Supp. Figures

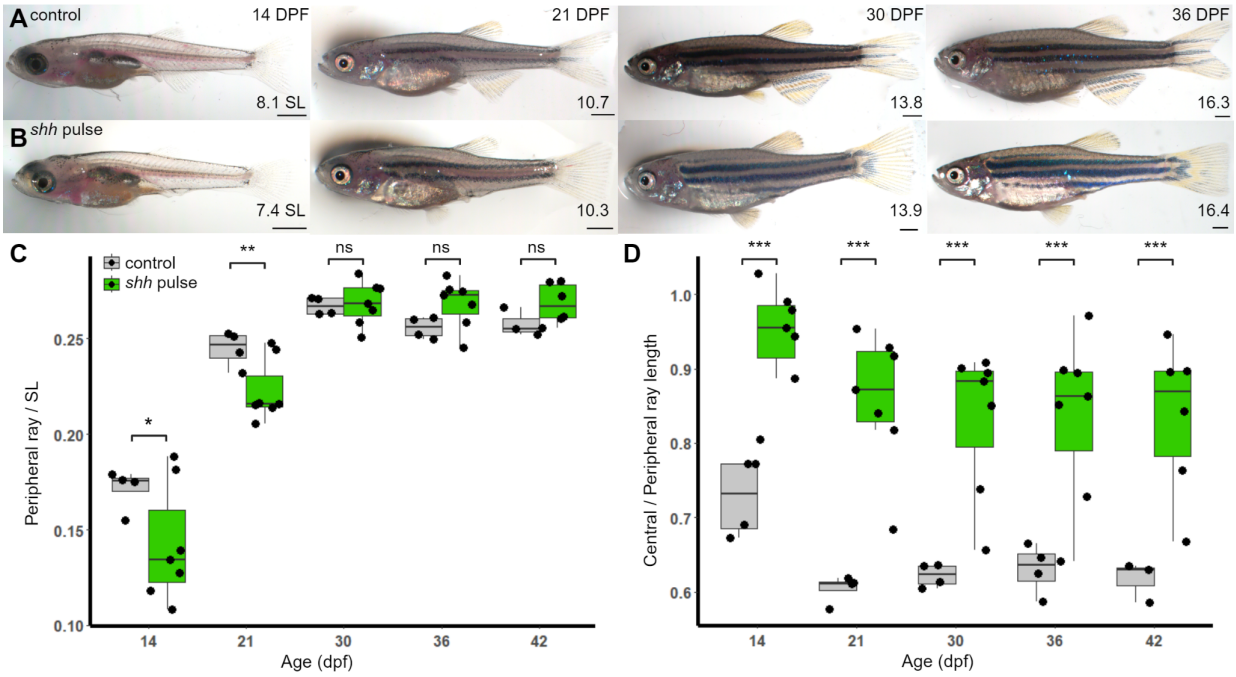

Fig. S1: Growth of body and fins under different *shha* profiles. *A-B*) Whole body images of (*A*) sibling control and (*B*) *shh* pulse-treated fish from 14-36dpf. Scale bars, 500 μm. (*C*) The overall length of the caudal fin gfas measured by the length of the peripheral ray) relative to the standard length of the fish. By 30 dpf, truncate fins were the same size as forked fins of control siblings. (*D*) The difference in caudal fin shape between conditions is evident by 14dpf. Significance within each time point determined by Welch's two-sample T-tests.

