

Data S1

DCTN2 inhibited cellular senescence through targeting TRIM21 mediated MST2 ubiquitination and activation in hepatocellular carcinoma

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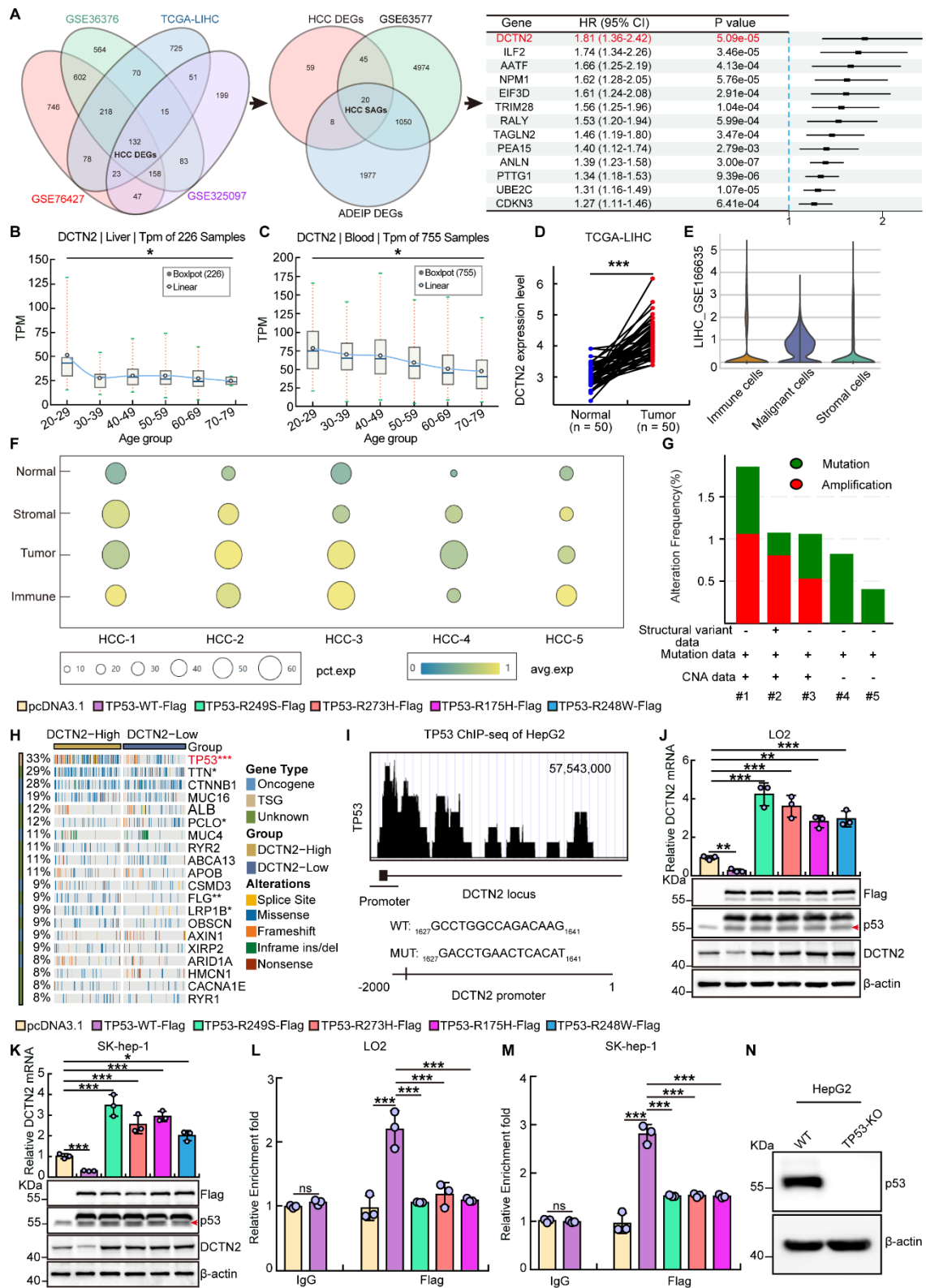


Figure S1. Senescence-related gene DCTN2 was up-regulated by TP53 mutation in HCC. (A)

