Table S1. Meiotic crossovers on chromosome *2L* in *mei-218^{FL}* and *mei-218$^{\Delta N}$*.

Interval	*mei-218^{FL}*	*mei-218$^{\Delta N}$*	Fold Change	*P* Value
net-ho	4.87 (1.53)	5.9 (1.08)	1.21	n.s.
ho-dp	5.79 (1.66)	7.49 (1.21)	1.29	<0.0001
dp-b	25.39 (3.1)	21.87 (1.91)	0.86	<0.0001
b-pr	11.71 (2.29)	13.55 (1.58)	1.16	n.s.
pr-cn	6.32 (1.73)	7.11 (1.18)	1.13	n.s.
Total *n*	759	1815		

Crossover frequency shown as map units (centimorgans). Numbers in parentheses represent 95% confidence intervals. Fold change = *mei-218^{FL}* / *mei-218$^{\Delta N}$*. *P* values determined by chi-squared tests. Figure 2 shows distributions for *mei-218^{FL}* and *mei-218$^{\Delta N}$*.

Table S2. Nondisjunction of *WT*, *rec$^-$ / rec$^+$*, and *rec^{DA} / rec$^+$*.

Genotype	*XX* females	*XY* males	*XXY* females	*XO* males	Total *n*	NDJ
wild type (y w)	1551	1481	0	1	**3034**	0.07%
rec$^-$ / rec$^+$	880	775	0	0	**1655**	0%
rec^{DA} / rec$^+$	1072	863	10	4	**1963**	1.43%

XX females and *XY* males are normal, whereas *XXY* females and *XO* males are karyotypes genotypes resulting from nondisjunction. Total *n* calculates in exceptional progeny that do not survive (*XXX* and *XO*).

Supplemental Table S3. Crossovers in each interval on chromosome *2L* for all mutants discussed.

Progeny		WT	*mei-218*	*mei-218* [FL]	*mei-218* [ΔN]	*rec*	*rec*[KA]	*rec*[DA]	*rec*[DA] / *rec*[+]	*mei-9*	*mei-9; rec*	*mei-9; rec*[KA]	*mei-9; rec*[DA]	*Blm*	*Blm rec*	*Blm rec*[KA]	*Blm rec*[DA]
	Parental	2376	1693	396	942	2129	1061	3452	1597	2366	490	3650	1360	844	705	684	445
SCO	1 (*net-ho*)	176	4	24	75	8	54	3	73	6	0	7	0	23	31	27	13
	2 (*ho-dp*)	290	6	33	93	10	100	5	137	11	3	13	1	22	29	35	10
	3 (*dp-b*)	1099	16	168	315	53	464	29	679	40	11	43	5	89	136	116	98
	4 (*b-pr*)	154	18	65	168	13	94	12	201	8	5	20	5	104	103	95	78
	5 (*pr-cn*)	39	7	29	80	20	44	6	30	2	2	19	4	61	87	78	64
DCO	1 and 2	1	0	0	0	0	0	0	0	0	0	0	0	1	0	4	0
	1 and 3	11	0	3	13	0	7	0	4	0	0	0	0	4	11	4	0
	1 and 4	10	0	4	11	0	4	0	2	0	0	0	0	2	7	0	3
	1 and 5	2	0	6	8	0	0	0	2	0	0	0	0	1	0	3	2
	2 and 3	6	0	3	13	0	3	0	3	0	0	0	0	1	5	1	6
	2 and 4	7	0	6	18	0	1	0	9	0	0	0	0	2	7	5	2
	2 and 5	13	0	1	12	0	2	0	3	0	0	0	0	2	2	1	4
	3 and 4	19	0	10	38	0	14	0	14	0	0	0	0	5	19	5	18
	3 and 5	17	0	8	18	0	4	0	7	0	0	0	0	7	21	17	12
	4 and 5	2	0	2	11	0	3	0	3	0	0	0	0	2	8	9	10
	TCO	0	0	1	0	0	0	0	0	0	0	0	0	1	10	7	7
	Total *n*	4222	1744	759	1815	2233	1855	3507	2764	2433	511	3752	1375	1171	1181	1091	774

Each row shows the number of parental (P), single (SCO), double (DCO), and triple (TCO) crossovers for each genotype and each mutant discussed in the article. Total *n* represents all parental and recombinant flies scored for each genotype. Wild-type data are from Hatkevich *et al.* 2017. Data for *mei-218 Blm*, and *Blm rec* are from Kohl, Jones, and Sekelsky 2012. The *mei-9; rec* experiment had six apparent double crossovers and one triple crossovers. Because all of these were *b pr*[+] *cn* and no multiple crossover events were observed in the 2.7x larger dataset of Blanton *et al.* (2005), we suspect these were from some non-meiotic event(s); these flies were therefore removed from this analysis.