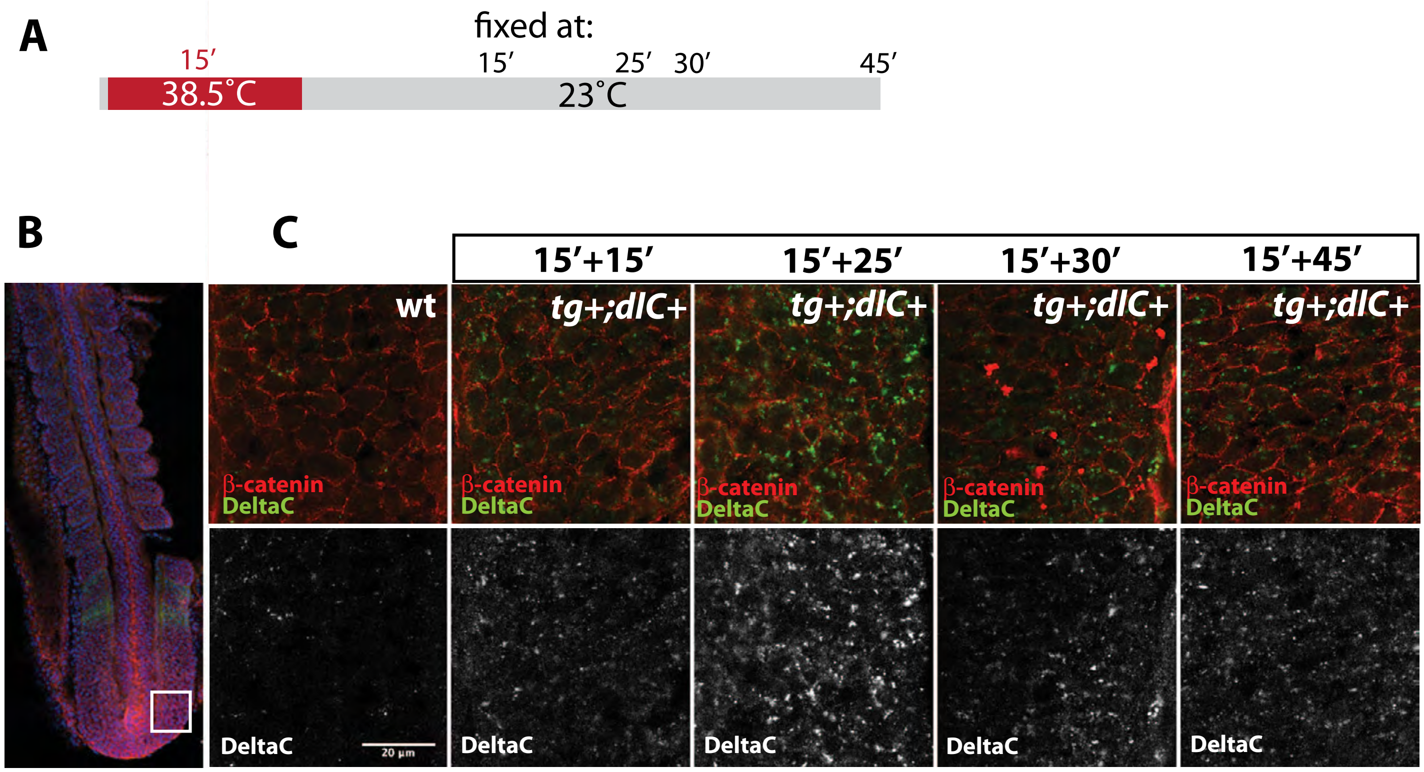
Model details.

Supplementary file M1. Mathematica notebook file representing a two-dimensional array of noisy oscillatory PSM cells coupled (or, in the mutant case, not coupled) by Delta-Notch signalling. The program is essentially as in Hanisch et al. (Hanisch et al., 2013), annotated to explain the principles of the computation, and with a preamble outlining the key equations that define the model mathematically. Readers who have Mathematica can easily adapt the notebook to explore alternative assumptions.

