SUPPLEMENTARY FIGURES
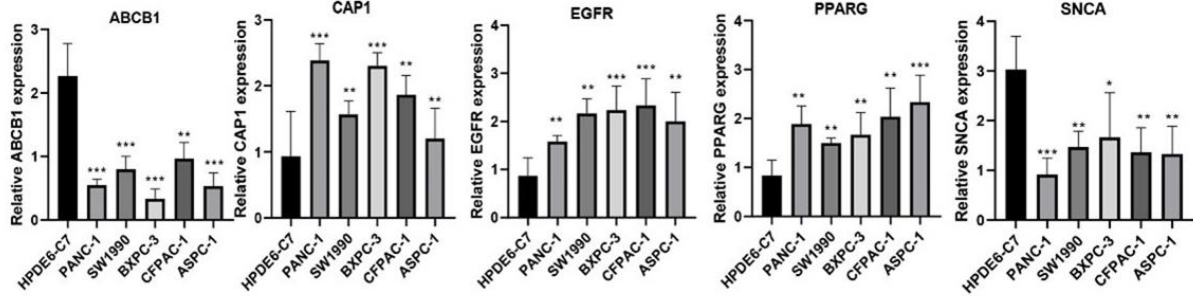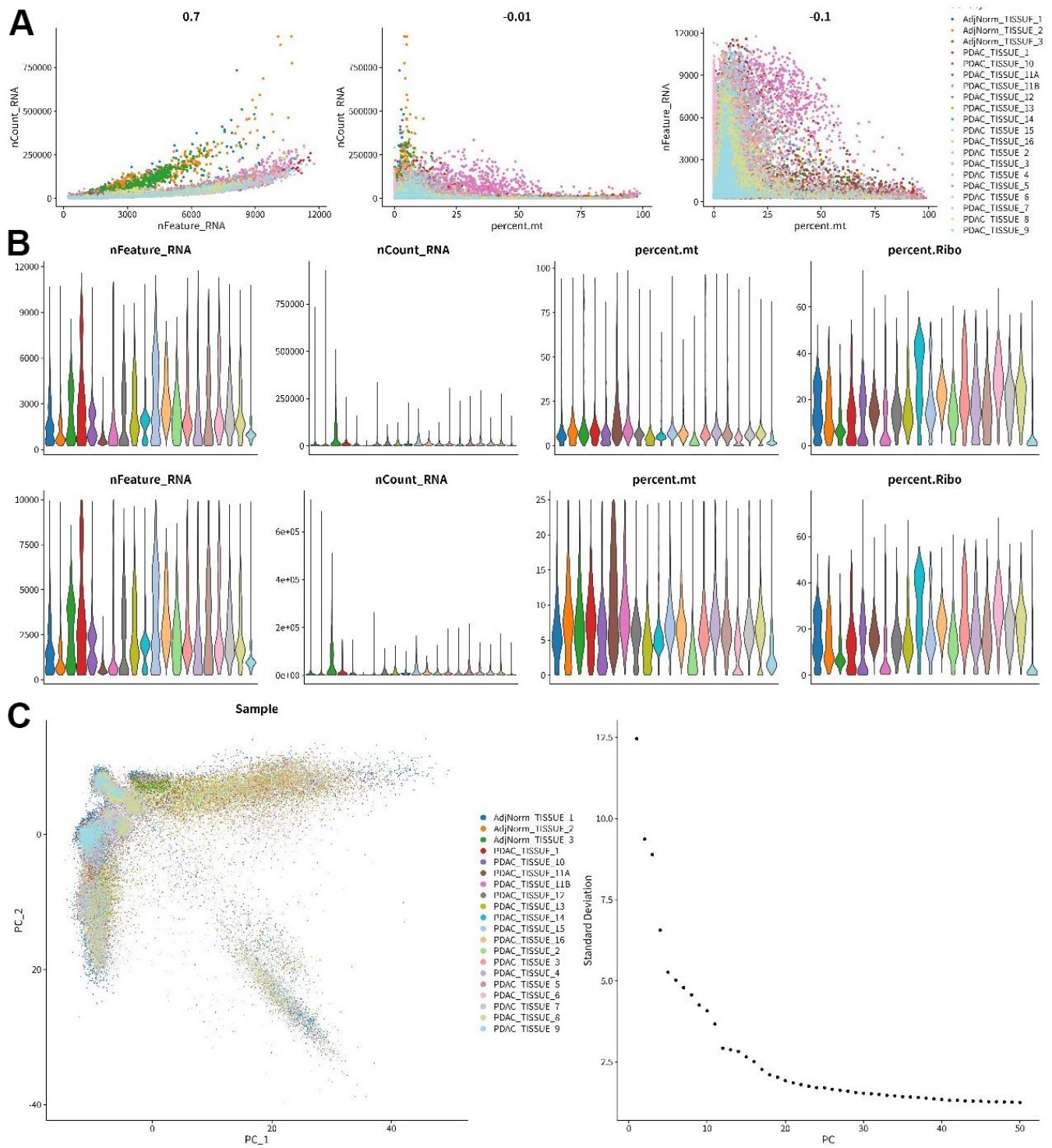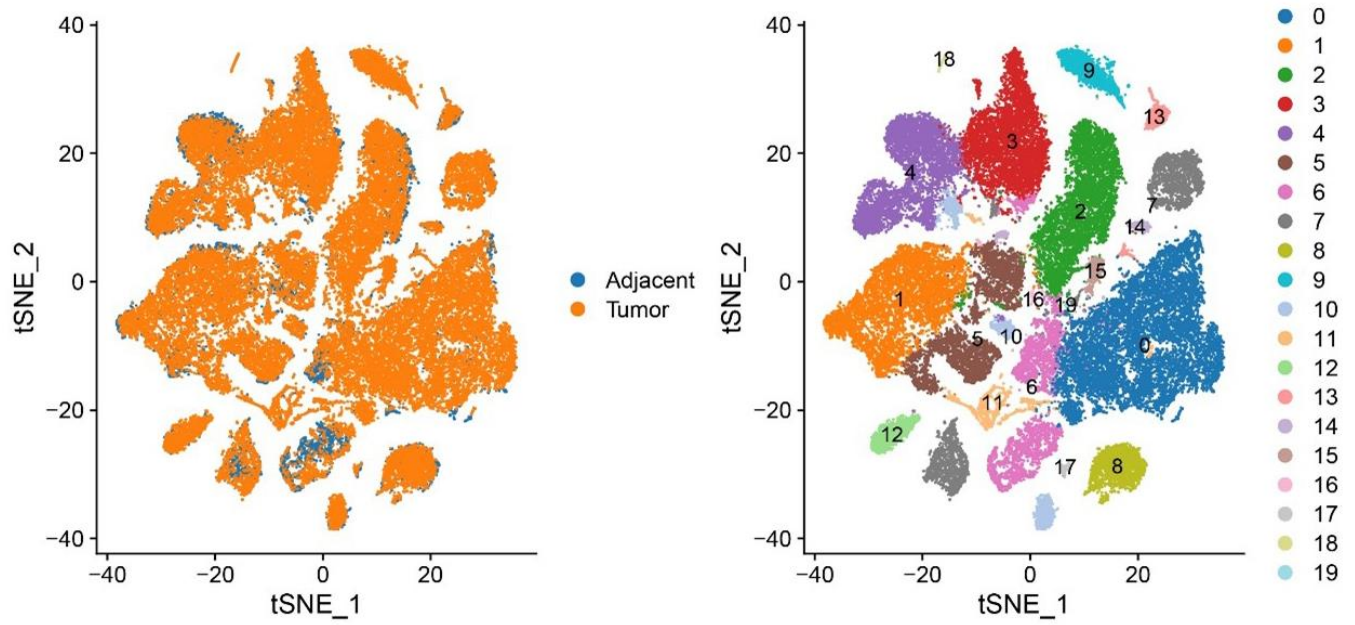
A

B

Supplementary Figure 1. (**A**) The expression of the 5 hub genes in pancreatic cancer cell lines comparing to pancreatic normal cell lines. ** means P-value <0.01, *** means P-value <0.001. (**B**) Correlation analysis of GSVA enrichment score and identified risk score in pan-cancer.