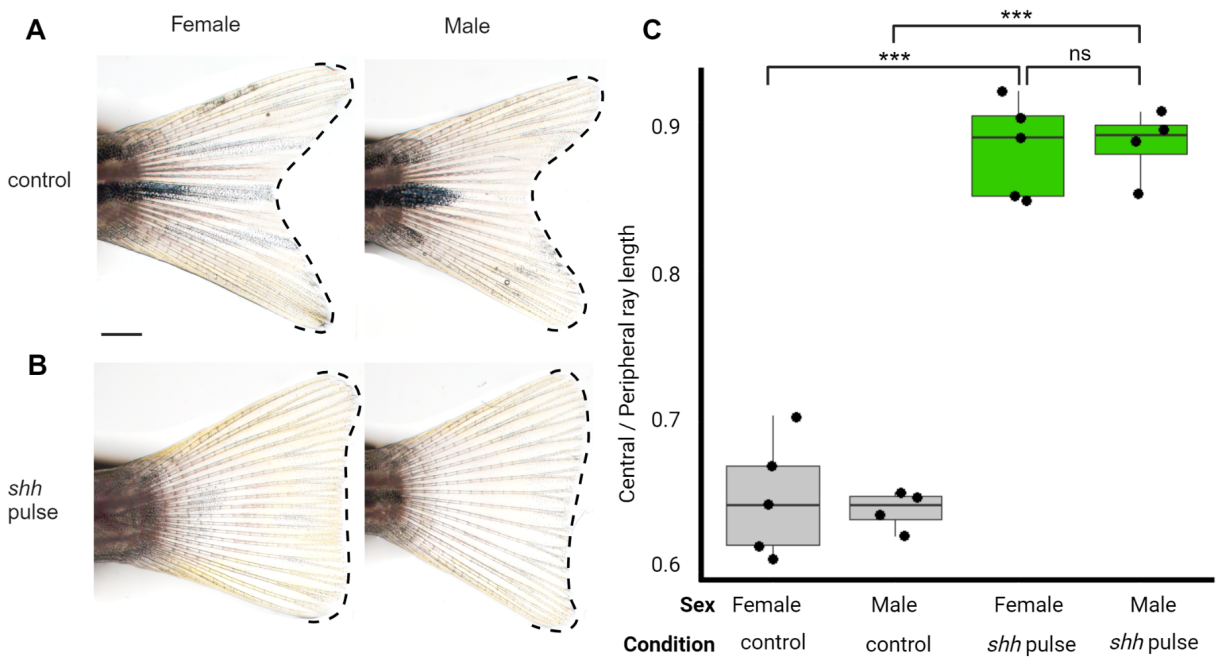

Figure S2: Fin shape shows no interaction with sex. Representative caudal fins of male and female (*A*) control and (*B*) *shh* pulse-treated sibling fish. Bar, 1mm. (*C*) There was no difference in fin shape between sexes in either control or *shh* pulse-treated fish. Significance determined by ANOVA followed by Tukey's post hoc test.

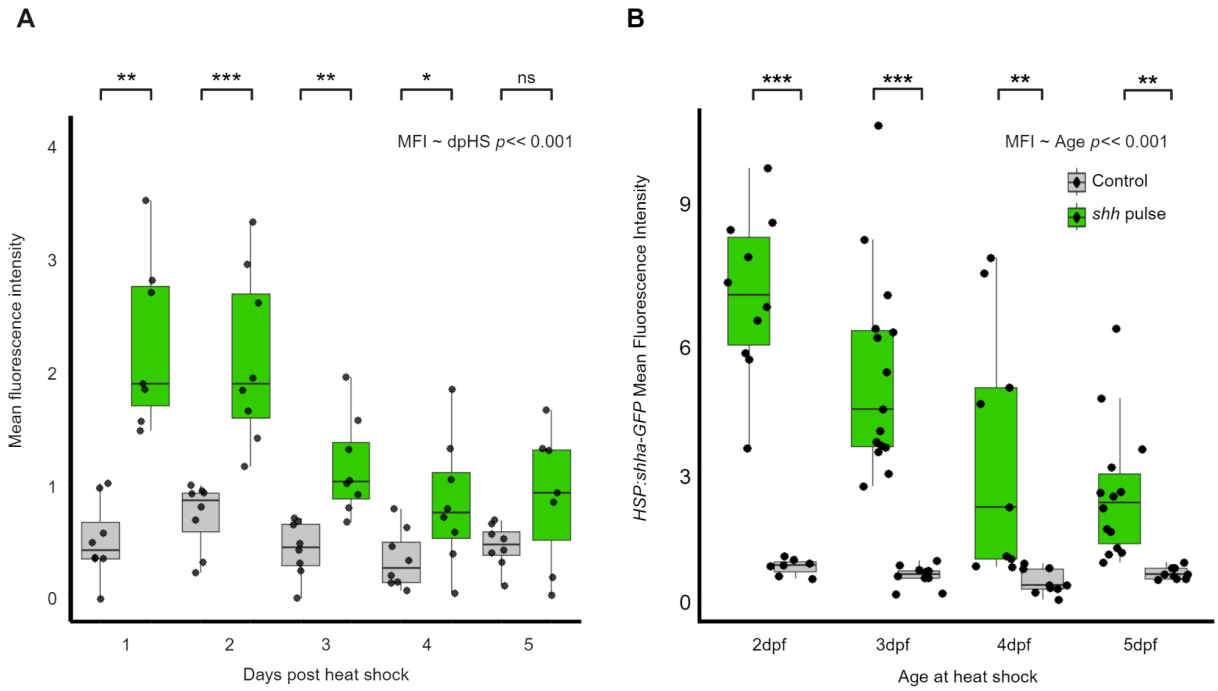

Fig. S3: Effect of development on heat-shock promoter efsiciency and GFP perdurance following *shh* pulse (*A*) GFP fluorescence is detectable for several days following heat shock. (*B*) Amount of GFP induced decreases with later heat shocks. GFP measured by fluorescence intensity 24 h after heat shock. Significance between conditions per day determined using Welch's two-sample T-tests, and the correlation between readout and time following heat shock / age of heat shock determined by linear-mixed effects model.

