

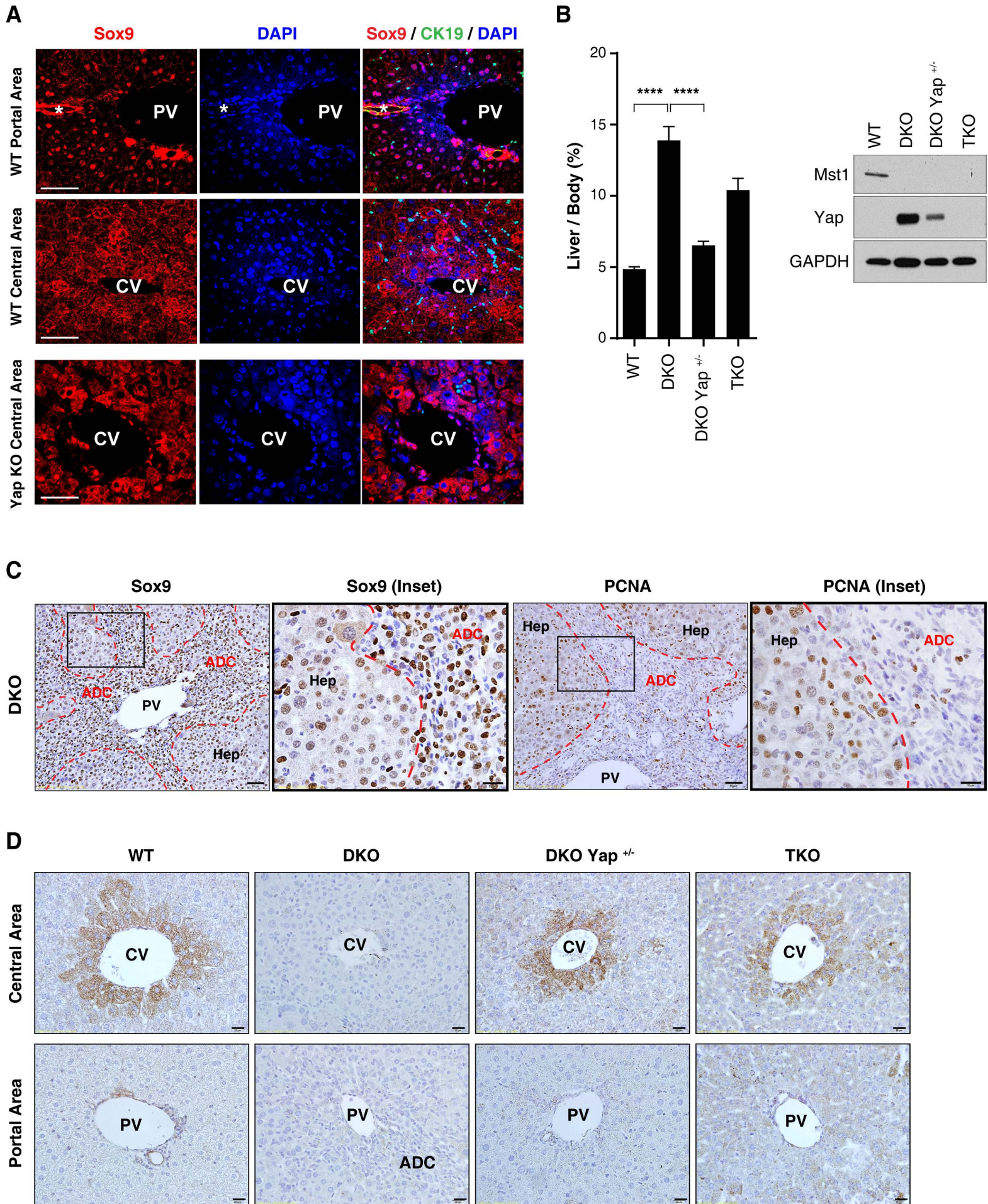
**Cell Reports**

**Supplemental Information**

## **YAP Inhibition Restores Hepatocyte Differentiation in Advanced HCC leading to Tumor Regression**

**Julien Fitamant, Filippos Kottakis, Samira Benhamouche, Helen S. Tian, Nicolas Chivin, Christine A. Parachoniak, Julia M. Nagle, Rushika M. Perera, Marjorie Lapouge, Vikram Deshpande, Andrew X. Zhu, Albert Lai, Bosun Min, Yujin Hoshida, Joseph Avruch, Daniela Sia, Genís Campreciós, Andrea I. McClatchey, Josep M. Llovet, David Morrissey, Lakshmi Raj, and Nabeel Bardeesy**

**Figure S1 (related to Figure 1)**



**Figure S1. The Hippo pathway controls hepatocyte identity (related to Figure 1).**

(A) SOX9 immunofluorescence in livers from WT and *Yap* KO mice. CK19 is a biliary marker. Bile ducts are indicated by an asterisk. Scale bar, 50 $\mu$ m.

(B) *Left panel:* Quantification of liver mass to body mass in mice of the indicated genotypes. N= 7 mice per group. Error bars indicate S.E.M. \*\*\*\* $p < 0.0001$ . *Right panel:* Immunoblot analysis of Mst1 and Yap in whole liver extracts of the indicated genotypes.

(C) PCNA and SOX9 staining in livers from DKO mice in regions with hepatocyte (Hep) and atypical ductal cell (ADC) morphology. Note that a higher proportion of the hepatocyte-like cells stain positively for PCNA as compared to the ADCs. Scale bars: 50  $\mu$ m and 20  $\mu$ m (Inset).

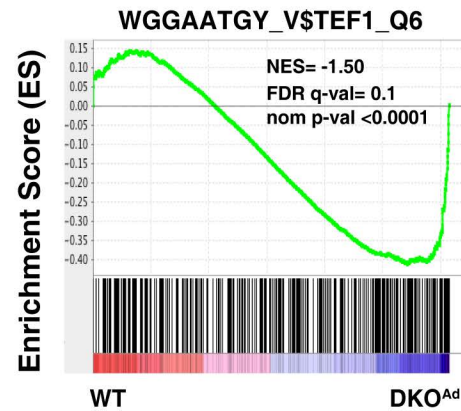
(D) Immunohistochemical analysis for the pericentral marker ornithine aminotransferase (OAT) in 7-week old livers of the indicated genotypes. Scale bar: 20 $\mu$ m.

