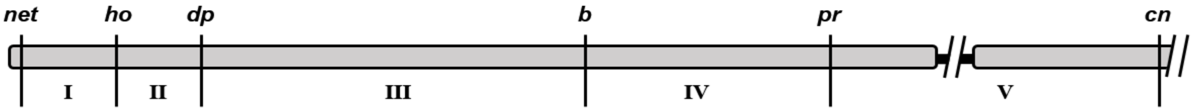
Table S1. Meiotic crossovers on chromosome *2L*.



Progeny		**Maternal Genotype**					
		WT1	***WT2***	***WT1+2***	***mei-41***	***mei-9***	***mei-9 mei-41***
Parental		1053	1223	2376	6667	2366	904
SCO	I	70	106	176	87	6	22
	II	127	163	290	119	11	5
	III	497	602	1099	530	40	69
	IV	89	65	154	286	8	39
	V	23	16	39	71	2	11
DCO	I / II	1	0	1	3	0	3
	I / III	4	7	11	6	0	0
	I / IV	7	3	10	4	0	0
	I / V	0	2	2	1	0	0
	II / III	1	5	6	7	0	2
	II / IV	5	2	7	2	0	1
	II / V	8	5	13	2	0	0
	III / IV	10	9	19	8	0	0
	III / V	7	10	17	6	0	1
	IV / V	1	1	2	2	0	1
TCO		0	0	0	0	0	1
n		1903	2319	4222	7801	2433	1059

Table S1. Meiotic crossovers on chromosome *2L*. Each row lists the number of total progeny from parental or single (SCO), double (DCO), or triple (TCO) crossover classes for wild-type (*WT*) and *mei-41* null mutants. Intervals I to V correspond to schematic above. Wild-type data were collected by different individuals in different years (see Material and Methods); the individual datasets and the summed set, which was used in all analyses, are given. The TCO in *mei-9 mei-41* was intervals I/II/IV. Wild-type data are from Hatkevich *et al.* (2017), used with permission (RightsLink license 4217090536151, 27 Oct 2017).

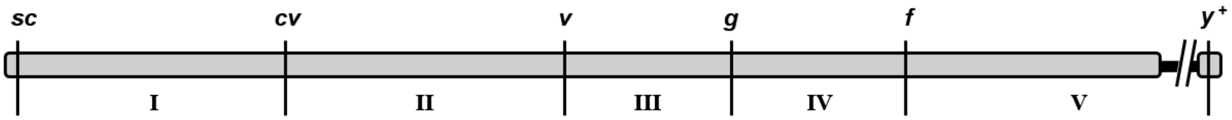


Table S2. Meiotic crossovers on chromosome *X*.

Progeny		**Maternal Genotype**	
		WT	***mei-41***
Parental		1015	3929
SCO	I	148	178
	II	333	370
	III	162	121
	IV	155	174
	V	166	258
DCO	I–II	5	15
	I–III	18	14
	I–IV	20	8
	I–V	29	10
	II–III	25	20
	II–IV	44	22
	II–V	26	24
	III–IV	6	7
	III–V	14	6
	IV-V	10	11
TCO		3	7
n		2179	5174

Table S2. Meiotic crossovers on chromosome *X*. Each row lists the number of progeny from parental or single (SCO), double (DCO), or triple (TCO) crossover classes for wild-type (*WT*) and *mei–41* null mutants. Intervals I to V correspond to schematic above. The TCOs in wild/type flies were one each in intervals (II/III/V), (II/IV/V), and (III/IV/V). TCOs in *mei/41* were one each intervals (I/II/III), (I/II/IV), (I/II/V), (I/III/V), and (II/IV/V) and two each in intervals (II/III/IV) and (II/IV/V). Wild/type data are from Hatkevich *et al.* (2017), used with permission (RightsLink license 4217090536151, 27 Oct 2017).

Table S3a. Genetic distances and crossover densities on chromosome *2*.

