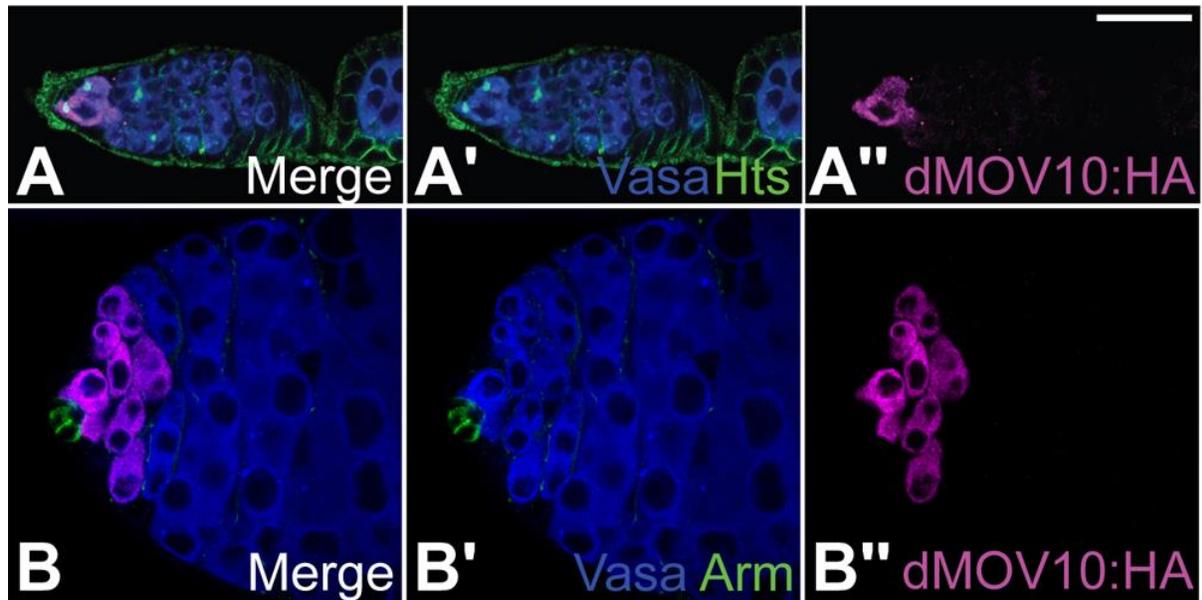
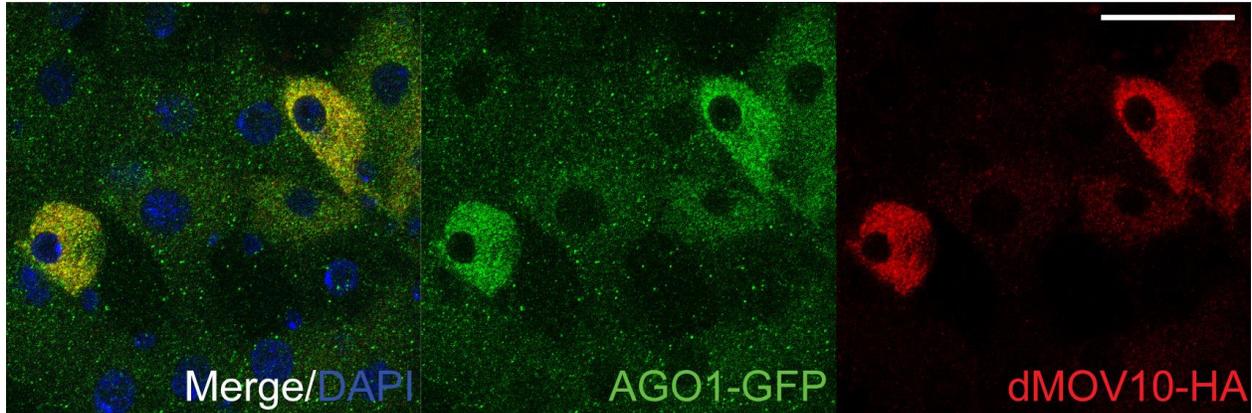


