Supplementary Information

Spontaneously Evolved Progenitor Niches Escape Yap Oncogene Addiction in Advanced Pancreatic Ductal Adenocarcinomas

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KPYYF_TAM 29d

Supplementary Figure 1. TAM treatment prolongs the survival of tumor-bearing mice despite divergent rates of Yap ablation. a. Scatter plot showing the tumor recombination rates calculated by dividing Tm+ area over Tm+ and GFP+ area and the corresponding days of TAM treatment of individual KPF, KPYF and KPYYF mice. Symbols represent genotypes whether KPF (circle), KPYF (square), or KPYYF (triangle). KPYY tumors are further grouped into three classes: Tm^LYap^H (low percentages of Tm⁺ cells and high Yap expression; filled triangle), Tm^HYap^L (high percentages of Tm⁺ cells with low Yap expression; half-filled triangle), and Tm^HYap^{KO} (high percentages of Tm⁺ cells with complete knockout Yap; open triangle). Trendlines indicate the average changes in recombination rates over time among KPF (black dash), KPYF (blue dash), and all of the KPYYF mice (red lines), respectively. b. Representative IHC images for Yap and Tm in PDAC tumors from KPF and the three major types of KPYYF mice. The days of TAM treatment for individual mice were shown at the bottom of images. Scale bars indicate 250 mm (left) or 100 µm (middle, right). Experiments were performed on KPF (n=9), KPYYF (Tm^LYap^H ;n=6), KPYYF (Tm^HYap^L ;n=11), and KPYYF (Tm^HYap^{KO} ;n=7). c. Kaplan-Meier survival curve from KPF (n = 42) and KPYYF (n = 92) mice. Mantel-Cox Long Rank test. **d.** Percentage of CC3+ area within GFP+ or Tm+ areas in KPF (n = 9) and KPYYF $(Tm^{H}Yap^{L} and Tm^{H}Yap^{KO}; n = 15)$ tumors. Unpaired, one-tailed, Student's t-test. e. Representative IHC images of indicated antibodies at relapsing (yellow) and regressing (red) regions of a KPYYF PDAC tumor after 29 days of TAM treatment matching Figure 1c. Scale bars indicate 50 µm. Experiments were performed on at 13 different KPYY mice. Source data are provided as a Source Data file.



а



Supplementary Figure 2. The gene signature upregulated in relapsed KPYYF tumors is correlated with worse survival in human PDAC patients. a. Gating strategy for fluorescenceactivated cell sorting (FACS) of GFP+ or Tm+ PDAC cells from the pancreata of KPF or KPYYF mice. b. Leading-edge analysis of the top-enriched Gene Sets in Tm+/Yap- or GFP+/Yap+ PDAC cells according to GSEA from Figure 1d. Gene Sets related to epithelial differentiation and cell-cell junctions are colored in green; Gene Sets related to Myc targets are colored in brown; Gene Sets related to pluripotent/progenitor and embryonic stem cells, undifferentiation and EMT are highlighted in yellow. c. WB analysis of indicated proteins in parental human Panc1 cells or YAP CRISPR knockout clones generated using two different YAP gRNAs (gYAP #1 and #2). VINC was used as the loading control. Shown is representative of three independent experiments. d. Left: Heatmaps depicting results from unsupervised clustering of TCGA (top; n = 176) and CPTAC (bottom: n = 140) PDAC tumors based on the mRNA expression of Yap-KO relapse-associated genes identified by RNA-seq of Tm+/Yap- and GFP+/Yap+ murine PDAC cells from Figure 1d (right). Right: Kaplan Meier survival analysis of TCGA (top) and CPTAC (bottom) PDAC patients expressing high (H) or low (L) levels of Yap-KO relapse-associated genes. TCGA (top): Relapse_H (n=163) and Relapse_L (n=13), and CPTAC (bottom): Relapse_H (n=14) and Relapse_L (n=126), respectively. Mantel-Cox Long Rank test. Source data are provided as a Source Data file.

b





Sox2 Yap

С

A matched region from an advanced KPF tumor



Supplementary Figure 3. PTF-expressing progenitor niches are present in both advanced murine and human PDAC tumors. a. Heatmaps of representative IHC staining of Sox5, Twist2, and Nr2f1 in three different advanced PDAC tumors from KPF mice. b. Heatmaps of representative IHC staining of SOX2 and ECAD at a matched region of an invasive PDAC tumor from a human patient. c. IHC images of Sox2 and Yap at a matched region of advanced PDAC tumor from a KPF mouse with two boxes marking two representative Sox2+ (yellow) and Sox2- (red) subregions. Scale bar indicates 200 μ m. IHC staining for the same set of antibodies was performed on 16 different mice. d. IHC images of SOX2, SOX5 and NR2F1 with matching images of YAP, Δ TP63 and ECAD at different regions of an invasive PDAC tumor from a human patient. IHC staining for the same set of antibodies was performed on five human PDAC tumor from a human patient. IHC staining for the same set of antibodies was performed on five human PDAC tumor from a human patient. IHC staining for the same set of antibodies was performed on five human PDAC tumor from a human patient. IHC staining for the same set of antibodies was performed on five human PDAC tumor from a human patient. IHC staining for the same set of antibodies was performed on five human PDAC tumor from a human patient. IHC staining for the same set of antibodies was performed on five human PDAC tumor from a human patient. IHC staining for the same set of antibodies was performed on five human PDAC tumor samples. Scale bar indicates 100 μ m.



