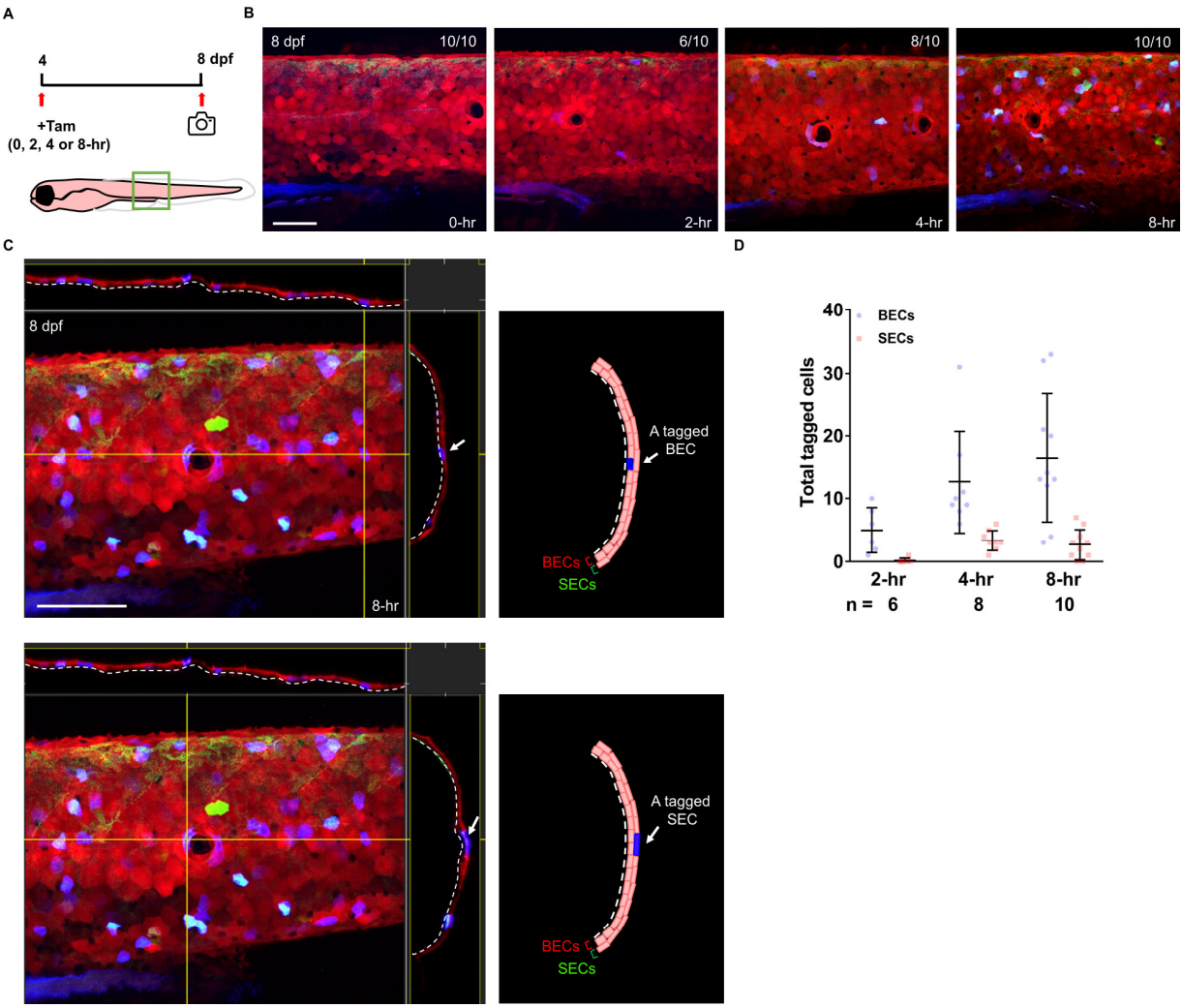

Fig. S1. The length of Tam treatment determines the number of the tagged BECs.

(A) Timeline depicting the cell tagging and imaging scheme. Green box indicates imaged body regions. Tam, Tamoxifen. dpf, days post fertilization.

