**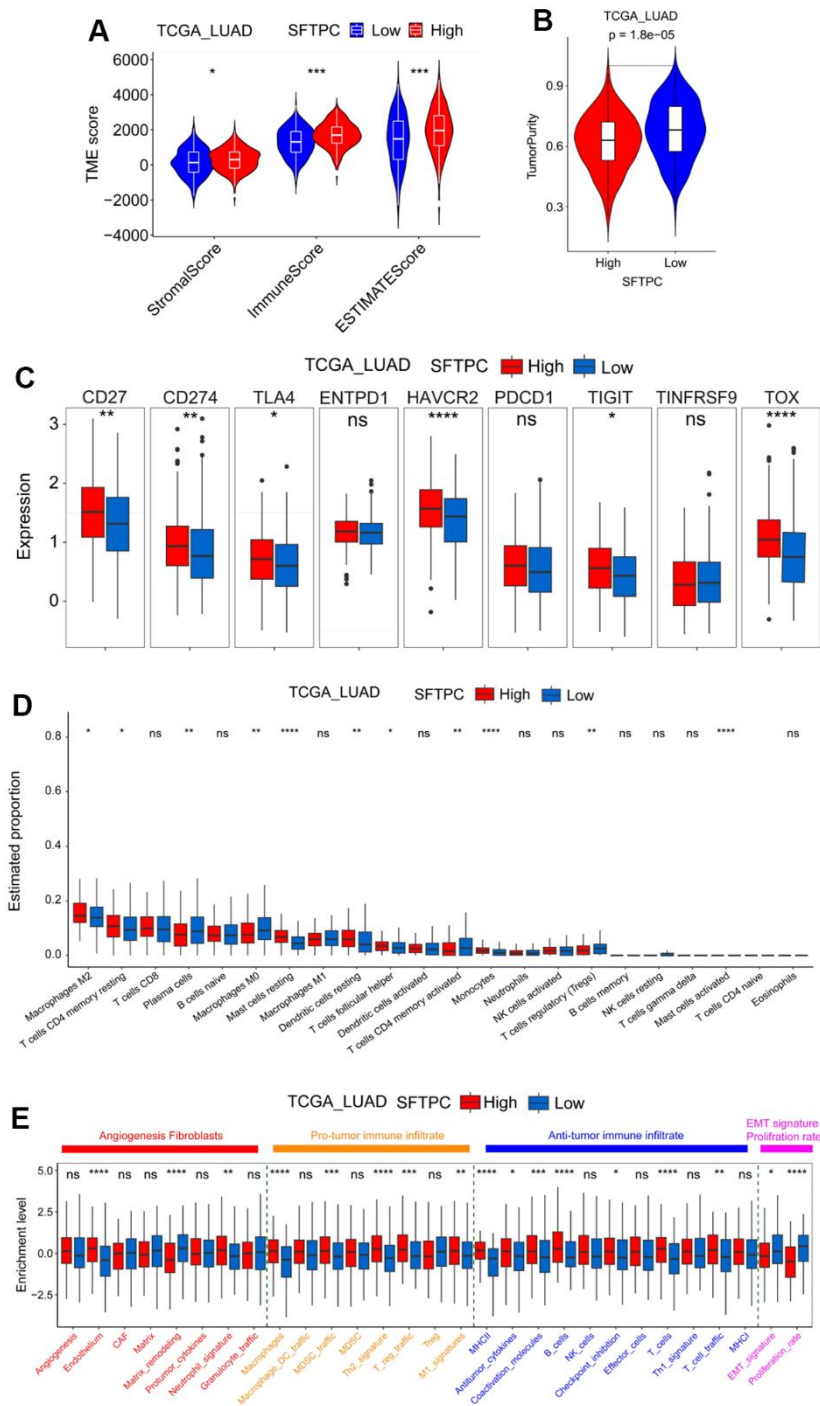Supplementary Figure 1. Tumor microenvironment landscape of SFTPC-based classification.** (**A**) The immune and stromal scores based on SFTPC classification in the TCGA_LUAD cohort. (**B**) The tumor purity based on SFTPC classification in the TCGA_LUAD cohort. (**C**) Expression of immune checkpoint genes based on SFTPC classification in the TCGA_LUAD cohort. (**D**) Distribution of infiltrating immune cells based on SFTPC classification in the TCGA_LUAD cohort. (**E**) Heatmap showed the 29 Fges based on SFTPC classification in the TCGA_LUAD cohort.
