

Supplementary Material

Supplementary Figures

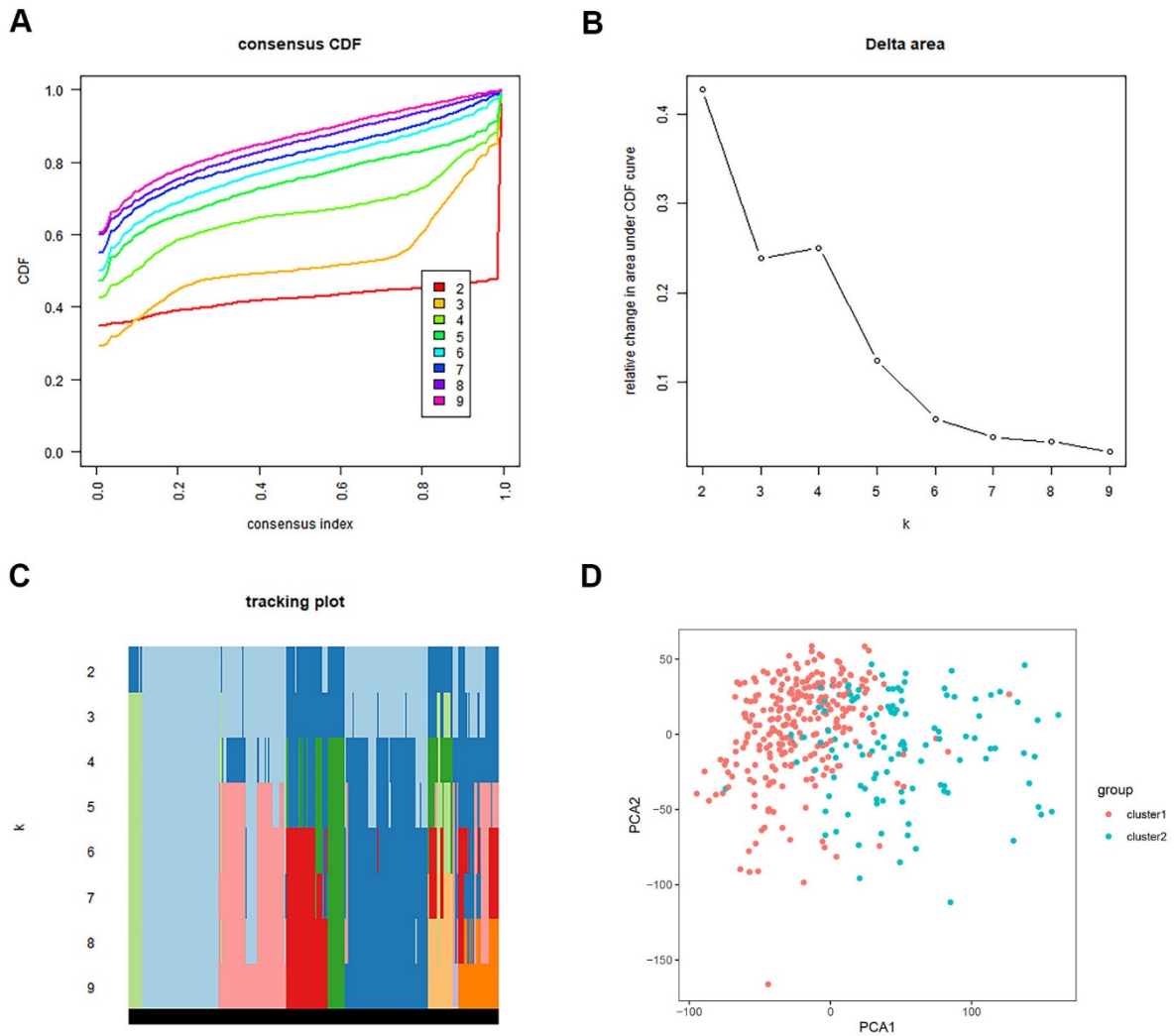


Figure S1. (A-C), consensus CDF, relative change in area under the CDF curve, and tracking plot for $k=2$ to 9 . (D), PCA plot of mRNA expression profiles in HCC.

