

Figure S1 Box plot of expression levels of eight genes in patients with pancreatic cancer and normal controls in The Cancer Genome Atlas dataset. *, P<0.05; **, P<0.01; ***, P<0.001.

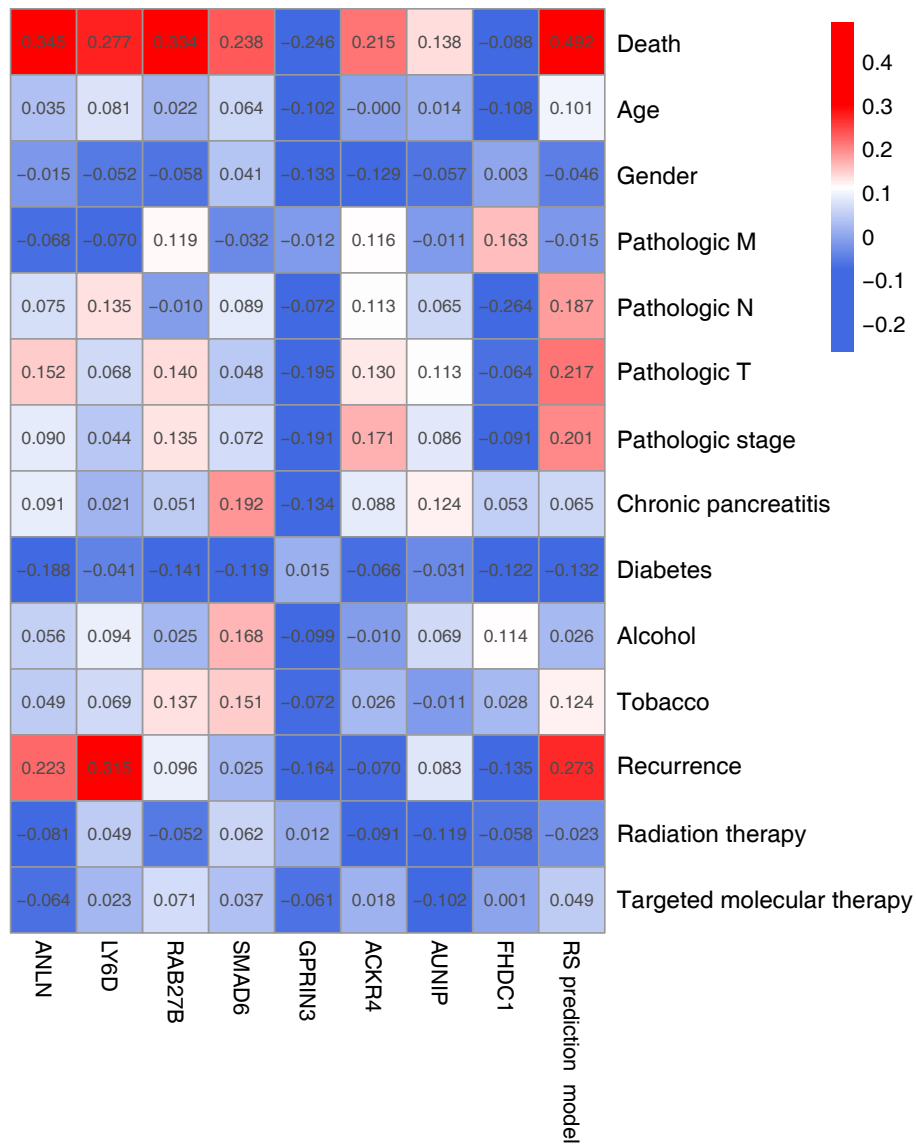


Figure S2 Heat map of correlation between each clinical information and expression levels of eight characteristic factors.

