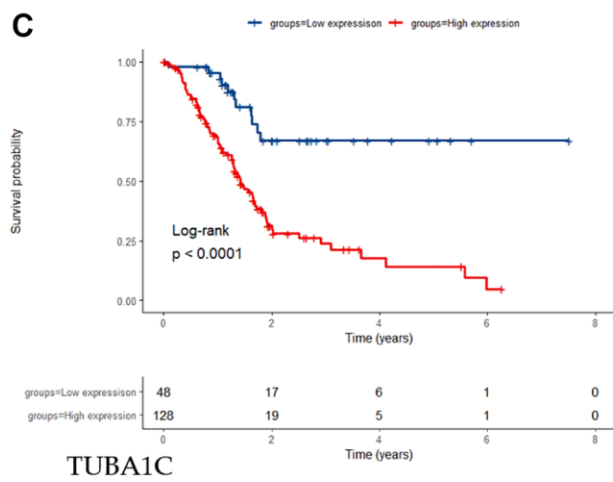
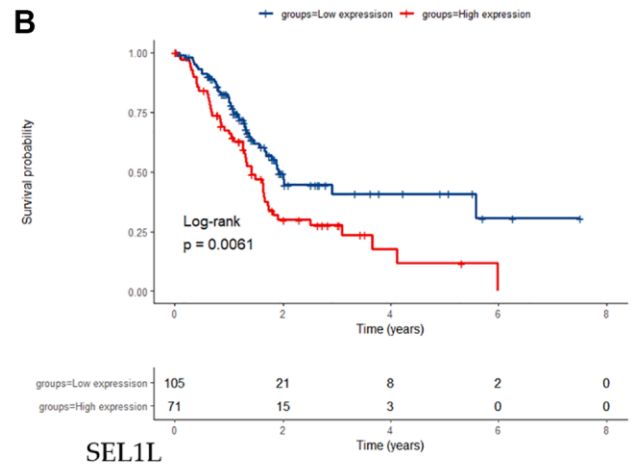
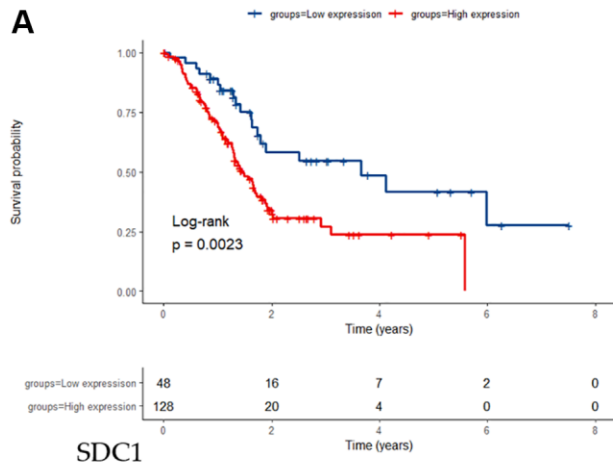
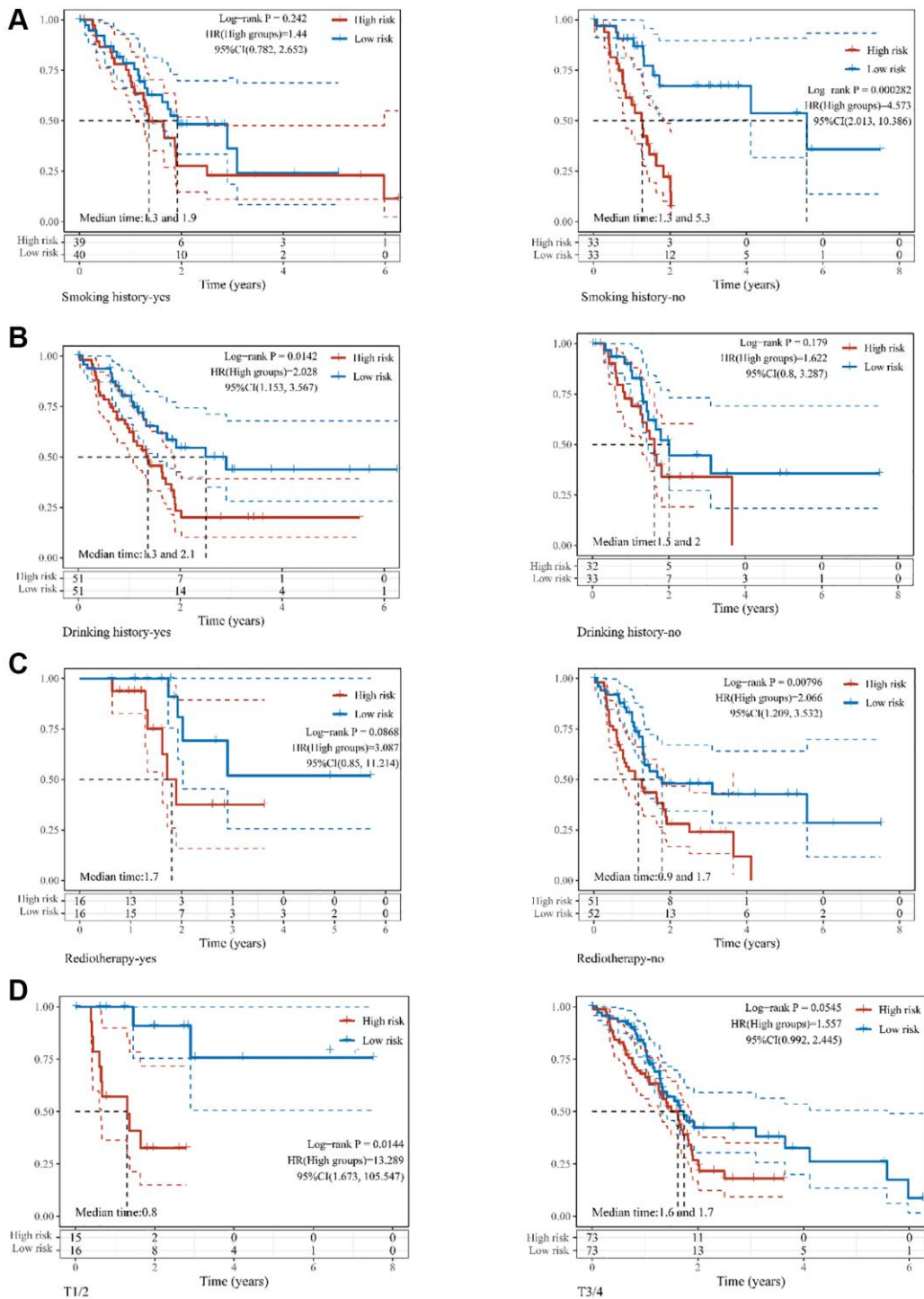


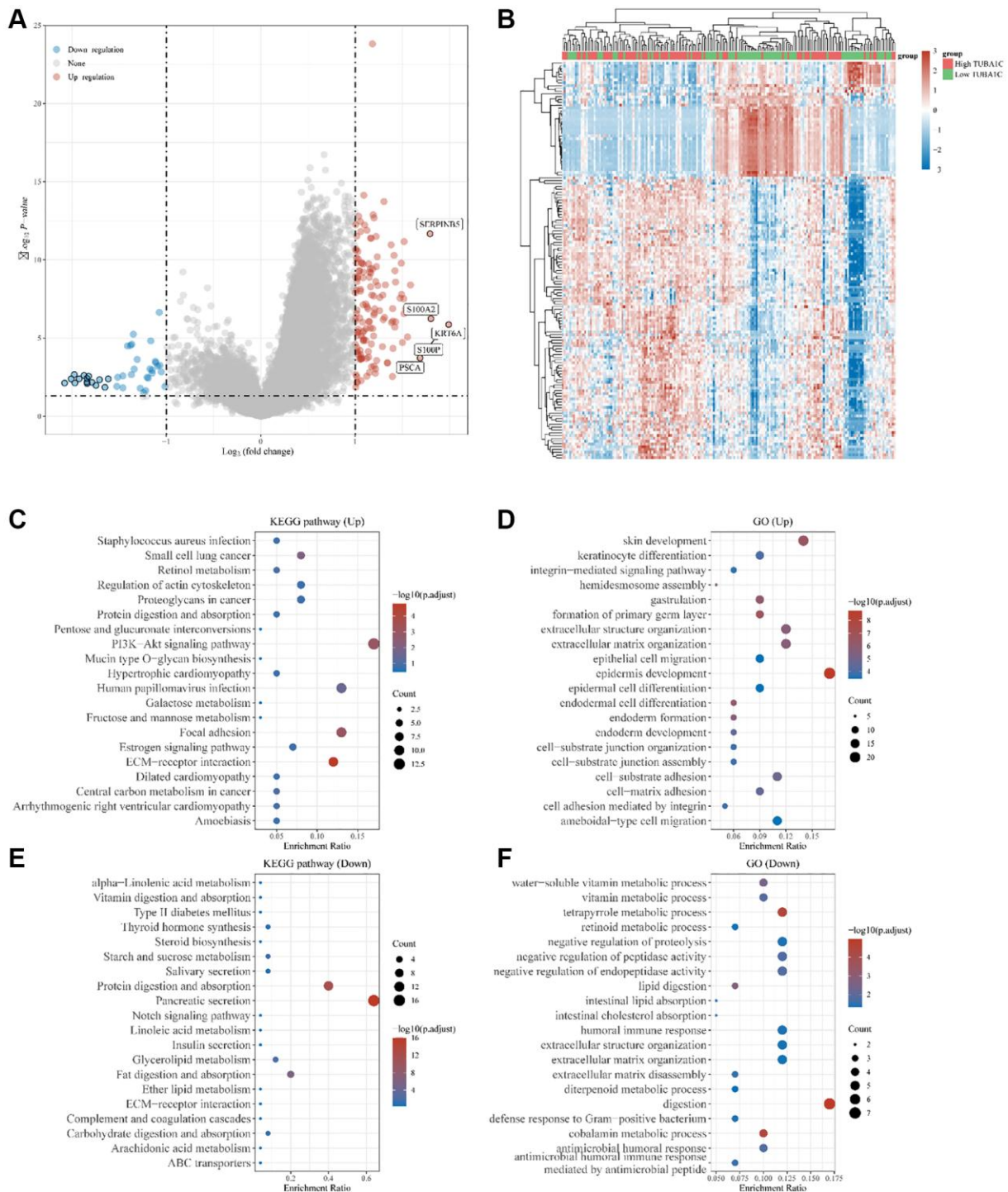
SUPPLEMENTARY FIGURES



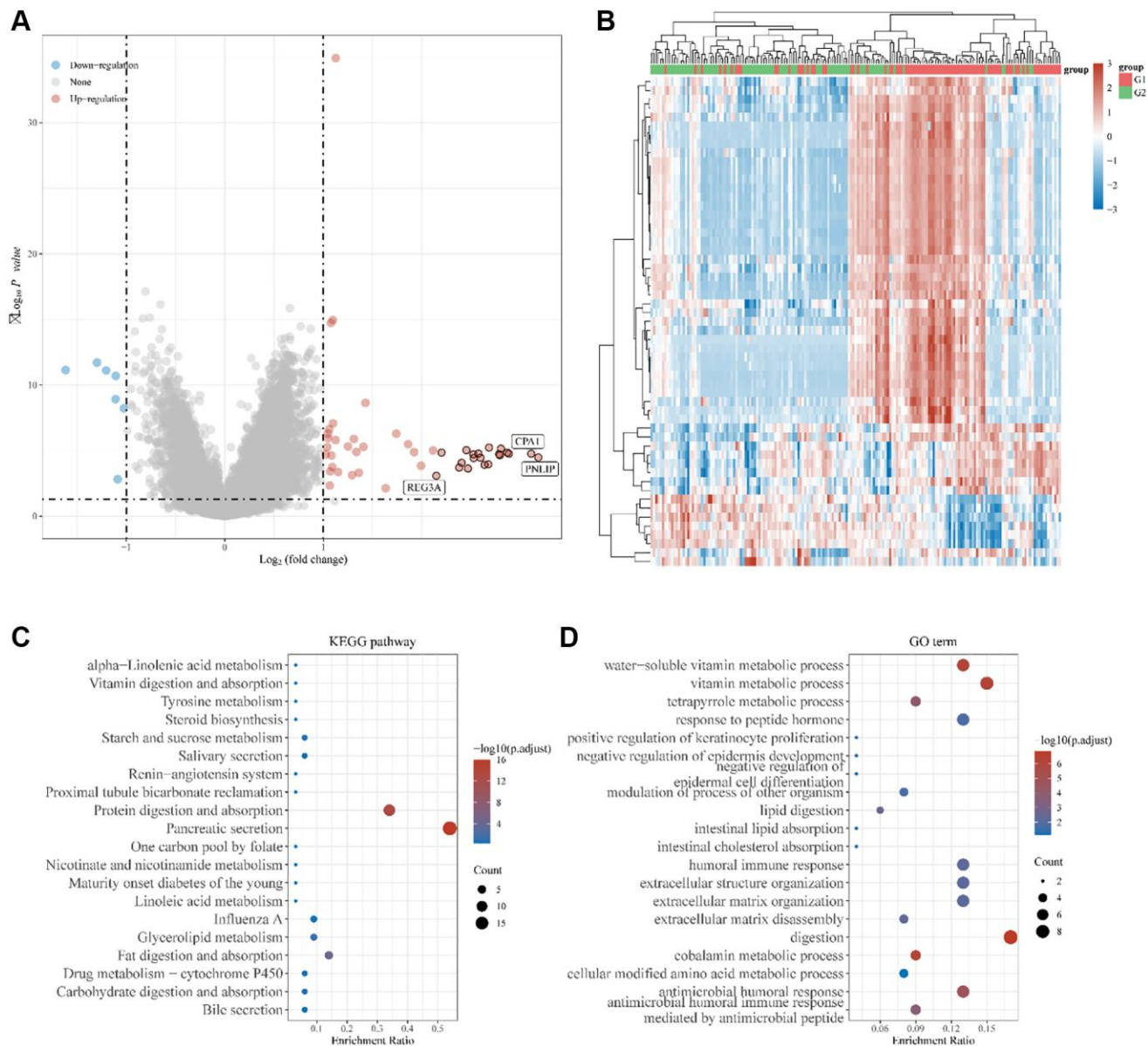
Supplementary Figure 1. Relationship between the expression of three glycosylation-related genes and the prognosis of PC patients. Survival analyses using the TCGA-pancreatic cancer dataset with the expression of SDC1 (A), SEL1L (B), TUBA1C (C).



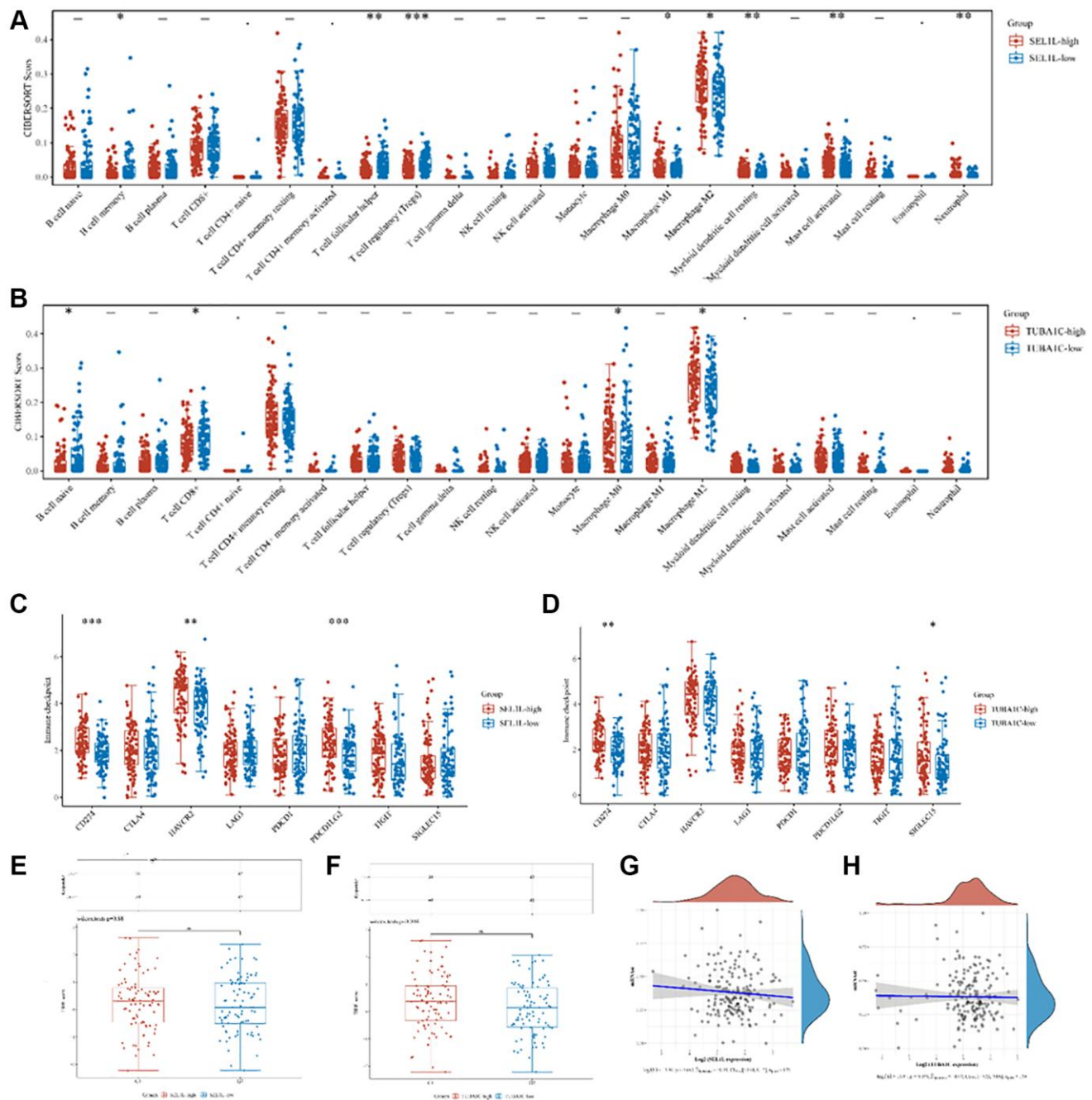