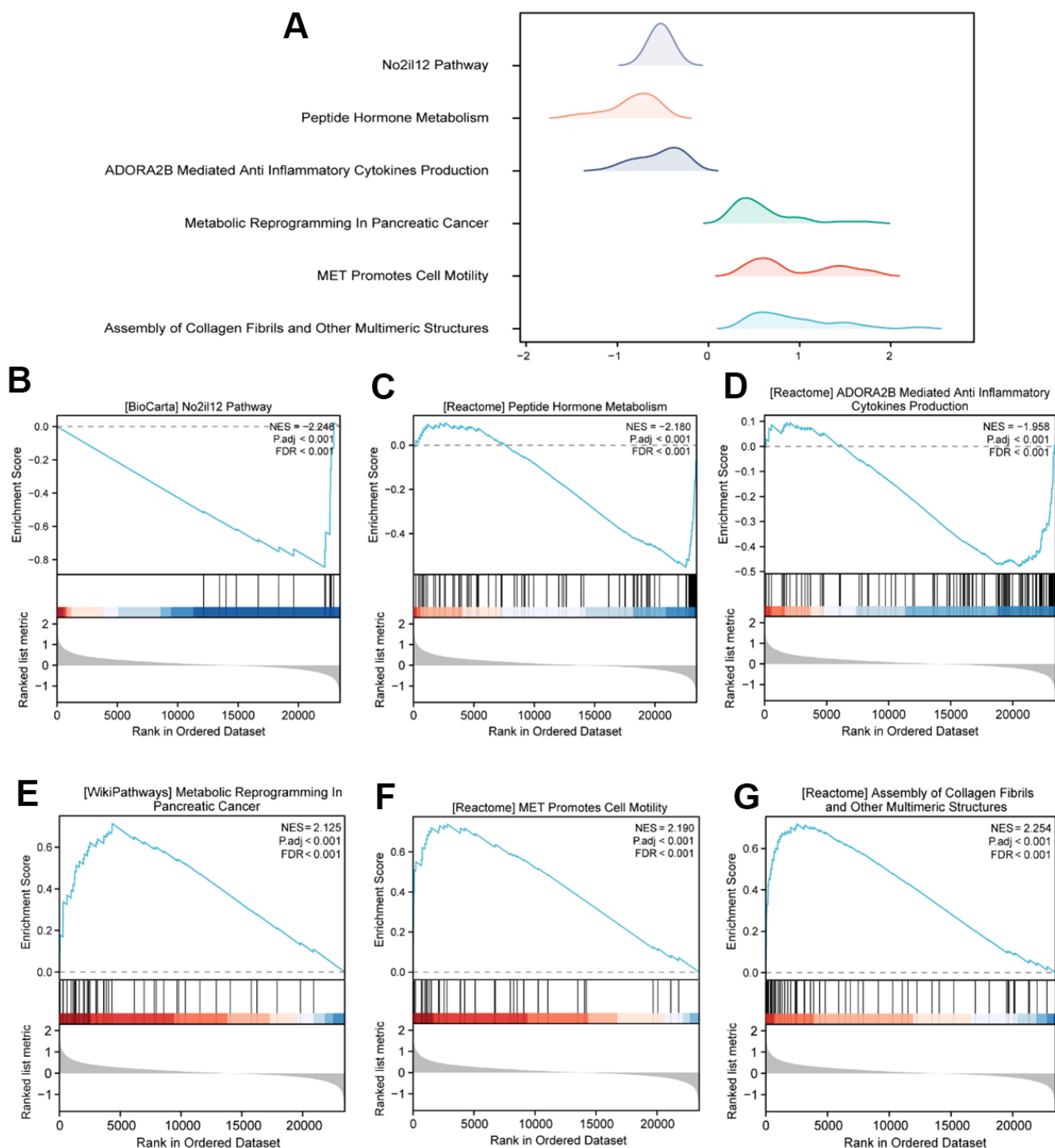
**Supplementary Figure 2.** (**A**–**C**) The quality of the enrolled single-cell sequencing data.
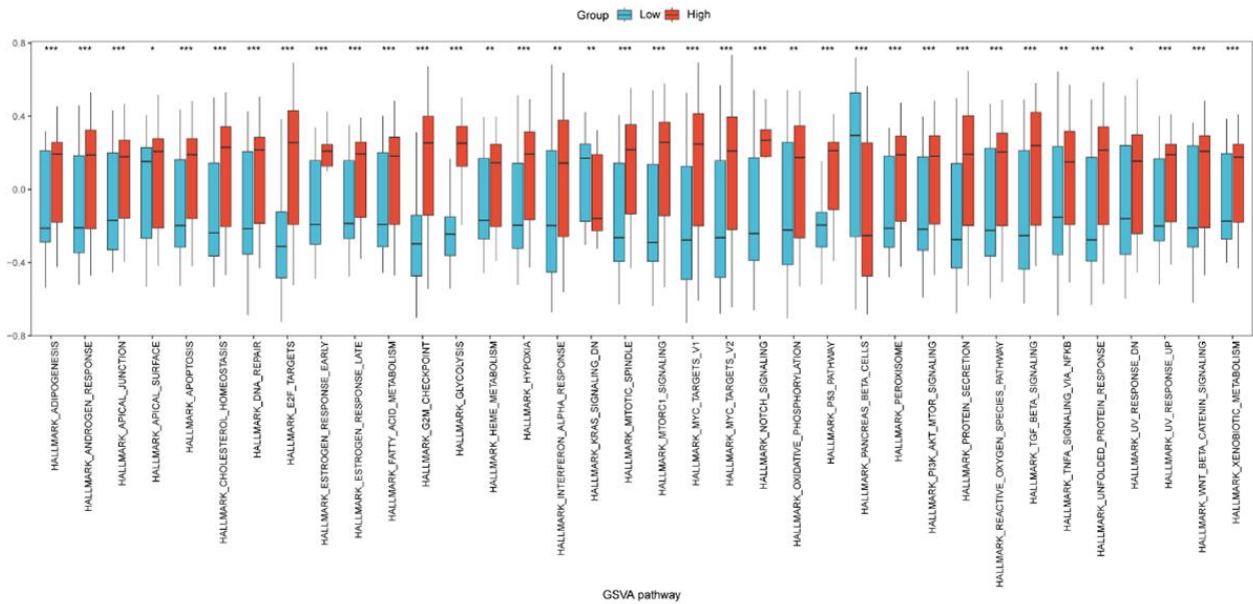
Supplementary Figure 3. Left: The tSNE