

Figure S1. Transcription and promoter methylation level of PAXIP1 in subgroups of patients with HCC stratified based on sex, age and ethnicity. Boxplots showing relative PAXIP1 expression in healthy controls and HCC samples based on (A) sex, (B) age and (C) ethnicity. One-way ANOVA. \* $P < 0.05$ , \*\* $P < 0.01$ , \*\*\* $P < 0.001$ . The sample sizes (n) were as indicated. Boxplots showing relative promoter methylation level of PAXIP1 in healthy controls and HCC samples based on (D) sex, (E) age and (F) ethnicity. One-way ANOVA. \* $P < 0.05$ , \*\* $P < 0.01$ , \*\*\* $P < 0.001$ . The sample sizes (n) were as indicated. HCC, hepatocellular carcinoma; NS, not significant; PAXIP1, PAX-interacting protein 1.

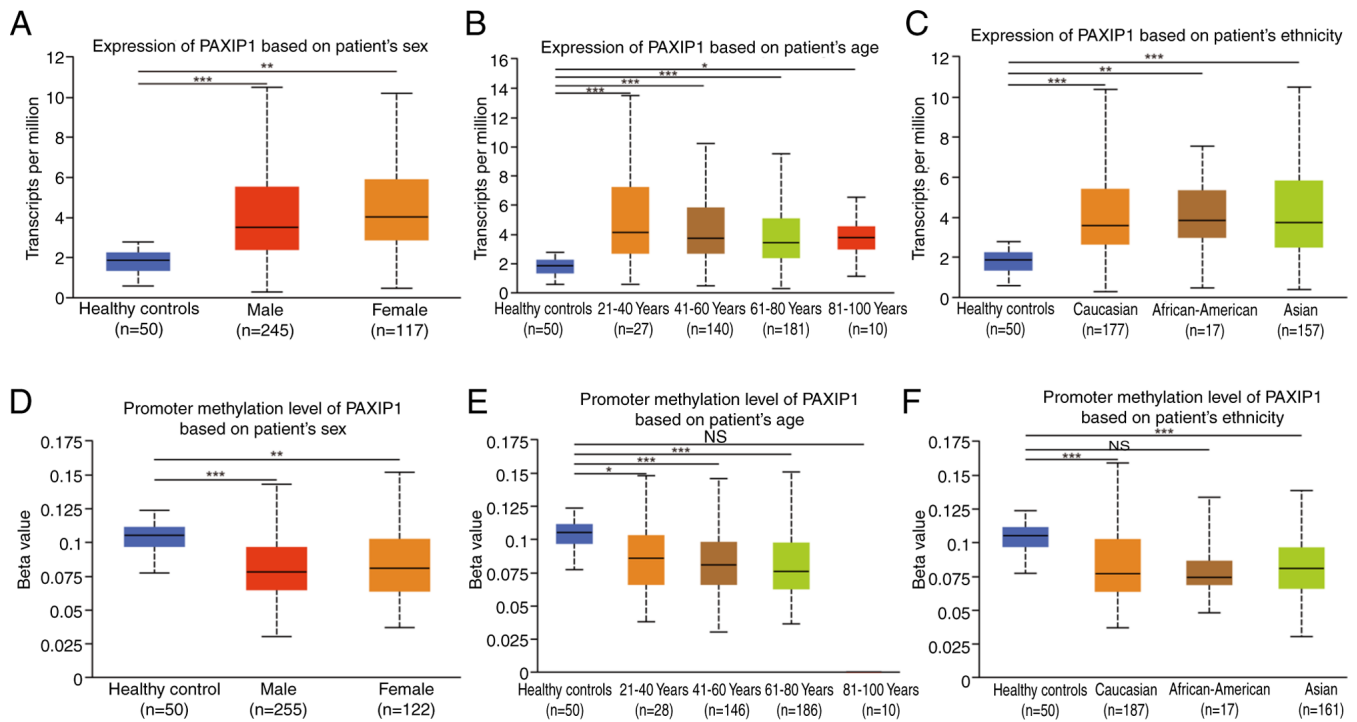


Figure S2. Overall survival rate of patients with hepatocellular carcinoma with low or high (A) CREB1, (B) ELF1, (C) GABPA, (D) REST, (E) SIN3A, (F) SP1, (G) TAF1 and (H) YY1 expression. The P-value was calculated using the log-rank test (n=362). HR, hazard ratio; TPM, transcripts per million.