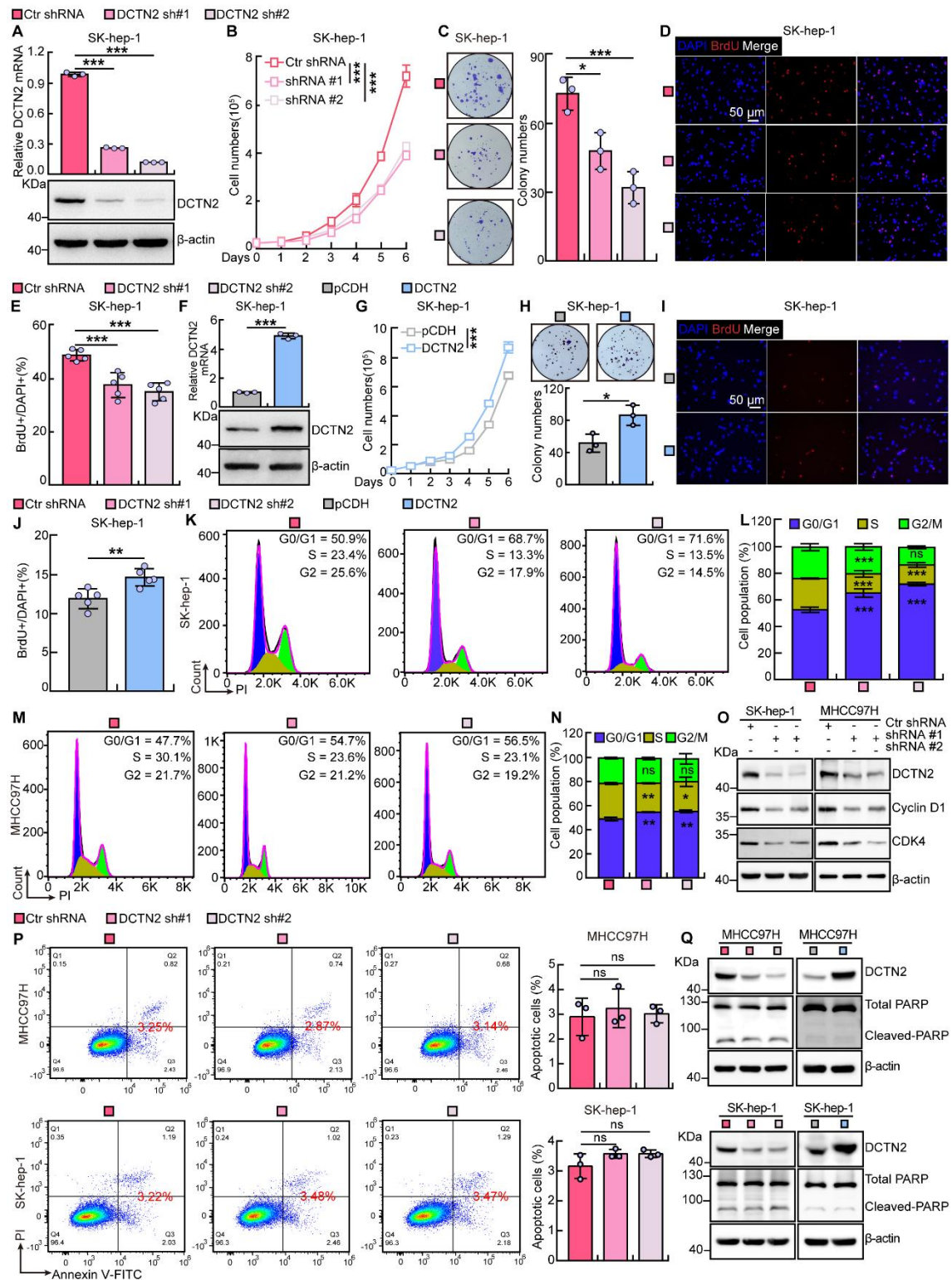
Identification of 20 core HCC senescence-associated genes via Venn diagram intersection of multi-dataset DEGs including GSE76427 ($|\text{LogFC}| > 0.58$, $P < 1\text{E-}10$), GSE36376 ($|\text{LogFC}| > 0.58$, $P < 1\text{E-}10$), GSE325097 ($|\text{LogFC}| > 1$, $P < 0.05$), TCGA-LIHC GSE63577 ($P < 0.05$) and ADEIP DEGs ($P < 0.05$), accompanying with Cox proportional hazards model analysis for these 20 genes in TCGA-LIHC dataset.

(B-C) The mean *DCTN2* transcripts per million across six age groups were retrieved from the ADEIP database for both 226 liver samples and 755 blood samples derived from healthy individuals. **(D)** Expression levels of *DCTN2* in paired normal and tumor tissues extracted from the TCGA-LIHC dataset.

(E) Distribution of *DCTN2* expression across distinct cell types (immune cells, malignant cells and stromal cells) in the single-cell RNA sequencing (scRNA-seq) analysis from GSE166635 dataset, visualized as a violin plot. **(F)** Cell-type-specific spatial expression of *DCTN2* from five HCC samples, visualized across four cellular compartments. Dot size = proportion of expressing cells; color = average expression intensity.

(G) Alteration frequency of *DCTN2* (mutation and amplification) in diverse hepatocellular carcinoma cohorts from online cBioPortal repository, indicating CNA, mutation, and structural variant data availability. The datasets were denoted as #5: HCC (CLCA, Nature 2024), #4: HCC (INSERM, Nat Genet 2015), #3: HCC (TCGA GDC, 2025), #2: LIHC (TCGA, PanCancer Atlas), #1: LIHC (TCGA, Firehose Legacy). **(H)** Waterfall plot showed the mutation distribution of the top 20 most frequently mutated genes in TCGA-LIHC cohort from CAMOIP database, grouped by *DCTN2* expression status. **(I)** The *DCTN2* promoter contained a predicted TP53 binding site identified by ChIP-seq. Data were obtained from the ENCODE project. **(J-K)** The relative expression levels of *DCTN2* were detected via RT-qPCR (top) and immunoblotting (bottom) in LO2 (J) and SK-hep-1 (K) cells transfected with pcDNA3.1, TP53-WT-Flag, TP53-R249S-Flag, TP53-R175H-Flag, TP53-R248W-Flag, and TP53-R273H-Flag. The red arrow marked

the endogenous p53 protein band. **(L-M)** CUT&Tag and qPCR assays showed the enrichment of Flag-tagged TP53 and mutants at the DCTN2 promoter in LO2 (L) and SK-hep-1 (M) cells, with IgG serving as a negative control. **(N)** Immunoblotting was applied to assess TP53 knockout efficacy in HepG2 cells. Bars indicate mean $\pm$ SD. ns, no significant difference. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.



by daily counting. **(C)** DCTN2 knockdown reduced the colony formation ability of SK-hep-1 cells. **(D-E)** DCTN2 knockdown reduced BrdU positive staining cells determined by the BrdU incorporation assay in SK-hep-1 cells. **(E)** Quantification data for **(D)**. Scale bar = 50 μ m. **(F)** Establishment of DCTN2 overexpression in SK-hep-1 cells, verified by RT-qPCR (top) and immunoblot (bottom). **(G)** The indicated cell growth was examined by daily counting. **(H)** DCTN2 overexpression elevated the colony formation ability of SK-hep-1 cells. **(I-J)** In SK-hep-1 cells, BrdU incorporation assay showed DCTN2 overexpression increased BrdU-positive cells. **(J)** Quantification data for **(I)**. Scale bar = 50 μ m. **(K-N)** DCTN2 knockdown increased G0/G1 phase cell populations as examined by FACS analysis. **(L, N)** Quantitative data corresponding to **(K, M)** respectively. **(O)** Depletion of DCTN2 decreased CyclinD1 and CDK4 expression. **(P)** Annexin V/PI flow cytometry quantification of apoptotic MHCC97H and SK-hep-1 cells with DCTN2 knockdown. **(Q)** Immunoblotting for DCTN2, total/cleaved PARP in DCTN2 silenced HCC cells. Bars indicate mean $\pm$ SD. ns, no significant difference. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.