PV: Portal vein, CV: Central vein, ADC: Atypical ductal cells.

Figure S2 (related to Figure 2)

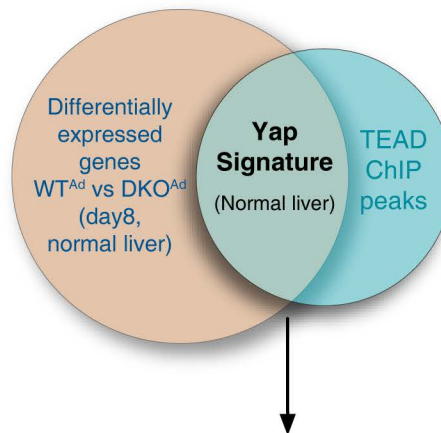
A

TEAD/TEF1 enrichment binding sites



B

Prediction of Yap-regulated transcriptional circuitry (normal liver)



Identification of enriched transcription factors  
(among 281 analyzed) using ENCODE ChIP-seq data

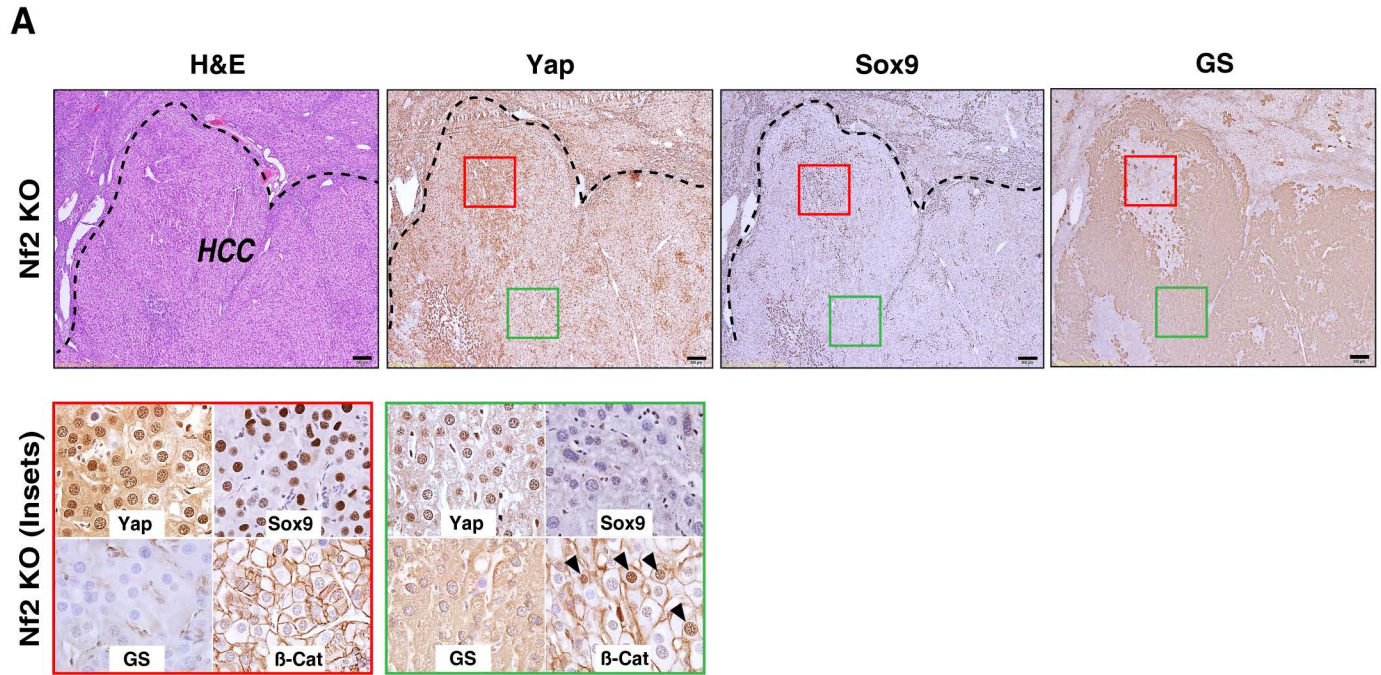
Factor	Total genes bound by factor	YAP/TEAD targets bound (out of 912)	Q-value (Hypergeometric test: Benjamini-Hochberg)	Factor rank
P300	11814	726	1.975E-42	1
Foxa1	8765	574	5.162E-33	2
Hnf4g	3740	320	5.162E-33	3
Hdac2	7939	535	8.517E-33	4
Tbp	12799	740	1.196E-32	5
Nfic	6462	462	2.701E-32	6
Mxi1	11719	696	5.151E-32	7
Hnf4a	3876	324	6.113E-32	8
Taf1	13370	759	6.528E-32	9
Cebpd	5434	408	7.106E-32	10

**Figure S2. Identification of candidate direct YAP targets following acute *Mst1/Mst2* inactivation in the adult liver (related to Figure 2).**

(A) GSEA of differentially expressed genes in DKO<sup>Ad</sup> versus WT<sup>Ad</sup> livers (8 days after Adeno-Cre administration) showing a significant enrichment of the consensus TEAD/TEF-1 DNA binding motif in the promoter sequences of this gene set.

(B) *Top panel:* To predict transcriptional networks regulated by YAP, we first identified presumptive direct YAP target genes (YAP signature) by integrating the set of differentially expressed genes observed in DKO<sup>Ad</sup> versus WT<sup>Ad</sup> livers (day 8) with ChIP-seq data for TEAD binding sites in hepatic cells (HepG2 cells) from the ENCODE database: <http://encodeqt.simple-encode.org/>). We then determined the enrichment of additional transcription factor binding sites in the region from -5 kb to +2.5 kb relative to the transcriptional start sites of this gene set using the data from ENCODE (comprising ChIP-seq data for 281 transcription factors). *Bottom panel:* The chart shows strong enrichment for FOXA1 and HNF4A binding to this set of candidate YAP targets, suggesting interplay of YAP and these transcription factors in regulating hepatocyte quiescence and differentiation. The top ranked transcription factors by enrichment score are shown. General transcription factors are greyed-out.

