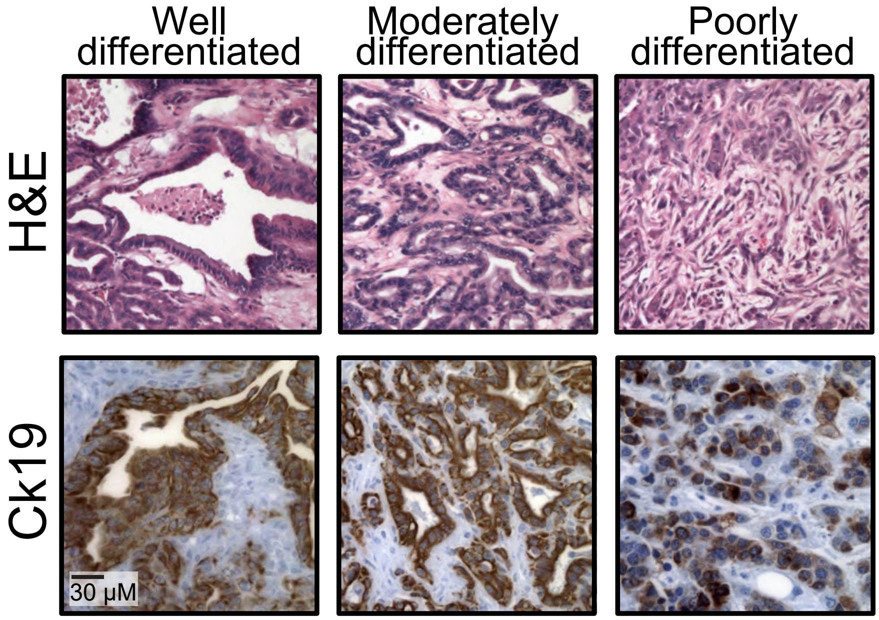

Figure S1, related to Figure 1. Differentiation states in mouse PDAC
Representative H&E and Ck19 immunostaining images showing pancreatic cancers of various differentiation states in 3 different *Kras*$^{+/LSL\text{-}G12D}$,*Pdx1-Cre*,*p53*$^{+/LSL\text{-}25,26,53,54}$ mice. The scale bar applies to all images in the panel.

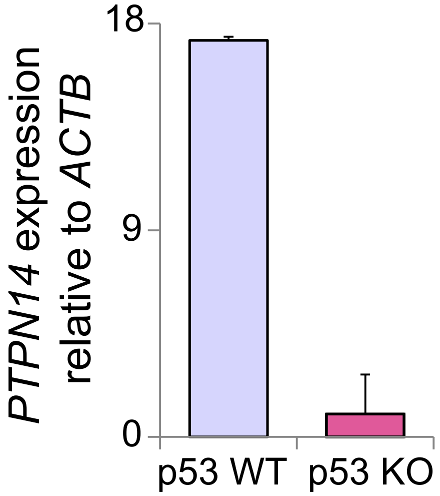

Figure S2, related to Figure 3. Ptpn14 expression is p53-dependent in human colorectal cancer cells
qRT-PCR analysis of *PTPN14* expression in doxorubicin-treated (0.2 µg/mL) human HCT116 colorectal cancer cells with and without p53. The cells were collected 24 hr post-treatment. *PTPN14* expression is shown relative to *ACTB*.

