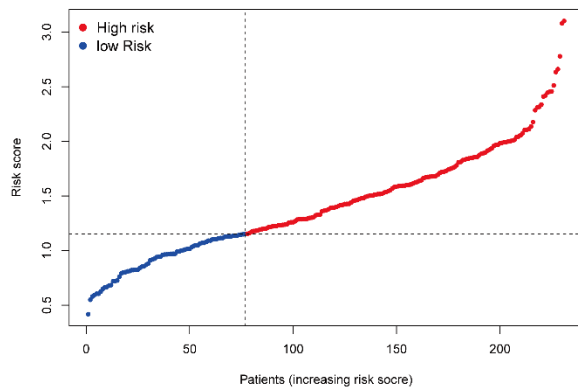
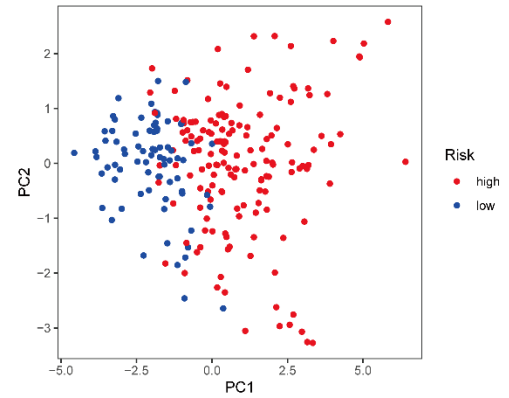


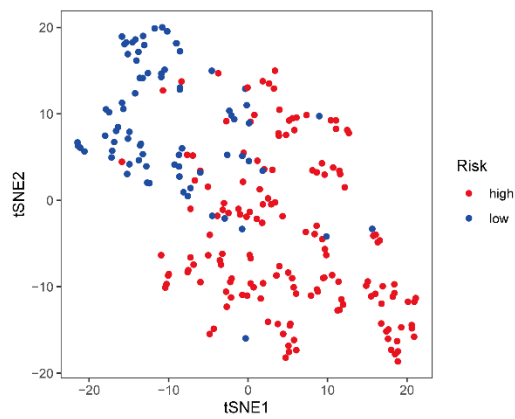
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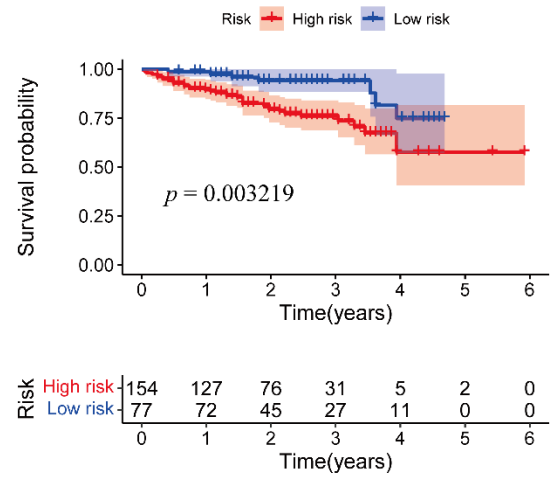
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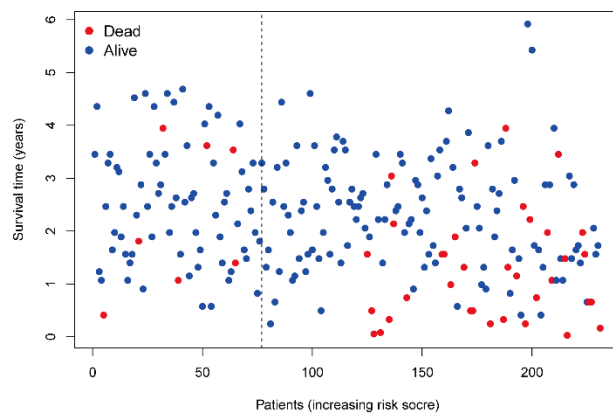
C



