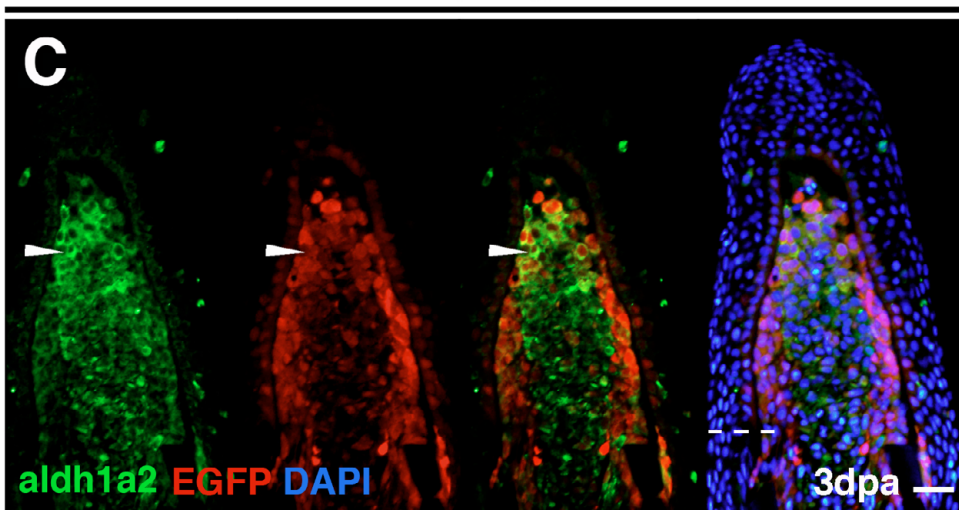
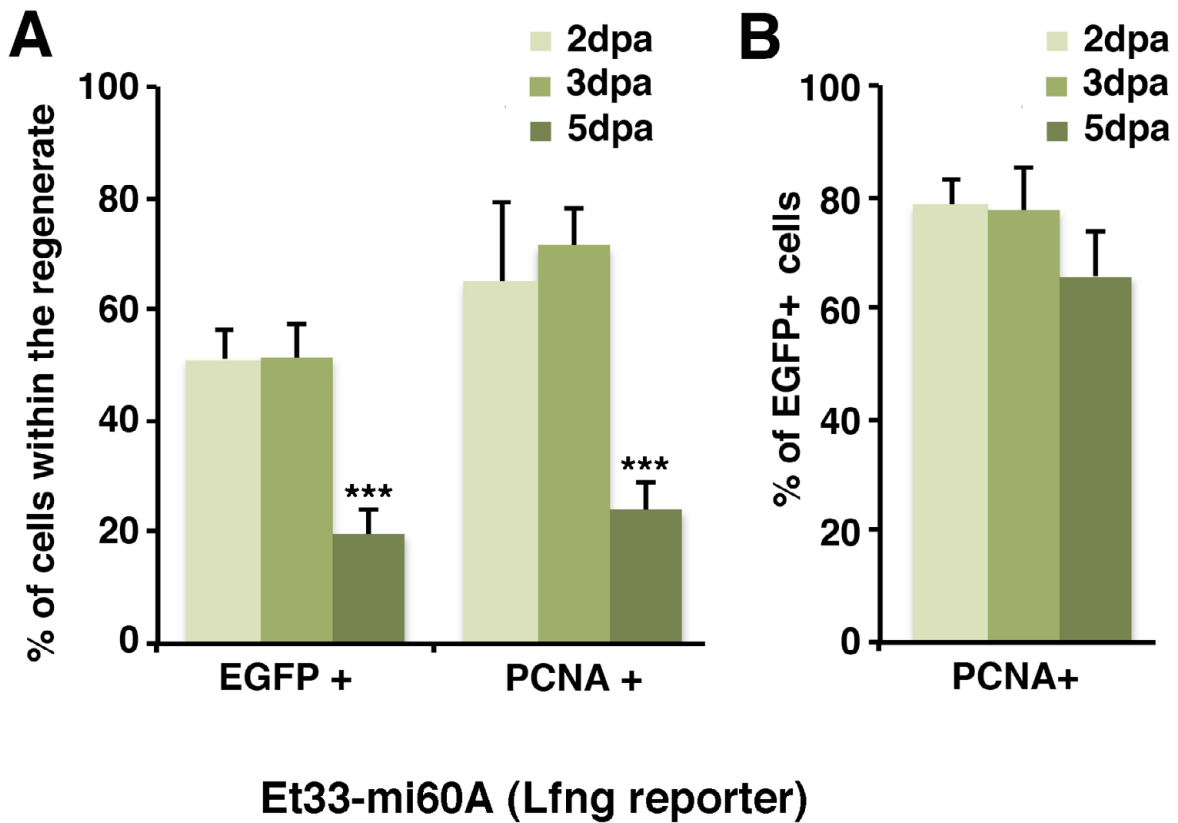
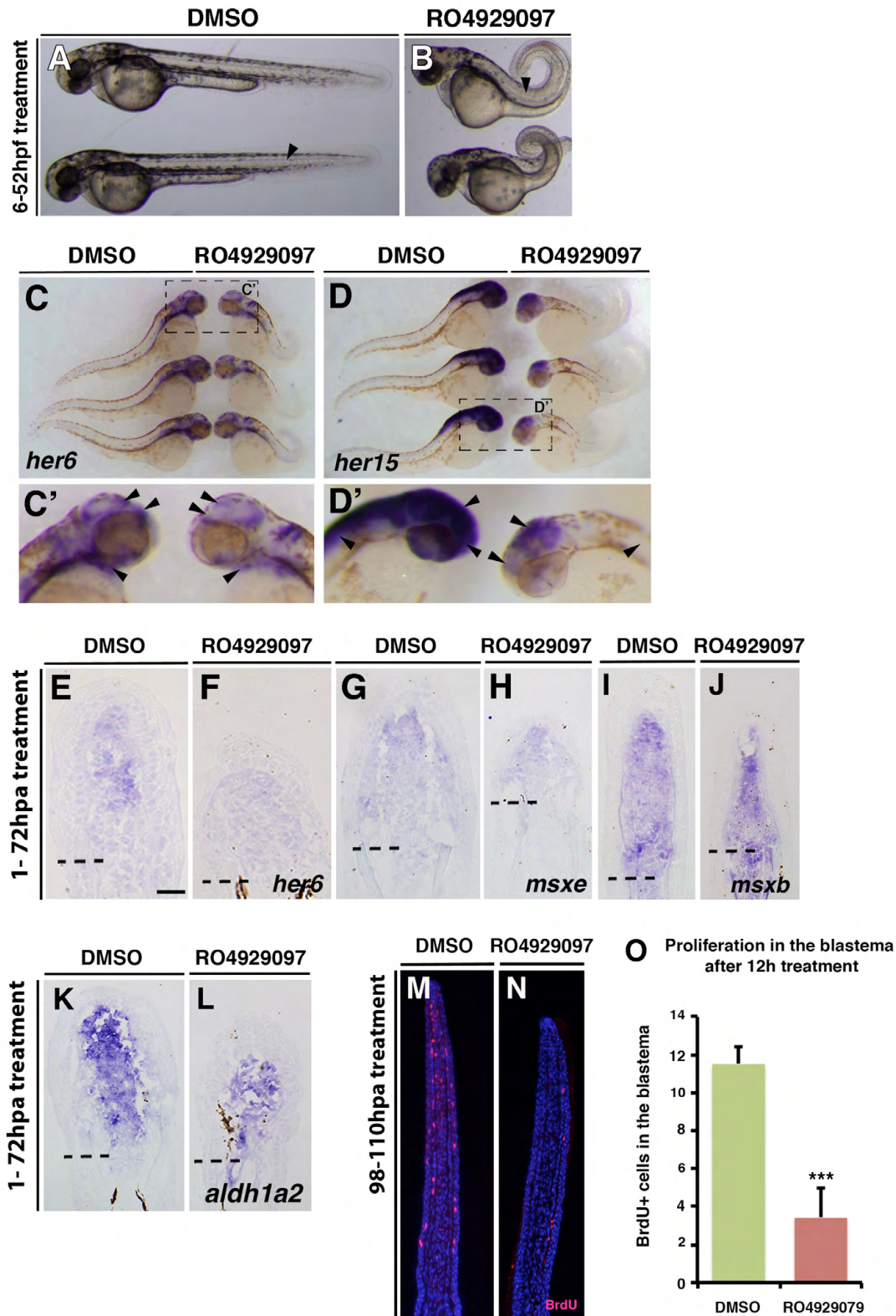


**Fig. S1. Notch signalling is active in the blastema.** (A) qPCR determination of *deltaC*, *deltaD*, *jag1b* and *notch1a* transcripts in regenerating fins at 3 dpa relative to non-amputated fins (0 dpa). (B,C,E) *In situ* hybridization on 3 dpa fin sections. *msxb* is expressed in the whole blastema (B) whereas *msxe* (C) and *aldh1a2* (E) expression is restricted to the distal region (arrowheads) but absent in the proximal region (arrows). (D) BrdU-labelled cells are densely packed in the distal region of the blastema (arrowhead), but dispersed proximally (arrow). (F-K) *In situ* hybridization on 5 dpa fin sections. *jag1b* (F), *lfng* (G) and *her6* (H) are expressed in the distal region of the blastema (arrowheads) but not in the more proximal differentiation zone, similar to *msxe* (I) and *aldh1a2* (K). Scale bar: 10  $\mu$ m in E,K. Broken lines mark the amputation plane.



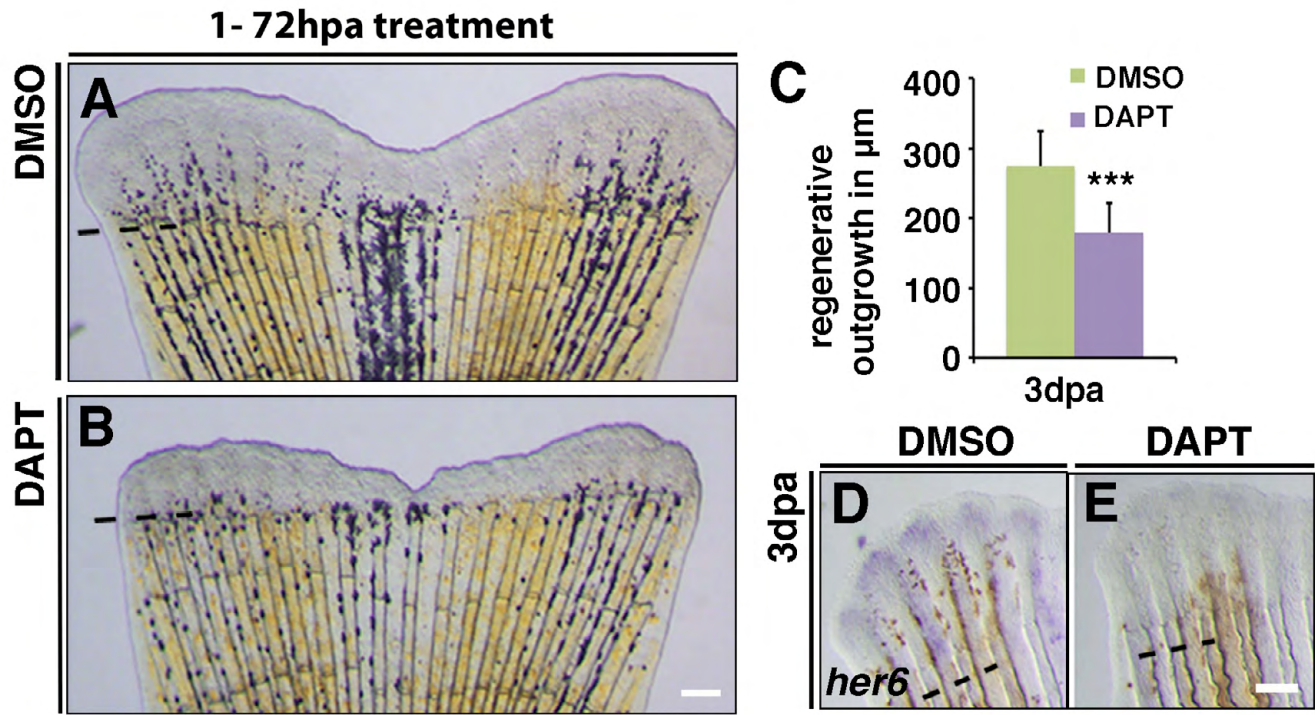