## Supplemental Figures



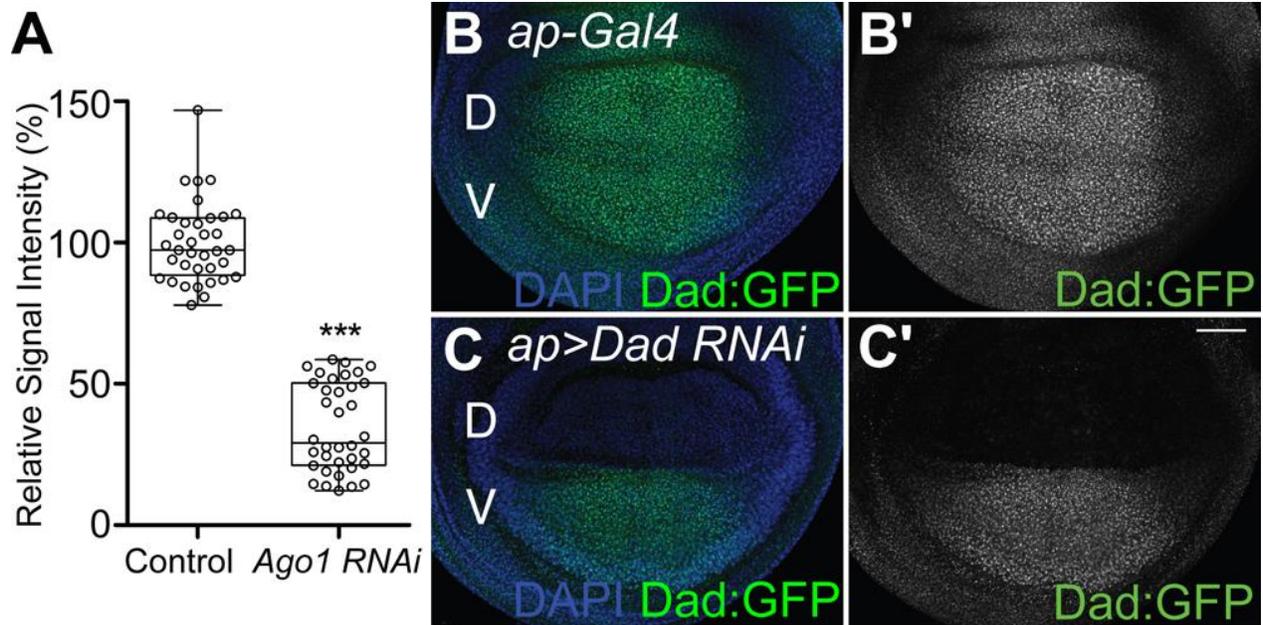
**Figure S1. dMOV10 expression in the ovary and testis.**

(A) A germarium, the most anterior structure of the ovary, of *dMOV10-HA* allele was dissected from female flies on day-4 after eclosion. The sample was stained for dMOV10-HA (magenta), Hu-li tai-shao (Hts, green), Vasa (blue; germline cells). Hts marks round spectrosomes characteristic of germline stem cells (GSCs). (B) A testis of *dMOV10-HA* stained for dMOV10-HA (magenta), Armadillo (Arm; a hub marker, green), and Vasa (blue). Scale bars: 50  $\mu$ m.