D



E



F

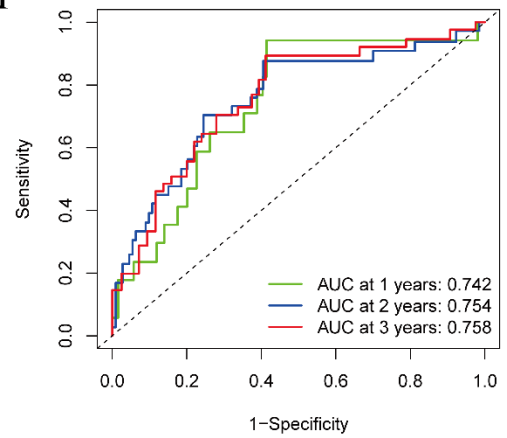
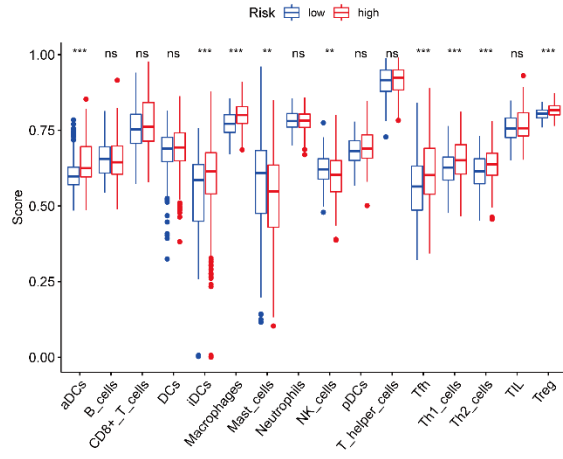
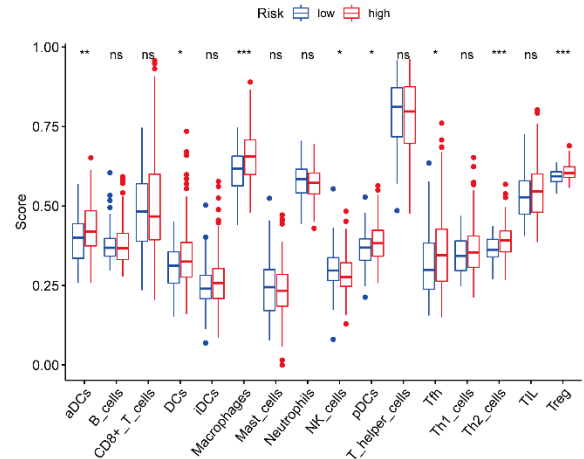


Figure S1. Validation of the prognostic signature in the ICGC cohort.(A) Distribution of the risk score in the ICGC cohort.(B) PCA analysis of patients in ICGC cohort.(C) T-SNE analysis of patients in ICGC cohort.(D) Kaplan-Meier survival curve of HCC overall survival in the ICGC cohort.(E) Distribution of survival status with increasing risk score in the ICGC cohort.(F) ROC curve showed that the 8-gene prognostic signature had satisfactory predictive efficacy in the ICGC cohort.

