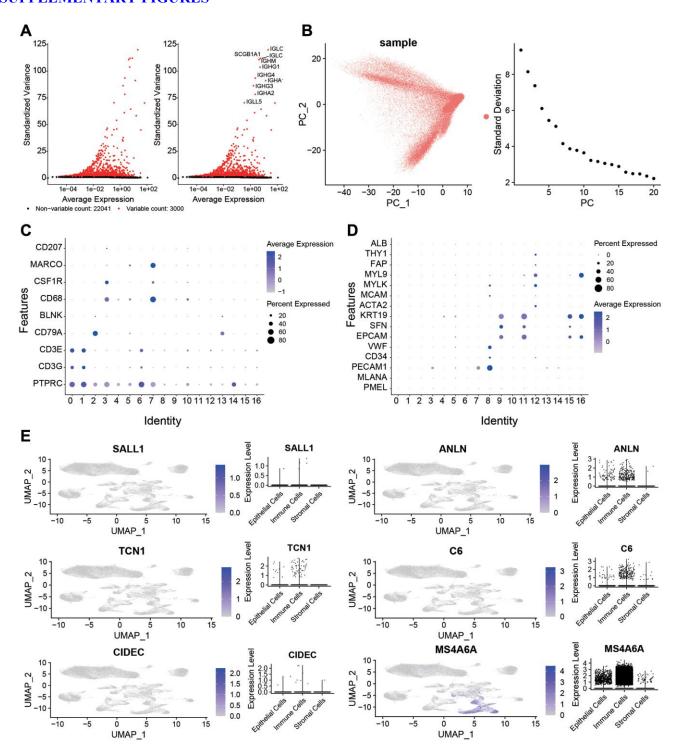
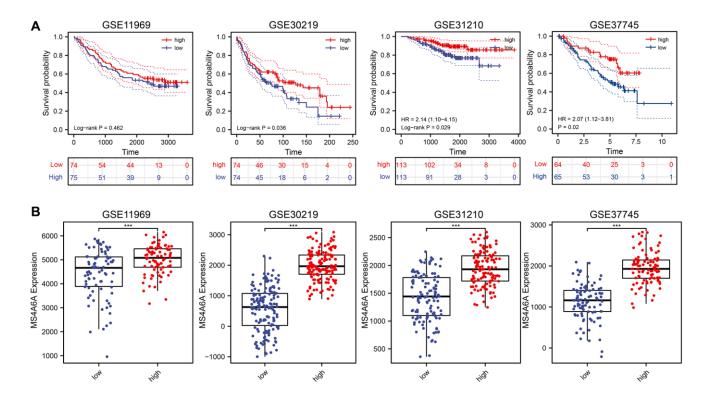
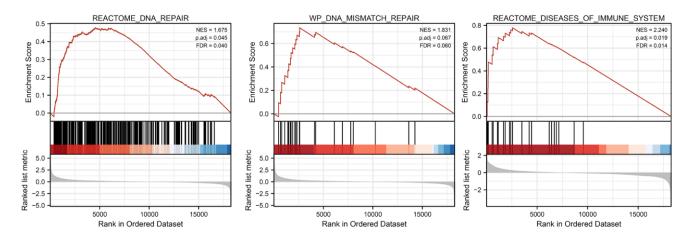
SUPPLEMENTARY FIGURES



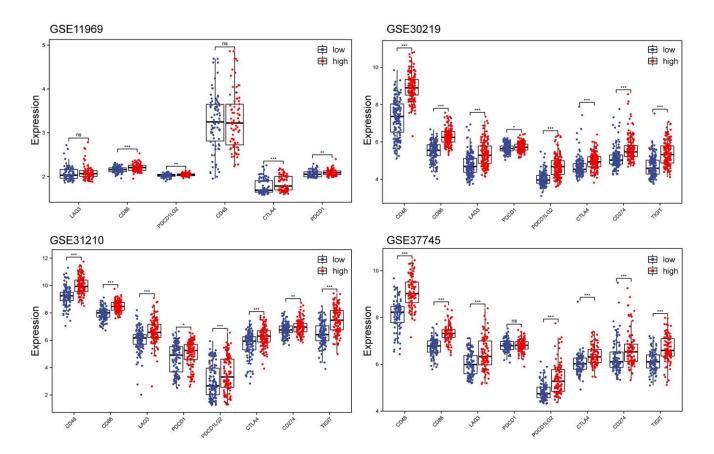
Supplementary Figure 1. scRNA-seq analysis. (A) The Variable Features plot identified the top 3000 variable genes, and the top 10 were highlighted. (B) PCA dimension reduction, 15 PCs were applied for cell clustering. (C) Bubble plot depicting the biomarkers of immune cells across 0–16 subsets. (D) Bubble plot depicting the biomarkers of epithelial and stromal cells across 0–16 subsets. (E) Distribution of 6 genes in different types of cells.



Supplementary Figure 2. Comparison of *MS4A6A* survival analysis and immune scores in GEO dataset. (A) KM survival curves of *MS4A6A* in the GSE11969, GSE30219, GSE31210, and GSE37745 datasets. (B) Differences in *MS4A6A* expression levels were compared in GSE11969, GSE30219, GSE31210, and GSE37745 in the high-low immune infiltration groups. *MS4A6A* expression was elevated in the high immune infiltration group.



Supplementary Figure 3. GSEA of high and low expression patterns of *MS4A6A***.** GSEA results revealed that the DNA repair, DNA mismatch repair, and immune system-related pathways were significantly enriched in the *MS4A6A*-positive group.



Supplementary Figure 4. Validation of relationship between *MS4A6A* **gene and immune checkpoint expression in GEO dataset.** Box plots demonstrate that *MS4A6A* high expression group in GSE11969, GSE30219, GSE31210, and GSE37745 datasets, as well as immune checkpoints, exhibited consistent elevated expression results with the TCGA-LUAD cohort.

Supplementary Figure 5. Immunohistochemical analysis of MS4A6A in normal lung vs. LUAD tissues. (A) Immunohistochemistry of MS4A6A in LUAD tissue. **(B)** Immunohistochemistry of MS4A6A in normal lung tissue.