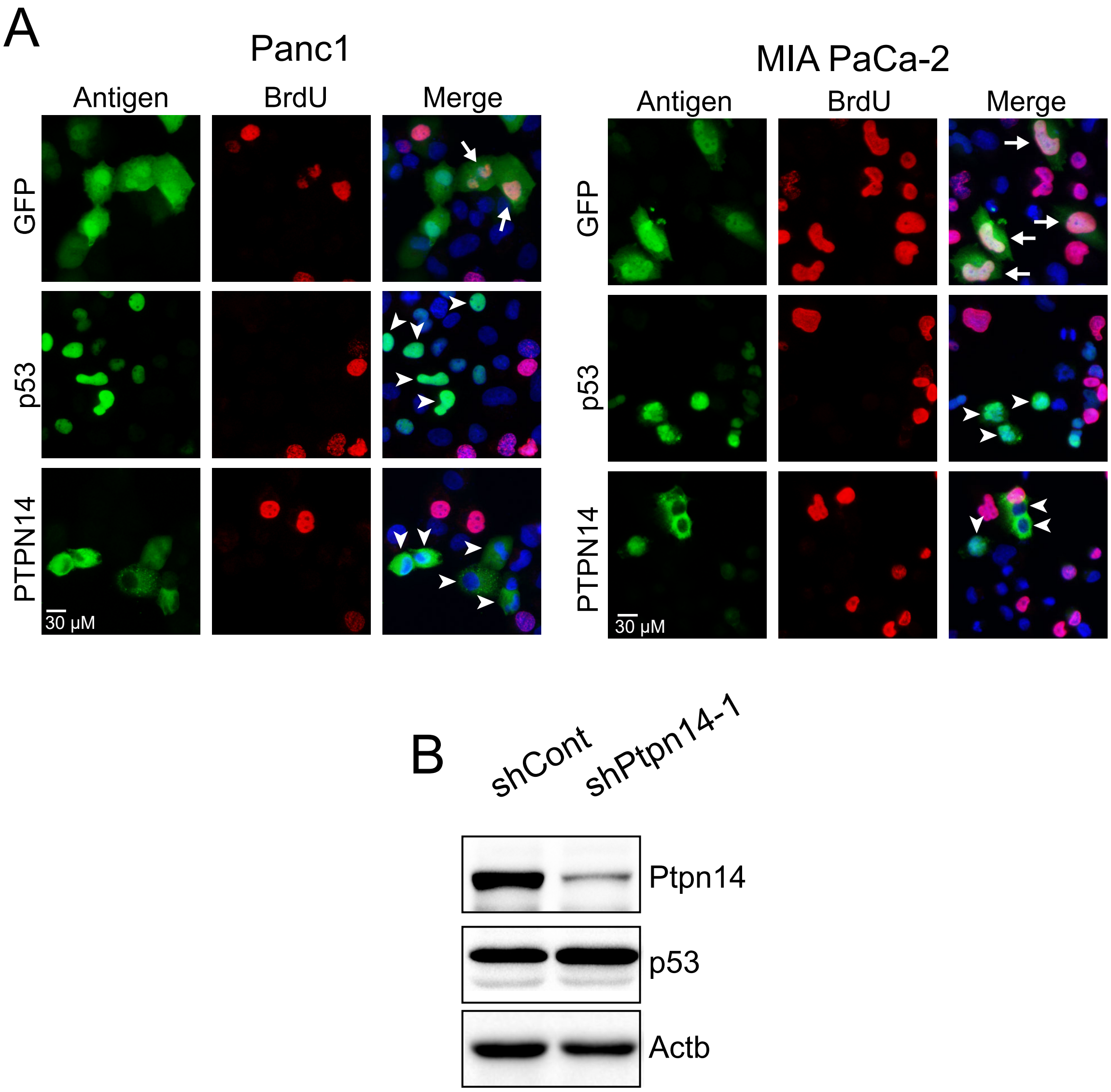

Figure S3, related to Figure 4. Ptpn14 inhibits cell proliferation in human pancreatic cancer cells
(A) The effect of HA-GFP, HA-Ptpn14 or HA-p53 expression on cell cycle progression in PANC-1 and MIA PaCa-2 human PDAC cells was examined by BrdU immunostaining. BrdU-positivity of cells expressing each antigen (detected by green fluorescence or HA immunofluorescence) was assessed. Representative images with arrows pointing to BrdU$^+$ cells and arrowheads pointing to BrdU$^-$ cells are depicted. The scale bar applies to all images in the panel. (B) Western blot examining Ptpn14 levels in p53-overexpressing PDAC cells from *Kras*$^{+/LSL\text{-}G12D}$*;Pdx1-Cre;Trp53*$^{fl/fl}$ (KPC) mice which were also transduced with either shControl or shPtpn14-1. The cells were used for BrdU incorporation experiments (quantification shown in Figure 4E). Actb is a loading control.