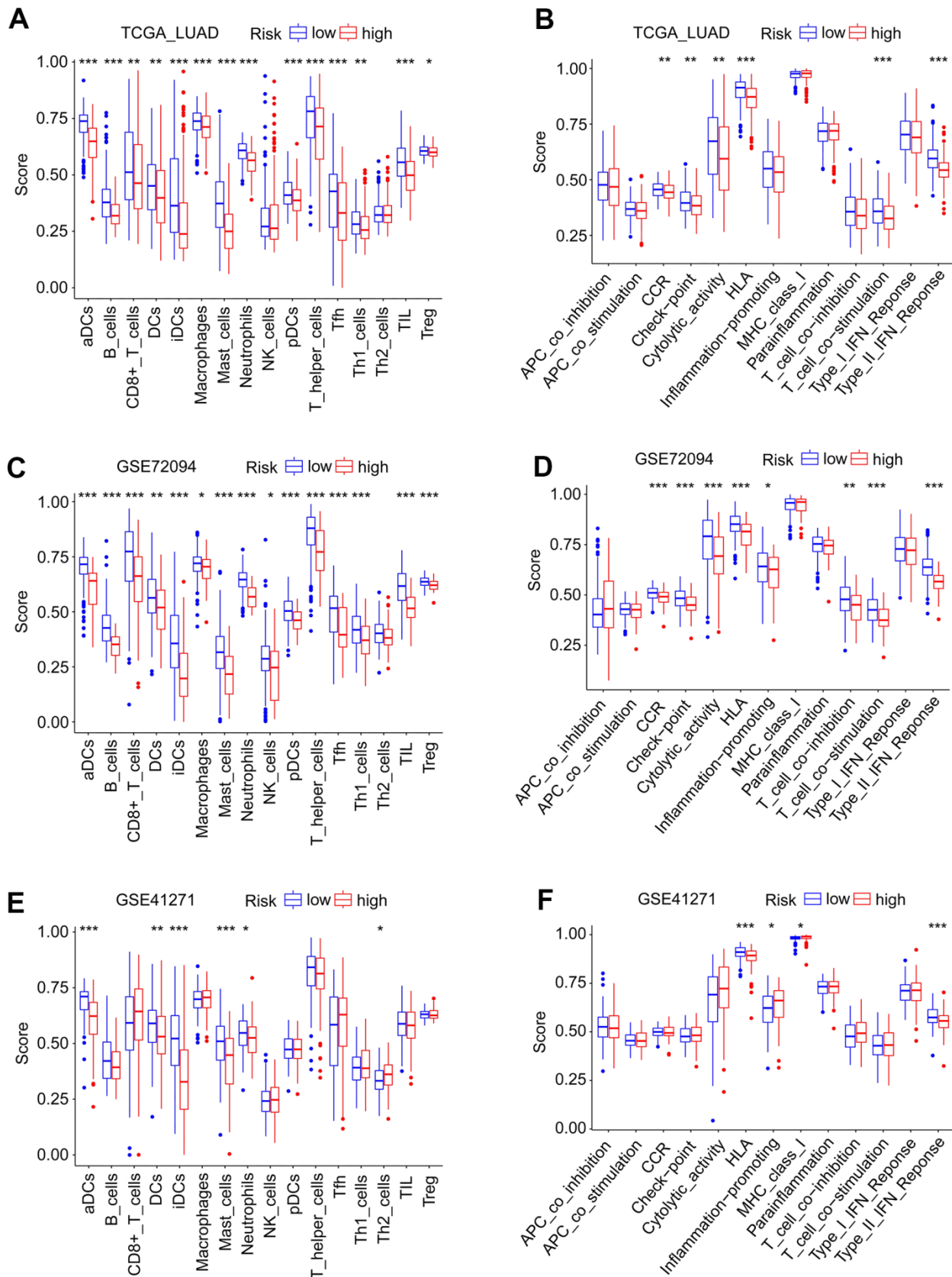
**Supplementary Figure 2. Boxplot of immune cell score and immune function score based on PRRS.** (**A**–**E**) Boxplot of immune cell score and immune function score based on risk score classification in TCGA_LUAD (**A**, **B**), GSE72094 (**C**, **D**), and GSE41271 (**E**, **F**) cohorts.