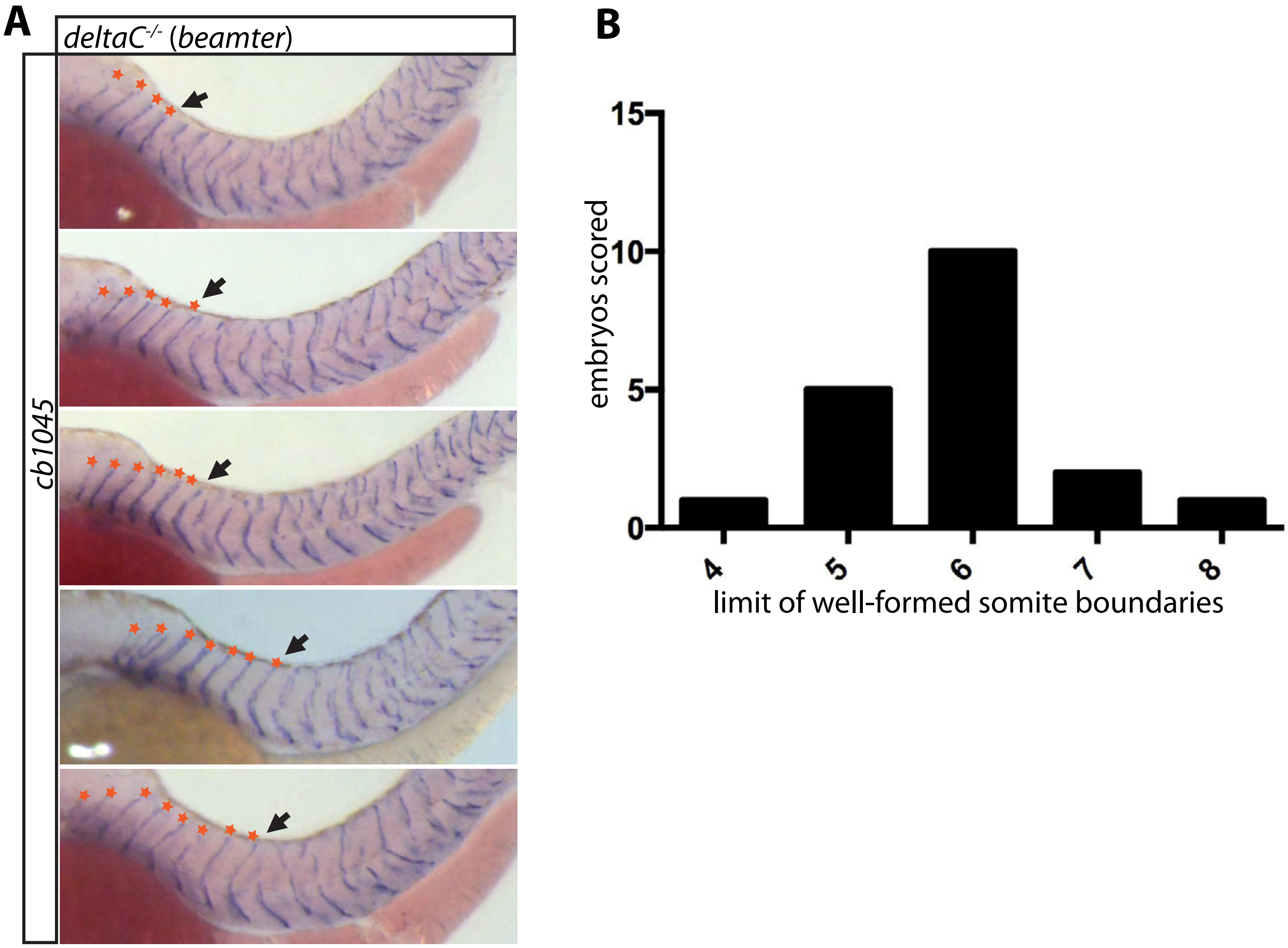
Download File M1

Supplementary file M2. The same Mathematica notebook as in M1, but displayed as a PDF file. This is not executable, but allows readers without Mathematica to see the full details of the model.