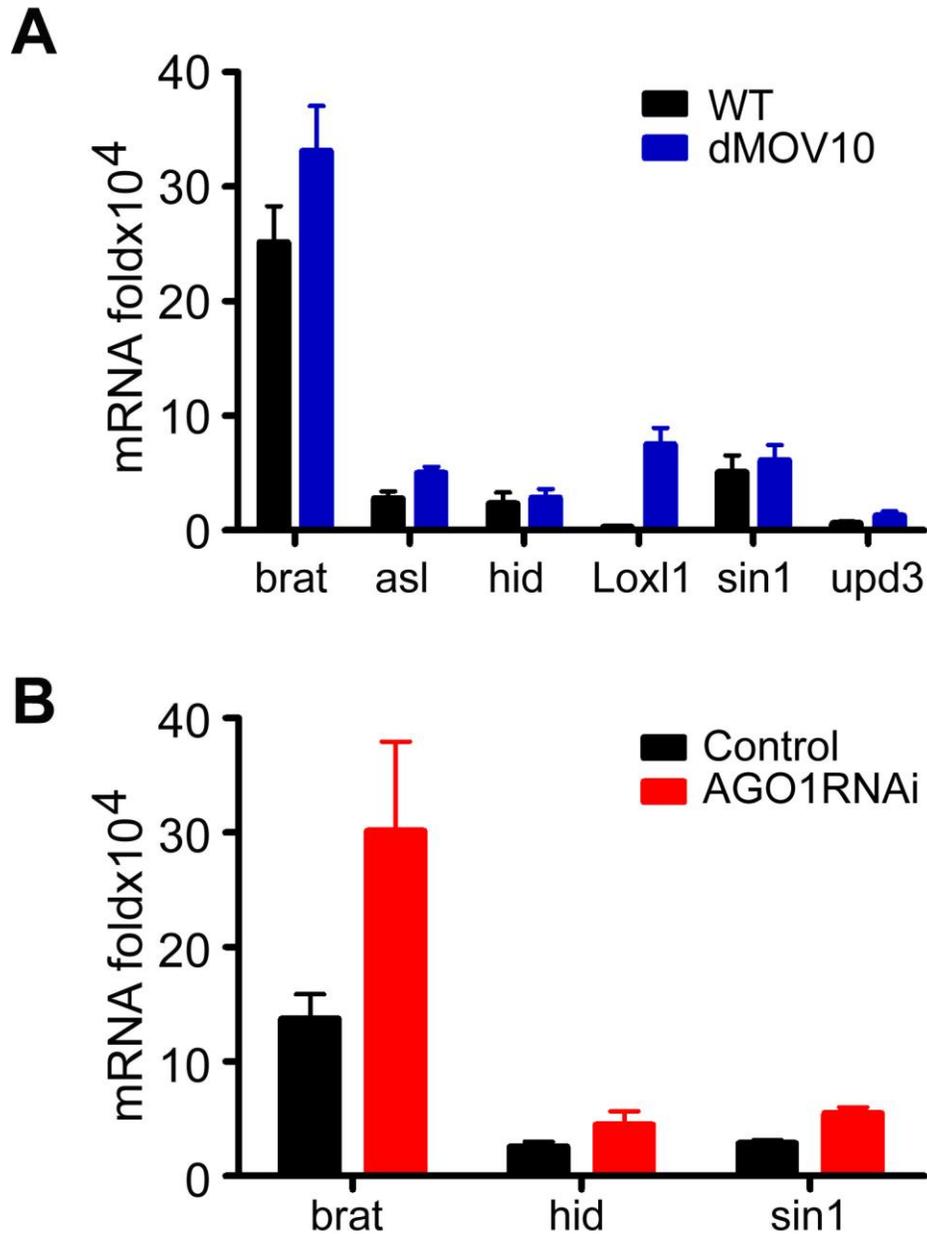
**Figure S2. Colocalization of AGO1 and dMOV10.**

A midgut sample from adult flies bearing AGO1-GFP and dMOV10-HA transgenes was dissected at day-3 after *Pe* infection. AGO1 and dMOV10 protein expression was revealed by staining with anti-GFP (green) and anti-HA (red) antibodies, respectively. Scale bar: 25  $\mu$ m.



**Figure S3. Validation of RNAi knockdown for *AGO1* and *Dad*.**

(A) Efficacy of *AGO1* RNAi knockdown. Relative signal intensity of *AGO1*-GFP in tdTomato-positive cells in control midgut (*esg<sup>ts</sup>>tdTomato*) and midgut expressing *UAS-AGO1 RNAi* (*esg<sup>ts</sup>>AGO1<sup>RNAi</sup>*) was quantified (see also Fig. 5C and D). \*\*\* $P < 0.001$ . The P value was calculated using the Wilcoxon rank sum test. (B-C) Wing discs showing the *Dad:GFP* expression. *Dad* is widely expressed in the wing disc with higher levels in the central domain (B). Expression of *UAS-Dad RNAi* using *ap-GAL4* depletes *Dad* expression in the dorsal compartment of the wing disc (C). D and V show the positions of the dorsal and ventral compartments, respectively. *Dad:GFP*, green; DAPI, blue. Scale bar: 50  $\mu\text{m}$ .



**Figure S4. Late miRNA targets are affected by *dMOV10* and *AGO1*.**

(A) RT-qPCR results comparing the levels of *brat*, *asl*, *hid*, *Loxl1*, *sin1*, and *upd3* mRNAs in wild-type (WT) and *dMOV10<sup>KO</sup>/dMOV10<sup>18</sup>* (*dMOV10*) at day-3 after *Pe* infection. Higher levels of these transcripts were detected in *dMOV10* mutants compared to wild-type control at various degrees. (B) RT-qPCR results comparing the levels of *brat*, *hid*, and *sin1* mRNAs in *esg<sup>ts</sup>-Gal4* (Control) and *esg<sup>ts</sup>>AGO1<sup>RNAi</sup>* (*AGO1RNAi*) at day-3 after *Pe* infection.