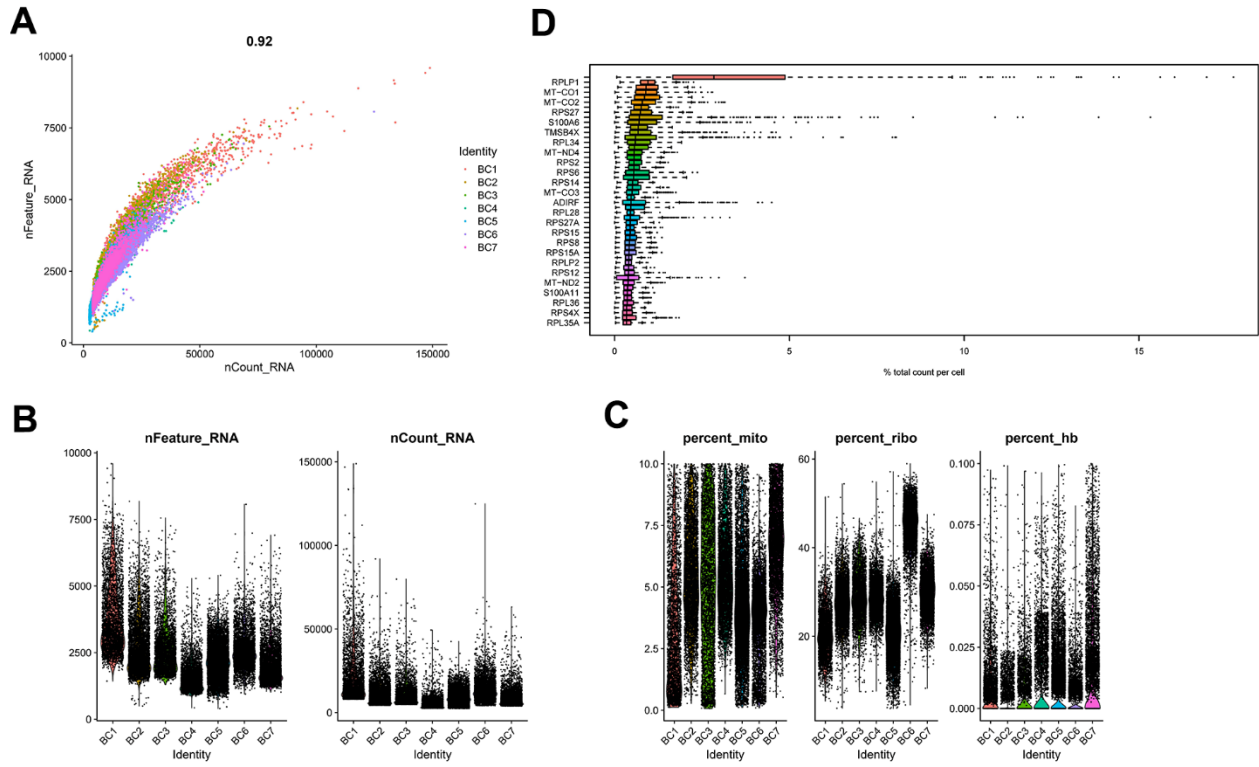
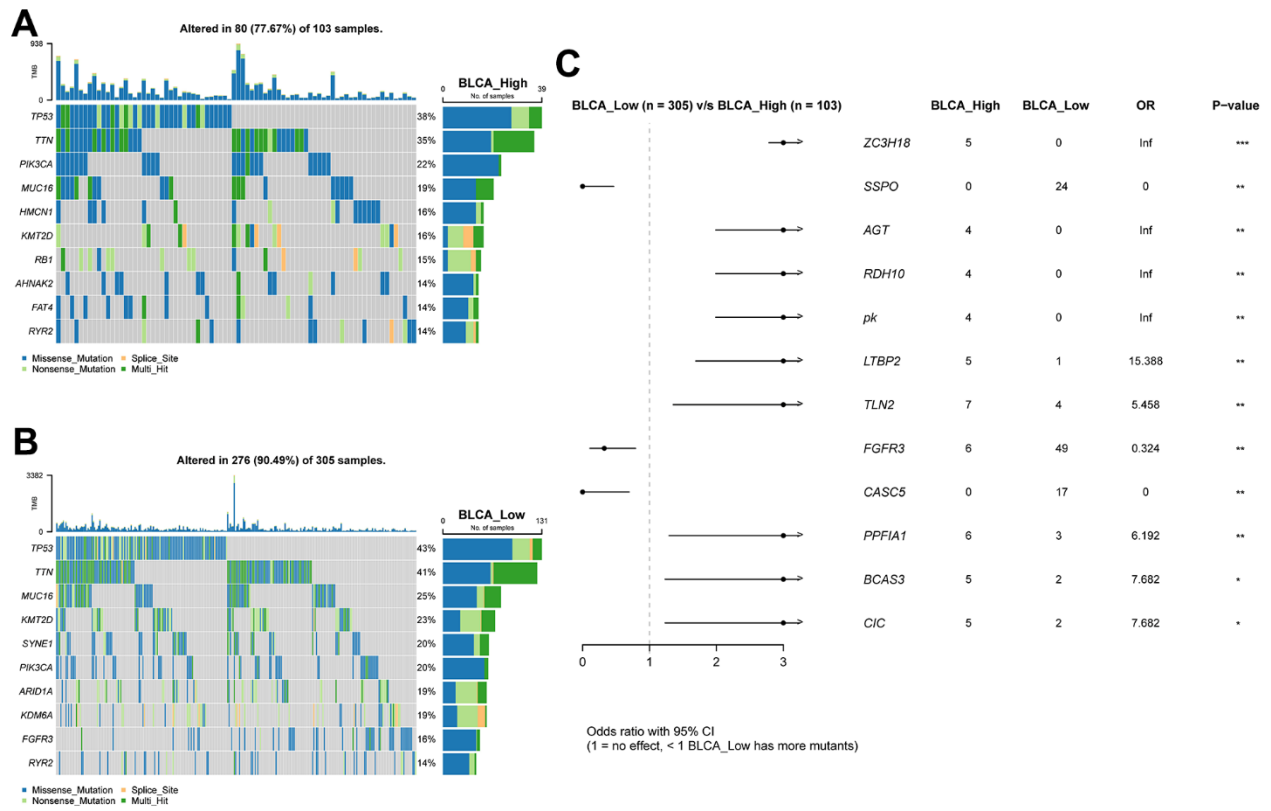