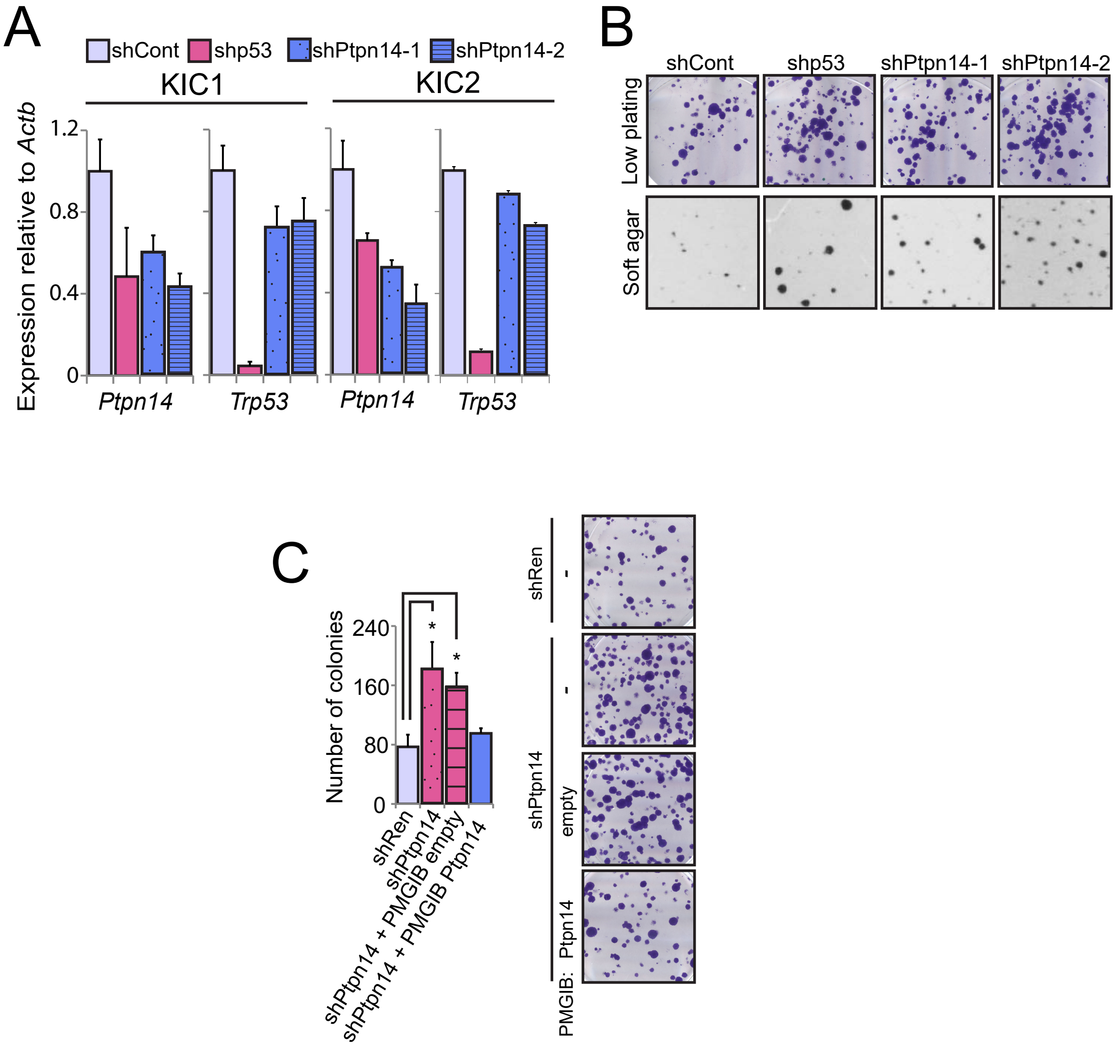

Figure S4, related to Figure 5. Ptpn14 displays tumor suppressor activity
(A) qRT-PCR to examine knockdown of *Ptpn14* in two different lines of PDAC cells from *Kras*$^{LSL\text{-}G12D/+}$*;Pdx1-Cre;Cdkn2a*$^{fl/fl}$ (KIC) mice after infection with a luciferase control shRNA or either of two Ptpn14 shRNAs (n=3). Knockdown of *Trp53* with p53 shRNA is also shown. (B) (Upper) Representative images of low plating experiments in a second KIC cell line after introduction of control shRNA, p53 shRNA, Ptpn14 shRNA-1 or Ptpn14 shRNA-2 (n=3, quantification shown in Figure 5B). (Lower) Representative images of soft agar experiment in a second KIC cell line after introduction of luciferase control shRNA, p53 shRNA, Ptpn14 shRNA-1 or Ptpn14 shRNA-2 (n=3, quantification shown in Figure 5C). (C) (Left) Low plating experiment quantification, showing the average colony number ± SD after introduction of luciferase control shRNA, p53 shRNA, Ptpn14 shRNA-1 or Ptpn14 shRNA-2, and rescue with a PMGIB-Ptpn14 overexpression construct. The experiments were performed in two PDAC KIC cell lines (n=2). (Right) Representative images show the crystal violet-stained colonies 2 weeks after seeding. * $p \leq 0.05$; ** $p \leq 0.001$, based on the two-tailed unpaired Student's t-test.