(B) Confocal images of tagged cells in an 8 dpf *basebow* (n = 10 animals in each treatment group). Scale bar, 100 µm.

(C) Images of optical sections and illustrations depicting the positon of a tagged BEC and SEC. White dashed lines mark basement membrane. SECs, Superficial epithelial cells. BECs, Basal epithelial cells. Scale bar, 100 µm.

(D) Quantification of total tagged BECs and SECs (465 µm x 465 µm; n = 6, 8, 10 animals, respectively; mean ± SD).

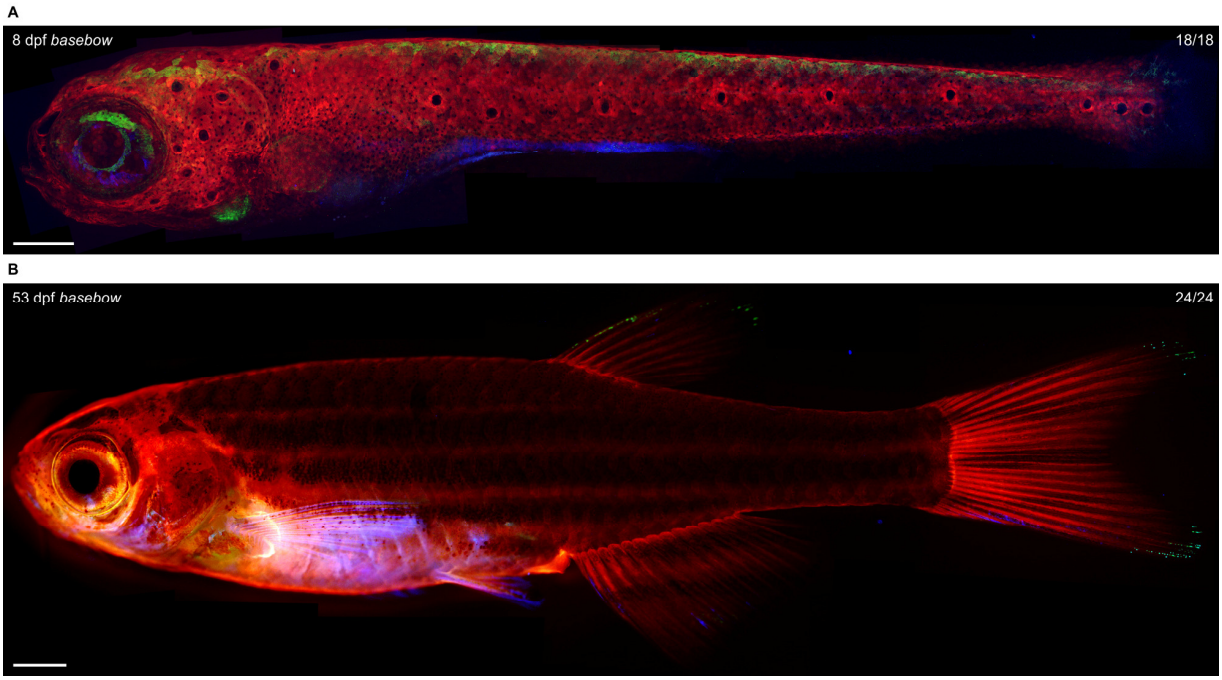

Fig. S2. *Basebow* zebrafish has no leaky Cre activity during long-term monitoring.

(A) Whole-mount confocal image of an 8 dpf *basebow* (stitched; n = 18 animals). Scale bar, 200 µm.

(B) Whole-mount epifluorescence image of a 53 dpf *basebow* (stitched; n = 24 animals). Scale bar, 1 mm.

