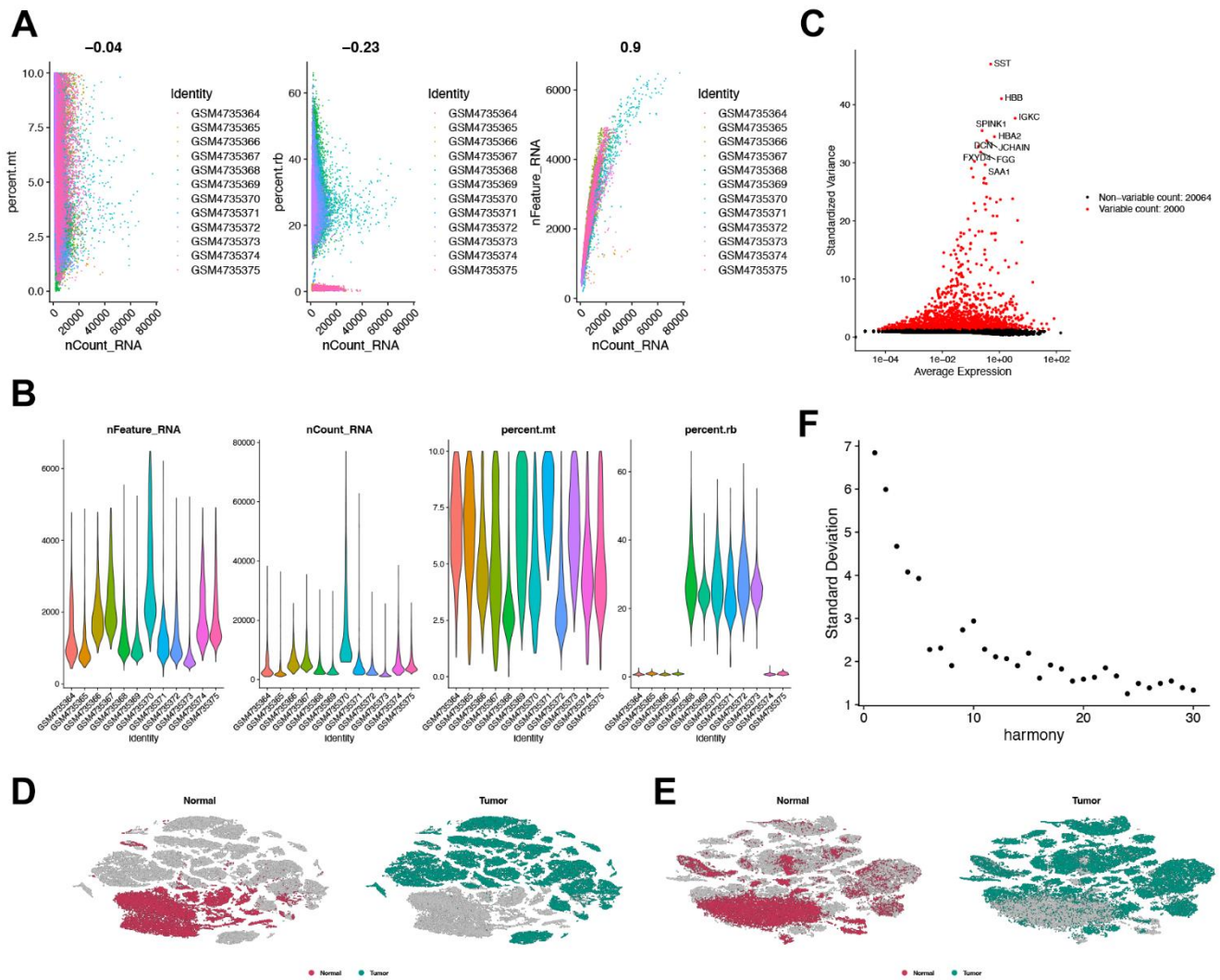
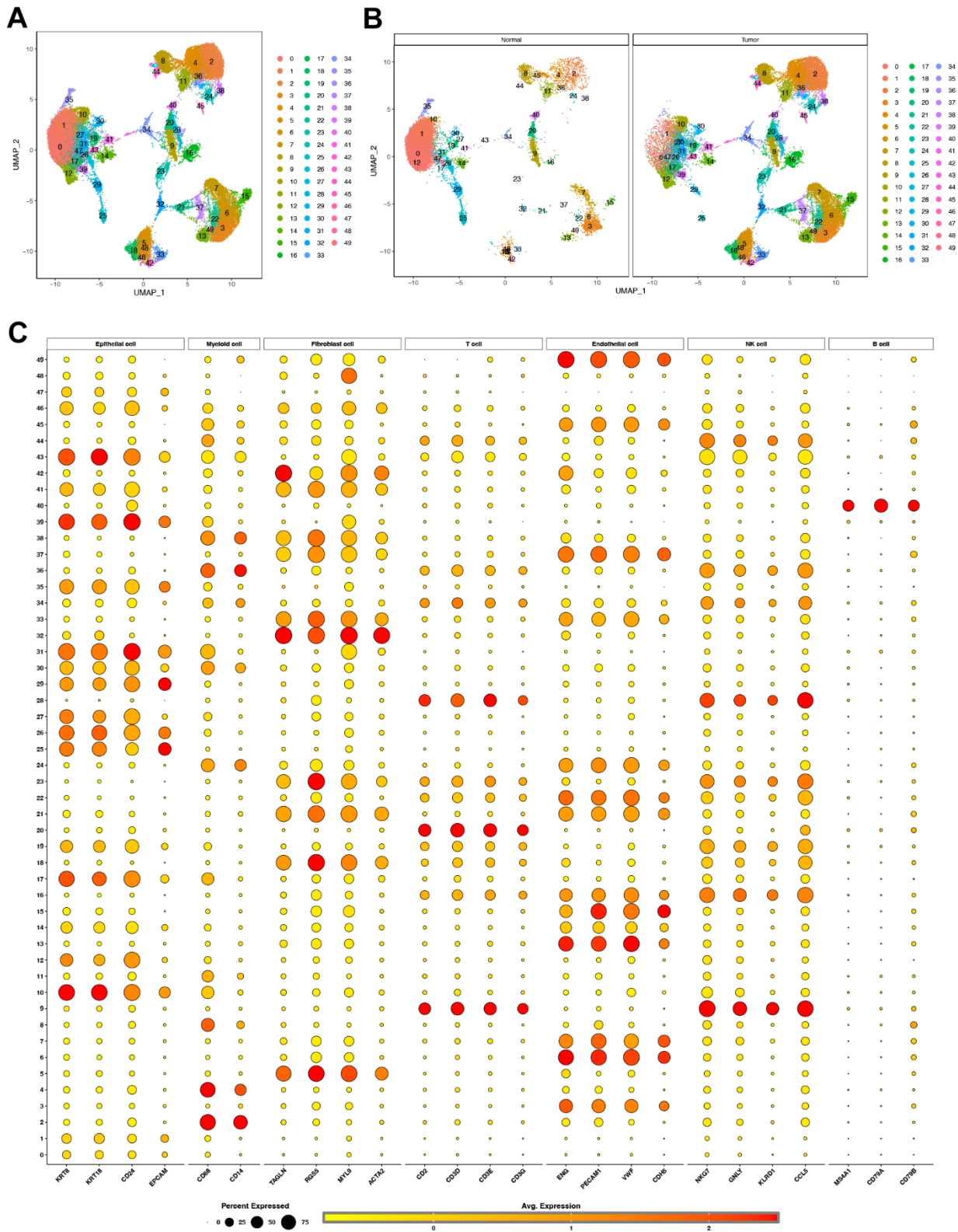


SUPPLEMENTARY FIGURES



Supplementary Figure 1. Single-cell data processing process. (A, B) Quality control of the scRNA-seq data. (C) Highly variable genes in the data. (D, E) Cell distribution before and after removing the batch effect with Harmony. (F) ElbowPlot for identifying an appropriate number of principal components.



Supplementary Figure 2. Single-cell dimension reduction and cell annotation. (A) UMAP plots for all samples. (B) UMAP plots for normal and tumor groups. (C) The expression of cell markers in each cluster.