**Supporting Information**

**Supporting Methods**

**Genotyping of *egfra* and *sox9b* mutants**

For *egfra* genotyping, genomic DNA was amplified with a forward (5'-ACTTCCAGGATGAAGGGACA-3') and a reverse (5'-CTTACGTGGGCATGTCTTGA-3') primer pair; the wild-type and mutant allele displayed 137-bp and 153-bp PCR products, respectively. For *sox9b* genotyping, genomic DNA was amplified with either wild-type allele- (5'-AGACCAGTCGTAGCCCTT-3') or mutant allele-specific (5'-AGACCAGTCGTAGCCCTA-3') reverse primer and a common forward primer (5'-TGAGTGTGTCCGGAGCTCCGA-3').

**Generation of the *Tg(fabp10a:rtTA,TRE:Venus-KRAS)* line**

Gateway cloning (Thermo fisher Scientific) was used to make the *fabp10a:rtTA-pA,TRE:CFP-pA* construct with three entry clones (p5E_the *fabp10a* promoter, pME_*rtTA-pA*, and p3E_*TRE:CFP-pA*) and a destination vector having two *I-SceI* sites. The *Venus-KRAS-pA* construct was made by fusing *Venus* to the human $KRAS^{G12V}$ gene. To make the final *fabp10a:rtTA-pA,TRE:Venus-KRAS-pA* construct, the *CFP-pA* region in the *fabp10a:rtTA-pA,TRE:CFP-pA* construct was replaced with *Venus-KRAS-pA* by regular cloning. One nl of the solution containing the final construct (20 ng/ul) and *I-SceI* meganuclease was microinjected into one-cell stage embryos as previously described (1). The injected embryos/larvae were treated with 10 ug/ml doxycycline from 3 to 4 dpf and larvae expressing Venus in the liver were selected at 4 or 5 dpf and raised to adulthood. Embryos from these adult fish were treated with doxycycline to identify founder fish with germline integration. F1 larvae, which expressed strong Venus expression in the entire liver, were selected and raised to establish the line.

**In situ hybridization and immunostaining**

Whole-mount (2) and section (3) in situ hybridization was performed as previously described. cDNA from 3- or 5-dpf larvae was used as a template for PCR to amplify genes-of-interest; PCR products were used to make in situ probes. The primers used for the probe synthesis are listed in Table S2. Immunostaining was performed as previously described (4), using the following antibodies: mouse anti-Bhmt (1:500; gift from Jinrong Peng at Zhejiang University), rabbit anti-Tp53 (1:200; gift from Jinrong Peng), mouse anti-Alcama (1:20; ZIRC, zn-5), mouse anti-Anxa4 (1:300; Abcam, ab71286), rabbit anti-Abcb11 (1:1000; Kamiya Biomedical, PC-064), rabbit anti-DsRed (1:200; Clontech, 632496), rabbit anti-Collagen I (1:100; Abcam, ab34710), rabbit anti-pH2AX (1:100; GeneTex, GTX127342), mouse anti-pErk1/2 (1:100; Sigma, M8159), rabbit anti-Sox9b (1:50; gift from Mizuki Azuma at the University of Kansas), and Alexa Fluor 488-, 568-, and 647-conjugated secondary antibodies (1:500; Thermo Fisher Scientific). For section, larvae were fixed

with 4% paraformaldehyde/PBS, embedded in Tissue Freezing Medium (Ted Fella), and cryo-sectioned to 12-µm thickness.

**qPCR**

Total RNA was extracted from 30-40 dissected livers for each condition using the RNeasy Micro Kit (Qiagen); cDNA was synthesized from the RNA using the SuperScript® III First-Strand Synthesis SuperMix (Thermo Fisher Scientific) according to the kit protocols. qPCR was performed as previously described (5), using the QuantStudio 12K Flex machine (Applied Biosystems) with the iTaq™ Universal SYBR® Green Supermix (Bio-Rad). *eef1a1l1* was used for normalization as previously described (6). At least three independent experiments were performed. The primers used for qPCR are listed in Table S3.

**Cre/loxP-mediated lineage tracing**

*Tg(Tp1:CreERT2)*;*Tg(fabp10a:pt-β-catenin)*, *Tg(fabp10a:CreERT2)*;*Tg(fabp10a:pt-β-catenin)*, *Tg(Tp1:CreERT2)*;*Tg(fabp10a:UHRF1-GFP)*, and *Tg(fabp10a:CreERT2)*;*Tg(fabp10a:UHRF1-GFP)* fish were crossed to the Cre reporter line, *Tg(ubb:loxP-GFP-loxP-mCherry)*. Larvae from the crosses were treated with 10 µM 4-OHT (Sigma) from 60 to 96 hours post-fertilization for 36 hours. The larvae were harvested at 15 or 30 dpf for *Tg(fabp10a:pt-β-catenin)* fish and at 20 dpf for *Tg(fabp10a:UHRF1-GFP)* fish and processed for immunostaining to reveal lineage-traced mCherry$^{+}$ cells as previously described (7).

**Cre/loxP-mediated overexpression of Sox9b and dnSox9b**

*Tg(fabp10a:CreERT2)*;*Tg(fabp10a:pt-β-catenin)* larvae containing the *ubb:loxP-CFP-loxP-sox9b-2A-mCherry* or *ubb:loxP-CFP-loxP-dnsox9b-2A-mCherry* transgene were treated with 10 µM 4-OHT from 11 to 12 dpf for 24 hours. The larvae were harvested at 15 dpf for dnSox9b overexpression and 20 dpf for Sox9b overexpression and processed for immunostaining.

**Tetracycline-inducible overexpression of KRAS**

*Tg(fabp10a:rtTA,TRE:KRAS)*;*Tg(fabp10a:pt-β-catenin)* larvae were treated with 10 µg/ml doxycycline (Sigma) from 12 to 14 dpf. The larvae were harvested at 14 dpf and processed for immunostaining.

