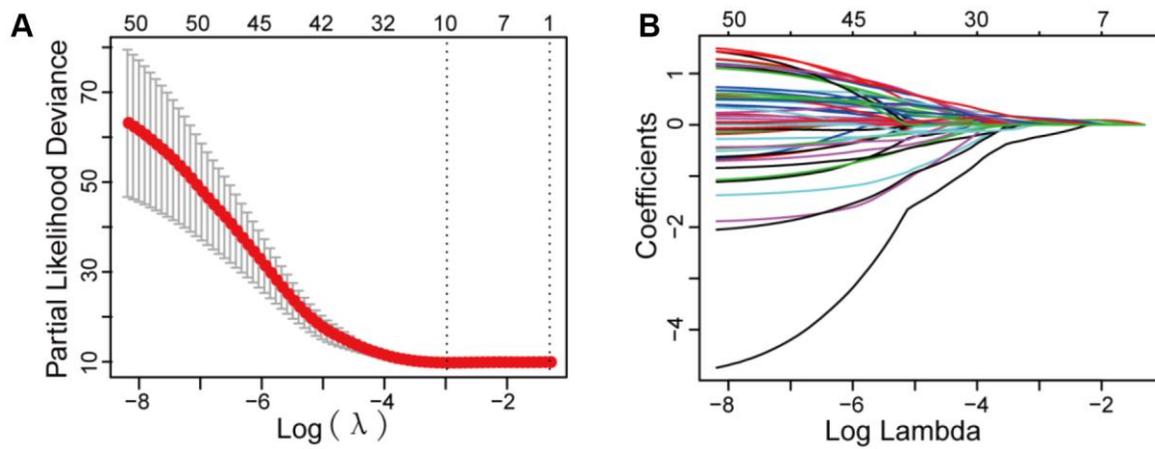
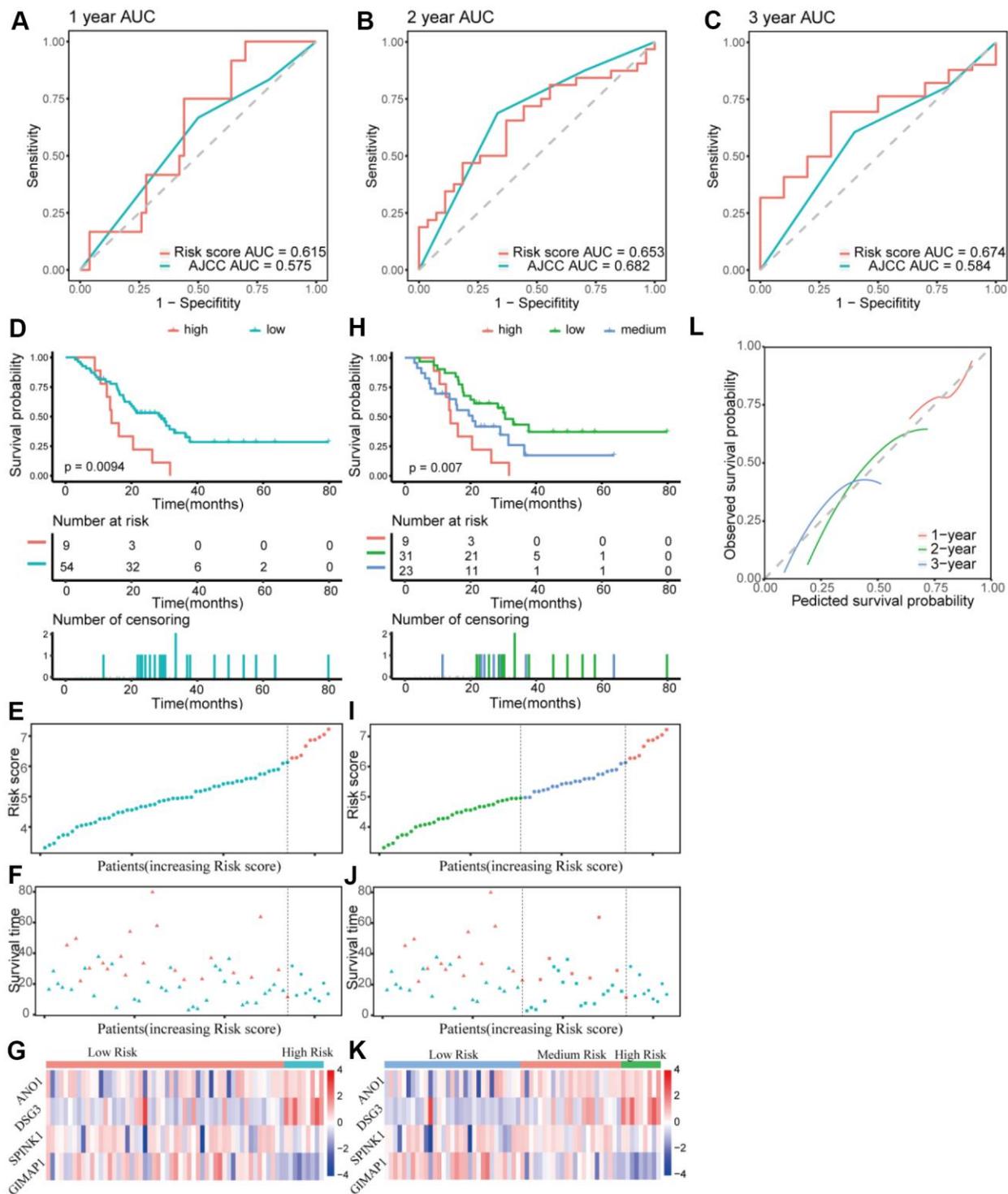