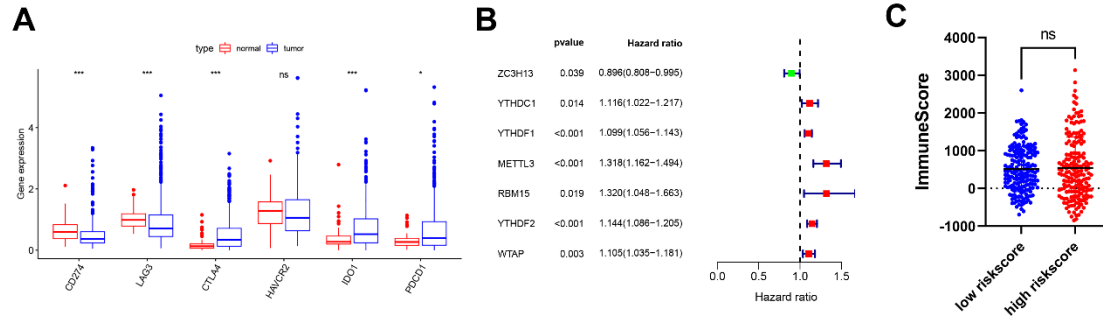
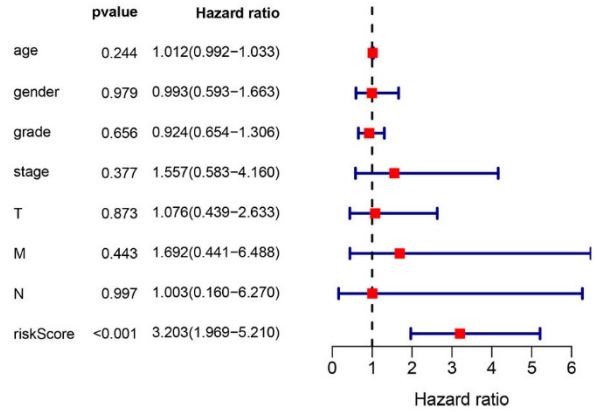
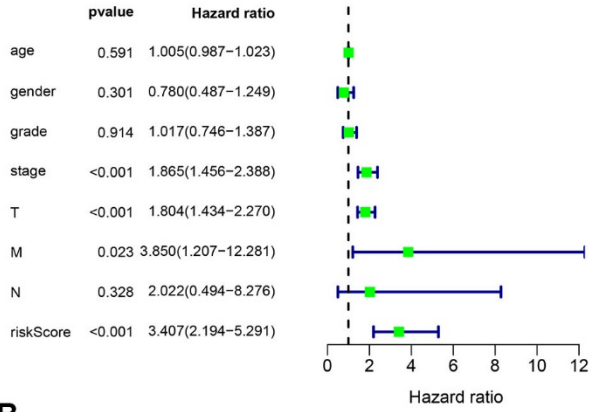
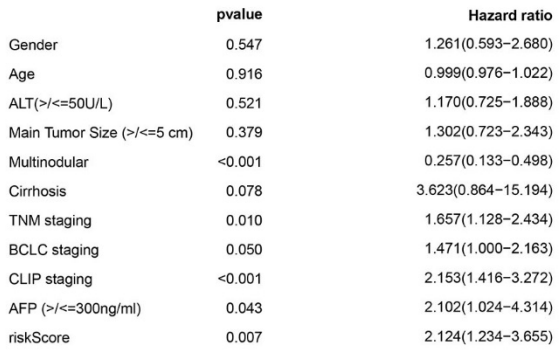
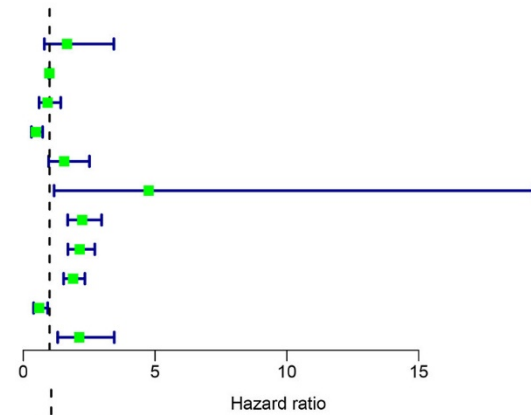
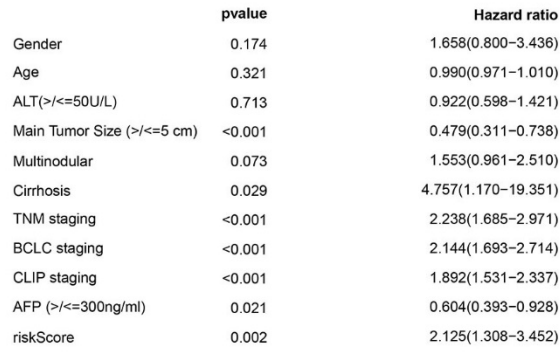


Figure S2. (A), the expression level of immune checkpoints between HCC and normal samples. (B), the forest plot of seven prognostic m6A genes filtered out by univariate Cox regression. (C), the relationship between risk score and immune score.

A



B



C

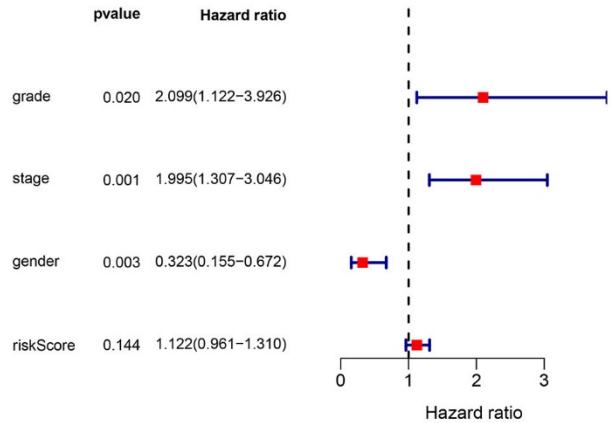
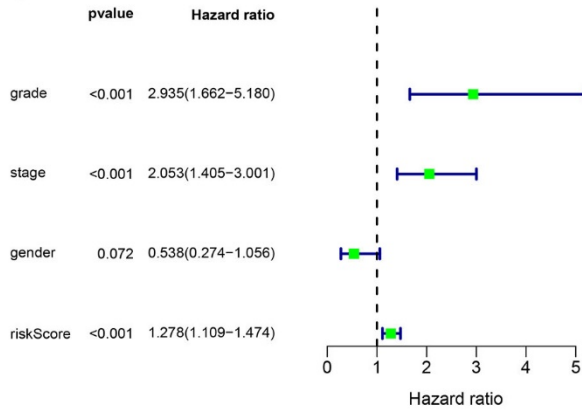