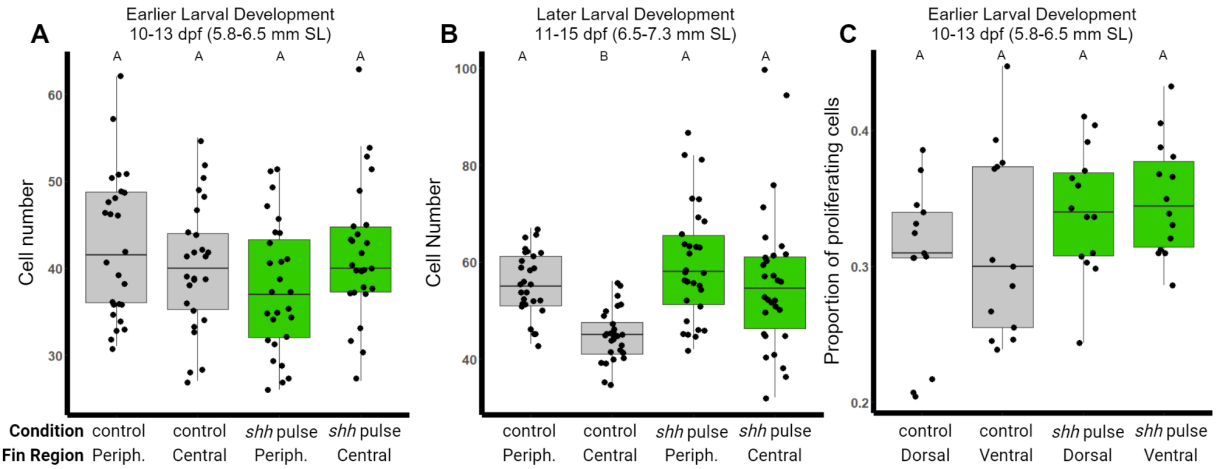

Fig. S4: *shh* pulse leads to larger cell populations in central regions of fins. (*A*) At earlier stages of larval development (SL = 5.8-6.5 mm) there is no difference in cell number between central and peripheral fin regions in either condition . (*B*) At later stages of larval development (SL = 6.5-7.2 mm), there is a central / peripheral differential in cell number in control individuals, but proliferation is the same in both regions of fish treated with *shh* pulse . (*C*) There is no difference in proliferation between dorsal compared to ventral fin regions . Significance determined by ANOVA followed by Tukey's post hoc test. Statistically indistinguishable groups are shown with the same letter (threshold for significance $p < 0.05$).