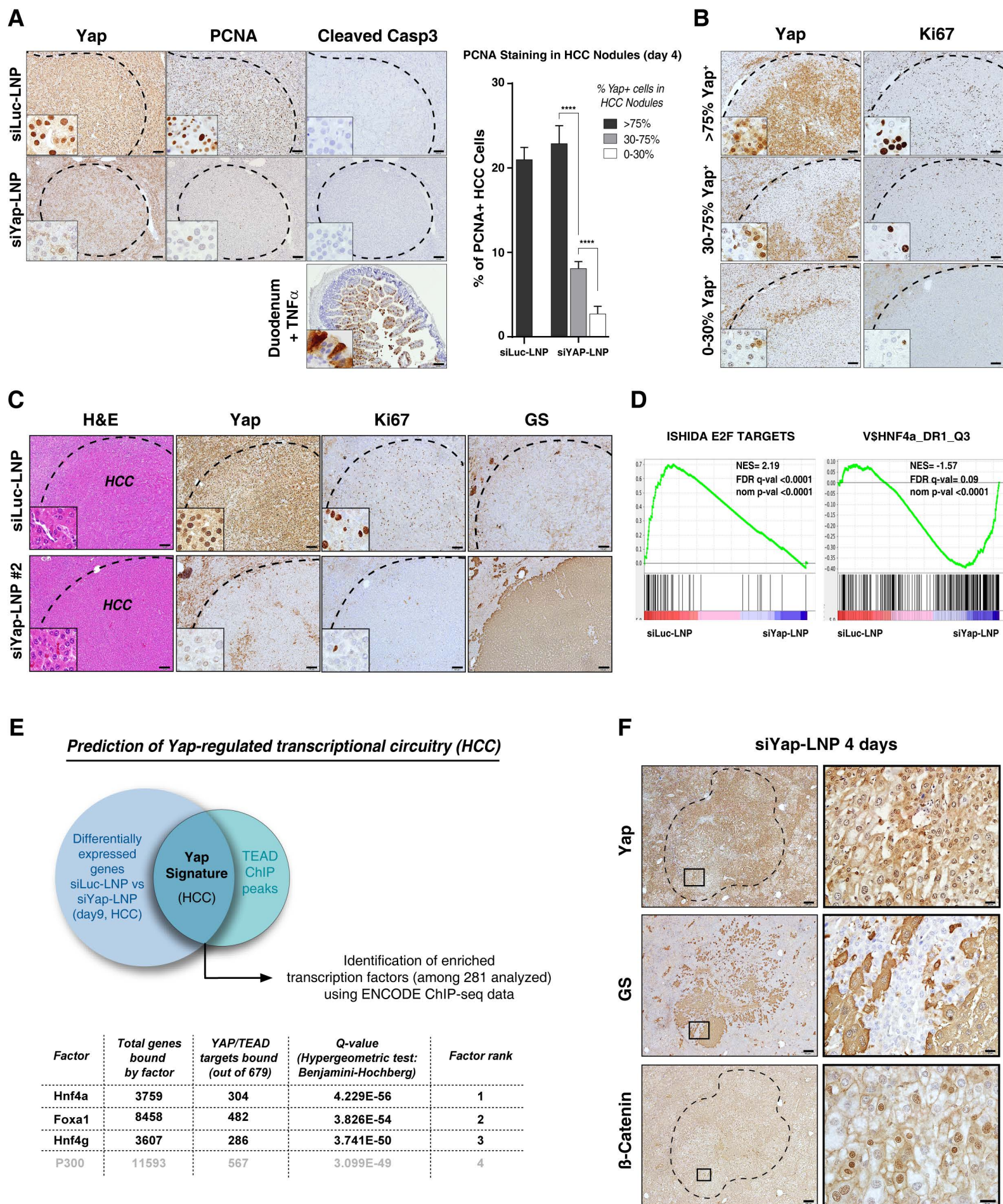
Figure S3 (related to Figure 3)



**Figure S3. Analysis of *Nf2* KO HCCs (related to Figure 3).**

(A) HCCs in mice with liver-specific *Nf2* KO show tumor variable levels of YAP staining, with high YAP specifically correlating with nuclear SOX9 and absence of GS and nuclear  $\beta$ -catenin. Arrowheads indicate nuclear  $\beta$ -catenin. The insets show high magnification views and are color-coded with the corresponding boxed regions. Scale bar: 200  $\mu$ m.

**Figure S4 (related to Figure 4)**





**Figure S4. siYap-LNPs induce proliferative arrest and reactivate a hepatocyte differentiation program in advanced HCC (related to Figure 4).**

(A) Representative immunohistochemical staining for YAP, PCNA and cleaved caspase-3 (Casp3) in HCCs following 4 days treatment with the indicated siRNA-LNP formulations. The bottom panel shows a positive control for cleaved caspase-3 staining (duodenal tissue from mouse treated with  $TNF\alpha$ ). The PCNA staining data are quantified in the graph (*right* panel). The chart shows % PCNA-positive HCC cells in different tumor nodules grouped according to degree of *Yap* knockdown. Note that the decrease in PCNA staining correlates with effectiveness of *Yap* knockdown. N= 87 tumors (siLuc; from treated 5 mice) and 87 tumors (siYap; from 4 treated mice). Error bars indicate S.E.M. \*\*\*\* $p < 0.0001$ . Scale bar: 100  $\mu\text{m}$ .

(B) Immunohistochemical staining for YAP and Ki67 in HCCs following 9 days treatment with siYap-LNP formulation showing representative nodules with varying degrees of *Yap* knockdown. Note that the decreased proliferation of HCC cells is directly correlated with the proportion of *Yap* knockdown. The percentage of YAP-positive HCC cells following treatment is indicated on the left side.

(C) Representative immunohistochemical staining for YAP, Ki67 and GS in HCCs following 9 days treatment with a second siYap-LNP formulation (siYap-LNP#2). Scale bar: 100  $\mu\text{m}$ .

(D) GSEA of differentially expressed genes in siLuc-LNPs versus siYap-LNPs-treated HCCs following 9 days of treatment. *Yap* knockdown results in downregulation of proliferation/E2F target gene signature and by reactivation of known Hnf4 $\alpha$  target genes.

