**Table S1.** Core genes of 6 solid tumors.

**Table S2.** Multivariable Cox regression analysis of predictors of survival outcomes in the TCGA discovery cohort for 6 solid tumors.

**Table S3.** The clinicopathological characteristics of the HCC patients enrolled in the TCGA cohort.

**Table S4.** The clinicopathological characteristics of the HCC patients enrolled in the GEO cohort.

**Table S5.** The clinicopathological characteristics of the HCC patients enrolled in the ICGC cohort.

**Figure S1.** **a** Distribution of NES value and FDR q value in GSEA analysis results. (**b-e**) Gene Ontology (GO) enrichment analysis and KEGG pathways enriched core genes form GSEA results.

**Figure S2.** Detailed GSEA analyses in 6 solid tumors.

**Figure S3.** The performance of ROC curves in BLCA, BRCA, HNSC, LIHC, LUAD, and LUSC.

**Figure S4.** K-M survival analysis in different clinicopathological subgroups in the TCGA cohort.

**Figure S5.** K-M analysis of patients stratified by Age (**a, b**), Gender (**c, d**), T classification (**e, f**), Stage (**g, h**), Grade (**i, j**), and Tumor Status (**k, l**) in TCGA cohort. Patients in the high-risk group achieved shorter overall survival.

**Figure S6.** K-M analysis of patients stratified by Family Cancer History (**a, b**), Hepatitis virus infection (**c, d**), Child-Pugh Score (**e, f**), BMI (**g, h**), and AFP level (**i, j**) in TCGA cohort. Patients in the high-risk group achieved shorter overall survival.

**Figure S7.** K-M survival analysis in different clinicopathological subgroups in the GEO cohort.

**Figure S8.** K-M analysis of patients stratified by Age (**a, b**), Gender (**c, d**), Stage (**e, f**), BCLC Staging (**g, h**), Child-Pugh Score (**i, j**), and Cirrhosis status (**k, l**) in GEO cohort. Patients in the high-risk group achieved shorter overall survival.

**Figure S9.** K-M analysis of patients stratified by Muti Nodular status (**a, b**), Tumor Size (**c, d**), AFP level (**e, f**), and ALT level (**g, h**) in GEO cohort. Patients in the high-risk group achieved shorter overall survival.

**Figure S10.** K-M survival analysis in different clinicopathological subgroups in the ICGC cohort.

**Figure S11.** K-M analysis of patients stratified by Age (**a, b**), Gender (**c, d**), Stage (**e, f**), Grade (**g, h**), Family Cancer History (**i, j**), and Prior Malignancy (**k, l**) in GEO cohort. Patients in the high-risk group achieved shorter overall survival.

**Figure S12.** The performance of a nomogram integrated the GRGPI model and clinicopathological characteristics in the GEO cohort. A Nomograph for predicting overall survival probability of HCC patients. (**b-c**) The Nomogram model improves the identification of high-risk patients, and 221 HCC patients are reclassified between the standard model and the Nomogram model. **d** ROC curve for Nomogram model. (**e, f**) Decision curve and calibration curves analyses of Nomogram for 1-, 2-, and 3-year.

**Figure S13.** The performance of a nomogram integrated the GRGPI model and clinicopathological characteristics in the ICGC cohort. A Nomograph for predicting overall survival probability of HCC patients. (**b-c**) The Nomogram model improves the identification of high-risk patients, and 221 HCC patients are reclassified between the standard model and the Nomogram model. **d** ROC curve for Nomogram model. (**e, f**) Decision curve and calibration curves analyses of Nomogram for 1-, 2-, and 3-year.