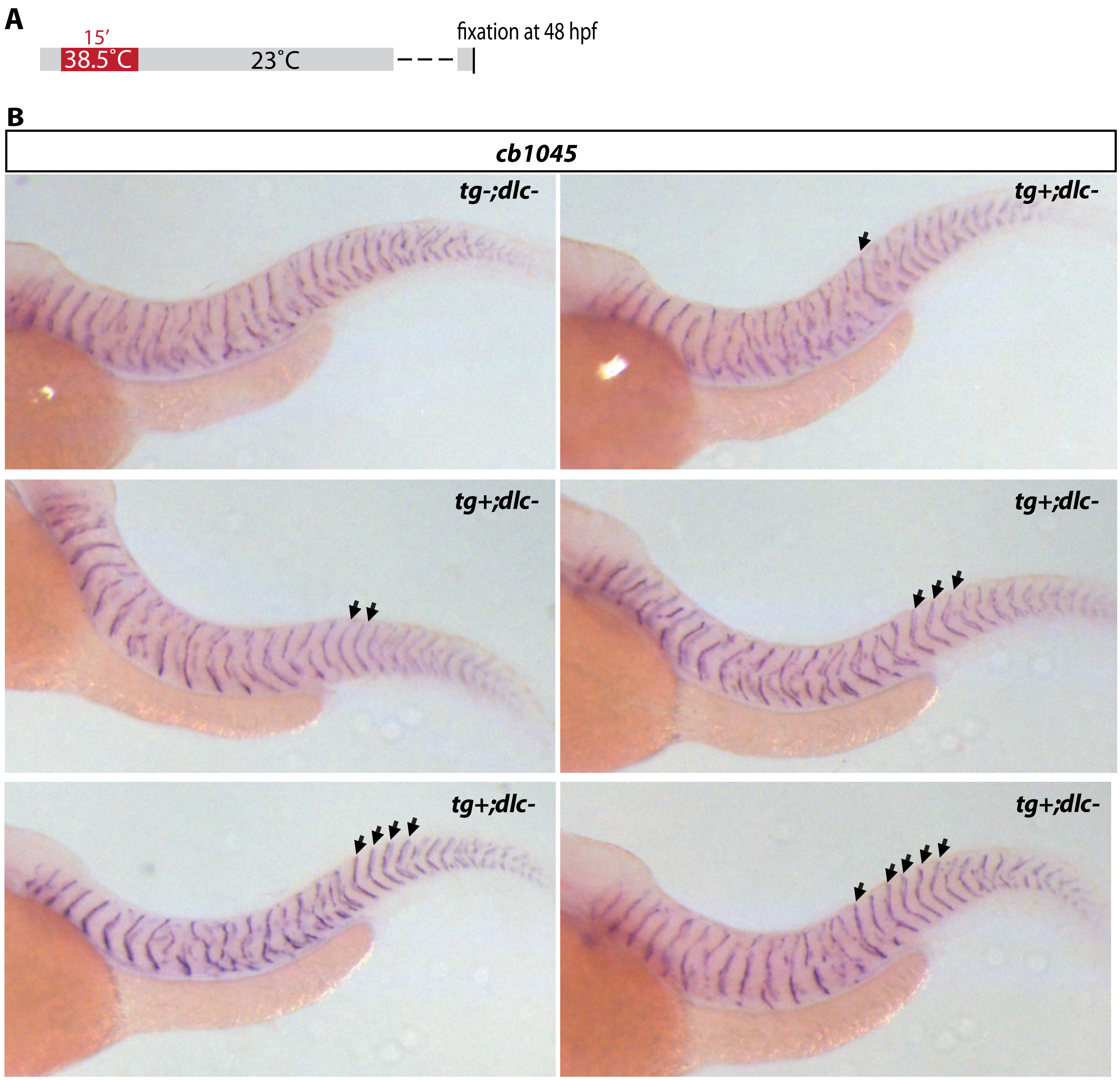
Download File M2



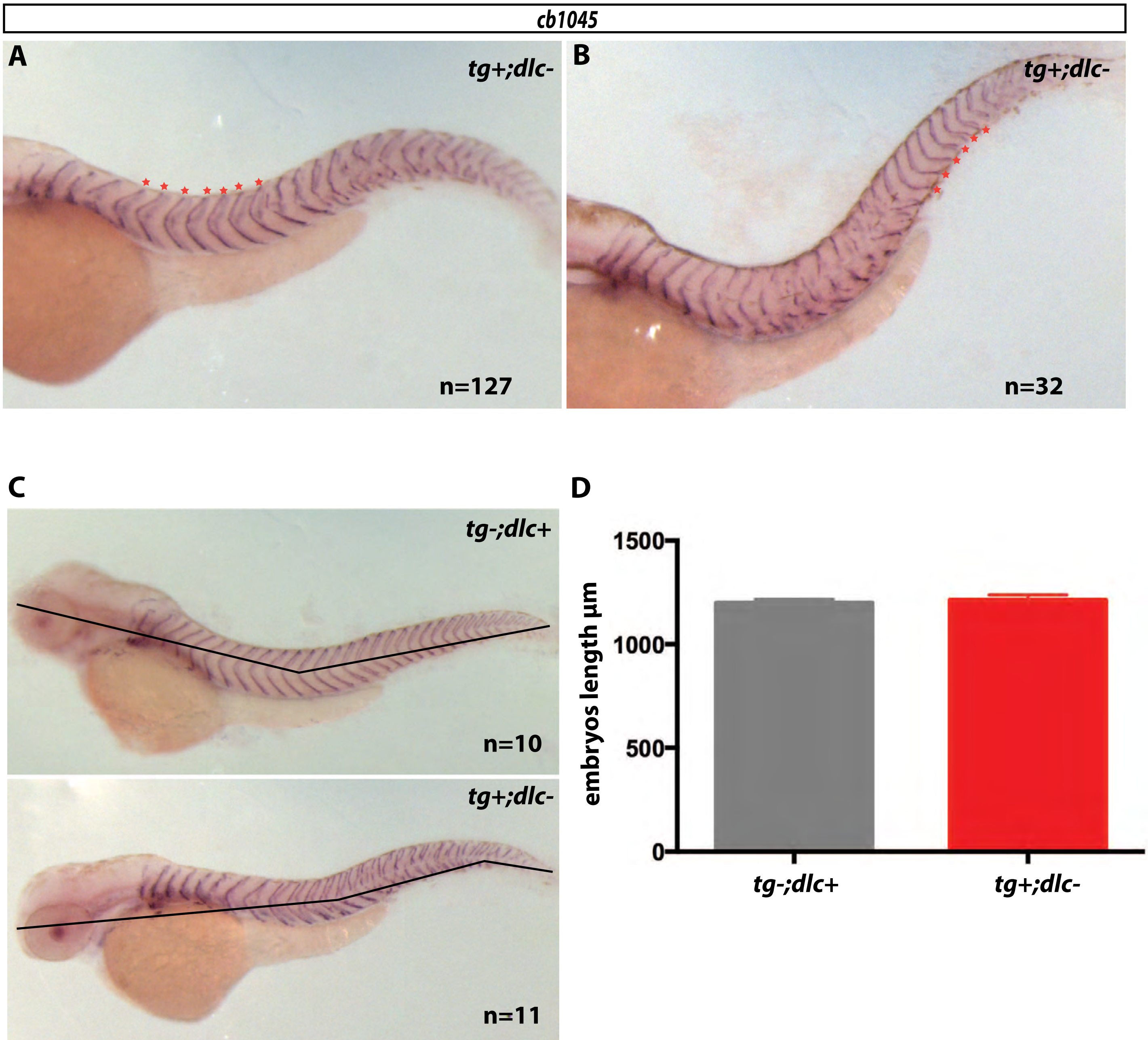
Supplementary Fig. S1. Time course of DeltaC protein expression in *tg+;dlC+* transgenic embryos after a single heat-shock. 15 hpf embryos were heat-shocked at 38.5 ºC for 15 minutes and left to recover at 23˚C for varying lengths of time before fixation. **(A)** Scheme of the treatment. **(B)** Flat-mounted embryo, dorsal view; white box shows region of posterior PSM selected for analysis. **(C)** Enlargements of boxed region marked in B, for a series of embryos fixed at the indicated times and immunostained for DeltaC (green) and beta-catenin (red, marking plasma membrane); confocal imaging. Levels of cell-surface-associated DeltaC have begun to increase at 15+15 minutes, reach a peak at 15+25 minutes, and have declined markedly by 15+30 minutes. Pictures are representative of 5 transgenic embryos analysed by confocal microscopy at each time point.



