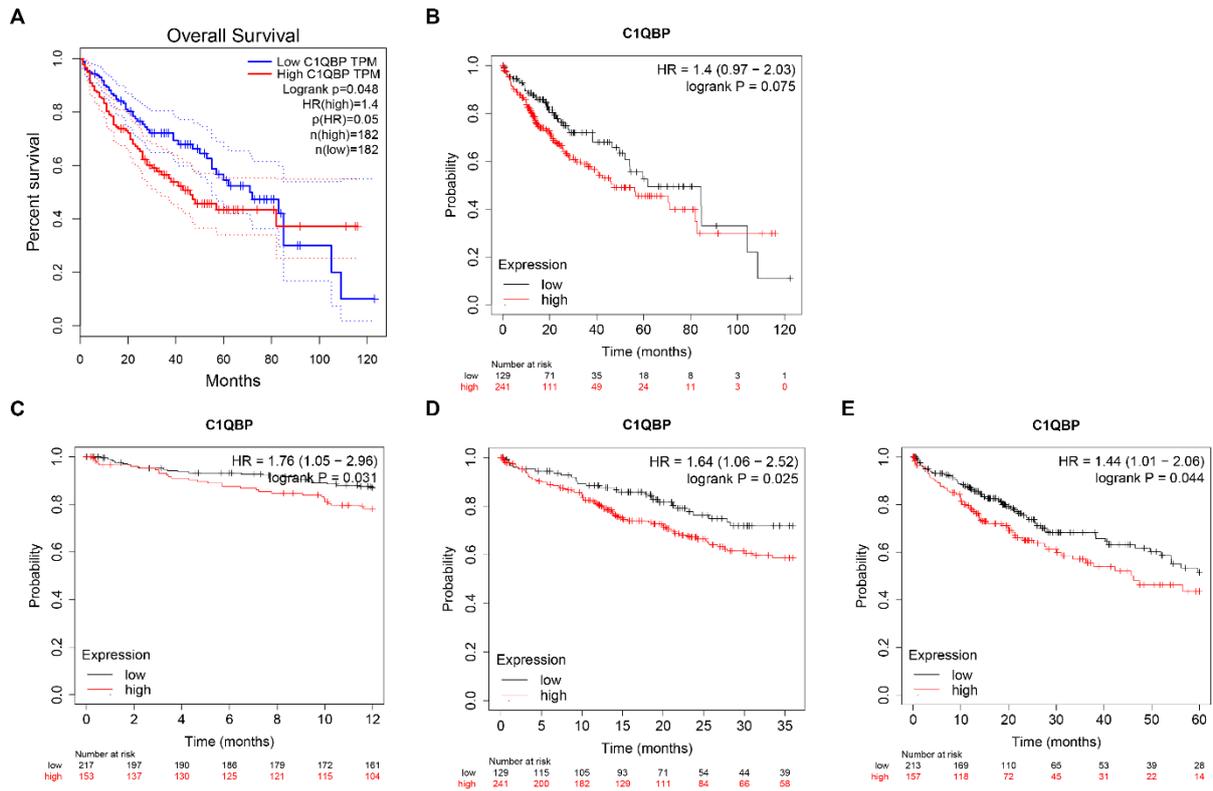


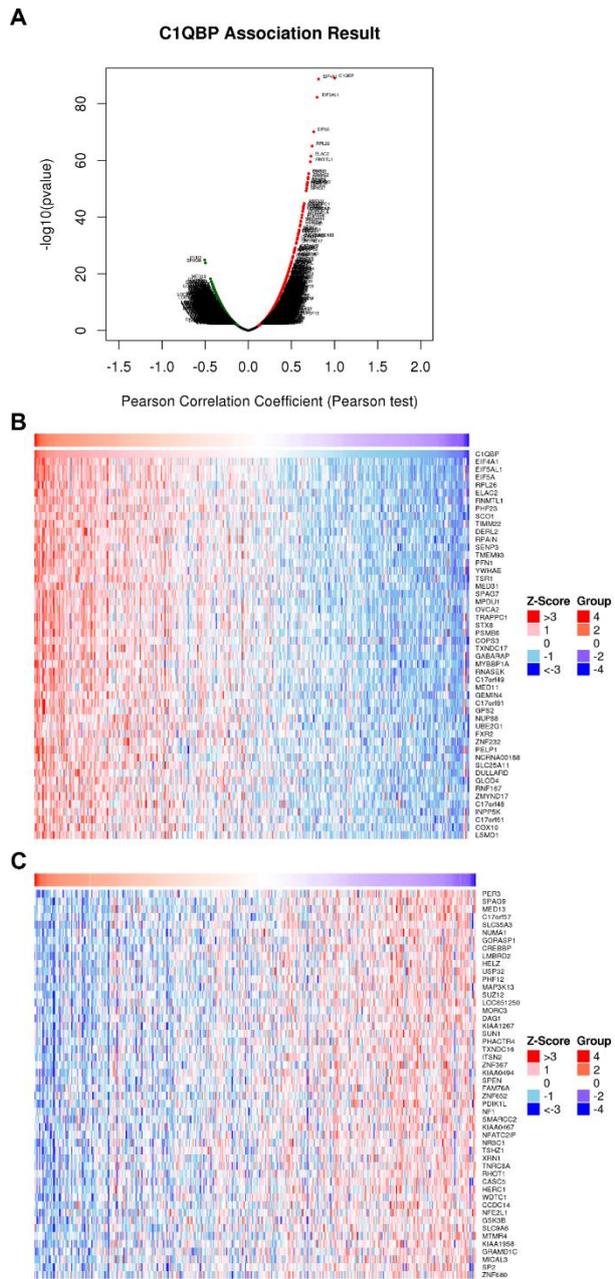
**Figure S2. Differential expression analysis of *CIQBP* in diverse databases**