**Senescence-associated β-galactosidase staining**

Senescence-associated β-galactosidase staining was performed as described in the protocol of the Senescence β-galactosidase Staining Kit (Cell Signaling). Briefly, larvae were fixed with fixative solution in

the kit overnight. One ml of the β-galactosidase staining solution was added into each tube and the larvae were incubated at 37 °C overnight.

**TUNEL assay**

TUNEL labeling was performed as described in the protocol of the In Situ Cell Death Detection Kit, TMR red (Roche). Sectioned samples on slides were treated with 200 ul of TUNEL reaction mixture and incubated at 37 ºC for 1 hour.

**BODIPY C5 staining**

BODIPY C5 assay was performed by treating larvae with 0.5 μM BODIPY C5 (Thermo Fisher Scientific) for 2 hours, as previously described (8). BODIPY C5-treated larvae were briefly rinsed, anesthetized with 0.016% tricaine/egg water, and then mounted in 1% low-melting agarose for live confocal imaging.

**H&E staining**

Liver tissue samples were fixed with Dietrich's fixative (9) (3.7% formaldehyde, 2% glacial acetic acid, 30% ethanol) at room temperature for 24 hours and processed for paraffin embedding. Paraffin block was prepared as previously described (10). Samples were cut into 5-μm sections, deparaffinized and stained with hematoxylin and eosin (Thermo Fisher Scientific), followed by dehydration to xylene and application of a coverslip with Cytoseal™ XYL (Thermo Fisher Scientific). Images were taken using a Zeiss Axioskop 40 bright-field microscope.

**Heat-shock condition**

*Tg(hsp70l:dnHRAS)* larvae were heat-shocked twice at 13 and 14 dpf by transferring them into system water pre-warmed to 38 °C and keeping them at this temperature only for 30 minutes as previously described (11).

**Survival assays**

For *Tg(fabp10a:pt-β-catenin)* survival assay, each 30 *Tg(fabp10a:pt-β-catenin)* larvae were first treated with DMSO or AG1478 from 13 to 15 dpf and then with 10 μM 4-OHT from 15 to 16 dpf. At 16 dpf, the number of survived larvae was counted. For *Tg(fabp10a:UHRF1-GFP)* survival assay, each 100 *Tg(fabp10a:UHRF1-GFP)* larvae were treated with DMSO or AG1478 from 9 to 10 dpf. At 20 dpf, the number of survived larvae was counted. Three independent experiments were performed.

**Hepatocyte ablation using the *Tg(fabp10a:CFP-NTR)* line**

*Tg(fabp10a:CFP-NTR)* fish express cyan fluorescent protein (CFP) and nitroreductase (NTR) fusion proteins under the hepatocyte-specific *fabp10a* promoter. NTR converts the nontoxic prodrug, metronidazole (Mtz), into a cytotoxic drug, thereby ablating only NTR-expressing cells (12, 13). Hepatocyte ablation was performed by treating *Tg(fabp10a:CFP-NTR)* larvae with 10 mM Mtz in egg water supplemented with 0.2% DMSO and 0.2 mM 1-phenyl-2-thiourea from 3.5 to 5 dpf for 36 hours, as previously described (7). The larvae were treated with 2 μM AG1478 from A20h (ablation 20 hour) to R6h (regeneration 6 hour) and harvested at R6h for subsequent whole-mount in situ hybridization.

**Quantification of Bhmt$^+$ liver area**

Confocal images of anti-Bhmt immunostaining and *fabp10a:*CFP intrinsic fluorescence were used to quantify Bhmt$^+$ liver area. Both Bhmt$^+$ and *fabp10a*:CFP$^+$ areas in the liver were calculated by ImageJ and the former area was divided by the latter.

**Image acquisition, processing, and statistical analysis**

Zeiss LSM700 confocal, Axioskop 40 bright-field, and Leica MZ16 microscopes were used to obtain image data. Confocal stacks were analyzed using the Zen 2009 software. All figures, labels, arrows, scale bars, and outlines were assembled or drawn using the Adobe Illustrator software. Statistical analyses were performed using the GraphPad Prism software. Differences among groups were tested by unpaired Student's t-tests or one-way ANOVA. Differences were considered statistically significant when $P < 0.05$ (*$P < 0.05$, **$P < 0.01$, ***$P < 0.001$, ****$P < 0.0001$).