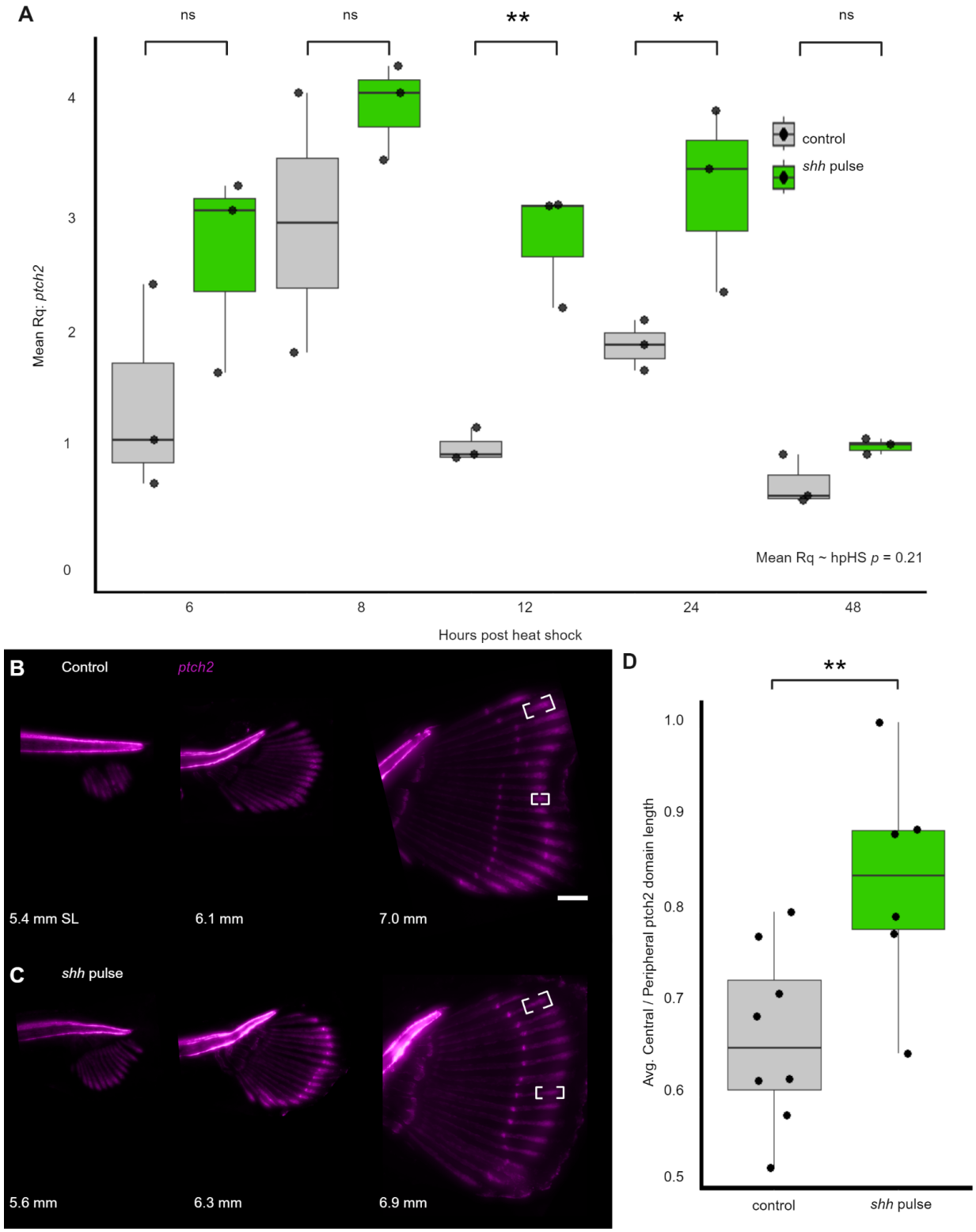

Fig. S5: Length of *ptch2* domain correlates to relative ray length. (*A*) *shh* pulse induces moderate upregulation of *ptch2* for 24 hours following heat-shock before returning to WT levels of expression. Significance within time points determined using Welch's two-sample T-test.

Relationship between mean Rq and time following heat shock also captured by linear-mixed effects model. (*B*-*C*) Fluorescent image series of individual *ptch2:kaede* transgenic larvae during early caudal fin development. (*B*) In control caudal fin *ptch2:kaede* is expressed in relatively longer domains of activity in peripheral rays compared to central rays. (*C*) Following *shh* pulse, the activity domains are of similar lengths. Bar, 100μm. (*D*) The average domain length of the peripheral to the central region between conditions. Significance determined using Welch's two-sample T-test.