Genotype	Interval on Chromosome *2*					
	I	II	III	IV	V	I - V
Genetic Size (cM ±95% CI)						
WT	4.74 ±0.64	7.51 ±0.80	27.29 ±1.35	4.55 ±0.52	1.73 ±0.39	45.81 ±0.90
mei-41	1.29 ±0.25	1.70 ±0.28	7.14 ±0.57	3.87 ±0.43	1.05 ±0.23	15.06 ±0.79
mei-9 mei-41	2.46 ±0.93	1.13 ±0.64	6.80 ±1.52	3.87 ±1.16	1.32 ±0.69	15.58 ±2.18
mei-9	0.25 ±0.20	0.46 ±0.27	1.64 ±0.51	0.33 ±0.23	0.08 ±0.11	2.75 ±0.65
Mb w/o TEs	2.312	2.004	9.006	5.639	9.438	28.399
WT	2.05 ±0.28	3.75 ±0.40	3.03 ±0.15	0.81 ±0.09	0.18 ±0.04	1.61 ±0.05
mei-41	0.56 ±0.09	0.86 ±0.14	0.79 ±0.06	0.69 ±0.08	0.11 ±0.03	0.53 ±0.03
mei-9 mei-41	1.06 ±0.40	0.57 ±0.33	0.75 ±0.16	0.69 ±0.19	0.14 ±0.07	0.55 ±0.08
mei-9	0.11 ±0.09	0.23 ±0.14	0.18 ±0.05	0.06 ±0.04	0.01 ±0.01	0.10 ±0.03
Mb w/ TEs	2.394	2.052	9.292	6.253	11.724	31.715
WT	1.98 ±0.27	3.66 ±0.39	2.94 ±0.15	0.73 ±0.10	0.15 ±0.04	1.44 ±0.04
mei-41	0.54 ±0.10	0.83 ±0.14	0.77 ±0.06	0.62 ±0.08	0.09 ±0.02	0.47 ±0.02
mei-9 mei-41	1.03 ±0.39	0.55 ±0.31	0.73 ±0.16	0.62 ±0.19	0.11 ±0.06	0.49 ±0.07
mei-9	0.10 ±0.08	0.22 ±0.13	0.18 ±0.06	0.05 ±0.03	0.01 ±0.01	0.09 ±0.02

Table S3b. Genetic distances and crossover densities on chromosome *X*

Genotype	Interval on Chromosome *X*					
	I	II	III	IV	V	I - V
Genetic Size (cM ±95% CI)						
WT	10.09 ±1.26	20.00 ±1.68	10.41 ±1.28	10.92 ±1.31	11.42 ±1.34	62.84 ±2.03
mei-41	4.40 ±0.67	8.87 ±0.77	3.34 ±0.49	4.39 ±0.56	6.07 ±0.65	27.09 ±1.21
Mb w/o TEs	5.018	5.089	2.732	3.385	5.568	21.792
WT	2.01 ±0.25	3.93 ±0.33	3.81 ±0.47	3.23 ±0.39	2.05 ±0.24	2.88 ±0.09
mei-41	0.88 ±0.11	1.74 ±0.15	1.22 ±0.18	1.30 ±0.17	1.09 ±0.12	1.24 ±0.05
Mb w/ TEs	5.295	5.233	2.810	3.521	6.291	23.150
WT	1.91 ±0.24	3.82 ±0.32	3.71 ±0.46	3.10 ±0.37	1.82 ±0.22	2.71 ±0.08
mei-41	0.84 ±0.11	1.69 ±0.14	1.19 ±0.17	1.25 ±0.16	0.96 ±0.10	1.17 ±0.05

Table S3. Genetic distances and crossover densities. The top section of each table gives calculated genetic distances (in cM, with 95% confidence intervals (CI); see Materials and Methods) for the five intervals on *2L* (see Tables S1) and *X* (see Table S3). The rightmost column has the summed distance across all five intervals. The lower two sections give crossover density (cM/Mb) calculated without including transposable elements (middle) or including transposable elements (bottom). Transposable element lengths are from the *Drosophila melanogaster* reference genome and are not necessarily the same in the chromosomes we used.

