**SUPPLEMENTARY FIGURE LEGENDS**

**Supplemental Figure 1:**

Cytoplasmic lysates from larva **(A)** and adults **(B)** were fractionated through sucrose gradients. Continuous A254 readings from the fraction collector for one of the three biological replicates used in Figure 1D and 1E are shown. Pooled fractions used for RNA extraction are highlighted as 40S/60S, monosome, low polysome and high polysome.

**Supplemental Figure 2:**

**(A)** Schematic depicting CRISPR-Cas9 editing scheme to delete the *AdhDIST* promoter region. A double-strand break (DSB) was made at the PAM site (green) using Cas9 nuclease (grey) and short guide RNA (sgRNA) (yellow), which binds ~730 base pairs (bp) upstream of the AdhDISTtranscription start site. The DNA region in red signifies the region that was deleted. The DNA region in black and brown signifies the DNA sequence flanking the deleted region. The blue arrow refers to the transcription start site of AdhDIST. Figure is not drawn to scale.

 **(B)** Expression levels of AdhPROX were measured by RT-qPCR using isoform specific primers. Data were normalized to *αTUB84B* and then to wild-type larvae levels to show fold change over wild type (1X). The mean of three independent biological replicates is shown. Error bars represent SEM.

**Supplemental Figure 3:**

Data from 5’ Rapid amplification of cDNA ends (5’ RACE) analysis for AdhPROX, AdhDIST, and AdhUAS. At the top are diagrams of the wild-type *Adh* locus and the *AdhUAS* locus with the GAL4/UAS induction system*.* At the *AdhUAS* locus, 10 consecutive GAL4 binding sites (UAS) (shown in yellow) are placed immediately upstream of the AdhDIS*T* TSS followed by the minimal *hsp70* promoter (black). Coding (grey) and non-coding (white) exons are shown. Arrows represent TSSs of AdhPROX(orange), AdhDIST(blue) and AdhDIST\* (light blue). Numbers below the *Adh* locus refer to distance in base pairs (bp) from the AdhPROXTSS. Diagrams for each isoform’s mRNA transcript are shown above the sequence results. Genomic DNA sequence is bolded with aligned transcript sequences listed below. Eight clones were analyzed and sequenced for each transcript isoform; successful sequencing reactions are shown.