Figure S1 Gating of flow cytometry analysis for HCC. Diagram showing the application of gating for flow cytometry. SSC-A, side scatter area; FSC-A, forward scatter area; FSC-H, forward scatter height; SSC-H, side scatter height.
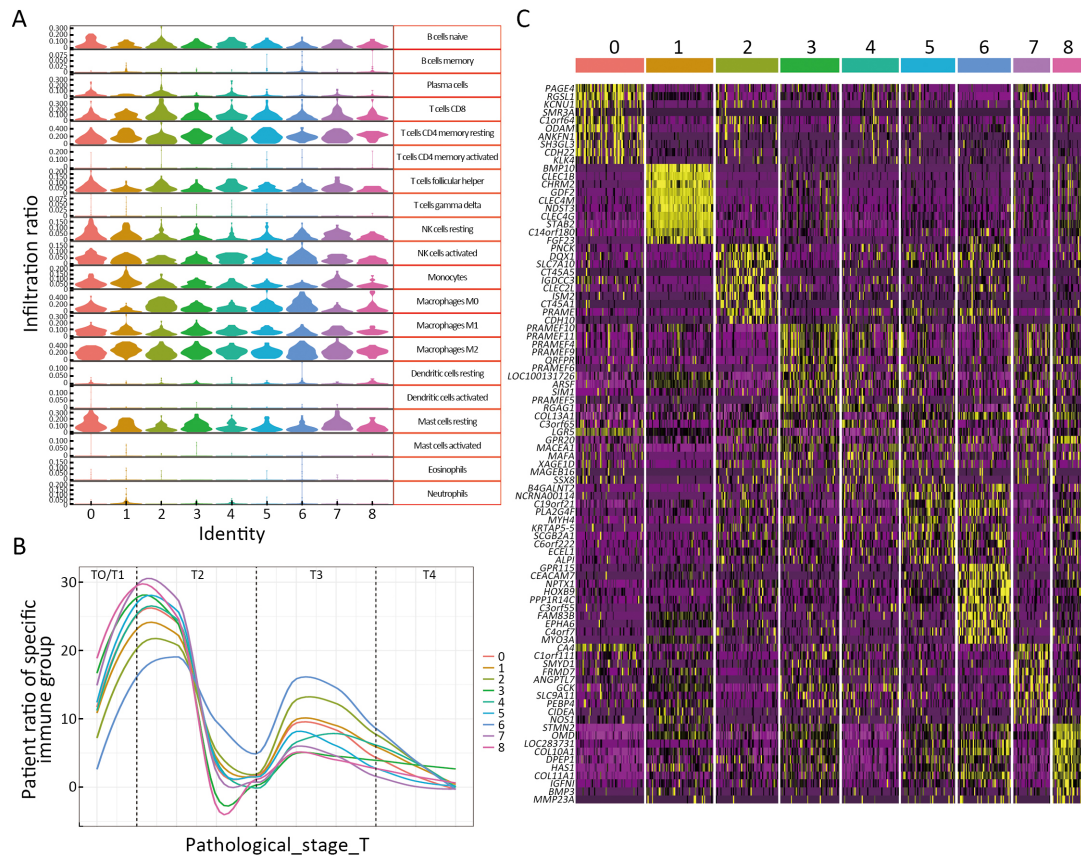
Figure S2 High expression of *ZNF296* promotes progression of HCC. (A) Violin plot shows 20 immune cell infiltration ratios for the nine immune infiltration subtypes of LIHC; (B) Pathological stages of nine LIHC immune infiltration subtypes; (C) Marker gene heatmap of nine immune infiltration subtypes of LIHC. HCC, hepatocellular carcinoma; LIHC, liver hepatocellular carcinoma.