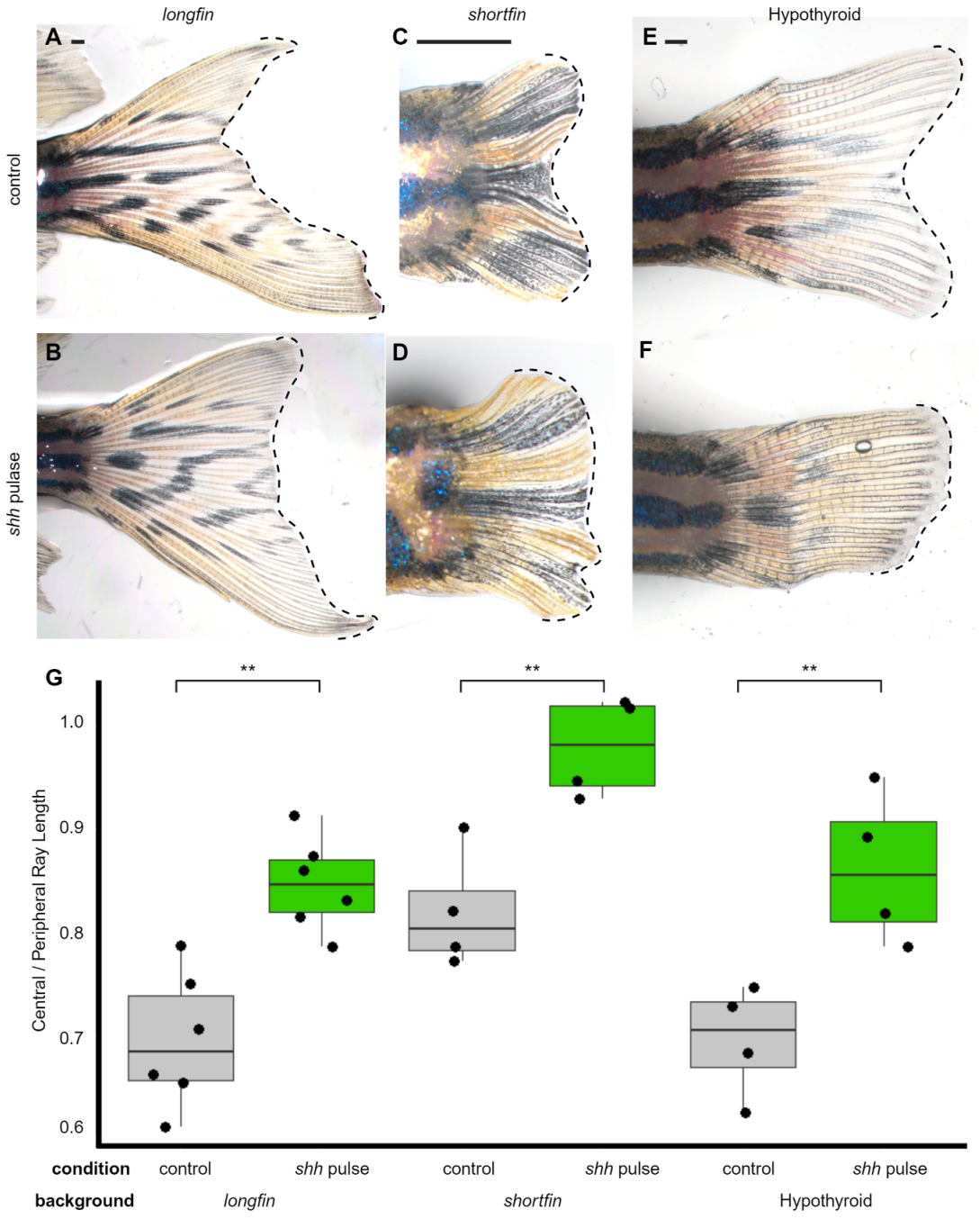

Fig. S6: *shha* pulse induces a truncate phenotype in *longfin* and *shortfin* mutants and in hypothyroid backgrounds. (*A, C, E*) *longfin* mutants, *shortfin* mutants, and hypothyroid zebrafish all show forked fin shape. (*B, D, F*) Treated with a *shh* pulse, truncate fin shape can be induced in all three backgrounds. (G) Quantification of fin shape in different backgrounds. Significance within each background is determined by Welch's two-sample T-tests. Scale bars, 500μm.

Table S1: Primer sets used for qPCR and RT-qPCR

Ptch2_F – RT-qPCR amp. of *ptch2* cDNA, forward	TGTGCTGTTTCTACAGTCCCTG
Ptch2_R – RT-qPCR amp. of *ptch2* cDNA, reverse	GCACGCTGATGGTTGTCATT
Shha_F – RT-qPCR amp. of *shha* cDNA, forward	AGAGCCGGACAAAAGGTGAT
Shha_R – RT-qPCR amp. of *shha* cDNA, reverse	AATGGTCCCATGTGCAGTCA
Actb1_F – RT-qPCR amp. of *actb1* cDNA, forward	CGACCAGAAGCGTACAGAGA
Actb1_R – RT-qPCR amp. of *actb1* cDNA, reverse	AATCCCAAAGCCAACAGAGA
EGFP_F – qPCR amp. of *EGFP* gDNA, forward	ACGACGGCAACTACAAGACC
EGFP_R – qPCR amp. of *EGFP* gDNA, reverse	TTGCCGTCCTCCTTGAAGTC
Actb1_F – qPCR amp. of *actb1* gDNA, forward	GATGCGGAAACTGGAAAGGG
Actb1_R – qPCR amp. of *actb1* gDNA, reverse	GGAGGGCAAAGTGGTAAACG