plot between tumor and adjacent tumor. Right: The tSNE plot of 19 group after clustered.
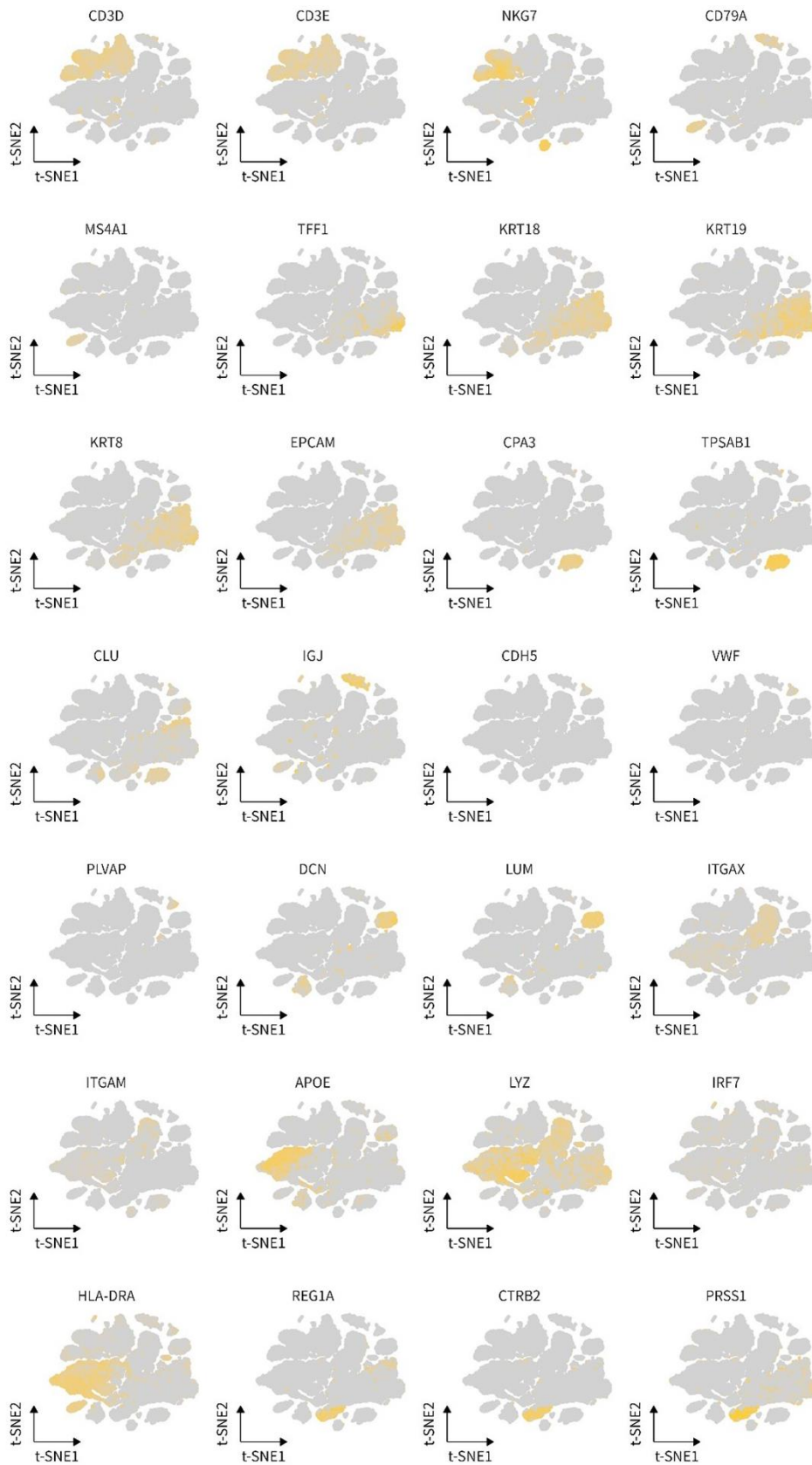
Supplementary Figure 4. The t-SNE plot of multiple markers in single-cell sequencing data.