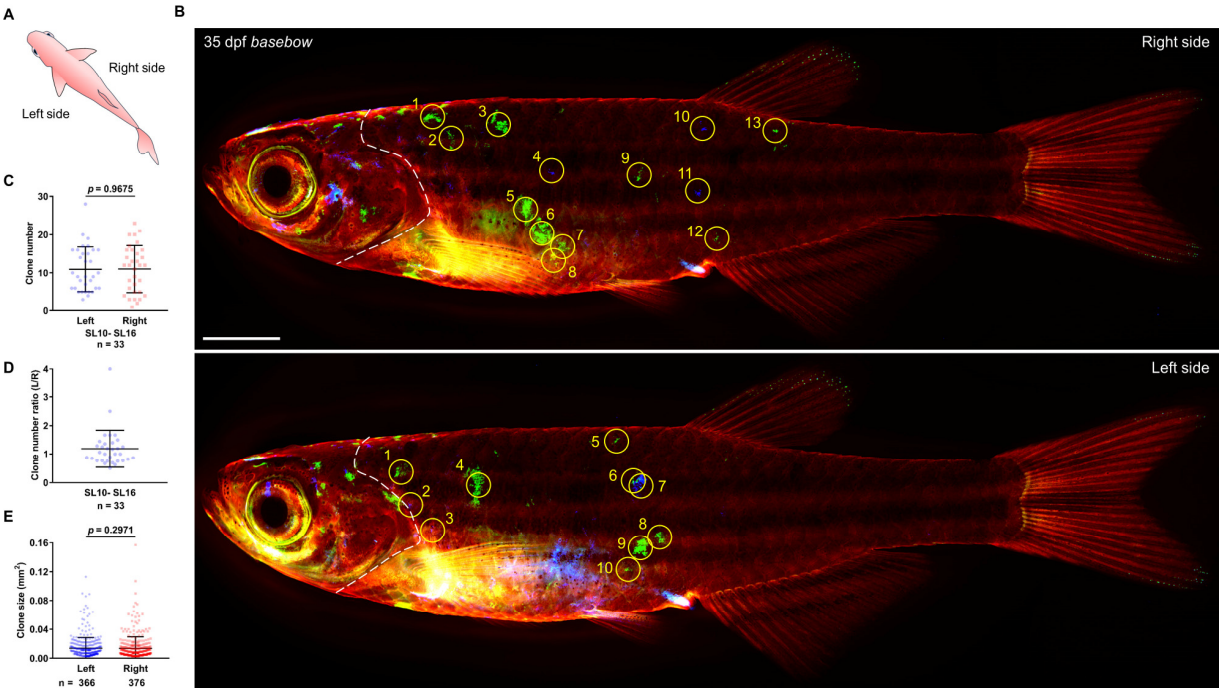

Fig. S3. Clonal behaviors on both sides of the fish body surface are symmetrical.

(A) Illustration depicting the left and the right side of the fish body.

(B) Representative whole-mount epifluorescence images of a 35 dpf *basebow* (stitched). Right side, top. Left side, bottom. Yellow circles mark examined BEC clones. Scale bar, 1 mm

(C) Quantification of clone numbers (n = 33 animals; mean ± SD; two-tailed Student's *t*-test).

(D) Quantification of clone number ratios. Clone numbers on both sides of the animal are symmetrical as the average ratio is close to one (n = 33 animals; mean ± SD).

(E) Quantification of clone size (n = 33 animals; mean ± SD; two-tailed Mann-Whitney test).

