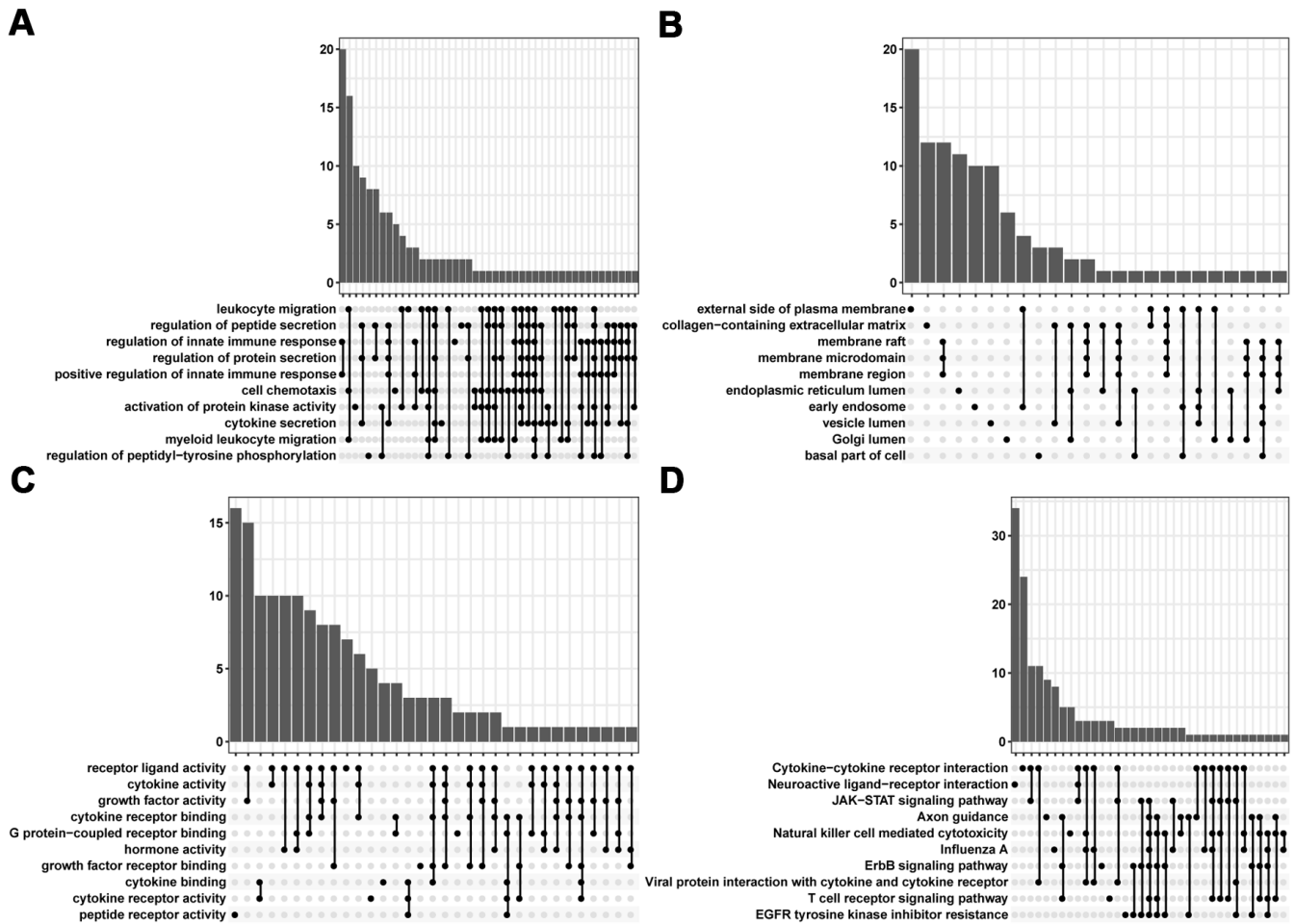
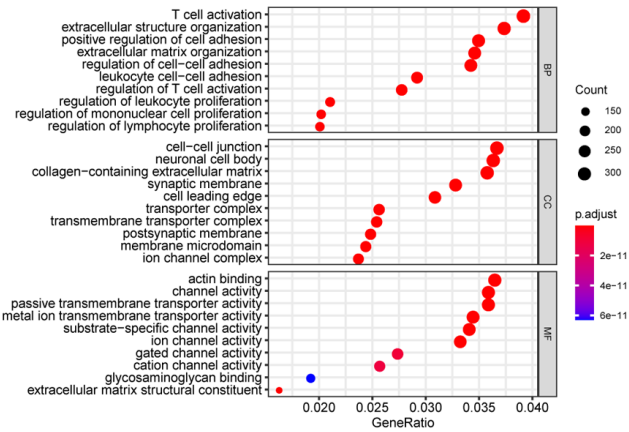
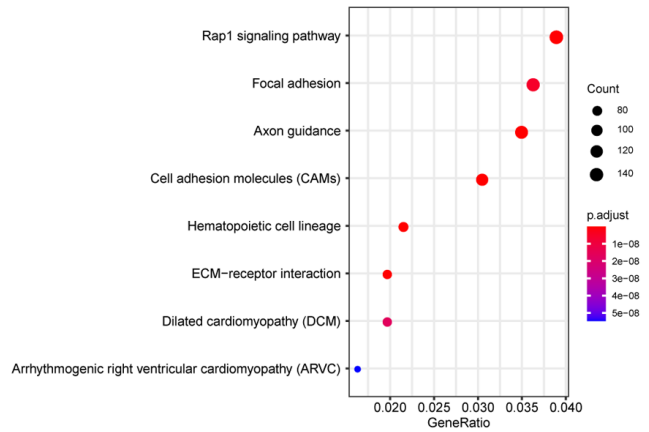