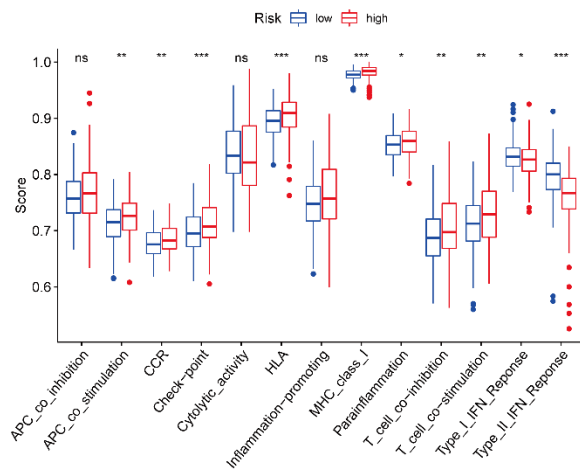
A



B



C



D

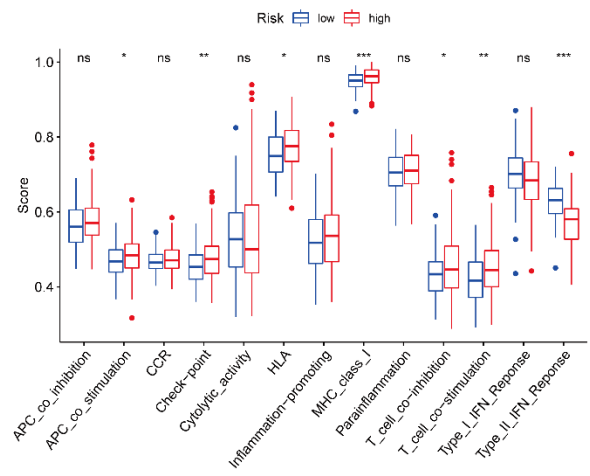


Figure S2. Results of TIME landscape analysis in the TCGA and ICGC cohorts.(A) The abundance of immune cells in the TCGA cohort.(B) The abundance of immune cells in the ICGC cohort.(C) Immune function pathway analysis in the TCGA cohort.(D) Immune function pathway analysis in the ICGC cohort. (* $p < 0.05$, ** $p < 0.01$ and *** $p < 0.001$.).

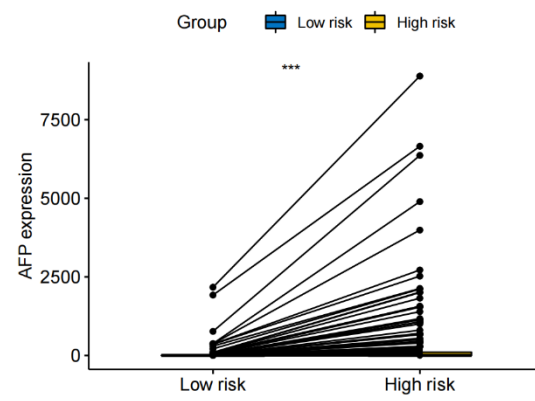


Figure S3. The AFP expression level was significantly higher in the high-risk group than in the low-risk group (** $p < 0.001$).

Gene Signature in Colorectal Cancer Patients

To test if the gene signature can be used to predict prognosis of other cancer patients, we obtained mRNA transcriptome profile of colorectal cancer (CRC) samples in TCGA cohort (372 patients) and analyzed the gene expression level and clinical outcome data. Subsequently the patients were divided into two groups by the risk score calculated by the gene signature established in HCC patients. Result showed that there was no significant difference of overall survival between the high-risk and low-risk group ($p = 0.96$). The conclusion is that the gene signature can not be used in CRC patients.

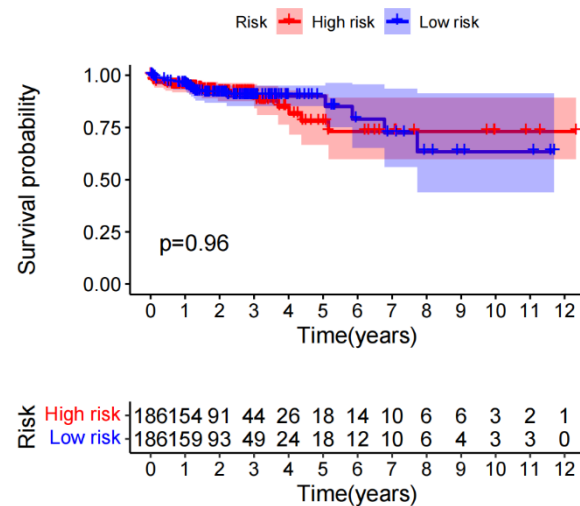


Figure S4. High-risk and low-risk group according to the risk score calculated by the gene signature.