**Supporting figures**

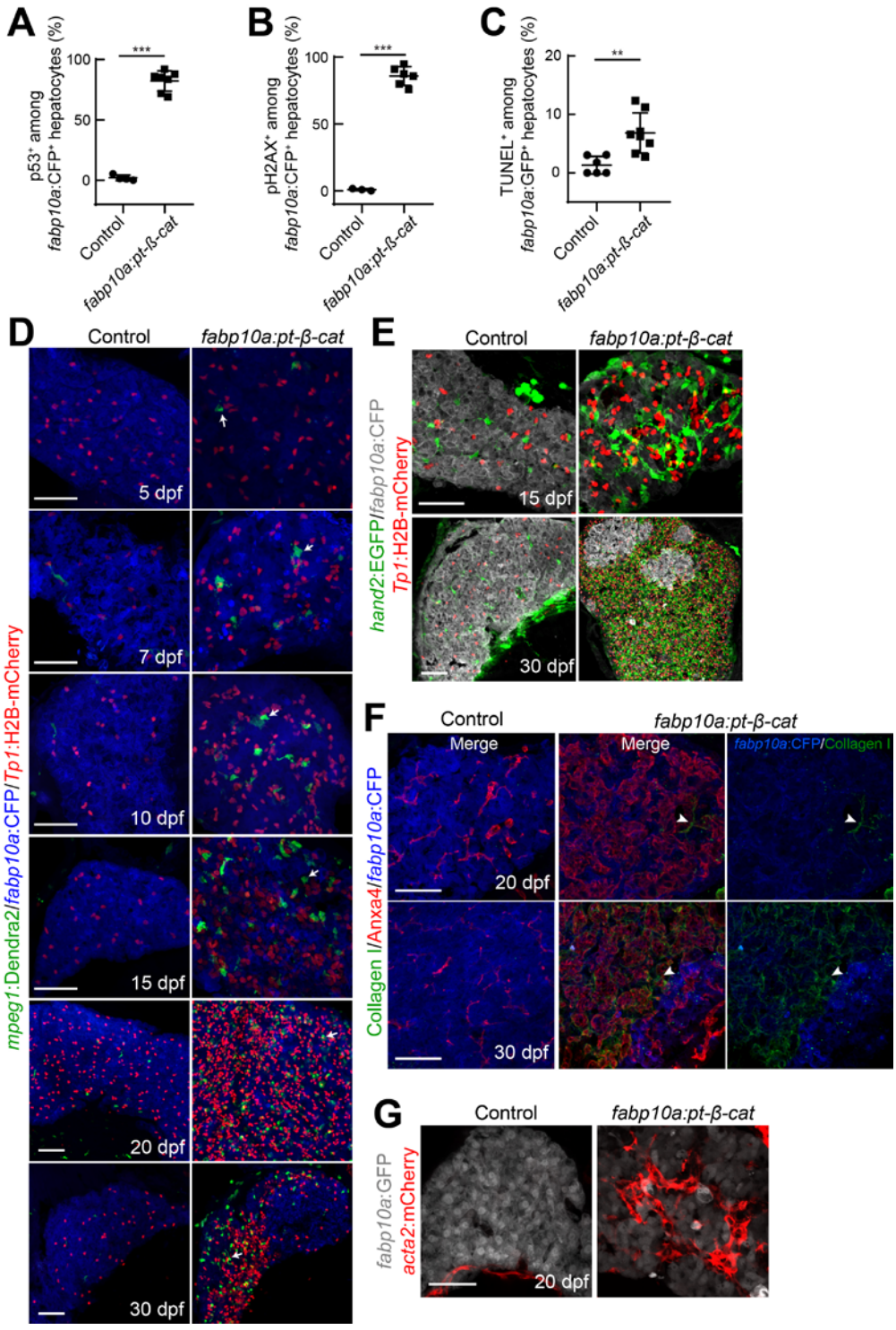


**Figure S1. Hepatocyte-specific overexpression of pt-β-catenin induces hepatocyte damage, inflammation and fibrosis in the liver.** (**A**) Quantification of the percentage of p53-positive cells among *fabp10a:*CFP$^{+}$ hepatocytes in the liver of *Tg(fabp10a:pt-β-catenin)* and control larvae at 7 dpf. (**B, C**) Quantification of the percentage of pH2AX$^{+}$ (B) or TUNEL$^{+}$ (C) cells among *fabp10a:*CFP$^{+}$ hepatocytes in

the liver of *Tg(fabp10a:pt-β-catenin)* and control larvae at 10 dpf. (**D**) Confocal images showing the hepatic expression of *fabp10a*:CFP, *Tp1*:H2B-mCherry, and *mpeg1*:Dendra2 (macrophages) at 5, 7, 10, 15, 20, and 30 dpf. Arrows point to macrophages. (**E**) Confocal images showing the hepatic expression of *fabp10a*:CFP, *Tp1*:H2B-mCherry, and *hand2*:EGFP (HSCs) at 15 and 30 dpf. (**F**) Confocal images showing the hepatic expression of *fabp10a*:CFP, Anxa4 (BECs/LPCs), and Collagen I (fibrosis) at 20 and 30 dpf. Arrowheads point to Collagen I-positive cells. (**G**) Confocal images showing the hepatic expression of *fabp10a*:GFP and *acta2:*mCherry (fibrosis) at 20 dpf. Scale bars, 50 μm. Data are presented as mean ± s.d. ***P*<0.01, ****P*<0.001; statistical significance was calculated using an unpaired two-tailed t-test.

