

Figure S1. Flowchart of this study. NSCLC, non-small cell lung cancer; PPI, protein-protein interaction; GSEA, gene set enrichment analysis; GO, gene ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; WGCNA, weighted gene co-expression network analysis; miRNA, microRNA; TF, transcription factor; LASSO, least absolute shrinkage and selection operator.

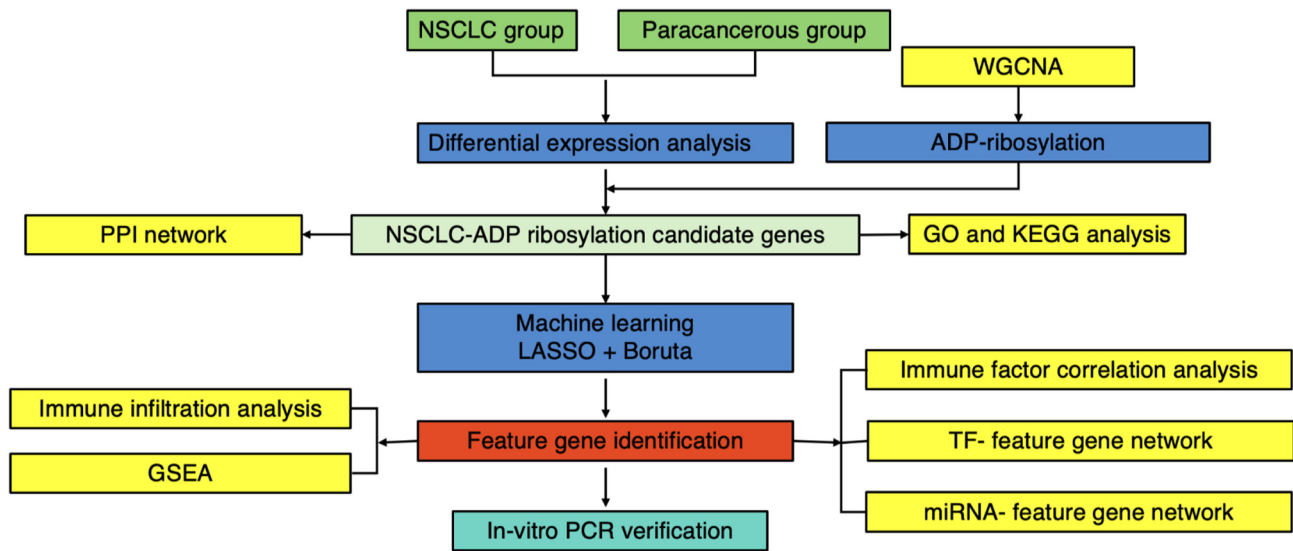


Figure S2. Parameter selection for weighted gene co-expression network analysis. (A) Hierarchical clustering of samples after introducing sample traits. (B and C) Soft-threshold screening: (B) Scale-free fit index (y-axis) under different soft-thresholds (x-axis) and (C) network connectivity under different soft-thresholds. ADPRGs, ADP-ribosylation-related genes.

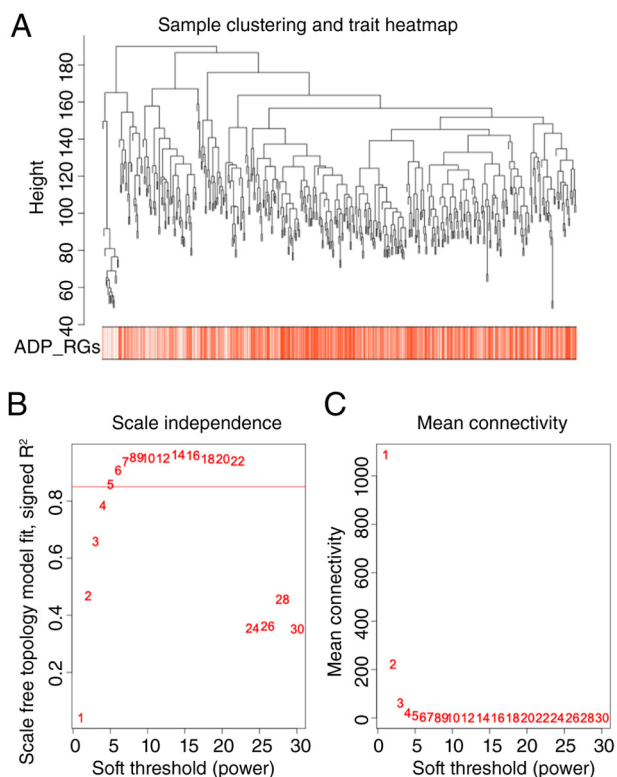


Figure S3. External validation of the three-gene signature in the independent The Cancer Genome Atlas LUAD cohort (GSE68465). (A) ROC curves for individual signature genes (HBZ, HLA-DRA and CCL4), with AUC values of 0.632, 0.805 and 0.633, respectively. (B) ROC curve for the combined three-gene signature for the first principal component, yielding an AUC of 0.772 (95% CI: 0.721-0.823), demonstrating robust discriminative capacity between LUAD tumor and adjacent normal tissues. LUAD, lung adenocarcinoma; ROC, receiver operating characteristic; AUC, area under the ROC curve.

