

Supplementary Table 2. GO analysis of genes differentially expressed in *piwi-MatKD* #2 0-1.5h embryos, as compared to *GFP-MatKD* embryos

Up-regulated genes in <i>piwi-MatKD</i> #2 vs <i>GFP-MatKD</i>						
GO biological process	#	# in reference	# expected	Fold Enrichment	raw P value	FDR
proteasomal ubiquitin-independent protein catabolic process	16	14	0.19	72.62	6.84E-20	4.08E-17
proteasomal protein catabolic process	194	38	2.34	16.26	2.02E-33	7.82E-30
proteolysis involved in cellular protein catabolic process	290	39	3.49	11.16	9.03E-29	9.99E-26
cellular macromolecule catabolic process	396	40	4.77	8.38	3.37E-25	2.61E-22
protein catabolic process	307	40	3.7	10.81	4.65E-29	6.00E-26
positive regulation of RNA polymerase II transcriptional preinitiation complex assembly	8	7	0.1	72.62	1.71E-10	6.96E-08
proteasome assembly	13	8	0.16	51.07	5.78E-11	2.49E-08
proteasome-mediated ubiquitin-dependent protein catabolic process	185	38	2.23	17.05	4.22E-34	3.27E-30
signaling	1033	41	12.45	3.29	4.59E-12	2.09E-09

Down-regulated genes in <i>piwi-MatKD</i> #2 vs <i>GFP-MatKD</i>						
GO biological process	#	# in reference	# expected	Fold Enrichment	raw P value	FDR
posterior Malpighian tubule development	3	3	0.07	45.83	1.83E-04	6.43E-03
Malpighian tubule development	65	16	1.42	11.28	1.09E-11	3.84E-09
renal tubule development	65	16	1.42	11.28	1.09E-11	3.67E-09
epithelium development	903	48	19.7	2.44	1.22E-08	1.26E-06
renal system development	74	16	1.61	9.91	5.87E-11	1.47E-08
animal organ development	1126	70	24.57	2.85	7.49E-16	1.16E-12
sex determination, establishment of X:A ratio	5	5	0.11	45.83	9.82E-07	6.98E-05
primary sex determination, soma	11	5	0.24	20.83	1.53E-05	7.61E-04
somatic sex determination	18	5	0.39	12.73	1.04E-04	3.95E-03
primary sex determination	16	5	0.35	14.32	6.54E-05	2.63E-03
amioserosa formation	8	7	0.17	40.1	1.03E-08	1.11E-06
gastrulation involving germ band extension	43	12	0.94	12.79	1.32E-09	1.96E-07
gastrulation with mouth forming first	43	12	0.94	12.79	1.32E-09	1.93E-07
anatomical structure formation involved in morphogenesis	485	34	10.58	3.21	4.36E-09	5.63E-07
positive regulator of activin receptor signaling pathway	4	3	0.09	34.37	3.16E-04	1.02E-02