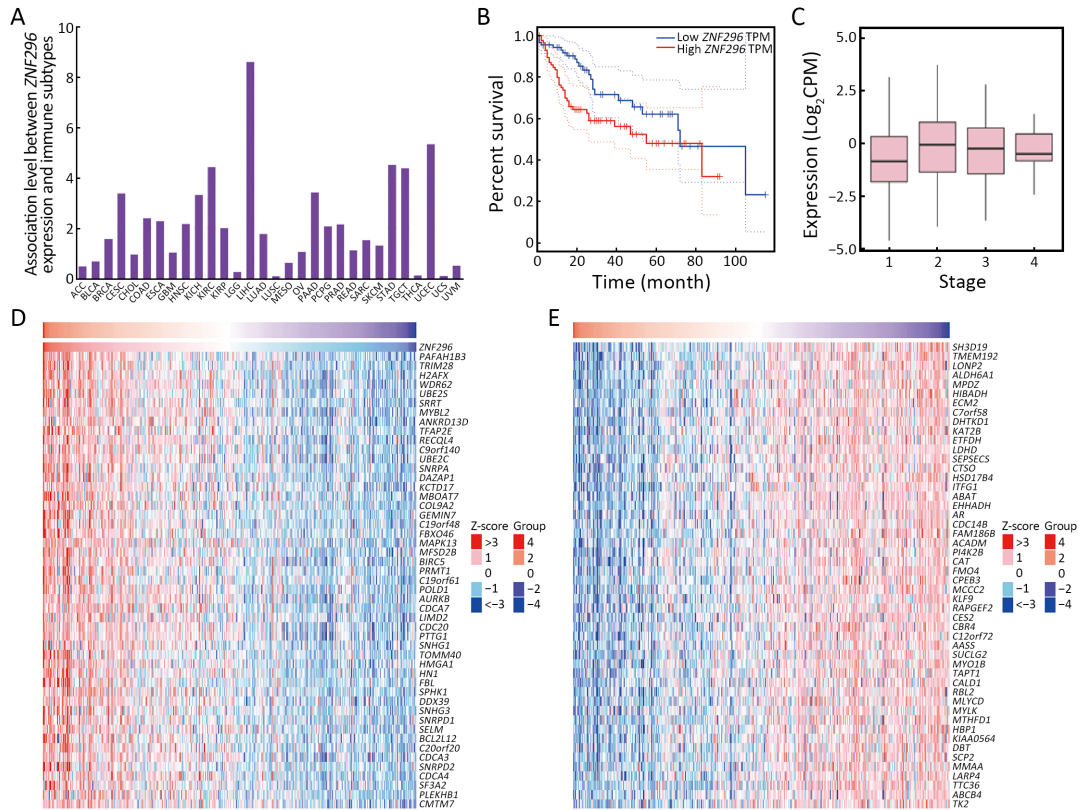
Figure S3 *ZNF296* is the specific high-expression molecule of HCC with poor prognosis. (A) Histogram showing the association between *ZNF296* expression and immune subtypes in human cancers; (B) Kaplan-Meier analysis of TCGA database of OS of patients with high or low *ZNF296* expression (Log-rank P=0.023); (C) Boxplot showing the associations between the expression of *ZNF296* and LIHC stage (r=0.14, P=0.007); (D,E) Heatmap after differential analysis shows the upregulated (D) and downregulated (E) genes in the high-expression samples of ZNF296. HCC, hepatocellular carcinoma; TCGA, The Cancer Genome Atlas; OS, overall survival; TPM, transcripts per million mapped reads; CPM, counts per million; ACC, adrenocortical carcinoma; BLCA, bladder urothelial carcinoma; BRCA, breast invasive carcinoma; CESC, cervical squamous cell carcinoma and endocervical adenocarcinoma; CHOL, cholangiocarcinoma; COAD, colon adenocarcinoma; ESCA, esophageal carcinoma; GBM, glioblastoma multiforme; HNSC, head and neck squamous cell carcinoma; KICH, kidney chromophobe; KIRC, kidney renal clear cell carcinoma; KIRP, kidney renal papillary cell carcinoma; LGG, lower grade glioma; LIHC, liver hepatocellular carcinoma; LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma; MESO, mesothelioma; OV, ovarian serous cystadenocarcinoma; PAAD, pancreatic adenocarcinoma; PCPG, pheochromocytoma and paraganglioma; PRAD, prostate adenocarcinoma; READ, rectum adenocarcinoma; SARC, sarcoma; SKCM, skin cutaneous melanoma; STAD, stomach adenocarcinoma; TGCT, testicular germ cell tumor; THCA, thyroid carcinoma; LICEC, large intestinal cancer; UCS, uterine carcinosarcoma; UVM, uveal melanoma.
