



Supplemental Fig. 3. The evolutionary history comparing *Anolis carolinensis* with other vertebrates for delta and jagged/serrate classes of notch ligands (A), notch receptors (B), mesoderm posterior (mesp) genes (C), *fgf8* (D), and *wnt3* genes (E) compared with other vertebrate developmental model systems was inferred using the Neighbor-Joining method displaying the optimal tree using MEGA 5 (Tamura et al., 2011). Values shown are the percentage of replicate trees in which the associated taxa clustered together using the bootstrap test with 500 replicates. Evolutionary distances were estimated using the Poisson correction method and are in units of amino acid substitutions per site. The *A. carolinensis* genome contains duplications of the *hes6* and *hes7* orthologues similar to *Xenopus tropicalis* but unlike other amniotes. G, Phylogenetic tree of *hes/hey* genes was similarly obtained comparing *Drosophila*, zebrafish, *X. tropicalis*, *A. carolinensis*, chick, and mouse. The lizard has duplication of *hes* genes including *hes6a* and *hes6b* and *hes7a* and *hes7b*. The ancestral arrangement of the *hes6* paralogs is unclear based on analysis of the mouse, chicken, anole, *X. laevis*, and zebrafish. Specifically, both the anole and *X. tropicalis* have tandem *hes6a* and *hes6b* orthologues, but the orientation of the tandem group is inverted *X. tropicalis* relative to the anole. In zebrafish, the *hes6* orthologue is not present in a tandem group. The chicken appears to have retained a single *hes6b*-like orthologue, and the mouse appears to have a single, divergent orthologue equidistantly divergent from both *hes6a* and *hes6b*. *In situ* hybridization analysis of green anole embryos with *hes6b* and *hes7b* identified expression within the developing neural tube but not in the PSM (data not shown).