

**Table S1. Phenotypic crossover mapping in WT and *Blm***

Genotype	Arm	Interval	Size (Mb) <sup>1</sup>	cM / Mb
WT	X	<i>sc - cv</i>	5.56	3.23
WT	X	<i>cv - v</i>	4.96	3.81
WT	X	<i>v - g</i>	2.81	3.93
WT	X	<i>g - f</i>	3.50	2.01
WT	X	<i>f - 20C</i> <sup>2</sup>	5.57	1.83
WT	X	<i>20C - end</i> <sup>3</sup>	0.72	0.00
WT	2L	<i>net - ho</i>	0.08	2.05
WT	2L	<i>ho - dp</i>	2.43	3.75
WT	2L	<i>dp - b</i>	4.48	3.03
WT	2L	<i>b - pr</i>	13.82	1.70
WT	2L	<i>pr - end</i> <sup>4</sup>	3.45	0.26
WT	2R	<i>end - cn</i>	7.78	0.26
WT	2R	<i>cn - vg</i>	12.88	1.40
WT	2R	<i>vg-Bc</i>	17.89	3.40
WT	2R	<i>Bc - px</i>	22.49	3.47
WT	3L	<i>ru - h</i>	7.31	3.23
WT	3L	<i>h - th</i>	7.37	2.81
WT	3L	<i>th - st</i>	0.45	0.31
WT	3L	<i>st - end</i>	11.61	0.19
WT	3R	<i>end - cu</i>	11.20	0.17
WT	3R	<i>cu - sr</i>	7.70	0.99
WT	3R	<i>sr - e</i>	3.14	2.10
WT	3R	<i>e - ca</i>	8.58	3.65
<i>Blm</i>	2L	<i>net - ho</i>	5.56	1.17
<i>Blm</i>	2L	<i>ho - dp</i>	4.96	1.21
<i>Blm</i>	2L	<i>dp - b</i>	2.81	0.86
<i>Blm</i>	2L	<i>b - pr</i>	3.50	1.31
<i>Blm</i>	2L	<i>pr - cn</i>	5.57	0.57

<sup>1</sup> Interval sizes were determined from approximate mid-points of genes on genome assembly. "End" refers to the most proximal PCR marker assembled genome was included (not the unassembled satellite sequences).

<sup>2</sup> The 20C location is defined by the insertion of *M{3xP3-RFP.attP}ZHb0C*.

<sup>3</sup> XR refers to the *Dp(1;1)y+* insertion to the right of the centromere.

