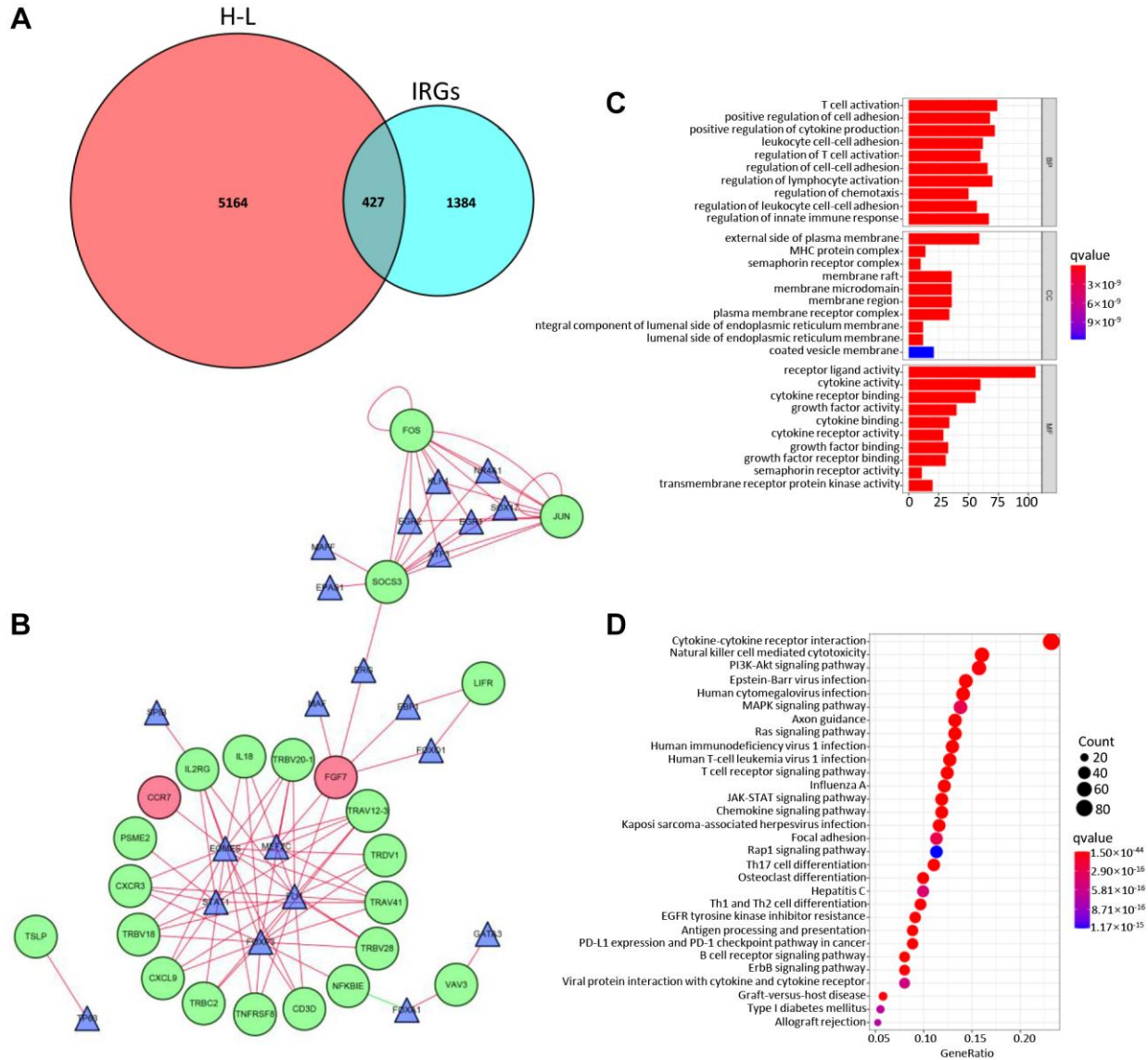
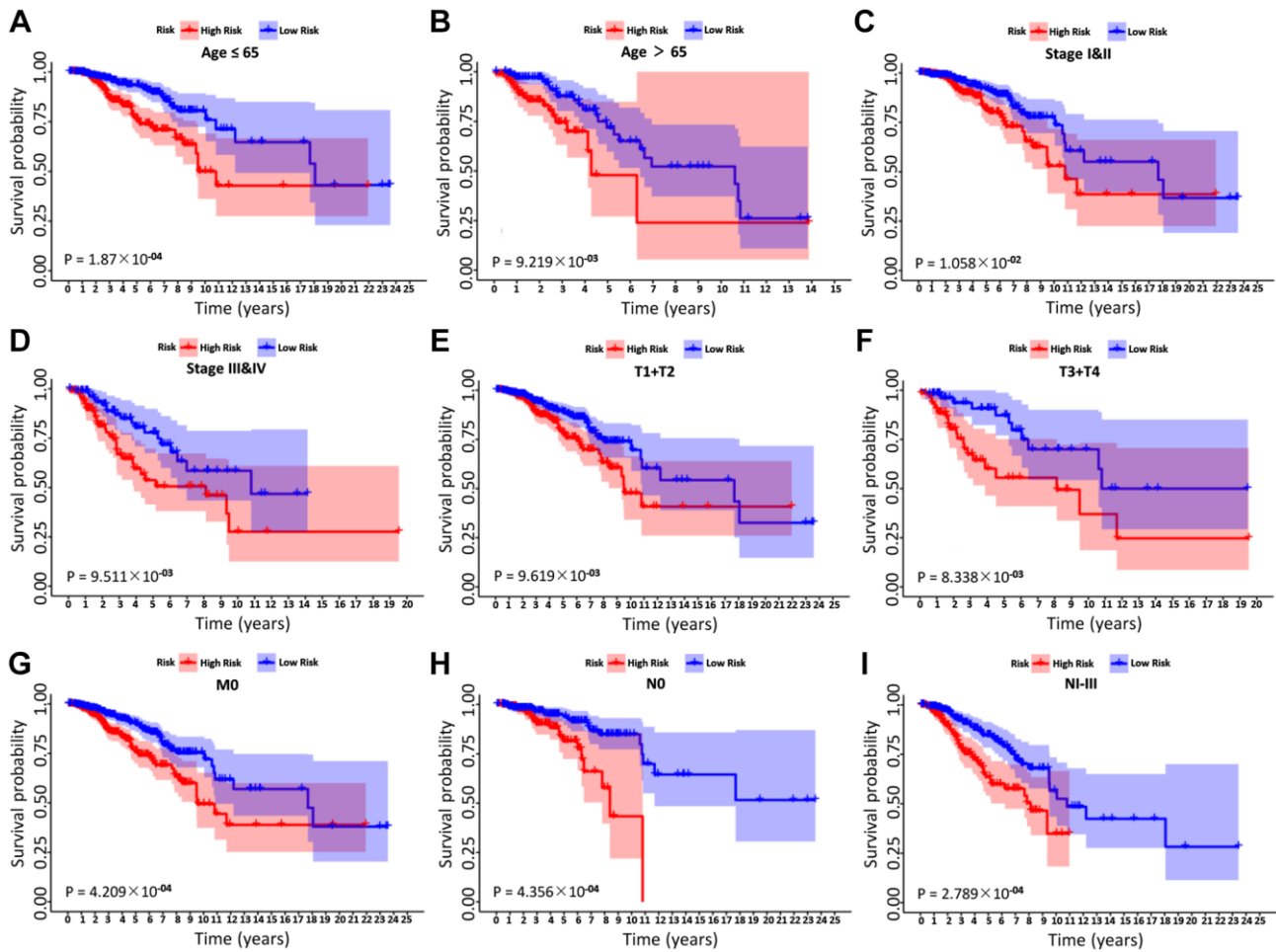


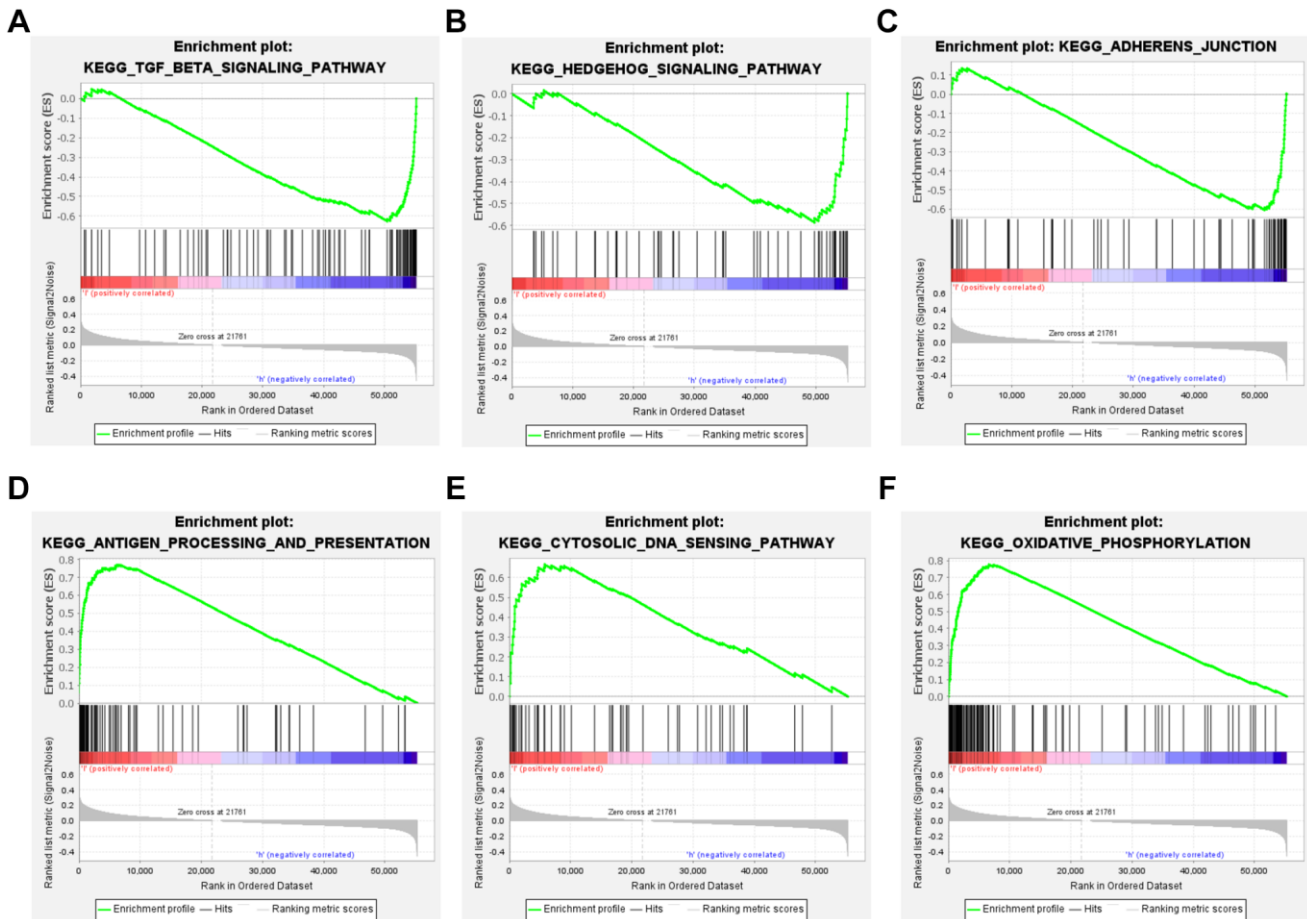
SUPPLEMENTARY FIGURES



Supplementary Figure 1. The 427 immune-related differential genes in high- and low-risk groups were shown in Venn diagram (A). The regulatory network of transcription factors (TFs) and (IRGs). Regulatory networks based on survival-related TFs and IRGs in breast cancer. Pink circles indicated high-risk genes, green circles indicate low-risk genes, and purple triangles indicated transcription factors in the regulatory network (B). GO functional annotation (C) and KEGG (D) enrichment analysis were performed for the IRGs.



Supplementary Figure 2. The OS differences under different classification between the high-risk group and the low-risk group. Age (A, B), stage (C, D), T stage (E, F), distant metastasis (G) and lymph node metastasis (H, I).



Supplementary Figure 3. KEGG pathway analysis from gene set enrichment analysis (GSEA). GSEA results showing (A), Hedgehog signaling pathway (B), Adherens junction enriched in the low-risk group (C), while Antigen processing and presentation (D), Cytosolic DNA sensing pathway (E), Oxidative phosphorylation were enriched in the high-risk group (F).