

Table S1. Strain list

NKY1551	<i>MATα</i> , <i>ho::LYS2</i> ⁺ , <i>lys2</i> ⁺ , <i>ura3</i> ⁺ , <i>leu2::hisG</i> ⁺ , <i>his4X-LEU2(BamHI)-URA3/his4B-LEU2(MluI)</i> , <i>arg4-nsp/arg4-bgl</i>
MSY717	NKY1551 with <i>rad24::LEU2</i>
MSY2820	NKY1551 with <i>zip1::LEU2</i>
MSY2122	NKY1551 with <i>rad24::LEU2</i> , <i>zip1::LEU2</i>
MSY620	<i>MATα</i> , <i>ho::LYS2</i> , <i>lys2</i> , <i>leu2::hisG</i> , <i>ura3</i> , <i>hom3-10</i> , <i>trp2</i>
S2921	<i>MATα</i> , <i>ho::LYS2</i> , <i>lys2</i> , <i>leu2::hisG</i> , <i>can1-R</i>
MSY1172	<i>MATα</i> , <i>ho::LYS2</i> , <i>lys2</i> , <i>ura3</i> , <i>hom3-10</i> , <i>trp2</i>
MSY1174	<i>MATα</i> , <i>ho::LYS2</i> , <i>lys2</i> , <i>can1-R</i>
MSY654	S2921 with <i>rad24::LEU2</i>
MSY655	MSY620 with <i>rad24::LEU2</i>
MSY1222	S2921 with <i>mec1::LEU2</i> , <i>sml1-X</i>
MSY1275	MSY620 with <i>mec1::LEU2</i> , <i>sml1-X</i>
MSY4245	<i>MATα</i> , <i>ho::LYS2</i> , <i>lys2</i> , <i>hml::KanMX6</i> , <i>HIS4-LEU2-URA3</i> , <i>cyh2-R</i> , <i>arg4-bgl</i>
MSY4303	<i>MATα</i> , <i>ho::LYS2</i> , <i>lys2</i> , <i>his4B-leu2-E</i> , <i>cup2-B</i> , <i>met13-B</i> , <i>trp5-S</i> , <i>ade6-B</i> , <i>arg4-bgl</i>
MSY4360	MSY4245 with <i>mec1-1 sml1-X</i>
MSY4358	MSY4360 with <i>mec1-1 sml1-X</i>
MSY4417	MSY4245 with <i>sml1-X</i>
MSY4419	MSY4245 with <i>mec1-kd::XbaI</i> , <i>sml1-X</i>
MSY4429	MSY4360 with <i>sml1-X</i>
MSY4435	MSY4360 with <i>mec1-kd::XbaI</i> , <i>sml1-X</i>
MSY5247	MSY4245 with <i>rad24::HygMX6</i>
MSY5330	MSY4360 with <i>rad24::HygMX6</i>

Table S2. Coincidence of crossovers on chromosome *V*

	Double crossovers in <i>CAN1-URA3-HOM3</i>			Double crossovers in <i>URA3-HOM3-TRP2</i>		
	Observed ^a (Total)	Expected ^b	Ratio (P-value) ^c	Observed ^a (Total)	Expected ^b	Ratio (P-value)
WT	0.43 (1067)	0.48	0.90 (0.018)	0.15 (1067)	0.16	0.94 (0.41)
<i>rad24</i>	0.16 (1167)	0.12	1.33 (8.0X10 ⁻⁵)	0.069 (1167)	0.043	1.60 (1.8X10 ⁻⁵)
<i>mec1</i>	0.28 (1170)	0.20	1.4 (9.4X10 ⁻¹⁰)	0.15 (1170)	0.10	1.5 (6.4X10 ⁻⁸)

^aThe number of tetrads with two adjacent intervals, both of which show crossovers (either tetratype or non-parental ditype), was counted. In parenthesis, a total number of tetrads checked is shown.

^bExpected is the products of the numbers given for two adjacent intervals with crossovers from the number of a crossover in single intervals.

^cP-value reflects the likelihood for the differences between the expected and observed frequencies is attributable to a chance as determined by χ^2 test.