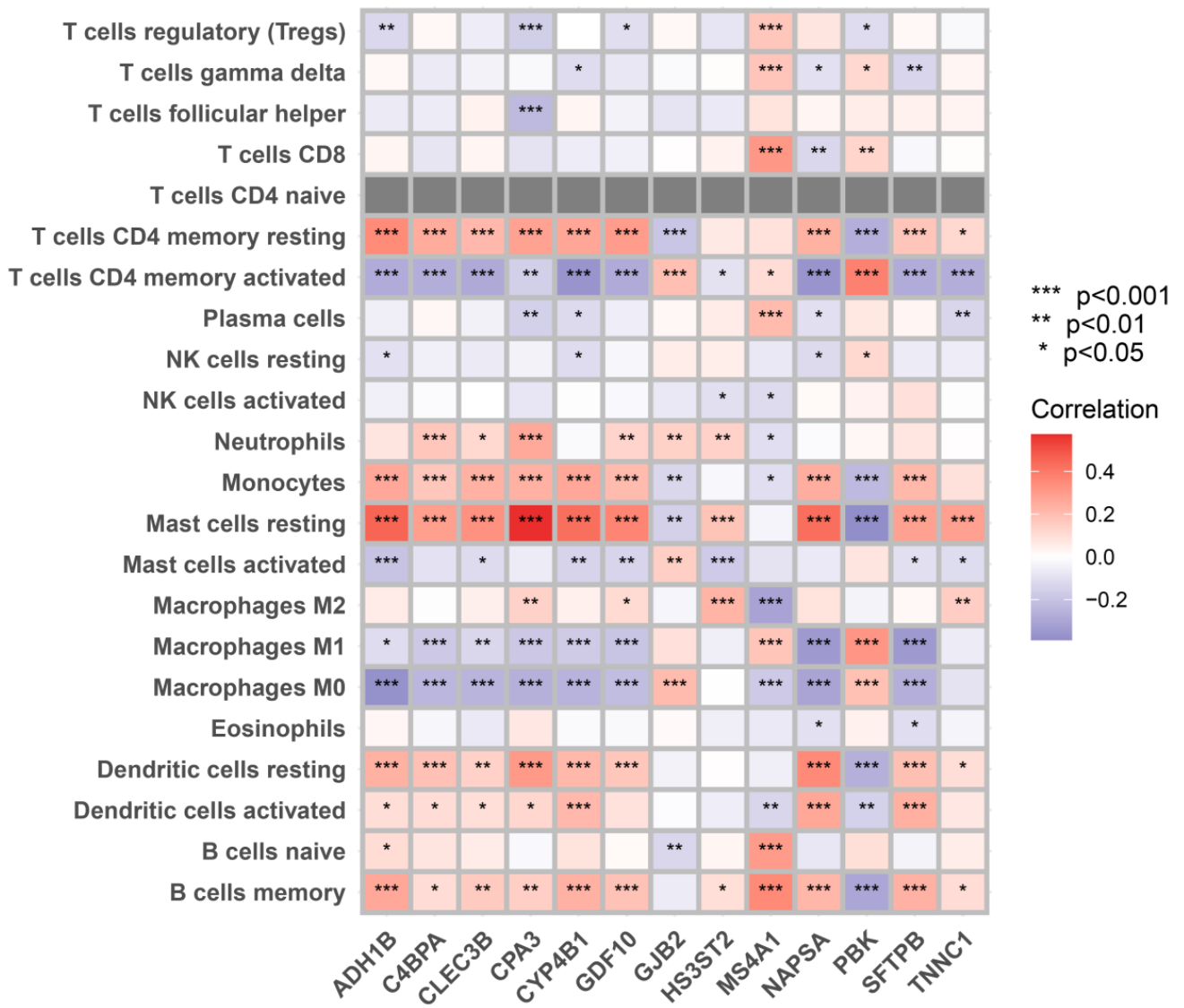
Supplementary Figure 3. Heatmap of correlation between immune cells and the 13 crucial genes.