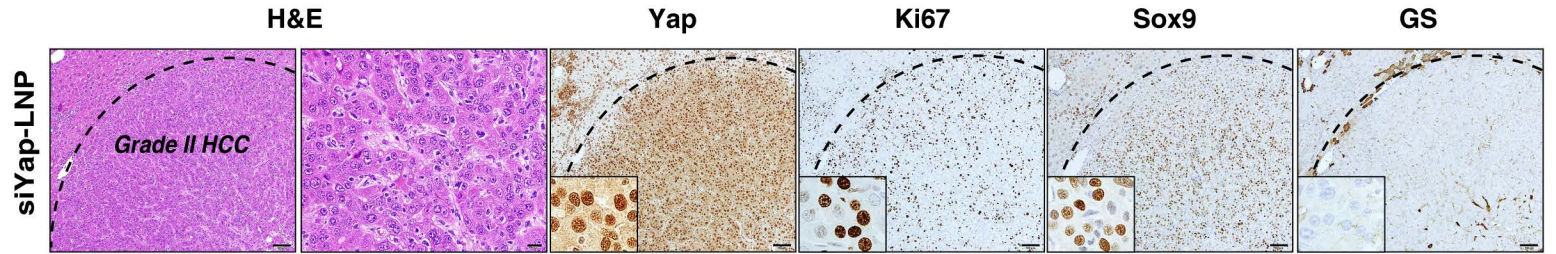
(E) *Top panel*: A YAP-specific activation signature in HCC was established by integrating the set of differentially expressed genes observed in siLuc-LNP-treated vs siYap-LNP-treated HCCs at day 9 with ChIP-seq data for TEAD binding sites in hepatic cells (ENCODE database). This allowed the identification of differentially expressed genes with predicted TEAD binding sites in their promoters to be analyzed for other enriched binding sites (-5 kb to +2.5 kb from the

transcriptional start sites). *Bottom panel:* the chart shows most enriched transcription factors (from Encode database, which includes CHIP-seq profiles for 281 transcription factors). Key regulators of liver differentiation are highlighted. General transcription factors are greyed-out.

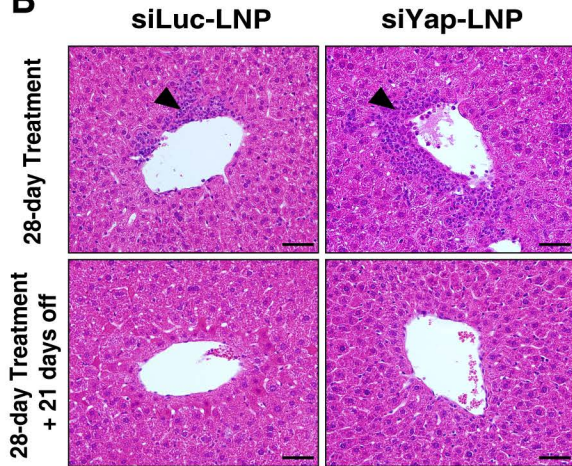
(F) Representative immunohistochemical staining for YAP, GS and  $\beta$ -catenin showing that siYap-LNPs induce partial reactivation of a WNT/ $\beta$ -catenin program in a subset of HCC nodules after only 3 days of treatment. Areas of  $\beta$ -catenin reactivation correlate with regions displaying low YAP staining. Scale bars: 200  $\mu$ m and 20  $\mu$ m (Inset).

Figure S5 (related to Figure 5)

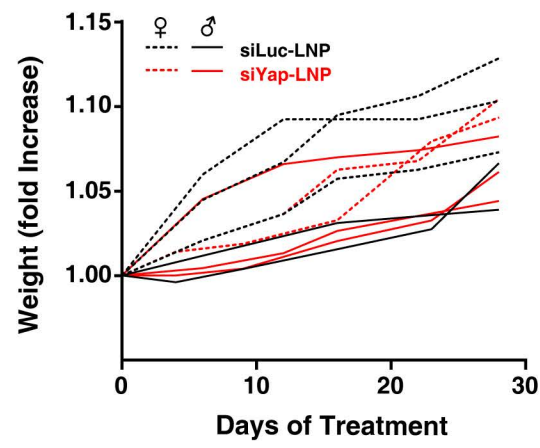
A



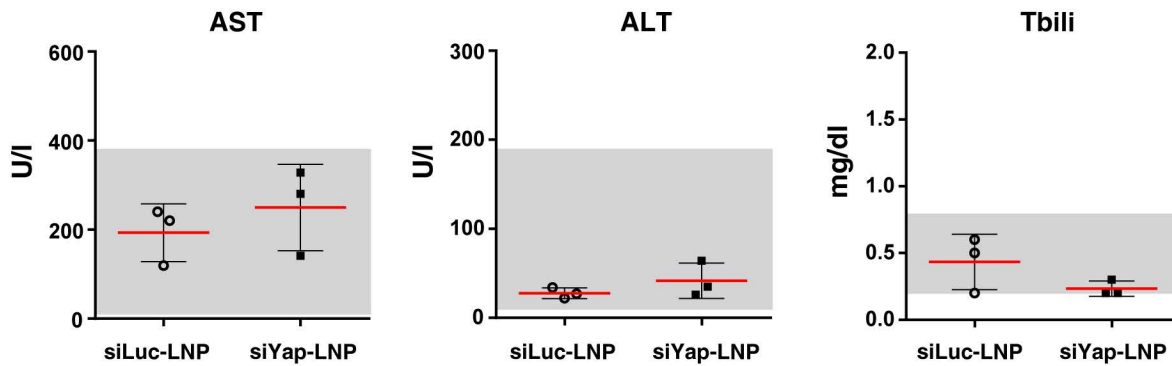
B



C



D



**Figure S5. Response to long-term administration of siLNP formulations (related to Figure 5).**

(A) While siYap-LNP treatment for 28 days greatly reduced the tumor burden in DKO mice, rare HCC foci were observed. Representative images of a resistant tumor are shown. These resistant tumors were high grade HCC that remained strongly positive for YAP, had high a level of Ki67 staining and expressed SOX9. Scale bar: 100  $\mu\text{m}$  (H&E *left panel*, Yap, Ki67, Sox9, GS) and 20  $\mu\text{m}$  (H&E *right panel*).

(B-D) Impact of siLNP treatment on liver function in WT mice. B) Representative H&E stained section showing a moderate inflammatory reaction (arrow heads) following 28 days treatment with the indicated siRNA-LNP formulations (*upper panels*). Inflammation was resolved within 3 weeks following discontinuation of the treatment (*lower panels*). Scale bar = 50  $\mu\text{m}$ . C) No weight loss was observed during the course of treatment. D) Treatment with the indicated siRNA-LNP formulations for 28 days does not result in significant liver toxicity as reflected by normal levels of serum Aspartate Aminotransferase (AST), Alanine Transaminase (ALT) and Total Bilirubin (Tbili). The grey areas indicate normal range of serum concentrations for the indicated factors.



