

## Supplementary Information for

### **p73 $\alpha$ 1, a p73 C-terminal isoform, regulates tumor suppression and the inflammatory response via Notch1**

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## Supplementary Information Text

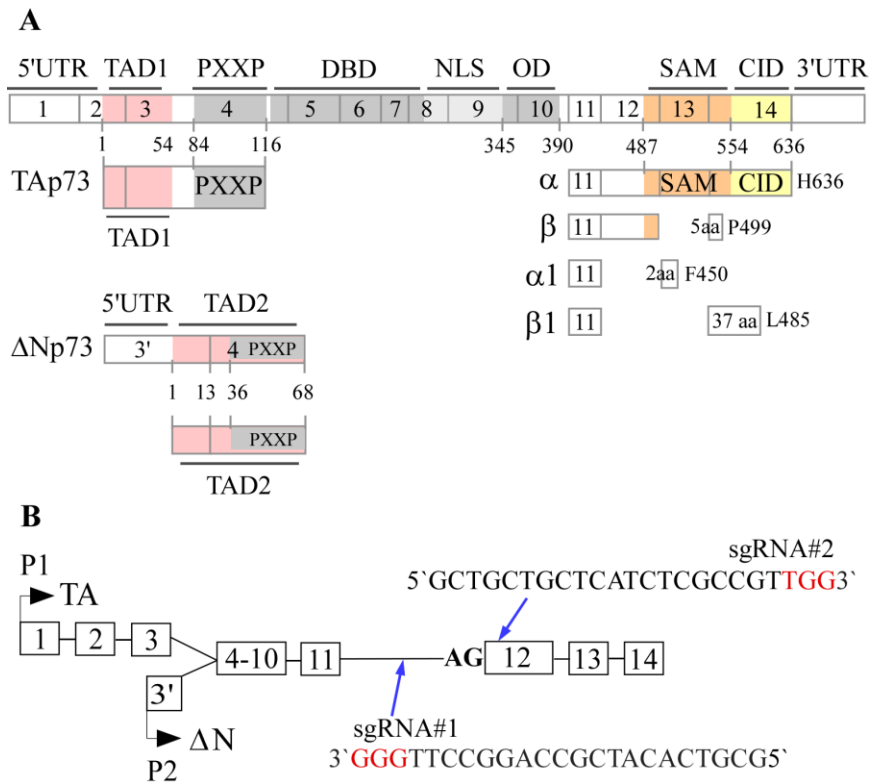
### Materials and Methods

#### *Cell Culture and Cell Line Generation*

MIA PaCa-2 cells and their derivatives, SK-N-AS, U373, T98G, and H12975 cells were cultured in DMEM with 10% FBS. MIA PaCa-2, SK-N-AS, U373, T98G, and H12975 cell lines were purchased from ATCC, tested negative for mycoplasma, and used at passage 20 or lower. We did not authenticate the cell lines because ATCC rigorously authenticates their cell lines. To generate *TAp73<sup>-/-</sup>*, *ΔNp73<sup>-/-</sup>*, and *E12<sup>-/-</sup>* MIA PaCa-2 cell lines, parental cells were transfected with the previously described pSpCas9(BB)-2A-Puro plasmids. Cells were puromycin-selected for 2-3 weeks and clones were confirmed via DNA-sequencing and/or Western blotting.

#### *RNA-seq Data*

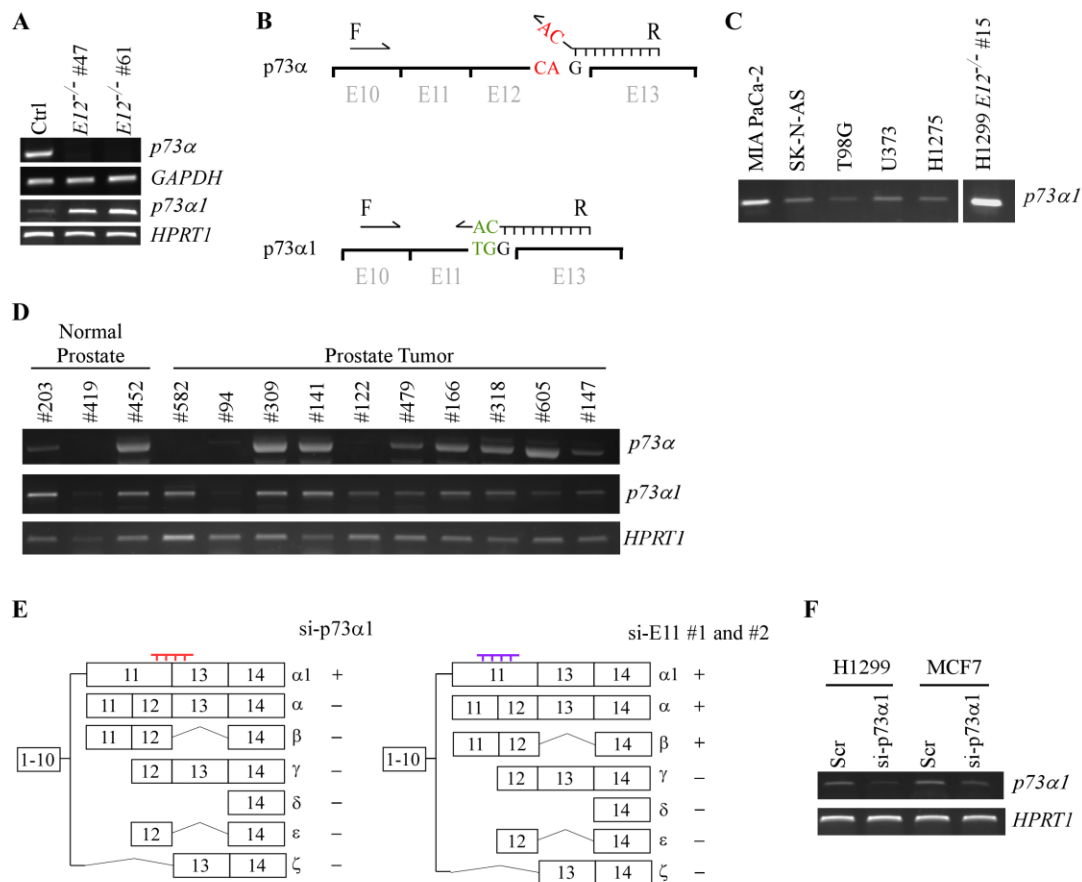
Isogenic control and E12-KO H1299 cells were collected in Trizol and sent to Novogene (Beijing, China) for analysis. To generate heat maps showing differential gene expression, z-score was calculated for each gene in the corresponding cell line and GraphPad Prism 9 was used to make the heat maps.



