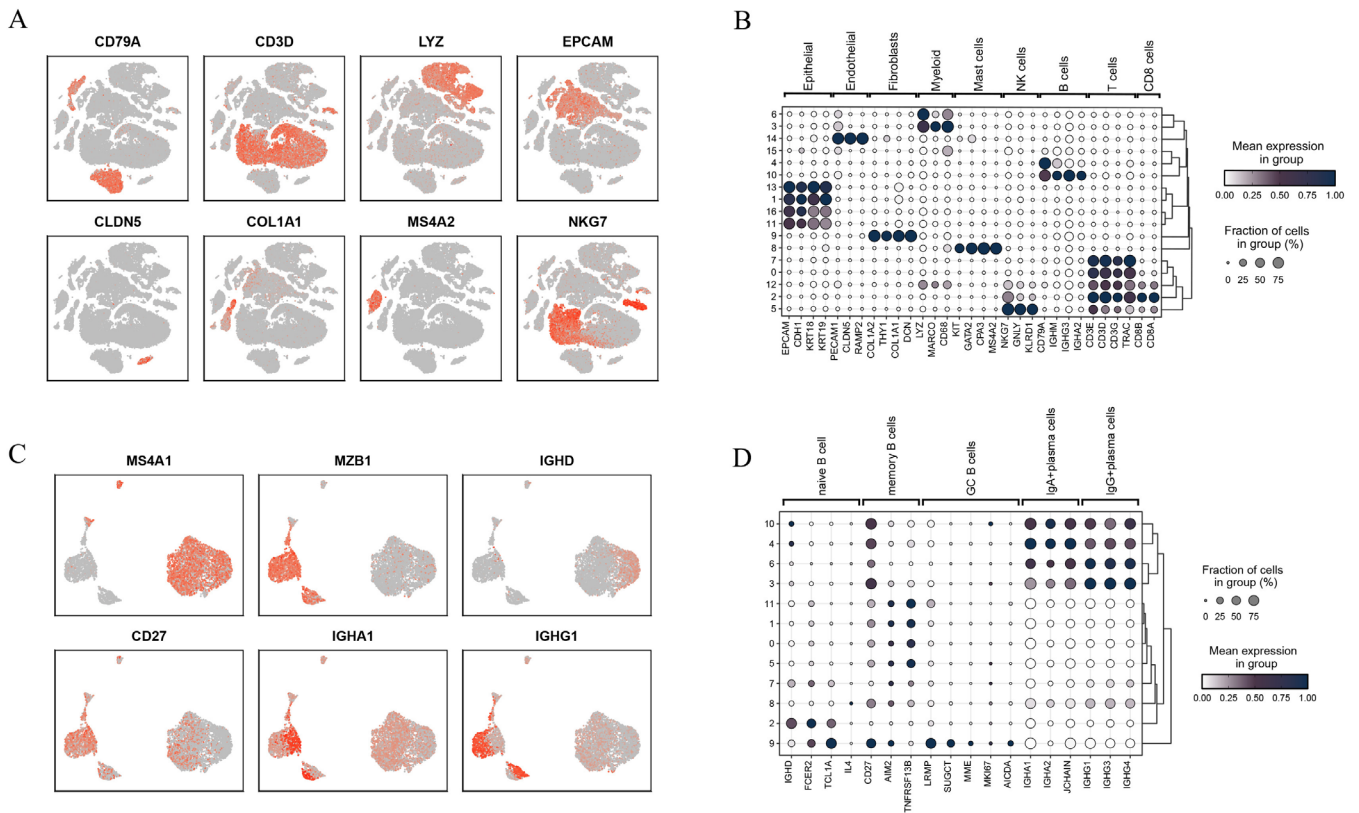A

B

Figure S1 Quality control of scRNA-seq analysis. (A) Based on the feature genes, the percentage of each feature set in the cell was calculated. The figure showed the number of genes and mRNA in each cell, as well as the percentage of hemoglobin, mitochondria, and ribosomes. (B) The graph showed the correlation between the features. scRNA-seq, single-cell RNA sequencing.

Figure S2 Visualization of marker genes. (A) Visualization of marker genes of different cell types on t-SNE map. (B) The dot plot showed the expression of marker genes of each cell cluster. The color of the dots represents the average expression level of the marker gene in the cluster, while the size of the dots indicates the proportion of cells expressing the marker gene in each cluster. (C) Visualization of marker genes of B cells subtypes. (D) The dot plot showed the expression of marker genes of B cells subtypes. t-SNE, t-distributed stochastic neighbor embedding.