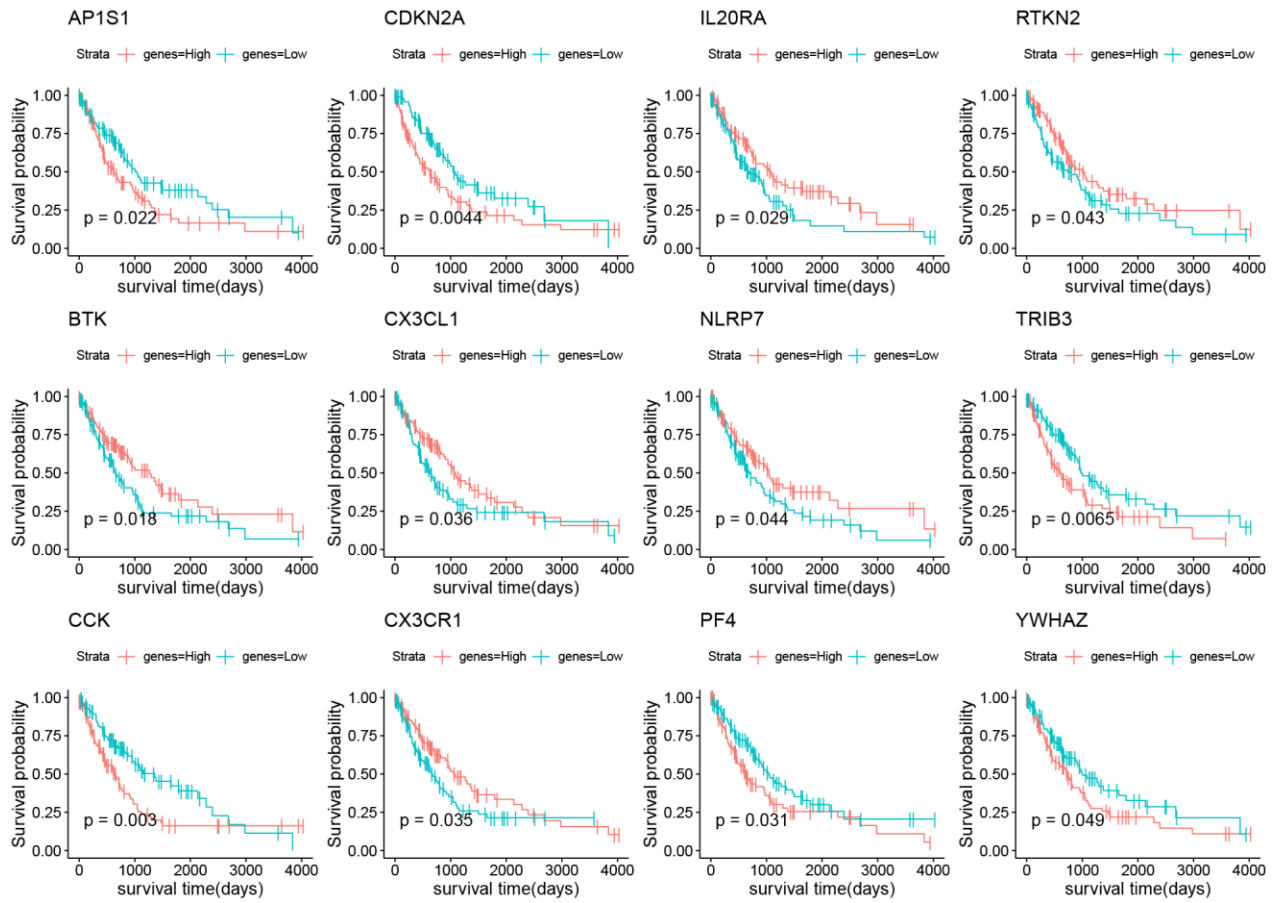
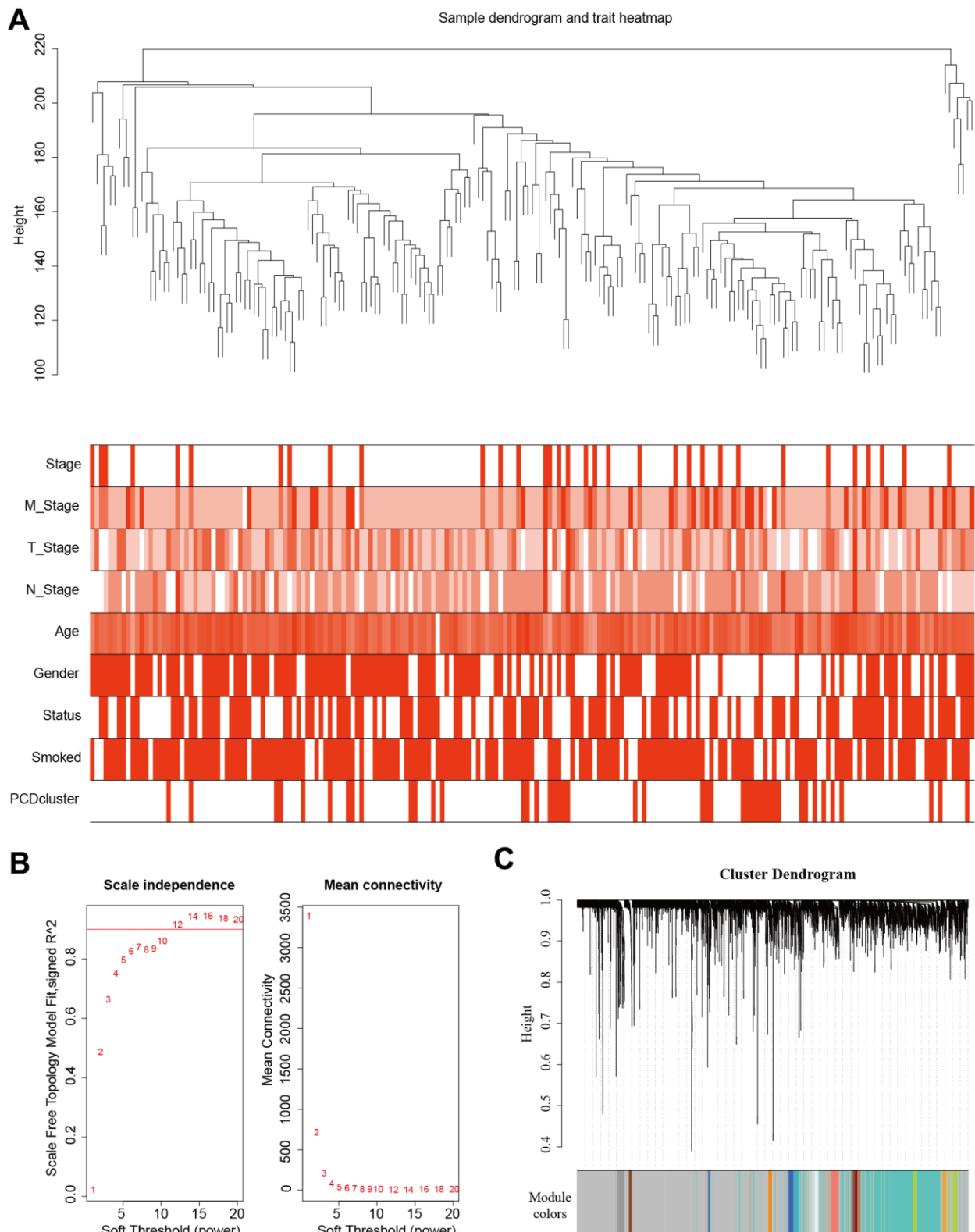


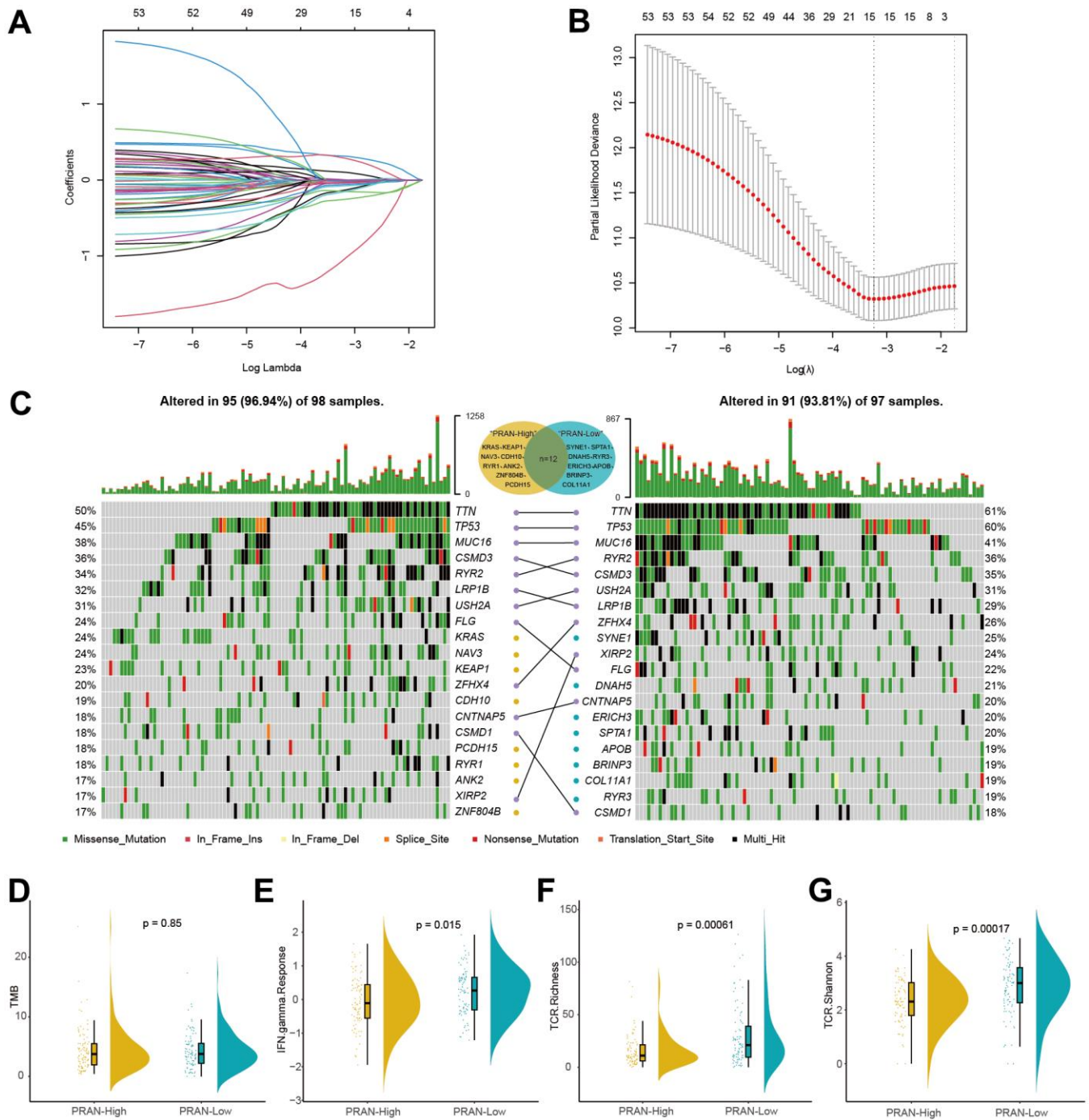
# SUPPLEMENTARY FIGURES



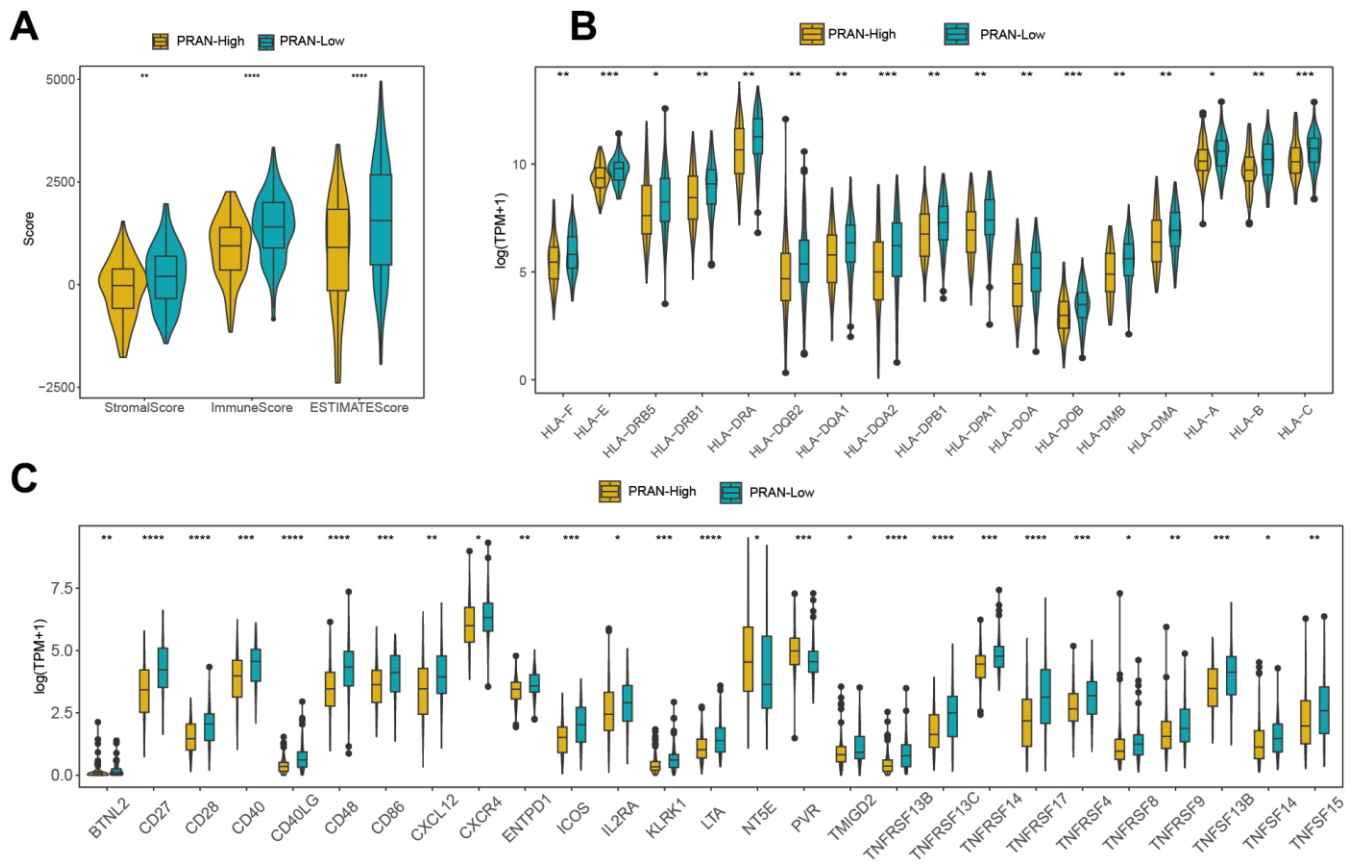
Supplementary Figure 1. The prognostic value of the 12 prognosis-related PCD genes.



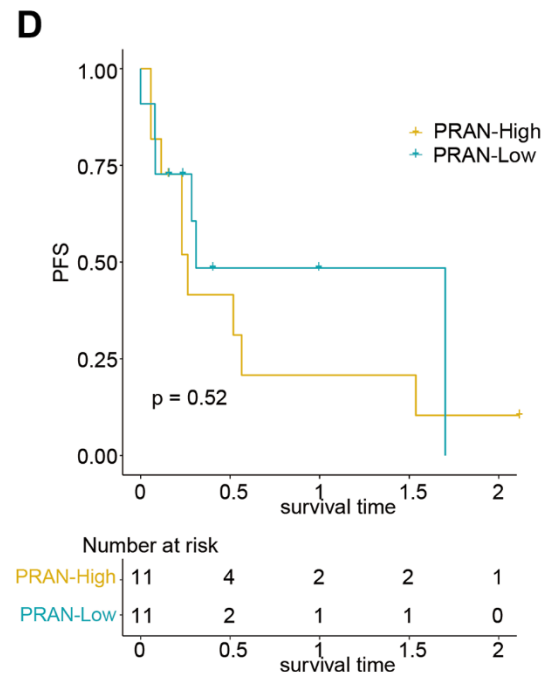
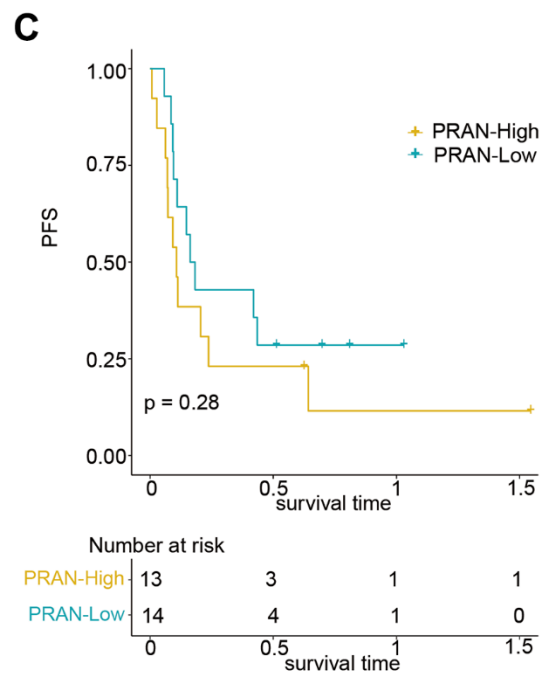
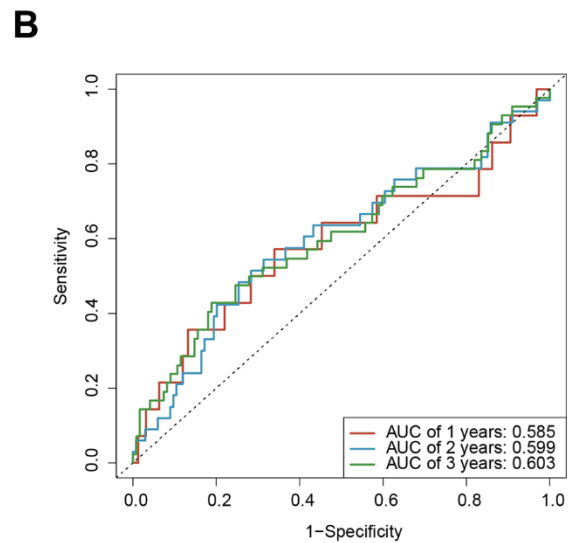
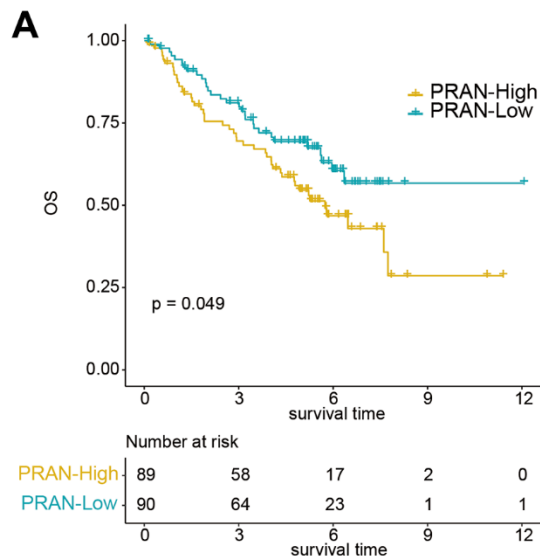
**Supplementary Figure 2. Identification of modules by WGCNA.