Supplementary Figure 4. PTF expression is associated with EMT. Representative images from IF (top panel) analysis of primary PDAC cell lines against Ecad (red) and Sox2 (green) and from IHC analysis of the corresponding primary PDAC tumors with indicated antibodies. N= 8, 6 and 6 mice for Epithelial, Intermediate, and Mesenchymal groups, respectively. Scale bars indicate 100 μm.

d а #5596 #6032-3 #6055-1 #5520 #6389 #6516 #6547-1 #5346 #5601 #6749 #6484 -+ - + -+ -+ • + -+ -+ - + -+ - + -+ Cre DepMap CRISPR KO Effect 75_ 0.0 Yap 63 Taz 50--0.5 37. Sox2 Sox5 100 — -1.0 25 Twist2 50 -Nr2f1 -1.5 Nr2f2 50 -50 JunB 50 Jun DepMap CRISPR KO Effect 150 0.0 Ecad 100 -35 -Slug -0.5 150 Vinc 100--1.0 1 PTF 0 2 -1.5 #6032-1#6547-2 #6597 #6055-2 #6134 #5462 #6394 #6139 + + - + -+ -+ -+ - + -+ -2.0 --Cre 75. Yap 63. Taz 10.00 - 1 81 8 50 — 37. Sox2 100 -Sox5 25 Twist2 е Nr2f1 50 -#6389 #6516 Nr2f2 50 -+ -+ 50 JunB 37 50 50 Jun 150 Ecad 100 35 + -Slug 150 100 Vinc 100 50 3 4 5 PTF -+ + 25b **Colony numbers** 20 50 С CRE 80 -150 50 100 200 60 40 20 5 #6394 g #6389 p<0.0001 p=0.0001 + + + ***** | p=0.0012 63 9 #5462 #6516 p<0.0001 + ക 50 50 #6516 ***** #6389 🎖 | ns . #5462 ns + 1 0 10 15 20 8 || 2D 5 ÷ 0 T #6394 ns p=0.0005 T Days post co-culture 3D

Supplementary Figure 5

hPDAC lines

YAP

••••

<=2 >=3

PTF

TAZ

<=2 >=3

PTF

SOX2

SOX2

Actin

SOX5

SOX5

Actin

TWIST2

TWIST2

Actin

NR2F2

NR2F2

Actin

ŝ

p=0.0012

Supplementary Figure 5. PTF expression reduces PDAC cell dependency on Yap. a. WB analysis of primary PDAC lines infected Ad-GFP (-) or Ad-Cre (+) with indicated antibodies. Font colors of mouse IDs represent the differentiation statuses of tumors and corresponding primary PDAC cells (EP: blue; Inter: grey; MS: red). PTF scores (PTF) are indicated by the bottom bars. Vinc was used as loading control. Shown is representative of three independent experiments. **b.** Representative linear regression graphs showing the changes over time in the ratios of Tm+Yap- cells in co-cultures of primary PDAC cells pre-treated with Ad-GFP or Ad-Cre as outlined in Figure 3a. c. Bar graphs showing average colony numbers from 2D or 3D colony formation assays of the indicated primary PDAC lines infected Ad-GFP (-) or Ad-Cre (+). 3D: #6389 (n=4 independent experiments), #6516 (n=3 independent experiments), #5462 (n=3 independent experiments), and #6394 (n=4 independent experiments) and 2D: #6389 (n=4 independent experiments), #6516 (n=3 independent experiments), #5462 (n=3 independent experiments), #6394 (n=5 independent experiments), respectively. Unpaired, two-tailed, Student's t-test. Data are presented as mean value +/- SEM. d. Dot plots showing the KO effects of YAP or TAZ in individual human PDAC cell lines with PTF scores <=2 and >=3 according to the DepMap 22Q2 CRISPR screen. Data are presented as mean value +/- SEM. e. WB analysis confirming the exogenous expression of indicated PTFs in #6389 and #6516 cells at comparable levels as their endogenous expression in #5462. Actin was used as loading control. Shown is representative of three independent experiments. Source data are provided as a Source Data file.







Supplementary Figure 6. Nutrient deprivation, hypoxia and DNA/histone methylation inhibitors induce PTF expression in PDAC cells. Representative images and heatmaps depicting the percentage of randomly selected 10x microscopic fields positive for Sox2, Sox5 or Twist2 according to IF analysis of #6389 and #6516 cells after 2 weeks of culturing under indicated conditions (n = 12 fields per condition). Scale bar indicates 200 μ m. Source data are provided as a Source Data file.







