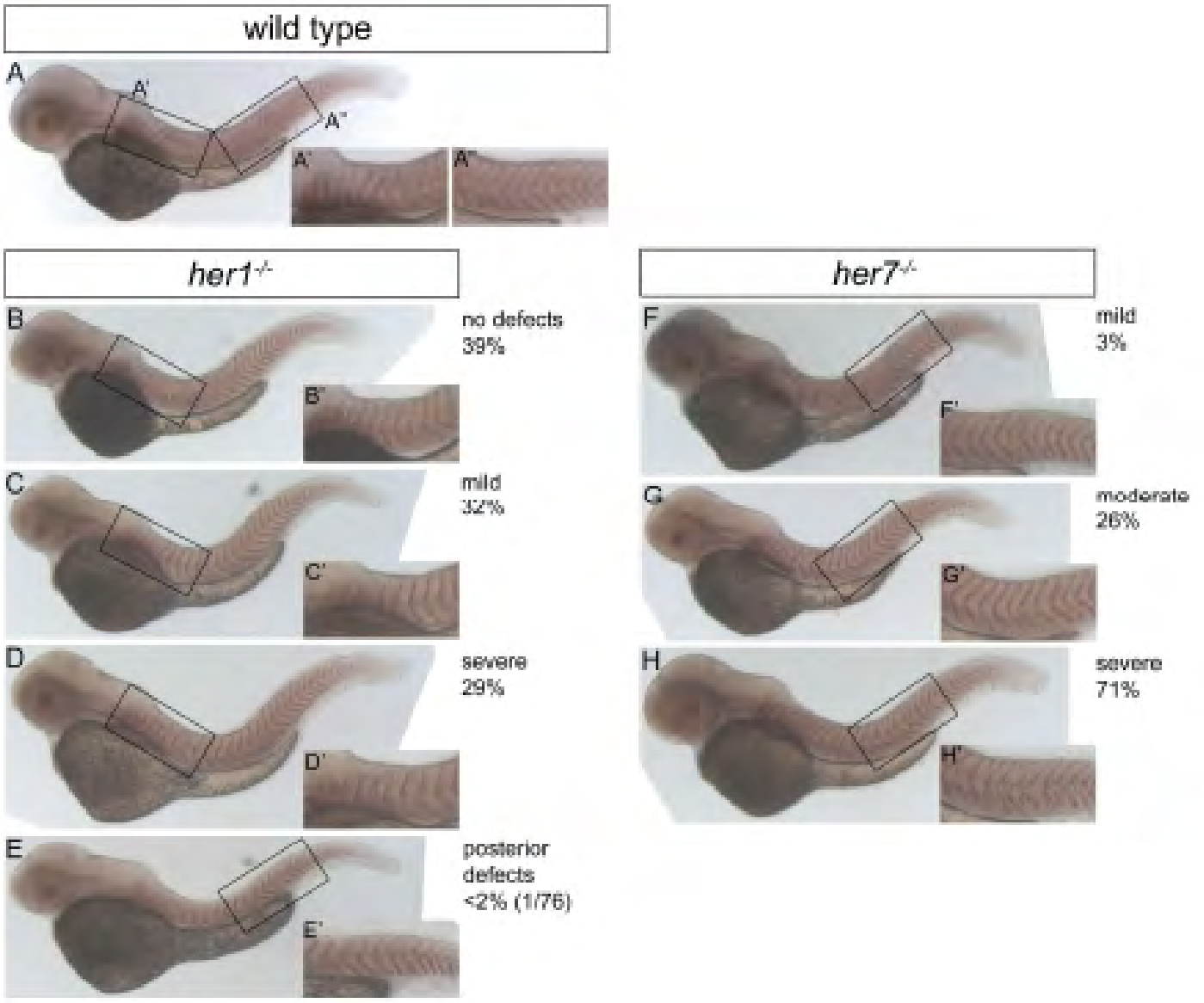

Fig. S1. Variability in the phenotype of *her1*$^{-/-}$ and *her7*$^{-/-}$ embryos. Embryos fixed at 48 hpf and stained with *cb1045* ISH probe to show somite boundaries (lateral views). (**A-A″**) Wild type; (**B-E′**) *her1*$^{-/-}$ mutant; (**F-H′**) *her7*$^{-/-}$ mutant. Insets show regions affected by segmentation irregularities in more detail. (B-E) A large proportion (~40%) of *her1*$^{-/-}$ embryos show no segmentation defects with the *cb1045* probe. The remaining ~60% of the embryos present one ('mild') or two to three ('severe') absent, broken or abnormally shaped somite boundaries in the anterior of the body. We only found one specimen in which posterior segments were affected (E; *n*=76). (F-H) All *her7*$^{-/-}$ embryos present somite boundary defects (*n*=88). These comprise broken or absent boundaries and boundaries that are misaligned on the two sides of the body. Defects always affect segments in the mid to posterior trunk rather than anterior segments. A small proportion of embryos are almost phenotypically normal ('mild', zero or one segment boundary affected), but most have defects in two to four ('moderate') or more than five ('severe') segment boundaries.