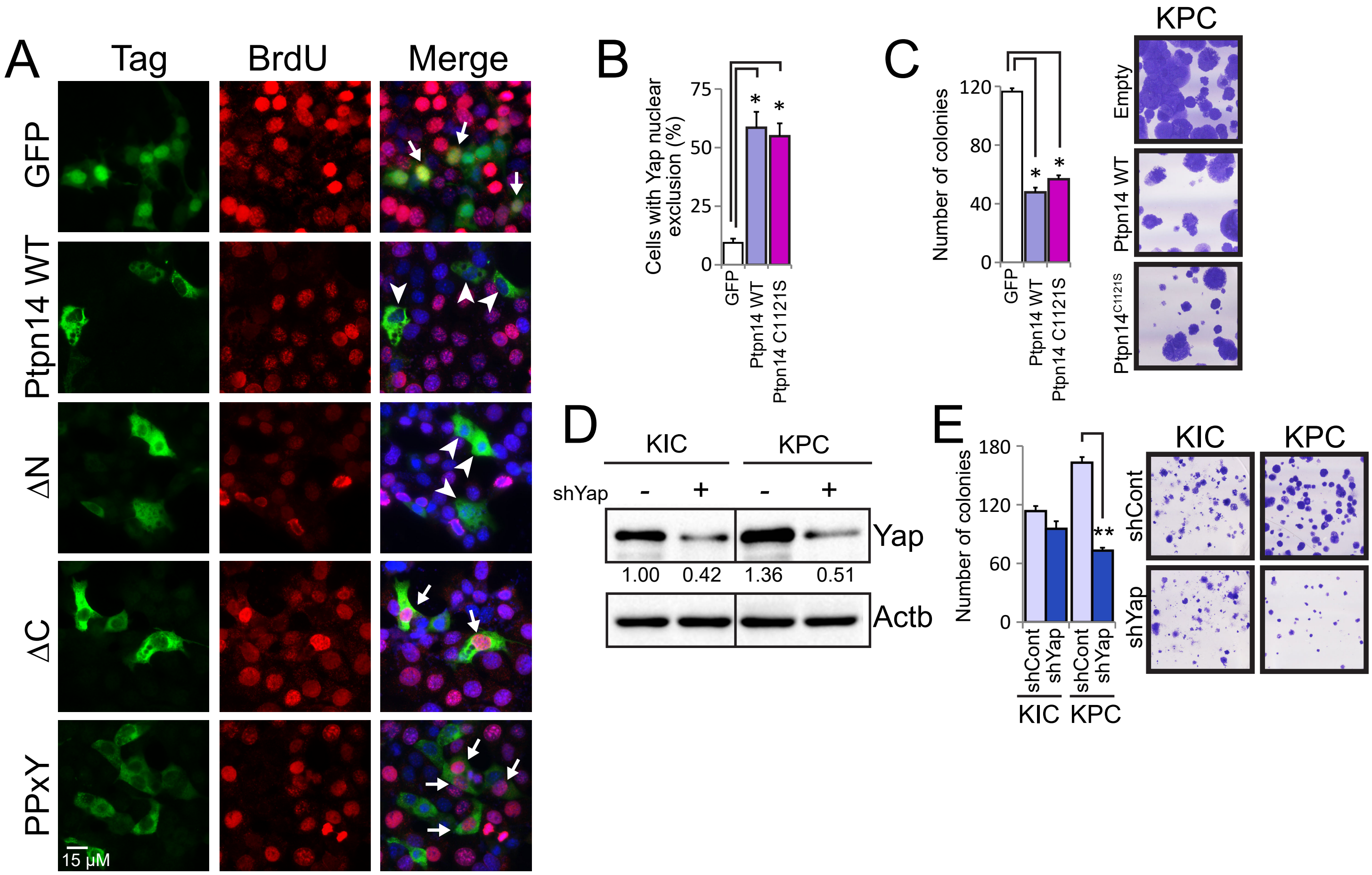

Figure S5, related to Figure 6. Ptpn14 inhibits proliferation through effects on Yap activity
(A) HA-GFP or different Ptpn14 variants were expressed in *$Kras^{+/LSL-G12D}$;Pdx1-Cre;$Trp53^{fl/fl}$* (KPC) mouse PDAC cells and BrdU-positivity of cells expressing each antigen (detected by green fluorescence or V5/HA immunofluorescence) was assessed. Representative images with arrows pointing to dividing (BrdU^{+}) cells and arrowheads pointing to arresting (BrdU^{-}) cells are depicted. The scale bar applies to all images in the panel. (B) Effects of HA-Ptpn14 or the phosphatase mutant HA-Ptpn14-C1121S expression on Yap localization in KPC cells, compared to HA-GFP. The graph shows the percentage of cells with Yap nuclear exclusion +/- SD (n=3). At least 50 cells were analyzed per experiment (C) Colony forming ability of KPC cells overexpressing HA-Ptpn14 or the phosphatase mutant HA-Ptpn14-C1121S. (Left) Low plating experiment quantification, showing the average colony number ± SD (n=3). (Right) Representative images show the crystal violet-stained colonies 2 weeks after seeding. (D) Western blot confirming knockdown of Yap protein in PDAC cells from KIC and KPC cells after introduction of a luciferase control shRNA or a Yap shRNA. Actb is a loading control. (E) Colony forming ability of KIC and KPC cells expressing luciferase control or Yap shRNAs. (Left) Low plating experiment quantification, showing the average colony number ± SD (n=3). (Right) Representative images show the crystal violet-stained colonies 2 weeks after seeding. * $p \le 0.05$; ** $p \le 0.001$, based on the two-tailed unpaired Student's t-test.

Table S1, related to Figure 6. List of 42 Yap target genes depicted in heatmap on Figure 6G.

1	*Rgcc*
2	*Tgm2*
3	*Serpine1*
4	*Phgdh*
5	*Ndrg1*
6	*Tnnt2*
7	*Schip1*
8	*Slit2*
9	*Fstl1*
10	*Lhfp*
11	*Axl*
12	*Camk4*
13	*Hexb*
14	*Msn*
15	*Dut*
16	*Itgb5*
17	*Tk1*
18	*Cdk6*
19	*Shcbp1*
20	*Anln*
21	*Sgk1*
22	*Samsn1*
23	*Mdfic*
24	*Shisa4*
25	*Stmn1*
26	*Ccrn4l*
27	*Cdc20*
28	*Cenpf*
29	*Birc5*
30	*Top2a*
31	*Hmmr*
32	*Rpn2*
33	*Mocs2*
34	*Nras*
35	*Siae*
36	*Gas2l3*
37	*Dram2*
38	*Ect2*
39	*Thbs1*
40	*Rhoq*
41	*Msrb3*
42	*Ctgf*