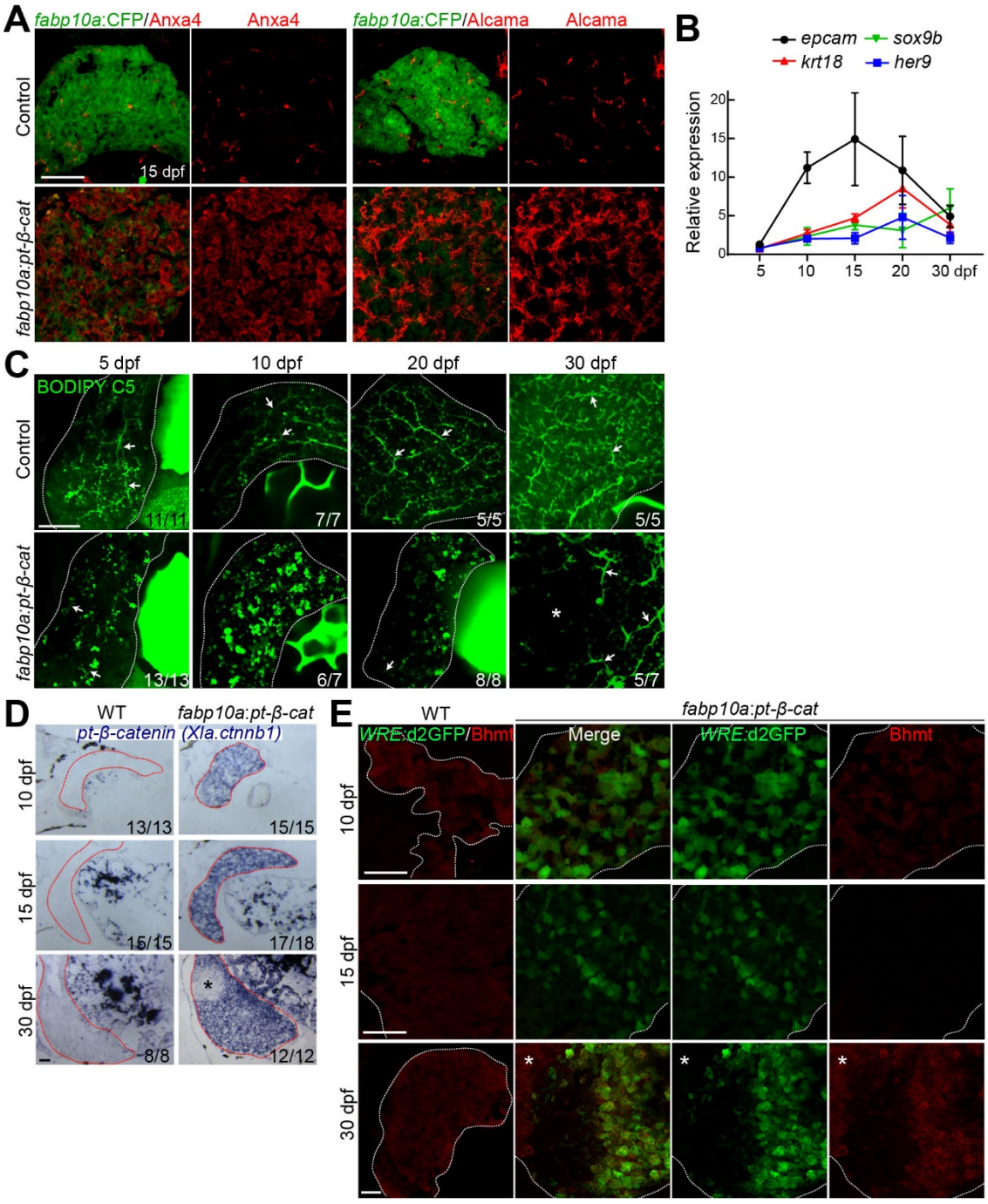


**Figure S2. The process of liver recovery in *Tg(fabp10a:pt-β-catenin)* zebrafish.** (**A**) Confocal images showing the hepatic expression of Anxa4 or Alcama (LPCs/BECs) and *fabp10a*:CFP at 15 dpf. (**B**) qPCR data showing the relative expression levels of *epcam*, *her9*, *krt18*, and *sox9b* between *Tg(fabp10a:pt-β-catenin)* and control livers at 5, 10, 15, 20, and 30 dpf. Data are presented as mean ± s.e.m. (**C**) Confocal images showing BODIPY C5 staining in the liver (dotted lines) at 5, 10, 20, and 30 dpf. Arrows point to labeled bile ductules; an asterisk indicates the region without bile flow. (**D**) Section in situ hybridization images showing the hepatic expression of *pt-β-catenin* (*Xla.ctnnb1*) in control and *Tg(fabp10a:pt-β-catenin)* larvae at 10, 15, and 30 dpf. The asterisk denotes the region without *pt-β-catenin* expression. (**E**) Confocal images showing the expression of *WRE*:d2GFP (Wnt/β-catenin activity) and Bhmt (hepatocytes) in the liver

at 10, 15, and 30 dpf. The asterisk denotes Bhmt-positive but *WRE:*d2GFP-negative region. Numbers in the lower right corner indicate the proportion of larvae exhibiting the phenotype shown. Scale bars, 50 μm.