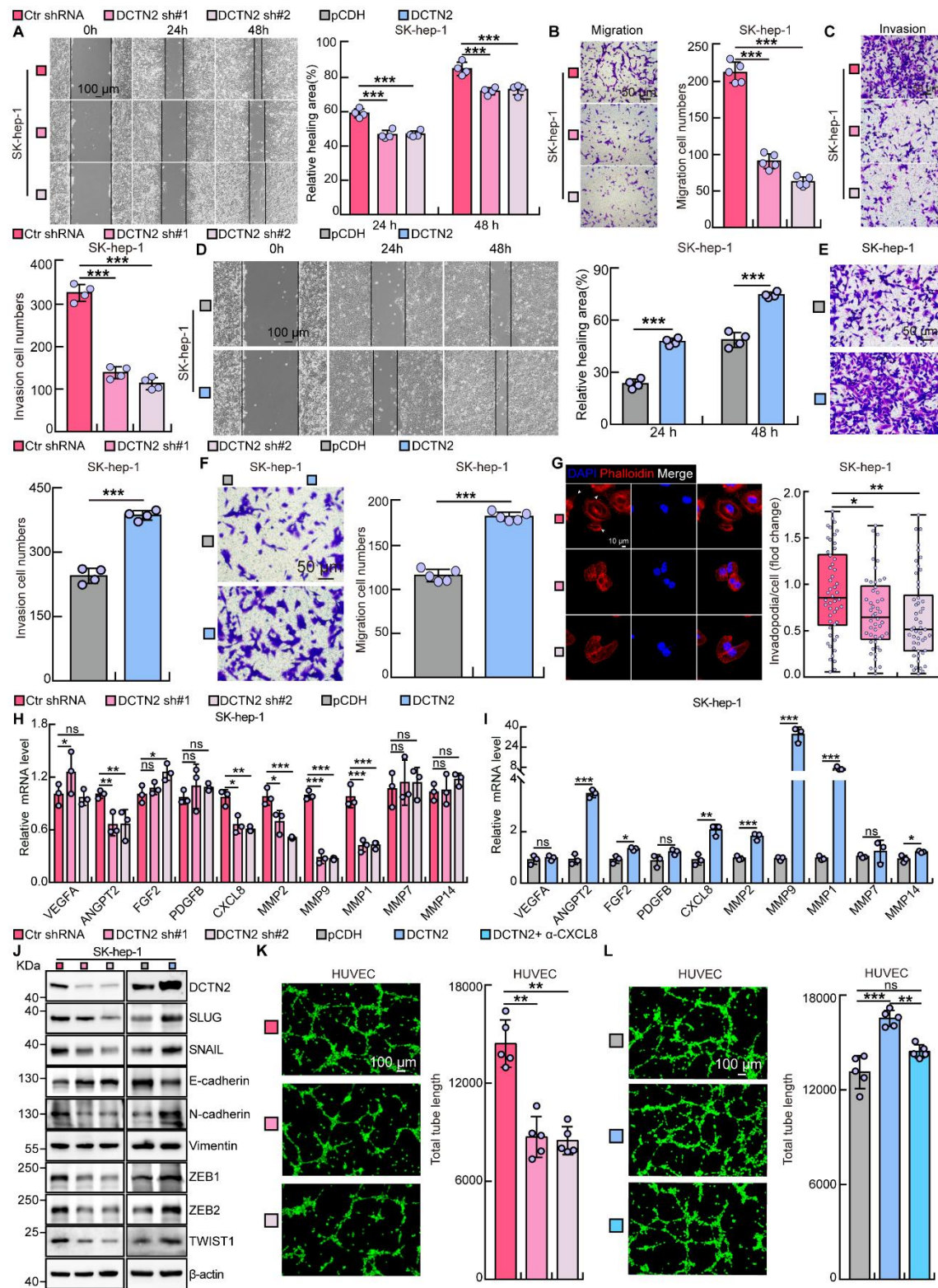
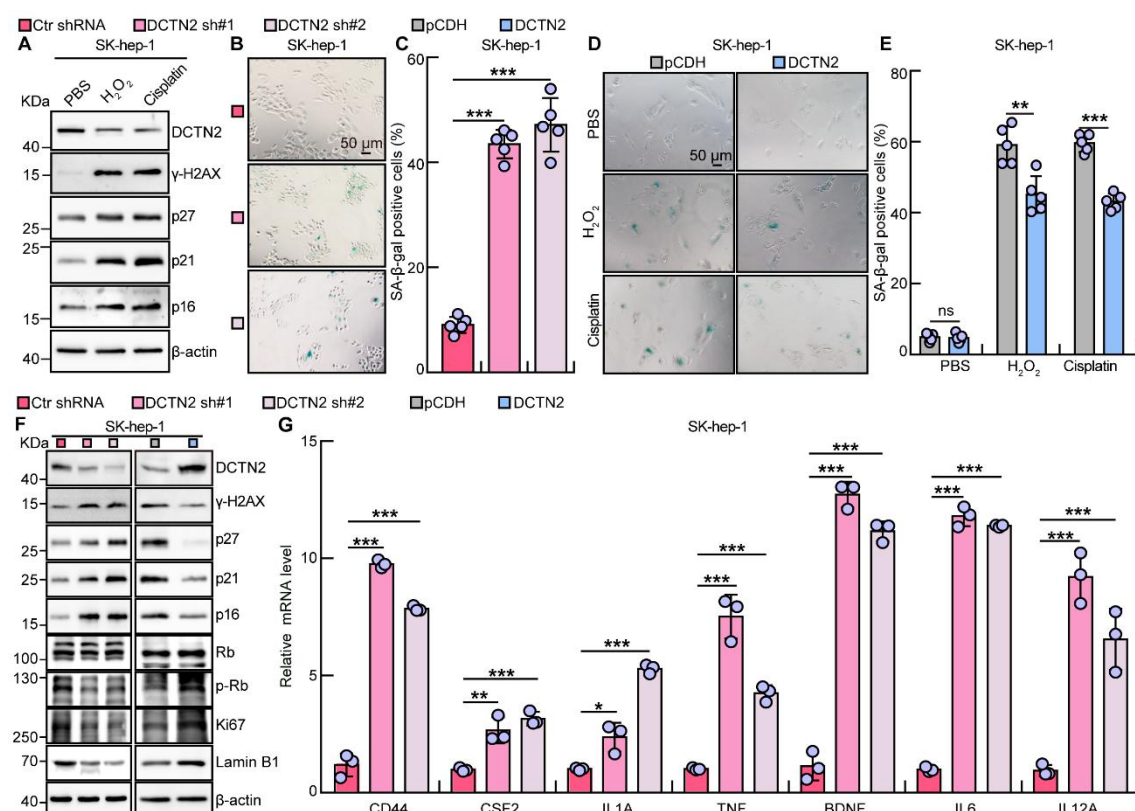