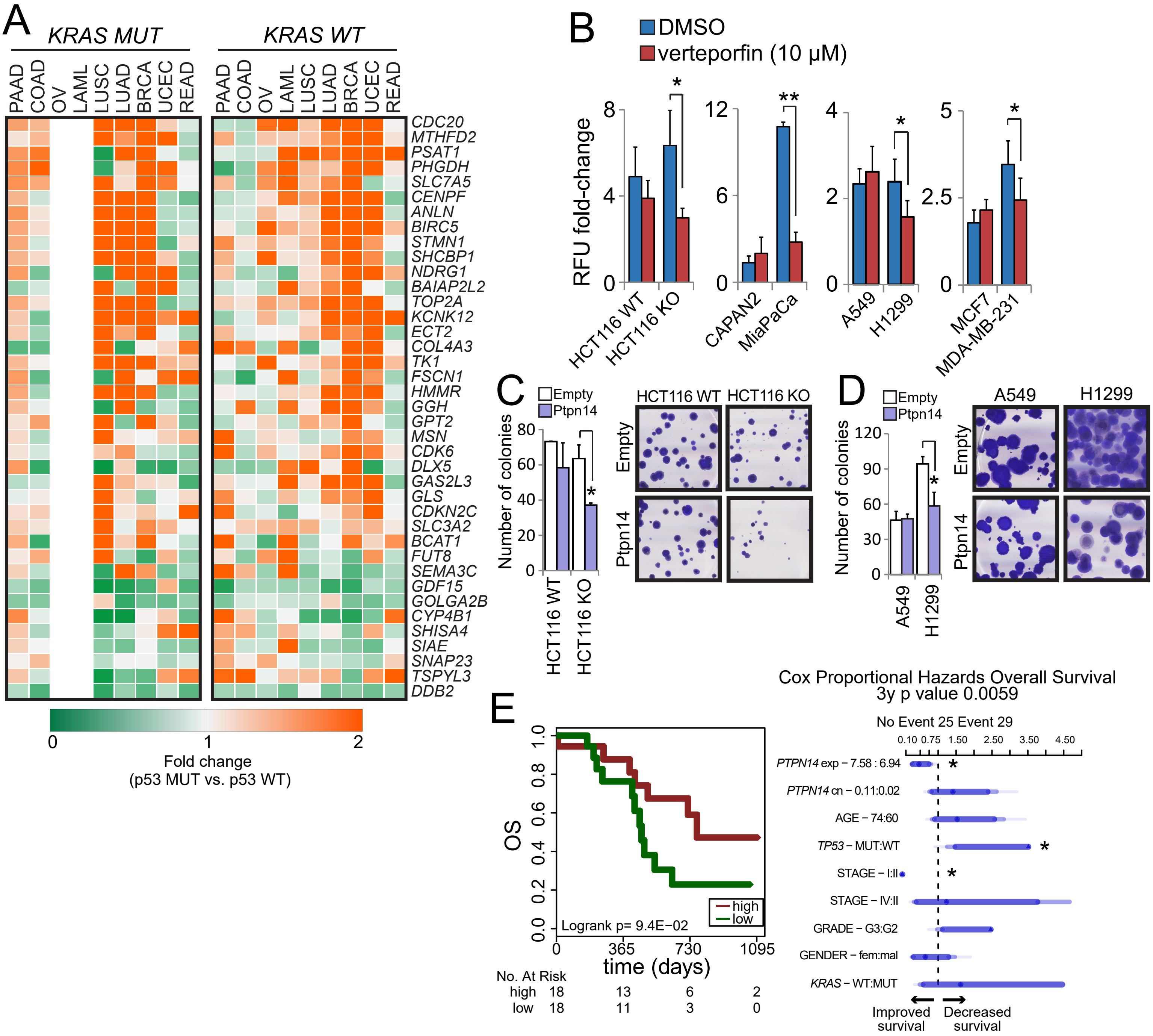

Figure S6, related to Figure 7. The p53-Ptpn14-Yap tumor suppressive axis is important in human cancer
(A) Heat map illustrating the fold-change in the expression of Yap-activated genes in tumor samples harboring *TP53* mutations relative to tumors with wild-type *TP53*. For each cancer the samples were further divided into those expressing mutant and wild-type *KRAS* (except OV and LAML, where there are no *KRAS* mutations), to assess the effect of *KRAS* mutations on p53-dependent Yap inhibition. (B) Quantification of viable cells using the Cell Titer-Blue assay in a variety of p53-proficient and deficient human cancer cells treated with DMSO or the Yap inhibitor verteporfin (10 μM). Colorectal (HCT116 p53 WT and HCT116 p53 KO), pancreatic (CAPAN2-p53 WT and MIA PaCa-2-p53 MUT), lung (A549-p53 WT and H1299-p53 MUT) and breast (MCF7-p53 WT and MDA-MB-231-p53 MUT) cancer cells were assessed 48 hours after verteporfin treatment. The Relative Fluorescence Units (RFU) reads were normalized based on initial fluorescence and background fluorescence values. (C) Colony formation ability of HCT116 cells proficient or deficient for p53 after introduction of a plasmid expressing HA-Ptpn14. (Left) Low plating experiment quantification, showing the average colony number ± SD (n=3). (Right) Representative images show the crystal violet-stained colonies 2 weeks after seeding. (D) Colony formation ability of A549 (p53 wild-type) or H1299 (p53 mutant) cells after introduction of a plasmid expressing HA-Ptpn14. (Left) Low plating experiment quantification, showing the average colony number ± SD (n=2). (Right) Representative images show the Crystal Violet-stained colonies 2 weeks after seeding. (E) Analysis of overall survival of PDAC patients from the International Cancer Genome Consortium (ICGC) pancreatic cancer project (Code: PACA-AU) divided by *PTPN14* expression levels. (Left) Kaplan-Meier analysis for overall survival of patients with tumors manifesting either high or low expression values of *PTPN14*. Survival analysis was based on those individuals without *PTPN14* copy number variations. High value correspond to the high tercile of the adjusted expression value, and low value to lowest tercile. (Right) Hazard plot of Cox Proportional Hazards for the association between overall survival and *PTPN14* expression levels, CN, grade, age, stage, gender and *KRAS* and *TP53* mutation status. Asterisks indicate the factors that significantly affect overall survival.

Table S2, related to Figure 7. Sample size for each cohort and breakdown of *TP53* mutant vs *TP53* wild-type cases used to determine changes in gene expression of Yap-induced genes, in Figure 7C.

Cancer type	Dataset	Total	p53 wild-type	p53 mutant
Rectum adenocarcinoma	READ	35	14	21
Colon adenocarcinoma	COAD	65	31	34
Ovarian serous cystadenocarcinoma	OV	162	7	155
Lung squamous cell carcinoma	LUSC	177	36	141
Lung adenocarcinoma	LUAD	163	82	81
Breast invasive carcinoma	BRCA	751	498	253
Bladder urothelial carcinoma	BLCA	95	47	48
Kidney renal clear cell carcinoma	KIRC	391	383	8
Head and Neck squamous cell carcinoma	HNSC	271	75	196
Glioblastoma multiforme	GBM	142	97	45
Uterine Corpus Endometrial Carcinoma	UCEC	239	171	68
Acute Myeloid Leukemia	LAML	169	156	13
Pancreatic adenocarcinoma	PAAD	121	40	81

Table S3, related to Figure 7. Combined statistics of Yap-induced genes, comparing expression levels in *TP53* mutant and *TP53* wild-type samples across different types of cancer, for each gene shown in Figure 7C.