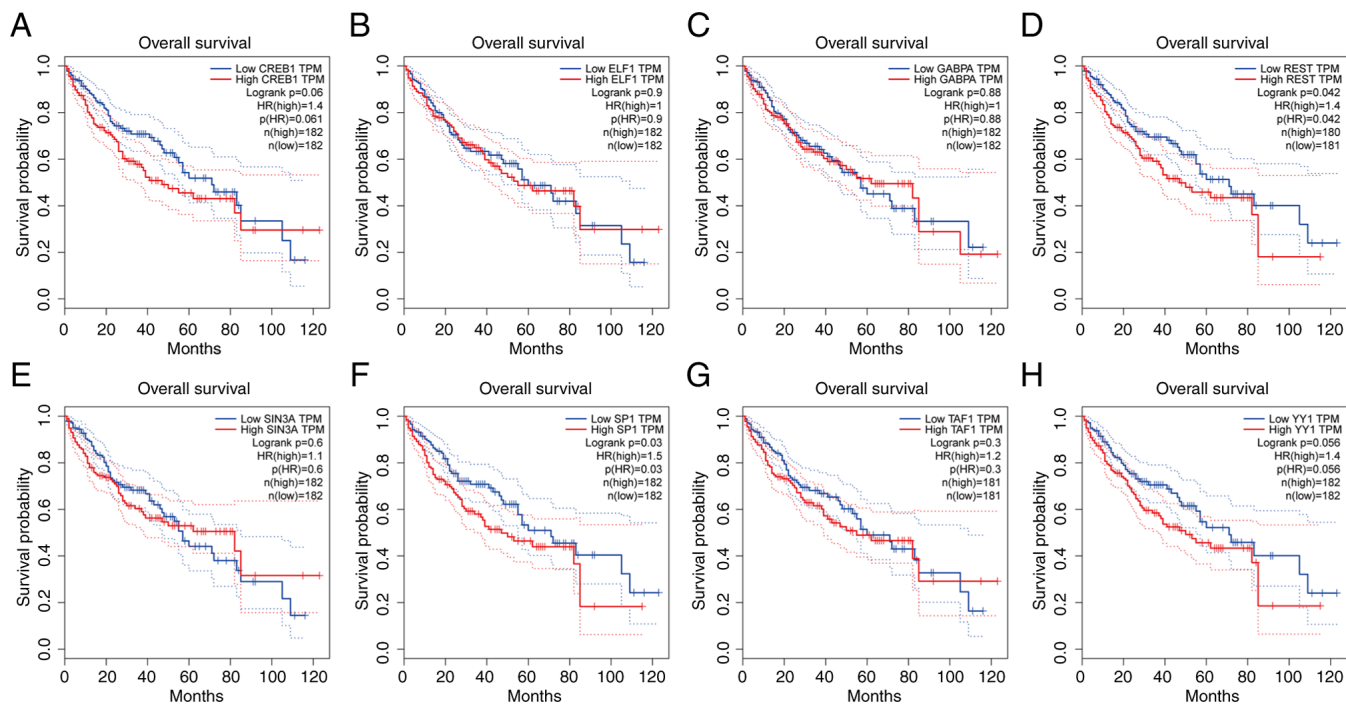


Figure S3. PAXIP1 expression is correlated with CD274, CTLA4 and PDCD1 expression in HCC. (A) Heatmap illustrating the correlation between PAXIP1 expression and immune checkpoint genes based on The Cancer Genome Atlas data. Kolmogorov-Smirnov and Wilcoxon rank sum tests. The P-value represents the comparison between the PAXIP1-high group and the PAXIP1-low group. \* $P < 0.05$ , \*\*\* $P < 0.001$ . (B) Spearman's correlation between HCC tumor purity and PAXIP1 expression. (C) Spearman correlation analysis of PAXIP1 expression and PDCD1, CD274 and CTLA4 expression in The Cancer Genome Atlas dataset of HCC, adjusted for tumor purity using Tumor Immune Estimation Resource 2.0. The Spearman correlation coefficient and P-value calculated using Spearman's test are indicated. Correlation of PAXIP1 expression with (D) PDCD1, (E) CD274 and (F) CTLA4 expression in HCC as assessed using the Gene Expression Profiling Interactive Analysis database. Pearson correlation coefficient and the P-value calculated using the Pearson test are indicated. CTLA4, cytotoxic T-lymphocyte associated protein 4; HCC, hepatocellular carcinoma; PAXIP1, PAX-interacting protein 1; PDCD1, programmed cell death 1; TPM, transcripts per million