С







Supplementary Figure /7. Global epigenetic reprogramming associated with EMT is linked to reduced dependency of PDAC cells on Yap. a. Unsupervised clustering of all 19 primary PDAC lines based on pairwise Spearman correlation co-efficiencies of H3K27ac, BRD4 or Yap Cut&Tag signals across the entire genome. b. RRHO representation of Kendal correlation coefficiencies calculated by comparing BRD4 and H3K27ac Cut&Tag signal variations for each genomic locus against the corresponding Yap dependency scores across all 19 primary PDAC lines. c. Heatmap depicting the overall Yap-binding statuses at genomic loci associated with either high (YapD^H) or low (YapD^L) Yap dependency from Figure 3B. d. Heatmap depicting unsupervised clustering of all 19 primary PDAC lines based on the signals of Yap Cut&Tag peaks overlapping the genomic loci associated with either high (YapD^H, black bars, n=151) or low (YapD^L, red bars, n=205) Yap dependency from Figure 4B. e. Heatmap depicting unsupervised clustering of all 19 primary PDAC lines based on the BRD4 Cut&Tag signals at the TSS sites corresponding to the PDAC squamous signature genes defined by Somerville et al. **f.** PCA plots segregating human PDAC lines based on the mRNA expression of PDAC squamous signature genes as shown in e. Each PDAC line is represented as a dot colored according to its YAP dependency score from the DepMap 22Q2 CRISPR screen. Source data are provided as a Source Data file.



Supplementary Figure 8. PTFs and Jun co-occupy active enhancer sites associated with Yap independency. a. Top10 most differentially enriched motifs according to HOMER differential motif enrichment analysis of BRD4 Cut&Tag peaks overlapping with genomic loci associated with either high (YapD^H) or low (YapD^L) Yap dependency from Figure 4b. b. Linear regression graphs showing the changes over time in the ratios of JunDN cells in co-cultures with parental primary PDAC cells as outlined in Figure 3a. n=3 independent experiments. Unpaired, two-tailed, Student's t-test. Data are presented as mean value +/- SEM. c. Cut&Tag signal heatmaps from the indicated antibodies within +/-3kb from the peak centers from PTF-high #5462 and PTF-low #6547-1 cells. d. Chow-Ruskey Venn diagram of the numbers of overlapping H3K27ac, Sox2, Sox5, and Twist2 Cut&Tag peaks in #5462 cells. e. Summary of the ratio of H3K27ac and BRD4 peaks at RE (gray) and SE (red) regions with different binding statuses by Jun, Sox2, Sox5, and/or Twist2 in #5462 cells. f. Peak distributions of each TF at active TSS (light blue), inactive TSS (dark blue), active CRE (light brown) and inactive CRE (dark brown) sites. g. Percentage of peaks containing the top most differentially enriched motifs according to HOMER differential motif enrichment analysis between Jun, Sox2, Sox5 or Twist2 peaks overlapping with active (light brown) or inactive (dark brown) CRE sites from f. Source data are provided within a Source Data file. Cut&Tag data are deposited in the GEO database under accession code GSE224566.



Supplementary Figure 9. PTFs are recruited to AP-1 sites by Jun and cooperate with Jun to activate transcription. a. Differential Jun, Sox2, Sox5, and Twist2 footprint scores (diffFPscore) and the corresponding -log10 P-values between active and inactive CRE at the sites of individual JASPAR motifs as determined by TOBIAS. Motifs with diffFPscore greater than 1.5 and -log10 P-values greater than 20 are highlighted in red. Dots corresponding to the AP-1 family of motifs are circled by blue dashed lines. **b.** Aggregated signal centering the Jun MA0489.2 motif (marked by grey dashed lines) within the Sox2, Sox5 or Twist2 peaks with (+, pink) or without (-, green) Jun co-binding. c. Aggregated signal centering the indicated motifs (marked by grey dashed lines) within the Jun, Sox2, or Twist2 peaks at active (blue) or inactive CRE (gray), or CRE bound by Jun and all the PTFs (red). d. Representative brightfield (left panel) and IF (right panel) images of Ecad (green) and Sox2 (purple) in indicated primary PDAC cells following extended treatments with TGFb or control medium. Scale bar indicates 50 µm on the left panel and 100 µm on the right panel. Shown is representative images from three independent experiments. e. Log2 FC in mRNA expression of indicated genes in indicated PDAC cells treated with TGFb relative to control. n = 3 independent experiments. Unpaired, two-tailed, Student's t-test. Data are presented as mean value +/- SEM. Source data are provided within a Source Data file.

а b С Days post Cre 1.0 #5346 Panc1 Relative Growth Rate (Yap-KD vs Parental) 0.0 Tm/GFP ratio 0 7 17 35 0.8 37 Sox2 -0.2 0.6 100 Sox5 0.4 -0.4 0.2 20 0 Twist2 -0.6 8 0.0 30 Ō 10 20 Nr2f1 50 -0.8 p=0.0009 Days post co-culture Nr2f2 50 Yap 75 150 d Vinc 100 Panc1 #5346 Normalized Growth Rate (Yap-KD v Parental) 0 -2 -1 1 2 ABBV-075 OTX015 SGC-CBP30 е Yap Cut&Tag (#6516) A-196 ML-324 TEAD2_MA1121.1 Jun MA0489.2 5-Aza 10 12 BI-7273 Aggegated Signal 10 8 AM580 PCI 34051 8 6 Bound 4 6 - Unbound CAY10603 2 JIB-04 4 — All 2 0 PFI-5 I-BRD9 0 -2 GSK2801 -2 -4 BAZ2-ICR -4 -6 AMI-1 -60 -40 -20 Ò 20 40 60 -60 -40 -20 0 20 40 60 MI-136 bp from motif center bp from motif center HDAC3-i **Nexturastat A** MS-275 EX-527