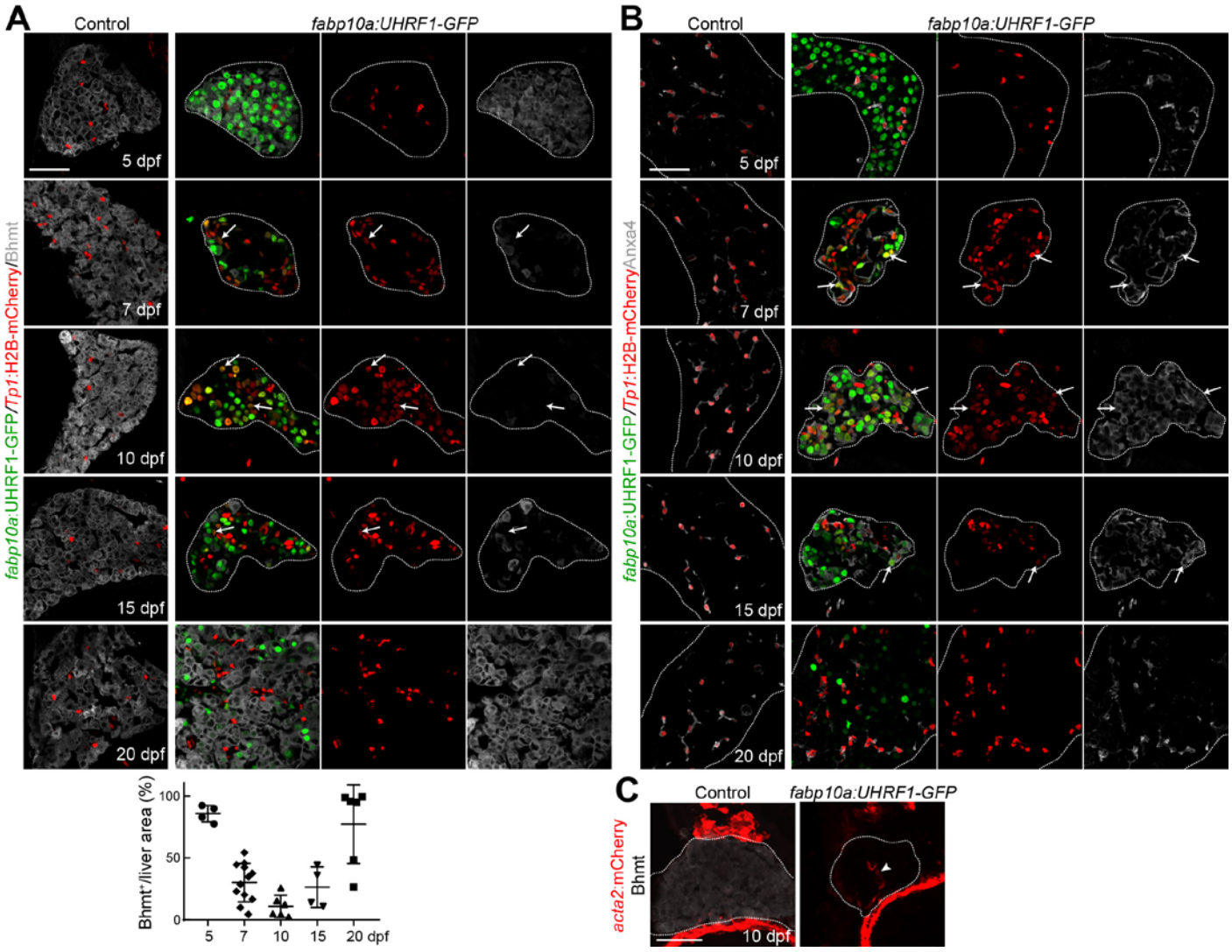


**Figure S3. The process of liver regeneration and recovery in *Tg(fabp10a:UHRF1-GFP)* fish.** (**A**) Confocal images showing the hepatic expression of *fabp10a*:UHRF1-GFP, *Tp1*:H2B-mCherry, and Bhmt at 5, 7, 10, 15, and 20 dpf. Quantification of Bhmt-positive area in *Tg(fabp10a:pt-β-catenin)* livers is shown. Data are presented as mean ± s.d. (**B**) Confocal images showing the hepatic expression of *fabp10a*:UHRF1-GFP, *Tp1*:H2B-mCherry, and Anxa4 at 5, 7, 10, 15, and 20 dpf. Arrows point to LPCs. (**C**) Confocal images showing the hepatic expression of *fabp10a*:UHRF1-GFP, Bhmt, and *acta2:*mCherry (fibrosis) at 10 dpf. Arrowheads point to *acta2:*mCherry$^{+}$ cells. Dotted lines outline livers. Scale bars, 50 μm.

