

Figure S1. Comparisons between the high and low PSS groups in The Cancer Genome Atlas. Comparison of (A) platelet counts, inflammatory factors: (B) IL10, (C) TGFB1 and (D) IFNG, and (E) hallmarks between the high and low PSS groups. ns, not significant; PSS, platelet signature score.

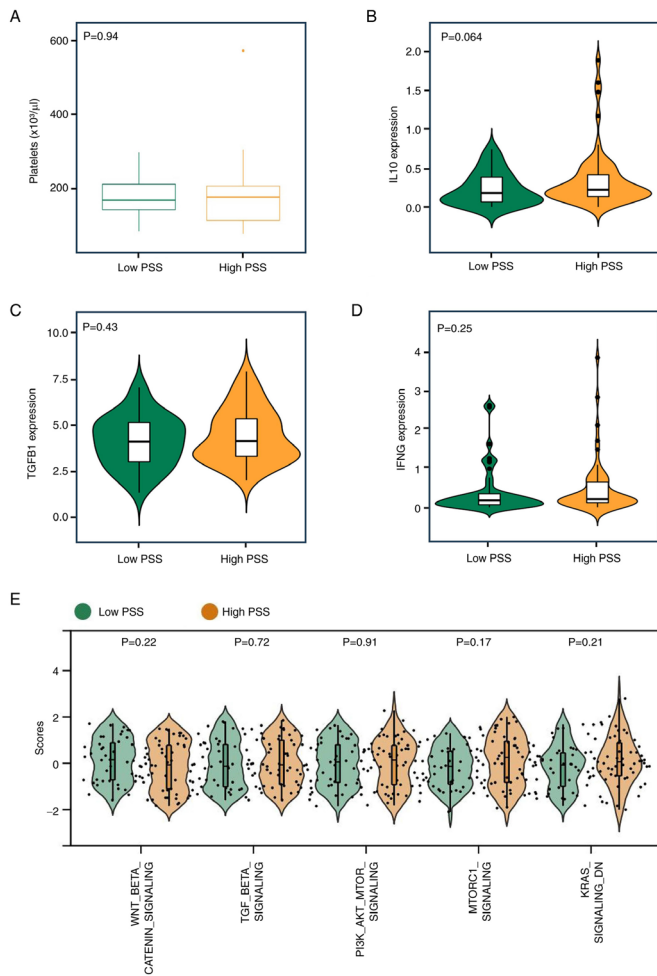


Figure S2. Comparison of the infiltration of immune cells between the high and low PSS groups using CIBERSORT. *P<0.05; ***P<0.001. ns, not significant; PSS, platelet signature score; NK, natural killer.