**Table S2. Primers used in fine mapping of crossovers**

Arm	Interval Boundary	Genomic Location	Forward Primer Sequence	Genomic Location	Reverse Primer Sequence
X	1 prox.	22649701	GATCTTTGCAATCCACGGAAG	22649922	CGCCAGAATCATGGCTGTG
X	1 - 2	21400408	CAGTCGACACGGCCTTCAC	21400805	GGACTACAGGAGAACTGAG
X	2 - 3	20596878	CGTCGTAGCTTTACATGAC	20597242	CGATCTCTGTTCCAGTGC
X	3 - 4	20065852	GTTGAACTTAATGGTCTTCTTAAAG	20066087	CTGGCCTTTTCATCACGTTTG
X	4 - 5	19541473	CAAATGTTTATAGATGTCACAG	19541898	CTTCAAACGAGGCAACCGTGC
X	5 - 6	18947554	CCACATGGCCCTGTAATC	18948141	CTTTAAGAGAATCACGCAGTG
X	6 - 7	18552184	CACGTTGCGCAAGTTGCC	18552373	GCACAGAGTGGCCATGATATG
X	7 - 8	18152965	CATGGATCGGCGAGAATCC	18153356	AAGCGCTAGTTGCTGGCTG
X	9 distal	17476509	CGTCTCTTTTGCCGCCTATG	17477114	TTCGTTCAAGGTTGTGTGTTAC
2L	1 prox.	23424573	TTTGTGGACTAACATTGGA	23424795	TTAGGACGAAACACAATTGG
2L	1 - 2	22073133	TACTCTAAGATTAGTGGATAT	22073251	TGACTACCGCACTTTCAAC
2L	2 - 3	21675849	GGACTAATACCATTGTAAAG	21676016	CCTATACTGGCCAGTCTCC
2L	3 - 4	21108908	GTAATCAGCTGTTGAAAAC	21109483	GAATTCGGCGTTCCTTAATCG
2L	4 - 5	20618378	GCCTGCGGCCGTGTCATG	20618548	CATGTTGCCAACGATTCCGG
2L	5 - 6	20041502	CCATTCCGATCCACTTGCG	20042067	CCACTTTCTGCTCTCCGC
2L	6 - 7	19070295	GCACGCACATGGTCAACTC	19070868	CATGTGGACAATTGGAACC
2L	7 - 8	17836891	CGCGAACTTCTCACACTC	17837185	AACAGCTCTGGCGGGAAATC
2L	8 - 9	17492746	CATCAGCTAATGGCAGGAGTTTG	17493189	GACTCAAGCCAGTCGAGCG
2L	9 - 10	17153268	GGGTTGCCAATTCTGCTTC	17153555	AAAGCCAGCCAACGGAACT
2L	10 - 11	16809718	CGTCTGTCTGTACGTTATTC	16810155	TCCTTCATTAAGCAATCGC
2L	11 - 12	16583646	GCCAATGCTGGGTCCACTC	16584204	CAGACACGCCACGAGGATGAC
2L	12 - 13	16339184	GATACGCTTCGCTGTGAATAAC	16339575	GTCCGGGATCTAGTGGTGC
2L	13 - 14	15866603	GTAGCTACCACCTGGATTAG	15867237	CACAGCCCATTTCTCAAG
2L	14 distal	14707226	GCGAGCCTGAAGGTTATCG	14707459	CGTGTAATCATCTCCTACC
2R	1 prox.	639629	GGAAGTTAGAGCTCAGACACAA	640253	GACTCTCTAATTCGTGGAC
2R	1 - 2	1097861	GCTCTCCCCTCTATTAGC	1098657	GTAAATTGGGTAAACATCGTCA
2R	2 - 3	2598095	GAAGGAGACAATTAATCAC	2598893	AGCAATCTACCCTACCAAGG
2R	3 - 4	3076813	CTCAAACCGCGTAGCCATC	3077426	ACACTTCCCTGTGGAATTCTT
2R	4 - 5	4377398	CTAGATGTTTCTACAGTTTC	4377786	GATACCCGTTACTGAGTGTGG
2R	5 - 6	5043317	CAAACCTGTAAGTCTGCAC	5043483	TTCTTATATCTACCGTAAAATGC
2R	6 - 7	5476458	GATGACCTCCAGTGCGAATC	5476859	GTCGTCAAGTGATGCTGCAC
2R	7 - 8	6111492	GTAGAAGTAGAAGATCGACG	6112190	GAAGGTTGTGGCCTGACTC
2R	8 - 9	6784660	CAAGTGCTGGGTCAATGTG	6785039	GATGTTTTCCGGCCCATTTC
2R	9 - 10	7459353	GCTAAAGTCTAGGCATATTTG	7459964	CAGAAGATTCGACGAAGCC
2R	10 - 11	7989635	AGTGTGGTGCCGTGTGGC	7990035	GATCGCTGGAACAGGTTG
2R	11 - 12	8338722	GACTTGACTTTCTTAAGTCTTAC	8338935	CCTGCAAGAAATTAGCGCCTG
2R	12 - 13	8769813	GGATTTTGAACATAGCCTTACG	8770212	CCAGCTGCCAGACGATTAAG
2R	13 - 14	9280320	GTTGCTTTTGGCACCATCCAATC	9280938	GTCTTGAGCTTCCACTTTCTCC
2R	14 - 15	10020451	GTGCCGCTCCGCTTATC	10020784	CAAATGGGATTTACTTGTCTGTG
2R	15 - 16	10794962	GTGTCTATGCGTGCCTGTTTTGTG	10795211	CGATGAGCAGACTTTGGGCAGC

