

Animal development is controlled by a tightly regulated network of gene expression where genes are often reused across multiple life stages and tissues (Cardoso-Moreira et al., 2020). The signaling pathways and genes making up this network show deep conservation across the animal family tree (Carroll, 2008). Our current understanding of the underlying mechanisms regulating the same gene in multiple tissues is limited to a few genes. Recent studies have also demonstrated that paralogous genes with co-expression can share cis-regulatory modules (CRMs) (Baudouin-Gonzalez et al., 2017; Bourbon et al., 2022, Lan and Pritchard 2016; Levo et al. 2022; Loker and Mann, 2022; Stevens et al. 2022). The T-box (Tbx) transcription factors are an ancient family of genes in animals (Sebé-Pedrós et al., 2013). The *Drosophila* Tbx20 homologs *midline* (*mid*) and *H15* demonstrate conserved functions across arthropods, with roles in the determination of posterior fate during oogenesis, axis formation in the developing limbs, specification of neurons, and formation of the heart tube in developing embryos (Buescher et al., 2004; Buescher et al., 2006; Miskolczi-McCallum et al., 2005; Prpic et al., 2005; Pyrowolakis et al., 2017; Svendsen et al., 2009). Additionally, these two genes sit within an isolated topologically associating domain (TAD) that contains no other genes, making *mid/H15* an excellent system for expanding our understanding of developmental gene regulation. We examined the roles of three CRMs on *mid/H15* patterning and tissue development. Using CRISPR-Cas9 gene editing, we deleted combinations of the three CRMs. Two (G04 and F11) are associated with *mid/H15* expression in the ovarian follicle cells. The third, the ventral leg enhancer (VLE), had been predicted to regulate their expression in the ventral domain of the leg disc (Levo et al., 2022; Revaitis et al., 2017, Svendsen et al., 2015). Impacts from the deletion of G04 and F11 were only evident in the ovaries (Stevens et al., 2022). Deletion of the VLE led to pleiotropic effects on leg and wing morphogenesis.