Figure S3. Univariate and multivariate Cox regression analyses in the TCGA cohort (A), the GEO cohort (B), and the ICGC cohort (C).

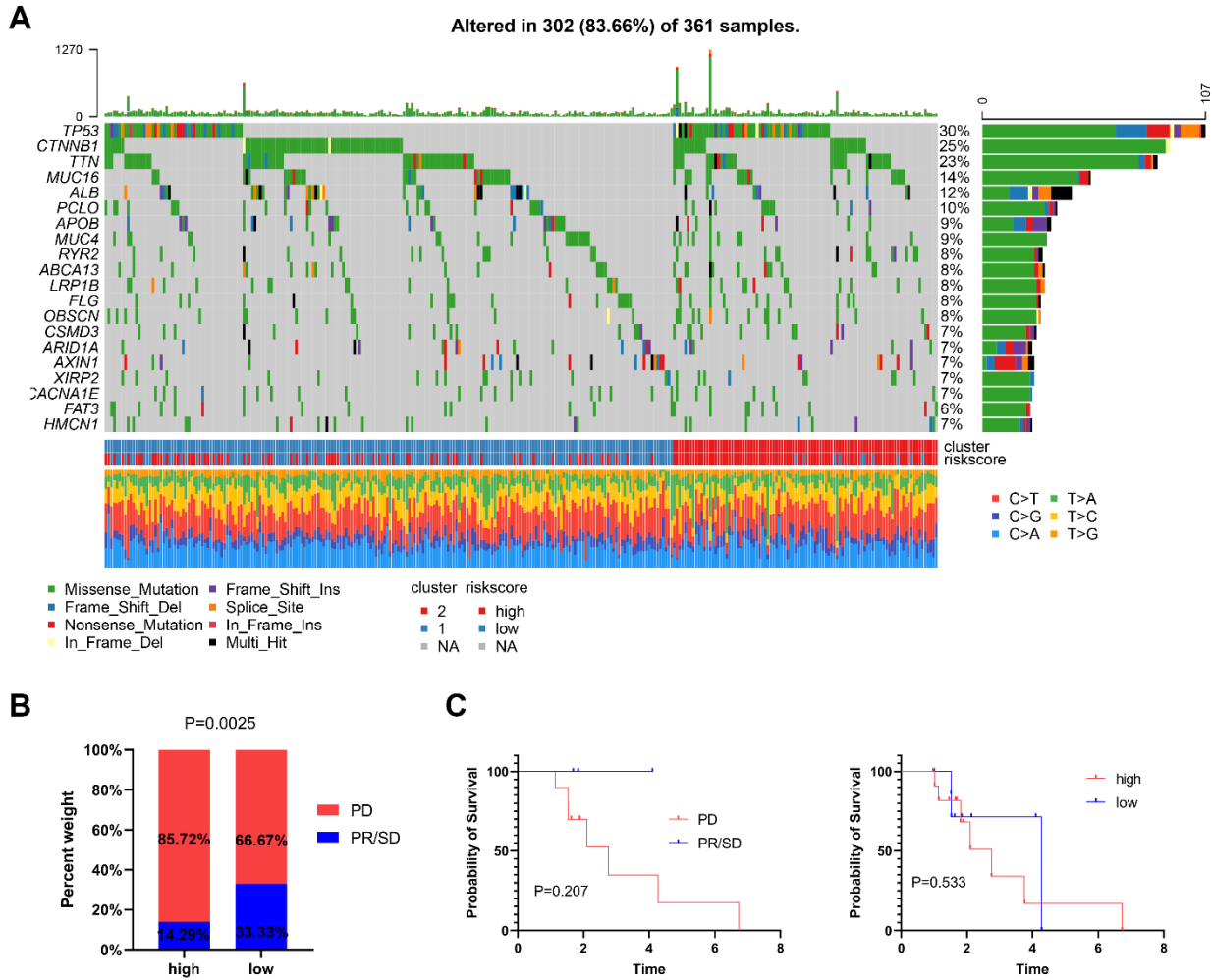


Figure S4. (A), the landscape of mutation in HCC stratified by cluster and risk signature. (B), Response to sorafenib treatment in the high-risk and low-risk patients in TCGA cohort. (C), Kaplan-Meier curve of the sorafenib-treated patients in TCGA cohort, stratified by response or risk score.