

Figure S1. Expression and correlation of curcumin target genes in HCC. (A) The interactive relationship among curcumin target genes. The Search Tool for the Retrieval of Interacting Genes/Proteins online tool (cn.string-db.org/cgi/input.pl) was utilized to analyze the relationship of the target genes by using the confidence interaction score of 0.7. (B) The Gene Ontology (bioconductor.org/packages/release/data/annotation/html/GO.db.html) and Kyoto Encyclopedia of Genes and Genomes ([https://bioconductor.org/packages/2.7/data/annotation/html/KEGG.db.html](http://bioconductor.org/packages/2.7/data/annotation/html/KEGG.db.html)) enrichment of the curcumin target genes. ID conversion of the candidate target genes using the org.Hs.eg.db package (version 3.11.4), enrichment analysis was performed using clusterProfiler package (version 3.12.0) and bubble plots were generated using the ggplot2 package (version 2.0.0). (C) mRNA expression levels of the curcumin target genes in HCC. RNA sequencing data in the TCGA-LIHC cohort (<http://portal.gdc.cancer.gov>) was used. P-values are indicated by ns ($P>0.05$), $**P\leq 0.01$ and $***P\leq 0.001$. (D) The expression correlations of the curcumin target genes. The RNA sequencing data in the TCGA-LIHC cohort (<http://portal.gdc.cancer.gov>) was used to determine the correlations between the gene expression levels using Pearson's correlation test. The data presented in the grid are the correlation coefficients. HCC, hepatocellular carcinoma; PTPN1, protein tyrosine phosphatase non-receptor type 1; HSP90AA1, heat shock protein 90 α -family class a member 1; KCNH2, potassium voltage-gated channel subfamily h member 2; F10, coagulation factor X; TCGA, The Cancer Genome Atlas; LIHC, liver hepatocellular carcinoma; ns, not significant; TPM, transcripts per kilobase million.