**Fig. S2. Lunatic-fringe-mediated Notch signalling is activated in proliferating, *aldh1a2*-expressing cells.** (A) Mean percentage of EGFP-expressing cells in the regenerate of *ET33-mi60A* fin sections at 2 dpa, 3 dpa and 5 dpa. \*\*\* $P < 0.05$ . (B) Mean percentage of EGFP<sup>+</sup> blastema cells co-labelled for PCNA in fin sections at 2 dpa, 3 dpa and 5 dpa. (C) Representative immunohistochemistry for EGFP and *aldh1a2* in a 3 dpa fin section. Cells are double positive in the distal region of the blastema (arrowhead). Scale bars: 100  $\mu$ m in C. Broken line marks the amputation plane.



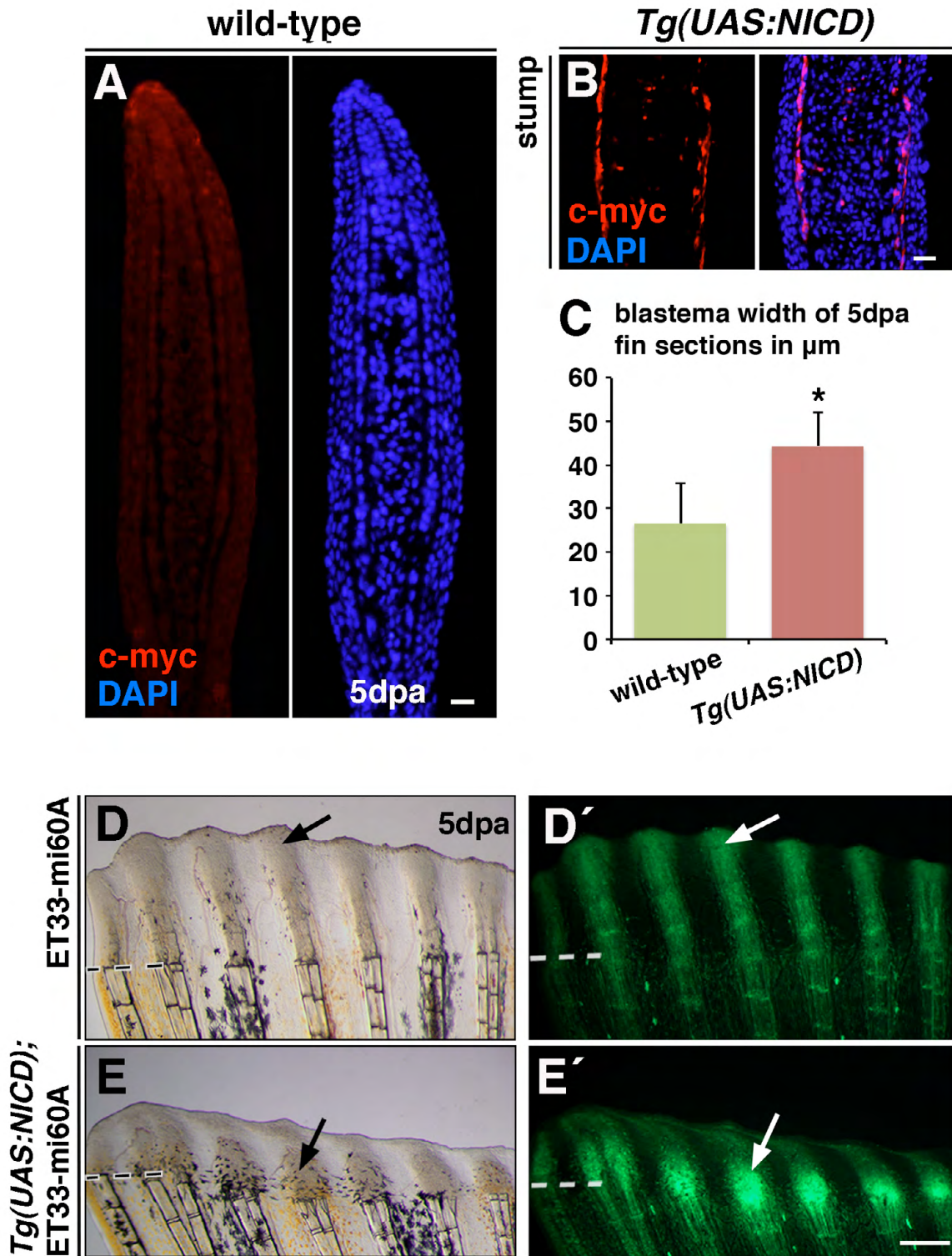