Table S3. Coincidence of crossovers on chromosome III

	Double crossovers in <i>HML-URA3-LEU2</i>			Double crossovers in <i>URA3-LEU2-HIS4</i>			Double crossovers in <i>LEU2-HIS4-MAT</i>		
	Observed ^a (Total)	Expected ^b	Ratio (P-value)	Observed ^a (Total)	Expected ^b	Ratio (P-value)	Observed ^a (Total)	Expected ^b	Ratio (P-value)
WT	0.033 (1104)	0.061	0.53 (1.7X10 ⁻⁴)	0.0091 (1104)	0.013	0.7 (0.26)	0.021 (1212)	0.03	0.7 (0.084)
<i>rad24</i>	0.0078 (1160)	0.0078	1 (1)	0 (1160)	0.0012	NA	0.0078 (1319)	0.0050	1.6 (0.18)
<i>mec1-1</i>	0.011 (1061)	0.014	0.79 (0.41)	0.0038 (1061)	0.0034	1.1 (0.82)	0.0076 (1213)	0.01	0.76 (0.42)
<i>mec1-kd</i>	0.039 (1033)	0.034	1.1 (0.38)	0.012 (1033)	0.0085	1.4 (0.22)	0.015 (1226)	0.022	0.7 (0.13)

^aThe number of tetrads with two adjacent intervals, both of which show crossovers (either tetratype or non-parental ditype), was counted. In parenthesis, a total number of tetrads checked is shown.

^bExpected is the products of the numbers given for two adjacent intervals with crossovers from the number of a crossover in single intervals.

^cP-value reflects the likelihood for the differences between the expected and observed frequencies is attributable to a chance as determined by χ^2 test.

Table S4. Coincidence of crossovers on chromosome VII

	Double crossovers in <i>CUP2-MET13-CYH2</i>			Double crossovers in <i>MET13-CYH2-TRP5</i>			Double crossovers in <i>CYH2-TRP5-ADE6</i>		
	Observed ^a (Total)	Expected ^b	Ratio (P-value)	Observed ^a (Total)	Expected ^b	Ratio (P-value)	Observed ^a (Total)	Expected ^b	Ratio (P-value)
WT	0.070 (1054)	0.12	0.57 (3.7X10 ⁻⁵)	0.13 (1054)	0.15	0.86 (0.094)	0.45 (1054)	0.47	0.95 (0.34)
<i>rad24</i>	0.099 (1092)	0.087	1.1 (0.17)	0.12 (1092)	0.11	1.10 (0.32)	0.41 (1092)	0.38	1.1 (0.11)
<i>mec1-1</i>	0.13 (932)	0.14	0.93 (0.41)	0.16 (932)	0.16	1 (1)	0.47 (932)	0.48	0.98 (0.66)
<i>mec1-kd</i>	0.15 (955)	0.17	0.87 (0.13)	0.18 (955)	0.20	0.90 (0.17)	0.53 (955)	0.53	1 (1)

^aThe number of tetrads with two adjacent intervals, both of which show crossovers (either tetratype or non-parental ditype), was counted. In parenthesis, a total number of tetrads checked is shown.

^bExpected is the products of the numbers given for two adjacent intervals with crossovers from the number of a crossover in single intervals.

^cP-value reflects the likelihood for the differences between the expected and observed frequencies is attributable to a chance as determined by χ^2 test.

Table S5. Chromatid Interference in various strains

Chromosome III

	Intervals	2 chromatids	3 chromatids	4 chromatids	Total	<i>P</i> -value ^a
Wild type	<i>HML-URA3-LEU2</i>	8	16	3	27	0.25
	<i>URA3-LEU2-HIS4</i>	5	3	0	8	0.03
	<i>LEU2-HIS4-MAT</i>	6	12	3	21	0.37
<i>rad24</i>	<i>HML-URA3-LEU2</i>	2	6	2	10	0.82
	<i>URA3-LEU2-HIS4</i>	0	0	0	0	-
	<i>LEU2-HIS4-MAT</i>	2	2	4	8	0.22
<i>mec1</i>	<i>HML-URA3-LEU2</i>	6	4	4	14	0.21
<i>sml1-X</i>	<i>URA3-LEU2-HIS4</i>	0	1	1	2	0.81
	<i>LEU2-HIS4-MAT</i>	0	5	1	6	0.22
<i>mec1-kd</i>	<i>HML-URA3-LEU2</i>	10	22	7	39	0.58
<i>sml1-X</i>	<i>URA3-LEU2-HIS4</i>	6	4	1	11	0.07
	<i>LEU2-HIS4-MAT</i>	6	5	4	15	0.33

