**Prognostic Value and Regulatory Network of Immune-Related Genes in Hepatocellular Carcinoma**

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**Supplementary Materials:**

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**Fig. S1: The expression level of PIRDEGs in tumor tissues and normal tissues.** These samples’ data of HCC were imported from TCGA and analyzed on the GIEPA website. (A) *HSPA4*. (B) *IL17D*. (C) *MAPT*. (D) *NDRG1*. (E) *NRAS*. (F) *PAMD14*. (G) *RBP2*. (H) *TRAF3*.



**Fig. S2: The overall survival of PIRDEGs. The overall survival of PIRDEGs was verified through a single gene input on the GIEPA website.** (A) *HSPA4*. (B) *TRAF3*. (C) *MAPT*. (D) *NDRG1*. (E) *NRAS*. (F) *PAMD14*. (G) *RBP2*. (H) *IL17D*.



**Fig. S3: The correlation between tumor immune microenvironment and the risk score of the prognostic model.** There were a little dependency between (A) immune score, (B) stromal score, (C)tumor purity, and (D) ESTIMATE score, and the risk score.



**Fig. S4: The correlation analysis between risk score and tumor-infiltrating immune cells (TIIC).** (A-P) the relationship between twenty types of immune infiltrating cells and risk score respectively. (A) naïve B cells. (B) memory B cells. (C) resting mast cells. (D) M0 macrophages. (E) M1 macrophages. (F) gamma delta T cells. (G) CD8+ T cells. (H) activated NK cells. (I) resting NK cells. (J) monocytes. (K) neutrophils. (L) activated dendritic cells. (M) resting dendritic cells. (N) regulatory T cells (Tregs). (O) activated mast cells. (P) resting CD4+ memory T cells.