(A-E) Differential expression analysis of *CIQBP* 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).



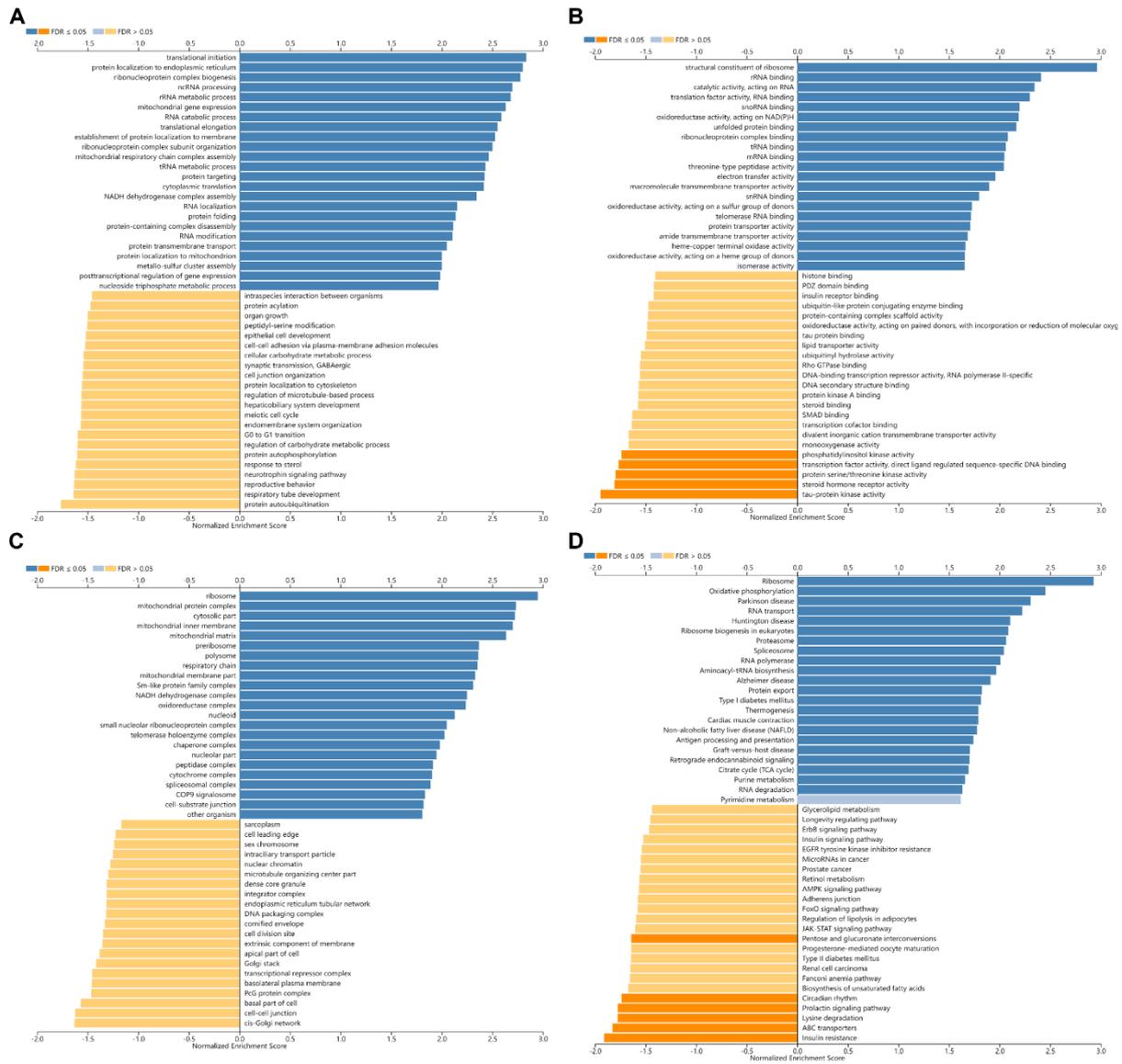
**Figure S3. Survival analysis of *CIQBP* in databases**

(A) Overall survival analysis of HCC patients stratified by *CIQBP* 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 *CIQBP* expression in the Kaplan-Meier Plotter database.