**Fig. S3. RO929097 treatment leads to Notch signalling knockdown in embryos and regenerating fins and reduces proliferation.**

(A-D) Embryos treated with either DMSO or 10  $\mu$ M RO929097 from 6 to 52 hpf. RO929097-treated embryos show defects in somitogenesis (arrow) and a looped tail (B). (C,D) Whole-mount *in situ* hybridization: *her6* gene expression is reduced in the brain and the gill mesenchyme of RO929097-treated embryos (arrowheads). *her15* gene expression is reduced in the brain and spinal cord of RO929097-treated embryos (arrowheads). (E-L) *In situ* on fin sections after 72 hours of DMSO or 10  $\mu$ M RO929097 treatment. *her6* gene expression is reduced in RO929097-treated fins (E,F), but *msxe* (H), *msxb* (J) and *aldh1a2* (L) expression seems to be unchanged in RO929097-treated compared with DMSO-treated fins (G,I,K). (M-O) Anti-BrdU-stained fin sections and quantification of BrdU<sup>+</sup> cells within the distal most 300  $\mu$ m of the mesenchyme. RO929097-treated fins ( $n=4$ ) (N) exhibit fewer BrdU-labelled cells than DMSO-treated fins (M) ( $n=4$ ). \*\*\* $P<0.001$ .



