



Supplemental Fig. 2. Syntenic conservation for *Anolis carolinensis* *hes6* (A), *hes7* (B), and *dll3* (C) orthologues compared with other vertebrates, including mouse, chicken, anole, and frog *Xenopus tropicalis* based on Ensembl database version 62.2a annotation of Anocar2.0 genome build. Gene symbols in red indicate the highlighted gene, in blue for orthologues identified in all vertebrates shown, in green for orthologues identified except for mouse, and in purple for orthologues identified only in amniotes. Genomic regions are shown to scale, and for *hes6* orthologues regions represented are: A. *carolinensis* chromosome 3, 27973077–28273076; mouse chromosome 1, 93209338–93459337, and X. *tropicalis* scaffold GL172691.1, 1423168–1623167. For *hes7* orthologues, the genomic regions represented are: A. *carolinensis* scaffold GL343400.1, 498000–952338; mouse chromosome 11, 68853906–69057557; X. *tropicalis* scaffold GL173687.1, 1–219716. C, Syntenic regions in the chicken and turkey corresponding to 5' and 3' flanking genes for lizard *dll3*, mouse *Dll3*, and X. *tropicalis* *dlc* (orthologous to X. *laevis* X-*Delta-2*) are shown. Genomic regions represented are: A. *carolinensis* scaffold GL343635.1, 1–430722; mouse chromosome 7, 29030000–29139000; X. *tropicalis* scaffold GL173025.1, 353000–465000; chicken scaffold Un_random, 38452086–38574565; turkey (*Meleagris gallopavo*) scaffold GL426281.1, 1–1,012.