Figure S3. Ablation of DCTN2 suppressed tumor cell migration. (A-C) Wound healing (A), trans-well

(C), and invasion (E) assays were conducted for evaluating how DCTN2 knockdown affected the migration

ability of SK-hep-1 cells, and quantification data were displayed in the panel on the right. Scale bars = 100 μm (A), 50 μm (B, C). **(D-F)** Wound healing (D), invasion (E), and trans-well (F) assays were used to detect the migratory ability of SK-hep-1 cells with DCTN2 overexpression. **(G)** The indicated cells underwent IF staining with phalloidin, and white head arrows highlighted structures that took on a pseudopodia-like appearance. Scale bar = 10 μm . **(H-I)** RT-qPCR quantification of pro-angiogenic mediators in SK-hep-1 cells with DCTN2 knockdown (H) or overexpression (I). **(J)** The protein expressions of SLUG, SNAIL, E-cadherin, N-cadherin, Vimentin, ZEB1, ZEB2 and TWIST1 in SK-hep-1 knockdown or overexpression cell extracts. **(K)** The capacity of primary HUVECs to form tubes was inhibited when treated with CM collected from SK-hep-1 cells with DCTN2 knockdown. Scale bar = 100 μm . **(L)** Ectopic DCTN2 overexpression promoted HUVEC angiogenesis, whereas neutralizing CXCL8 (3 $\mu\text{g/mL}$) partially abrogated this phenotype. Scale bar = 100 μm . Bars indicate mean $\pm$ SD. ns, no significant difference. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.



