**Supplementary Figure Legend:**

**Supplementary Figure S1. Comparative analysis of immune infiltration and functionality between clusters.** A. Degree of immune cell infiltration across different clusters. B. Comparison of ImmuneScore, StromalScore, and ESTIMATEScore between clusters. C. Expression levels of immune-related genes across clusters. D-I. Differences in TIDE, IFNG, dysfunction score, exclusion score, and proportions of TAM M2 and MDSC between clusters. (\**p* < 0.05, \*\**p* < 0.01, \*\*\**p* < 0.001, \*\*\*\**p* < 0.0001, ns indicates non-significant)

**Supplementary Figure S2. Differential gene expression and functional enrichment analysis.** A. Volcano plot illustrating the results of differential expression analysis, with blue representing down-regulated DEGs, red representing up-regulated DEGs, and gray indicating genes with no significant difference. B. Results from GO enrichment analysis. C. Results from KEGG enrichment analysis.

**Supplementary Figure S3. Validation of prognostic analysis across multiple external datasets.** A-E. Kaplan-Meier analyses and corresponding ROC analysis results based on the GSE68465, GSE3141, GSE31210, GSE37745, and GSE50081 datasets.

**Supplementary Figure S4. Risk score distribution across various clinical subgroups.** A-F. Box plots displaying risk scores across various age groups, TNM stages, tumor stages, and sex. (\**p* < 0.05)

**Supplementary Figure S5. Correlation of prognostic genes with pathways and functional enrichment in LUAD.** A. Heatmap showing correlations between prognostic genes and signature pathways based on the TCGA-LUAD dataset. B. Heatmap illustrating the expression of prognostic genes and functional enrichment for each tumor sample based on the TCGA-LUAD dataset. (\**p* < 0.05, \*\**p* < 0.01, \*\*\**p* < 0.001)

**Supplementary Figure S6. Cell type scoring and trajectory analysis in KRAS/TP53 MUT and WT groups.** A. Violin plot displaying the prognostic gene set scores for ten cell types in the KRAS/TP53 MUT and WT groups based on different algorithms. B. Violin plot showing the scoring of ten cell types on the prognostic gene set between the KRAS/TP53 MUT and WT groups. C. Trajectories illustrating pseudo-time-dependent cellular states of epithelial cells in the KRAS/TP53 MUT group. (\*\**p* < 0.01, \*\*\*\**p* < 0.0001, ns indicates non-significant)