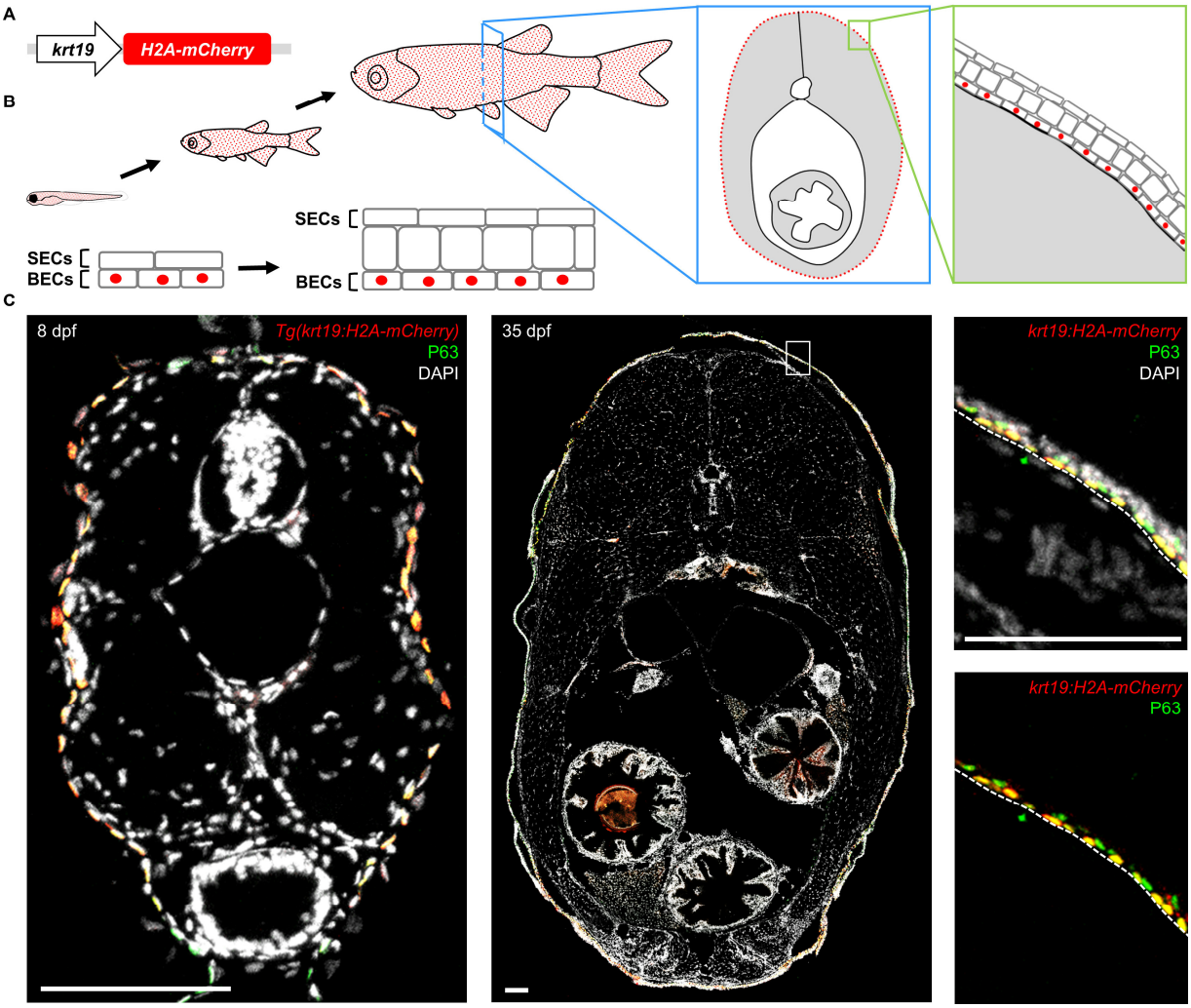

Fig. S4. *Tg(krt19:H2A-mCherry)* line labels only the BEC stem cell population.

(A) The *Tg(krt19:H2A-mCherry)* transgenic construct.

(B) Illustration depicting the development of zebrafish skin epidermis and the cell populations that are labeled in the *Tg(krt19:H2A-mCherry)*^{as54} line. SECs, Superficial epithelial cells. BECs, Basal epithelial cells.

(C) Cross-sections of the *Tg(krt19:H2A-mCherry)*^{as54} line at 8 and 35 dpf. P63 Ab staining marks the BEC layer (green). DAPI stains all cells (white). 35 dpf images are stitched. White box indicates magnified area shown in the right-most images. White dashed lines mark basement membrane. dpf, days post fertilization. Scale bar, 100 µm.