**Figure S6. Modulation of *Yap* expression primary HCC cultures from DKO GEM model (related to Figure 6).**

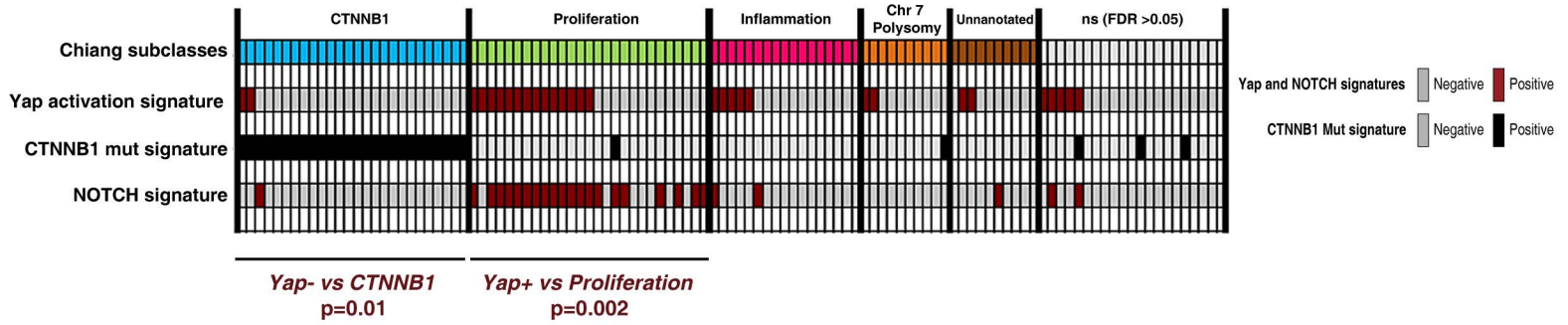
(A) qRT-PCR analysis of *Yap* levels in DKO cells 4 days following RNAi-mediated *Yap* knockdown. N= number of independent cell lines tested. Error bars indicate S.E.M. \*\*\*\*p<0.0001.

(B) Immunoblot analysis for YAP, phospho-Rb (p-Rb), Rb and GAPDH proteins of GFP-infected and hYAP-infected TKO cells treated with the CDK 4/6 inhibitor, PD-0332991, at the indicated concentrations.

Figure S7 (related to Figure 7)

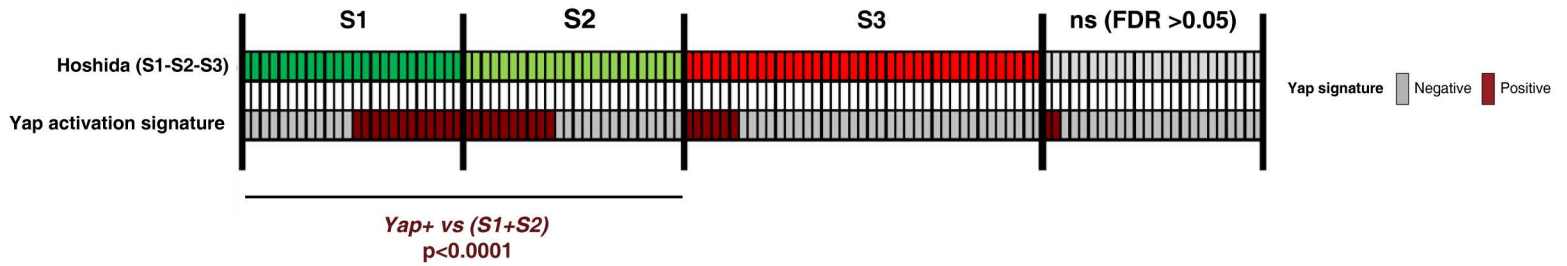
A

Association of Yap Signature with Chiang HCC subclasses



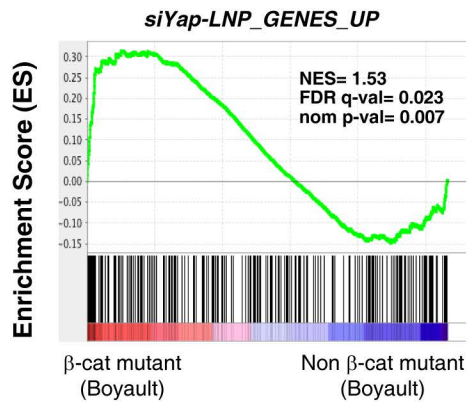
B

Association of Yap Signature with Hoshida subclasses



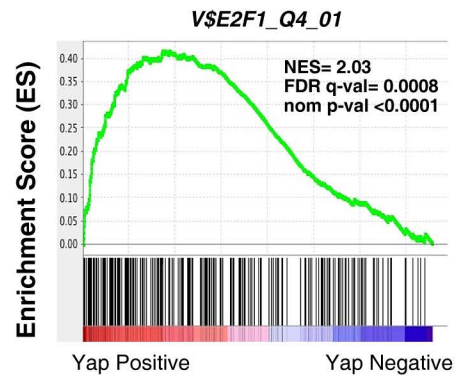
C

Association of Yap Signature with Boyault subclasses



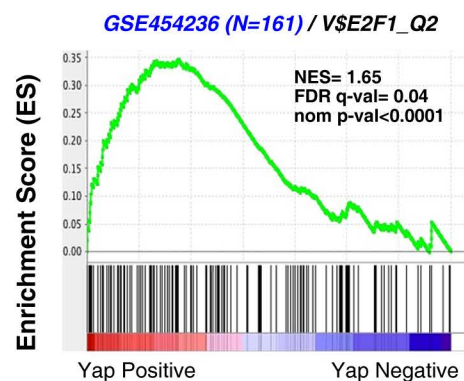
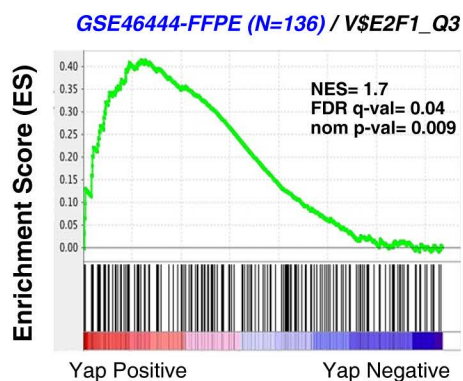
D

Yap-associated E2F activation in CCLE liver cell lines



E

Yap-associated E2F activation in Human HCC Cohorts



**Figure S7. Association of Yap signature with distinct molecular subclasses of human HCC (related to Figure 7).**

(A) Distribution of the YAP-activated (Yap+, red squares) and YAP-non activated (Yap-, grey squares) HCC samples according to the Chiang molecular classification (Chiang et al., 2008).

