

Figure S1 ROC curve expression in 19 tumors. ROC curves are presented for 19 cancer types where sufficient data remained after excluding missing values, while other cancers lacked sufficient outcome diversity for ROC analysis.



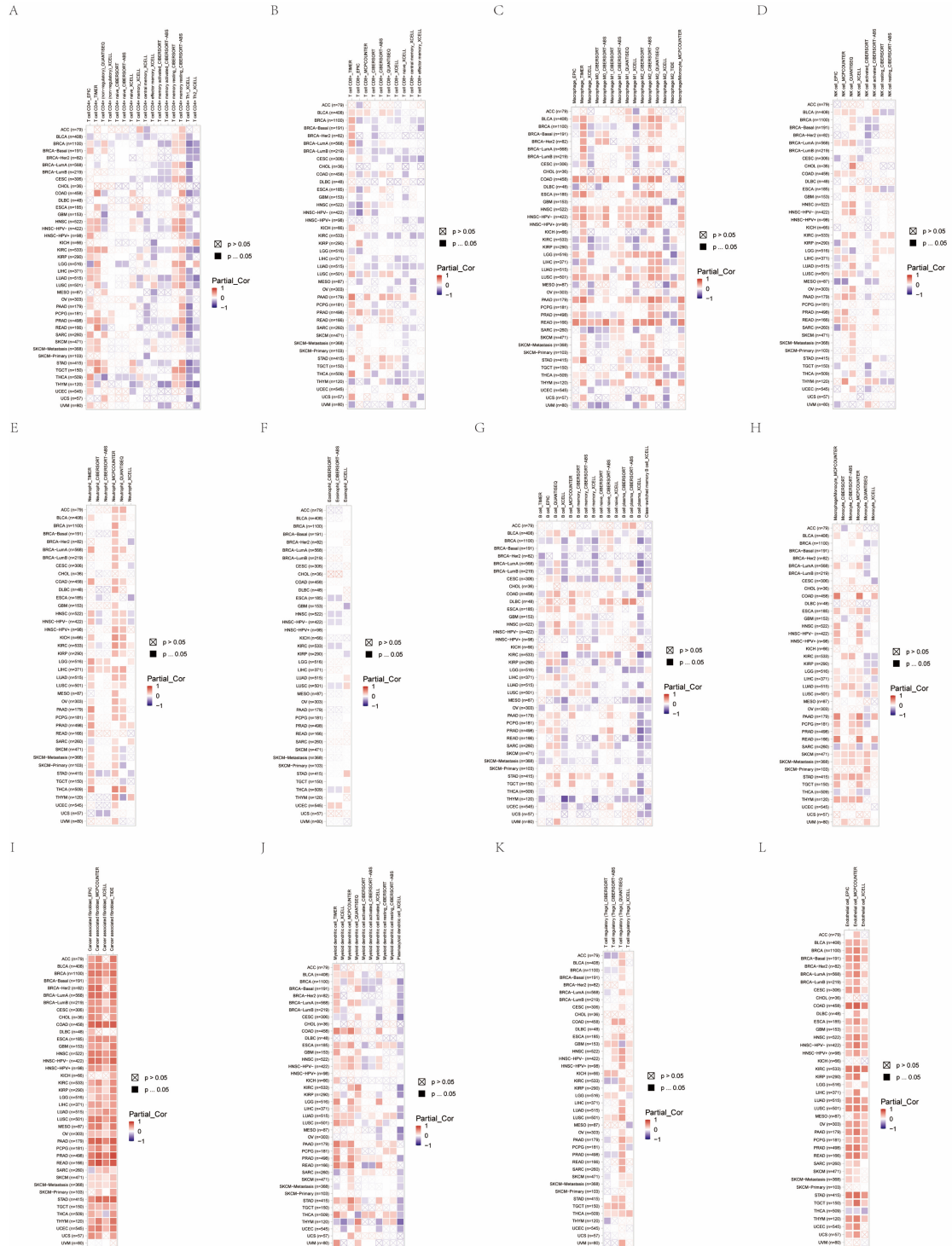


Figure S2 Correlation Between KANK2 Expression and Immune Cell Infiltration in 33 Cancer Types. Correlation analysis between KANK2 expression and various immune cells (e.g., CD4+ T cells, CD8+ T cells, macrophages, NK cells, neutrophils, Eosinophil, B cells, monocytes, cancer-associated fibroblasts, myeloid dendritic cell, Tregs, and endothelial cells) in 33 cancers, based on TIMER2.0 database results.

