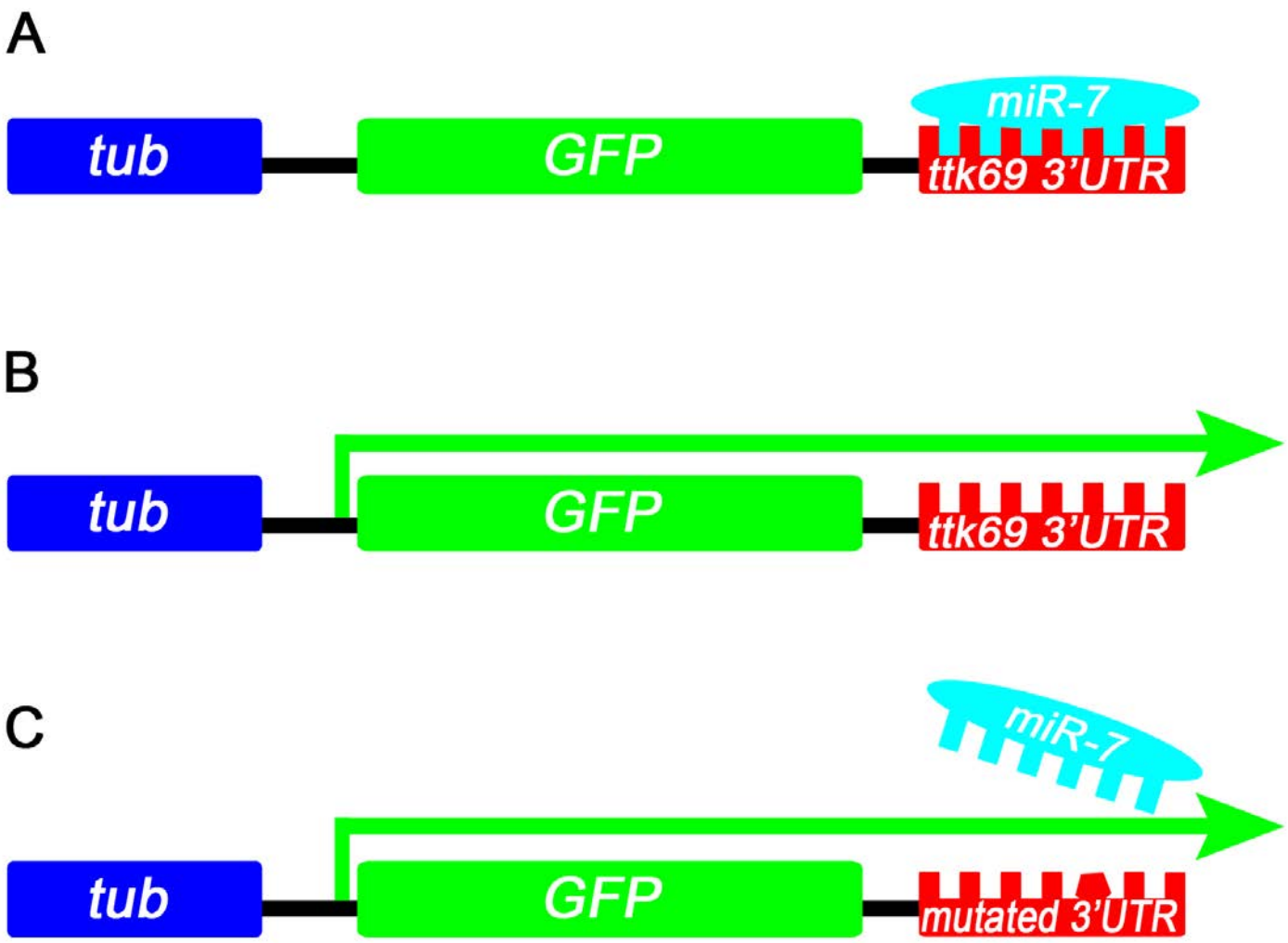

Fig. S1. The *ttk69* 3′UTR sensor, which contains a tubulin promoter, a GFP open reading frame and *ttk69* 3′ UTR. (**A**) In the wild type, miR-7 binds to the target sequence at the *ttk69* 3′UTR and represses GFP expression. (**B**) Without *miR-7*, GFP expression is derepressed. (**C**) miR-7 cannot bind to the mutated target sequence at the *ttk69* 3′UTR to repress GFP expression.