symbol	entrez	hazard ratio	coef	se	lower	upper	p value
CDC20	991	2.094023592	0.739087379	0.04490542	1.91759993	2.28667864	7.60E-70
DDB2	1643	0.576812072	-0.55023876	0.02836685	0.54561768	0.60978993	1.96E-62
MTHFD2	10797	1.618500652	0.481500197	0.03288903	1.51746151	1.72626742	1.68E-48
PSAT1	29968	2.108227848	0.745847712	0.06237312	1.86562972	2.38237235	7.73E-47
PHGDH	26227	2.130141535	0.756188426	0.05882446	1.89817823	2.39045148	4.40E-46
SLC7A5	8140	1.87768378	0.630038986	0.0558943	1.68284896	2.09507594	1.99E-45
CENPF	1063	1.663376468	0.508849554	0.04550483	1.5214468	1.81854619	1.50E-44
ANLN	54443	1.760670926	0.565694945	0.045798	1.6095144	1.92602322	8.85E-44
BIRC5	332	1.839817143	0.609666188	0.04843366	1.67320001	2.02302599	9.34E-43
STMN1	3925	1.571826328	0.452238209	0.03977591	1.45394254	1.69926798	1.06E-40
SHCBP1	79801	1.530228936	0.425417356	0.03898074	1.4176726	1.6517217	1.13E-37
SEMA3C	10512	0.743242314	-0.29673316	0.05903436	0.66203399	0.83441205	6.07E-35
NDRG1	10397	1.533696421	0.427680783	0.05142128	1.38665855	1.69632583	4.81E-34
FUT8	2530	0.798620745	-0.22486911	0.03710925	0.74259691	0.85887119	1.21E-31
BAIAP2L2	80115	1.7685119	0.570138459	0.06797384	1.54792012	2.02053989	7.64E-30
GDF15	9518	0.389564551	-0.9427257	0.07839485	0.33407933	0.45426497	3.89E-29
TOP2A	7153	1.476531596	0.389695821	0.04657222	1.34772226	1.61765196	4.43E-25
GOLGA2B	55592	0.585077465	-0.53601102	0.04864919	0.53186707	0.64361126	1.21E-24
KCNK12	56660	1.841883996	0.610788959	0.0583998	1.64267736	2.06524832	2.05E-24
ECT2	1894	1.429318723	0.357197913	0.03844948	1.32556438	1.5411941	2.26E-24
COL4A3	1285	1.518993871	0.418048189	0.07997103	1.29862738	1.77675476	2.99E-24
TK1	7083	1.508696074	0.411245751	0.04213628	1.38910569	1.63858219	5.34E-24
CYP4B1	1580	0.726034251	-0.32015809	0.06455541	0.6397458	0.82396123	2.24E-23
FSCN1	6624	1.56748183	0.449470402	0.04746944	1.42822443	1.72031736	2.33E-23
HMMR	3161	1.493797566	0.40132158	0.04728785	1.36157088	1.63886522	4.79E-23
SHISA4	149345	0.856474549	-0.15493068	0.0416797	0.78929007	0.92937778	2.53E-22
GGH	8836	1.407337757	0.341699804	0.0478529	1.28134441	1.54571991	6.28E-22
SIAE	54414	0.686035571	-0.3768258	0.03787608	0.63695164	0.73890195	1.77E-21
GPT2	84706	1.440034945	0.364667381	0.04333849	1.32276667	1.56769949	3.06E-21
MSN	4478	1.260445113	0.231464923	0.03306569	1.18134942	1.34483656	6.06E-21
SNAP23	8773	0.855321243	-0.15627816	0.02080519	0.82114499	0.89091991	7.57E-21
CDK6	1021	1.51828401	0.417580756	0.05121109	1.37328937	1.67858748	2.76E-19
DLX5	1749	1.615782962	0.479819645	0.07385031	1.39804621	1.86743082	4.83E-19
GAS2L3	283431	1.369986422	0.314800829	0.05232951	1.23644074	1.51795613	5.26E-19
TSPYL3	128854	0.782662148	-0.24505416	0.0494982	0.71029929	0.86239708	1.38E-17
GLS	2744	1.286809474	0.252165879	0.03501741	1.20145464	1.37822817	3.53E-17
CDKN2C	1031	1.235226491	0.211254347	0.04110371	1.13961736	1.33885682	4.89E-17
SLC3A2	6520	1.284518259	0.250383753	0.02741842	1.21731137	1.35543559	8.01E-17
BCAT1	586	1.524064242	0.42138061	0.06238223	1.34866295	1.72227747	9.80E-17
C16orf87	388272	1.27163929	0.240306847	0.02823076	1.20318905	1.34398371	4.10E-16
C17orf58	284018	0.901492104	-0.103704	0.0316528	0.8472645	0.95919044	4.47E-16
ASAP1	50807	1.332040624	0.28671207	0.03001045	1.25595051	1.41274056	9.67E-16
CRIM1	51232	0.881088209	-0.12659753	0.03909926	0.81608996	0.9512633	1.77E-15
XAGE2	9502	1.095832883	0.091514697	0.02057801	1.052515	1.14093358	4.03E-15
SCHIP1	29970	1.395684567	0.333385024	0.04301163	1.28284951	1.51844421	7.56E-15
SDPR	8436	0.682062944	-0.38263333	0.06096507	0.60524456	0.76863121	9.04E-15
PRRG1	5638	1.313755689	0.272889974	0.04656698	1.19915888	1.43930386	2.03E-14
ATP2C1	27032	1.129596671	0.121860641	0.02107155	1.08389513	1.17722518	6.31E-14
GNB4	59345	1.213455177	0.193471809	0.04028393	1.12133144	1.3131474	1.25E-13
DLC1	10395	0.687670249	-0.37444585	0.04617651	0.62816642	0.75281065	1.47E-13
MYC	4609	1.45750143	0.37672362	0.04734415	1.328341	1.5992207	2.98E-13
RPN2	6185	1.187092082	0.171506688	0.02331236	1.13407268	1.24259021	5.59E-13
TNNT2	7139	1.18149987	0.166784708	0.05658898	1.05746269	1.32008623	6.95E-13
PMP22	5376	0.78023429	-0.24816103	0.0446778	0.71481758	0.85163763	5.64E-12
GKAP1	80318	0.763050806	-0.27043066	0.03982253	0.70575905	0.82499336	5.69E-12
ITGB5	3693	0.947058912	-0.05439398	0.03618247	0.88222308	1.01665962	5.96E-12