**Fig. S1. p73 functional domains and gene structure.**

(A) p73 functional domains. TAD1: Transactivation Domain 1. TAD2: Transactivation Domain 2. PXXP: Proline-rich Domain. DBD: DNA-Binding Domain. NLS: Nuclear Localization Signal. OD: Oligomerization Domain. SAM: Sterile Alpha Motif. CID: C-terminal Inhibitory Domain.

(B) Schematic representation of sgRNA #1 and #2 used to generate *E12*<sup>-/-</sup> cell lines.



**Fig. S2. Endogenous expression of *p73α1*.**

(A) The level of *p73α*, *p73α1*, *GAPDH*, and *HPRT1* transcripts was measured in isogenic control and *E12<sup>-/-</sup>* MIA PaCa-2 cells.

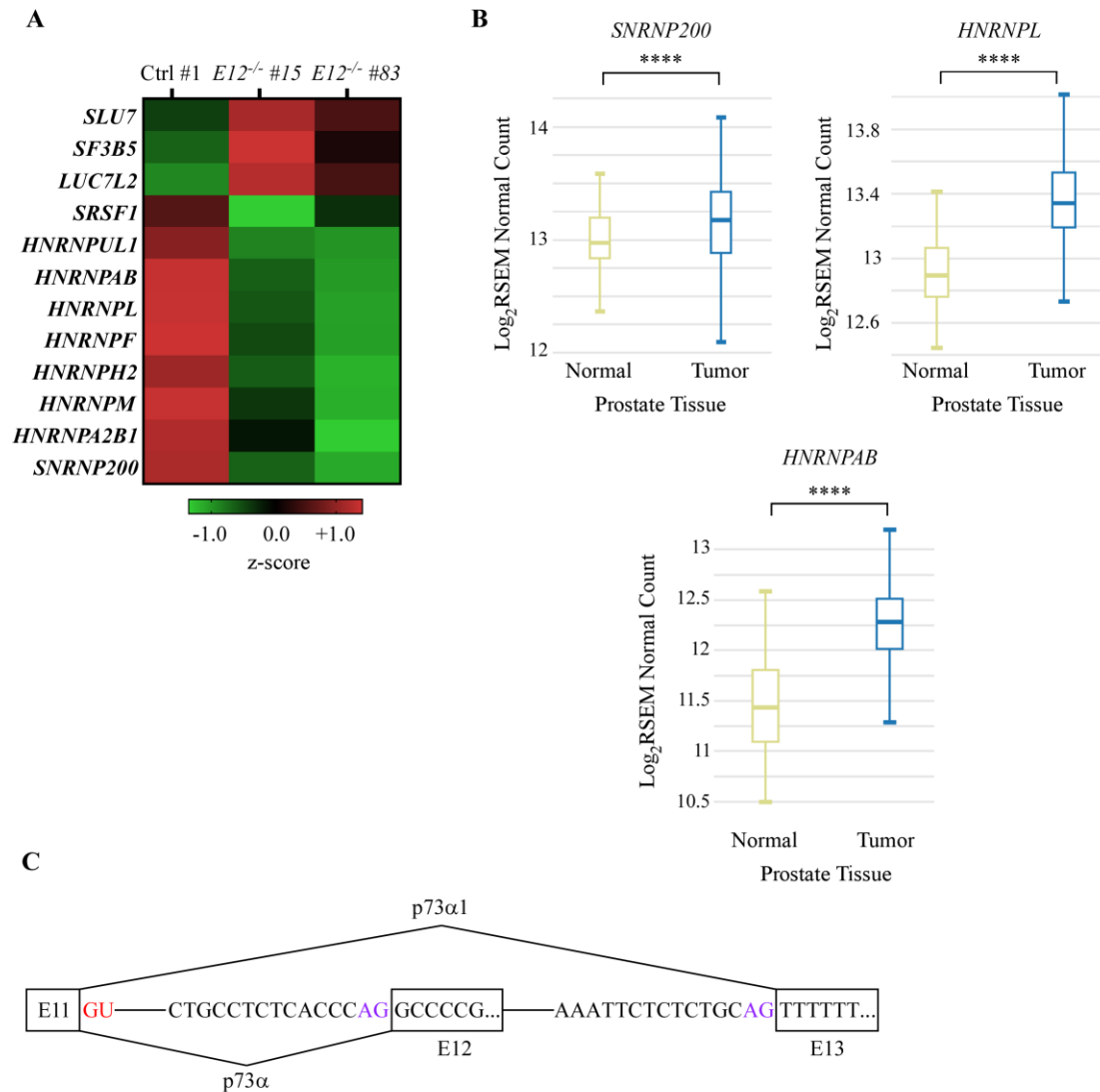
(B) Schematic diagram of the reverse primer that specifically amplifies *p73α1*, but not *p73α*.

(C) The level of *p73α1* transcript was measured in MIA PaCa-2, SK-N-AS, T98G, U373, H1275, and H1299 *E12<sup>-/-</sup>* cells.

(D) The level of *p73α*, *p73α1*, and *HPRT1* transcripts was measured in normal human and tumor prostate tissues.

(E) Diagram of the locations targeted by si-*p73α1* and si-E11 #1 and 2 and the effect on each *p73* isoform. + : knockdown; - : no effect.

(F) The level of *p73α1* and *HPRT1* transcripts was measured in H1299 and MCF7 cells transiently transfected with Scrambled siRNA (Scr) or si-*p73α1* for 3 days.

