

Supplementary Figure S1. (A) Patients with hepatocellular carcinoma are divided into two clusters based on *EIF4E3* and *LARP1*. (B) Patients with hepatocellular carcinoma are divided into two clusters based on *EIF4E3* and *NUDT10*. (C) Patients with hepatocellular carcinoma are divided into two clusters based on *EIF4E3* and *NUDT11*. (D) Kaplan-Meier curves of overall survival in the *EIF4E3* high and low groups. (E) Kaplan-Meier curves of overall survival in the *LARP1* high and low groups.



Supplementary Figure S2. (A) Kyoto Encyclopedia of Genes and Genomes (KEGG) analyses. (B) Comparison of the abundance of immune infiltrating cells in two clusters.



Supplementary Figure S3. Comparison of immunomodulatory drug targets in HCC between two clusters. (ns, no significance, ${}^{*}P < 0.05$; ${}^{**}P < 0.01$, ${}^{***}P < 0.001$).



Supplementary Figure S4. Identification of immune-related modules by the WGCNA. (A) Analysis of network topology for soft powers. (B) The number of genes expressed in each module. (C) Gene dendrogram and module colors. (D) Heatmap between module eigengenes and cluster, ESTIMATE results. (E) Scatter plot of module eigengenes in the yellow module.



Supplementary Figure S5. Analysis of 18 hub genes. (A) PPI network of hub genes. (B) Correlation between hub genes. (C) The KEGG analysis of hub genes. (D) Correlation between hub genes and results of ESTIMATE. (E) Correlation between hub genes and expression of immune cells.



Supplementary Figure S6. GSE112790 validation of immune contexture between two clusters. (ns, no significance, ${}^{*}P < 0.05$; ${}^{**}P < 0.01$, ${}^{***}P < 0.001$). *EIF4E3* and *LARP1* influence tumor immunity in HCC.