** (A) Clustering dendrogram of TCGA-Advanced NSCLC samples and corresponding heatmap displaying clinical traits. The color band beneath the dendrogram represents the tissue trait status. (B) Evaluation of the scale-free fit index (left) and mean connectivity (right) across various soft threshold power values. The appropriate power value was determined for subsequent module identification. (C) Cluster dendrogram representing 39 distinct colored modules, based on a dissimilarity measure (1-TOM).



**Supplementary Figure 3. The candidate genes screen by LASSO regression and association analysis of mutation profiles and immunological factors with PRAN risk score in the TCGA-Advanced NSCLC cohort. (A)** The LASSO coefficient profiles of PCD-related genes. **(B)** Two dotted vertical lines are drawn at the optimal values according to the minimum criterion (right) and the Mean-Squared Error criterion (left). The horizontal axis represents the log value of lambda, and the vertical axis represents the Mean-Squared Error criterion of the independent variable. **(C)** The mutation profiles revealing the different mutation frequency between the two PRAN risk groups. **(D)** Box plot representing the comparison of Tumor Mutation Burden (TMB) levels between the two PRAN risk groups. **(E)** Box plot displaying the comparison of Interferon Gamma (IFN- $\gamma$ ) levels between the two PRAN risk groups. **(F)** Box plot showing the comparison of T-cell Receptor (TCR) richness levels between the two PRAN risk groups. **(G)** Box plot illustrating the comparison of T-cell Receptor (TCR) Shannon diversity index between the two PRAN risk groups.



**Supplementary Figure 4. Immune cell infiltration analysis between the two PRAN risk groups in the TCGA-Advanced NSCLC cohort.** (A) Stromal score, immune score, and ESTIMATE score between PRAN-High and PRAN-Low groups. The expression of (B) HLA genes, and (C) immunostimulatory genes between PRAN-High and PRAN-Low groups. P value: \* < 0.05; \*\* < 0.01; \*\*\* < 0.001; \*\*\*\* < 0.0001.



**Supplementary Figure 5. The predicting performance validation of the PRAN risk model in multiple GEO cohorts. (A)** Kaplan-Meier survival analysis in validation cohort GSE50081. **(B)** Time-dependent ROC curves between PRAN-High and PRAN-Low groups in validation cohort GSE50081. **(C, D)** Kaplan-Meier survival analysis in validation cohort GSE135222, and GSE93157.