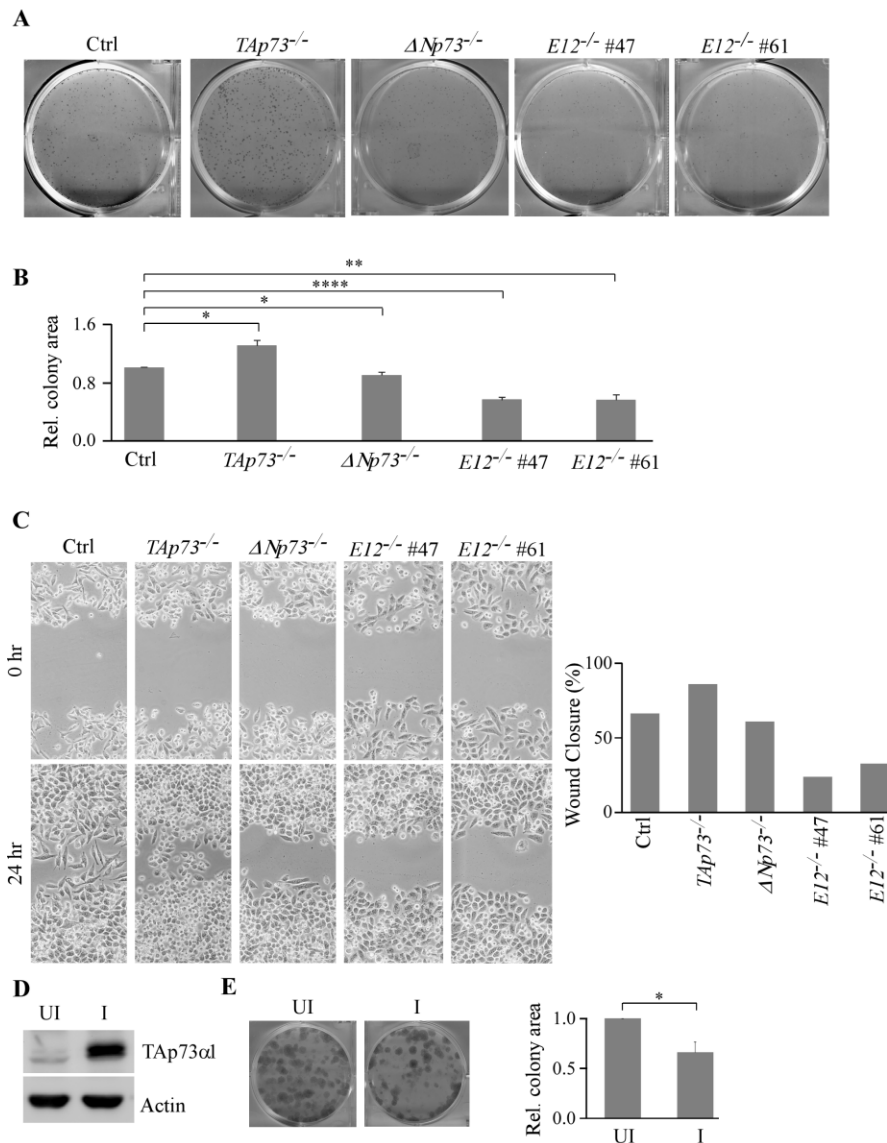


**Fig. S3. E12-KO differentially regulates splicing-associated genes.**

(A) Heatmap of splicing-associated genes and their differential expression in isogenic control and *E12*<sup>-/-</sup> H1299 cells.

(B) RSEM values of *SNRNP200*, *HNRNPL*, and *HNRNPAB* in normal human and prostate cancer samples from GTEx and TCGA databases, respectively. Data was analyzed using UCSC Xena Browser (TCGA Target GTEx).

(C) Diagram showing donor splice site (red) in intron 11 and the splice acceptor sites (purple) in introns 11 and 12.



**Fig. S4. p73 $\alpha$ 1 inhibits cell growth and migration.**

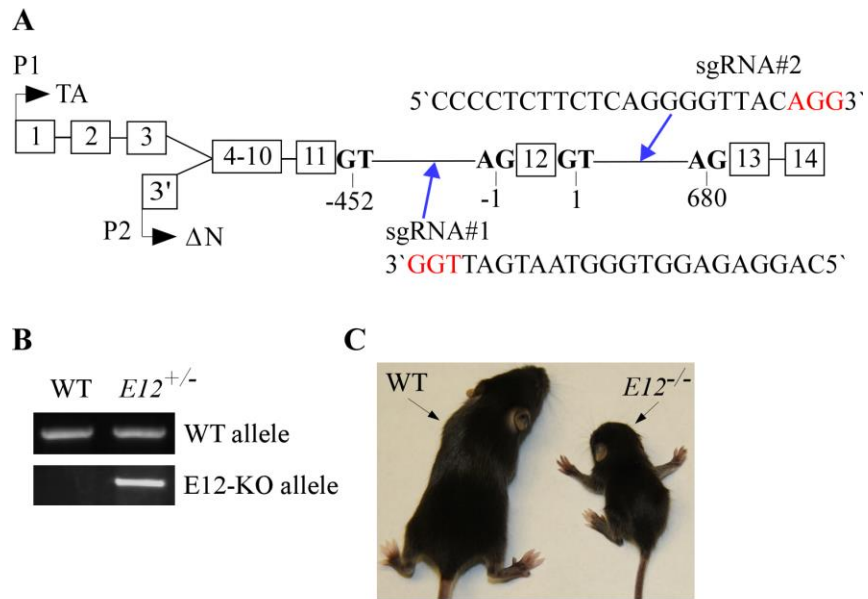
(A) Colony formation assay was performed in isogenic control, *TAp73*<sup>-/-</sup>,  $\Delta Np73$ <sup>-/-</sup>, and *E12*<sup>-/-</sup> MIA PaCa-2 cells.

(B) Quantification of colony formation assay shown in (A) using relative colony area. The relative colony area in isogenic control cells was arbitrarily set as 1.0. Data are presented as the mean  $\pm$  SEM of three independent experiments. One-way ANOVA was used to calculate p-values. \* p < 0.05; \*\* p < 0.01; \*\*\*\* p < 0.0001.

(C) Isogenic control, *TAp73*<sup>-/-</sup>,  $\Delta Np73$ <sup>-/-</sup>, and *E12*<sup>-/-</sup> MIA PaCa-2 cells were used for scratch assays. Microscopic images were taken immediately after scratch (0 hr) and 24 hr later to monitor cell migration. Wound closure percentages were calculated and presented to the right.

(D) The level of TAp73 $\alpha$ 1 and actin proteins was examined in H1299 cells that were uninduced (UI) or induced (I) to express TAp73 $\alpha$ 1 for 24 hr.