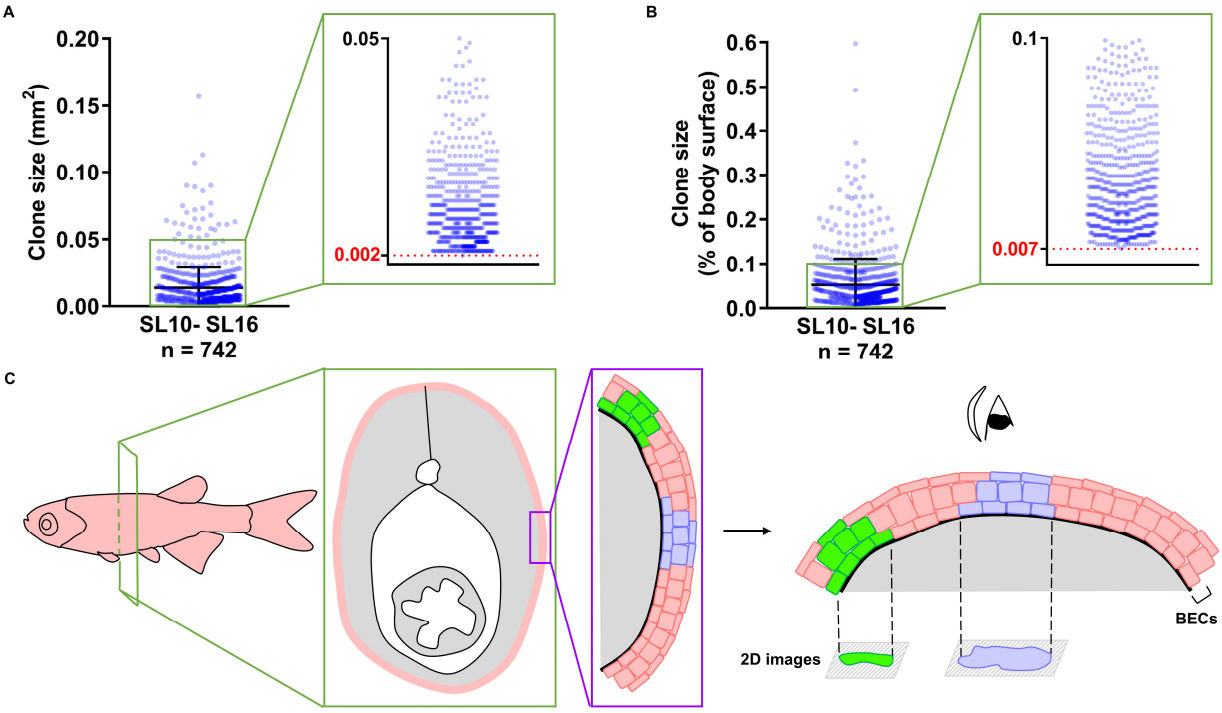

Fig. S5. Macroscopic imaging platform detects BEC clones larger than 0.002 mm² in size.

(A) Quantification of absolute clone size from all examined clones. BEC clones smaller than 0.002 mm² are below the detection limit of the imaging platform. The sizes of animals examined here ranged from SL10 to SL16 mm (n = 742 clones; mean ± SD).

(B) Quantification of relative clone size as percentage of body surface area. BEC clones smaller than 0.007% of the body surface area are below the detection limit of the imaging platform (n = 742 clones; mean ± SD).

(C) Illustration depicting how 2D maximum intensity projection clone images may underestimate actual clone size.