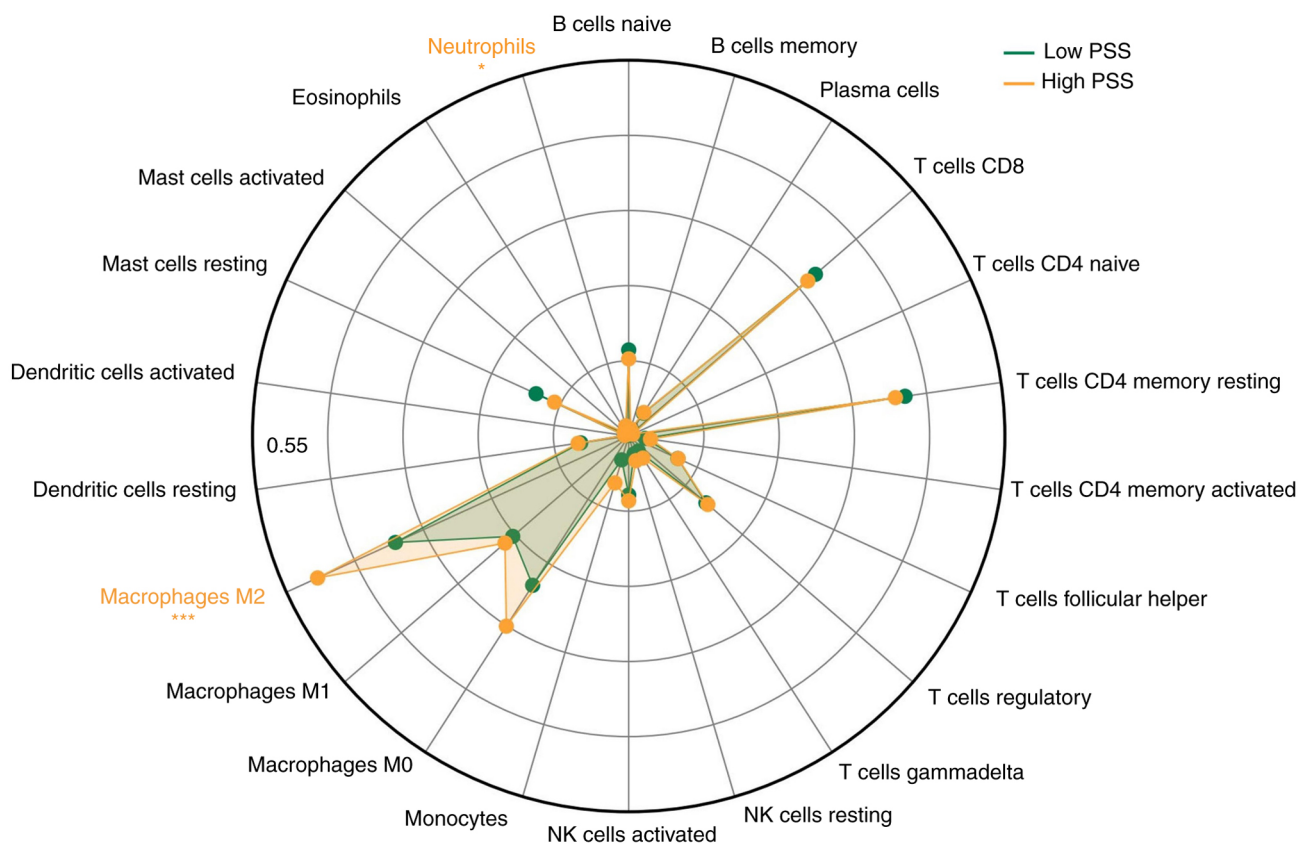


Figure S3. Expression and overall survival of 3 genes (CCNJL, NR0B1 and TRIM54) in patients with HCC. (A) Kaplan-Meier curve showing the prognosis of patients with HCC with virus infection in the International Cancer Genome Consortium. (B) Sankey diagram showing the distribution of PSS, virus infection, RS and survival status in patients with virus-related HCC from The Cancer Genome Atlas. CCNB1 was (C) highly expressed in HCC and (D) associated with poor prognosis (UALCAN). NR0B1 was (E) highly expressed in HCC and (F) associated with poor prognosis (UALCAN). TRIM54 was (G) highly expressed in HCC and (H) associated with poor prognosis (UALCAN). Immunohistochemical staining showed the protein expression levels of (I) CCNJL and (J) TRIM54 in HCC and normal tissues (Human Protein Atlas). * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$; **** $P < 0.0001$. CCNJL, Cyclin-J-Like protein; NR0B1, nuclear receptor subfamily 0 group B member 1; TRIM54, tripartite motif containing 54; HCC, hepatocellular carcinoma; PSS, platelet signature score; RS, risk score; HBV, hepatitis B virus; HCV, hepatitis C virus; UALCAN, University of ALabama at Birmingham CANcer data analysis Portal; ns, not significant.