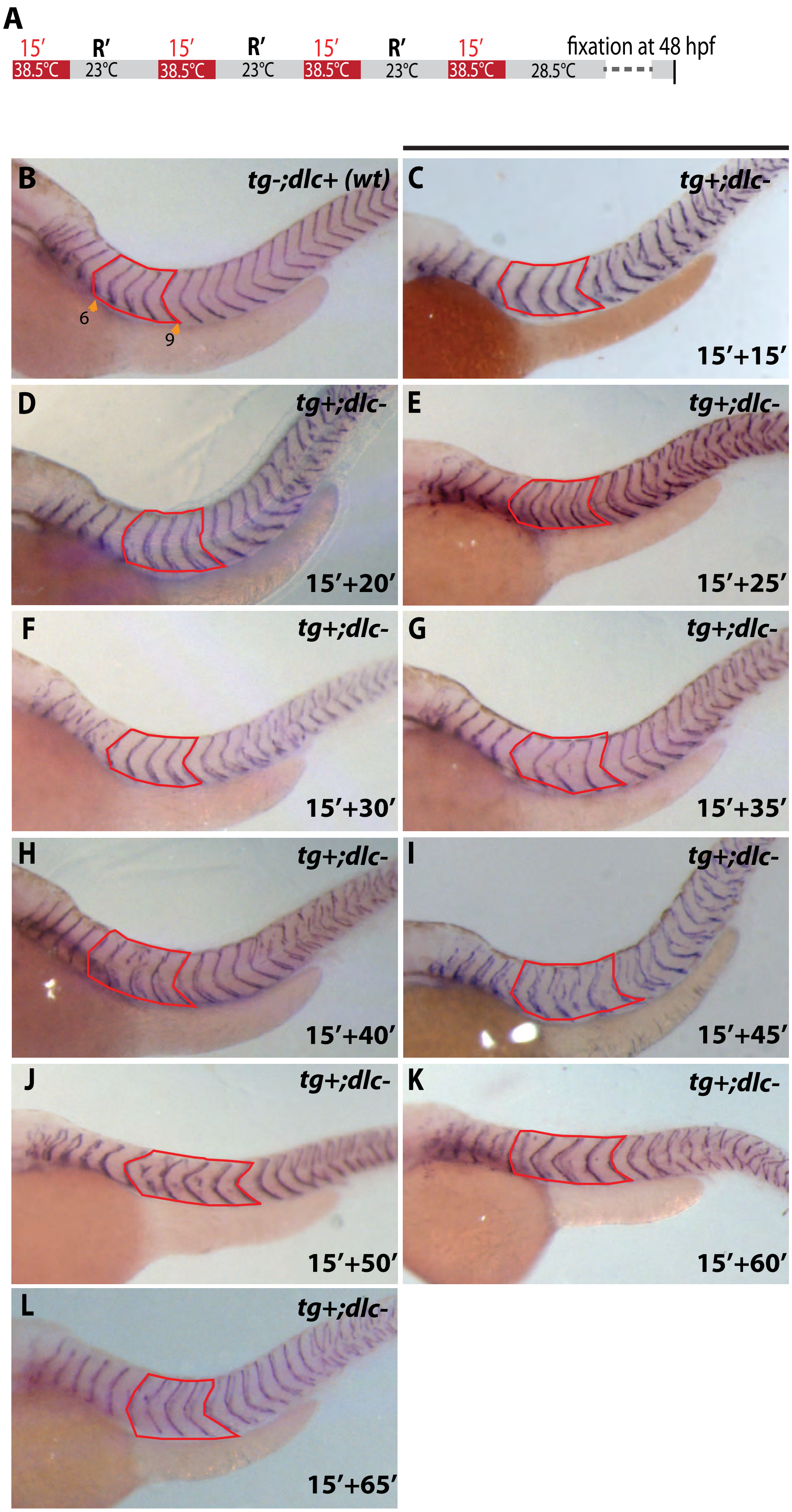
Supplementary Fig. S2. (A) Examples of *dlc*$^{tw212b/tw212b}$ (*tg-;dlc-*, *beamter*) embryos, stained by ISH with *cb1045* at 48hpf. Asterisks mark well-formed boundaries; arrows mark the posterior limit of segmentation. **(B)** Histogram showing the frequency with which different numbers of somite boundaries are formed anteriorly before segmentation breaks down. Note that the numbers of regular segments on the two sides of the embryo do not always match. The histogram shows data for one side of the embryo.