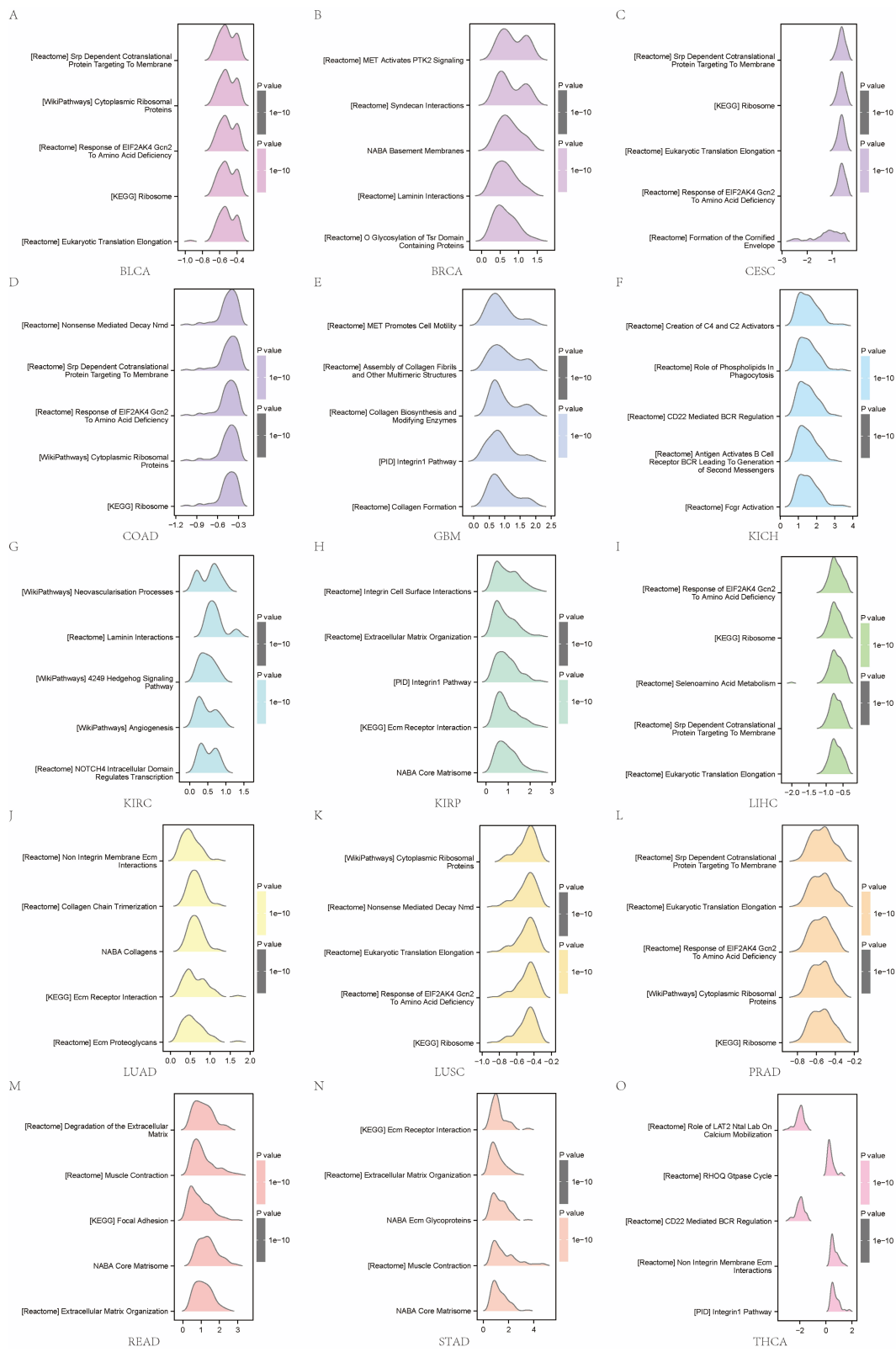


Figure S3. GSEA functional enrichment analysis of KANK2 expression in 15 cancers. A-O shows the top 5 GSEA functional enrichment pathways of KANK2 in BLCA, BRCA, CESC, COAD, GBM, KICH, KIRC, KIRP, LIHC, LUAD, LUSC, PRAD, READ, STAD, THCA. The Y-axis represents one gene set and the X-axis is the distribution of logFC corresponding to the core molecules in each gene set.