Arm	Interval Boundary	Genomic Location	Forward Primer Sequence	Genomic Location	Reverse Primer Sequence
2R	16 - 17	11889879	G TTCATTGTCCAAGTGTGAGC	11890485	GTCAGCGTTTGCCTTGCTTTTGGC
2R	17 distal	12284348	CCCAAGATATTTTCCCTTTTACCG	12285113	GCAGGATATGGATGTGGTTTC
3L	1 prox.	27398795	GCGTCATCTGGATGCCAC	27399291	CTCTGTACGCTTCCGTTATTCCTAA
3L	1 - 2	26699659	GCCTTGACAGTGTTCATCAG	26700239	GGATTCTGCGGTGACATC
3L	2 - 3	26003222	GTTTGTGACCCATGTTGTC	26003611	GAATCCTGAGAGGATTGTGC
3L	3 - 4	25068055	GAAAATCCACGCGTAAGCTGCC	25068669	CTTCAGATACCGTGATATGGATTG
3L	4 - 5	24515924	GCTAGGAGGCAGGATGGAATACTAC	24516307	CTTCATCAGCTCCACCGCTC
3L	5 - 6	23632568	GGAACATAATTCAACCAAATTTCG	23633162	GCTGTAAACTCTTCCGTGC
3L	6 - 7	22980628	TGCTTTAGTGACACTTCCTCATTG	22980989	CTATAAAGCGATAGCTTGAAGG
3L	7 - 8	21997309	ATCCTTCTTATGGGGTGGCAG	21997682	GTTTTGACCCGTCCCACACG
3L	8 - 9	21501188	CCAGTATACCAAAGACCCTAG	21501580	CCACTGTCACCGTAGCTG
3L	9 - 10	21082261	GATTTTTCTTGCTTTCCTCGAC	21082465	GTACGAATATCGAACGAATAC
3L	10 - 11	20462623	GTAATCAAATCATGGCTGTTT	20463199	GTTGCGCAGTTGCATGTGAG
3L	11 - 12	18948357	GAAGGAGGCTGGGAGCCAAAAG	18948563	CATGCGAGAAATCGAAATTCAG
3L	12 - 13	18590308	CATCACAGCATCTGCATGC	18591113	GCTTATTCGTGGGGATGTTGAG
3L	13 - 14	17507475	CAAATGGAGCAACAGGTTGG	17507899	CATCGCCATTGCTCTTCGTC
3L	14 - 15	17006414	GGTGTCTCGTTGAGCTTCCGTT	17006615	GTTGATAGCAGTGTATGGCG
3L	15 - 16	15446067	ACACAGAAAGCTCGTGGTG	15446468	GTGGCTTTGGAAGACATGC
3L	16 - 17	14867724	GTGGTATAACTACTGGTCATGC	14868335	CAAATTGCATCGCCATACGAAAC
3L	17 - 18	13799750	CTATCTTCTTTGGCCCTTATTC	13799988	GTGTTTGAATGTGCGAGTGTG
3L	18 - 19	12647591	GCACCAACACGATCCTCAATG	12647997	TAGCCCCATAACAAGGTTTCC
3L	19 - 20	11349437	CATTACATACAATCCAGCAACC	11349993	GTGTAACACAGCAAGTGCGC
3L	20 distal	9732472	ATCAACTCATAGAAAGCTTCC	9733062	CACAATGCTCTAAAGCAATGC
3R	1 prox.	1153007	CATCCAAAGCATCCGTTACTGTC	1153418	CGAGAATAGTGAAGAGGAAGAAGCG
3R	1 - 2	1521153	CGCTTCGATCATCTTCCGC	1521700	GATAATGTGACAGACCATGTG
3R	2 - 3	2080717	CAATCTTTGTAAATTAGGTCTCA	2080936	CTATCGATGACAAATACCCAATTC
3R	3 - 4	2460409	GTAAGAGGAAGCACAAAGGTATCC	2460800	CATATCCATCTTACATAATCGTCCG
3R	4 - 5	3526413	GACAAACTAACGGGATACGC	3526605	CTTACTGCTCCGCTACCTC
3R	5 - 6	4622421	GCGTTTGCGGTGAGTTGACATTC	4623036	CGCAGCTCGAACTATCACTAAG
3R	6 - 7	4966057	GCGTATTAAGTATCGCCAGG	4966844	GATCAACACCATCCGCCGATTC
3R	7 - 8	5584425	GCTTGCACGTTGGAGTTGCTTG	5584877	CTCGCCATAATCTTCCGAAAC
3R	8 - 9	5989386	GACCCTCTGCAAATGTGCAAG	5989567	CCGATGTCGATGCCTTTGCC
3R	9 - 10	6604707	GCGCACAACAGCATTGTCAG	6605100	CTGCACCCAGCTTGTCCATC
3R	10 - 11	7026906	GTTCCCATTCGGCGCCTTTTC	7027518	GAACGCAAGTCGGCAAAGACG
3R	11 - 12	7503742	TATTGTACCTTCCCAAGTGACC	7504533	CTTCCATGGCTGCATTTGATC
3R	12 - 13	7977701	GCGAAATGAACGCGGTGAAG	7978303	TTTAGTGTGTGCCAATACATGA
3R	13 - 14	9062678	CTGAAAGATACAACTGTACCGACC	9063061	CTTGGCAGGTTGACTTATCGAC
3R	14 - 15	9497822	GTCTGTGGAGCGAGTACGAAGA	9498450	CCTTCAAGCGAACTCAACTG
3R	15 - 16	10000797	GTGCTTGTACCGCTTACATT	10000965	CACCCATCAAGAGCATAATGAAC
3R	16 - 17	10543465	CCTTGCCAGCATTCAACC	10543855	GCGTGCTATATGTCTGACCAAC
3R	17 - 18	12038967	GGAATTTCCCAAAAACCGAC	12039148	CCACTTTTCATGCCAAATTTTCG
3R	18 - 19	13964694	ACGTATGCAATTCTTATTCGAAC	13965268	CATGCTGCTCCGTTTCATCG