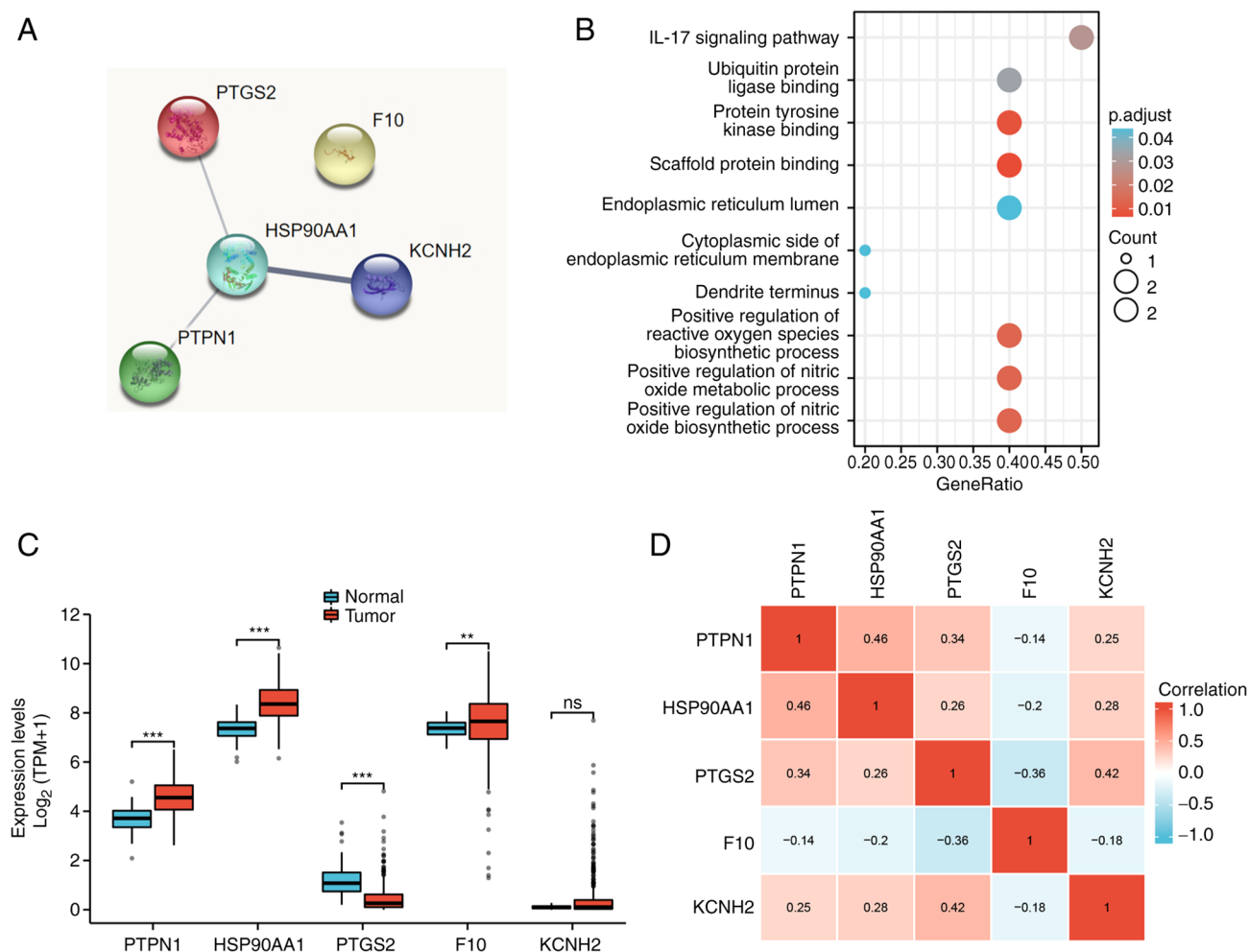


Figure S2. Prognostic analyses of the curcumin target genes. Overall survival of patients with HCC and high or low expression of (A) PTPN1, (B) HSP90AA1, (C) PTGS2, (D) KCNH2 and (E) F10. Disease specific survival of patients with HCC and high or low expression of (F) PTPN1, (G) HSP90AA1, (H) PTGS2, (I) KCNH2 and (J) F10. Progress free interval of patients with HCC and high or low expression of (K) PTPN1, (L) HSP90AA1, (M) PTGS2, (N) KCNH2 and (O) F10. The Kaplan-Meier plots were made using survminer (version 0.4.4) in R (version 4.0.3) and the two-stage test using the TSHRC (version 0.1.6) package based on the RNA sequencing data in the TCGA-LIHC cohort (portal.gdc.cancer.gov). TSPV, P-value of the two-stage test; HCC, hepatocellular carcinoma; PTPN1, protein tyrosine phosphatase non-receptor type 1; HSP90AA1, heat shock protein 90 α -family class a member 1; KCNH2, potassium voltage-gated channel subfamily h member 2; F10, coagulation factor X; HR, hazard ratio; TCGA, The Cancer Genome Atlas; LIHC, liver hepatocellular carcinoma.