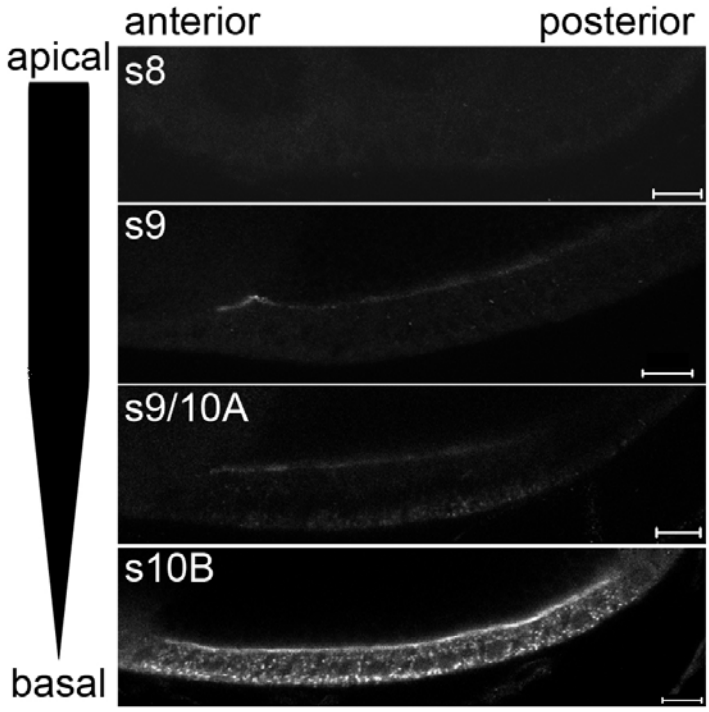

Fig. S2. The VM32E expression pattern during stages 8-10B of oogenesis. Posterior is towards the right. VM32E (white). Scale bars: 10 μm