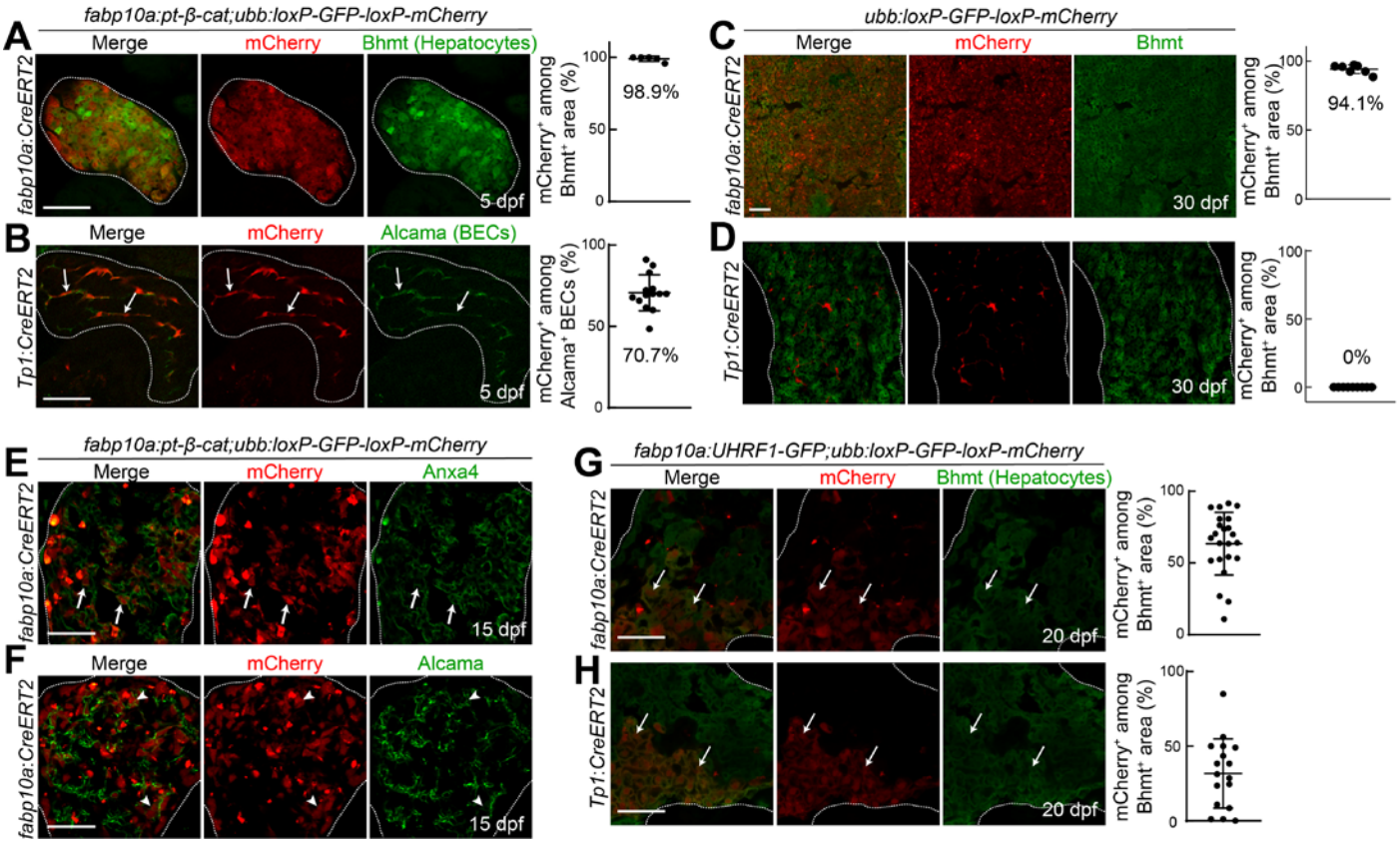


**Figure S4. Lineage tracing in *Tg(fabp10a:pt-β-catenin)* and *Tg(fabp10a:UHRF1-GFP)* zebrafish.** (**A**, **B**) Labeling efficacy of the *fabp10a:CreERT2* and *Tp1:CreERT2* lines in the *Tg(fabp10a:pt-β-catenin)* background. Confocal images showing the hepatic expression of mCherry (lineage-traced cells) and Bhmt (hepatocytes, A) or Alcama (BECs, B) in *Tg(fabp10a:pt-β-catenin)* larvae at 5 dpf. Arrows point to mCherry/Alcama double-positive hepatocytes. (**C, D**) Hepatocyte-labeling efficacy of the *fabp10a:CreERT2* and *Tp1:CreERT2* lines in the control background. Confocal images showing the hepatic expression of mCherry (lineage-traced cells) and Bhmt (hepatocytes) in control larvae at 30 dpf. (**E**, **F**) Confocal images showing the expression of mCherry (lineage-traced cells) and Anxa4 (E) or Alcama (F) in *Tg(fabp10a:pt-β-catenin)* livers at 15 dpf. Arrows point to mCherry/Anxa4 double-positive cells; arrowheads point to mCherry/Alcama double-positive cells. (**G**, **H**) Confocal images showing the expression of mCherry (lineage-traced cells) and Bhmt (hepatocytes) in *Tg(fabp10a:UHRF1-GFP)* livers at 20 dpf. Arrows point to mCherry/Bhmt double-positive hepatocytes. For Cre-mediated cell labeling, embryos/larvae were treated with 4-OHT from 2.5 to 4 dpf. Dotted lines outline livers. Data are presented as mean ± s.d. Scale bars, 50 μm.

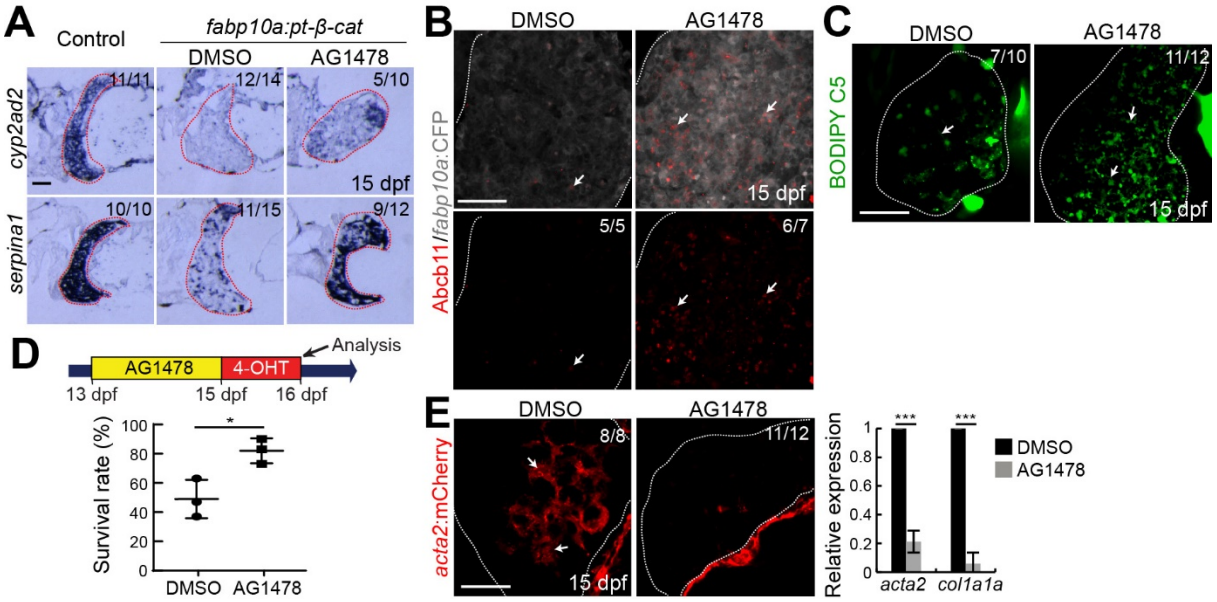


**Figure S5. EGFR inhibition promotes liver recovery.** (**A**) Section in situ hybridization images showing the expression of hepatocyte markers (*cyp2ad2* and *serpina1*) in control and *Tg(fabp10a:pt-β-catenin)* larvae at 15 dpf. (**B**) Confocal images showing the hepatic expression of Abcb11 (bile canaliculus, arrows) and *fabp10a:*CFP in 15-dpf *Tg(fabp10a:pt-β-catenin)* larvae (**C**) Confocal projection images showing BODIPY C5 labeling in *Tg(fabp10a:pt-β-catenin)* livers at 15 dpf. Arrows point to labeled bile ductules. (**D**) Scheme illustrates AG1478 and 4-OHT treatments and analysis stage for survival assay. Quantification shows the survival rate of *Tg(fabp10a:pt-β-catenin)* larvae. 30 larvae were used for each condition. (**E**) Confocal images showing the hepatic expression of *acta2*:mCherry (arrows) in 15-dpf *Tg(fabp10a:pt-β-catenin)* larvae. qPCR data show the relative expression levels of fibrosis markers (*acta2* and *col1a1a*) between DMSO- and AG1478-treated *Tg(fabp10a:pt-β-catenin)* livers. Scale bars, 50 µm. Dotted lines outline livers. Data are presented as mean ± s.d. **P*<0.05, ****P*<0.001; statistical significance was calculated using an unpaired two-tailed t-test.