Arm	Interval Boundary	Genomic Location	Forward Primer Sequence	Genomic Location	Reverse Primer Sequence
3R	19 - 20	14915739	GCCAGCCGGGTTGAATATC	14916114	CATAAGTCAACCCGTGAGTAG
3R	20 - 21	15933596	CGTTGTAGCGACTTCGTC	15933796	TAGCTATATCATCGAGAATCG
3R	21 - 22	17012997	GTAAGTGGGCGTTTCAACCG	17013362	CCATGGACCTGTTTTGTGCG
3R	22 - 23	18507653	AGCTGATCAGGTGTTTGTTCAT	18507838	CTGGCATTGACAACCGAATAGC
3R	23 - 24	18968137	GGTGGATTCGCTTATCGTACGAC	18968292	CCTGCTCTGCTTCAGTCACAATTG
3R	24 - 25	19559552	GCCACTCACTCTGCGAATGG	19559961	CAAGGGAATGGCATCTTCTGCAGC
3R	25 - 26	20054762	CTGTACTGAGGTTATACTTTAC	20055162	GATGGGATTGGGGGACTCAAAG
3R	26 distal	20512391	GATCCGTTCCGGTGGACAGCACTG	20512983	GCTATTGATACTGAAACTTAAATG

Each primer pair amplifies sequence from one of the two isogenized strains used in each cross, and each pair defines the boundary between two intervals (or the proximal boundary of interval one or the distal boundary of the most distal interval).