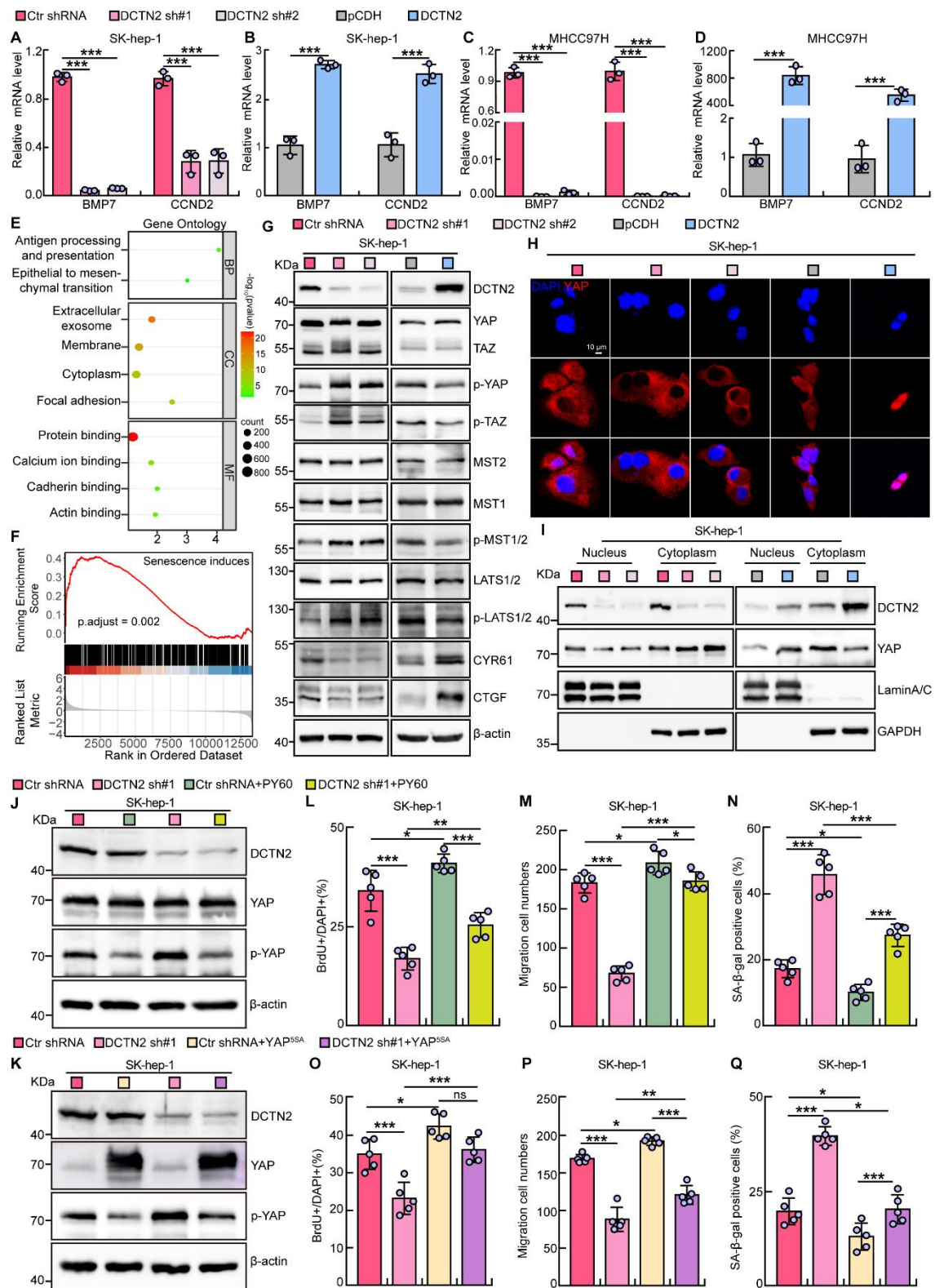


Figure S5. DCTN2 restrained the Hippo signaling pathway. (A-D) RT-qPCR was performed to validate BMP7 and CCND2, the downstream genes of DCTN2 identified from RNA-seq results. (E) GO enrichment

analysis of DEGs identified relevant pathways perturbed by DCTN2 depletion. **(F)** GSEA analysis from RNA-seq data indicated the involvement of DCTN2 in HCC cellular senescence. **(G)** Western blot was used to detect the protein levels of key Hippo signaling pathway components and its downstream target genes CYR61, CTGF in SK-hep-1 cells under DCTN2 overexpression or knockdown. **(H-I)** Immunofluorescence staining (H) and western blot of nucleus-cytoplasm fractionation (I) were utilized to determine the subcellular localization of YAP in SK-hep-1 cells. Scale bar = 10 μ m. **(J-K)** Immunoblotting was employed to validate the protein levels of DCTN2, YAP and p-YAP in indicated SK-hep-1 cells. **(L-Q)** Treatment with PY60 or ectopic expression of YAP^{5SA} was able to restore the phenotypes in DCTN2-deleted SK-hep-1 cells. Bars indicate mean $\pm$ SD. ns, no significant difference. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.

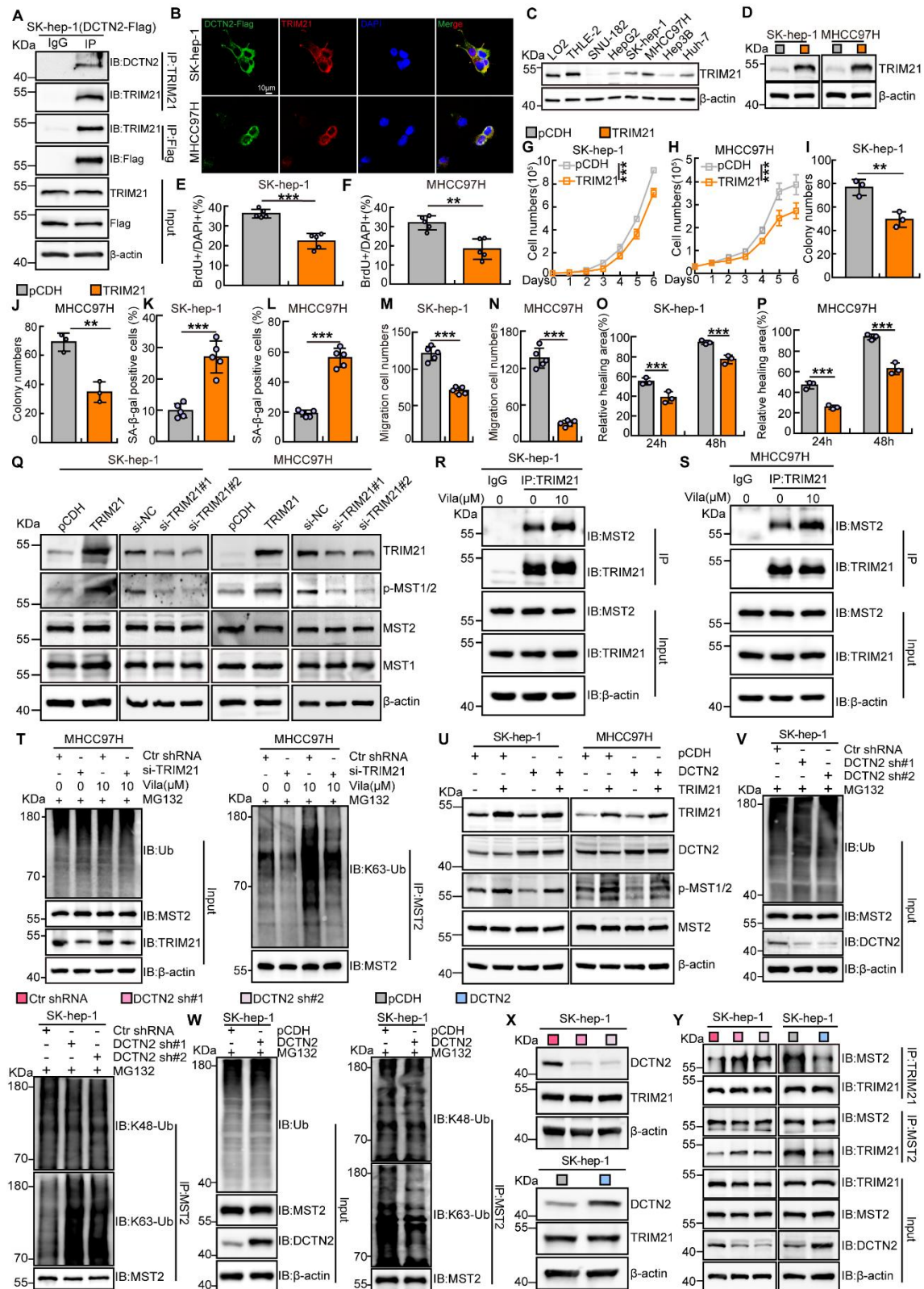


Figure S6. TRIM21 suppressed HCC malignancy. (A) Co-IP assay using Flag and TRIM21 antibodies

in DCTN2-Flag overexpressing SK-hep-1 cells. IgG was used as a negative control. (B)