Fisher's exact test was used for statistical analysis.

(B) Distribution of the YAP-activated (Yap+, red squares) and YAP-non activated (grey squares) HCC samples according to the Hoshida molecular classification (Chiang et al., 2008)

(C) Gene set enrichment analysis showing a positive association between the expression profile of siYap-LNP treated HCC (day 9) and the  $\beta$ -Catenin mutant human subclass according to Boyault classification (Boyault et al., 2007).

(D) YAP levels show significant correlation with an E2F signature in human HCC cell lines.

(E) YAP levels show close correlation with E2F signatures across two independent human HCC cohorts (N= 136 and 161 samples respectively).





**Table S1. Predicted direct Yap targets following Mst1/Mst2 DKO (related to Figure 2).**

Gene set based on the integration of differentially expressed genes following acute activation of endogenous YAP (DKO<sup>Ad</sup> versus WT<sup>Ad</sup> livers at day 8) with chromatin immunoprecipitation data for TEAD binding sites in hepatic cells (ENCODE database) (see also [Fig. S2B](#)). Genes are ranked based on p-value.



**Table S2. Yap signature in advanced HCC (related to Figure 4).**

Gene set defining a YAP-specific signature based on the integration of differentially expressed genes observed in siLuc-LNP-treated versus siYap-LNP-treated HCCs in DKO mice (day 9) with chromatin immunoprecipitation data for TEAD binding sites in hepatic cells (ENCODE database) (see also [Fig. S4E](#)). Genes are ranked based on fold-change expression.

**Table S3**

<i>Gene name</i>	<i>Forward primer (5' to 3')</i>	<i>Reverse primer (5' to 3')</i>
18S	TGCCTTCCTTGATGTGGTAG	CGTCTGCCCTATCAACTTTCCG
AKR1D1	TGGAGTGCCACCCGTATTTTC	GGCTATGTGCGACAATGACG
B2M	GGTCTTTCTGGTGCTTGTCTCA	GTTCCGGCTTCCCATTCTCC
BDH1	GGTGGAACCTGGCAACTTCAT	GGTCATCCCACATCTTCTTGG
CDC6	CTGAAGAGTGCAAAGCTCCG	GCTTGTGTCTGGGATCTGGT
CDK1	AAGTGTGGCCAGAAGTCGAG	TCGTCCAGGTTCTTGACGTG
CDT1	TTACCAGCTCACCATCGAGC	TCCTTGACACGTTCCACCAG
CIDEB	CAATGGCCTGCTAAGGTCAGT	GATCACAGACACGGAAGGGTC
CLML4	AAGCAGGCATTGAACCAAACG	AGGAATGGTGATCCTCTGGATAA
CTGF	AGCTGACCTGGAGGAAAACA	GACAGGCTTGGCGATTTTAG
DBF4	GACATTCGATACTACATTGAACAGA	TCTCCCTGTTCTTGTCTTTTGT
DHRS1	AAAAGCCTGTTTCGAGCAAGTAG	CGCCAGCATAGGCATTATTGAC
DIO1	AGAGACTCGTAGATGACTTTGCC	GCCGGATGTCCACGTTGTT
E2F1	CAGCAACTGCAGGAGAGTGA	GTCCTGGCAGGTCACATAGG
ETFDH	TCTTCCGATGAACAATCATGGC	AGTGGCGATTCTTTTACACTAC
HNF4a	GGTAGGGGAGAATGCGACTC	AAACTCCAGGGTGGTGTAGG
KI67	GCTCACCTGGTCACCATCAA	TGACACTACAGGCAGCTGGA
LGR5	CAGTGTGTGCATTTGGGGG	CAAGGTCCCGCTCATCTTGA
MCM4	CAGGGGACAGAGTGAACGTC	ATGCAGACGTTTTGCATCCG
MCM6	CCTGAGAGAAACACGCTGGT	GGTCTTCAAGGCTCGACACA
MCM7	GCGCTTAAGGACTACGCGAT	CCGATGAGCCAGATGAACCA
MELK	GGCATCCTCCTGTATGTGCT	GCTACTGGGAGAGAGCCACT
NCPAG	GCCAAGTTTGTTACTTCATTTACC	CTGCACTGCTGTTTGCTTCAT
NUF2	CGGCTGGAGCACTTCTACAT	CCGGCAAATGGGCATAAAGG
ORC1	TACGTGTTGTAGCCGTGGTC	GCCTTGGAGGTAGGATGGC
PBK	TGTTGGCGGGAGGGAG	TCCTTCCATTGTAGCAATCACG
POLA1	GACTGTAAACTGGAGGCAAGC	TCTCCCAGCTTTAGCCTTTTT
RFC3	TGGCCCAGTCACAACAACCTT	GTTCTGCGTAAGGCATGCTG
SOX9	GAGCCGGATCTGAAGAGGGA	GCTTGACGTGTGGCTTGTTT
TBX3	ATCACGAAGTCAGGAAGGCG	TATCGACAGTCGTCAGCAGC
UBE2T	TGGGGAAGGAGTCCCCTTTCTA	AGGTCTGGCGGGGGTGTA
YAP	GGATGTCTCAGGAATTGAGAACA	ATGCTGTAGCTGCTCATGCTGA

**Table S3. Primer sets used in this study.**

Set of primers used for expression analysis (qRT-PCR) for the indicated genes.