Supplementary Figure 5. (**A**) The identified GSEA pathways between the high and low-risk group. (**B**–**G**) The enrichment score of identified GSEA pathway.
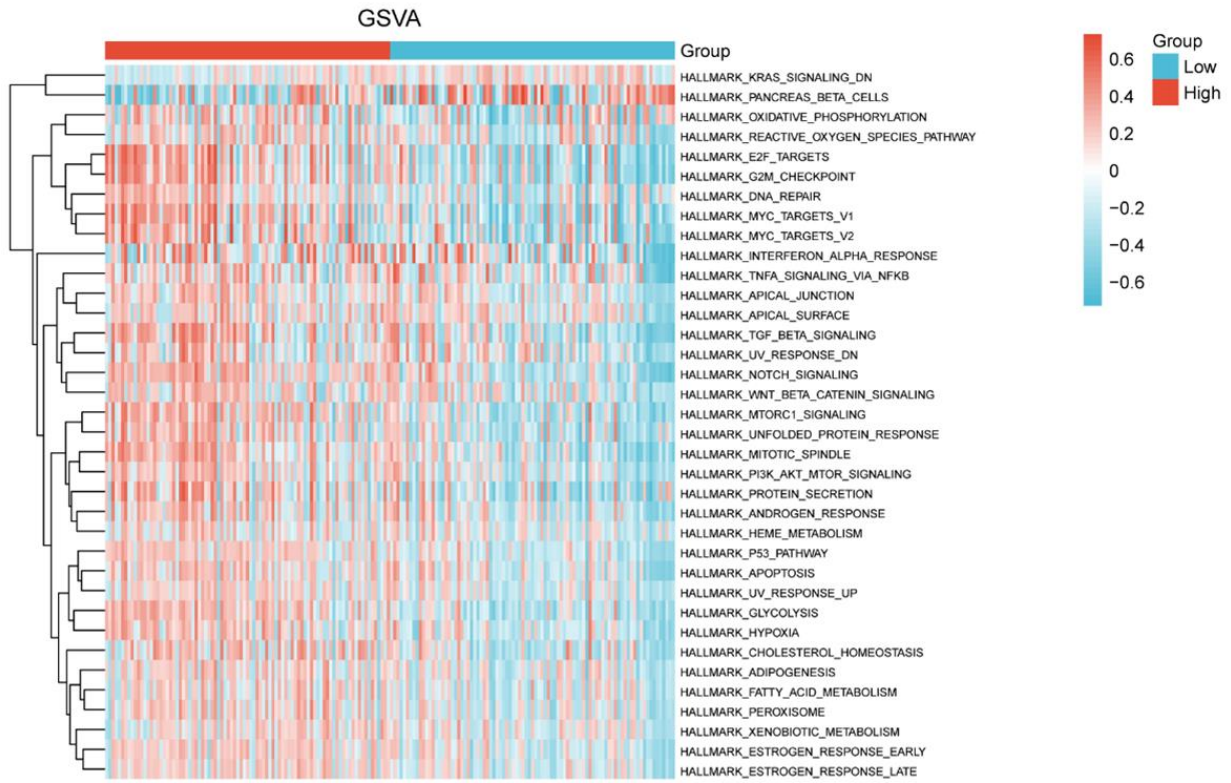
Supplementary Figure 6. (**A**) The identified GSVA pathways in the high and low-risk groups. (**B**) The identified GSEA pathways in the high and low-risk groups.