ETV5	2119	1.199160898	0.18162206	0.04524258	1.09740493	1.3103521	2.24E-11
DUSP1	1843	0.693222327	-0.36640451	0.05653462	0.620512	0.7744527	2.29E-11
CDIPT	10423	1.010886152	0.010827324	0.02093783	0.9702417	1.05323324	3.67E-11
MYO1C	4641	0.864976094	-0.14505341	0.02714058	0.82016645	0.91223391	4.91E-11
TRIB3	57761	1.462237681	0.379967921	0.04633025	1.33530843	1.60123233	6.77E-11
MOCS2	4338	0.799114381	-0.22425119	0.02789709	0.75659402	0.84402438	7.16E-11
AGFG2	3268	0.830330544	-0.18593141	0.03107582	0.78126654	0.8824758	1.32E-10
FLNA	2316	1.333201344	0.287583076	0.04358647	1.22403792	1.4521003	1.67E-10
NUAK2	81788	0.979437217	-0.02077714	0.04140376	0.90309545	1.06223242	2.01E-10
FAF2	23197	0.915519433	-0.08826369	0.01815191	0.8835205	0.94867728	1.17E-09
ARHGAP29	9411	1.052772775	0.051427422	0.04692835	0.96026071	1.15419751	1.42E-09
MARCKS	4082	1.246322358	0.220197101	0.03355461	1.16699407	1.33104311	2.43E-09
CXorf56	63932	1.197974491	0.180632206	0.02263583	1.14598759	1.25231974	4.57E-09
C8orf48	157773	0.808807779	-0.21219399	0.05993774	0.71916115	0.90962925	5.22E-09
SLIT2	9353	0.907046149	-0.09756195	0.07325861	0.78572676	1.04709774	5.98E-09
GLIS2	84662	1.09476084	0.090535929	0.04147712	1.00928512	1.18747545	6.15E-09
TNS1	7145	0.858703724	-0.15233132	0.04281859	0.78957992	0.93387898	8.49E-09
RHOQ	23433	1.143764098	0.134324664	0.0279565	1.08277904	1.208184	1.35E-08
ANKRD1	27063	1.146212487	0.136463018	0.08261426	0.97486337	1.34767918	1.67E-08
AMOTL2	51421	1.074567893	0.071918621	0.03661467	1.00015521	1.15451697	3.15E-08
EDN2	1907	1.157424463	0.146197246	0.07681303	0.99565595	1.34547621	3.92E-08
PPP1R3B	79660	0.822554929	-0.19534002	0.04045633	0.75985097	0.89043331	8.71E-08
THBS1	7057	0.881475213	-0.1261584	0.0544967	0.79217737	0.98083912	1.00E-07
FAM167A	83648	0.981904901	-0.01826082	0.06992941	0.85614122	1.12614276	1.06E-07
LHFP	10186	0.80749185	-0.21382232	0.04117605	0.74488466	0.87536114	3.54E-07
NEB	4703	1.45891892	0.377695695	0.06933692	1.2735367	1.67128627	4.52E-07
NRAS	4893	1.150687509	0.140359597	0.02752856	1.09024736	1.21447828	4.79E-07
MAML2	84441	1.223727454	0.201901491	0.0471695	1.11566537	1.34225631	6.44E-07
TSPAN3	10099	0.883693267	-0.12364526	0.02761151	0.83714095	0.93283429	6.70E-07
EDN1	1906	1.179250793	0.164879315	0.05902602	1.05042038	1.3238818	7.37E-07
ITGB2	3689	1.175089064	0.161343944	0.05389096	1.05730118	1.30599903	1.11E-06
FLOT1	10211	0.998454663	-0.00154653	0.02516008	0.95041231	1.04892551	1.21E-06
TGM2	7052	1.221716949	0.200257205	0.05337604	1.10036517	1.35645179	1.36E-06
TEAD1	7003	0.948572046	-0.05279754	0.03199995	0.89090606	1.00997059	1.41E-06
GTPBP3	84705	1.193333929	0.176751011	0.02679268	1.13228569	1.25767364	1.85E-06
SEC14L1	6397	1.066248312	0.064146237	0.0266572	1.01197016	1.12343773	1.93E-06
SLC5A3	6526	1.148903042	0.13880761	0.03753393	1.0674178	1.23660876	1.95E-06
AKR1C2	1646	1.255814814	0.227784616	0.10050855	1.03127044	1.52925051	2.00E-06
DDAH1	23576	0.809916886	-0.21082365	0.03804147	0.75172588	0.87261245	2.28E-06
HEXB	3074	0.892295556	-0.11395786	0.02437499	0.85066919	0.93595886	5.63E-06
GAS6	2621	0.864550485	-0.14554558	0.04520045	0.79125354	0.94463721	5.84E-06
TGFB2	7042	1.148844124	0.138756327	0.06592214	1.00959707	1.30729661	1.79E-05
MSRB3	253827	0.825609957	-0.19163282	0.0524956	0.74488733	0.91508041	3.15E-05
GADD45B	4616	0.827712529	-0.18908937	0.04093408	0.76389977	0.89685592	3.45E-05
TMEM49	81671	0.921936813	-0.08127859	0.02793621	0.87281422	0.97382406	4.17E-05
FAM35A	54537	0.919459876	-0.08396887	0.02181562	0.88097441	0.95962659	4.52E-05
ARHGEF10	9639	0.940921509	-0.06089555	0.03708115	0.87496336	1.01185184	5.55E-05
C8orf58	541565	0.892810688	-0.11338072	0.026945	0.84688366	0.94122837	6.78E-05
SH2D4A	63898	0.713913338	-0.3369937	0.04787515	0.64997117	0.78414594	0.000178
SAMSN1	64092	1.02352418	0.02325175	0.05352814	0.92158388	1.13674053	0.000258
MDFIC	29969	0.977932235	-0.0223149	0.03962498	0.90485692	1.05690903	0.000289
EMP2	2013	0.893456417	-0.11265772	0.04057818	0.82515049	0.96741671	0.000584
MACF1	23499	0.953920312	-0.04717514	0.03148541	0.89683318	1.01464128	0.00064
SNX7	51375	1.052507141	0.051175071	0.03619679	0.98042481	1.12988908	0.000926
CCDC8	83987	0.980581655	-0.01960936	0.06667872	0.86045217	1.11748266	0.000955
DAB2	1601	0.923451104	-0.07963743	0.04286808	0.84903292	1.00439208	0.000989
SFRS2IP	9169	0.919615549	-0.08379958	0.02190473	0.88096968	0.95995671	0.00139
GOLGA7	51125	1.03284246	0.032314672	0.02756697	0.97851849	1.09018231	0.001823
CNIH	10175	0.964007279	-0.03665643	0.02500586	0.91789983	1.01243077	0.001853
SERTAD4	56256	1.161193494	0.14944835	0.06317691	1.025955	1.31425875	0.001855
RAB40C	57799	0.913780073	-0.09016536	0.02833216	0.86442099	0.96595759	0.001905