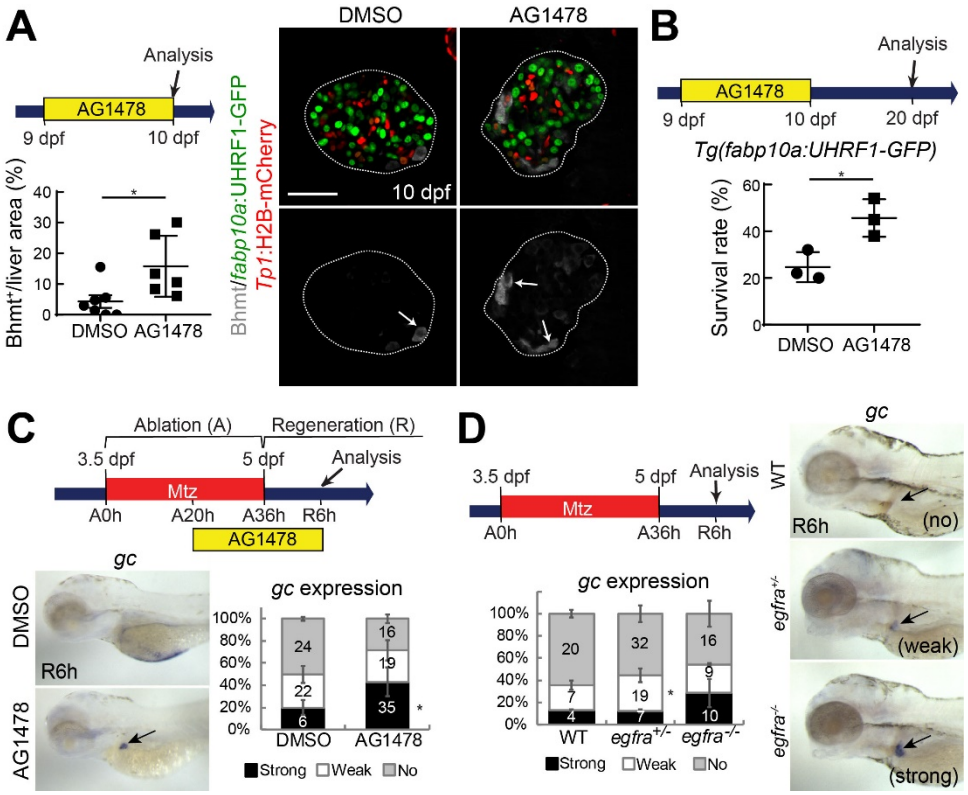


**Figure S6. EGFR inhibition promotes LPC-to-hepatocyte differentiation in two additional liver injury models, *Tg(fabp10a:UHRF1-GFP)* and *Tg(fabp10a:CFP-NTR)*.** (**A**) Scheme illustrates AG1478 treatment and analysis stage. Confocal images show the hepatic expression of Bhmt, *Tp1:*H2B-mCherry, and *fabp10a:*UHRF1-GFP in 10-dpf *Tg(fabp10a:UHRF1-GFP)* larvae. Quantification of the percentage of Bhmt-positive liver area is shown. Arrows point to Bhmt$^{+}$ hepatocytes. (**B**) Scheme illustrates AG1478 treatment and analysis stage. Quantification of the survival rate of *Tg(fabp10a:UHRF1-GFP)* larvae at 20 dpf is shown. 100 larvae were used for each condition. (**C**) Scheme illustrates the periods of metronidazole (Mtz; hepatocyte ablation) and AG1478 treatments and analysis stage. Whole-mount in situ hybridization images show *gc* expression in regenerating *Tg(fabp10a:CFP-NTR)* livers at R6h (Regeneration 6 hours). (**D**) Scheme illustrates the period of Mtz treatment and analysis stage. Whole-mount in situ hybridization images show *gc* expression in regenerating *Tg(fabp10a:CFP-NTR)* livers at R6h in the *egfra* mutant background. Based on the level of hepatic *gc* expression, larvae were divided into three groups: no, weak, and strong. Numbers in the graph indicate the number of larvae in each group. An arrow points to the liver. Data are presented as mean ± s.d. (A, B, D) or ± s.e.m. (C). *$P$<0.05; statistical significance was calculated using an unpaired two-tailed t-test.

**Supporting tables**

**Table S1. Transgenic and mutant zebrafish lines used in this study**

| Names | Official names (ZFIN database) | Allele # |
|---|---|---|
| *Tg(fabp10a:pt-β-catenin)* | *Tg(fabp10a:Xla.Ctnnb1,cryaa:Venus)* | s704 |
| *Tg(fabp10a:UHRF1-GFP)* | *Tg(fabp10a:Hsa.UHRF1-EGFP)* | mss1a |
| *Tg(mpeg1:Dendra2)* | *Tg(mpeg1.1:Dendra2)* | uwm12 |
| *Tg(hand2:EGFP)* | *TgBAC(hand2:EGFP)* | pd24 |
| *Tg(acta2:mCherry)* | *Tg2(acta2:mCherry)* | uto5 |
| *Tg(fabp10a:GFP)* | *Tg(-2.8fabp10a:EGFP)* | as3 |
| *Tg(fabp10a:CFP)* | *Tg(fabp10a:CFP-NTR)* | s931 |
| *Tg(WRE:d2GFP)* | *Tg(OTM:d2EGFP)* | kyu1 |
| *Tg(Tp1:VenusPEST)* | *Tg(EPV.Tp1-Mmu.Hbb:Venus-Mmu.Odc1)* | s940 |
| *Tg(Tp1:H2B-mCherry)* | *Tg(EPV.Tp1-Mmu.Hbb:hist2h2l-mCherry)* | s939 |
| *Tg(fabp10a:CreERT2)* | *Tg(fabp10a:Cre-ERT2,cryaa:ECFP)* | pt602 |
| *Tg(Tp1:CreERT2)* | *Tg(EPV.Tp1-Mmu.Hbb:Cre-ERT2,cryaa:mCherry)* | s959 |
| *Tg(ubb:loxP-GFP-loxP-mCherry)* | *Tg(-3.5ubb:loxP-EGFP-loxP-mCherry)* | cz1701 |
| *Tg(hsp70l:dnHRAS)* | *Tg(hsp70l:dnHRAS,cryaa:EGFP)* | pd7 |
| *Tg(fabp10a:rtTA,TRE:Venus-KRAS)* | *Tg(fabp10a:rtTA,TRE:Venus-KRAS$^{G12V}$)* | pt618 |
| *Tg(ubb:loxP-CFP-loxP-sox9b-2A-mCherry)* | *Tg(ubb:loxP-eCFP-loxP-sox9b-2A-mCherry)* | jh47 |
| *Tg(ubb:loxP-CFP-loxP-dnsox9b-2A-mCherry)* | *Tg(ubb:loxP-eCFP-loxP-trsox9b-2A-mCherry)* | jh48 |
| *egfra* | *egfra* | ct870 |
| *sox9b* | *sox9b* | fh313 |

