## Table S1. Cycle threshold (CT) of qPCR detecting expression levels of mature miRNAs *miR-8* and *miR-278*

Cycle threshold	miR-8	miR-278
FRT42D	22.95±0.039	30.64±0.156
FRT42DmiR-278 <sup>ĸo</sup>	22.55±0.569	39.22±0.390*

Mean±s.e. is shown.

\*The maximum PCR cycle is 40. If the fluorescent signal of the PCR products is not higher than the threshold after 40 cycles, the CT is assigned as 40.

## Table S2. Number of progeny generated by each GSC in regions 1-2A of germarium and number of progeny produced by the heterozygous neighboring control GSC

Genotypes (days after larval/pupal heat shock)	Cysts/GSC*
FRT42D/FRT42DGFP (14 d)	3.45±0.27
<i>FRT42D/FRT42D</i> (14 d)	3.60±0.14
<i>FRT42DmiR-278<sup>ko</sup>/FRT42DGFP</i> (14 d)	3.29±0.09
<i>FRT42DmiR-278<sup>k0</sup>/FRT42DmiR-278<sup>k0</sup></i> (14 d)	2.47±0.15
FRT42DmiR-278 <sup>Gal4KI</sup> /FRT42DGFP (14 d)	3.38±0.02
<i>FRT42DmiR-278<sup>Gal4KI</sup>/FRT42DmiR-278<sup>KIGal4</sup></i> (14 d)	2.66±0.11
<i>FRT42DmiR-7<sup>∆1</sup>/FRT42DGFP</i> (8 d)	4.40±0.11
<i>FRT42DmiR-7<sup>Δ1</sup>/FRT42DmiR-7<sup>Δ1</sup></i> (8 d)	4.33±0.29
CyO/+;FRT82BInR <sup>ex52.1</sup> /+ (8 d)	4.21±0.16
CyO/+;FRT82BInR <sup>ex52.1</sup> /FRT82BInR <sup>ex52.1</sup> (8 d)	1.68±0.09
FRT42Bdap <sup>4</sup> /+;FRT82BInR <sup>ex52.1</sup> /+ (8 d)	3.95±0.13
FRT42Bdap <sup>4</sup> /+;FRT82BInR <sup>ex52.1</sup> /FRT82BInR <sup>ex52.1</sup> (8 d)	2.37±0.20

\*Mean±s.e. of three repeats. At least ten mosaic germaria were counted in each repeat.