**Fig. S1.** **RNA-seq data suggests a low level of *tou-RB* transcript.** (A) Rows 1-4: ChIP-seq distributions of H3K27me3, H3K36me3, CP190 and PolII over a part of *tou* in WT. Rows 5-6: RNA-seq data derived from WT brains and discs of third instar larvae (Brown *et al.* 2018) at two different scales, the scale represents FPKM (fragments per kilobase per million). A *tou-RB* specific exon (boxed in red) is evident on the 0-1000 scale suggesting a low level of *tou-RB* is made. Note that the first exon of *touRB* is 20bp and would not have been detected in our analysis. (B) RNA FISH with probe targeting all *tou* isoforms except *tou-RB*, in WT and *eZ-λ-eG* larval wing discs (*tou-big* probe, green box). Two representative wing discs (medium expression, high expression) from both genotypes are shown, along with the percentage of each typeobserved(total counted: 29 discs from WT and 30 discs from *eZ-λ-eG*).

**Fig. S2.** **Transgene inserted just upstream of *tou-RF* does not alter the *inv-en* domain boundary.** (A) ChIP-seq distribution of H3K27me3, H3K36me3, CP190 and CTCF over *inv-en* domain in WT. *en*PRE1 and 2 are indicated by red lines at the bottom. The locations of transgenes in *tou-MiMIC* and P[*en*3]-*tou* are indicated by vertical black lines. (B) ß-gal staining in the transgenic lines with (P[*en*3]-*tou*) and without (P[*en*3(-PREs)]-*tou*) *en*PREs in the transgene [data is reproduced from (DeVido *et al.* 2008)]. (C) ChIP-seq data of H3K27me3 in WT and P[*en*3]-*tou* is shown in a custom track that includes *lacZ* and *mw*,representing the transgene. H3K27me3 is deposited over *lacZ* and *mw.* We did not observe spreading of H3K27me3 flanking the transgene insertion site, and this transgene does not change the H3K36me3 distribution over *tou*.