Table S4. Progeny counts from *dp–Sp–b* interference experiment

Progeny		Maternal Genotype	
		WT	***mei-41^{29D}***
Parental	+ + +	1510	5200
	dp Sp b	1897	3686
SCO	+ *Sp b*	172	195
	dp + +	144	164
	+ + *b*	344	272
	dp Sp +	258	297
DCO	+ *Sp* +	4	17
	dp + *b*	1	5
n		3330	9836

Table S4. Progeny counts from *dp–Sp–b* interference experiment. Each row lists the number of progeny from parental and single (SCO), or double (DCO) classes for wild-type (*WT*) and *mei-41* null mutants.

Table S5a. *X* nondisjunction.

	Maternal Genotype	Normal Progeny	Nondisjunction Progeny		*X* NDJ (%)	
			XO ♂♂	*XXY* ♀♀		
1	*mei-41*^{1}	815	24	15	8.7	± 2.7
2	*mei-41*^{29D}	3791	144	155	13.6	± 1.5
3	*mei-9*^{a}	287	25	27	26.5	± 6.7
4	*mei-9*^{a} *mei-41*^{29D}	499	27	20	15.9	± 4.4
5	*mei-9*^{a} *mei-41*^{29D} / *mei-9*^{a}	354	31	37	27.7	± 6.1
6	*mei-9*^{a} *mei-41*^{29D} / *mei-9*^{a}	521	36	52	25.3	± 4.9

Table S5a. *X* nondisjunction. *X* chromosome nondisjunction (NDJ) was scored as described in Materials and Methods. Genotypes 1-4 were homozygous for the indicated mutant alleles. All *mei-41*^{29D} experiments had the *M*{*UASp::mei-41*} and *P*{*mata::GAL4*} transgenes described in the text. Genotypes 5 and 6 were made by crossing each of the two stocks that were used to generate *mei-9 mei-41* double mutants to *mei-9*^{a} single mutants to test for the presence of *mei-9*^{a} in the stock. The males used to generate genotype 5 were *y M*{*UASp::mei-41*} *mei-9*^{a} *mei-41*^{29D} on the *X* chromosome. The males used to generate genotype 6 were *y mei-9*^{a} *mei-41*^{29D} on the *X*. Statistical analyses are in Table S5b, below. *p* values are not corrected for multiple comparisons, but such corrections would not change any conclusions.

Table S5b. Statistical comparisons of *X* nondisjunction.

Genotypes	*p*	Interpretation
1 *vs.* 2	0.0020	NDJ is significantly higher in *mei-41*^{29D} than in *mei-41*^{1}, supporting the conclusion that *mei-41*^{1} is a hypomorphic allele.
2 *vs.* 3	0.0002	NDJ is significantly higher in *mei-41*^{29D} than in *mei-9*^{a}. (Genotypes 5 and 6 were homozygous for *mei-9*^{a} and heterozygous for *mei-41*^{29D}
2 *vs.* 5	<0.0001	
2 *vs.* 6	<0.0001	
2 *vs.* 4	0.3420	NDJ in *mei-9*^{a} *mei-41*^{29D} double mutants is not significantly different from NDJ in *mei-41*^{29D} single mutants.
3 *vs.* 5	0.8033	NDJ is not significantly different between the three *mei-9* single mutants, confirming the presence of the *mei-9*^{a} mutation in the stocks used to generate *mei-9*^{a} *mei-41*^{29D} double mutants (also confirmed by allele-specific PCR).
3 *vs.* 6	0.7516	
5 *vs.* 6	0.5324	

Table S5b. Statistical comparisons of *X* nondisjunction. Methods of Zeng *et al.* (2010) was used to calculate *X* nondisjunction (NDJ) with 95% confidence intervals and to calculate *p* values based *Z* tests. *p* values are not corrected for multiple comparisons, but such corrections would not change any conclusions.

Hatkevich, T., K. P. Kohl, S. McMahan, M. A. Hartmann, A. M. Williams, and J. Sekelsky, 2017 Bloom syndrome helicase promotes meiotic crossover patterning and homolog disjunction. Curr Biol **27:** 1-5.

Zeng, Y., H. Li, N. M. Schweppe, R. S. Hawley and W. D. Gilliland, 2010 Statistical analysis of nondisjunction assays in *Drosophila*. Genetics **186:** 505-513.