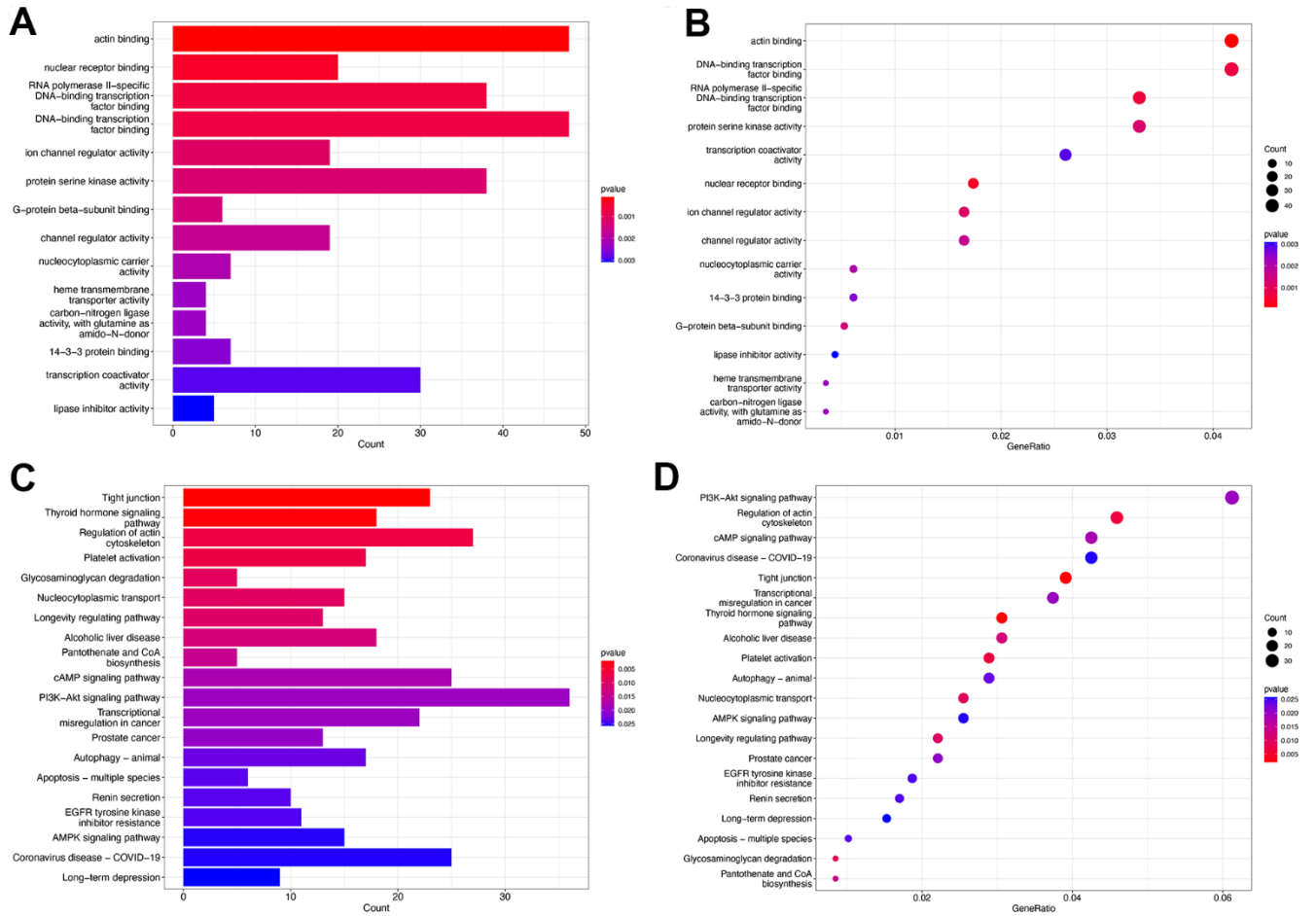