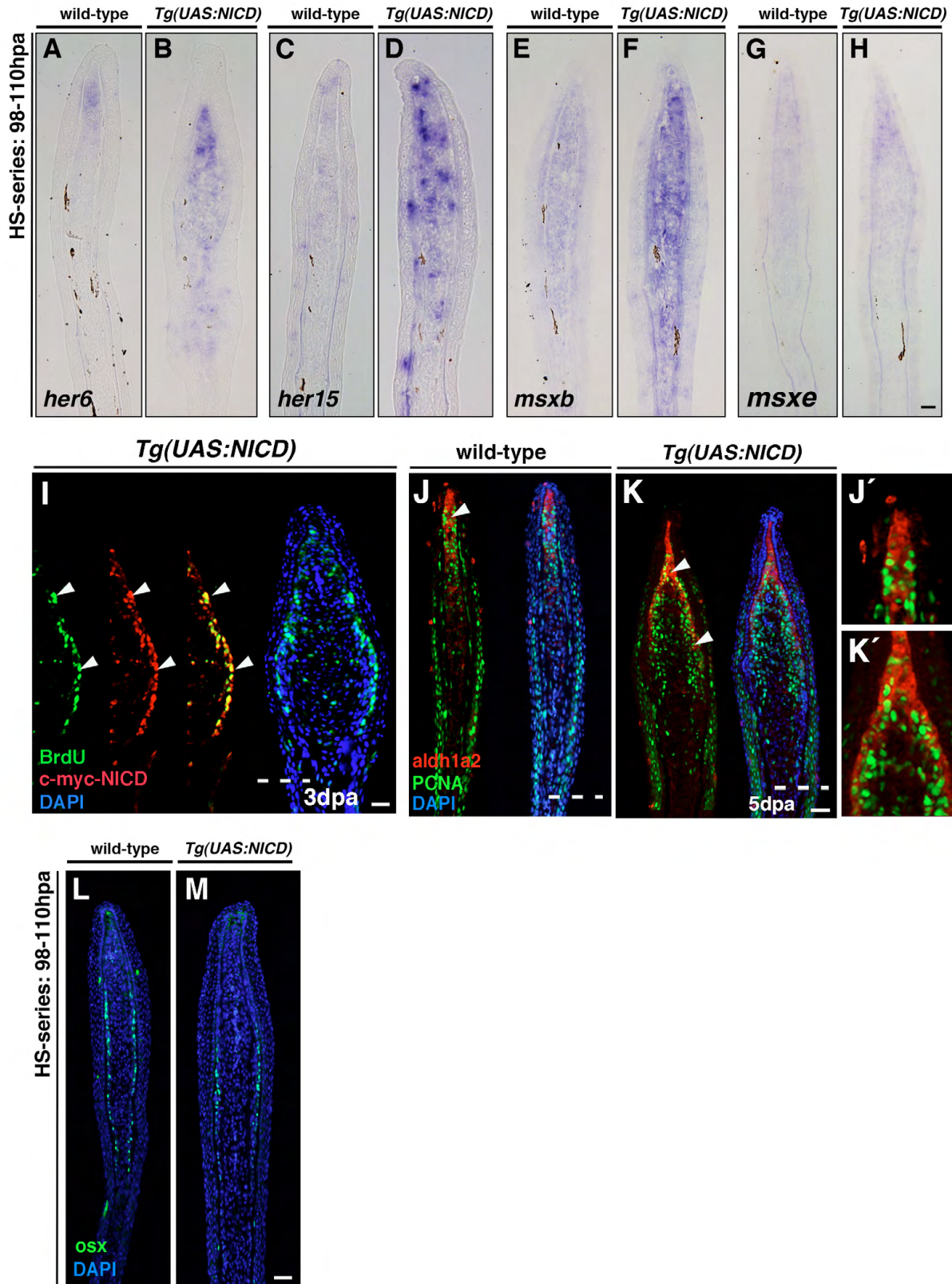


**Fig. S4. DAPT treatment leads to Notch signalling downregulation in regenerating fins and reduces regenerative outgrowth.** (A,B) Juvenile fish treated with 50  $\mu\text{M}$  DMSO or DAPT for 3 days. Fin regeneration is impaired by DAPT treatment. (C) Mean length of fin regenerates; DAPT treatment ( $n=10$ ) decreased regenerate length compared with DMSO-treated fins ( $n=6$ ); \*\*\* $P < 0.005$ . (D,E) *her6* whole-mount *in situ* hybridization reveals Notch activity in DMSO-treated fins (D) but not in DAPT-treated fins (E).