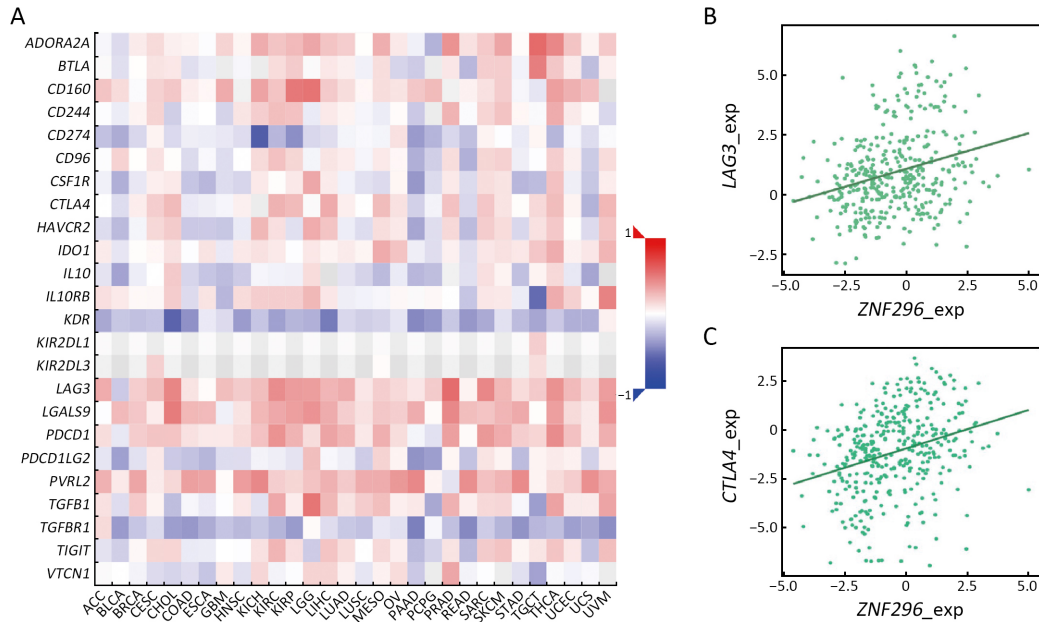
Figure S4 High expression of *ZNF296* is correlated with expression of *LAG3* and *CTLA4*. (A) Heatmap showing Spearman correlations between the expression of *ZNF296* and immune inhibitors in human cancers; (B) Scatter plot showing the correlation between *ZNF296* and *LAG3* expression (r=0.27); (C) Scatter plot showing the correlation between *ZNF296* and *CTLA4* expression (r=0.31). *LAG3*, lymphocyte activation gene-3; *CTLA4,* cytotoxic T-lymphocyte associated protein 4; ACC, adrenocortical carcinoma; BLCA, bladder urothelial carcinoma; BRCA, breast invasive carcinoma; CESC, cervical squamous cell carcinoma and endocervical adenocarcinoma; CHOL, cholangiocarcinoma; COAD, colon adenocarcinoma; ESCA, esophageal carcinoma; GBM, glioblastoma multiforme; HNSC, head and neck squamous cell carcinoma; KICH, kidney chromophobe; KIRC, kidney renal clear cell carcinoma; KIRP, kidney renal papillary cell carcinoma; LGG, lower grade glioma; LIHC, liver hepatocellular carcinoma; LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma; MESO, mesothelioma; OV, ovarian serous cystadenocarcinoma; PAAD, pancreatic adenocarcinoma; PCPG, pheochromocytoma and paraganglioma; PRAD, prostate adenocarcinoma; READ, rectum adenocarcinoma; SARC, sarcoma; SKCM, skin cutaneous melanoma; STAD, stomach adenocarcinoma; TGCT, testicular germ cell tumors; THCA, thyroid carcinoma; LICEC, large intestinal cancer; UCS, uterine carcinosarcoma; UVM, uveal melanoma.