EED226 TC-E 5003 EPZ015666

Supplementary Figure 10

Supplementary Figure 10. BET inhibitors sensitize human and murine PDAC cells to Yap inhibition in vitro and in vivo. a. Changes in the ratios of #5346 cells pretreated with Ad-Cre (Tm+Yap-) or Ad-GFP (GFP+Yap-) and co-cultured over indicated time. **b.** WB of indicated proteins in #5346 cells at the indicated days post infection with Ad-CRE. Vinc was used as the loading control. Shown is representative of three independent experiments. c. Log2 relative growth rates of Yap-KD versus parental Panc1 cells. n=3 independent experiments. Unpaired, two-tailed, Student's t-test. Data are presented as mean value \pm -SEM. d. Log2 relative growth rates of Yap-KD versus parental Panc1 cells co-cultured over a 2-month period in the presence of indicated epigenetic inhibitors normalized to DMSO. BET inhibitors are highlighted with red. e. Aggregated signals from bound (red), unbound (blue), or all (gray) Yap peaks centered on the indicated motif sites (marked by grey dashed lines) in #6516 cells. The total numbers of bound, unbound and all peaks for each motif are: TEAD2 MA1121.1:711, 2492 and 3203; Jun MA0489.2: 798, 5481 and 6279. f. Log2 relative growth rates of Yap-KD versus parental mT3 and mT4 cells. n=3 independent experiments. Data are presented as mean value +/- SEM. Unpaired, two-tailed, Student's t-test. g. WB analysis of indicated proteins in CRISPR Yap KO clones derived from mT3 and mT4 cells. Shown is representative of three independent experiments. h. Relative growth rate of Yap-KD to parental mT4 cells after co-culturing in the presence of indicated concentrations of ABBV-075. n=3 independent experiments. Data are presented as mean value +/- SEM. Unpaired, two-tailed, Student's t-test. Source data are provided within a Source Data file. Cut&Tag data are deposited in the GEO database under accession code GSE224566.



е



f





Supplementary Figure 11. BET inhibitor ABBV-075 reduces PTF expression and the growth of Yap-independent murine PDAC tumors. a-b. Kaplan-Meier survival curve of mice carrying subcutaneous xenografts derived from mT4 (a) and #5462 cells (b) treated with ABBV (light blue), VT103 (blue), ABBV+VT103 (A+V) (pink) or DMSO (black). n = 6 mice for each treatment arm. Log-rank (Mantel-Cox) test. c-d. Representative IHC images with indicated antibodies of mT4 (c) and #5462 (d) xenografts treated with treated with ABBV (light blue), VT103 (blue), ABBV+VT103 (A+V) (pink) or DMSO (black). Experiments were performed on three different mice from each treatment. Scale bar indicates 100 μ m. e. WB analysis of indicated proteins in two primary PDAC lines derived from relapsed Yap-KO tumors from TAM-treated KPYYF mice. Vinc was used as the loading control. Shown is representative of three independent experiments. f. Changes in relative tumor size (left) and overall survival (right) of nude mice bearing #6385 Yap-KO Relapsed xenografts treated with ABBV (red; n=7 mice) or DMSO (black; n=6 mice). Left: Two-way ANOVA test. Right: Log-rank (Mantel-Cox) test. Data are presented as mean value +/- SEM. Source data are provided as a Source Data file.

Tumor ID	Mouse ID	Gender	Genotype	Age (davs)	TAM (davs)
#6028-				(]-/	(
T00	#6028	Female	KPF	121	4
#6028-					
T01	#6028	Female	KPF	121	4
#6114-	110020	i onnaio		121	•
T00	#6114	Female	KPF	41	6
#4921-		i omaio			Ū
T00	#4921	Female	KPF	61	9
#4921-	# 10 <u></u>	i onnaio		01	0
T01	#4921	Female	KPF	61	9
#4921-					-
T02	#4921	Female	KPF	61	9
#4921-					
T03	#4921	Female	KPF	61	9
#4921-					
T04	#4921	Female	KPF	61	9
#6149-					
Т00	#6149	Female	KPF	116	11
#5997-					
Т00	#5997	Female	KPF	143	23
#5897-					
Т00	#5897	Female	KPF	149	30
#5996-					
T00	#5996	Male	KPF	152	32
#4785-					
Т00	#4785	Male	KPF	106	36
#4785-					
T01	#4785	Male	KPF	106	36
#4785-					
T02	#4785	Male	KPF	106	36
#4785-					
T03	#4785	Male	KPF	106	36
#4943-					
100	#4943	Male	KPF	149	79
#5376-				1.10	10
100	#5376	Male	KPYF	149	40
#4808-	#4000	E		77	40
100	#4808	Female	KPYF	11	43
#5379-	#5070	Mala		170	60
100	#5379	male	KPTF	1/8	69
#4892- T00	#1050	Mala		150	70
100	#4002	male	NPTF	150	12
#3024- T00	#5004	Fomolo		174	04
100	#3024	remale	NETE	174	94
#3130- T00	#5136	Malo	KDVE	170	102
100 #1802-	#3130	INIGIE	KPYYE	170	102
#4032- T00	#1802	Fomale	(Tm ^H Van ^{KO})	100	26
#8224-	H-1032		KPYYE	122	50
T00	#8224	Male	(Tm ^H Yap ^{KO})	109	48
			(····· · · · · · · · · · · · · · · · ·	100	-10