**Table S2. Sequences of primers used for in situ probe synthesis**

| Gene | Primer | Nucleotide sequence (5' to 3') |
|---|---|---|
| *tp53* | forward | AAGAACAGCCTCAGCCATCC |
| *tp53* | reverse | TAATACGACTCACTATAGGGTCCATTCAGCACCAAGCTGT |
| *cdkn1a* | forward | CAAGCGGATCCTACGTTCAC |
| *cdkn1a* | reverse | TAATACGACTCACTATAGGGCTGGGGTTTTCTCCACTTCA |
| *ces2* | forward | GGAATATTAGGATACTTCAGCACAG |
| *ces2* | reverse | TAATACGACTCACTATAGGGAAAATCTGGGGGAGCATCCA |
| *ces3* | forward | GGCTTCAGAAGCCAATGGAATC |
| *ces3* | reverse | TAATACGACTCACTATAGGGTCAGGCTGTATGAAGTGCAGC |
| *tdo2a* | forward | AACCAGCCTCGGAGAGGAAG |
| *tdo2a* | reverse | TAATACGACTCACTATAGGGATCTTCTCCTCATTCCTCCATC |
| *cyp2ad2* | forward | CACCACCATGATCCTGCACCTG |
| *cyp2ad2* | reverse | TAATACGACTCACTATAGGGAACCTCCTATGTGACCGCCAG |
| *serpina1* | forward | CATGTTGGGTCACAGTCAGG |
| *serpina1* | reverse | TAATACGACTCACTATAGGGGCCTTTGTAGGGCACCATCAT |
| *egfra* | forward | TCCCGCACACAACTGCTGCA |
| *egfra* | reverse | TAATACGACTCACTATAGGGATCTGCTAGTGCACCTCCAG |
| *Xla.ctnnb1* | forward | GAAACTGCTTAATGACGAGGACC |
| *Xla.ctnnb1* | reverse | TAATACGACTCACTATAGGGCACCAGCTTCAACTATAGCAGGC |

Underlined are T7 primer sequences.

**Table S3. Sequences of primers used for qPCR**

| Gene | Primer | Nucleotide sequence (5' to 3') |
|---|---|---|
| *eef1a1l1* | forward | CTGGAGGCCAGCTCAAACAT |
| *eef1a1l1* | reverse | ATCAAGAAGAGTAGTACCGCTAGCATTAC |
| *tp53* | forward | CTCTCCCACCAACATCCACT |
| *tp53* | reverse | GATTGCCCTCCACTCTTATCA |
| *cdkn1a* | forward | CCGCATGAAGTGGAGAAAAC |
| *cdkn1a* | reverse | ACGCTTCTTGGCTTGGTAGA |
| *mdm2* | forward | CCTCCTCTTCCTCGACACTG |
| *mdm2* | reverse | GGGTCTCTTCCTGACTGCTG |
| *bhmt* | forward | CTGATCGCTGAGTACTTTG |
| *bhmt* | reverse | CAATGAAGCCCTGGCAGC |
| *ces2* | forward | GGAATATTAGGATACTTCAGCACAG |
| *ces2* | reverse | CTGTAAAGCTGCGATCTGG |
| *ces3* | forward | TGAAAGTTACAGGAACACTCAC |
| *ces3* | reverse | TACGAACAAAGTTAGCCCAG |
| *cyp2ad2* | forward | CACTCAGAATGATAGCTTCGT |
| *cyp2ad2* | reverse | CTCATTGTTAAACCGATTCCC |
| *cyp7a1a* | forward | CCTACCATGCTGTCATCCGTC |
| *cyp7a1a* | reverse | TCTCATGACCAAATGCCTTCGC |
| *gc* | forward | CAAGCATGGGTTTCTTGGG |
| *gc* | reverse | AACCTCCTCTGTCAGTTTCTG |
| *serpina1* | forward | CATGTTGGGTCACAGTCAGG |
| *serpina1* | reverse | CGATTTCAGGCTTGGAGAA |
| *tdo2a* | forward | GATGATTGGCAGTAAAGACGG |
| *tdo2a* | reverse | ACCTTGTAGCGATCACTGAC |
| *epcam* | forward | CTTGTTTGTTGTGGCATTGG |
| *epcam* | reverse | TTGACGCACCAGCATACTTC |
| *krt18* | forward | CGTCGCCGCTTACAAGAAAGAAC |
| *krt18* | reverse | ATGTGTCTCCGCAGATGTCGTC |
| *sox9b* | forward | CAGAAACACCCGACTCCAG |
| *sox9b* | reverse | CACACCGGCAGATCTGTTT |
| *her9* | forward | AATGCCAGCGAGCATAGAAAGTC |
| *her9* | reverse | TGCCCAAGGCTCTCGTTGATTC |
| *acta2* | forward | CCGTGATCTCACTGACTACC |
| *acta2* | reverse | ACGATTTCTCTTTCAGCAGTG |
| *col1a1a* | forward | GGTAAAGATGGCATTCGTGG |
| *col1a1a* | reverse | AGATTCTCCCTTGTCACCAG |
| *egfra* | forward | GCCAGAGAATGACGAAAGTG |
| *egfra* | reverse | CATTACAGCAGTCAATGGGTC |

**Supporting references**

1. Grabher C, Joly JS, Wittbrodt J. Highly efficient zebrafish transgenesis mediated by the meganuclease I-SceI. Methods Cell Biol 2004;77:381-401.
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