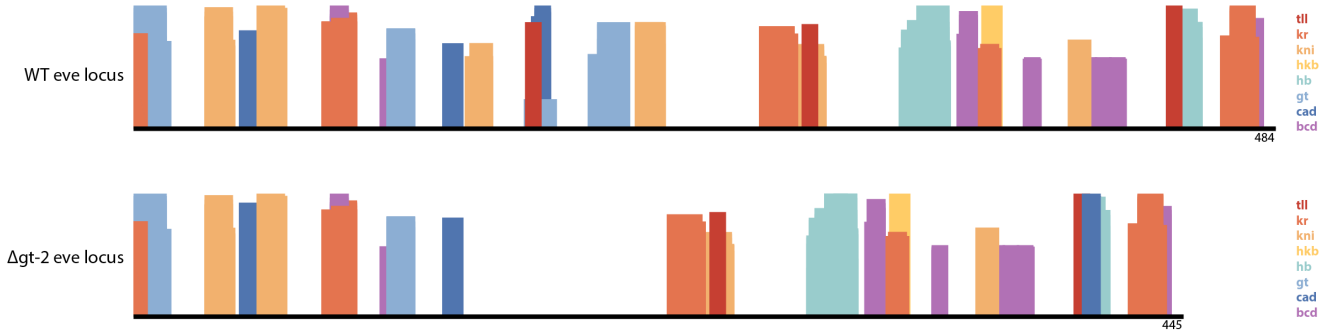

Figure S6: Binding site plots showing changes to predicted binding sites in the *eve* locus after CRISPR deletion of gt-2. To identify all predicting binding sites, we used multiple available PWMs for each *eve* regulator (Bicoid, Caudal, Giant, Hunchback, Huckebein, Knirps, Krüppel, Tailless, and Zelda), totalling 87 PWMs. These PWMs were used with the PATSER program to predict binding sites within the *eve* minimal stripe 2 enhancer sequences using a p-value of 0.001 (File S1). The transcription factor binding site locations are included for the minimal *eve* stripe 2 WT *eve* locus and the Δgt-2 *eve* locus (File S2 and File S3 respectively). All binding site plots have been aligned to the left. Note that removal of gt-2 in the Δgt-2 *eve* locus could have potentially disrupted predicted tailless, caudal and huckebein sites. We did notice the addition of a SNP on the 3' end of the Δgt-2 *eve* locus, which may create an additional Caudal binding site (File S1).