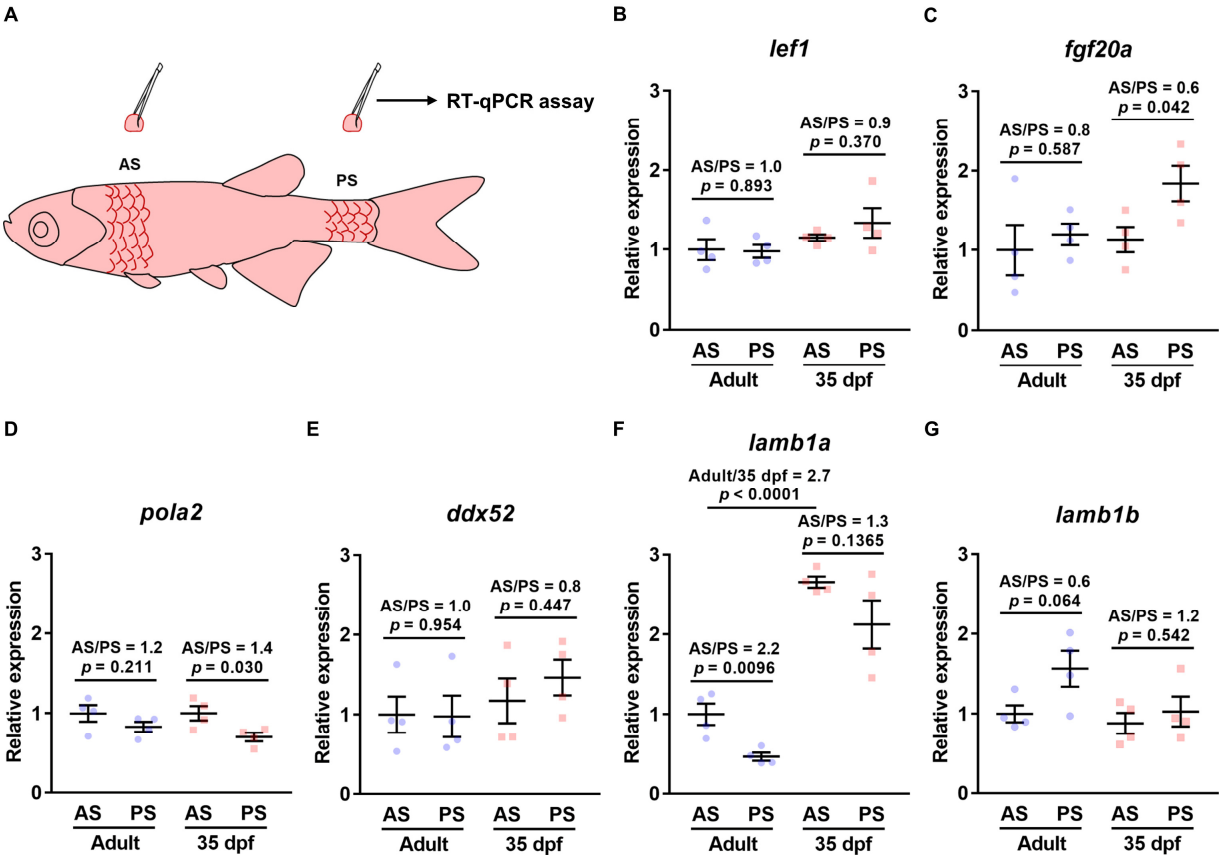

Fig. S6. Lamb1a expression is spatially regulated in developing and homeostatic skin tissues.

(A) Illustration depicting scale-plucking from either AS or PS region of the animal body surface. Plucked scales containing skin BECs from distinct body regions were subjected to RT-qPCR analyses.

(B-G) RT-qPCR analyses of *lef1*, *fgf20a*, *pola2*, *ddx52*, *lamb1a*, and *lamb1b* expression in skin tissues collected from either the AS or PS region of the animal body surface. (n = 4 biological replicates in each data point; mean ± SEM; two-tailed Student's *t*-test).