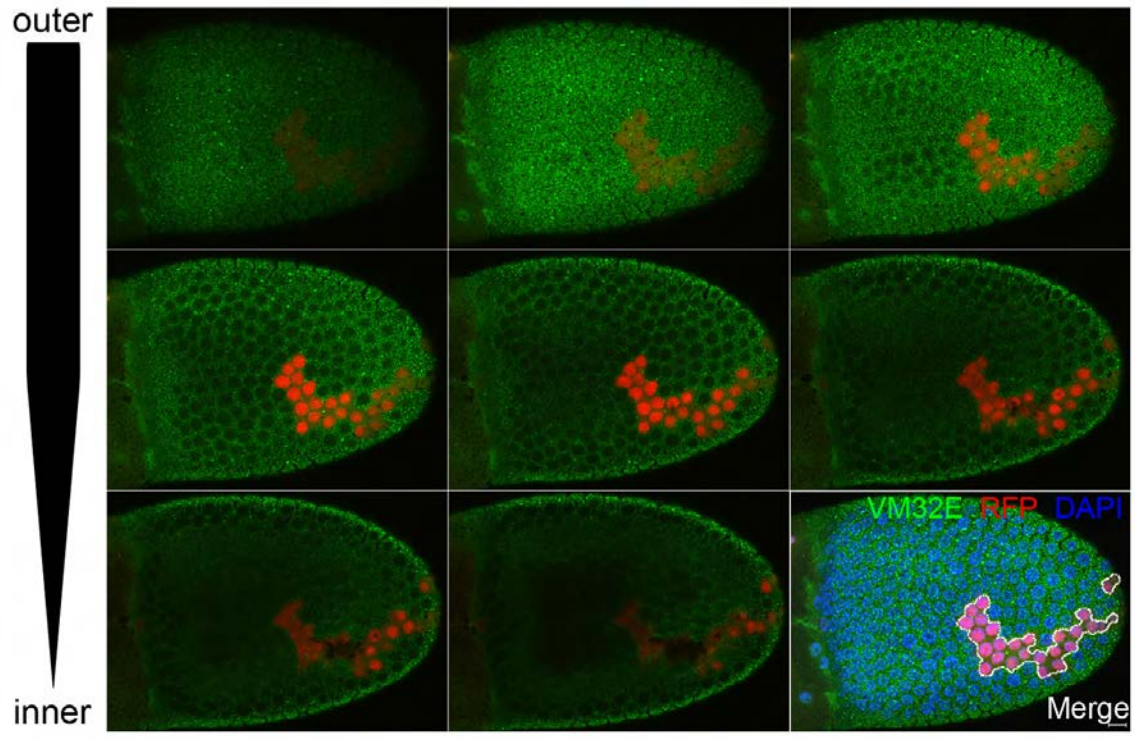

Fig. S3. A gallery of sectional images that were used to project Fig. 6B. Posterior is towards the right. VM32E, green; clone cells, red. Scale bars: 10 μm

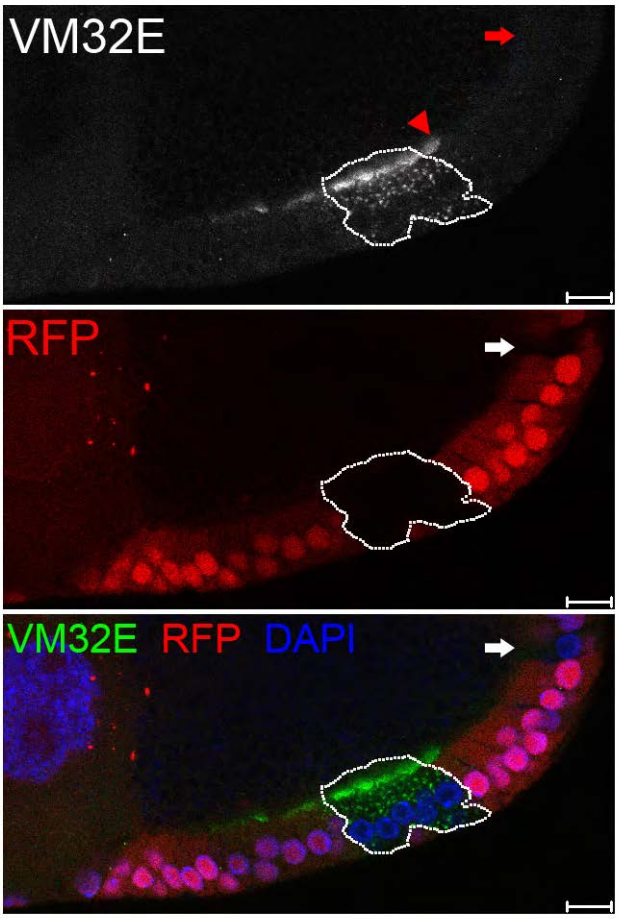

Fig. S4. A larger area of the egg chamber that contains the cropped image area Fig. 6C. This is a different section from the one shown in Fig. 6C. In addition to increased VM32E expression (green) in *miR-7* mutant cells (lack of RFP, outlined), high levels of VM32E appear to be diffused onto the surface of an adjacent wild-type cell (arrowhead). Posterior is towards the right. DAPI (blue) was used to mark cell nuclei. Scale bars: 10 µm