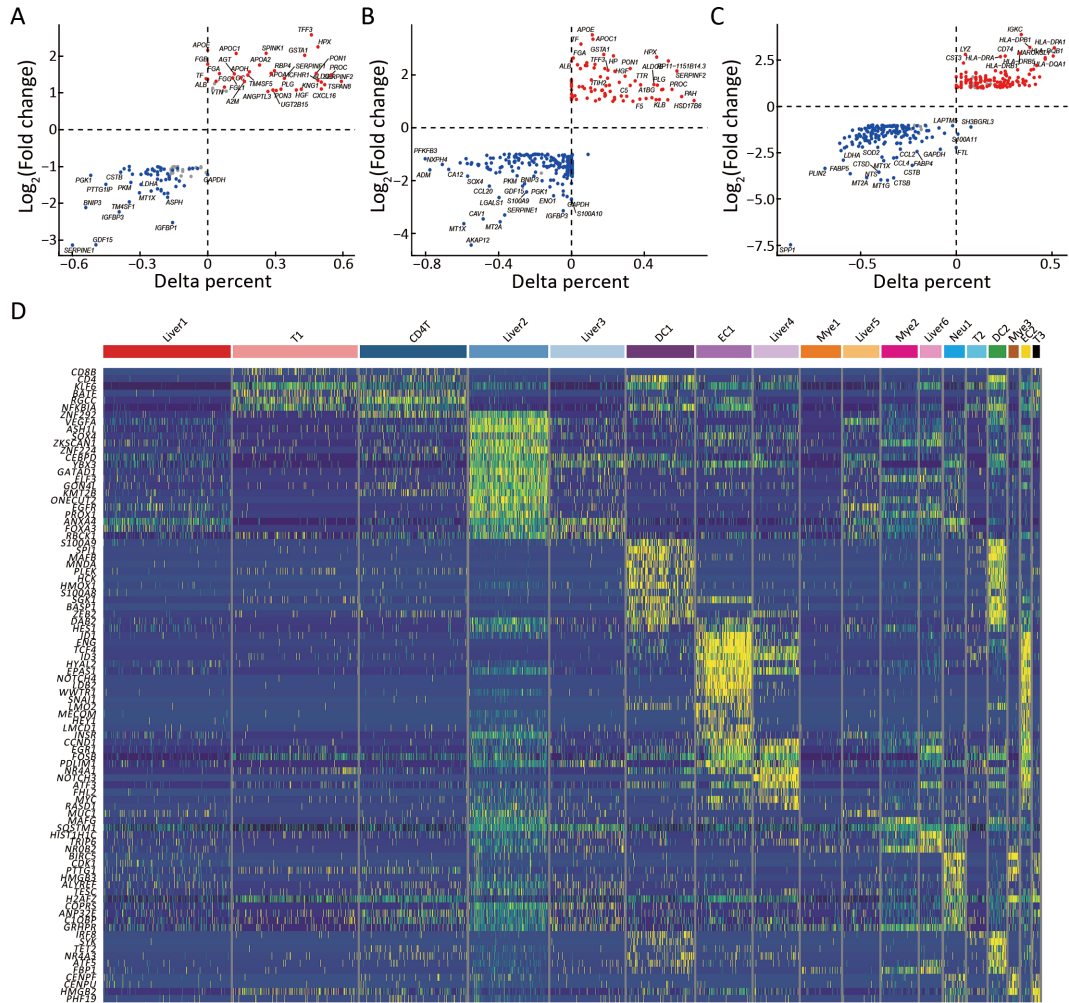
Figure S5 Survival of patients with HCC depends on the normal function of liver and DC cells. (A–C) Differential expression analysis was performed to identify genes enriched in Liver 1 (A), Liver 2 (B), and DC1 (C) cells. For each subtype, the average log fold change and percentage of cells expressing the gene above background were compared between the two clusters (right); (D) Heatmap showing the top-expressed TFs of the 18 cell clusters. HCC, hepatocellular carcinoma; T, CD8+ T cell; CD4T, CD4+ T cell; DC, dendritic cell; EC, endothelial cell; Neu, neutrophil; Liver, liver cell; Mye, myeloid cell.