

Figure S1. scRNA-seq analysis identified cell subpopulations of PDAC. (A-F) The t-SNE plots showing the original cluster (A-C) and named cell subpopulations (D-F) for multiple human scRNA-seq datasets; (G) The forest plot showing the prognostic values of signatures in established prognostic model.

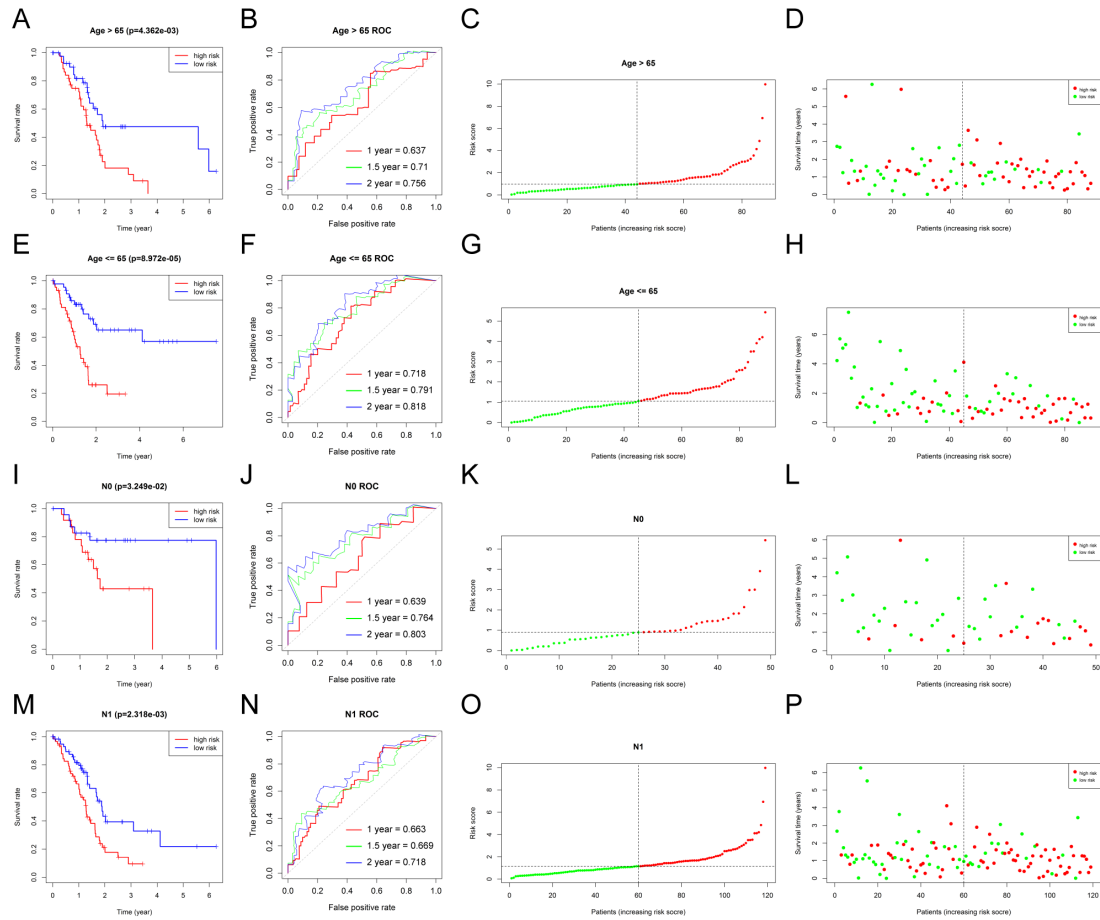


Figure S2. The performance of established prognostic model in different age and N stage subgroups. (A-H) The performance of prognostic model in different age subgroups, KM curve showing different OSs between high and low risk groups (A, E), ROC curve was used to evaluate the accuracy of prognostic model for 1-/1.5-/2-year OSs (B, F), risk score distribution of subjects in train set (C, G) and survival status scatter plot (D, H); (I-P) The performance of prognostic model in different N stage subgroups.