**Table S3. Fine crossover mapping in wild-type flies**

Arm	Interval	Width (Mb)	Cross(es) <sup>1</sup>	Flies	COs	cM / Mb	95% CI	Genes	TEs
X	1	1.24929	1	1595	1	0.05	0.01 - 0.28	52	200
X	2	0.80353	1	1595	19	1.48	0.95 - 2.30	74	88
X	3	0.53103	1	1595	20	2.36	1.53 - 3.62	74	44
X	4	0.52438	1	1595	23	2.75	1.83 - 2.75	102	40
X	5	0.59392	1	1595	38	4.01	2.93 - 5.47	60	21
X	6	0.39537	1	1595	23	3.65	2.43 - 3.64	51	7
X	7	0.39922	1	1595	11	1.73	0.98 - 3.08	53	5
X	8	0.67646	1	1595	16	1.48	0.92 - 2.39	69	11
X	9	0.24357	1	1595	9	2.32	1.19 - 4.35	18	6
2L	1	1.35144	2La	7399	3	0.03	0.01 - 0.09	46	220
2L	2	0.39728	2La	7399	5	0.07	0.03 - 0.17	40	136
2L	3	0.56694	2La	7399	2	0.06	0.02 - 0.20	198	163
2L	4	0.49053	2La	7399	7	0.16	0.07 - 0.33	85	26
2L	5	0.57688	2La	7399	16	0.37	0.24 - 0.62	77	83
2L	6	0.97121	2Lb	1460	16	1.13	0.70 - 1.83	137	28
2L	7	1.23340	2Lb	1460	14	0.78	0.46 - 1.30	194	26
2L	8	0.34415	2Lb	1460	4	0.80	0.29 - 2.03	16	7
2L	9	0.33948	2Lb	1460	3	0.61	0.21 - 1.80	42	8
2L	10	0.34355	2Lb	1460	4	0.80	0.29 - 2.04	40	9
2L	11	0.22607	2Lb	1460	10	3.03	1.64 - 5.53	40	5
2L	12	0.24446	2Lb	1460	11	3.08	1.72 - 5.48	22	1
2L	13	0.47258	2Lb	1460	15	2.17	1.33 - 3.58	65	12
2L	14	1.15938	2Lb	1460	35	2.07	1.49 - 2.86	150	20
2L	15	0.88325	2Lb	1460	28	2.17	1.51 - 3.12	108	10
2R	1	0.63963	2La, 2Lc	15115	0	0.00	0.00 - 0.05	4	3
2R	2	0.45823	2La, 2Lc	15115	0	0.00	0.00 - 0.07	16	20
2R	3	1.50023	2La, 2Lc	15115	0	0.00	0.00 - 0.02	3	5
2R	4	0.47872	2La, 2Lc	15115	3	0.04	0.02 - 0.13	13	10
2R	5	1.30059	2La, 2Lc	15115	6	0.03	0.02 - 0.07	20	400
2R	6	0.66592	2La, 2Lc	15115	8	0.08	0.03 - 0.15	18	297
2R	7	0.43314	2La, 2Lc	15115	45	0.69	0.51 - 0.92	51	229
2R	8	0.63503	2La, 2Lc	15115	42	0.44	0.33 - 0.60	80	128
2R	9	0.67317	2La, 2Lc	15115	44	0.43	0.33 - 0.58	118	31
2R	10	0.67469	2La, 2Lc	15115	22	0.22	0.15 - 0.34	58	8
2R	11	0.32344	2R	2389	12	1.55	0.90 - 2.69	118	15
2R	12	0.55593	2R	2389	9	0.68	0.36 - 1.30	73	14
2R	13	0.43109	2R	2389	5	0.49	0.21 - 1.14	98	7
2R	14	0.51051	2R	2389	16	1.31	0.80 - 2.14	120	22
2R	15	0.74013	2R	2389	32	1.81	1.28 - 2.55	114	11
2R	16	0.77451	2R	2389	50	2.70	2.05 - 3.55	173	24
2R	17	1.09492	2R	2389	18	0.69	0.43 - 1.08	82	4
2R	18	0.99475	2R	2389	30	1.26	0.88 - 1.8	132	13
3L	1	0.70121	3a	3744	0	0.00	0.00 - 0.14	3	3
3L	2	0.69914	3a	3744	14	0.53	0.31 - 0.89	10	7
3L	3	0.69644	3a	3744	0	0.00	0.00 - 0.14	4	5
3L	4	0.93517	3a	3744	0	0.00	0.00 - 0.11	10	12
3L	5	0.55213	3a	3744	0	0.00	0.00 - 0.18	8	3
3L	6	0.88336	3a	3744	0	0.00	0.00 - 0.11	14	162