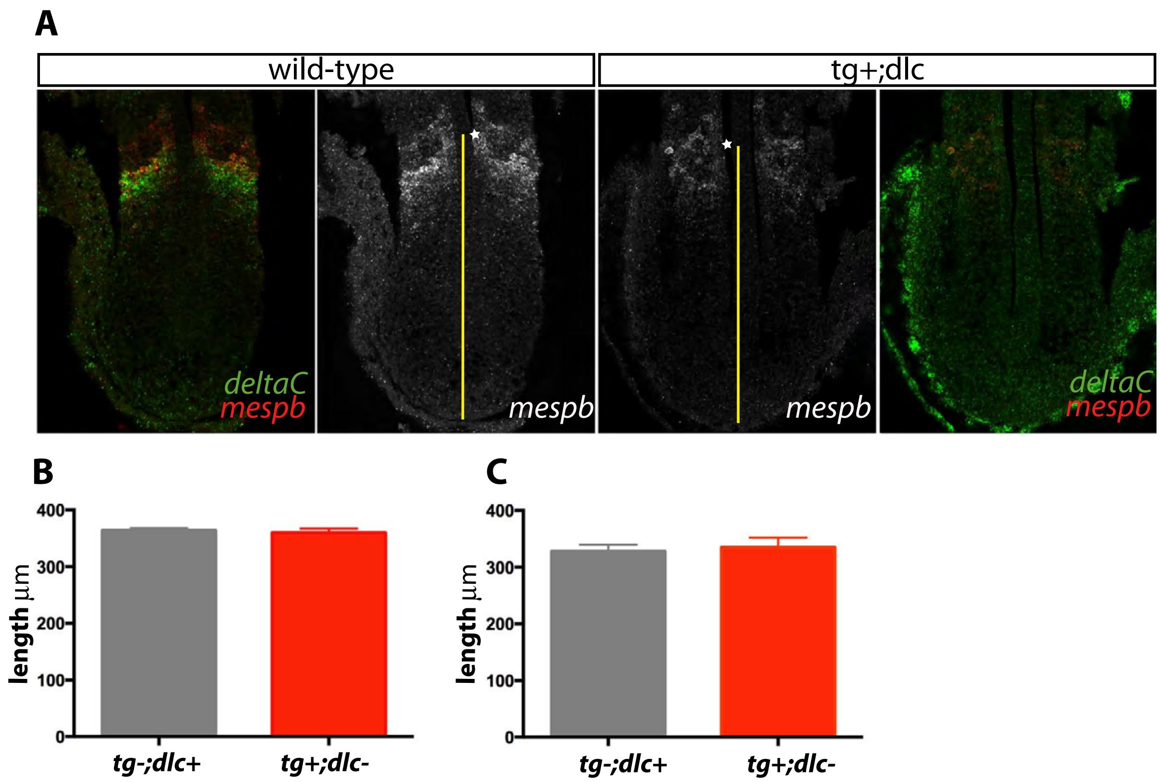
Supplementary Fig. S3. Responses of *tg+;dlc-* embryos to a single standard heat-shock, showing the range of variation in the number of rescued somite boundaries. **(A)** Scheme of the experiment. **(B)** Results. Details of staining etc. as in Fig. 3.



