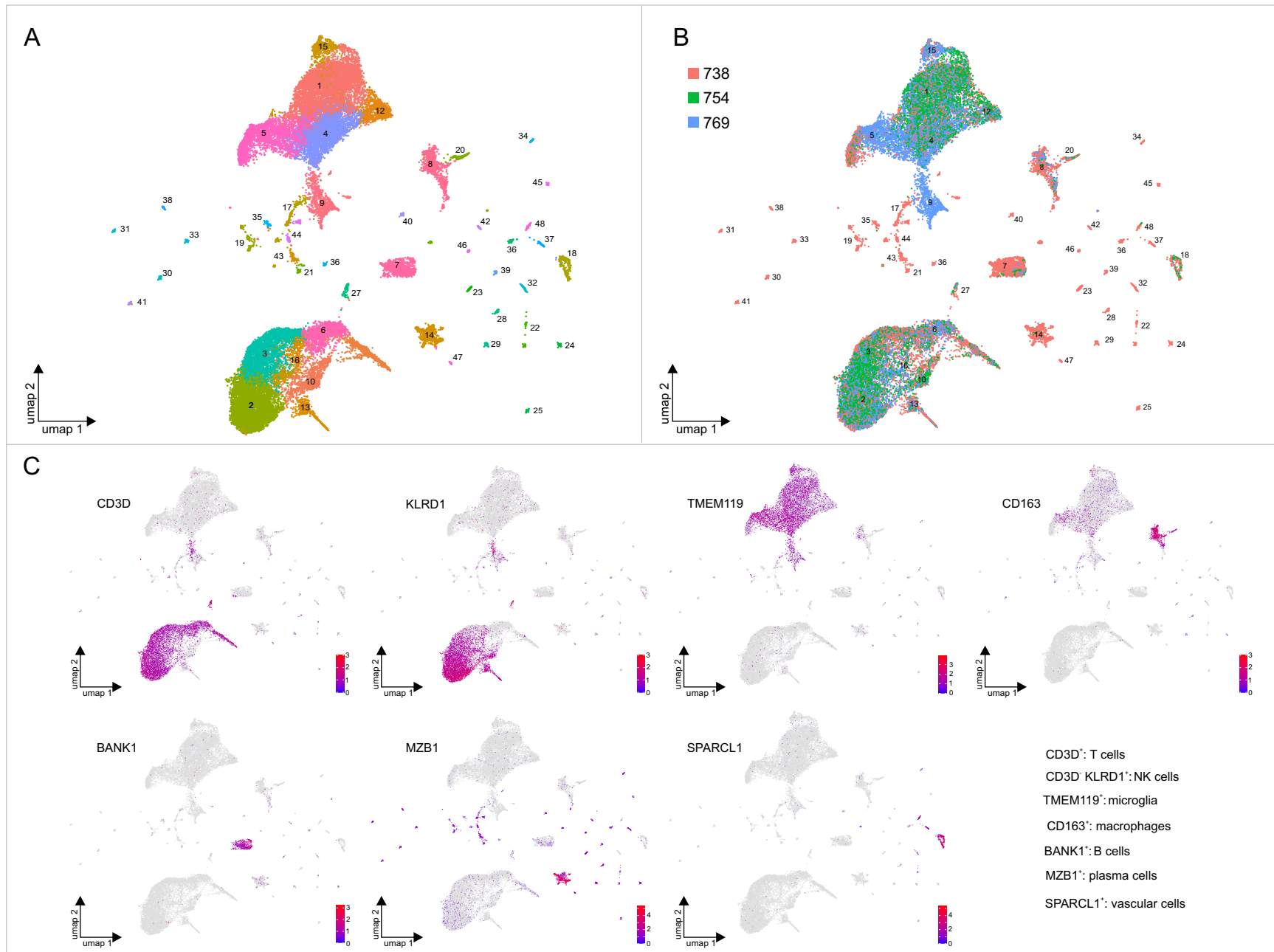


Fig. S2: Cell clusters obtained by integrating the scRNA-seq gene expression data from the three surgical specimens. (A) UMAP showing the number of clusters. (B) UMAP showing the distribution of the cells from each surgical specimen among the clusters. (C) Assignment of cell types to each cluster based on the expression of a specific marker gene.