Chromosome VII

	Intervals	2 chromatids	3 chromatids	4 chromatids	Total	<i>P</i> -value
Wild type	<i>CUP2-MET13- CYH2</i>	29	44	19	92	0.31
	<i>MET13-CYH2-TRP5</i>	43	69	24	136	0.07
	<i>CYH2-TRP5-ADE6</i>	132	214	113	459	0.16
<i>rad24</i>	<i>CUP2-MET13- CYH2</i>	27	52	27	106	0.98
	<i>MET13-CYH2-TRP5</i>	35	71	26	132	0.37
	<i>CYH2-TRP5-ADE6</i>	108	195	98	401	0.67
<i>mec1</i>	<i>CUP2-MET13- CYH2</i>	29	68	28	125	0.61
<i>sml1-X</i>	<i>MET13-CYH2-TRP5</i>	51	77	38	166	0.20
	<i>CYH2-TRP5-ADE6</i>	110	198	98	406	0.62
<i>mec1-kd</i>	<i>CUP2-MET13- CYH2</i>	28	85	35	148	0.15
<i>sml1-X</i>	<i>MET13-CYH2-TRP5</i>	60	77	39	176	0.02
	<i>CYH2-TRP5-ADE6</i>	101	218	126	445	0.22

Chromosome V

	Intervals	2 chromatids	3 chromatids	4 chromatids	Total	P-value
Wild type	<i>CAN1-URA3-HOM3</i>	120	230	143	493	0.35
	<i>URA3-HOM3-TRP2</i>	33	72	44	149	0.85
<i>rad24</i>	<i>CAN1-URA3-HOM3</i>	43	70	52	165	0.32
	<i>URA3-HOM3-TRP2</i>	15	36	15	66	0.88
<i>mec1- sml1-X</i>	<i>CAN1-URA3-HOM3</i>	83	160	135	378	<0.0001
	<i>URA3-HOM3-TRP2</i>	33	97	70	194	0.00059

^aNumbers of tetrads with 2-, 3- and 4-strand double crossovers in two adjacent intervals were counted. Expected number of each class are simply calculated from 1:2:1 ratio for 2-, 3- and 4-strand double crossovers.

^bP-values were calculated using the chi-square independent test.

Differences between observed and expected ratio were calculated using chi-square independent test.

Table S6. Genetic analysis of crossovers in adjacent intervals-Chromosome III

	PD:NPD:TT cM (\pm S.E.)				
	<i>HML-URA3</i>	<i>URA3-LEU2</i>	<i>LEU2-HIS4</i>	<i>HIS4-MAT</i>	
Wild type	-	661:7:284 17.1(\pm 1.1)	880:0:51 2.7(\pm 0.4)	384:42:581 41.4(\pm 1.9)	
	+	244:0:28 5.2(\pm 0.9)	268:0:4 0.7(\pm 0.4)	145:7:133 30.7(\pm 2.9)	
	661:2:242 14.0(\pm 0.9)	-	852:0:47 2.6(\pm 0.4)	317:44:531 44.6(\pm 2.1)	
	291:0:28 4.4(\pm 0.8)	+	309:0:8 1.3(\pm 0.4)	177:2:138 23.7(\pm 1.9)	
	880:2:256 11.8(\pm 0.7)	852:6:303 14.6(\pm 0.9)	-	463:46:655 40.0(\pm 1.7)	
	51:0:4 3.6(\pm 1.8)	47:1:7 11.8(\pm 5.7)	+	34:0:21 19.1(\pm 3.3)	
	381:1:144 14.3(\pm 1.1)	317:3:174 19.4(\pm 1.5)	463:0:34 3.4(\pm 0.6)	-	
	655:2:151 10.1(\pm 0.9)	615:5:146 11.5(\pm 1.1)	752:0:21 1.4(\pm 0.3)	+	
	<i>rad24</i>	-	987:2:113 5.7(\pm 0.6)	1077:0:12 0.6(\pm 0.2)	674:32:444 27.7(\pm 1.5)
		+	81:0:10 5.5(\pm 1.6)	87:0:2 1.1(\pm 0.8)	45:4:51 37.5(\pm 0.6)
		987:1:80 4.0(\pm 0.5)	-	1042:0:14 0.7(\pm 0.2)	621:30:389 27.4(\pm 1.6)
		115:0:10 4.0(\pm 1.2)	+	125:0:0 0	58:5:59 36.5(\pm 5.4)
		1077:1:86 4.0 (\pm 0.5)	1042:2:123 5.8 (\pm 0.6)	-	685:33:444 27.6(\pm 1.5)
		12:0:2 7.1 (\pm 4.7)	14:0:0 0	+	6:2:7 63.3(\pm 24.8)
674:0:45 3.1(\pm 0.5)		621:1:57 4.6(\pm 0.7)	685:0:6 0.4(\pm 0.2)	-	
476:1:54 5.7(\pm 0.9)		419:1:63 7.1(\pm 1.0)	471:0:9 0.9(\pm 0.3)	+	
<i>mec1 sml1-X</i>		-	824:3:176 9.7(\pm 0.8)	981:0:20 1.0(\pm 0.2)	503:47:504 37.3(\pm 1.9)
		+	71:2:14 14.9(\pm 5.1)	82:0:2 1.2(\pm 0.8)	42:5:40 40.2(\pm 7.4)
	824:1:70 4.3(\pm 0.6)	-	873:0:19 1.1(\pm 0.2)	430:36:406 35.7(\pm 2.0)	
	179:1:15 5.4(\pm 1.8)	+	191:0:3 0.8(\pm 0.4)	84:11:94 42.3(\pm 5.0)	
	981:2:80 4.3(\pm 0.6)	873:4:187 9.9(\pm 0.8)	-	506:47:508 37.2(\pm 1.9)	
	20:0:2 4.6(\pm 3.1)	19:1:2 18.2(\pm 13.5)	+	13:0:7 17.5(\pm 5.3)	