## **Supplemental Experimental Procedures**

### **Materials**

Reagents were obtained from the following sources: antibodies against YAP (Cell Signaling cat. #4912), SOX9 (Millipore cat. #AB5535), MST1 (Cell Signaling cat. #3682), Glutamine Synthetase (BD Transduction Laboratories cat. #610517), Ornithine aminotransferase (Abcam cat. #ab137679),  $\beta$ -Catenin (BD Transduction Laboratories cat. #610154), PCNA (Cell Signaling cat. #13110), Ki67 (Abcam cat. #ab15580), Cleaved Caspase-3 (Cell Signaling cat. #9661), GAPDH (Millipore cat. #AB374); biotinylated goat anti-rabbit (cat. #BA-1000) and anti-mouse (cat. #BA-9200) secondary antibodies from Vector Laboratories; RPMI, DMEM, DMEM:F12, Sodium Pyruvate (cat. #11360070), Insulin-Transferrin-Selenium-X (cat. #51500056), Insulin (cat. #12585014) and fetal bovine serum (FBS) from Life Technologies, Recombinant Human IGF-II (cat. #100-12) and EGF (cat. #AF-100-15) from PeproTech; Ad5CMV-Cre Adenovirus was purchased from the Gene Transfer Vector Core, University of Iowa (<http://www.uiowa.edu/~gene/>); Liquid Isoflurane for inhalation was purchased from Baxter (Forane, cat. # 1001936040).

### **siRNA-mediated *in vitro* knockdown**

siRNA were transfected by using **Lipofectamine**<sup>®</sup> RNAiMAX Transfection Reagent (Life Technologies) at a final concentration of 20 nM. Control siRNA was purchased from Ambion (Negative Control #1 cat. #4390843) and anti-*Yap* siRNA was provided by Novartis (target sequence: 5'-TTAAGAAGTATCTTTGACC-3').

### **SDS-PAGE analysis**

Cells or liver tissues were lysed in ice-cold RIPA lysis buffer (150 mM NaCl, 50 mM Tris-HCl (pH 8), 1mM EDTA, 1% NP-40, 0.5% Sodium Deoxycholate, 0.1% Sodium Dodecyl Sulfate) supplemented with one tablet of EDTA-free protease inhibitors [Roche] per 10 ml, Serine/threonine phosphatase inhibitor and Tyrosine Phosphatase inhibitor [Calbiochem]. Samples were sonicated and clarified by centrifugation and protein content measured using BCA protein assay kit (Thermo Scientific). 10µg protein was resolved on 10% SDS-PAGE gels and transferred onto PVDF membranes (GE Healthcare Life Sciences, Pittsburgh, PA). Membranes were blocked in Tris-buffered saline (TBS) containing 10% non-fat dry milk and 0.1% Tween 20 (TBS-T), prior to incubation with primary antibody overnight at 4°C. The membranes were then washed with TBS-T followed by exposure to the appropriate horseradish peroxidase-conjugated secondary antibody for 45 min and visualized on Kodak X-ray film using the enhanced chemiluminescence (ECL) detection system (Thermo Scientific).

### **Ultrasound imaging**

Mice were anesthetized by inhalation of isoflurane at a starting dose of 4% with O<sub>2</sub> 1-2L/min and maintenance dose of 2% O<sub>2</sub>, and placed on a 40°C heating platform in order to maintain their body temperature. Abdominal hair is shaved off using a Remington groomer. Aquasonic 100, an ultrasound transmission gel, was applied to the shaved abdomen and liver imaging was performed using a high frequency Broadband transducer that allows the detection of lesions up to 0.5 mm. Images were captured using the associated Vevo software.

### **RNA Extraction from mouse HCC**

6-10 mm<sup>3</sup> pieces of previously frozen liver tumors were homogenized in 700 µl of Trizol using scissors and syringe. 140 µl of Chloroform was added to the specimens before being vortexed for 30 seconds and incubated for 10 minutes at room temperature. The RNA-containing



aqueous upper phase was collected on ice after centrifugation (15min, 12,000g, 4°C) and mixed with ½ volume of High-salt solution (1.2 M NaCl; 0.8 M Sodium Citrate) and one volume of Isopropanol. Supernatant was removed after a 10min centrifugation (12,000g, 4°C) and the precipitated RNA was washed with ice-cold 80% ethanol. Washed RNA was spin down for 5min (7,500g, 4°C) and allowed to air-dry before resuspension in RNase-free water.

### **Quantitative RT-PCR**

Reverse transcription from total cellular RNA was performed from 2 µg of total RNA using the QuantiTect Reverse Transcription Kit (Qiagen). Quantitative RT-PCR was performed with FastStart Universal SYBR Green (Roche) in a MX3005P continuous fluorescence detector (Stratagene) or using a Lightcycler 480 (Roche). PCR reactions were performed in duplicate and the relative amount of cDNA was calculated by the comparative CT method using the 18S ribosomal RNA sequences or beta-2 microglobulin (B2M) as a control. Primer sequences can be found in [Table S3](#).

### **Cell proliferation assay**

Cells were plated in 6-well plates at 60,000-120,000 cells per well in 2 mL of complete culture media. At the indicated time points, cells were trypsinized and counted using a Countess automated cell counter (Invitrogen).

### **Cell Culture**

DKO and TKO murine cell lines were generated from liver tumors that arose in *Mst1*<sup>-/-</sup>, *Mst2*<sup>Flox</sup>, and *Mst1*<sup>-/-</sup>, *Mst2*<sup>Flox</sup>, *Yap*<sup>Flox</sup> mice, respectively, by performing collagenase/dispase-based cell isolation and maintained at low passage numbers. Cells were grown on collagen-I-coated plates and cultured in DMEM:F12 supplemented with 5% heat inactivated FBS, Sodium Pyruvate (1 mM), Insulin-Transferrin-Selenium-X, human EGF (50ng/ml), human IGF-II (30 ng/ml) and

Insulin (10 µg/ml). Negative mycoplasma contamination status of all cell lines and primary cells used in the study was established using LookOut Mycoplasma PCR Kit (Sigma, MP0035). Forced expression of *YAP* in TKO cells was performed by stable infection with a pBabe retroviral expression vector encoding human YAP.