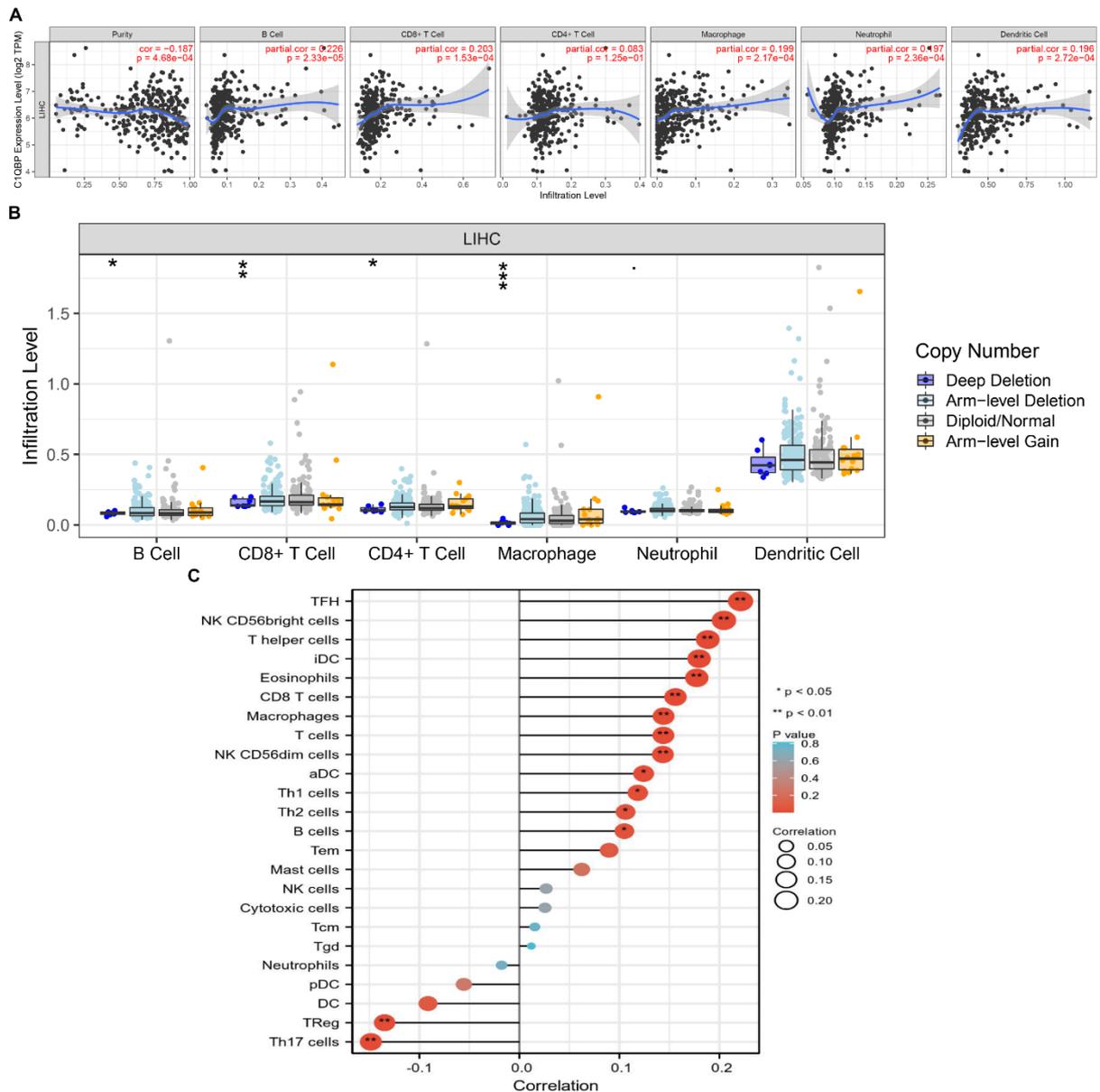
**Figure S4. Enrichment of *C1QBP* associated genes**

(A) Volcano plot showing the associated genes of *C1QBP*. (B, C) Heat map showing the positively (B) and negatively (C) correlated genes of *C1QBP*. All the associations were analyzed based on the TCGA-LIHC database using the LinkedOmics platform (<http://www.linkedomics.org/>).