	503:0:42 3.9(±0.6)	430:1:83 8.7(±1.0)	506:0:13 1.3(±0.3)	-
	551:2:43 4.6(±0.9)	442:4:101 11.4(±1.3)	555:0:7 0.6(±0.2)	+
<i>mec1-kd</i>	-	706:6:194 12.7(±1.0)	863:0:36 2.0(±0.3)	379:62:516 46.4(±2.3)
<i>sml1-X</i>	+	119:0:39 12.3(±1.7)	148:0:3 1.0(±0.6)	54:12:100 51.8(±5.7)
	706:1:118 7.5(±0.7)	-	786:0:28 1.7(±0.3)	306:52:428 47.1(±2.6)
	200:1:39 9.4(±1.7)	+	227:0:11 2.3(±0.7)	92:13:127 44.2(±4.4)
	863:2:147 7.9(±0.7)	786:6:221 12.7(±1.0)	-	383:68:558 47.9(±2.3)
	36:0:3 3.9(±2.1)	26:0:11 14.9(±3.8)	+	20:0:16 22.2(±4.1)
	379:2:53 7.5(±1.2)	306:1:91 12.2(±1.3)	383:0:20 2.5(±0.5)	
	578:0:112 8.1(±0.7)	480:5:135 13.3(±1.3)	626:0:16 1.3(±0.3)	

Map distances with S.E. were calculated using the Stahl Lab online tool (<https://elizabethhousworth.com/StahlLabOnlineTools>).