Arm	Interval	Width (Mb)	Cross(es) <sup>1</sup>	Flies	COs	cM / Mb	95% CI	Genes	TEs
3L	7	0.65194	3a	3744	0	0.00	0.00 - 0.15	16	416
3L	8	0.98332	3a	3744	0	0.00	0.00 - 0.10	122	98
3L	9	0.49612	3a	3744	1	0.05	0.02 - 0.32	89	26
3L	10	0.41893	3a	3744	1	0.06	0.02 - 0.38	69	23
3L	11	0.61964	3a	3744	1	0.04	0.02 - 0.26	93	26
3L	12	1.51427	3a	3744	17	0.30	0.18 - 0.48	258	49
3L	13	0.35805	3a	3744	6	0.45	0.20 - 0.98	67	9
3L	14	1.58389	3a	3744	20	0.34	0.21 - 0.52	192	41
3L	15	0.50595	3a	3744	17	0.90	0.55 - 1.42	76	7
3L	16	0.44743	3b	796	1	0.28	0.04 - 1.61	116	9
3L	17	0.60697	3b	796	5	1.03	0.21 - 0.51	113	5
3L	18	0.57834	3b	796	4	0.87	0.47 - 2.52	70	13
3L	19	1.06797	3b	796	7	0.82	0.40 - 1.69	105	19
3L	20	1.15216	3b	796	28	3.05	2.13 - 4.37	146	11
3L	21	1.29815	3b	796	38	3.68	2.69 - 4.99	224	13
3L	22	1.61697	3b	796	42	3.26	2.40 - 4.41	201	13
3L	23	1.05671	3b	796	27	3.21	0.00 - 0.14	177	17
3R	1	0.36815	3a	3744	0	0.00	0.00 - 0.27	1	6
3R	2	0.55956	3a	3744	0	0.00	0.00 - 0.18	1	0
3R	3	0.37969	3a	3744	10	0.70	0.40 - 1.29	1	6
3R	4	2.16201	3a	3744	0	0.00	0.00 - 0.05	90	162
3R	5	0.34364	3a	3744	0	0.00	0.00 - 0.29	40	39
3R	6	0.61837	3a	3744	2	0.09	0.02 - 0.31	81	22
3R	7	0.40496	3a	3744	1	0.07	0.02 - 0.40	87	18
3R	8	0.61532	3a	3744	0	0.00	0.00 - 0.16	80	20
3R	9	0.42220	3a	3744	3	0.19	0.07 - 0.57	56	12
3R	10	0.47684	3a	3744	1	0.06	0.02 - 0.34	94	19
3R	11	0.47396	3a	3744	0	0.00	0.00 - 0.21	56	22
3R	12	1.08498	3a	3744	10	0.25	0.14 - 0.45	197	18
3R	13	0.43514	3a	3744	2	0.12	0.02 - 0.44	51	4
3R	14	0.50298	3a	3744	10	0.53	0.30 - 0.97	104	3
3R	15	0.54267	3a	3744	6	0.30	0.13 - 0.64	74	8
3R	16	0.65213	3a	3744	9	0.37	0.20 - 0.71	80	7
3R	17	0.84338	3c	2310	13	0.67	0.39 - 1.14	141	7
3R	18	1.92573	3c	2310	29	0.65	0.46 - 0.93	309	56
3R	19	0.95105	3c	2310	35	1.59	1.16 - 2.22	126	11
3R	20	1.01786	3c	2310	25	1.06	0.72 - 1.56	153	14
3R	21	1.07940	3c	2310	21	0.84	0.56 - 1.29	148	8
3R	22	1.07781	3c	2310	28	1.12	0.78 - 1.61	158	16
3R	23	0.41685	3c	2411	26	2.59	1.78 - 3.79	66	10
3R	24	0.46048	3c	2411	48	4.32	3.26 - 5.71	54	4
3R	25	0.59142	3c	2411	32	2.24	1.59 - 3.16	65	9
3R	26	0.49521	3c	2411	17	1.42	0.89 - 2.34	75	5
3R	27	0.45763	3c	2411	28	2.54	1.75 - 3.65	1	11
3R	28	0.71741	3c	2411	37	2.14	1.55 - 2.93	127	12

Fine mapping data and data used for modeling analyses. Intervals are numbered from proximal to distal along each arm. See Materials and Methods for Cross Numbers.

<sup>1</sup> See Materials and Methods for descriptions of crosses. Some crosses were set up multiple times on different days. These are designated with a, b, etc.

**Table S4. *Blm* mutant fine mapping**

Interval	Width (Mb)	COs	Flies	cM / Mb	95% CI
1	1.35144	3	1070	0.21	0.07 - 0.61
2 + 3	0.96422	11	1070	1.07	0.60 - 1.90
4	0.49053	1	1070	1.91	1.04 - 3.49
5	0.57688	7	1070	1.13	0.54 - 2.32
6 + 7	2.20461	40	1070	1.70	1.25 - 2.29
8	0.34415	1	1070	0.27	0.06 - 1.51
9	0.33948	3	1070	0.83	0.29 - 2.42
10	0.34355	2	1070	0.54	0.15 - 1.98
11	0.22607	3	1070	1.24	0.44 - 3.63
12	0.24446	7	1070	2.68	1.27 - 5.48
13	0.47258	5	1070	0.99	0.42 - 2.31
14	1.15938	7	1070	0.56	0.27 - 1.16
15	0.88325	15	1070	1.59	0.96 - 2.60

**Table S5. Statistical analysis of crossover distributions**

Arm	$P_{prox}$	$P_{all}$
X	NA	1.000
2L	0.0030 (5)	<0.0001
2R	<0.0001 (10)	<0.0001
3L	<0.0001 (15)	<0.0001
3R	<0.0001 (8)	<0.0001
2L <i>Blm</i>	NA	0.9926

$P$  values are comparison of crossover distribution to the expected distribution if interval size is the only determinant of crossover number, calculated using deviat (see Materials and Methods). Because crossovers on autosomal arms in wild-type flies came from different crosses with different number of flies scored (Table S3), we analyzed the set of most-proximal intervals that came from a single cross ( $P_{prox}$ , number of intervals is in parentheses) and, separately, for all intervals ( $P_{all}$ ). For  $P_{all}$ , the number of crossovers in more distal intervals was normalized to number of flies scored in proximal intervals.