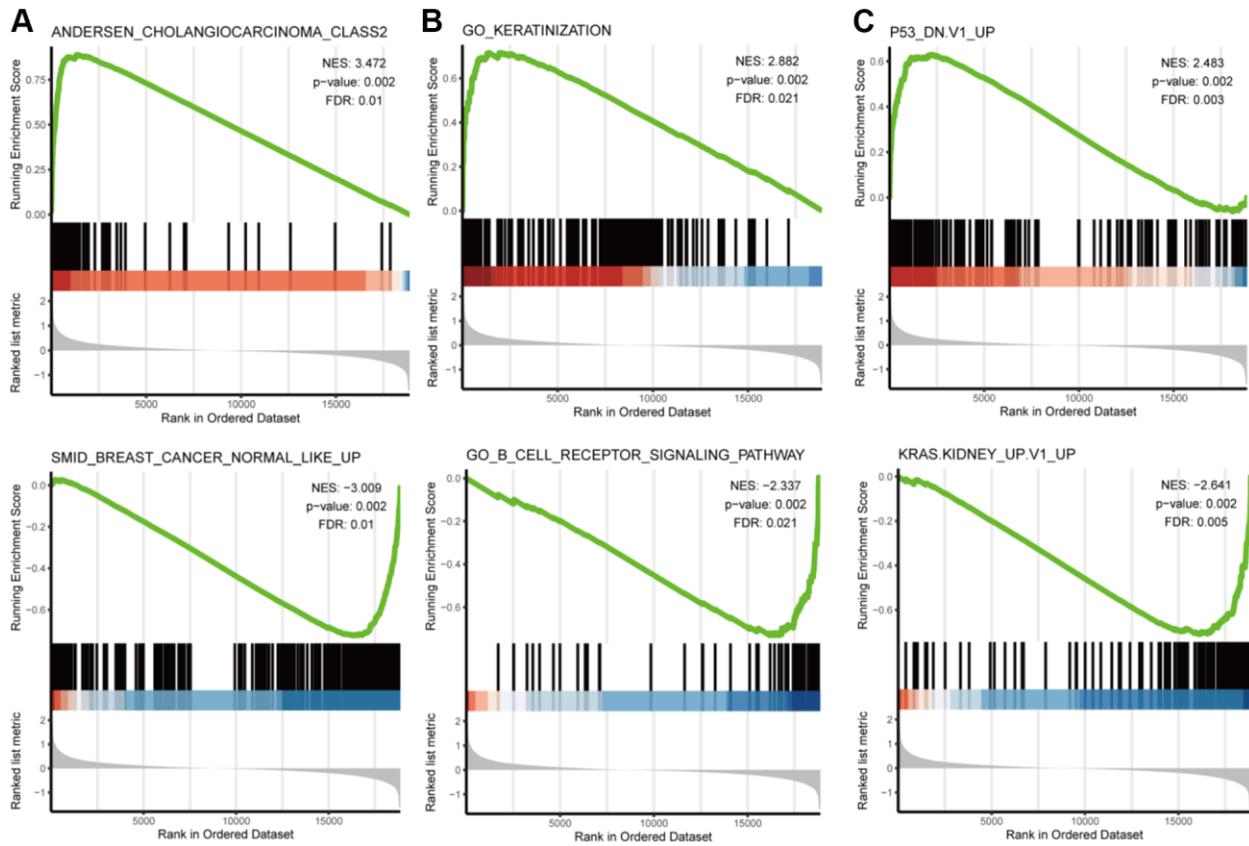
SUPPLEMENTARY FIGURES



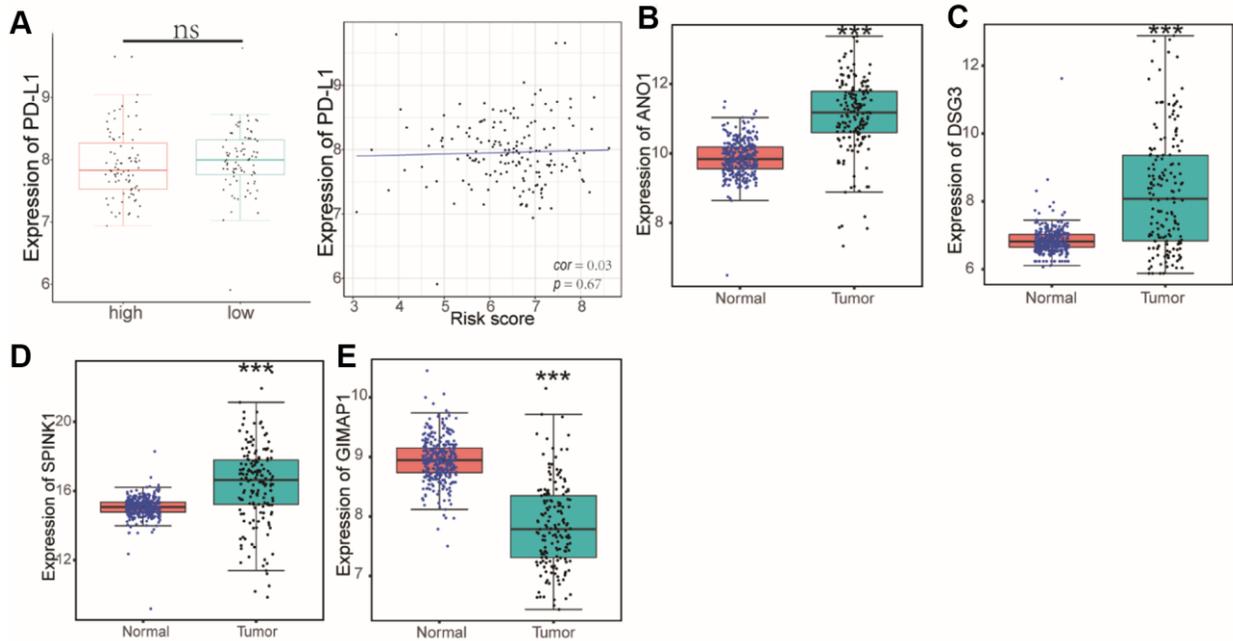
Supplementary Figure 1. Lasso analysis of the prognostic RRDEGs in pancreatic cancer. (A) Selection of tuning parameter (λ) in LASSO model. **(B)** LASSO coefficient profiles of all genes.



Supplementary Figure 2. External validation of the prognostic gene signature. (A–C) Time dependent ROC curves for 1-, 2- and 3-years overall survival predictions of genes signature in GSE57495, and AJCC stage is the control. (D–G) Kaplan-Meier survival curves of the four-gene signature and distribution of patient survival and risk score in different groups when patients in GSE57495 were divided into two groups. (D) Kaplan-Meier survival curves. (E) Distribution of the risk score. (F) Distribution of the survival time. Circle shape stands for high-risk group while triangle shape for low-risk group. Red stands for survival and green stands for dead. (G) Heatmap of the expression of the four genes. (H–K) Kaplan-Meier survival curves of the four-gene signature and distribution of patient survival and risk score in different groups when patients in GSE57495 were divided into three groups. (H) Kaplan-Meier survival curves. (I) Distribution of the risk score. (J) Distribution of the survival time. (K) Heatmap of the expression of the four genes. (L) Calibration plot for validation of the gene signature in GSE57495.



Supplementary Figure 3. GSEA for other MSigDB gene sets. Upregulated and downregulated enriched pathways with top NES were showed. (A) C2 (curated gene sets). (B) C5 (GO gene sets). (C) C6 (oncogenic gene sets).



Supplementary Figure 4. Expression of PD-L1 and four genes in signature. (A) Correlation between expression of PD-L1 and risk score. (B–E) The mRNA expression of four genes in signature.