Table S7. Genetic analysis of crossovers in adjacent intervals-Chromosome VII

	PD:NPD:TT cM (\pm S.E.)				
	<i>CUP2-MET13</i>	<i>MET13-CYH2</i>	<i>CYH2-TRP5</i>	<i>TRP5-ADE6</i>	
Wild type	-	360:0:170 16.0(\pm 1.0)	183:17:325 40.7(\pm 2.3)	161:26:334 47.0(\pm 2.7)	
	+	547:0:93 7.3(\pm 0.7)	252:21:357 38.3(\pm 2.2)	183:55:387 57.4(\pm 3.1)	
	360:16:531 34.6(\pm 1.4)	-	331:36:582 42.0(\pm 1.8)	287:66:585 52.3(\pm 2.3)	
	170:1:92 18.6(\pm 1.8)	+	129:7:136 32.7(\pm 3.0)	72:21:173 56.2(\pm 4.6)	
	183:5:247 31.8(\pm 1.8)	331:0:129 14.0(\pm 1.1)	-	124:45:305 60.7(\pm 3.7)	
	342:12:365 30.4(\pm 1.6)	617:0:143 9.4(\pm 0.7)	+	259:46:486 48.2(\pm 2.4)	
	161:6:177 31.0(\pm 2.4)	287:0:72 10.0(\pm 1.1)	124:16:243 44.3(\pm 3.0)	-	
	360:11:431 31.0(\pm 1.4)	651:0:194 11.5(\pm 0.7)	350:28:505 38.1(\pm 1.8)	+	
	<i>rad24</i>	-	525:0:109 8.6(\pm 0.8)	273:35:302 42.0(\pm 2.8)	255:41:307 45.9(\pm 3.0)
		+	406:3:113 12.6(\pm 1.3)	175:39:294 52.0(\pm 3.3)	143:42:313 56.7(\pm 3.5)
		525:34:372 30.9(\pm 1.9)	-	390:61:503 45.6(\pm 2.3)	340:75:512 51.9(\pm 2.5)
		109:7:109 33.6(\pm 3.6)	+	80:15:133 48.9(\pm 4.7)	75:15:134 50.0(\pm 4.7)
		273:8:167 24.0(\pm 2.1)	390:2:78 9.6(\pm 1.2)	-	210:35:239 46.4(\pm 3.4)
		337:31:302 36.4(\pm 2.4)	564:1:147 10.7(\pm 0.9)	+	237:58:448 53.6(\pm 2.8)
255:16:127 28.0 (\pm 3.0)		340:1:74 9.6 (\pm 1.2)	210:26:211 41.1 (\pm 3.3)	-	
348:24:331 33.8 (\pm 2.1)		587:2:147 10.8 (\pm 0.9)	274:52:454 49.1 (\pm 2.5)	+	
<i>mec1-1 sml1-X</i>		-	294:2:109 14.9(\pm 1.5)	135:30:228 51.9(\pm 3.8)	125:31:225 53.9(\pm 3.9)
		+	470:4:136 13.1(\pm 1.3)	162:53:367 58.9(\pm 3.3)	161:59:346 61.8(\pm 3.5)
		294:31:439 40.9(\pm 2.1)	-	248:72:481 57.0(\pm 2.8)	237:69:463 57.0(\pm 2.9)
		111:11:129 38.8(\pm 3.9)	+	80:19:172 52.8(\pm 4.3)	69:28:158 63.9(\pm 5.4)
		135:10:152 35.7(\pm 3.2)	248:0:80 12.2(\pm 1.2)	-	100:32:200 59.0(\pm 4.5)
		258:29:391 41.7(\pm 2.3)	553:5:186 14.5(\pm 1.2)	+	221:73:464 59.5(\pm 3.0)

	125:12:149 38.6(±3.5)	237:2:67 12.9(±1.8)	100:29:192 57.0(±4.5)	-
	256:28:377 41.2(±2.3)	532:3:183 14.0(±1.1)	232:62:475 55.0(±4.5)	+
<i>mec1-kd</i>	-	262:3:120 17.9(±1.7)	96:36:236 61.4(±4.3)	93:28:234 56.6(±4.0)
<i>sml1-X</i>	+	490:1:160 12.8(±1.0)	163:47:427 55.7(±2.9)	168:71:370 65.4(±3.6)
	261:34:455 43.9(±2.2)	-	182:62:533 58.2(±2.7)	198:65:469 58.7(±2.9)
	122:10:151 37.3(±3.3)	+	94:27:179 56.8(±4.6)	78:37:171 68.7(±5.4)
	96:8:155 39.2(±3.3)	183:0:94 17.0(±1.4)	-	77:18:191 52.3(±4.0)
	272:35:439 43.5(±2.3)	596:4:203 14.1(±1.1)	+	220:92:505 64.7(±3.0)
	93:10:158 41.8(±3.5)	197:1:77 15.1(±1.7)	77:19:201 53.0(±4.0)	+
	262:31:410 42.4(±2.3)	537:3:206 15.0(±1.1)	209:71:526 59.1(±2.7)	-

Map distances with S.E. were calculated using the Stahl Lab online tool (<https://elizabethhousworth.com/StahlLabOnlineTools>).

Table S8. Genetic analysis of crossovers in inter-chromosome -Chromosome III

	Reference Interval	PD:NPD:TT cM (\pm S.E.)				
		<i>TRP5-ADE6</i>	<i>HML-URA3</i>	<i>URA3-LEU2</i>	<i>LEU2-HIS4</i>	<i>HIS4-MAT</i>
Wild type	+	696:2:182 11.0(\pm 0.8)	604:5:219 15.0(\pm 1.1)	788:0:38 2.3(\pm 0.4)	359:31:487 38.4(\pm 1.9)	
	-	289:0:94 12.3(\pm 1.1)	278:2:86 13.4(\pm 1.6)	351:0:15 2.1(\pm 0.5)	161:15:167 38.8(\pm 3.0)	
<i>rad24</i>	+	721:0:56 3.6(\pm 0.5)	640:1:74 5.6(\pm 0.7)	706:0:8 0.6(\pm 0.2)	433:22:304 28.7(\pm 1.9)	
	-	402:1:41 5.3(\pm 1.0)	365:1:42 5.9(\pm 1.0)	403:0:6 0.7(\pm 0.3)	259:12:162 27.0(\pm 2.5)	
<i>mec1-1</i> <i>sml1-X</i>	+	698:1:62 4.5(\pm 0.6)	571:4:123 10.5(\pm 1.1)	694:0:15 1.1(\pm 0.3)	345:38:366 39.7(\pm 2.4)	
	-	304:1:17 3.6(\pm 1.1)	243:0:52 8.8(\pm 1.1)	293:0:5 0.8(\pm 0.4)	158:8:149 31.3(\pm 2.8)	
<i>mec1-kd</i> <i>sml1-X</i>	+	676:2:116 8.1(\pm 0.8)	557:5:149 12.6(\pm 1.2)	690:0:30 2.1(\pm 0.4)	294:56:420 49.1(\pm 2.7)	
	-	242:0:47 8.1(\pm 1.1)	196:0:66 12.6(\pm 1.3)	260:0:9 1.7(\pm 0.6)	109:16:161 44.9(\pm 3.9)	