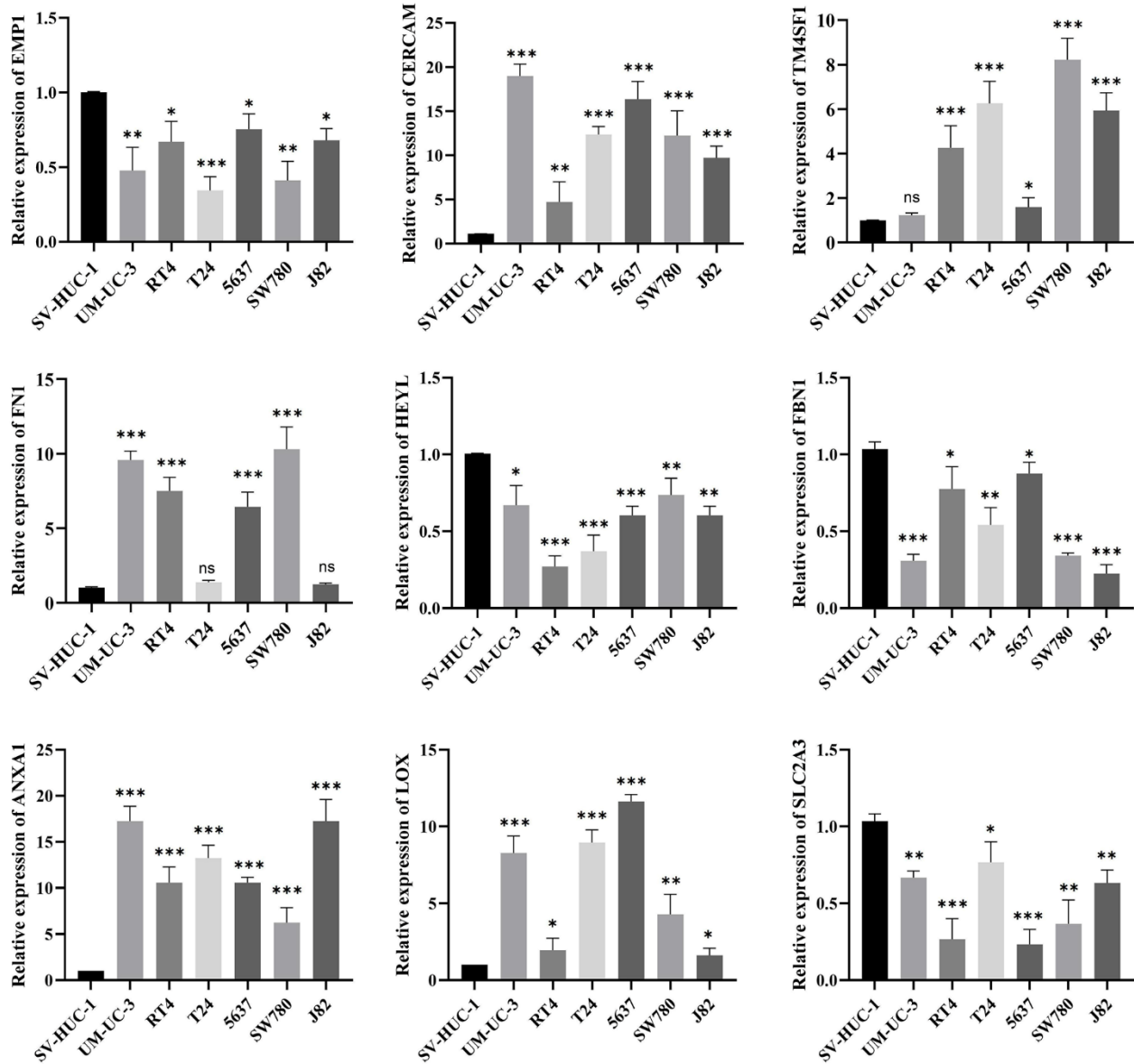
SUPPLEMENTARY FIGURES



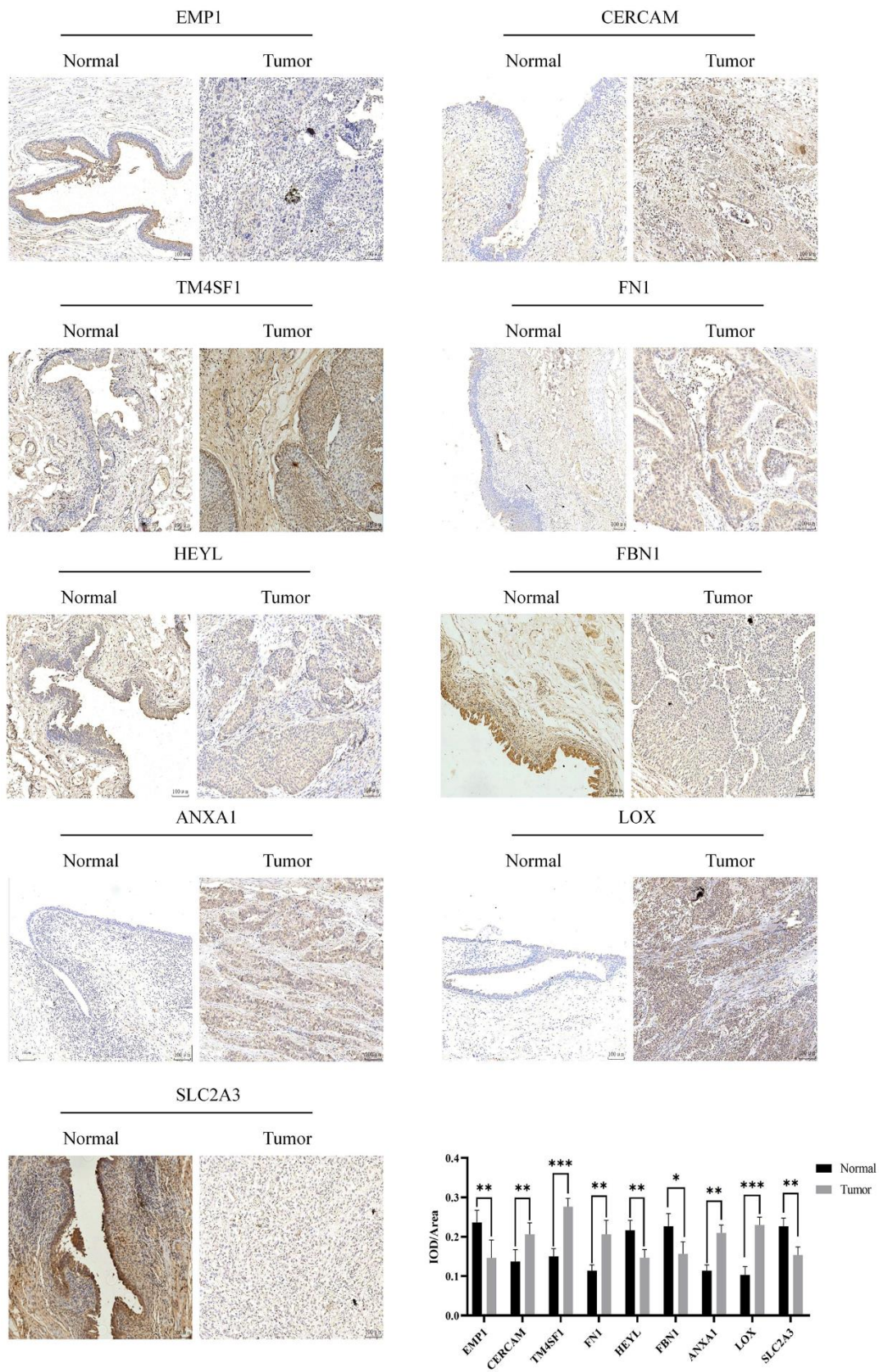
Supplementary Figure 1. Quality control of scRNA-seq data. (A) Correlation between nFeature_RNA and nCount_RNA. (B, C) Information of filtered scRNA-seq data from 7 BLCA samples. (D) The top 25 genes with the highest percentage of cellular expression.



Supplementary Figure 2. Gene mutations in the high- and low-score groups. (A, B) Distribution of gene mutations in the high- and low-score groups. **(C)** Comparison of the gene mutations in the high- and low-score groups.



Supplementary Figure 3. mRNA expression levels of model genes in bladder uroepithelial cell line (SV-HUC-1) and BLCA cells (UM-UC-3, RT4, T24, 5627, SW780, and J82).



Supplementary Figure 4. Reprehensive image of the expression of model genes in tumor and paired normal samples revealed by IHC.