Supplementary Table 1. The information of mice

#4449-			KPYYF		
Т00	#4449	Female	(Tm ^H Yap ^{KO})	126	51
#7783-			КРҮҮГ ́		
Т00	#7783	Female	(Tm ^н Yap ^{ко})	129	79
#7783-			KPYYF		
T01 #6385-	#7783	Female	(Tm ^H Yap ^{KO}) KPYYF	129	79
T00 #6385-	#6385	Male	(Tm ^н Yap ^{ко}) крууг	222	132
T01	#6385	Male	(Tm ^H Yap ^{KO})	222	132
#7041- T00 #7641	#7641	Female	(Tm ^H Yap ^{KO})	197	145
T01	#7641	Female	(Tm ^H Yap ^{KO})	197	145
#4097- T00 #4607	#4697	Female	(Tm ^H Yap ^{KO})	246	178
#4097- T01 #4607	#4697	Female	(Tm ^H Yap ^{KO})	246	178
#4697- T02 #4607	#4697	Female	(Tm ^H Yap ^{KO})	246	178
#4697- T03	#4697	Female	(Tm ^H Yap ^{KO})	246	178
#5720-	#5700	Famala		101	07
100 #4455	#5720	remale	KPTTF (III-Tap ¹⁰)	101	21
T00	#4455	Female	KPYYF (Tm ^H Yap ^L)	61	6
#0387- T00 #5601	#6387	Female	KPYYF (Tm ^н Yap [∟])	43	7
#5001- T00 #5601	#5601	Male	KPYYF (Tm ^H Yap ^L)	159	17
#5601- T01 #4644	#5601	Male	KPYYF (Tm ^H Yap ^L)	159	17
#4641- T00 #4641	#4641	Female	KPYYF (Tm ^H Yap ^L)	63	26
#4641- T01 #4901	#4641	Female	KPYYF (Tm ^н Yap [∟])	63	26
#4891- T00 #4028	#4891	Female	KPYYF (Tm ^H Yap ^L)	115	29
#4938- T00 #6265	#4938	Female	KPYYF (Tm ^H Yap ^L)	128	29
#0305- T00 #6265	#6365	Male	KPYYF (Tm ^н Yap [∟])	140	40
#0305- T01 #5522	#6365	Male	KPYYF (Tm ^H Yap ^L)	140	40
#5522- T01 #6028	#5522	Male	KPYYF (Tm ^H Yap ^L)	136	41
#0920- T00 #6028	#6928	Female	KPYYF (Tm ^н Yap [∟])	127	58
#0928- T01 #4546	#6928	Female	KPYYF (Tm ^H Yap ^L)	127	58
#4516- T01 #4610	#4516	Male	KPYYF (Tm [⊦] Yap [∟])	150	80
#4610- T01	#4610	Female	KPYYF (Tm ^н Yap [∟])	205	141
#0021- T00	#6821	Male	KPYYF (Tm ^L Yap ^H)	80	2

#5346-					
T00 #5596-	#5346	Male	KPYYF (Tm [∟] Yap ^H)	127	10
T00	#5596	Female	KPYYF (Tm [∟] Yap ^H)	155	13
#5522- T00	#5522	Male	KPYYF (Tm ^L Yap ^H)	136	41
#7369- T00	#7369	Male	KPYYF (Tm [∟] Yap ^н)	133	67
#4516- T00	#4516	Male	KPYYF (Tm ^L Yap ^H)	150	80
#4610-		E		005	
100	#4610	Female	KPYYF (Im-Yap'')	205	141

Supplementary Table 2. The HOMER motifs whose genomic locations were used to plot Sox2, Sox5, Twist2 and Jun Cut&Tag signals in Figure 5b.

Homer Motif Name	Homer Motif Profile
Sox2(HMG)/mES-Sox2- ChIP- Seq(GSE11431)/Homer (Motif 338)	SCCATTGTIC Reverse Opposite: SAACAATGGS
Sox6(HMG)/Myotubes-Sox6- ChIP- Seq(GSE32627)/Homer (Motif 341)	Reverse Opposite:
Twist2(bHLH)/Myoblast- Twist2.Ty1-ChIP- Seq(GSE127998)/Homer (Motif 391)	EXAMPLE 1 Reverse Opposite:
AP-1(bZIP)/ThioMac-PU.1- ChIP- Seq(GSE21512)/Homer (Motif 1)	ATGASTCASE Reverse Opposite: SETGASTCASE