(E) Colony formation assay was performed with H1299 cells that were uninduced (UI) or induced (I) to express TAp73 $\alpha$ 1 for 24 hr. (Right) Quantification of colony formation assay by using relative colony area. The relative colony area in UI cells was arbitrarily set as 1.0. Data are presented as the mean  $\pm$  SEM of three independent experiments. Student's t-test was used to calculate p-values. \* p < 0.05.

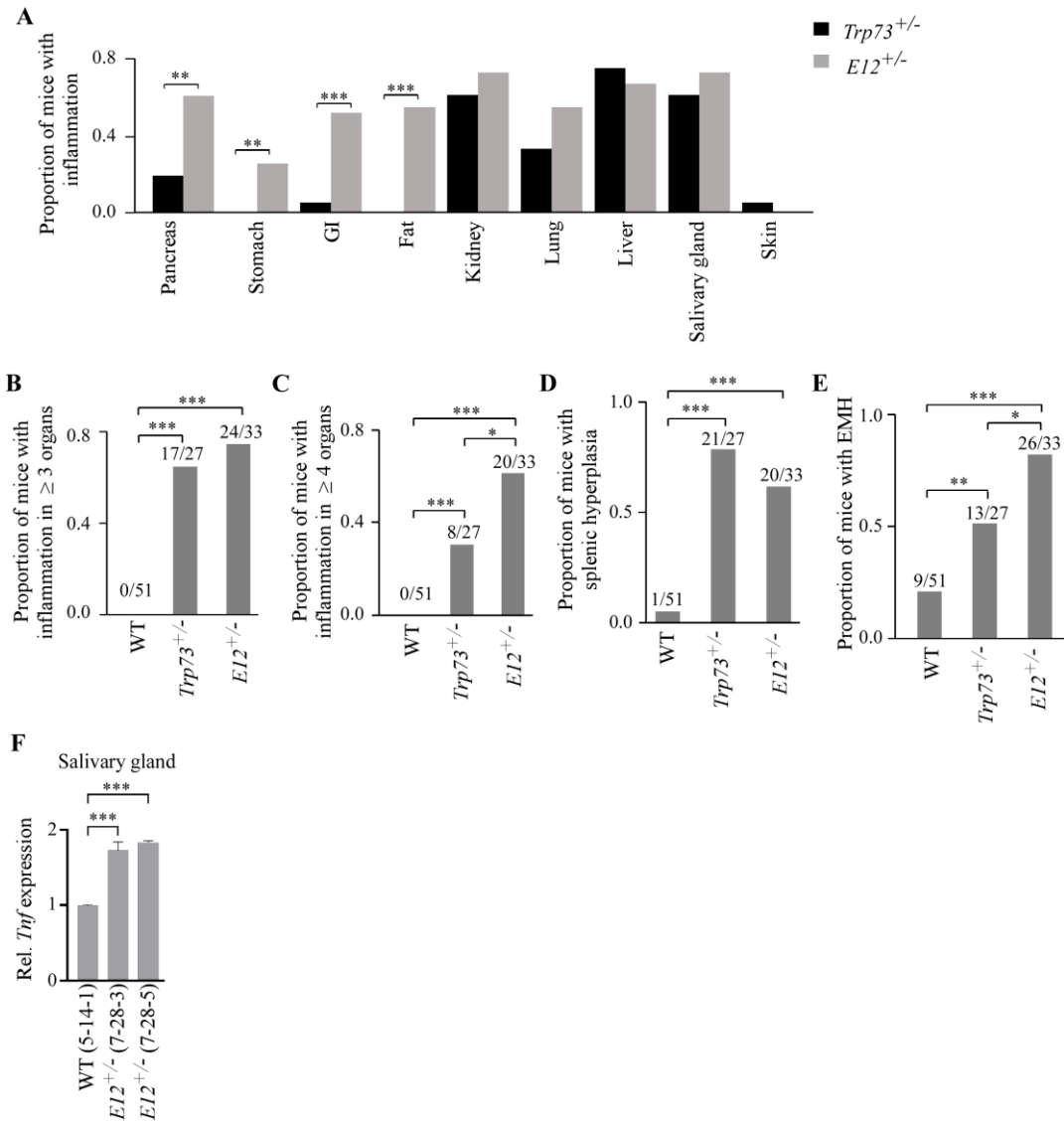


**Fig. S5. Generation of *E12*-deficient mice.**

(A) Schematic representation of *Trp73* gene structure and the locations of sgRNA #1 and #2 used to generate *E12*-deficient mice.

(B) Genotype of WT and  $E12^{+/-}$  mice.

(C) Image of WT and  $E12^{-/-}$  littermates at 13 weeks of age.



**Fig. S6. *E12*<sup>+/-</sup> mice exhibit widespread systemic inflammation.**

(A) Proportion of *Trp73*<sup>+/-</sup> and *E12*<sup>+/-</sup> with inflammation in the indicated organs. Fisher's exact test was used to calculate p-values. \*\*  $p < 0.01$ ; \*\*\*  $p < 0.001$ .

(B) Proportion of WT, *Trp73*<sup>+/-</sup>, and *E12*<sup>+/-</sup> with inflammation in three or more organs. Fisher's exact test was used to calculate p-values. \*\*\*  $p < 0.001$ .