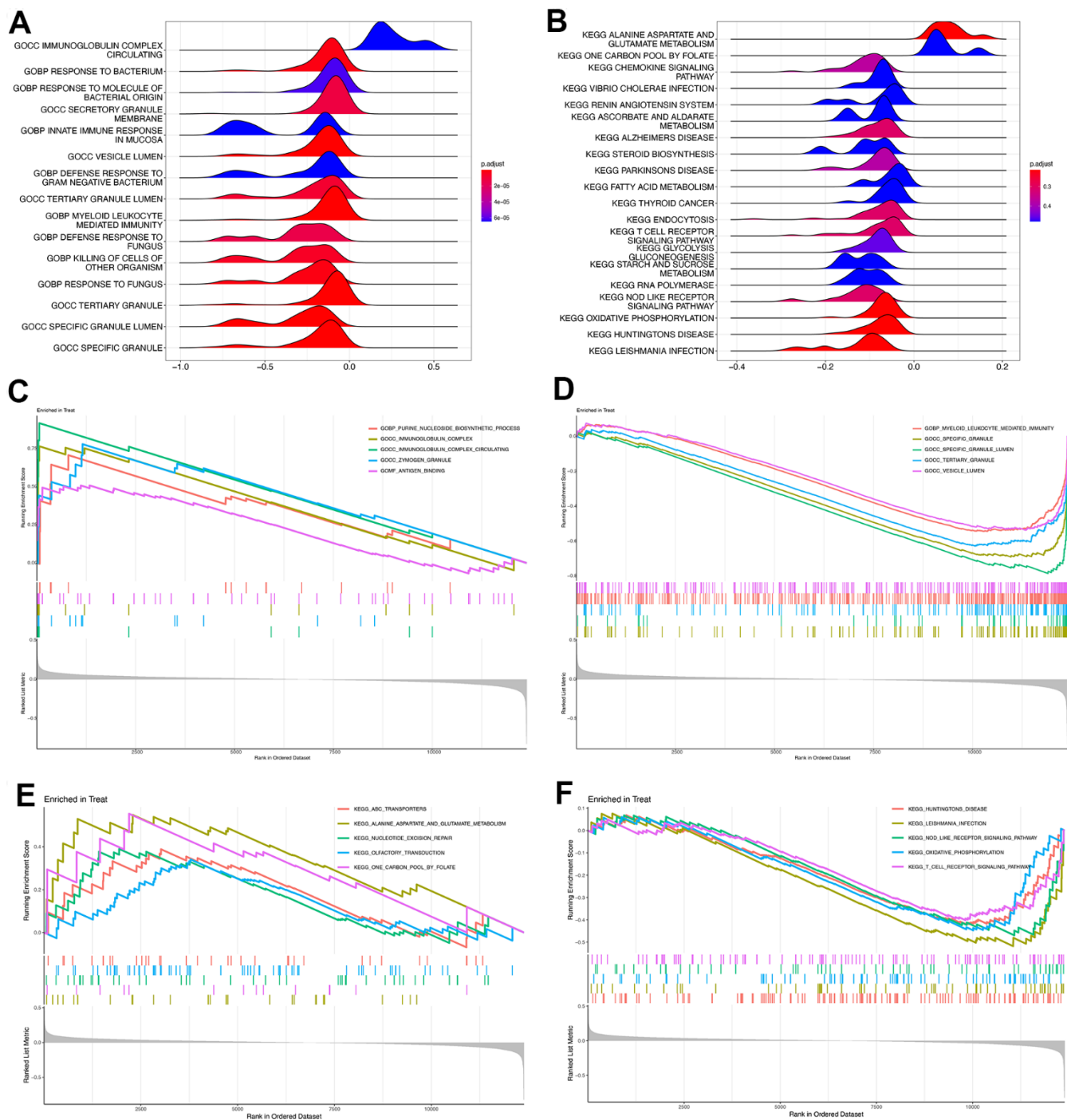