Immunofluorescence assay indicated the co-localization of DCTN2 with TRIM21 in SK-hep-1 and MHCC97H cells. **(C)** The relative expression level of TRIM21 in HCC cell lines including LO2, THLE-2, SNU-182, HepG2, SK-hep-1, MHCC97H, Hep3B and Huh7 examined by immunoblotting assay. **(D)** TRIM21-overexpressing SK-Hep-1 and MHCC97H cell lines were established and verified via western blot. **(E-J)** TRIM21 overexpression decreased SK-hep-1 and MHCC97H cells' proliferation abilities by BrdU incorporation (E, F), growth curve (G, H), and colony formation experiments (I, J). **(K-L)** β -gal staining quantification result of SK-hep-1 (K) and MHCC97H (L) cells with stable overexpression of DCTN2. **(M-P)** Forced expression of TRIM21 inhibited cell migration in trans-well assays (M, N) and wound healing (O, P). **(Q)** The protein expressions of TRIM21, p-MST1/2, MST2, and MST1 were detected by immunoblot with the indicated antibodies in SK-hep-1 and MHCC97H cell extracts. **(R-S)** Co-IP analysis demonstrating that vilazodone enhanced endogenous TRIM21-MST2 interaction in SK-hep-1 (R) and MHCC97H (S) HCC cells. Cells were exposed to 0 or 10 μ M vilazodone. IgG served as negative control for immunoprecipitation. **(T)** Ubiquitination analysis of MST2 in MHCC97H cells with TRIM21 knockdown and vilazodone intervention. **(U)** Western blot analysis of TRIM21, DCTN2, p-MST1/2 and MST2 expression in SK-hep-1 and MHCC97H cells transfected with or without DCTN2-expressing plasmid and TRIM21-expressing plasmid. **(V-W)** DCTN2 mainly mediated K63-linked polyubiquitination of MST2. SK-hep-1 cells with DCTN2 knockdown (V) or overexpression (W) were subjected to anti-MST2 immunoprecipitation, followed by *in vivo* ubiquitination assay to detect K48- and K63-linked polyubiquitination of MST2 using chain-specific antibodies. **(X)** Western blot was used to assess TRIM21 expression in MHCC97H cells with DCTN2 silencing or overexpression. **(Y)** Co-IP assay was performed to investigate the interaction between DCTN2 and TRIM21 in SK-hep-1 cells with DCTN2 overexpression

or knockdown. Bars indicate mean $\pm$ SD. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.