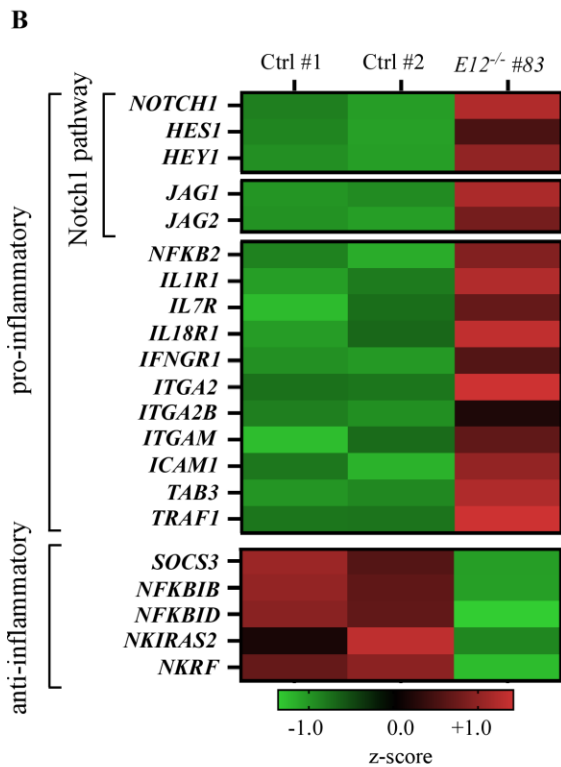
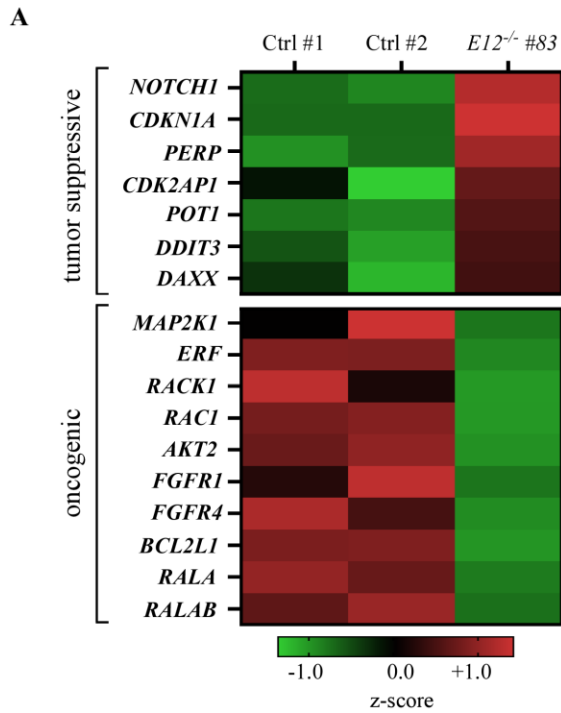
(C) Proportion of WT, *Trp73*<sup>+/-</sup>, and *E12*<sup>+/-</sup> with inflammation in four or more organs. Fisher's exact test was used to calculate p-values. \*  $p < 0.05$ ; \*\*\*  $p < 0.001$ .

(D) Proportion of WT, *Trp73*<sup>+/-</sup>, and *E12*<sup>+/-</sup> with splenic hyperplasia. Fisher's exact test was used to calculate p-values. \*\*\*  $p < 0.001$ .

(E) Proportion of WT, *Trp73*<sup>+/-</sup>, and *E12*<sup>+/-</sup> with EMH. Fisher's exact test was used to calculate p-values. \*  $p < 0.05$ ; \*\*  $p < 0.01$ ; \*\*\*  $p < 0.001$ .

(F) qPCR was used to quantify relative *Tnf* expression in salivary gland tissue from age- and sex-matched WT and *E12*<sup>+/-</sup> mice (100 wks; F). One-way ANOVA was used to calculate p-values. \*\*\*  $p < 0.001$ .

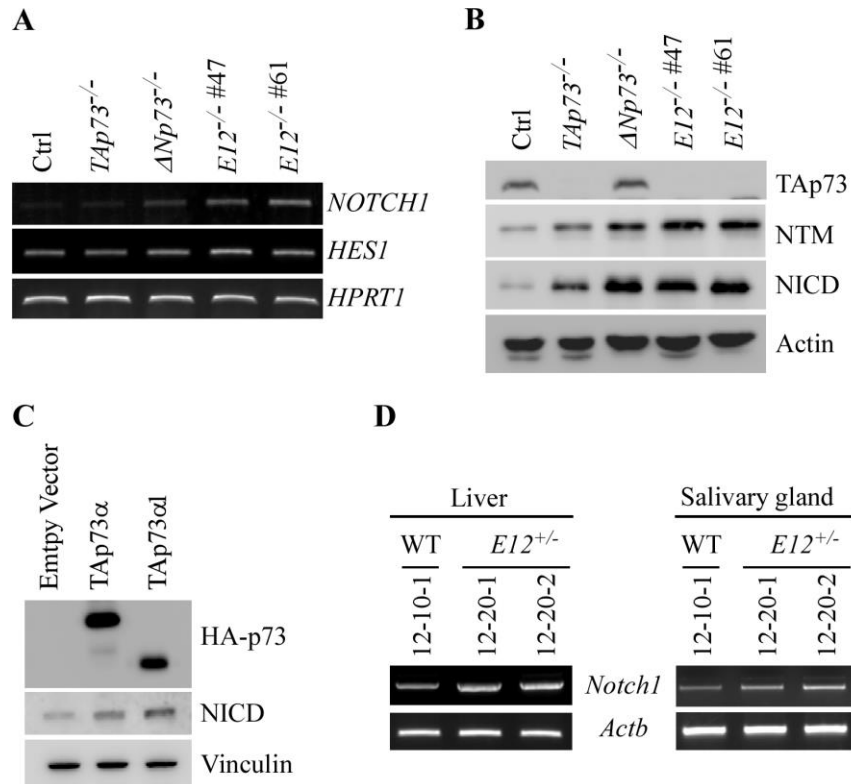




**Fig. S7. *E12*-KO differentially regulates cancer- and inflammation-associated genes.**

(A) Heatmap of cancer-associated genes and their differential expression in isogenic control and *E12*<sup>-/-</sup> H1299 cells.

(B) Heatmap of inflammation-associated genes and their differential expression in isogenic control and *E12*<sup>-/-</sup> H1299 cells.



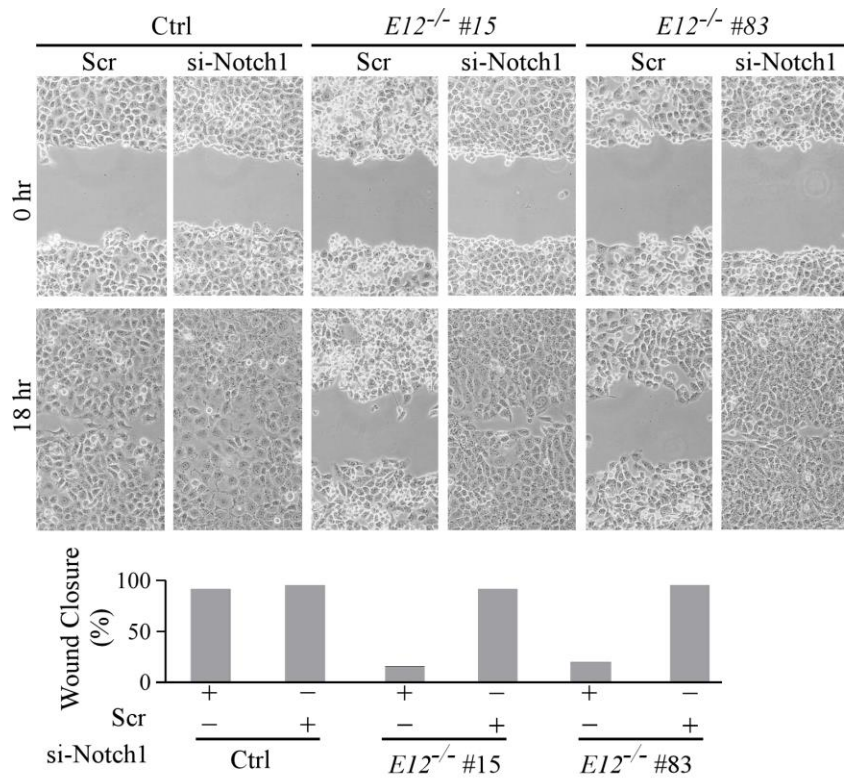
**Fig. S8. p73 $\alpha$ 1 regulates the Notch1 pathway.**

