Figure S1. Pan-cancer analysis of $C1QB$ expression

(A) Plot showing the expression of $C1QB$ in normal (left) or tumor (right) samples from multiple cancer types. The figure was generated based on the transcriptomic data from the TNMplot database (https://tnmplot.com/analysis/). (B) Plot indicating $C1QB$ levels in normal and tumor samples. The figure was generated on the transcriptomic data from the TIMER database (https://cistrome.shinyapps.io/timer/).
Figure S2. Differential expression analysis of *C1QBP* in diverse databases

(A-E) Differential expression analysis of *C1QBP* between normal (N) and HCC tumor samples (T) in the TNMplot database including all the samples (A) or only paired samples (B), in the UALCAN database (http://ualcan.path.uab.edu; C) and the GEPIA2 database (http://gepia2.cancer-pku.cn/) including all the samples (D) or without the GTEx normal samples (E).
Figure S3. Survival analysis of C1QBP in databases

(A) Overall survival analysis of HCC patients stratified by C1QBP expression in the GEPIA2 database. (B-E) Overall survival analysis (B), 1-year survival analysis (C), 3-year survival analysis (D) or 5-year survival analysis (E) of HCC patients stratified by C1QBP expression in the Kaplan-Meier Plotter database.
Figure S4. Enrichment of C1QBP associated genes

(A) Volcano plot showing the associated genes of C1QBP. (B, C) Heat map showing the positively (B) and negatively (C) corelated genes of C1QBP. All the associations were analyzed based on the TCGA-LIHC database using the LinkedOmics platform (http://www.linkedomics.org/).
Figure S5. GO and KEGG analysis of C1QBP associated processes and pathways

(A-C) GO analysis of C1QBP correlated biological process (BP; A), molecular function (MF; B) and cellular component (CC; C). (D) KEGG analysis of C1QBP correlated biological pathways.
Figure S6. Correlation between C1QBP expression and immune cell infiltration

(A) Plots showing the levels of C1QBP mRNA and infiltration of various immune cells. (B) Plots indicating the copy number variance of C1QBP gene and infiltration of various immune cells. The expression data for Figure A and B were derived from the TCGA-LIHC database and analyzed by the TIMER platform (https://cistrome.shinyapps.io/timer/). (C) Forest plot showing the correlation between C1QBP expression and 24 immune cells. Immune infiltration analysis was performed by single-sample gene set enrichment analysis (ssGSEA) in the “GSVA” R package, and the infiltration levels of 24 immune cell types were quantified from gene expression profiles.
Figure S7. Correlation between C1QBP expression and known immune-related gene expression

Plots showing the levels of C1QBP mRNA and expression of various known immune-related genes by the TIMER platform.