Map distances with S.E. were calculated using the Stahl Lab online tool (<https://elizabethhousworth.com/StahlLabOnlineTools>).

Table S9. Genetic analysis of crossovers in inter-chromosome-Chromosome VII

		PD:NPD:TT cM (\pm S.E.)			
	<i>HIS4-MAT</i>	<i>CUP2-MET13</i>	<i>MET13-CYH2</i>	<i>CYH2-TRP5</i>	<i>TRP5-ADE6</i>
Wild type	+	333:14:394 32.3(\pm 1.6)	610:0:161 10.4(\pm 0.7)	299:27:476 39.8(\pm 1.7)	232:66:494 56.2(\pm 2.7)
	-	211:4:256 29.7(\pm 1.6)	380:0:119 11.9(\pm 1.0)	198:19:302 40.1(\pm 2.5)	161:32:327 49.9(\pm 3.0)
<i>rad24</i>	+	252:21:195 34.3(\pm 2.9)	382:2:103 12.4(\pm 1.4)	204:35:266 47.1(\pm 3.3)	174:39:287 52.1(\pm 3.4)
	-	376:20:265 29.1(\pm 2.1)	569:0:123 8.9(\pm 0.7)	280:45:383 46.1(\pm 2.6)	259:52:381 50.1(\pm 2.9)
<i>mec1-1</i> <i>sml1-X</i>	+	191:24:293 43.0(\pm 2.3)	400:2:150 14.7(\pm 1.2)	158:43:371 55.0(\pm 3.1)	157:52:352 59.2(\pm 3.4)
	-	206:19:254 38.4(\pm 2.7)	394:4:117 13.7(\pm 1.5)	172:47:305 56.0(\pm 3.5)	158:51:294 59.6(\pm 3.7)
<i>mec1-kd</i> <i>sml1-X</i>	+	224:26:364 42.4(\pm 2.4)	469:2:181 14.8(\pm 1.1)	175:57:454 58.0(\pm 2.9)	177:64:412 61.0(\pm 3.2)
	-	148:19:208 42.9(\pm 3.3)	292:3:106 15.5(\pm 1.7)	108:36:274 58.5(\pm 3.8)	109:39:255 60.7(\pm 4.1)

Map distances with S.E. were calculated using the Stahl Lab online tool (<https://elizabethhousworth.com/StahlLabOnlineTools>).