(A) The level of *NOTCH1*, *HES1*, and *HPRT1* transcripts were measured in isogenic control, *TAp73*<sup>-/-</sup>,  $\Delta$ *Np73*<sup>-/-</sup>, and *E12*<sup>-/-</sup> MIA PaCa-2 cells.

(B) The level of TAp73, Notch1 transmembrane/intracellular region (NTM), Notch1 intracellular domain (NICD), and actin proteins was measured in isogenic control, *TAp73*<sup>-/-</sup>,  $\Delta$ *Np73*<sup>-/-</sup>, and *E12*<sup>-/-</sup> MIA PaCa-2 cells.

(C) H1299 cells were transfected with HA-TAp73 $\alpha$  or TAp73 $\alpha$ 1 plasmids and then subjected to Western blot analysis to detect HA-tagged p73, Notch1 intracellular domain (NICD), and vinculin proteins.

(D) The level of *Notch1* and *Actb* transcripts was measured in liver and salivary gland tissue from age- and sex-matched WT and *E12*<sup>+/-</sup> mice (78 wks; F).



**Fig. S9. p73 $\alpha$ 1 mediates Notch1 to inhibit cell migration in H1299 cells.**

Isogenic control and *E12*<sup>-/-</sup> H1299 cells were transiently transfected with Scrambled siRNA (Scr) or si-Notch1 for 3 days and used for scratch assays. Microscopic images were taken immediately after scratch (0 hr) and 18 hr later to monitor cell migration. Wound closure percentages were quantified and presented below.

**Table S1.** Wild type (WT) mice (n=56) survival time, tumor spectrum, inflammation, and other abnormalities

ID	Gender	Survival (wks)	Tumor	Inflammation	Other abnormalities
5	F	134	-	-	-
7	F	117	-	-	-
16	F	100	-	-	-
22	F	109	-	-	-
25	F	109	-	-	-
44	F	90	-	-	-
55	F	104	T-LBL	-	-
64	F	120	-	-	-
2	M	127	-	-	-
3	M	117	-	Liver	-
12	M	127	-	-	-
13	M	127	-	-	-
20	M	122	-	-	-
23	M	122	-	-	-
26	M	127	-	Liver/Salivary gland	-
34	M	124	DLBCL	-	-
37	M	134	-	-	-
62	M	128	-	-	-
45	M	133	-	-	-
49	M	117	-	-	-
50	M	113	T-LBL/ DLBCL	-	-
56	M	117	DLBCL	-	-
59	M	119	DLBCL	-	-
65	M	106	-	-	-
69	M	102	DLBCL	-	Splenic hyperplasia
70	M	103	-	-	Thymic hyperplasia
71	M	90	-	-	-
1-24-2	M	83	-	-	Steatosis
2-15-2	F	140	Lymphoma	-	EMH in liver
2-19-6	M	132	-	Pancreas	EMH in Spleen
2-19-2	F	143	-	-	EMH in Spleen
3-11-3	M	129	-	-	-
3-28-5	F	85	-	-	EMH in spleen/Steatosis
3-9-7	M	129	-	-	-
5-12-3	F	99	Lymphoma	-	EMH in Spleen
7-9-9	F	116	-	-	-
8-2-6	M	120	-	-	-
10-24-7	F	130	-	Pancreas	EMH in spleen
10-26-6	F	129	Histiocytic sarcoma	-	EMH in spleen/liver
11-10-7	M	121	-	-	-
11-7-3	F	121	-	-	-
11-29-2	F	144	-	-	EMH in spleen/Steatosis
12-2-4	F	113	-	-	-
12-20-7	F	115	-	-	EMH in Spleen
11-9-6	F	96	DLBCL	Skin	-
1-19-1	F	86	-	Skin	-
11-10-15	F	105	-	Skin/Pancreas	-
12-25-6	M	111	-	-	Hepatocirrhosis
1-19-5	F	109	Lymphoma	-	-
7-22-4	M	86	-	-	-
7-22-7	M	126	-	Kidney	-
11	M	111	N/A	-	Found dead
42	M	111	N/A	-	Found dead
43	M	107	N/A	-	Found dead
46	M	117	N/A	-	Found dead
52	M	101	N/A	-	Found dead

These mice were from published studies (Yang et al, 2017, PNAS, 114 (43) 11500-11505; Zhang et al, 2017, Genes & Dev, 31:1243-56)  
T-LBL: Thymic lymphoblastic lymphoma; DLBCL: Diffuse large B-cell lymphoma; N/A: not applicable; EMH: Extramedullary hematopoiesis  
5-14-1 (F, 105 wks), 11-29-6 (M, 110 wks), 12-10-1 (F, 80 wks)

**Table S2.** *Trp73<sup>+/-</sup>* mice (n=32) survival time, tumor spectrum, steatosis, inflammation, and other abnormalities