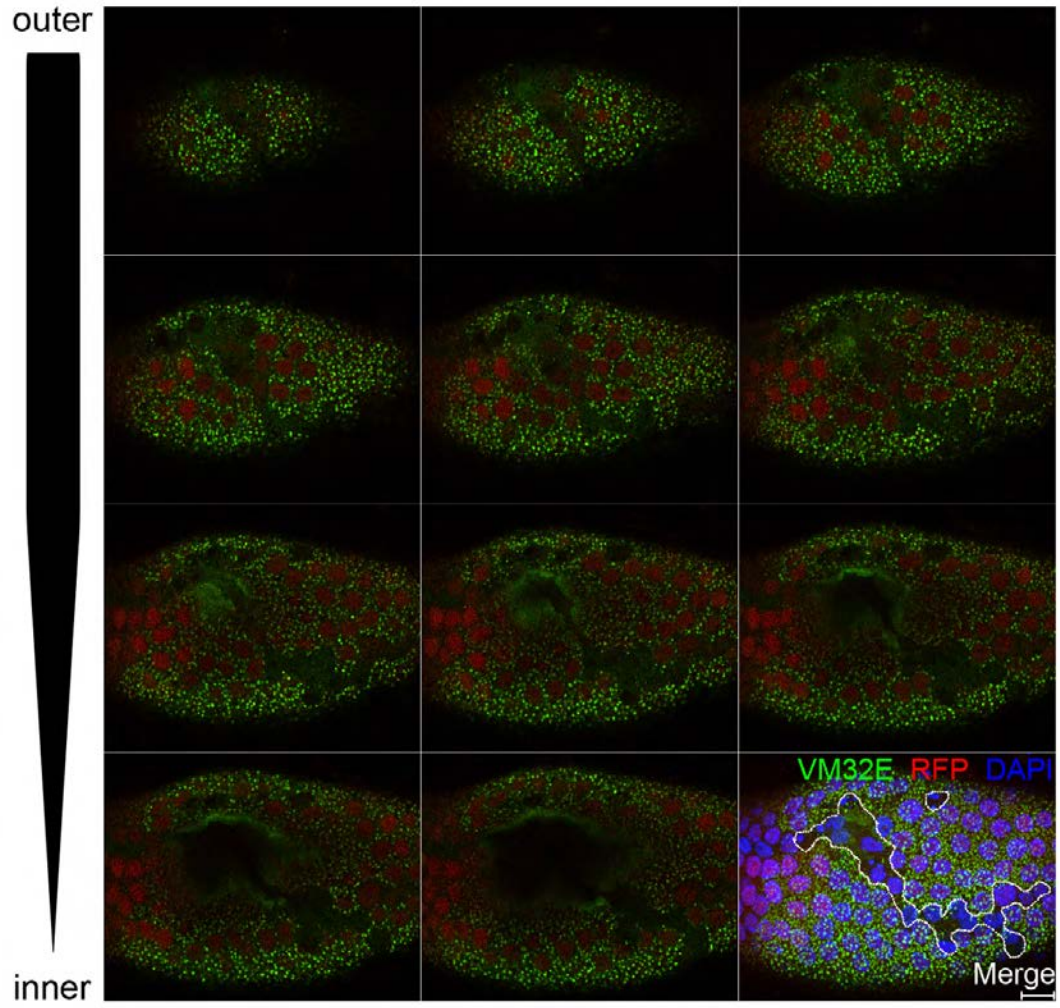

Fig. S5. A gallery of sectional images used to project Fig. 6E. Top and left panel is the outer layer. Posterior is towards the right. VM32E , green; clone cells, red. Scale bars: 10 μm