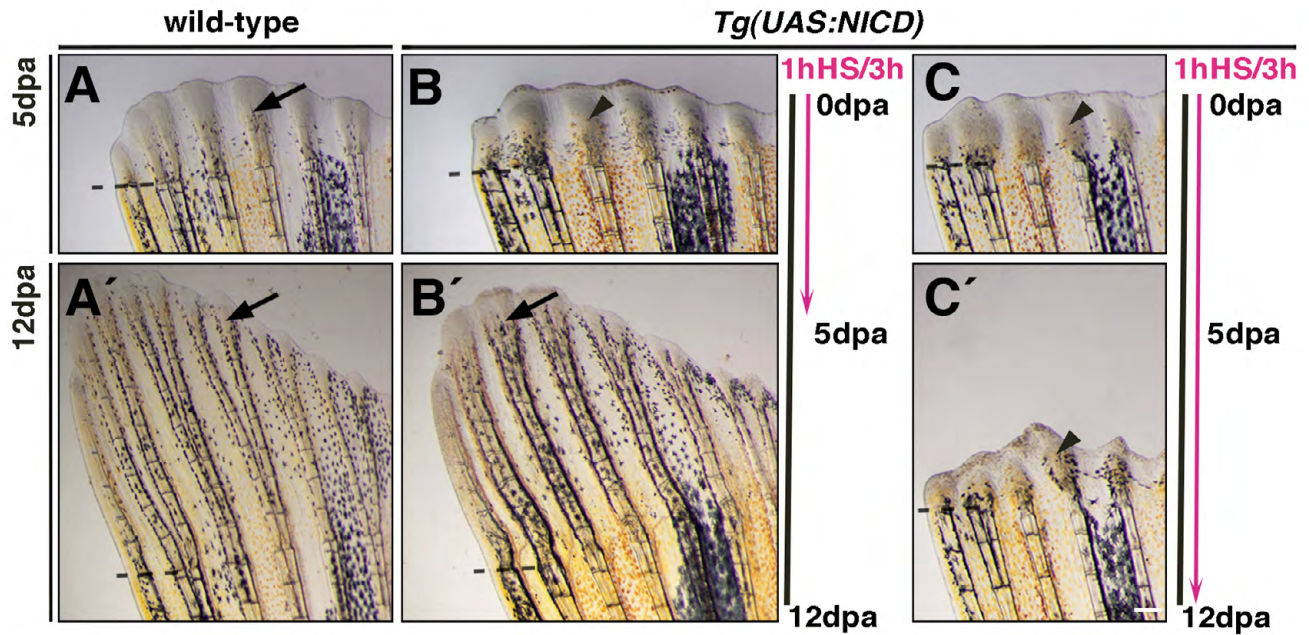


**Fig. S5. NICD overexpression leads to increased blastema width and increases EGFP expression in *Tg(UAS:NICD);Et33-mi60A* fish.** (A,B) Immunohistochemistry for Myc does not label wild-type fin sections (A), whereas Myc-NICD expression is detected in peripheral cells, most likely osteoblasts, and cells within the ray in the fin stump of *Tg(UAS:NICD)* fish (B). (C) Mean blastema width of wild-type and *Tg(UAS:NICD)* fin sections at 5 dpa. \*\*\* $P < 0.05$ . (D-E') *Tg(UAS:NICD)* fish were crossed with *Et33-mi60A* fish and the *Tg(UAS:NICD);Tg Et33-mi60A* fish were exposed to a series of heat shocks during 5 days of regeneration. EGFP expression is increased in *Tg(UAS:NICD);ET33-mi60A* fish at 5 dpa (E') compared with *ET33-mi60A* fish. Scale bars: 10  $\mu\text{m}$ . Broken lines mark the amputation plane.