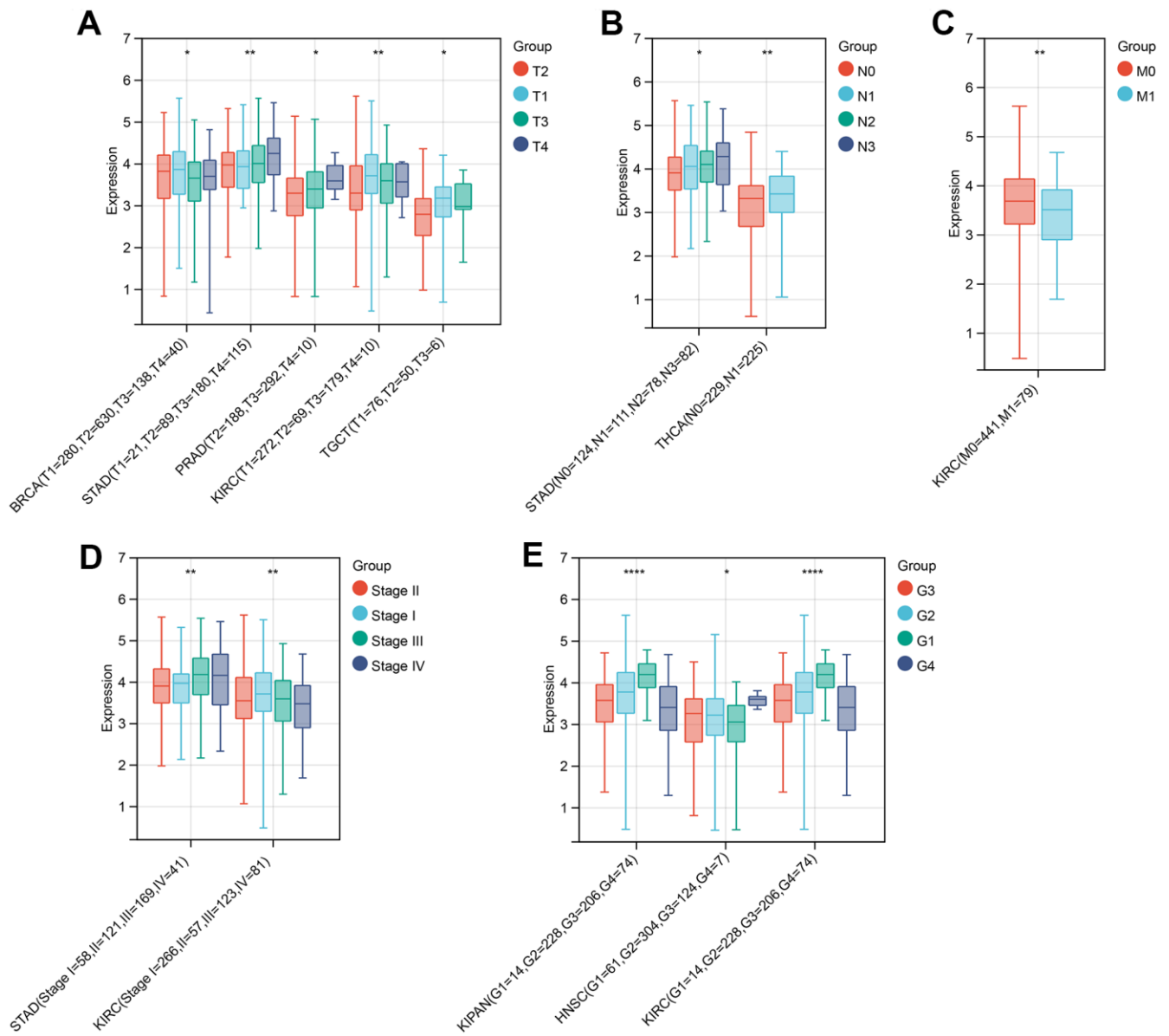
SUPPLEMENTARY FIGURES



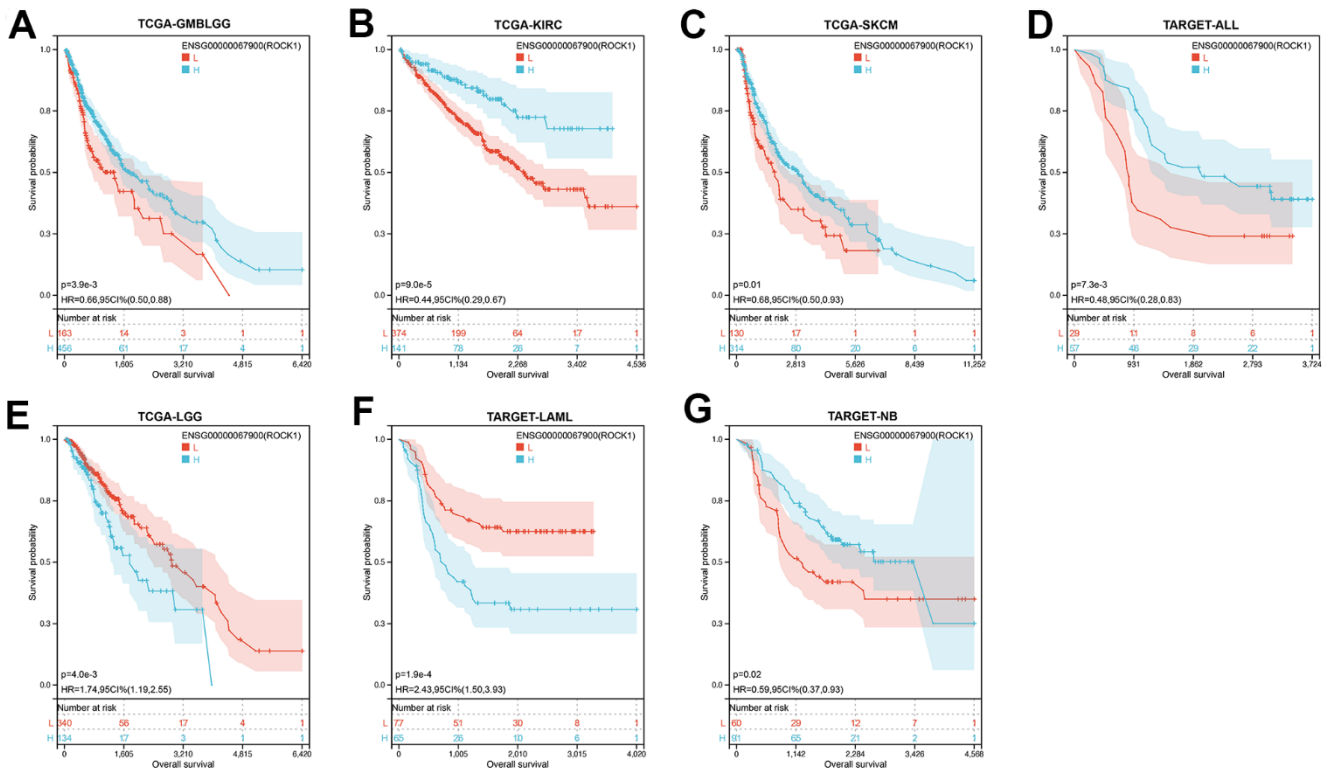
Supplementary Figure 1. Bar plot (A) and dot plot (B) showed the results of GO enrichment analysis of DEGs. Bar plot (C) and dot plot (D) showed the results of KEGG enrichment analysis of DEGs.