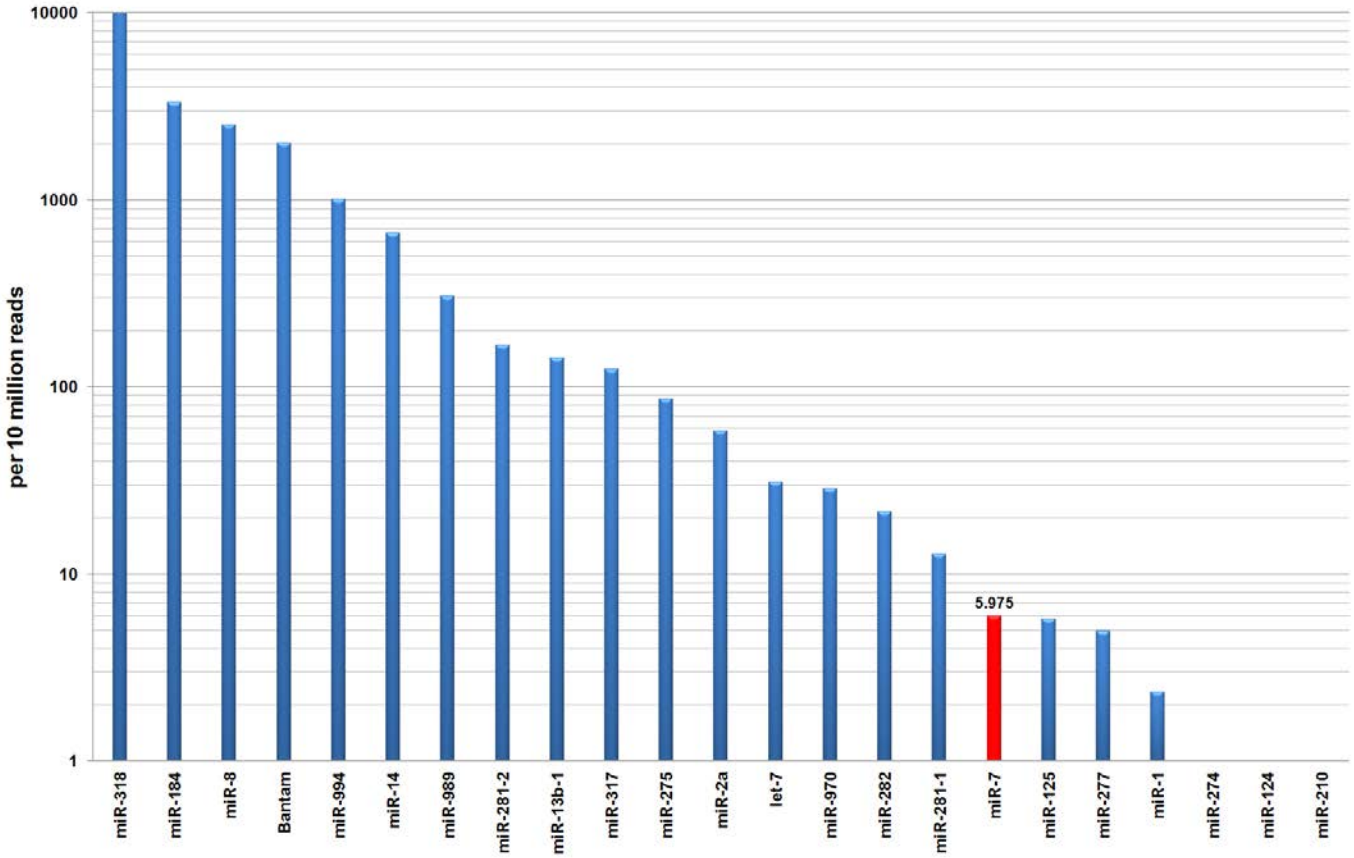

Fig. S6. Graphical results of relative expression levels of selected miRNAs in *w*^{1118} ovaries based on our RNA-seq analysis. Total RNA was isolated from *w*^{1118} ovaries by using the TRIzol reagent. Preparation of small RNA libraries was then carried out using the TreSeq small RNA preparation kit (Illumina) following the manufacturer's guide. Small RNA libraries (2 nM) were then sequenced on Illumina HiSeq 2000 system. Reads were demultiplexed and indexes removed with CASAVA v1.8.2 (Illumina). The 3′ adapter sequences were trimmed and reads with more than 10% containing a Sanger quality score of less than 25 were discarded with the FastX-toolkit (http://hannonlab.cshl.edu/fastx_toolkit/). We aligned the resulting reads to the FlyBase *Drosophila melanogaster* release 5.45 genome assembly (McQuilton et al., 2012) with Bowtie2 (Langmead and Salzberg, 2012) using default parameters. The per-base coverage was calculated per 10 million raw reads with BEDTools (Quinlan and Hall, 2010). The average coverage of two biological samples were used in subsequent data analysis. Different miRNAs are expressed at different levels in *Drosophila* ovaries. Among them, *miR-7* is expressed (read bar), but at a relatively low level. The *y*-axis shows the reads of each miRNA pre 10 million reads of total small RNA sequencing.