**Fig. S6. Notch signalling pathway overactivation leads to increased blastema marker expression and higher proliferation.** (A-H) *In situ* hybridization of fins after a 12-hour heat-shock period (98-110 hpa). *her6*, *her15*, *msxb* and *msxe* expression is present in the distal region of the blastema in wild-type fins (A,C,E,G). Gene expression is stronger and expanded proximally in *Tg(UAS:NICD)* fish (B,D,F,H). (I) Double immunohistochemistry reveals co-labeling of Myc-NICD and BrdU in many cells (arrowheads). (J-K') Immunohistochemistry of PCNA and *aldh1a2* on 5 dpa fin sections. Double labelled cells (J',K') are restricted to the distal region of the wild-type fin (J, arrowhead) but is expanded proximally in *Tg(UAS:NICD)* fins at 5 dpa (K, arrowheads). (L,M) Immunohistochemistry against Osx of fins after a 12-hour heat-shock period (98-110 hpa). Scale bars: 10 μm in H,I,K,M. Dashed lines indicate the amputation plane.



**Fig. S7. NICD-induced blastema expansion is reversible.** (A-C') Heat-shock cycles were applied over 5 days of regeneration (A-B') or 12 days (C,C'). Black line indicates time of regeneration. Pink line indicates time of heat-shock treatment (1 hour of heat-shock every 3 hours for 5 or 12 days). Arrows indicate regenerating radials. Arrowheads indicate expanded blastemas. Regeneration is inhibited in *Tg(UAS:NICD)* (B,C) fins but not in wild-type fins (A). Regeneration reverts to normal when heat-shock treatment is stopped (A',B', arrows) but the blastema remains close to the amputation plane (arrowhead) when heat-shocked continued up to 12 days (C'). Scale bars: 100  $\mu$ m. Dashed lines mark the amputation plane.

**Table S1. ISH probes**

<b>Probe</b>	<b>Reference</b>
<i>msxb</i>	(Akimenko et al., 1995)
<i>msxe</i>	(Akimenko et al., 1995)
<i>tcf7</i>	(Li et al., 2009)
<i>aldh1a2</i>	(Grandel et al., 2002)
<i>notch1b</i>	(Westin and Lardelli, 1997)
<i>jagged1b</i>	(Zuniga et al., 2010)
<i>her15</i>	(Shankaran et al., 2007)
<i>lunatic fringe</i>	(Prince et al., 2001)
<i>her6</i>	This report: Forward, 5'-CATCATTGCCGCACCA-3'; Reverse, 5'-TGTGTTTAGGGCAGCGGTCAT-3'



**Table S2. qPCR primers**

<b>Gene</b>	<b>Forward (5'-3')</b>	<b>Reverse (5'-3')</b>
<i>deltaC</i>	CGCAGAAACCTCTGACCAGT	CAGTCCTCACTGATAGCGAGTC
<i>deltaD</i>	GTTACCAACCCCATTCCTT	TGTGCAGCGCTTCAATAATC
<i>jag1b</i>	ACATGCGAGTGTCAAGAAGGT	CATGGGTTACTTTACAATCGTT
<i>notch1a</i>	TGTGAATGCACCCCAGGT	GACGCACACTCGTTGATGTC
<i>notch1b</i>	GGGCACCTGCGTACAGAA	CAAATTCCTGCCGACCTG
<i>lfng</i>	TCTGTTGAGGAGGACCCATC	GCACCAAGGAGTGTCTGGAT
<i>her6</i>	GGCTTCGGAACACAGAAAGT	TGACCCAAGCTTTCGTTG <sub>a</sub>
<i>her15</i>	TCGCTCTGCTCAGAAACA	ACCACTGGCTTTCGAAT
<i>msxb</i>	GGTCAAACCTTTCATCTTTCACATC	TCTTGTGCTTGCCTAAGGTG
<i>msxe</i>	GAGCGGAGCACATGGGTA	CCGGTTGGTTTTGTGTTTTC
<i>aldh1a2</i>	GGGGGAAGCTACTGTTCAAAT	TCCAGAGACTCCAGGGTAGC