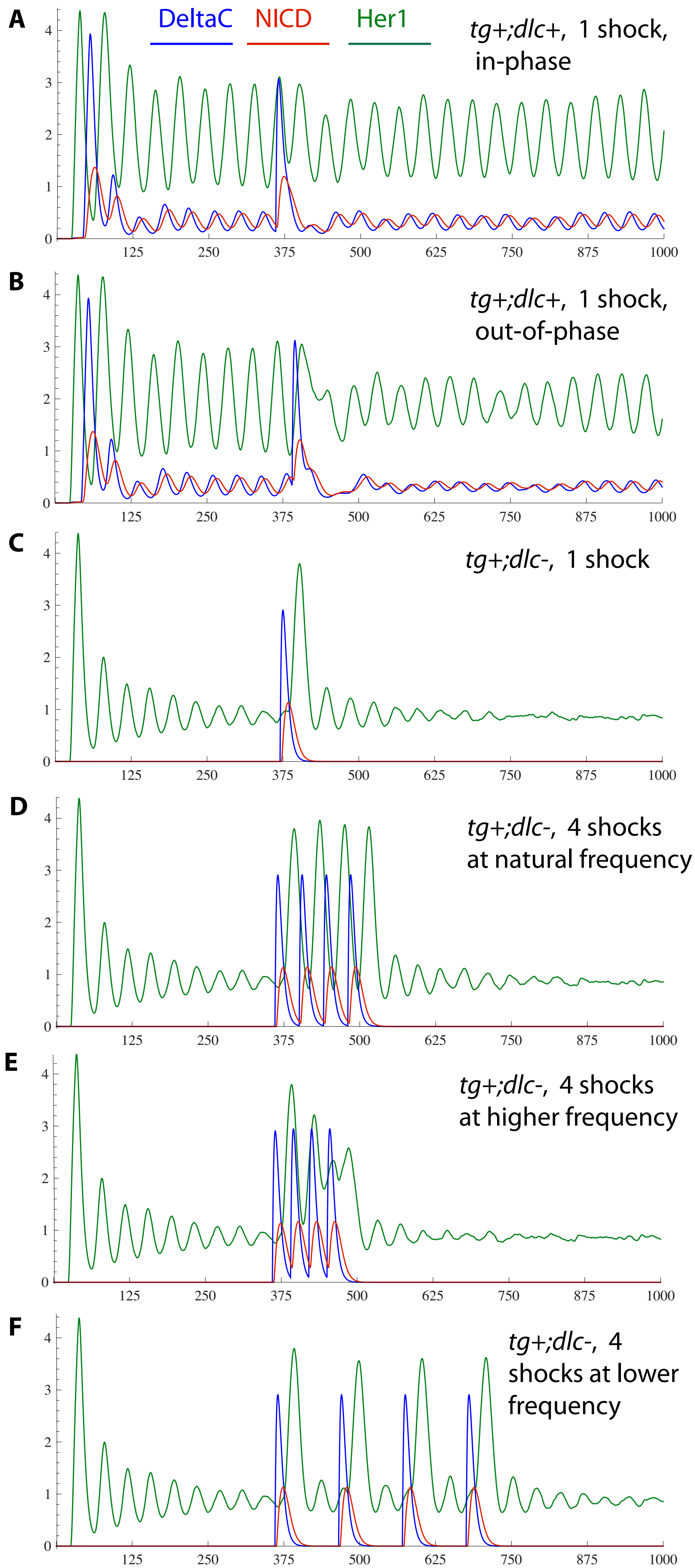
Supplementary Fig. S4. Responses of *tg+;dlc-* embryos to a series of 4 standard heat-shocks (15+25 minutes), delivered (A) at the 3-somite stage and (B) at the 13-15 somite stage, with fixation at 48hpf. Within each class, all embryos (n=127 for A, n=32 for B) showed a similar distribution of rescued somites – anterior for A, about 12 somite-widths further posterior for B – as illustrated by the photographs. In each case, the rescue of segmentation begins with a delay of 3 to 5 segmentation clock cycles relative to the time of heat-shock. Asterisks mark rescued somite boundaries. Details of staining etc. as in Fig. 3. (**C**) Measurement of whole *tg-;dlC+ and tg+dlC-* (15+60 minutes treatment) embryos. (**D)** Graph of embryo length measurements. Note that heat shocked *tg-;dlC*$^{+}$ (n=10) and *tg+dlC-* (n=11) embryos have similar body lengths.



Supplementary Fig. S5. Somite width can be modified by varying the interval between heat-shocks: typical results for each of the intervals studied. (A) diagram of the heat-shocking regime. **(B)** Wildtype control. **(C-L)** Examples from batches of *tg+;dlc-* embryos taken at the 3-somite stage and heat-shocked 4 times, but with different recovery times, R, between one heat-shock and the next, as indicated. The red box in each case outlines the set of 4 somites whose width was measured. See Fig. 4 legend for details.



