

Figure S1

Gene expressions levels of the prognostic model. **A–F** Gene expressions levels of the prognostic model in TCGA.

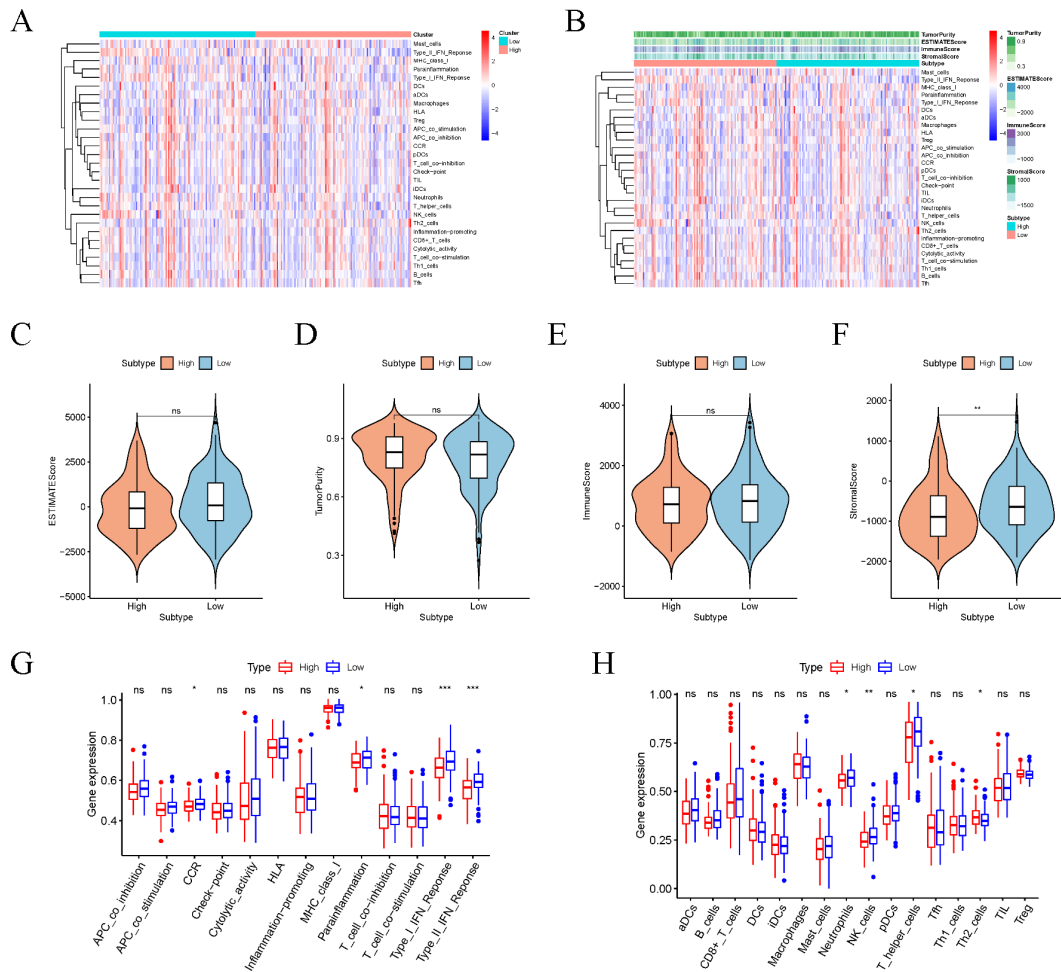


Figure S2

Risk score is closely related to tumor immune environment characteristics and immune infiltration in HCC. **A-B** Heat map (using "pheatmap" R package, <https://cran.r-project.org/bin/windows/base/old/4.1.3/>) distribution of risk score and various immune scores. **C-F** Comparison of estimate score, stromal score, immune score, and tumor purity between high-risk groups and low-risk groups. **G** The relationship between immune function and risk score in ICGC cohort. **H** The relationship between immune cell infiltration and risk score in the ICGC cohort.

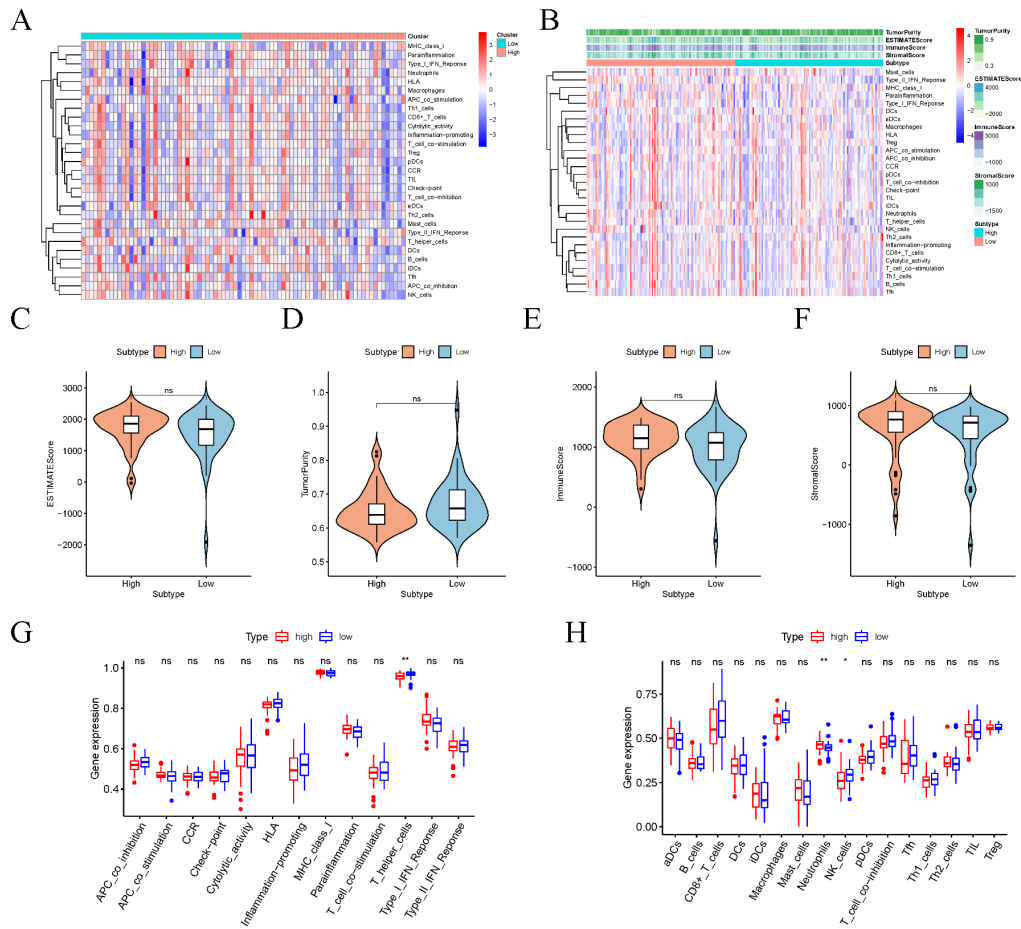


Figure S3

Risk score is closely related to tumor immune environment characteristics and immune infiltration in HCC. **A-B** Heat map (using " pheatmap" R package, <https://cran.r-project.org/bin/windows/base/old/4.1.3/>) distribution of risk score and various immune scores. **C-F** Comparison of estimate score, stromal score, immune score, and tumor purity between high-risk groups and low-risk groups. **G** The relationship between immune function and risk score in GSE54236 cohort. **H** The relationship between immune cell infiltration and risk score in the GSE54236 cohort.