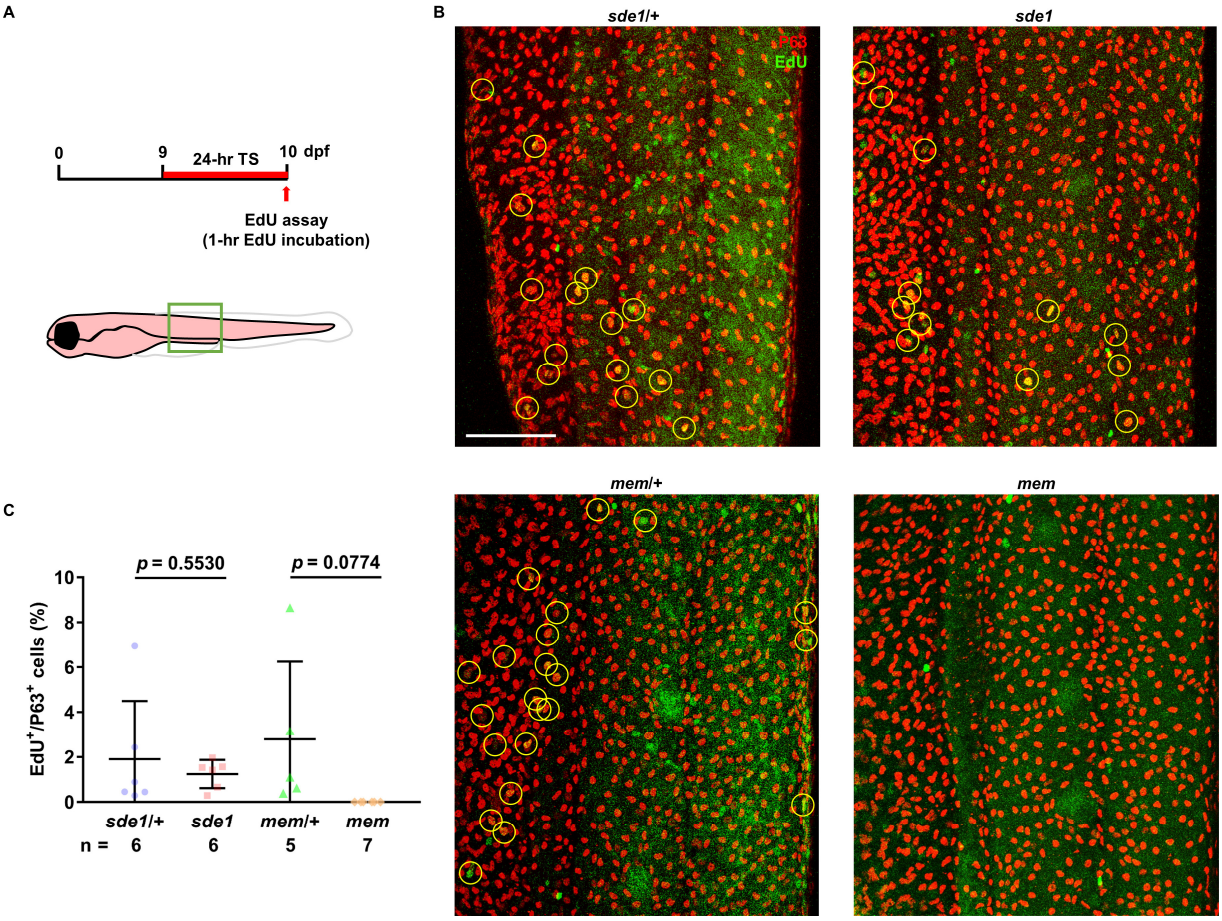

Fig. S7. Temporal inactivation of Lamb1a activity has no significant influence on BEC proliferation in developing skin tissues.

(A) Illustration depicting the temperature shift (TS) and EdU incubation scheme. Green box indicates imaged body region.

(B) Whole-mount EdU staining of *sde1* and *mem* mutant larvae. Proliferating BECs were visualized by double staining of P63 (red) and EdU (green). Yellow circles mark double-positive cells. Scale bar, 100 µm.

(C) Quantification of EdU^+ $P63^+$ double positive cells in *sde1* and *mem* mutant larvae upon heat treatment. The *mem* mutant, which carries a ts allele of the gene DNA polymerase alpha subunit 2 (*pola2*), was included as a positive control for the heat treatment (n = 6 *sde1*/+, 6 *sde1*; 5 *mem*/+, 7 *mem*; mean ± SD; two-tailed Student's *t*-test).

Table S1. List of primers used for RT-qPCR.

RT-qPCR		
Gene	Direction	Primer sequence
lef1	Forward	CTG GTC AAC GAG ACA GAA ATC A
	Reverse	CCT GTG CTT CTC ATG GTA AGA G
fgf20a	Forward	TGG ATA GCG GAT TGT ATC TGG
	Reverse	CAA ACT GCT CCC TGA ACA CA
pola2	Forward	GTT CGG ACC TTT TGT TGA TTC A
	Reverse	TCC ACT ATG CTG TCC ATA CAT C
ddx52	Forward	GGT CTG GAG CAA AGT TTG ATT T
	Reverse	ATC ACT TGC TTC TCC TTC TTC A
lamb1a	Forward	CCC CTG TCG ATG GAA CTG
	Reverse	TAC ACA TAC AAT GAC CAT GAA CCA
lamb1b	Forward	CTC CCA ACC GCC TTA AAA C
	Reverse	AAT CCA GCT GAA TGG TCA CA
actb	Forward	TAC ACA GCC ATG GAT GAG GAA AT
	Reverse	TCC CTG ATG TCT GGG TCG TC