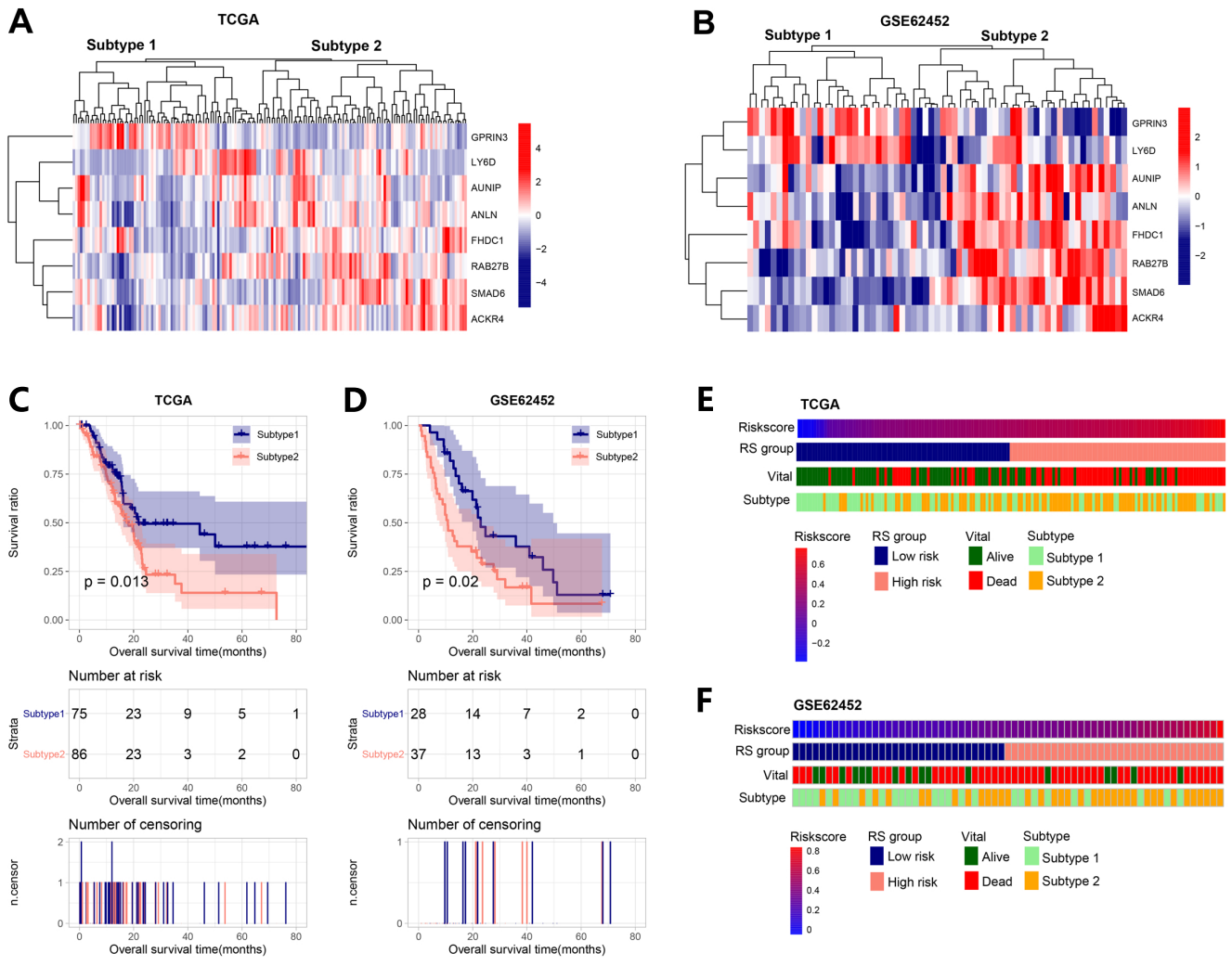


Figure S3 Risk groups of different subtypes and their association with survival prognosis. (A) Bidirectional hierarchical clustering based on the expression levels of 8 characteristic factors in TCGA; (B) Bidirectional hierarchical clustering based on the expression levels of 8 characteristic factors in GSE62452; (C) KM curve of the correlation between different types and survival prognosis based on clustering results in TCGA; (D) KM curve of the correlation between different types and survival prognosis based on clustering results GSE62452; (E) Heatmap display of classification based on Risk score; grouping, survival status and clustering in TCGA; (F) Heatmap display of classification based on Risk score; grouping, survival status and clustering in GSE62452.

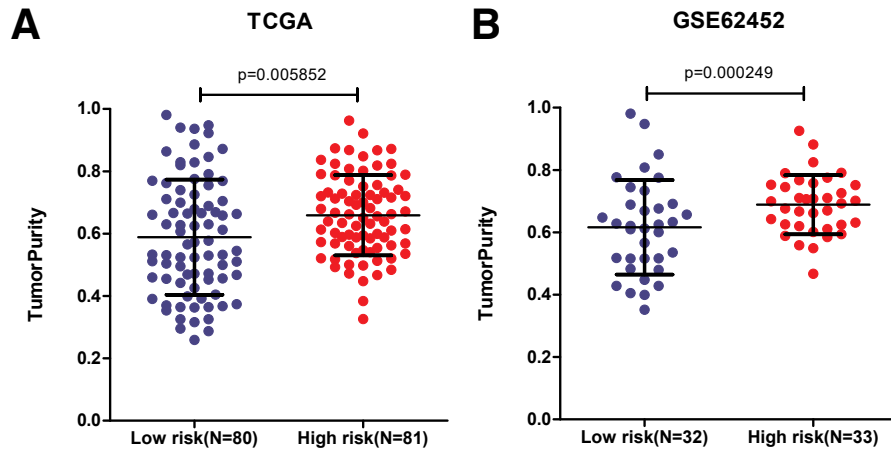


Figure S4 RTumor Purity and Risk Group. (A) Tumor Purity distribution of different risk groups in TCGA; (B) Tumor Purity distribution of different risk groups in GSE62452.