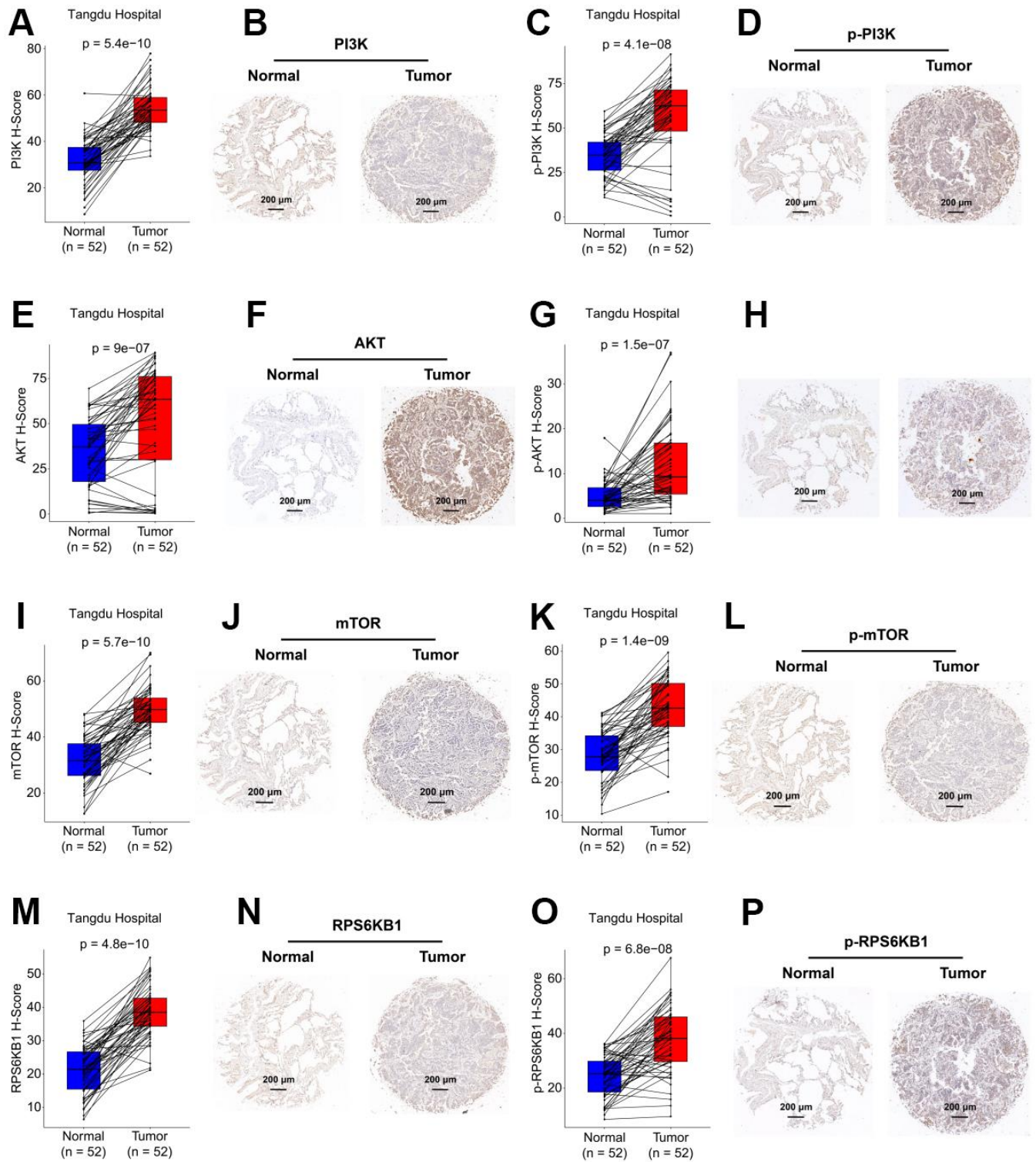
**Supplementary Figure 4. Immunohistochemical detection of target gene in Tangdu Hospital cohort.** (**A**–**P**) Protein levels of target genes in patients in Tangdu Hospital cohort, and representative IHC staining of indicated proteins in carcinoma and para-carcinoma tissues: PI3K (**A**, **B**), p-PI3K (**C**, **D**), AKT (**E**, **F**), p-AKT (**G**, **H**), mTOR (**I**, **J**), p-mTOR (**K**, **L**), RPS6KB1 (**M**, **N**), and p-RPS6KB1 (**O**, **P**).