



Research article

A novel immune checkpoint-related gene signature for hepatocellular carcinoma to predict clinical outcomes and therapeutic response

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Supplementary

Table S1. Immune checkpoint genes involved in this study.

ADORA2A	CD160	CD40LG	HAVCR2	HLA-DPA1	HLA-DRB5	KIR2DL2	KIR2DS4	PDCD1	TNFRSF4
BTLA	CD209	CD47	HLA-A	HLA-DPB1	HLA-E	KIR2DL3	KIR2DS5	PDCD1LG2	TNFRSF9
BTN2A1	CD226	CD70	HLK-B	HLA-DQA1	HLA-F	KIR2DL4	KIR3DL1	PVR	TNFSF14
BTN2A2	CD27	CD80	HLA-C	HLA-DQB1	HLA-G	KIR2DL5A	KIR3DL2	SIRPA	TNFSF18
BTN3A1	CD274	CD86	HLA-DMA	HLA-DRA	ICOS	KIR2DL5B	KIR3DL3	TDO2	TNFSF4
BTNL3	CD276	CD96	HLA-DMB	HLA-DRB1	ICOSLG	KIR2DS1	KIR3DS1	TIGIT	TNFSF9
BTNL9	CD28	CEACAM1	HLA-DOA	HLA-DRB3	IDO1	KIR2DS2	LAG3	TNFRSF14	VTCN1
C10orf54	CD40	CTLA4	HLA-DOB	HLA-DRB4	KIR2DL1	KIR2DS3	LGALS9	TNFRSF18	

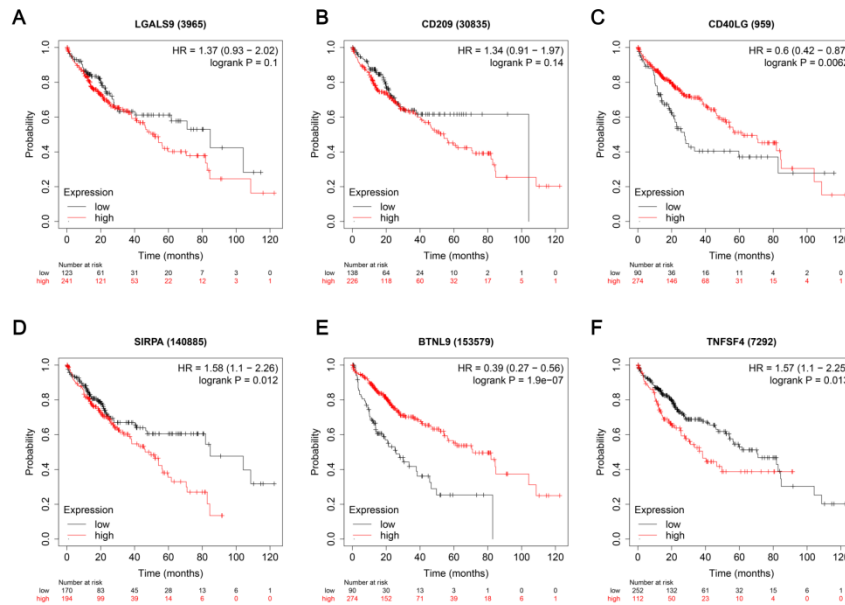


Figure S1. Verification of the hub immune checkpoint genes (ICGs) in the Kaplan-Meier plotter database.

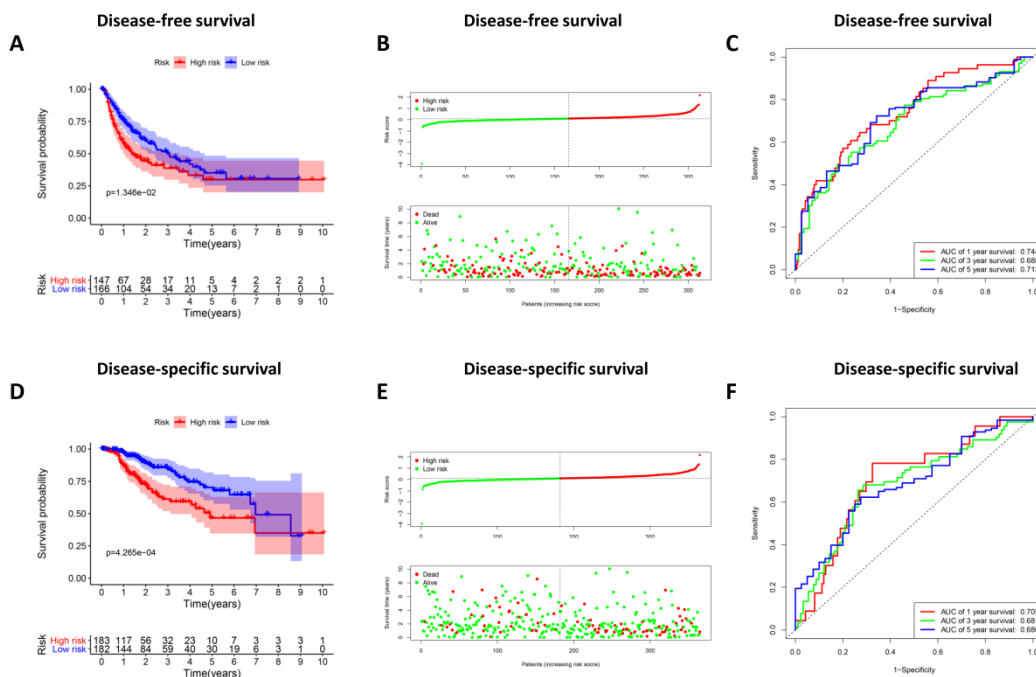


Figure S2. The predictive value of the gene signature for disease-free survival (DFS) and disease-specific survival (DSS) of HCC patients. (A) Disease-free survival analysis of high- and low-risk groups. (B) Risk score and DFS status of HCC patients. (C) ROC curves for predicting DFS based on risk score. (D) Disease-specific survival analysis of high- and low-risk groups. (E) Risk score and DSS status of HCC patients. (F) ROC curves for predicting DSS based on risk score.

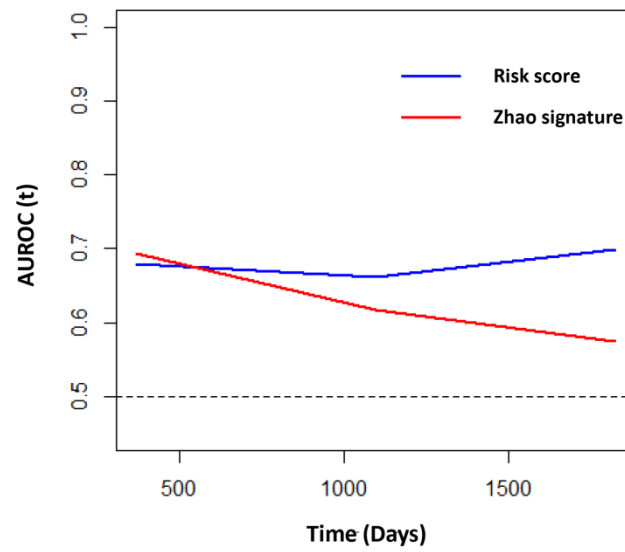


Figure S3. Comparison of the time-dependent ROC curves for our risk score and Zhao et al. signature.



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