**Table S6. Crossovers in WT and *bw<sup>D</sup>***

Genotype	Crossover	Parental	Total	cM	95% CI
<i>px + sp / +</i>	71	1287	1358	5.3	4.2 - 6.6
<i>px bw<sup>D</sup> sp / +</i>	73	1363	1436	5.1	4.1 - 6.3
<i>px + sp / bw<sup>D</sup></i>	53	1197	1250	4.2	3.3 - 5.5

**Table S7. Model averaged standardized effect sizes for each chromosome**

Arm	Estimate	SE	Lower 95	Upper 95
<b>Distance from centromere</b>				
X	0.363	0.378	-0.378	1.104
2L	1.179	0.152	0.881	1.477
2R	1.865	0.282	1.312	2.418
3L	1.291	0.237	0.825	1.756
3R	1.38	0.152	1.082	1.677
<b>Squared distance from centromere</b>				
X	-0.251	0.186	-0.616	0.114
2L	-0.461	0.039	-0.537	-0.386
2R	-0.412	0.131	-0.668	-0.156
3L	-0.285	0.127	-0.533	-0.036
3R	-0.292	0.115	-0.517	-0.068
<b>Gene Density</b>				
X	0.316	0.155	0.012	0.619
2L	0.005	0.025	-0.044	0.054
2R	0.768	0.158	0.459	1.077
3L	0.037	0.27	-0.492	0.565
3R	-0.313	0.141	-0.59	-0.036
<b>TE Density</b>				
X	-0.342	0.261	-0.853	0.169
2L	-0.505	0.075	-0.653	-0.357
2R	0.422	0.141	0.145	0.698
3L	-6.845	1.866	a0.501	-3.188
3R	-0.812	0.231	a.264	-0.36

Model-averaged parameter estimates along with estimated standard errors and 95% confidence intervals for wild type analysis. All variables were standardized by two times their standard deviation prior to model fittings. Model-averaged parameters and variance estimates were based on zero values for parameters if they were not included in model.



**Table S8. 95% confidence set for wild type chromosome analysis**

Arm	Dist	Dist <sup>2</sup>	Gene Dens	TE Dens	Arm * Dist	Arm * Dist <sup>2</sup>	Arm * GD	Arm * TE	df	Likelihood	Δ AICc	weight
X	X	X	X	X	X		X	X	22	-341.4	0	0.673
X	X	X	X	X	X	X	X	X	26	-335.2	1.44	0.327

Summary of models in 95% confidence set for wild type chromosome analysis. X indicates parameter was included in model. Interactions (\*) indicate separate parameter estimated for each chromosome.

**Table S9. Modeled averaged parameters for mutant comparison**

Chromosome	Estimate	SE	Lower 95	Upper 95
<b>Distance from centromere</b>				
Wild Type	1.818	0.118	1.586	2.049
<i>Blm</i>	0.439	0.318	-0.183	1.062
<b>Squared distance from centromere</b>				
Wild Type	-0.784	0.026	-0.835	-0.734
<i>Blm</i>	-0.198	0.162	-0.517	0.12
<b>TE Density</b>				
Wild Type	-0.073	0.042	-0.155	0.009
<i>Blm</i>	0.047	0.141	-0.228	0.323

Model averaged parameter estimates along with estimated standard errors and 95% confidence intervals for 2L mutant analysis. All variables were standardized by two times their standard deviation prior to model fittings. Model averaged parameters and variance estimates were based on zero values for parameters if they were not included in model.

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**Table S10. 95% confidence set for 2L *Blm* mutant chromosome analysis**

Arm	Dist	Dist <sup>2</sup>	TE Dens	Arm * Dist	Arm * Dist <sup>2</sup>	Arm * TE	df	Likelihood	Δ AICc	weight
X	X	X		X	X		7	a06.8	0	0.873
X	X	X	X			X	7	a08.7	3.85	0.127

95% confidence set for 2L *Blm* mutant chromosome analysis. X indicates variable(s) was in fit model. Interactions indicate separate parameter estimated for each chromosome.