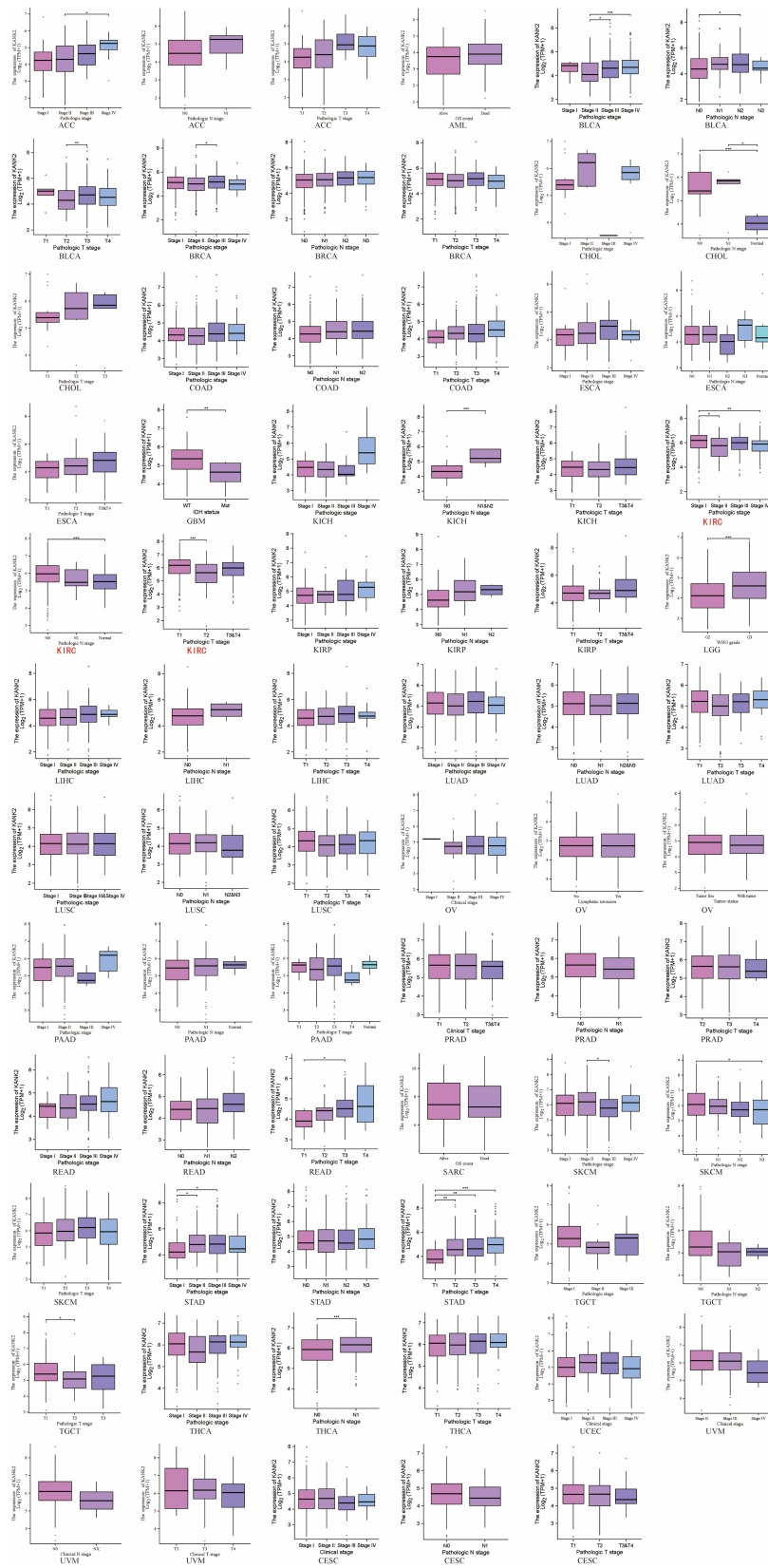


Figure S4. The correlation between KANK2 expression and the pathological stage, T stage, and N stage of 33 tumor types. Kidney Renal Clear Cell Carcinoma (KIRC) demonstrated the strongest association with diagnostic ROC, prognostic KM curves, and staging parameters.