ID#	Gender	Survival (Wks)	Tumor	Steatosis	Inflammation	Other abnormalities
1-30-11	F	82	-	-	Liver/Salivary gland/Kidney/Pancreas	SWPH/EMH
6-7-14	M	43	-	-	Liver/Lung/Kidney/Salivary gland/Skin	SWPH/EMH/TH
9-23-1	F	77	Hepatoma	-	Liver/Pancreas/Kidney	SWPH
12-14-3	F	46	-	-	Skin/Lung/Kidney/Liver/Salivary gland	SWPH/EMH
5-27-14	M	65	-	-	Liver/Salivary gland	SWPH/EMH
9-13-11	F	69	-	-	Liver/Salivary gland/Lung/Kidney	SWPH/EMH
11-6-1	F	55	TLBCL	-	Liver/Kidney/Salivary gland/Pancreas/Lung	SWPH/EMH
5-3-5	F	105	-	Y	Kidney/Liver/Pancreas/Salivary gland	SWPH/EMH/TH
11-6-5	F	88	DLBCL/Hemangioma	Y	Liver/Salivary gland	SWPH/EMH/TH
5-13-2	M	117	-	Y	Liver/Salivary gland/Kidney	SWPH/EMH/TH
11-13-1/5	M	99	-	-	Liver/Salivary gland	-
10-13-12	F	89	Lymphoma	-	-	-
11-5-7	F	102	DLBCL/Lymphoma	-	Kidney/Liver/Cecum	SWPH
6-11-6	M	108	Lymphoma	-	Liver	SWPH
10-3-11	F	99	-	-	Liver/Salivary gland/Lung	SWPH/TH
10-22-4	F	86	Histiocytic sarcoma	-	Kidney/Salivary gland	-
5-28-16	F	120	Lymphoma	-	-	-
11-13-4	F	74	Lymphoma	-	-	-
12-14-1	F	103	-	-	Liver/Pancreas/Salivary gland	SWPH
1-25-4	F	94	DLBCL	-	-	-
1-15-8	F	69	-	-	Liver/Kidney/Salivary gland	SWPH
10-31-4	F	88	Lymphoma	-	Liver/Kidney/Lung/Salivary gland	SRPH/EMH
11-6-4	F	62	Gastric Adenoma	-	Lung/Salivary gland/Liver/Kidney	SRPH/EMH
9-16-5	F	76	-	-	Kidney/Liver/Salivary gland	SRPH/EMH Liver multifocal necrosis
6-22-4	F	80	-	-	Kidney/Lung/liver	SRPH/EMH Liver multifocal necrosis
4-19-1	F	102	-	-	Liver/Heart	SWPH/FH
10-31-5	F	99	DLBCL	Y	Kidney/Lung/Salivary Gland	-
1-2-5	M	7	-	-		Hydrocephalus
11-13-2	M	11	-	-		Hydrocephalus
10-9-2	M	101	N/A			Found dead
2-10-3	M	57	N/A			Found dead
3-10-3	M	108	N/A			Found dead

These mice were from published studies (Zhang et al., 2019, PNAS, 116 (48) 24259-24267)

DLBCL: Diffuse large B-cell lymphoma; EMH: Extramedullary hematopoiesis; SWPH: Spleen white pulp hyperplasia; SRPH: Spleen red pulp hyperplasia; TH: Thymic hyperplasia; LBCL: Large B-cell lymphoma; FH: Follicular hyperplasia

**Table S3.** *E12*<sup>+/-</sup> mice (n=33) survival time, tumor spectrum, steatosis, inflammation, and other abnormalities.

ID	Sex	Survival (wks)	Tumor	Steatosis	Inflammation	Other Abnormalities
9-16-12	M	43.57	-	-	Salivary gland	SWPH/EMH
4-14-1	F	78.86	-	-	Kidney/Lung/Liver/Stomach/GI/Fat/Salivary gland	EMH/SWPH
6-21-1	F	91.57	-	-	Liver	EMH/SWPH/FH
9-18-3	F	80.14	DLBCL	-	Kidney/Salivary gland	-
9-13-7	F	89.43	-	-	Kidney/Lung/Pancreas/Liver/Stomach/GI/Fat/Salivary gland	EMH/FH
10-6-1	M	91.00	DLBCL	-	Salivary gland	EMH/TH
9-13-6	F	95.86	AC	-	Kidney/Pancreas/Liver/GI/Fat/Salivary gland	EMH/SWPH
9-13-3	M	95.86	DLBCL	-	-	EMH
4-7-9	F	67.43	DLBCL	-	-	EMH
11-22-1	M	87.71	HCC	-	Kidney/Lung/Liver/GI/Fat/Salivary gland	-
10-17-6	M	95.86	-	-	Kidney/Lung/Pancreas/Liver/GI/Fat/Salivary gland	EMH/SWPH
4-14-4	F	126.71	-	-	Kidney/Lung/Pancreas/GI/Fat/Salivary gland	SWPH
11-22-5	M	95.00	-	-	Kidney/Lung/Pancreas/Liver/Stomach/GI/Fat/Salivary gland	EMH/SWPH
10-6-4	M	101.71	-	-	Kidney/Lung/Pancreas/Liver/Stomach/GI/Fat/Salivary gland	EMH/SWPH
1-8-1	M	88.29	DLBCL	-	Kidney/Pancreas/Liver/GI/Salivary gland	EMH/SWPH
10-6-3	M	101.71	DLBCL	-	Kidney/Pancreas/Liver	-
11-8-2	F		-	-	Kidney/Lung/Pancreas/Liver/GI/Fat/Salivary gland	EMH/SWPH/TH
4-7-8	M	131.57	-	-	Lung/Pancreas/Liver/Stomach/GI/Fat/Salivary gland	SWPH
9-13-5	F	108.86	-	-	Kidney/Lung/Pancreas/Liver/GI/Salivary gland	EMH/SWPH
8-25-2	F	123.57	DLBCL	-	Stomach/GI	-
8-25-3	F	123.57	DLBCL	-	Kidney/Liver/Fat	-
5-11-12	F	92.57	DLBCL	-	Kidney/Pancreas/GI	EMH
3-15-11	F	102.57	DLBCL	-	-	EMH
3-15-7	M	110.71	-	-	Kidney/Lung/Pancreas/Liver/Stomach/GI/Fat/Salivary gland	EMH/SWPH
3-2-3	F	40.86	-	-	Lung/Pancreas/Liver/Stomach/GI/Fat/Salivary gland	EMH/SWPH
15	F	57.57	-	-	Kidney/Lung/Pancreas/Liver/GI/Salivary gland	EMH/SWPH
1		46.86	-	-	Kidney/Salivary gland	EMH/TH
7-28-3	F	94.43	-	-	Kidney/Heart/Lung/Pancreas/Liver/Fat/Salivary gland	EMH/SWPH
7-28-5	F	94.71	-	-	Kidney/Heart/Lung/Pancreas/Liver/Salivary gland	EMH/SWPH
7-28-8	F	94.43	-	Y	Kidney/Heart/Lung/Pancreas/Liver/Fat/Salivary gland	EMH/SWPH
12-20-1	F	78	-	Y	Kidney/Heart/Lung/Pancreas/Liver/Fat/Salivary gland	EMH/SWPH/TH
12-20-2	F	78	-	-	Kidney/Heart/Lung/Pancreas/Liver/Fat/Salivary gland	EMH/SWPH
12-20-3	F	78	-	-	Kidney/Fat/Salivary gland	EMH/SWPH