Table S10. Genetic analysis of crossovers in adjacent intervals-Chromosome V

		PD:NPD:TT cM (\pm S.E.)		
	<i>CAN1-URA3</i>	<i>URA3-HOM3</i>	<i>HOM3-TRP2</i>	
Wild type	-	79:21:208 54.2(\pm 4.0)	217:1:84 14.9(\pm 1.6)	
	+	259:22:481 40.2(\pm 1.8)	596:2:152 10.9(\pm 0.9)	
	79:10:249 45.7(\pm 2.7)	-	256:1:80 12.8(\pm 1.4)	
	229:19:484 40.9(\pm 1.8)	+	566:2:159 11.8(\pm 1.0)	
	217:22:574 43.4(\pm 1.7)	256:28:538 42.9(\pm 1.9)	-	
	85:6:148 38.5(\pm 3.1)	81:14:147 47.7(\pm 4.3)	+	
	<i>rad24</i>	-	554:13:230 19.3(\pm 1.5)	705:0:85 5.4(\pm 0.6)
		+	179:9:186 32.1(\pm 2.5)	308:1:60 8.9(\pm 1.2)
		554:12:167 16.3(\pm 1.6)	-	667:1:66 4.9(\pm 0.7)
		243:10:185 28.0(\pm 2.3)	+	352:1:80 9.9(\pm 1.2)
705:15:293 18.9 (\pm 1.3)		667:16:336 21.2(\pm 1.3)	-	
85:7:54 32.9(\pm 5.3)		67:5:76 35.8(\pm 4.5)	+	
<i>mec1 sml1-X</i>		-	238:27:217 39.3(\pm 3.1)	342:3:123 15.1(\pm 1.5)
		+	179:41:337 52.3(\pm 3.1)	370:14:156 22.2(\pm 2.2)
		238:19:160 32.9(\pm 3.1)	-	301:6:100 16.7(\pm 2.0)
		244:27:351 41.2(\pm 2.4)	+	417:11:183 20.4(\pm 1.8)
	342:27:343 35.5(\pm 2.2)	301:35:382 41.2(\pm 2.4)	-	
	126:15:155 41.4(\pm 3.8)	106:31:163 58.2(\pm 4.9)	+	

Map distances with S.E. were calculated using the Stahl Lab online tool (<https://elizabethhousworth.com/StahlLabOnlineTools>).

Table S11. Non-Mendelian segregation in *rad24* and *mec1* mutants

Crossover	Percent of non-Mendelian segregation ^a On Chromosome III (<i>P</i> -values ^b)						Percent of non-Mendelian segregation ^a On Chromosome VII (<i>P</i> -values ^b)					
	<i>URA3</i>		<i>LEU2</i>		<i>HIS4</i>		<i>MET13</i>		<i>CYH2</i>		<i>TRP5</i>	
	-	+	-	+	-	+	-	+	-	+	-	+
Wild type	0.41	0.74	1.90	3.71	0.17	0.33	0.83	2.3	0.08	0.02	0.17	1.07
<i>rad24</i>	0.45	0.61	2.73	4.32	0.23	0.91	1.29	4.47	0.38	0.61	0.68	2.43
	(0.002)	(0.002)	(4.2 X 10 ⁻⁵)	(3.7 X 10 ⁻⁴)	(0.0016)	(4.5X 10 ⁻⁷)	(1.5 X 10 ⁻⁴)	(3.7 X 10 ⁻¹¹)	(4.5 X 10 ⁻⁷)	(2.5 X 10 ⁻⁵)	(5.7 X 10 ⁻⁹)	(1.1 X 10 ⁻⁹)
<i>mec1</i>	0.66	1.15	2.56	4.37	0.41	0.16	1.65	3.87	0.49	0.91	0.58	3.05
<i>sml1-X</i>	(0.18)	(0.10)	(0.10)	(0.23)	(0.034)	(0.32)	(0.0016)	(3.3 X 10 ⁻⁴)	(5.7 X 10 ⁻⁷)	(3.9 X 10 ⁻⁶)	(4/1 X 10 ⁻⁴)	(2.8 X 10 ⁻¹¹)
<i>mec1-kd</i>	1.06	1.63	3.34	4.89	0.24	0.90	1.96	4.98	0.16	0.98	0.81	2.04
<i>sml1-X</i>	(3.2 X 10 ⁻⁴)	(2.3 X 10 ⁻⁴)	(1.6 X 10 ⁻⁴)	(0.023)	(0.42)	(4.3 X 10 ⁻⁴)	(8.8 X 10 ⁻⁶)	(4.1 X 10 ⁻¹⁰)	(0.28)	(1.9 X 10 ⁻⁷)	(1.4 X 10 ⁻⁸)	(8.0 X 10 ⁻⁴)

^aFrequencies of tetrads with 4⁺:0⁻, 3⁺:1⁻, 1⁺:3⁻ and 0⁺:4⁻ segregation for each marker were calculated.

At each locus showing no-Mendelian segregation, the locus was checked for exchange of flanking markers and are classified into crossover-negative (-) or -positive (+).

Supplementary Figure legends:

Figure S1. Distribution of viable spores in the *rad24* and *mec1* mutants.

- A. Distribution of viable spores per tetrad. Numbers of viable spores per tetrad were calculated for wild type (blue bars), the *rad24* (magenta bars) and *mec1 sml1-X* mutants (green bars).
- B. Distribution of viable spores per tetrad. Numbers of viable spores per tetrad were calculated for wild type (blue bars), the *rad24* (magenta bars), *mec1-1 sml1-X* mutants (green bars) and *mec1-kd sml1-X* mutants (light green bars).