_	Concentrat	ion (µM)
Inhibitor	mPDAC cells	Panc1
3-Deazaneplanoci (DZNep)	1	None
5-Azacytidine	2	0.66
A-196	10	2.5
ABBV-075	0.005	0.11
AM580	20	20
AMI-1	0.5	10
AR-42 (OSU-HDAC42)	1	None
BAZ2-ICR	25	25
BI-7273	1	20
BMS 493	5	None
BRD4884	1.88	2.5
CAY10603	1	0.022
EED226	20	6.66
EPZ015666	20	2.5
EPZ6438	1	None
EX-527	30	2.5
GSK126	2	None
GSK2801	15	15
GSK6853	20	None
HDAC3 inhibitor	1	20
I-BRD9	15	10
JIB-04	0.375	0.037
LE 135	4	None
MI-136	3.33	2.5
ML-324	0.83	1.66
MM-102	0.5	None
MS-275	10	1
MS023	5	None
Nexturastat A	2.5	1
OTX015	0.25	0.1
Panobinostat	0.5	None
PCI 24781	0.4	0.125
PCI 34051	20	20
PFI-3	30	None
PFI-5	15	15
PRT4165	72	None

Supplementary Table 3. The list of epigenetic inhibitors

PTC-209	0.5	None
SGC-CBP30	18	3
SGC707	12.5	None
TC-E 5002	30	30
TC-E 5003	0.75	0.75
Trichostatin A (TSA)	0.2	None
UNC0379	6.25	2.5

Supplementary Table 4. The list of reagents and resources

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Antibodies		
	Abcam Cat#ab13970;	
Chicken polyclonal anti-GFP	RRID:AB_300798	IHC 1:2000
Goat polyclonal anti-tdTomato	LifeSpan Cat#LS-C348313	IHC 1:2000
Ki67 Rabbit polyclonal antibody	MilliporeSigma Cat#ab9260; AB_RRID:2142366	IHC 1:500
HNF-4 alpha/NR2A1 Rabbit polyclonal antibody	NOVUS BIOLOGICALS Cat#NBP1-89679	IHC 1:1000
CDH2 rat mAb	DSHB Cat#MNCD2; RRID:AB_528119	IHC 1:200
Mouse monoclonal Anti-E- Cadherin (clone36)	BD Biosciences Cat#610182; RRID:AB_397581	IHC 1:2000; IF 1:500; WB 1:2000
Mouse monoclonal anti-Vinculin (Clone 7F9)	Santa Cruz Biotechnology Cat#sc- 73614; RRID:AB_1131294	WB 1:2000
Mouse monoclonal anti-β-Actin (Clone C4)	Santa Cruz Biotechnology Cat#sc- 47778; RRID:AB 2714189	WB 1:5000
ZEB1 (E2G6Y) XP Rabbit mAb	Cell Signaling Technology Cat#70512	IHC 1:500

	Cell Signaling Technology	
JunB (C37F9) Rabbit mAb	RRID:AB_2130002	1:1000
	Cell Signaling Technology	
(D3N8F)	Cat#13987; RRID:AB_2631168	WB 1:1000
	Cell Signaling Technology	IHC 1:500; WB
Rabbit polyclonal anti-YAP	Cat#4912; RRID:AB_221891	1:1000; Cut&Tag 1:50
	Cell Signaling Technology	IHC 1:500; IF
Rabbit monoclonal anti-SOX2 (Clone D6D9)	Cat#5024; RRID:AB 1904142	1:200; WB 1:1000; Cut&Tag 1:50
		IHC 1:500: IF
	Proteintech Cat#13216-1-	1:200; WB 1:1000;
SOX5 Polyclonal antibody	AP; RRID:AB=2196089	Cut& lag 1:50
	Proteintech Cat#11752-1-	IHC 1:500; IF 1:200: WB 1:1000:
TWIST2 Polyclonal antibody	AP; RRID:AB_2877791	Cut&Tag 1:100
COUP-TEL (D/H2) Rabbit mAb	Cell Signaling Technology	
antibody (NR2F1)	RRID:AB_11220432	1:1000
	Cell Signaling Technology	
mAb (NR2F2)	RRID:AB_11220428	1:1000
ETS 1 (D8O8A) Pabbit mAb	Cell Signaling Technology	WR 1:1000
	Cal#14009	
	Proteintech Cat#55013-1-	
MAF polyclonal antibody	AP; RRID:AB_10863127	WB 1:1000