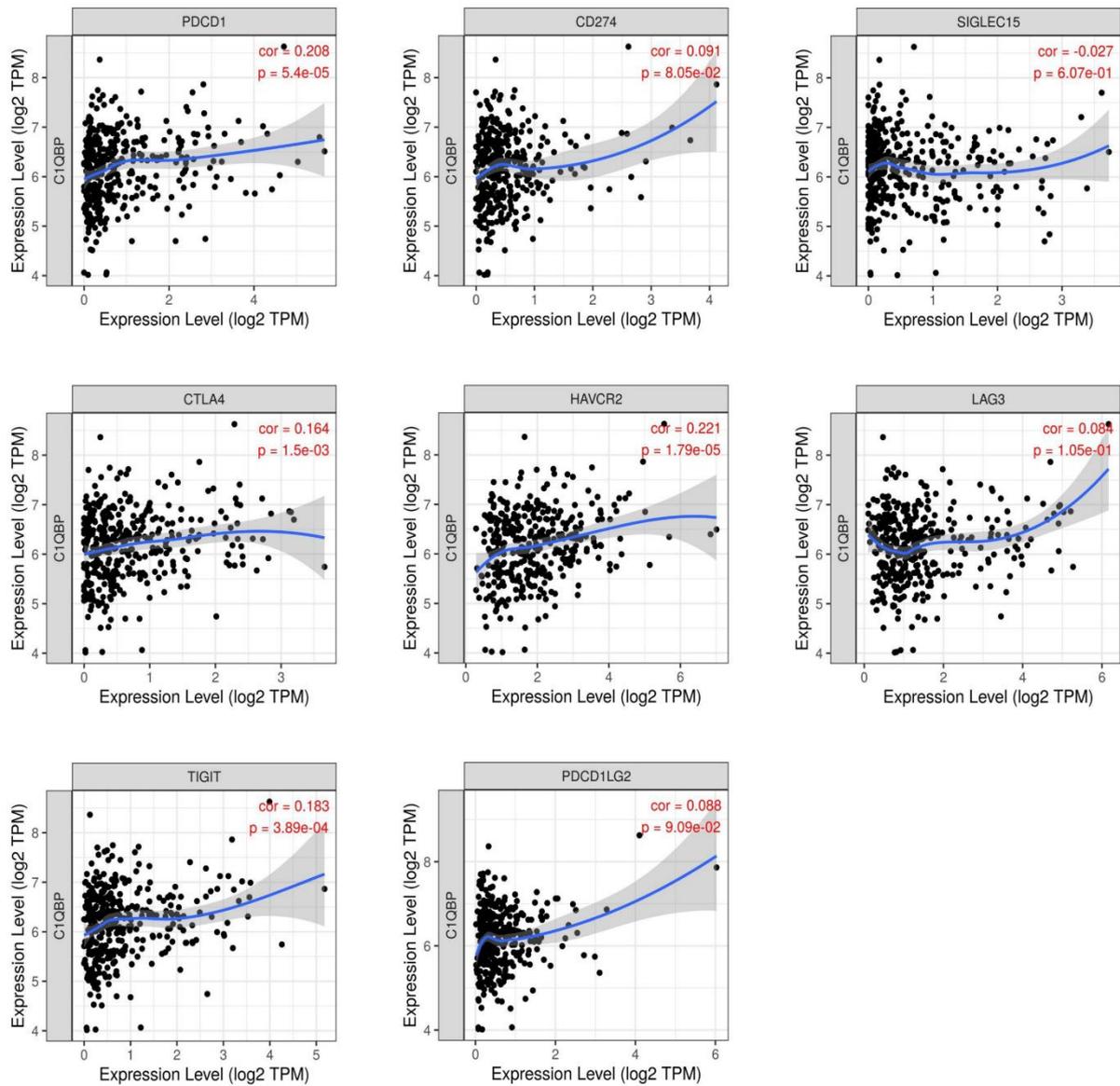
**Figure S5. GO and KEGG analysis of *CIQBP* associated processes and pathways**

(A-C) GO analysis of *CIQBP* correlated biological process (BP; A), molecular function (MF; B) and cellular component (CC; C). (D) KEGG analysis of *CIQBP* correlated biological pathways.



**Figure S6. Correlation between *CIQBP* expression and immune cell infiltration**

(A) Plots showing the levels of *CIQBP* mRNA and infiltration of various immune cells. (B) Plots indicating the copy number variance of *CIQBP* 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 *CIQBP* 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 *CIQBP* expression and known immune-related gene expression**

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