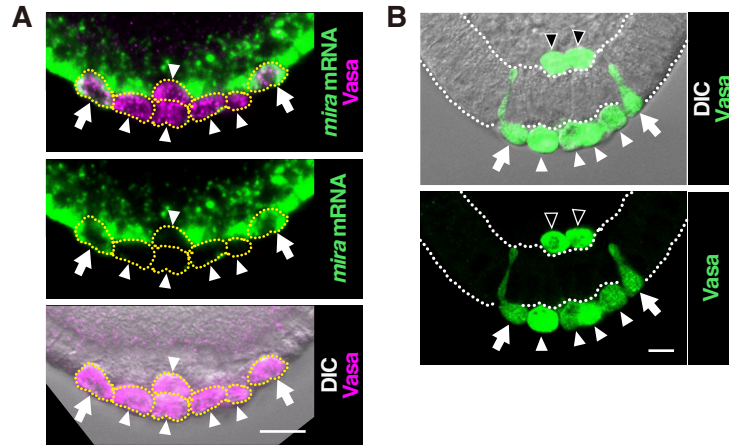




Appendix Figure S1. Misexpression of *mira* and protrusion formation were observed in peripheral pole cells in *pgc impa2OE* embryos.

(A) Representative confocal images of posterior pole region of *pgc impa2OE* embryos double-stained for *mira* mRNA and Vasa protein at stage 5 (n = 8 embryos, biological replicates). A DIC image merged with the Vasa signal is also shown (bottom). Yellow dotted lines outline pole cells.

(B) Representative images of posterior pole region of a *pgc impa2OE* embryos stained for Vasa protein at stage 6 (n = 8 embryos, biological replicates). A DIC image merged with the Vasa signal is also shown (upper). White dotted lines outline the somatic-cell layer. Black arrowheads indicate pole cells in the yolk region.

In **(A, B)**, arrows and arrowheads indicate peripheral and central pole cells, respectively.

Scale bars, 10 μ m.

23 **Appendix Table S1. Expression of transcripts encoding germ-plasm components**
24 **in *pgc⁻ impa2OE* and normal (*w*) pole cells.**

Transcript ID ^a	Gene symbol ^b	Log2 fold change ^c	FDR	TPM ^d (normal)	TPM ^d (<i>pgc⁻</i> <i>impa2OE</i>)
FBtr0088710	<i>gcl</i>	0.41	0.22	494.39	875.87
FBtr0339337	<i>gcl</i>	0.14	0.84	12.15	18.13
FBtr0083732	<i>nanos</i>	2.59	1.48E-23	86.87	692.81
FBtr0335019	<i>nanos</i>	-0.58	0.024	1869.52	1635.00
FBtr0081954	<i>osk</i>	0.63	0.021	81.61	162.83
FBtr0081956	<i>osk</i>	0.63	0.021	81.61	162.83
FBtr0080166	<i>piwi</i>	0.12	0.92	5.06	7.41
FBtr0340227	<i>piwi</i>	-0.42	0.14	109.53	106.93
FBtr0073763	<i>Prx2/jafrac1</i>	-0.19	0.64	257.92	296.67
FBtr0339699	<i>Prx2/jafrac1</i>	0.48	0.74	4.26	8.03
FBtr0339700	<i>Prx2/jafrac1</i>	0.77	0.87	0.93	2.53
FBtr0345161	<i>Prx2/jafrac1</i>	-3.25	0.11	5.00	1.15
FBtr0070848	<i>Tre1</i>	-0.22	0.53	260.74	291.22
FBtr0308339	<i>Tre1</i>	0.08	0.99	1.83	5.51
FBtr0340222	<i>Tre1</i>	-0.58	0.83	2.01	1.80
FBtr0088506	<i>wun2</i>	-0.18	0.64	96.64	115.77

25 ^a Transcript ID in Flybase.

26 ^b Gene symbol of corresponding transcript.

27 ^c log₂(fold change) values (*pgc⁻ impa2OE* / normal) were calculated using edgeR.

28 ^d TPM represents the average TPM (the transcripts per million) value among three
29 biological replicates of normal or *pgc⁻ impa2OE* pole cells.

30

31 **Appendix Table S2. Transcripts used for the calculation of the ‘mRNA level’ in**
32 **Figure 5B,C.**

mRNA ^a	List of transcripts examined ^b
<i>mira</i>	FBtr0083847, FBtr0083848, FBtr0335243
<i>gcl</i>	FBtr0088710, FBtr0339337
<i>nanos</i>	FBtr0083732, FBtr0335019
<i>osk</i>	FBtr0081956, FBtr0081954
<i>ovo-B</i>	FBtr0070740, FBtr0100408
<i>piwi</i>	FBtr0080166, FBtr0340227
<i>Prx2</i>	FBtr0073763, FBtr0073764, FBtr0339699, FBtr0339700, FBtr0345161
<i>Tre1</i>	FBtr0070848, FBtr0340222, FBtr0308339
<i>wun2</i>	FBtr0088506, FBtr0339380

33 ^a Names of mRNAs examined in Fig. 5.

34 ^b 'Transcript ID' in Flybase of corresponding transcripts are shown.