	Proteintech Cat#21305-1-	
SIX4 polyclonal antibody	AP; RRID:AB_10860258	WB 1:1000
	Santa Cruz Biotechnology	
	Cat#sc-271047;	
PRX (Prrx1; C-6) antibody	RRID:AB_10611937	WB 1:1000
	BIOCARE MEDICAL	
antibody	RRID:AB 2858274	IHC 1:500
Rat monoclonal anti-Keratin.	DSHB Cat#TROMA-III:	IHC 1:500: WB
type I; cytokeratin 19	RRID:AB_2133570	1:2000
	Sigma-Aldrich	
	Cat#HPA015055;	
Rabbit Anti-BRD4 antibody	RRID:AB_1845435"	Cut&Tag 1:50
Anti-acetyl-Histone H3 (Lys27)	MilliporeSigma Cat#07-360;	Cut&Tag 1:50
Antibody		
Anti-trimethyl-Histone H3 (Lys4)	MillinoreSigma Cat#07-473	
Antibody	RRID:AB_1977252	Cut&Tag 1:100
	Cell Signaling Technology	
c-Jun (60A8) Rabbit mAb	Cat#9165;	WB 1:1000;
antibody	RRID:AB_2130165	Cut&Tag 1:100
Anti-rabbit IgG, HRP-linked	Cell Signaling Technology	WB 1:5000
Anibody		VB 1.5000
Anti-mouse IaG HRP-linked	Cell Signaling Technology	
Antibody	Cat#7076	WB 1:5000
Chemicals, Pe	ptides, and Recombinant Prot	eins
5 Azacutidina	AnovRio	Cat#A1907; CAS:
		020-07-2
ABBV-075	Cayman	1445993-26-9

OTX015	Cayman	Cat#15947; CAS: 202590-98-5
JQ1	Cayman	Cat#11187; CAS: 1268524-70-4
ML-324	Cayman	Cat#17472; CAS: 1222800-79-4
PRT4165	Cayman	Cat#19093; CAS: 31083-55-3
MI-136	Cayman	Cat#19245; CAS: 1628316-74-4
TC-E 5003	Cayman	Cat#17718; CAS: 17328-16-4
PFI-3	Cayman	Cat#15267; CAS: 1819363-80-8
UNC0379	Cayman	Cat#16400; CAS: 1620401-82-2
PFI-5	Cayman	Cat#15267; CAS: 1819363-80-8
Trichostatin A	Cayman	Cat#89730; CAS: 58880-19-6
GSK126	Cayman	Cat#15415; CAS: 1346574-57-9
GSK484	Cayman	Cat#17488; CAS: 1652591-81-5
MM-102	Cayman	Cat#17699; CAS: 1417329-24-8
TP-472	Cayman	Cat#20030; CAS: 2079895-62-6
BRD4884	Cayman	Cat#19834; CAS: 1404559-91-6
BMS 453	Cayman	Cat#19076; CAS: 166977-43-1
UNC3866	Cayman	Cat#19237; CAS: 1872382-47-2
CD2665	Cayman	Cat#16031; CAS: 170355-78-9

MI192	Cayman	Cat#18288; CAS: 1415340-63-4
DZNep	Cayman	Cat#13828; CAS: 102052-95-9
TC-E 5002	Cayman	Cat#17717; CAS: 1453071-47-0
(R)-PFI-2	Cayman	Cat#14678; CAS: 1627607-87-7
EPZ5676	Cayman	Cat#16175; CAS: 1380288-87-8
BAY-6035	Cayman	Cat#25925; CAS: 2247890-13-5
UNC1215	Cayman	Cat#13968; CAS: 1415800-43-9
C646	Cayman	Cat#10549; CAS: 328968-36-1
JIB-04	Cayman	Cat#15338; CAS: 199596-05-9
CAY10603	Cayman	Cat#13146; CAS: 1045792-66-2
Furamidine	Cayman	Cat#19121; CAS: 55368-40-6
BI-7273	Cayman	Cat#20311; CAS: 1883429-21-7
SGC3027	SGC	Cat#6825; CAS:None
GSK-LSD1	Cayman	Cat#16439; CAS: 2102933-95-7
MRK-740	MedChemExpress	Cat#HY-114209; CAS: 2387510-80-5
NI-57	Cayman	Cat#17662; CAS: 1883548-89-7
GSK6853	Cayman	Cat#20985; CAS: 1910124-24-1
AR-42	Cayman	Cat#17531; CAS: 1798310-55-0

AM580	Cayman	Cat#15261; CAS: 102121-60-8
BIX 01294	Cayman	Cat#13124; CAS: 1808255-64-2
OICR-9429	Cayman	Cat#16095; CAS: 1801787-56-3
BAZ2-ICR	Cayman	Cat#17448; CAS: 1665195-94-7
EED226	Cayman	Cat#22031; CAS: 2083627-02-3
EPZ015666	Cayman	Cat#17285; CAS: 1616391-65-1
EPZ020411	Cayman	Cat#19160; CAS: 1700663-41-7
PTC-209	Cayman	Cat#16277; CAS: 315704-66-6
MS-275	Cayman	Cat#13284; CAS: 209783-80-2
TMP269	Cayman	Cat#17738; CAS: 1314890-29-3
EX-527	Cayman	Cat#10009798; CAS: 49843-98-3
SGC707	Cayman	Cat#17017; CAS: 1687736-54-4
AMI-1	Cayman	Cat#13965; CAS: None
BMS493	Cayman	Cat#17418; CAS: 215030-90-3
Panobistat	MedChemExpress	Cat#HY-10224; CAS: 404950-80-7
PCI 34051	Cayman	Cat#10444; CAS: 950762-95-5
A-196	Cayman	Cat#18317; CAS: 1982372-88-2
LE 135	Cayman	Cat#14415; CAS: 155877-83-1