DLBCL: Diffuse large B-cell lymphoma; AC: Adenocarcinoma; HCC: Hepatocellular carcinoma; EMH: Extramedullary hematopoiesis; SWPH: Spleen white pulp hyperplasia; TH: thymic hyperplasia

**Table S4.** Primers used to generate expression vectors

Name	Oligonucleotide	Sequence
TAp73-sgRNA-1	Sense	5`-ACCGCTTCCCCACGCCGGCCTCCG-3`
	Antisense	5`-AAACCGGAGGCCGGCGTGGGGAAGC-3`
TAp73-sgRNA-2	Sense	5`-CACCGTCAAACGTGGTGCCCCCATC-3`
	Antisense	5`-AAACGATGGGGGCACCACGTTTGAC-3`
$\Delta$ Np73-sgRNA-1	Sense	5`-CACCGTACAGCATGGTAGGCGCCG-3`
	Antisense	5`-AAACCGGCGCCTACCATGCTGTAC-3`
$\Delta$ Np73-sgRNA-2	Sense	5`-CACCGCGTCACACCTACCGTGGCG-3`
	Antisense	5`-AAACCGCCACGGTAGGTGTGACGC-3`
p73-E12-gRNA-1	Sense	5`-CACCGCGTCACATCGCCAGGCCTT-3`
	Antisense	5`-AAACAAGGCCTGGCGATGTGACGC-3`
p73-E12-gRNA-2	Sense	5`-CACCGCTGCTGCTCATCTCGCCGT-3`
	Antisense	5`-AAACACGGCGAGATGAGCAGCAGC-3`
HA-TAp73 $\alpha$ 1	Sense	5`-ACGGAATTCACCACCATCCTG-3`
	Antisense	5`-CTCGAGTTAAAAACCACGGGCCCCAG-3`
HA-TAp73 $\beta$ 1	Sense	5`-ACGGAATTCACCACCATCCTG-3`
	Antisense	5`-CTCGAGCTAGAGCGGAGCAGCTGCTG-3`

**Table S5.** Primers used for RT-PCR, qPCR, and ChIP

Name	Oligonucleotide	Sequence
<i>TP73</i> -all-isoforms (human)	Sense	5'-ACCGTTCCCCACGCCGGCCTCCG-3'
	Antisense	5'-AAACCGGAGGCCGGCGTGGGGAAGC-3'
<i>TP73α1</i> (human)	Sense	5'-CACCGTCAAACGTGGTGCCCCATC-3'
	Antisense	5'-AAACGATGGGGGCACCACGTTTGAC-3'
<i>NOTCH1</i> (human)	Sense	5'-CACCGTACAGCATGGTAGGCGCCG-3'
	Antisense	5'-AAACCGGCGCCTACCATGCTGTAC-3'
<i>HES1</i> (human)	Sense	5'-CACCGCGTCACACCTACCGTGGCG-3'
	Antisense	5'-AAACCGCCACGGTAGGTGTGACGC-3'
<i>TNF</i> (human)	Sense	5'-ACCACCACTTCGAAACCTGG-3'
	Antisense	5'-GGCCTAAGGTCCACTTGTGT-3'
<i>HPRT1</i> (human)	Sense	5'-CACCGCGTCACATCGCCAGGCCTT-3'
	Antisense	5'-AAACAAGGCCTGGCGATGTGACGC-3'
<i>GAPDH</i> (human)	Sense	5'-CACCGCTGCTGCTCATCTCGCCGT-3'
	Antisense	5'-AAACACGGCGAGATGAGCAGCAGC-3'
<i>Tnf</i> (mouse)	Sense	5'-TGGCCTCCCTCTCATCAGTT-3'
	Antisense	5'-ACAAGGTACAACCCATCGGC-3'
<i>Cdkn1a</i> (mouse)	Sense	5'-CCCGTGGACAGTGAGCAGT-3'
	Antisense	5'-CAGCAGGGCAGAGGAAGTA-3'
<i>Cdkn2a</i> (mouse)	Sense	5'-AGGTTCTTGGTCACTGTGAGG-3'
	Antisense	5'-ACAACATGTTACGAAAGCCAG-3'
<i>Actb</i> (mouse)	Sense	5'-TCCATCATGAAGTGTGACGT-3'
	Antisense	5'-TGATCCACATCTGCTGGAAG-3'
<i>Notch1</i> (mouse)	Sense	5'-CAATCAGGGCACCTGTGAGCCACAT-3'
	Antisense	5'-TAGAGCGCTTGATTGGGTGCTTGCGC-3'
<i>Notch1</i> (mouse qPCR)	Sense	5'-TGTGGCTTCCTTCTACTGCG-3'
	Antisense	5'-CTTTGCCGTTGACAGGGTTG-3'
<i>Trp73α/α1</i> (mouse)	Sense	5'-GTCAACAACTGCCCTCCGTC-3'
	Antisense	5'-CCTTGGGAAGTGAAGCACTCG-3'
<i>Hes1</i> (mouse)	Sense	5'-GAAGAGGCGAAGGGCAAGAATAAATG-3'
	Antisense	5'-CAGGAAGCGGGTCACCTCGTTC-3'
<i>NOTCH1</i> -ChIP (human)	Sense	5'-TGACCGAGGAGCGTGTCGA-3'
	Antisense	5'-AGAGTGGCCTAGCCGTGTGT-3'
<i>CDKN1A</i> -ChIP (human)	Sense	5'-GGTCTGCTACTGTGTCTCC-3'
	Antisense	5'-CATCTGAACAGAAATCCCAC-3'
<i>GAPDH</i> -ChIP (human)	Sense	5'-AAAAGCGGGGAGAAAGTAGG-3'
	Antisense	5'-AAGAAGATGCGGCTGACTGT-3'