Supplementary Figure 2. Survival curves stratified by different clinical features in TCGA. Survival analyses using the glycosylation-related signature in patients with different smoking history (A), drinking history (B), radiotherapy history (C), and T staging (D).



Supplementary Figure 3. Differential expression and enrichment analysis of high and low TUBA1C expression groups. (A) Volcano plots show the differential gene expression between TUBA1C high expression and TUBA1C low expression groups using fold-change values and adjusted p -values. (B) Heatmap showing differential gene expression (only 50 genes were displayed due to a large number of genes). (C–F) KEGG and GO analyses revealed the signaling pathways associated with up-regulated and down-regulated genes in the TUBA1C high/low expressed groups; an enriched pathway is considered when $p < 0.05$ or FDR < 0.05 .



Supplementary Figure 4. Differential expression and enrichment analysis of high and low SEL1L expression groups. (A) Volcano plots show the differential gene expression between SEL1L high expression and SEL1L low expression groups using fold-change values and adjusted p -values. (B) Heatmap showing differential gene expression (only 50 genes were displayed due to a large number of genes). (C, D) KEGG and GO analyses revealed the signaling pathways associated with up-regulated and down-regulated genes in the SEL1L high/low expressed groups; An enriched pathway is considered when $p < 0.05$ or FDR < 0.05 .



Supplementary Figure 5. Comparison of immune status and stemness between groups that express high and low levels of SEL1L/TUBA1C. (A) An analysis of immune infiltration obtained using the CIBERSORT algorithm for the high/low expression group of SEL1L. (B) Comparison of immune-checkpoint gene expression in the high/low expression group of SEL1L. (C) Table showing immune response statistics and immune response scores for the high/low expression group of SEL1L. (D) Stemness for the high/low expression group of SEL1L. (E) An analysis of immune infiltration obtained using the CIBERSORT algorithm for the high/low expression group of TUBA1C. (F) Comparison of immune-checkpoint gene expression in the high/low expression group of TUBA1C. (G) Table showing immune response statistics and immune response scores for the high/low expression group of TUBA1C. (H) Stemness for the high/low expression group of TUBA1C. (A and E) The horizontal axis represents immune cells, while the vertical axis displays immune scores ($*p < 0.05$, $**p < 0.01$, $***p < 0.001$).