### **Histology and immunostaining**

Livers were harvested, submitted for histological examination, and analyzed in a blinded fashion by pathologist (V.D.). Tissue samples were fixed overnight in 4% buffered formaldehyde, and then embedded in paraffin and sectioned (5 µm thickness) by the DF/HCC Research Pathology Core. Haematoxylin and eosin staining was performed using standard methods. For immunohistochemistry, unstained slides were deparaffinized in xylenes (two treatments, 3 min each), rehydrated sequentially in ethanol (2 min in 100%, 2 min in 95%, 2 min in 80%), and washed for 3 min in water. Slides were incubated for 20 min with 3% H<sub>2</sub>O<sub>2</sub> at room temperature to block endogenous peroxidase activity and rinsed twice with water (3min each). Endogenous peroxidase activity was blocked by incubating deparaffinized tissue sections with 3% Hydrogen Peroxide (20 min; Fisher Scientific), and antigen retrieval was performed by boiling in 10 mM sodium citrate buffer (20 min, 95°C, pH 6). Sections were blocked 1 hour in TBS-0.05 % Tween 20 (Fisher Scientific)-10% Normal Goat Serum (Cell Signaling #5425), and incubated overnight at 4°C with primary antibody. Primary antibodies were diluted in blocking solution as follows: YAP (1:40), SOX9 (1:2000), Glutamine Synthetase (1:200), β-catenin (1:100), PCNA (1:10,000), Ki67 (1:100), Cleaved Caspase 3 (1:150), Ornithine aminotransferase (1:200). Specimens were then washed three times for 3 min each in PBST and incubated with biotinylated secondary antibodies (1:200, Vector Laboratories) in blocking solution for 45min at room temperature, followed by catalyzed signal amplification using the Vectastain Elite ABC kit (30 min; Vector Laboratories) Specimens were then washed three times in TBS-0.05 % Tween 20 and treated with ABC reagent (Vectastain ABC kit #PK-6100) for 30 min, followed by three washes for 3 min

each. Finally, slides were stained for peroxidase for 1-2 min with the DAB(di-aminebenzidine) substrate kit (SK-4100, Vector Laboratories), washed with water and counterstained with haematoxylin. Stained slides were photographed with an Olympus DP72 microscope. For quantification of Yap, Ki67 and PCNA staining in HCC following short term treatment with siYap-LNPs (Figure 4E,F and Figure S4A,B), % of positive HCC nuclei within individual tumor nodules were determined by IHC. One or two liver sections were stained per treated animal and every HCC nodule was analyzed.

### **Gene Expression Profiling**

RNA-sequencing was performed using total RNA isolated from HCC's from mice following treatment with siYap-LNPs and siLuc-LNPs for 9 days. RNA quality was measured using an Agilent Bioanalyzer and RNA was quantified using Qubit Fluorometer (Life Technologies) before sequencing library generation. RNAseq libraries were prepared using the ScriptSeq Complete Gold Kit (Epicentre). RNAseq libraries were uniquely indexed with custom primers (SriptSeq) and run on MiSeq (Illumina) to confirm quality of the library before sequencing to deeper coverage using a HiSeq2500 (Illumina). Approximately 50 million reads per sample were obtained. Data was processed using a standard RNA-seq pipeline that used Trimmomatic to clip and trim the reads, used tophat2 to align the reads to mm10, and used cuffdiff to calculate differential expression.

### **Image analysis and Statistics**

Image analysis was conducted using ImageJ software (NIH). To determine the percentage of GS positive hepatocytes (**Fig. 2C**), five to eight representative images of stained liver tissue per animal were acquired using a 4X objective lens on an Olympus DP72 microscope and processed in an 8-bit greyscale setting. All images were subjected to fixed thresholding to evaluate positively stained areas (in  $\mu\text{m}^2$ ), and a ratio between summed positive areas and the

total surface area of the tissue section (in  $\mu\text{m}^2$ , excluding the venous regions) was calculated for each image. Percentage of GS positive hepatocytes represents the average ratio for a given genotype. Statistical analyses of results are expressed as mean  $\pm$  SEM, unless otherwise specified. Significance was analyzed using 2-tailed Student's t test. A p value of less than 0.05 was considered statistically significant.

### **Liver function tests**

Following a 28-day treatment with siRNA-LNP formulations, blood from wild type mice was collected by retro-orbital puncture and mixed with 3.8% sodium citrate buffer using a ratio of 1 part citrate: 9 parts blood. The plasma-containing upper phases were collected on ice after centrifugation (15min, 1,500g, 4°C), and conserved at -80°C until analysis. Blood chemistry analyses (AST, ALT and Tbili) on samples were performed by the Center for Comparative Medicine platform (Massachusetts General Hospital, Boston MA 02115).

### **Analysis of human HCC**

Specimens from 111 HCC patients treated with surgical resection in 3 institutions belonging to the HCC Genomic Consortium: Mount Sinai School of Medicine in New York, Istituto Di Ricovero e Cura a Carattere Scientifico (IRCCS) Istituto Nazionale Tumori in Milan and Hospital Clinic in Barcelona. Gene expression data is published elsewhere (Chiang et al., 2008; Villanueva et al., 2011) (Villanueva et al Hepatology submitted). Presence of previously published signatures such as CTNNB1 mutation signature (Lachenmayer et al., 2012), NOTCH signature (Villanueva et al., 2012), Chiang 5 subclasses (Chiang et al., 2008) and Hoshida S1-S2-S3 classes (Hoshida et al., 2009) was determined using a nearest template prediction algorithm implemented in GenePattern as previously reported (Hoshida, 2010), based on a prediction confidence false discovery rate (FDR) cut-off of 0.05. Presence of YAP late activation signature was calculated using the same algorithm but a FDR of 0.25 was used as cut-off.

Presence of mutations in exon 3 of *CTNNB1* was analyzed by Sanger sequencing. Tissue sections were macrodissected to avoid contamination of non-cancerous liver tissue. Genomic DNA was isolated using the QIAamp® DNA FFPE tissue kit (Qiagen). One-hundred nanograms of DNA from both samples as well as positive and negative controls for *CTNNB1* mutations were then amplified by PCR using two sets of primers that span the whole exon 3: P1-F CAATCTACTAATGCTAATACTGTTTCG and P1-R CCTCAGGATTGCCTTTACCA (1); P2-F GATTTGATGGAGTTGGACATGG and P2-R TGTTCTTGAGTGAAGGACTGAG(2). PCR was performed in a volume of 20µL reaction mixture containing 1.5mM MgCl<sub>2</sub>, 0.2mM of each dNTP, 0.125mM of each primer and 1U of Platinum Taq DNA Polymerase (Invitrogen). PCR products were then purified using ExoSAP-IT® and sequenced.