

**Supplementary Figure 1: GO, and KEGG of DEGs in lung cancer tissues and adjacent tissues were analyzed.** (A) Heatmap of the 141 DEGs with |log2fold change | > 1, P <0 .05. Red: higher expression; blue: lower expression. (B) A volcano plot of 141 DEGs. Red: upregulation with |log2fold change | > 1, P <0 .05; blue: downregulation with |log2fold change | > 1, P <0 .05; black: unchanged genes. (C-F) GO and KEGG enrichment analysis on 141 differential genes. BP: biological process; CC: cellular component; MF: molecular function; KEGG: Kyoto Encyclopedia of Genes and Genomes.



**Supplementary Figure 2: Clinicopathological characteristics between clusters.** Different clinicopathological parameters between the clusters, including TNM classification (A-I), tumor stage (J-L), and drug response (M-O).



**Supplementary Figure 3: Venn diagram of genetic intersection.**



**Supplementary Figure 4: Gene differential expression map in Pan-cancer.** (A-E) Comparison of the expression levels of five hub genes (RRM2, HMMR, PFKP, TCN1 and TK1) in tumors and normal tissues.



**Supplementary Figure 5: Correlation map and survival map of genes and immune cells.** (A-D) Correlation map of HMMR, PFKP, TCN1 and TK1 with seven kinds of immune cells. (E-H) The survival time of HMMR, PFKP, TCN1 and TK1 expressions.