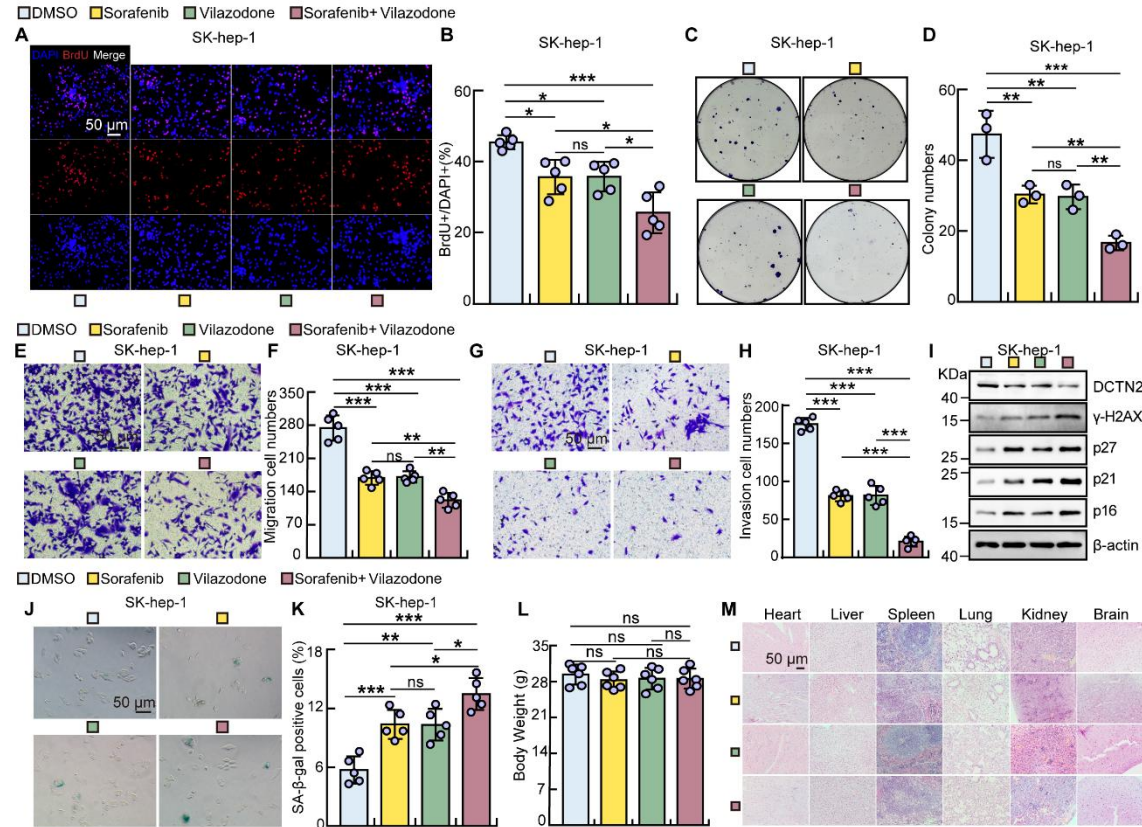


Figure S7. The TRIM21 activator vilazodone exhibited an additive therapeutic effect in combination with sorafenib. (A-D) The co-treatment with vilazodone and sorafenib led to an additive inhibition of SK-hep-1 cell proliferation, as evidenced by the BrdU incorporation assay (A) and colony formation assay (C). The statistical analyses for (A) and (C) were presented in (B) and (D), respectively. **(E-H)** The combination of vilazodone and sorafenib notably diminished the migration capacity of SK-hep-1 cells, as confirmed by trans-well assays (E) and invasion assays (G). The statistical data for (E) and (G) were presented in (F) and (H), respectively. **(I)** Western blot analysis was performed to assess the expression levels of DCTN2, γ -H2AX, p27, p21, and p16 proteins in SK-hep-1 cells treated with vilazodone and sorafenib. **(J-K)** The co-treatment with vilazodone and sorafenib resulted in an obvious induction of SK-hep-1 cell senescence, with

statistical data shown in (K) corresponding to (J). Scale bar = 50 μm . **(L)** There were no significant changes in the body weight of nude mice by treatment of SK-hep-1 with vilazodone in combination with sorafenib (n = 6 per group). **(M)** The heart, liver, spleen, lung, brain and kidney of nude mice were harvested, followed by H&E staining to assess potential drug toxicity. No noticeable morphological alterations were observed in the organs post-treatment with the drug. Scale bar = 50 μm . Bars indicate mean $\pm$ SD. ns, no significant difference. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.

Supplementary Tables

Table S1. Antibodies and oligos used in this study.

Antibody Name	Catalog number	Supplier	Species
p53	sc-126	Santa Cruz	Mouse
DCTN2	A2200	abclonal	Rabbit
p16	23200S	CST	Rabbit
β -actin	3700S	CST	Mouse
p21	2947S	CST	Rabbit
p27	3686S	CST	Rabbit
Ki67	RMA-0731	MXB	Rabbit
p-MST2	bs4634R	Bioss	Rabbit
p-MST1/2	AP1564	abclonal	Rabbit
CyclinD1	55506	CST	Rabbit
CDK4	553048	Biosciences	Mouse
γ -H2A.X	7631S	CST	Rabbit
YAP/TAZ	8418S	CST	Rabbit
p-YAP	4911S	CST	Rabbit
p-TAZ	AF4315	Affinity	Rabbit
MST1	22245-1-AP	proteintech	Rabbit
Snail	13099-1-AP	proteintech	Rabbit

Slug	12129-1-AP	proteintech	Rabbit
MST2	A9036	abclonal	Rabbit
MST2	PA5-29320	thermo	Mouse
LATS1/2	DF7517	Affinity	Rabbit
p-LATS1/2	AF8163	Affinity	Rabbit
K48-Ub	A3606	abclonal	Rabbit
K63-Ub	A18164	abclonal	Rabbit
CTGF	ER1802-69	HUABIO	Rabbit
CYR61	ER1905-70	HUABIO	Rabbit
YAP	14074S	CST	Rabbit
LaminA/C	81042-1-RR	proteintech	Rabbit
GAPDH	60004-1-Ig	proteintech	Mouse
Flag	14793S	CST	Rabbit
Flag	F1804	Sigma	Mouse
HA	SC-7392	Santa Cruz	Mouse
HA	3724S	CST	Rabbit
TRIM21	67136-1-Ig	proteintech	Mouse
TRIM21	DF6717	Affinity	Rabbit
Myc	2278S	CST	Rabbit
Ub	80992-1-RR	proteintech	Rabbit

RB	10048-2-Ig	proteintech	Rabbit
N-cadherin	22018-1-AP	proteintech	Rabbit
E-cadherin	20874-1-AP	proteintech	Rabbit
Vimentin	10366-1-AP	proteintech	Rabbit
PARP	9532S	CST	Rabbit
ZEB2	A5705	abclonal	Rabbit
ZEB1	EM1710-27	HUABIO	Mouse
TWIST1	25465-1-AP	Proteintech	Rabbit
P-RB	30376-1-AP	Proteintech	Rabbit
Ki-67	84192-4-RR	Proteintech	Rabbit
Lamin B1	13435S	CST	Rabbit
CXCL8	MAB208	R&D	Mouse
Primer Name	Primer Sequences (5'-3')		
Human β -actin_F	AAGTGTGACGTGGACATCCGC		
Human β -actin_R	CCGGACTCGTCATACTCCTGCT		
Human DCTN2_F	ATGGCGGACCCTAAATACGC		
Human DCTN2_R	TCAGGTAGGTCGCTAGTTTCATA		
Human p53_F	CAGCACATGACGGAGGTTGT		
Human p53_R	TCATCCAAATACTCCACACGC		
Ctr shRNA_F	GCACTACCAGAGCTAACTCAG		

Ctr shRNA_R	CTGAGTTAGCTCTGGTAGTGC
Human DCTN2 shRNA #1_F	GCCTCTGTAGAAGATGCAGAT
Human DCTN2 shRNA #1_R	ATCTGCATCTTCTACAGAGGC
Human DCTN2 shRNA #2_F	CAACTGTTTCTGACCATTAAA
Human DCTN2 shRNA #2_R	TTTAATGGTCAGAAACAGTTG
Negative Control siRNA_F	UUCUCCGAACGUGUCACGUTT
Negative Control siRNA_R	ACGUGACACGUUCGGAGAATT
Human p53 siRNA #1_F	CGGCGCACAGAGGAAGAGAAU
Human p53 siRNA #1_R	AUUCUCUUCCUCUGUGCGCCG
Human p53 siRNA #2_F	GUCCAGAUGAAGCUCCCAGAA
Human p53 siRNA #2_R	UUCUGGGAGCUUCAUCUGGAC
Human TRIM21 siRNA #1_F	GACUUCACCUGUUCUGUGATT
Human TRIM21 siRNA #1_R	UCACAGAACAGGUGAAGUCTT
Human TRIM21 siRNA #2_F	CAGCACGCUUGACAAUGAUTT
Human TRIM21 siRNA #2_R	AUCAUUGUCAAGCGUGCUGTT
Human CD44_F	GCCGCTTTGCAGGTGTATT
Human CD44_R	TCCATCTGGGCCATTGTG
Human CSF2_F	CCCTGGGAGCATGTGAAT
Human CSF2_R	GCCCTTGAGCTTGGTGAG
Human IL1A_F	GGTTGAGTTTAAGCCAATCCA