Supplementary Fig. S6. PSM length in heat-shocked *tg+;dlc-* embryos is the same as in heat-shocked wildtype. (A) *tg+;dlc-* embryos, along with wildtype controls, were taken at the 13 somite stage, given a series of heat-shocks and then stained by double FISH for *mespb* mRNA (red channel) and *deltaC* mRNA (green channel). The distance from the posterior tip of the embryo to the middle of the *mespb* expression domain (asterisk) was measured (yellow line). **(B)** Graph of length measurements for *tg-;dlC+* (n=5) and *tg+;dlC-* (n=5) embryos after 3 standard heat-shocks (15+25 minutes), fixed 25 minutes after the end of the last heat shock. The values for wildtype and mutant were respectively 364 ± 4 µm and 360 ± 7 µm (mean ± SEM). **(C)** Graph of length measurements for *tg-;dlC+* (n=6) and *tg+;dlC-* (n=5) embryos after 4 heat-shocks repeated with periodicity 15 + 65 minutes, fixed 65 minutes after the end of the last heat shock. The values for wildtype and mutant were respectively 328 ± 11.6 µm and 335 ± 17 µm (mean ± SEM). The differences in B and C are not statistically significant (two-tailed t-test).



A
DeltaC
NICD
Her1
tg+;dlc+, 1 shock, in-phase
B
tg+;dlc+, 1 shock, out-of-phase
C
tg+;dlc-, 1 shock
D
tg+;dlc-, 4 shocks at natural frequency
E
tg+;dlc-, 4 shocks at higher frequency
F
tg+;dlc-, 4 shocks at lower frequency
0
1
2
3
4
125
250
375
500
625
750
875
1000

Supplementary Fig. S7. Mathematical modelling predicts effects similar to those observed. Output is shown from a Mathematica program representing a two-dimensional array of noisy oscillatory PSM cells coupled (or in the mutant case, not coupled) by Delta-Notch signalling; see Supplementary Material M1 and M2 for full details. The graphs show, as a function of time (in minutes), the computed levels of DeltaC (blue), NICD (red), and Her1 (green) proteins (arbitrary units), following one or more DeltaC pulses. The segmentation behaviour is taken to correspond to the Her1 line. The calculation is done for an array of 10x10 cells and the plotted values are means over this set. When there is coordinated collective oscillation, these means show strong oscillation; when the individual cells oscillate asynchronously, the means show only small random fluctuations. **(A)** Wildtype (*tg+;dlc+*) system exposed to a single shock delivered approximately in-phase with the endogenous collective oscillation. **(B)** Wildtype (*tg+;dlc+)* system exposed to an out-of-phase shock. This resets the phase of the endogenous oscillation, giving a disturbance corresponding to an alteration in the size of one somite, after which normal oscillation resumes immediately. **(C)** Effect of a single shock in a mutant (*tg+;dlc-*) embryo where endogenous *deltaC* is non-functional. The shock forces the cells back into synchrony, which persists for a few cycles until they once again drift out of synchrony. **(D)** As in (C), but with 4 shocks, delivered at a repetition frequency roughly matching the frequency of the endogenous oscillator. **(E)** As in (D), but with the 4 shocks repeated with a repetition cycle length .75 times that of the endogenous clock. This gives a series of 4 accelerated segmentation clock cycles, corresponding to small somites, followed by a drift away from synchrony. **(F)** As in (D), but with the 4 shocks repeated with a repetition cycle length 2.6 times that of the endogenous clock. This gives a series of 4 prolonged segmentation clock cycles of abnormal shape, corresponding to enlarged somites with a blip in the middle of each. Note that parameter values in the model, although constrained by experimental data (Giudicelli et al., 2007; Lewis, 2003), are not known precisely. Thus the interest lies in the qualitative match to observed behaviour, rather than quantitative exactness. The model is relatively insensitive to the assumed strength of the DeltaC pulses: for values of this quantity ranging over an order of magnitude around the value used here, the model predictions as to the rescue of synchrony are essentially similar.