SGK1	6446	1.057896935	0.056282914	0.0441555	0.97019298	1.15352919	0.002076
ORC2L	4999	1.005613556	0.005597859	0.020467	0.96607218	1.04677337	0.002361
SLC38A1	81539	1.053941077	0.052536545	0.04140014	0.97179905	1.14302622	0.003289
SERPINE1	5054	1.067027143	0.06487641	0.06391258	0.94139736	1.20942226	0.003671
PTPMT1	114971	0.94817686	-0.05321423	0.02200488	0.90815246	0.98996523	0.004151
RFTN1	23180	0.962520831	-0.03819957	0.04038059	0.88927916	1.04179474	0.005328
AXL	558	0.941354985	-0.06043497	0.04288594	0.86546369	1.02390108	0.005535
ERRFI1	54206	1.062187922	0.060330858	0.04556523	0.97144041	1.16141265	0.006228
COX8A	1351	1.089728221	0.085928327	0.02626111	1.03505803	1.14728601	0.00639
FGF2	2247	0.827753134	-0.18904032	0.05985238	0.73612979	0.9307805	0.00713
DUT	1854	0.988714113	-0.01135006	0.02434486	0.94264539	1.0370343	0.008411
MYLK	4638	1.043757681	0.042827357	0.05129596	0.94392283	1.15415166	0.009906
F3	2152	0.808345341	-0.21276591	0.06478146	0.71195879	0.91778091	0.010827
CNP	1267	0.999476605	-0.00052353	0.02183194	0.95761128	1.04317222	0.015003
CDK14	5218	0.903518815	-0.10145834	0.04294601	0.83058004	0.98286283	0.016297
YAP1	10413	1.074151146	0.071530718	0.0345597	1.00380216	1.14943037	0.027103
FSTL1	11167	1.031786658	0.031291919	0.04585214	0.94310597	1.12880603	0.036856
KIAA1033	23325	0.958991192	-0.04187339	0.02376679	0.91534389	1.00471977	0.053691
LLGL1	3996	1.07518405	0.072491857	0.02716521	1.01943547	1.13398128	0.05473
DRAM2	128338	0.964263149	-0.03639105	0.02473698	0.91862744	1.01216596	0.063421
PDLIM2	64236	0.937252649	-0.0648024	0.03483205	0.8754021	1.00347318	0.079515
KLF6	1316	0.976919217	-0.02335132	0.03523937	0.91172287	1.04677769	0.110534
GLTSCR1	29998	0.958004414	-0.04290289	0.02555494	0.91120293	1.00720973	0.131301
BICC1	80114	1.121220364	0.114417703	0.07207945	0.97350198	1.29135341	0.239443
FAM45A	404636	0.986037408	-0.01406099	0.02098648	0.9463018	1.02744154	0.243106
CCRN4L	25819	1.096420042	0.092050365	0.03776258	1.01820072	1.18064826	0.273882
CAMK4	814	0.953738647	-0.0473656	0.05858306	0.8502828	1.06978221	0.320353
CYR61	3491	1.044917475	0.043937911	0.05530632	0.93757316	1.16455182	0.348566
PFKFB3	5209	0.960507091	-0.04029391	0.0423034	0.88408059	1.04354046	0.368723
CTGF	1490	1.021113128	0.020893334	0.05803639	0.91132481	1.14412777	0.449523
PRKACG	5568	1.00382085	0.003813569	0.0128564	0.97884252	1.02943659	0.663378
ATP6V1A	523	1.00433343	0.004324067	0.02194855	0.96204477	1.04848098	0.760478

Table S4, Related to STAR methods. qPCR primer list

Gene	Forward	Reverse
Abhd4	5'-AAGCTAGCTCTTCCCGATGC-3'	5'-TCTCCTACCCATGCCTTGTC-3'
Actb	5’-ATCCGCCGCCCGTCCACA-3’	5’-ACCATCACGCCCTGGTGCCT-3’
ACTB	5’-ATCCGCCGCCCGTCCACA-3’	5’-ACCATCACGCCCTGGTGCCT-3’
Bax	5'-TGAAGACAGGGGCCTTTTTG-3'	5'-AATTCGCCGGAGACACTCG-3'
Cdkn1a	5'-CTAGGGGAATTGGAGTCAGG-3'	5'-AGAGACAACGGCACACTTTG-3'
Crip2	5'-GGCCAGGTCTGGGATTTC-3'	5'-TCATGGAGAAATACGTGTCACC-3'
Phlda3	5'-GAGCGGTGGAACATGTAAGG-3'	5'-TCGTGCGATGCTACTCTCTC-3'
Ptpn14	5’-AGCACTACTCGGAGACCCAT-3’	5’-GAGAACGGCAGTACAAGGCT-3’
PTPN14	5’-CGACTTCTGGCAGATGGTGT-3’	5’-GTGGCTTTTGGTTCGTCCAC-3’