Human IL1A_R	TGCTGACCTAGGCTTGATGA
Human TNF_F	TCCAGGCGGTGCTTGTTTC
Human TNF_R	GGCTACAGGCTTGTCACCTCG
Human BDNF_F	CTCTTTCTGCTGGAGGAATACA
Human BDNF_R	CGCCGTTACCCACTCACT
Human IL6_F	GAAAGCAGCAAAGAGGCAC
Human IL6_R	GCTCTGGCTTGTTCTCACTAC
Human IL12A_F	TGGCTACCCTGGTCCTCCT
Human IL12A_R	GCCTCCACTGTGCTGGTTTTAT
Human BMP7_F	TCGGCACCCATGTTTCATGC
Human BMP7_R	GAGGAAATGGCTATCTTGCAGG
Human CCND2_F	TTTGCCATGTACCCACCGTC
Human CCND2_R	AGGGCATCACAAGTGAGCG
DNA Spike in Primer F	GCCTTCTTCCCATTCTGATCC
DNA Spike in Primer R	CACGAATCAGCGGTAAAGGT
hDCTN2 Cut&Tag qPCR primer_F	TCTGCTCAGCAACTGTCTGG
hDCTN2 Cut&Tag qPCR primer_R	TTCCCTTAAGATTCAAGGTAGGTT
Human VEGFA_F	AGGGCAGAATCATCACGAAGT
Human VEGFA_R	AGGGTCTCGATTGGATGGCA
Human ANGPT2_F	AACTTTCGGAAGAGCATGGAC

Human ANGPT2_R	CGAGTCATCGTATTCGAGCGG
Human FGF2_F	AGAAGAGCGACCCTCACATCA
Human FGF2_R	CGGTTAGCACACACTCCTTTG
Human PDGFB_F	CTCGATCCGCTCCTTTGATGA
Human PDGFB_R	CGTTGGTGCGGTCTATGAG
Human CXCL8_F	GACATACTCCAAACCTTTCCACC
Human CXCL8_R	AAACTTCTCCACAACCCTCTGC
Human MMP2_F	TACAGGATCATTGGCTACACACC
Human MMP2_R	GGTCACATCGCTCCAGACT
Human MMP9_F	TGTACCGCTATGGTTACACTCG
Human MMP9_R	GGCAGGGACAGTTGCTTCT
Human MMP1_F	AAAATTACACGCCAGATTGCCC
Human MMP1_R	GGTGTGACATTACTCCAGAGTTG
Human MMP7_F	GAGTGAGCTACAGTGGGAACA
Human MMP7_R	CTATGACGCGGGAGTTTAACAT
Human MMP14_F	GGCTACAGCAATATGGCTACC
Human MMP14_R	GATGGCCGCTGAGAGTGAC

Table S2. Bioinformatical databases used in this study.

Name	Link	Targets
ADEIP	https://gb.whu.edu.cn/ADEIP/	To investigate DCTN2 expression pattern in 226 liver and 755 blood samples across six age groups of healthy individuals.
HCCDB V2	http://lifeome.net/database/hccdb/home.html	To validate DCTN2 expression in the spatial transcriptomics data.
CAMOIP	http://www.zjyy-oncology.com:20002/	To explore the correlation between DCTN2 expression and TP53 mutation status.
GSEA	https://www.gsea-msigdb.org/gsea/index.jsp	To examine the correlation between DCTN2 and cellular senescence process.
KEGG	https://www.genome.jp/kegg/catalog/org_list.html	To examine DCTN2 regulated Hippo signaling pathway.
GO	http://geneontology.org/	To examine DCTN2 regulated Hippo signaling pathway.
Kaplan Meier Plotter	https://kmplot.com/analysis/index.php?p=background	To examine the correlation between DCTN2 and survival time of HCC patients.
ROC Plotter	https://www.rocplot.org/	To examine the correlation between DCTN2 and prognosis of HCC patients.

GEO	https://www.ncbi.nlm.nih.gov/geo/	To examine the expression of DCTN2 in different GEO datasets.
cBioPortal	http://www.cbioportal.org/	To examine the mutation and amplification status in HCC.
ENCODE	https://www.encodeproject.org/	To examine whether the DCTN2 promoter contains a predicted TP53 binding site

Table S3. Clinicopathological characteristics of liver cancer patients in this study.

Patient characteristics	Clinical parameters	Cases	Low expression	High expression	P value
Gender	Male	74	30	44	0.251
	Female	16	9	7	
Age (years)	< 60	68	39	29	0.199
	≥ 60	22	16	6	
Clinical stage	I/II	58	23	35	0.343
	III/IV	32	16	16	
Tumor size (cm)	< 5	44	21	23	0.411
	≥ 5	46	18	28	
Total bilirubin (μM)	< 17	64	30	34	0.287
	≥ 17	26	9	17	
ALT (U/L)	< 40	41	21	20	0.167
	≥ 40	49	18	31	
ALB (g/dL)	< 40	22	7	15	0.210
	≥ 40	68	32	36	
AFP (μg/L)	< 400	57	29	28	0.058
	≥ 400	33	10	23	
GGT (U/L)	< 50	35	22	13	0.003
	≥ 50	55	17	38	

ALT: Alanine Aminotransferase

ALB: Albumin

AFP: Alpha-fetoprotein

GGT: γ-glutamyl transpeptidase

Data S3. Full gels/blots images used in this study