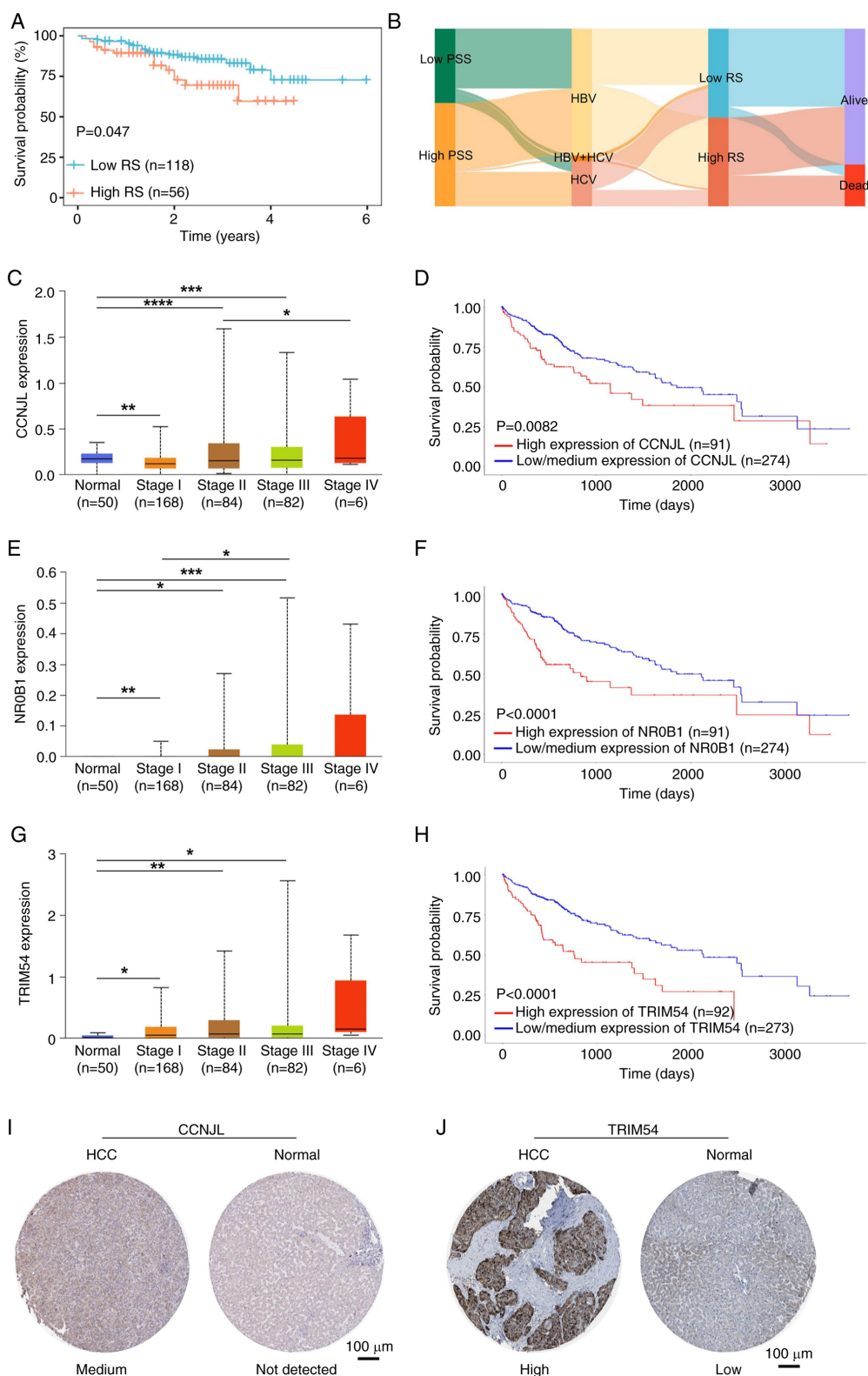


Figure S4. Spearman analysis of risk score and the mRNA expression levels of immune checkpoints. Spearman analysis showed that risk score did not have a linear relationship with (A) PDCD1, (B) CD274, (C) LAG3 or (D) TIGIT. PDCD1, programmed cell death protein 1; LAG3, lymphocyte-activation gene 3; TIGIT, T cell immunoreceptor with Ig and ITIM domains.

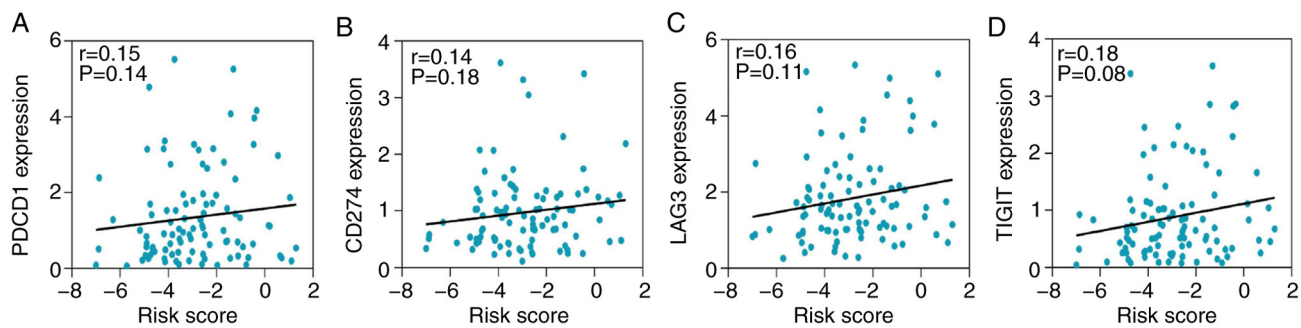


Figure S5. Comparison analysis in the four groups in The Cancer Genome Atlas. Comparison of the (A) WNT, (B) TGF, (C) TNFA and (D) PI3K signaling in the four groups. Comparison of the (E) inflammation response, (F) P53 pathway, (G) IL2, (H) KRAS-UP and (I) KRAS-DN signaling in the four groups. Comparison of (J) TGFB1, (K) IL6 and (L) IL10 among the four groups. *P<0.05; **P<0.01; ***P<0.001. RS, risk score; PSS, platelet signature score; ns, not significant.