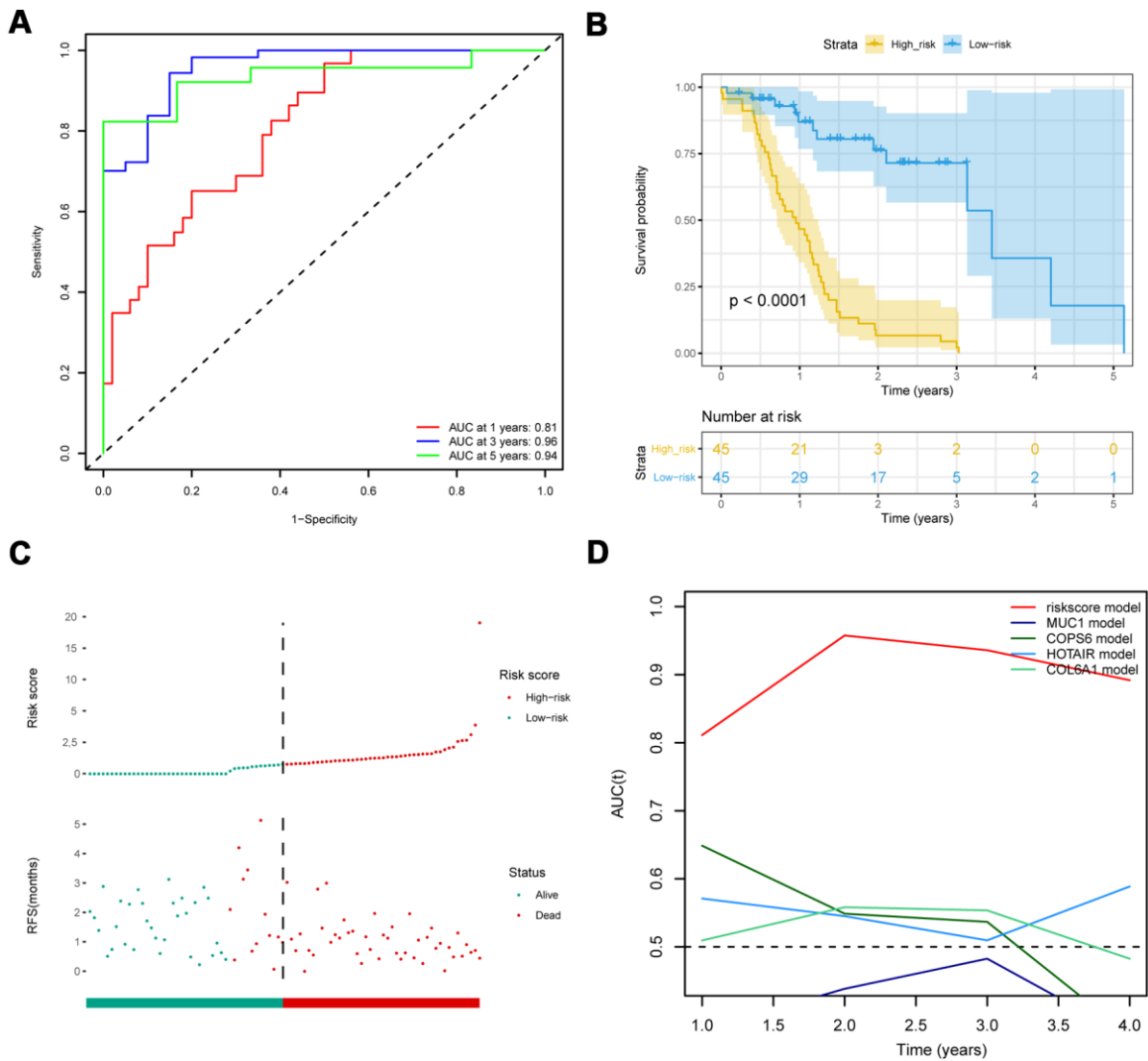
SUPPLEMENTARY FIGURES



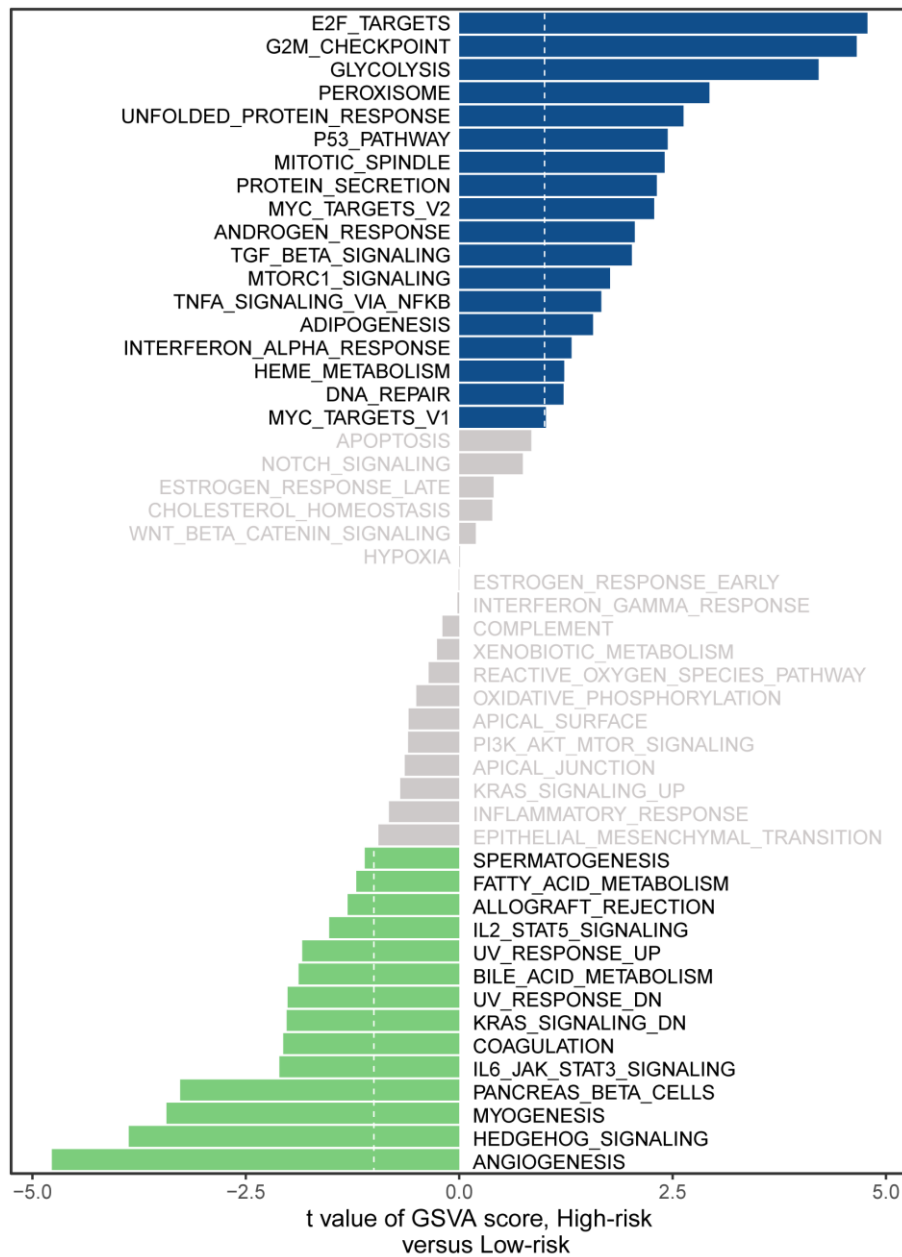
Supplementary Figure 1. Gene ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) enrichment analyses for prognostic IRGs. Biological process (BP) (A); Cellular component (CC) (B); Molecular function (MF) (C); KEGG signaling pathways (D).

A**B**

Supplementary Figure 2. Gene ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) enrichment analyses for IncRNA-targeted genes. (A) GO analysis including Biological process (BP), Cellular component (CC), and Molecular function (MF). (B) KEGG analysis including the main pathways. The X-axis indicates the gene ratio between the number of enriched genes and the total number of genes in GO terms, the Y-axis represents GO terms. The color represents the adjusted *P* value, and the point size denotes the number of genes.



Supplementary Figure 3. Comparison with other prognosis biomarkers and validation of the eight-IRlncRNA signature in the validation cohort (PACA-AU). (A) ROC curve of eight-IRlncRNA signature for 1, 3, 5- year survival. (B) Kaplan-Meier curves for the high- and low-risk groups. (C) Risk score distribution and the survival status for patients. (D) Time-dependent ROC curve of the eight-IRlncRNA signature compared with other prognosis biomarkers.



Supplementary Figure 4. Gene set variation analysis (GSVA) of high- and low-risk groups revealed significant difference in enrichment of h.all.v7.0.symbols.gmt.