

**Table S1. Analysis of fixed wild-type, *zyg-11(RNAi)*, *cul-2(RNAi)* and *cyb-3(RNAi)* embryos**

	Meiosis I		Metaphase II		Metaphase II late		Anaphase II		First S phase		First M phase*		Two-cell stage	
	%(MI)	<i>n</i>	%(MI)	<i>n</i>	%(MI)	<i>n</i>	%(MI)	<i>n</i>	%(MI)	<i>n</i>	%(MI)	<i>n</i>	%(MI)	<i>n</i>
Wild type	100	38	32	12	0	0	42	16	82	31	32	12	84	32
<i>zyg-11(RNAi)</i>	100	30	97	29	73	22	147	44	87	26	23	7	73	22
<i>cul-2(RNAi)</i>	100	35	103	36	97	34	114	40	80	28	23	8	77	27
<i>cyb-3(RNAi)</i>	100	25	168	42	0	0	44	11	160	40	108	27	140	35

Embryos of the indicated genotypes were fixed and stained with anti- $\alpha$ -tubulin antibodies, and counterstained with Hoechst to view DNA; staging was as in Table 1, except that metaphase I and anaphase I were pooled into the meiosis I category.

\*One-cell stage embryos after NEBD were placed into M phase category.

As the time between fertilization and the end of meiosis I is not altered following inactivation of *zyg-11*, *cul-2* or *cyb-3* (Fig. 1), we normalized each category to the number of embryos in meiosis I [% (MI)]. For instance, whereas metaphase II represents 32% (MI) for wild type, it corresponds to 170% (MI) in the case of *zyg-11(RNAi)* (pooling the Metaphase II and Metaphase II late categories).