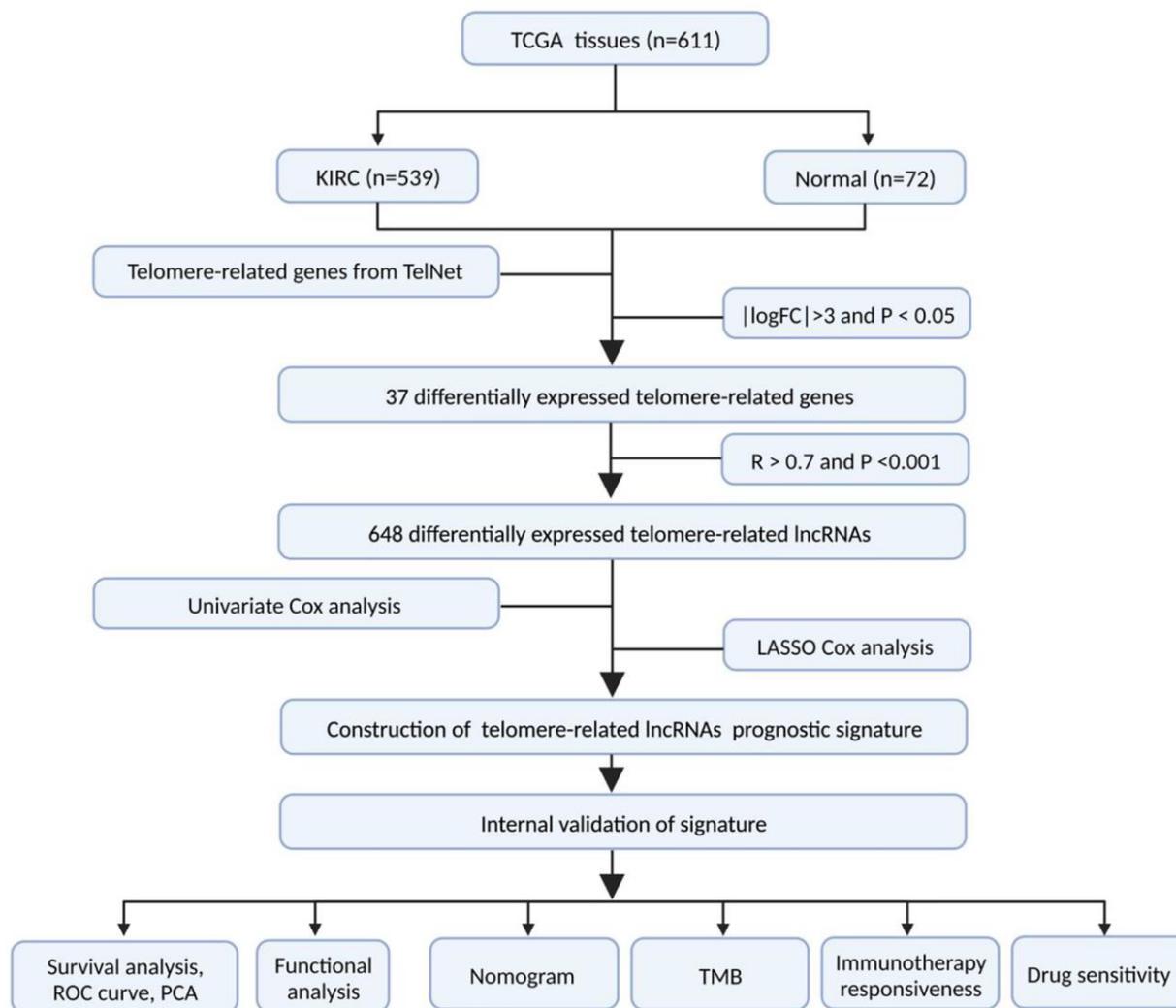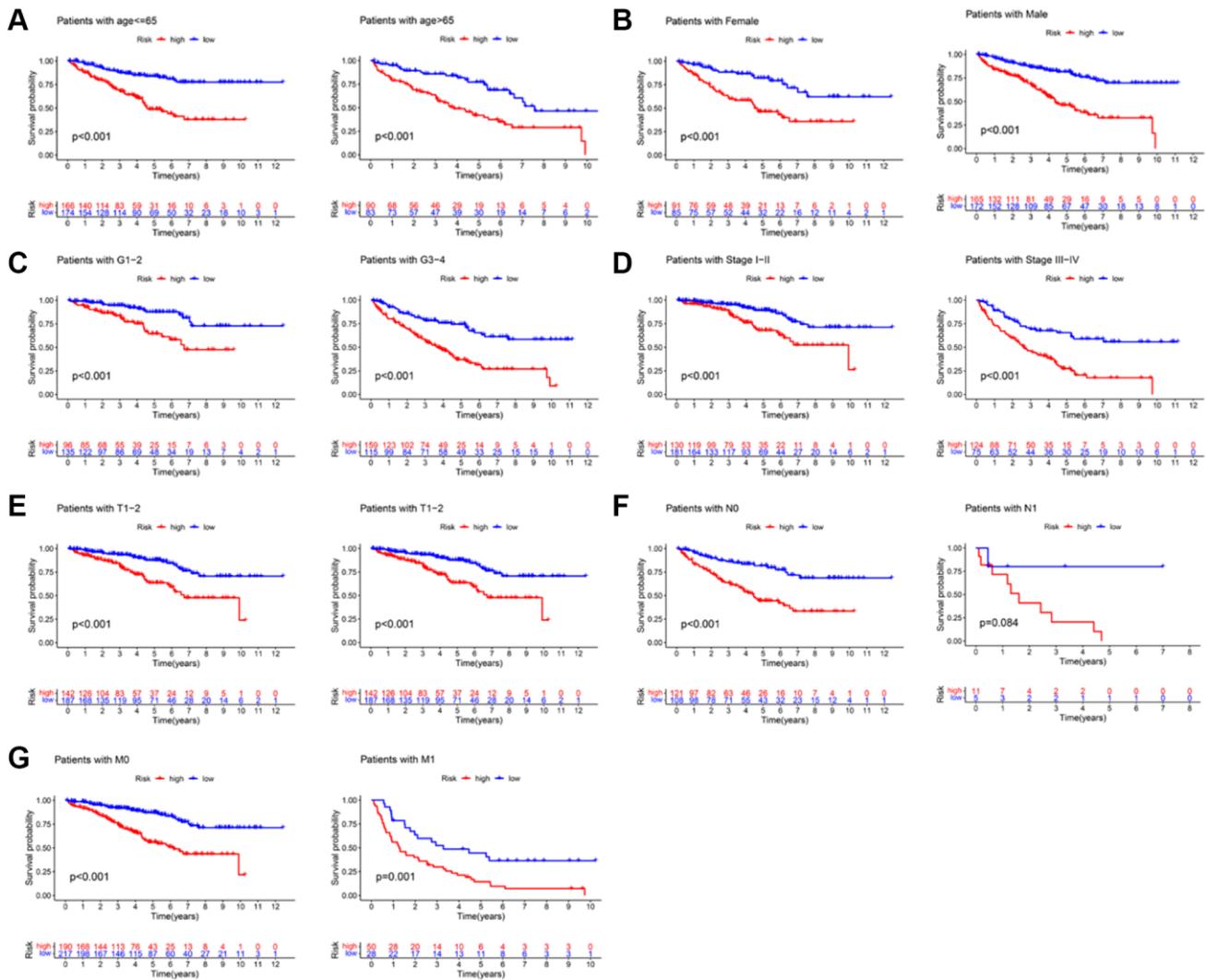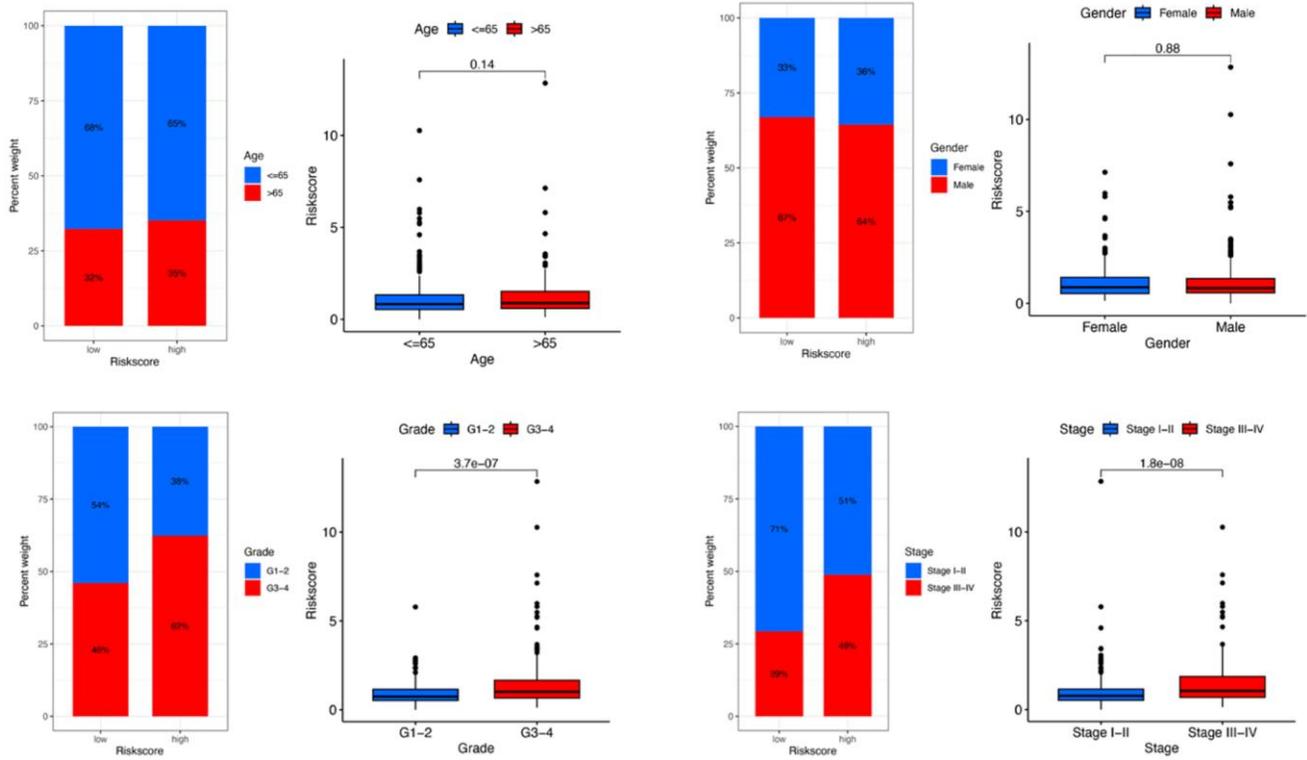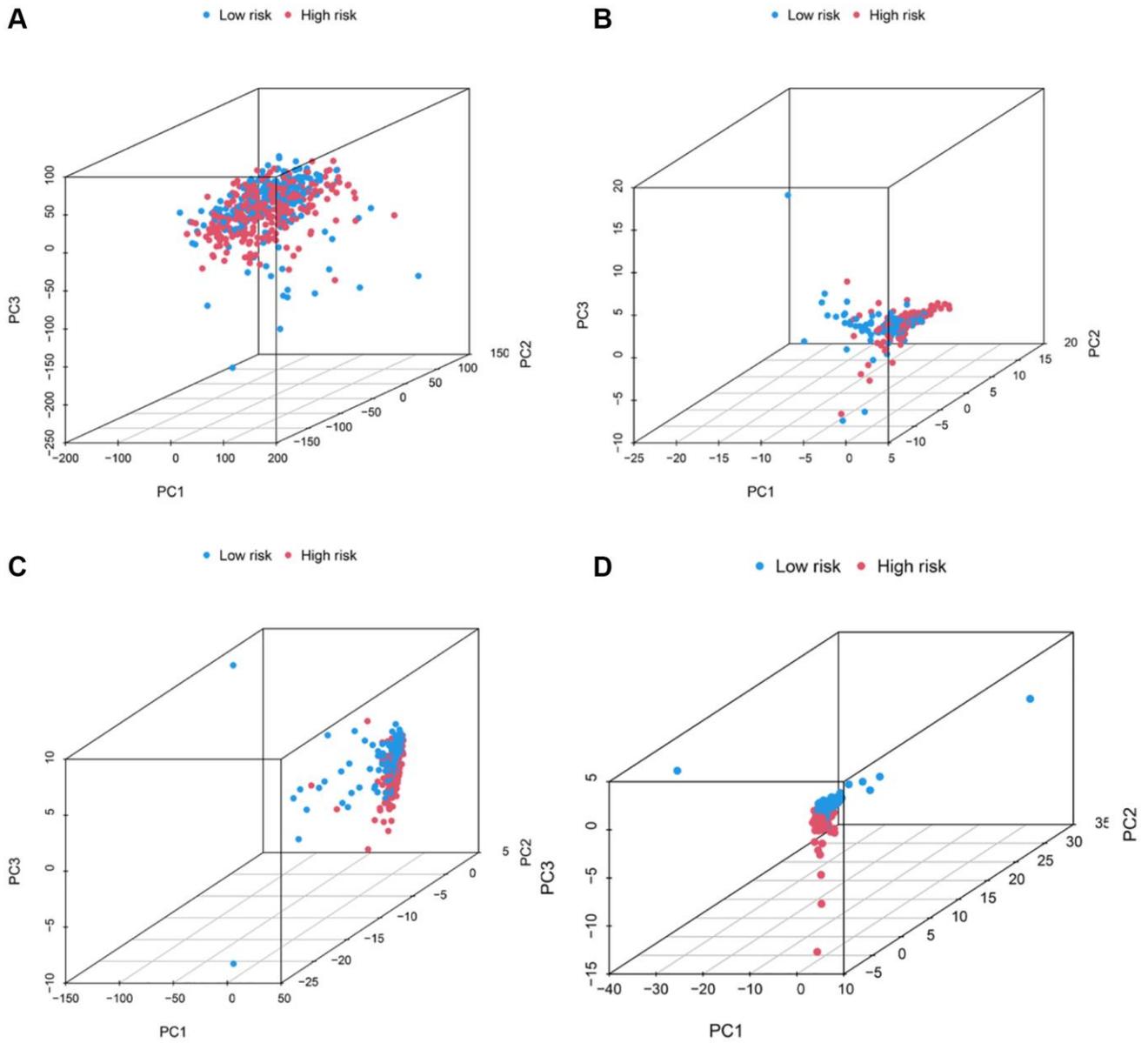# SUPPLEMENTARY FIGURES

**Supplementary Figure 1. The flowchart of our research.**

Supplementary Figure 2. Stratified survival analysis based on TRLs prognostic signature. The OS rates of different risk groups with different clinical features; including age (**A**); gender (**B**); grade (**C**); AJCC stage (**D**); T stage (**E**); N stage (**F**); and M stage (**G**).