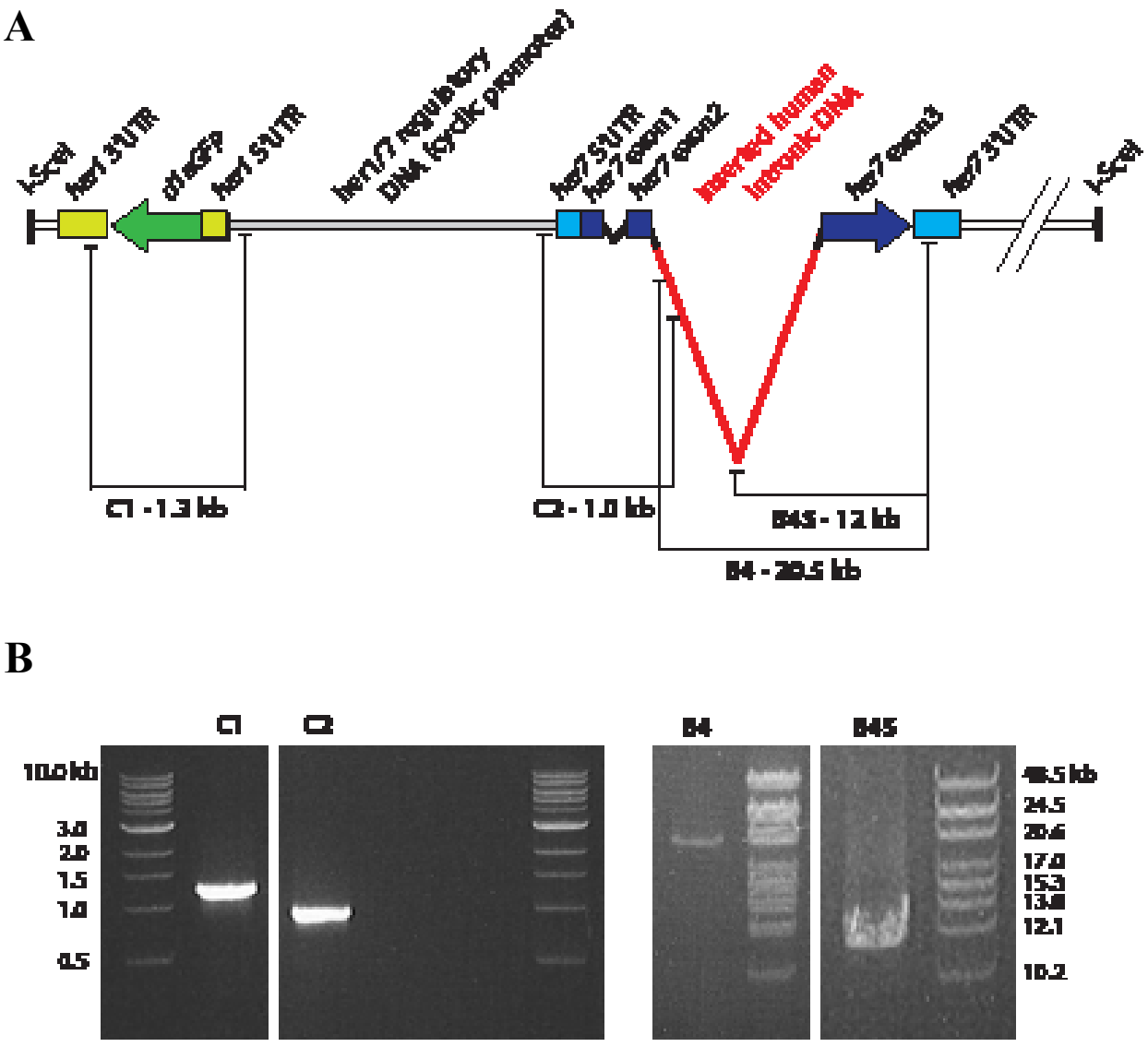

Fig. S2. PCR analysis of the integrated *her7*^{b21} transgene. (**A**) The *b21* BAC construct (not to scale), showing sites of PCR primers used for analysis in B. (**B**) PCR analysis of the DNA from a *b21* transgenic fish, demonstrating that the whole of the region including the 21 kb artificially enlarged intron is present and correctly linked to the *her1/7* cyclic promoter/enhancer. PCR primers (5′-3′) were: C1forward, GCTGTCCCAACACAAATCCG; C1reverse, GAGCAGCAGAACGCCATAAG; C2forward, GCAGCTCAGGGATTGGGTTAG; C2reverse, TGCTTGGTGGCATCTGTCTG; B4forward, TGGCTTGGTCATATTGGGAAAC; B4reverse, GGATTCTGCGTGCTGCTTTC; B4Sforward, AGATGGAAGCCTGGGGAGAG; B4S reverse, GGATTCTGCGTGCTGCTTTC. These conclusions were confirmed in an independent set of PCR analyses using a different set of primers that were more closely spaced, spanning the region from the first exon of *her7* through the enlarged intron to the second exon of *her7*, in nine overlapping steps. The identities of these PCR products were checked by sequencing.