**Supplementary Figure 2.** Ridge map showed the GO (A) and KEGG (B) enrichment analysis results by GSEA. GSEA plot with 112 ranked common genes and the top 5 up-regulated GO terms (C) or KEGG terms (D). GSEA plot with 112 ranked common genes and the top 5 down-regulated GO terms (E) or KEGG terms (F).

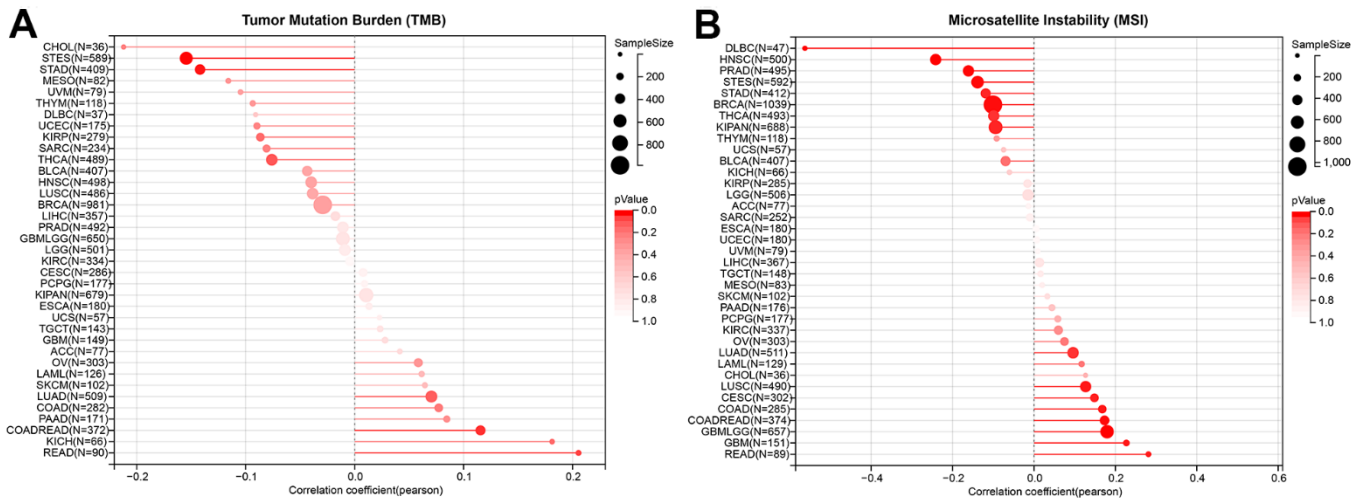


**Supplementary Figure 3.** Significantly different Pan-cancer expression levels of ROCK1 in T-stage (A), N-stage (B), M-stage (C), Stage (D), and Grade (E). \* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ , \*\*\*\* $p < 0.0001$ .



**Supplementary Figure 4. Analysis of the overall survival in multiple tumors with the best cut-off method.** The expression levels of ROCK1 are positively correlated with OS in TCGA-GMBLGG (A), TCGA-KIRC (B), TCGA-SKCM (C), and TARGET-ALL (D). The expression levels of ROCK1 are negatively correlated with OS in TCGA-LGG (E), TCGA-LAML (F), and TARGET-NB (G).





**Supplementary Figure 6.** (A) Correlation between the expression levels of ROCK1 and TMB pan-cancer. (B) Correlation between the expression levels of ROCK1 and MSI pan-cancer.