Supplementary Figure 3. The distribution of the risk scores in terms of age, gender, grade, and stage.

Supplementary Figure 4. Principal components analysis between low- and high-risk groups with different data sets. (**A**) The whole genome data. (**B**) The differentially expressed telomere-related genes. (**C**) TRLs. (**D**) The signature-based TRLs.
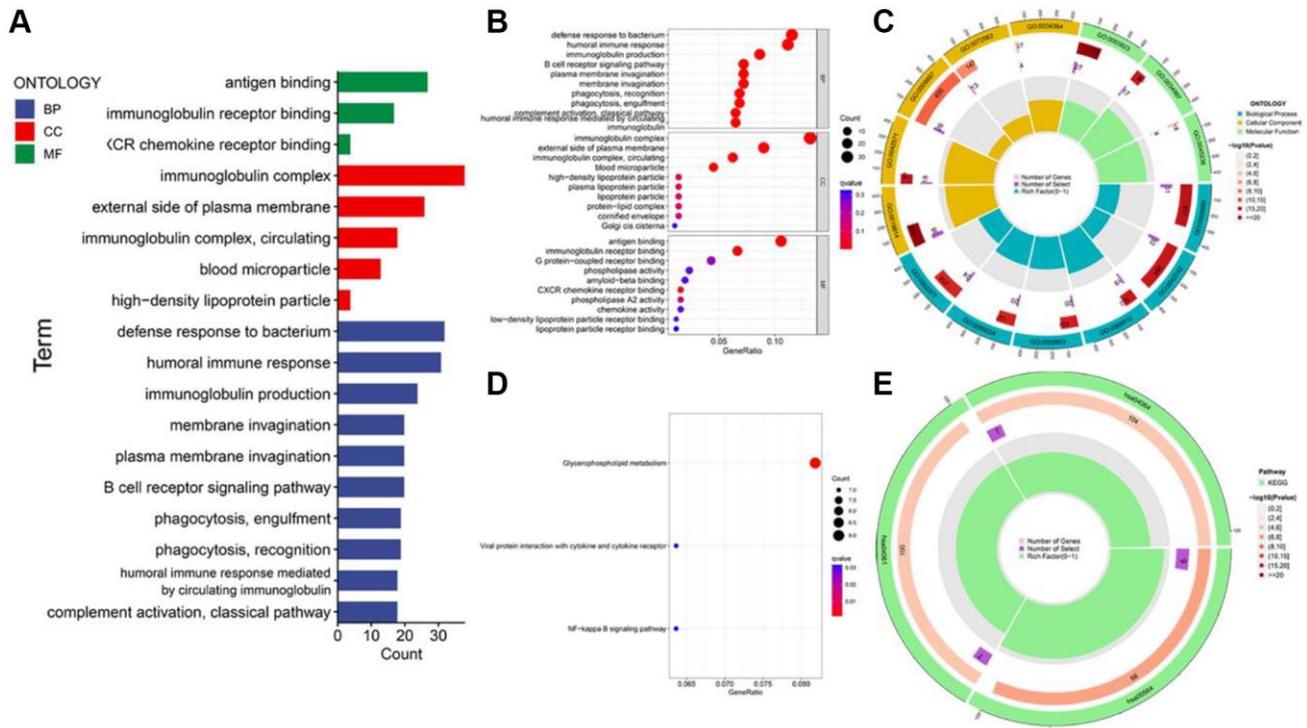
Supplementary Figure 5. Functional enrichment analysis of 548 genes with differential expression between low- and high-risk groups. (**A**–**C**) GO enrichment analysis. (**D**, **E**) KEGG enrichment analysis.