Figure S2. Inter-chromosomal intervals do not show crossover interference.

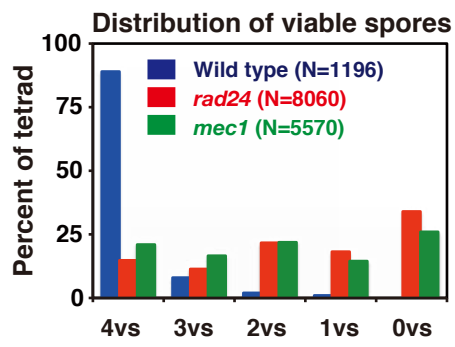
Crossover interference on chromosomes *III* and *VII* was measured by the method of Malkova et al. (2004). For *TRP5-ADE6* on chromosome *VII* (top) or *HIS4-MAT* on chromosome *III* (bottom), tetrads were classified into “+” for TT and NPD or “-” for PD. Map distances with S.E. for each class were calculated using the Stahl Lab online tool (<https://elizabethhousworth.com/StahlLabOnlineTools>). Error bars; S.E. See Table S8 and S9 for raw data. Wild type, blue; *rad24*, red; *mec1-1 sml1-x*, green; *mec1-kd sml1-x*, light green.

Figure S3. Analysis of crossover interference among intra-chromosomal intervals.

Crossover interference on chromosomes *V* was measured by the method of Malkova (2004). For each interval, tetrads were classified into “+” for TT and NPD or “-” for PD. Map distances with S.E. were calculated using the Stahl Lab online tool (<https://elizabethhousworth.com/StahlLabOnlineTools>). Error bars; S.E. See Table S10 for raw data. Wild type, blue; *rad24*, red; *mec1 sml1-x*, green.

Supplementary Figure 1. Miki Shinohara

A



B

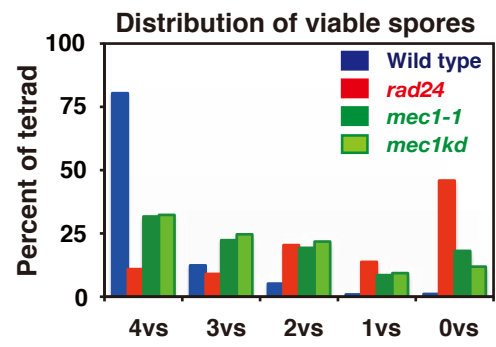


Figure S2. Miki Shinohara

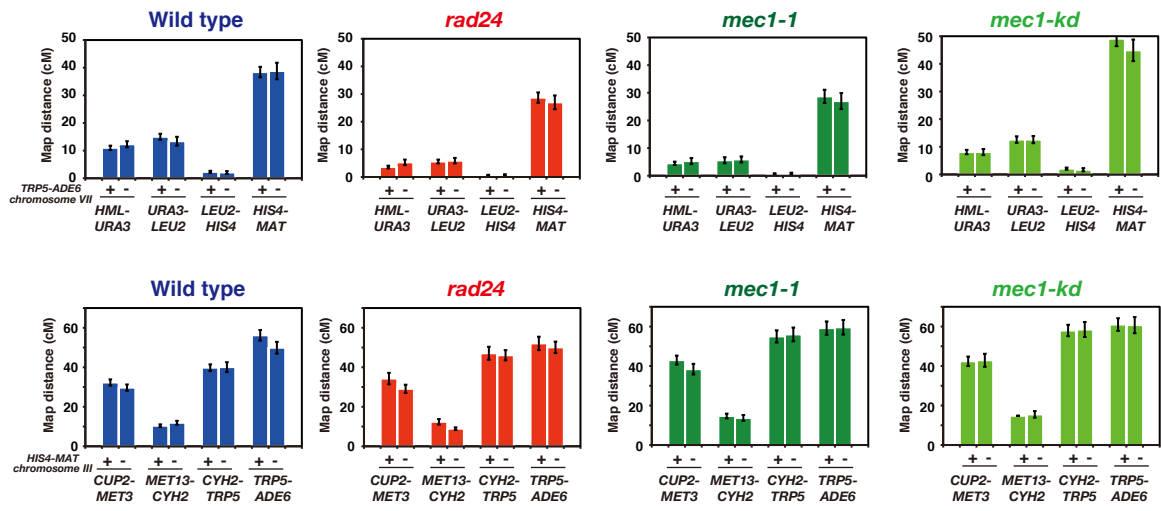


Figure S3. Miki Shinohara