Nextrastat A	Cayman	Cat#71462653; CAS No.1403783- 31-2		
GSK2801	Cayman	Cat#14120; CAS: 1619994-68-1		
GSK-J4	Cayman	Cat#12073; CAS: 1797983-09-5		
MS023	Cayman	Cat#34786; CAS: 1831110-54-3		
BRD73954	Cayman	Cat#16919; CAS: 1440209-96-0		
PCI24781	Cayman	Cat#20059; CAS: 783355-60-2		
SGC-CBP30	Cayman	Cat#14469; CAS: 1613695-14-9		
I-BRD9	Cayman	Cat#17749; CAS: 1714146-59-4		
EPZ6438	Cayman	Cat#16174; CAS: 1403254-99-8		
Vivace102 (V102)	Vivace Therapeutics	None		
Puromycin	Thermo Fisher Scientific	Cat# A1113803		
Doxycycline hydrochloride	Alfa Aesar	Cat#J60422; CAS: 10592-13-9		
TGFb1	MedChemExpress	HY-P7117		
Critical Commercial Assays				
GoTaq® Green Master Mix	Promega	Cat#M7122		
ImmPACT DAB EqV HRP substrate	Vector Laboratories	Cat#SK-4103		
IMMPRESS HRP Polymer Detection Kit	Vector Laboratories	Cat#MP-7401, MP- 7402, MP-7405		
iScript cDNA Synthesis Kit	Bio-Rad	Cat#1708890		
iTaq Universal SYBR Green Supermix	Bio-Rad	Cat#1725124		

Pierce BCA Protein Assay Kit	Thermo Fisher Scientific	Cat#23225
PrepEase Genomic DNA		
isolation kit	Affymetrix	Cat#78855
RNAeasy Mini Kit	Qiagen	Cat#74104
Tyramide Signal Amplification (TSA) kit	Thermo Fisher Scientific	Cat#T20932, T20933, T20936
NEBNext HiFi 2x PCR Master mix	NEB	Cat#M0541
BioMag®Plus Concanavalin A	Bangs Laboratories	Cat#BP531
Mag-Bind® TotalPure NGS beads	Omega Bio Tech	Cat#M1378
Exper	imental Models: Cell Lines	
Panc1	ATCC	CRL-1469
293T	ATCC	CRL-3216
mT3 and mT4	Sylvia F.Boj ea al., 2015	N/A
Primary mPDAC (KP)	This paper	N/A
Primary mPDAC (KPYY)	This paper	N/A
Experimen	ntal Models: Organizms/Strain	S
Athymic Nude Mouse	Charles River Laboratories (Croy and Chapeau, 1990)	Strain code #553
CL57/BL6 mice	Charles River Laboratories (Croy and Chapeau, 1990)	Strain code #027
Genetically engineered mouse strains	(Schönhuber et al., 2014 (Zhang et al., 2010)	N/A
	Recombinant DNA	
pTRIPZ lentiviral vector	GE Healthcare Dharmacon, Inc.	Cat#RHS4740
LentiCrispr v2	Addgene	Cat#52961
pCW57-MCS1-2A-MCS2	Addgene	Cat##71782

Ad-CMV-GFP	lowa viral vector core	Cat#lowa-1174		
Ad-CMV-CRE	lowa viral vector core	Cat#lowa-5		
		Cat#HsCD0033033		
pLenti6.2-V5-TWIST2	DNASU	1		
pl X304-SOX2	DNASU	Cat#HsCD0043632		
		Cat#HsCD0044263		
pLX304-SOX5	DNASU	8		
		Cat#HsCD0000521		
pDNR-Dual-NR2F2	DNASU	5		
pCW57-SOX2	This paper	N/A		
pCW57-SOX5	This paper	N/A		
pCW57-TWIST2	This paper	N/A		
pCW57-NR2F2	This paper	N/A		
pTRIPZ-shSox2	This paper	N/A		
pTRIPZ-shSox5#1	This paper	N/A		
pTRIPZ-Sox5#2	This paper	N/A		
pTRIPZ-shTwist2#1	This paper	N/A		
pTRIPZ-shTwist2#2	This paper	N/A		
pTRIPZ-shNr2f1#1	This paper	N/A		
pTRIPZ-shNr2f1#2	This paper	N/A		
pTRIPZ-shNr2f2#1	This paper	N/A		
pTRIPZ-shNr2f2#2	This paper	N/A		
TLCV2-sgNr2f2#1	This paper	N/A		
TLCV2-sgNr2f2#2	This paper	N/A		
3XFlag-pA-Tn5	Addgene	Cat#124601		
Oligonucleotides				
	Broad TRC RNAi shRNA			
A 3'	library	TRCN0000085748		
-				
Mouse Sox5_shRNA 5'	Broad TBC BNA: abBNA			
A 3'	library	TRCN0000421409		

Mouse Twist2_shRNA 5' AGCAAGAAATCGAGCGAAGA T 3'	Broad TRC RNAi shRNA library	TRCN0000086085
Mouse Nr2f1_shRNA 5' GTCCGCAGGAACTTAACTTA C 3'	Broad TRC RNAi shRNA library	TRCN0000350649
Mouse Nr2f2_shRNA 5' CTCGTACCTGTCCGGATATA T 3'	Broad TRC RNAi shRNA library	TRCN0000054475