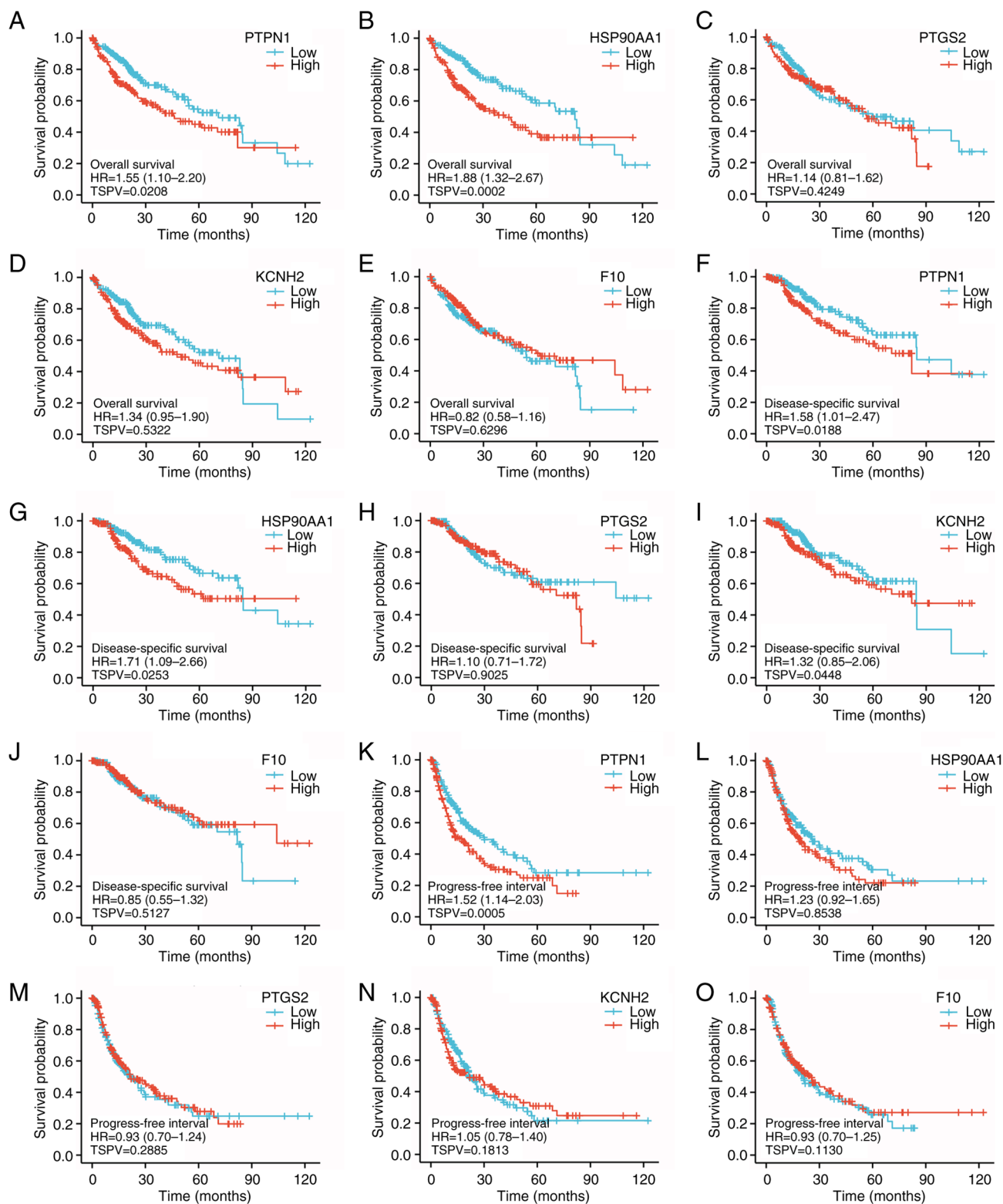


Figure S3. PTPN1 overexpression in different types of cancer. mRNA expression levels in 18 different types of cancer as determined using the RNA sequencing data in the TCGA-LIHC cohort (<http://portal.gdc.cancer.gov>). PTPN1 mRNA levels in normal (blue boxes) and cancer tissues (red boxes) of the bladder, thyroid, kidney, colon, lung, prostate, cervix uteri, bile duct and breast. ** $P \leq 0.01$, *** $P \leq 0.001$. TCGA, The Cancer Genome Atlas; PTPN1, protein tyrosine phosphatase non-receptor type 1; TPM, transcripts per kilobase million; BLCA, bile duct cancer; BRCA, breast cancer; CESC, cervical cancer; CHOL, colon and rectal cancer; COAD, colon cancer; ESCA, esophageal cancer; HNSC, head neck cancer; KIRC, kidney clear cell carcinoma; KIRP, kidney papillary cell carcinoma; LIHC, liver hepatocellular carcinoma; LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma; PAAD, pancreatic cancer; PRAD, prostate cancer; READ, rectal cancer; STAD, stomach cancer; THCA, thymoma; UCEC, endometrioid cancer.

