

Supplemental Material

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Five different classes of DNA sequence-specific meiotic recombination hotspots in *Schizosaccharomyces pombe* each function through chromatin remodeling

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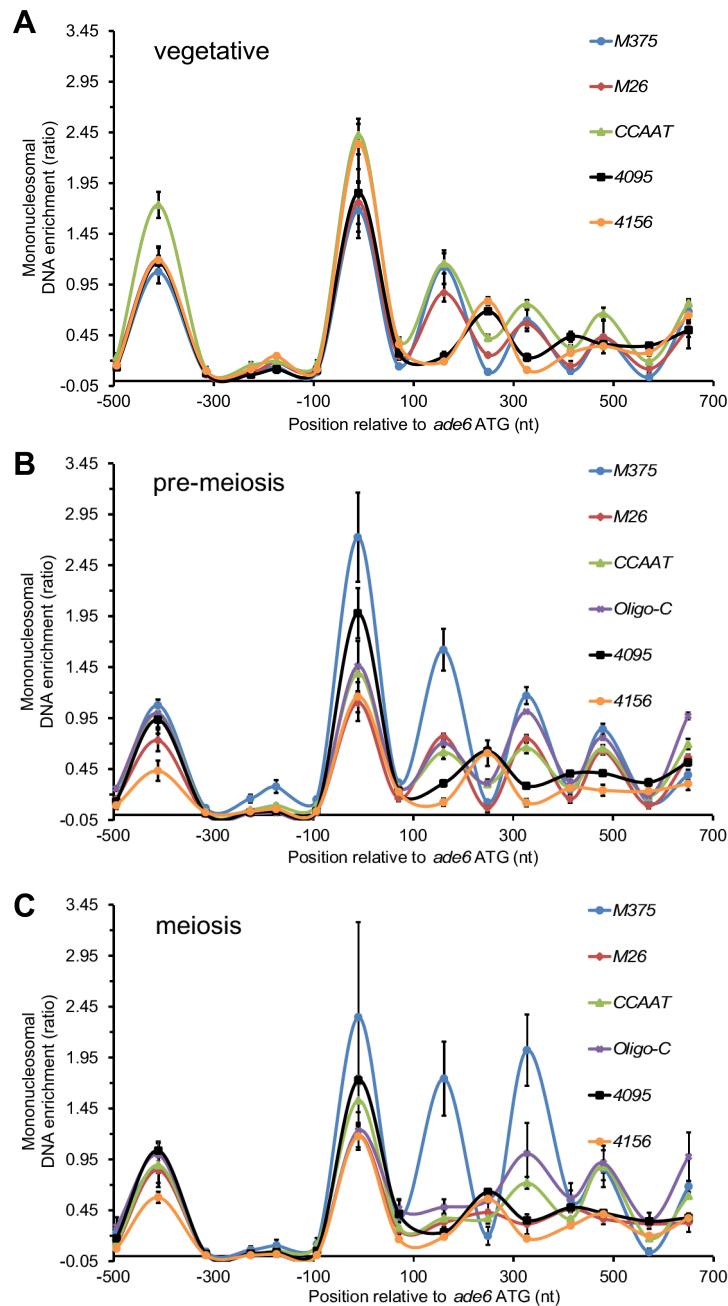


Figure S1. Hotspot-specific chromatin remodeling occurs during mitosis and meiosis.

Plot compares the chromatin maps of strains harboring the basal recombination control (*M375*) and hotspot DNA sequence motifs (*M26*, *CCAAT*, *Oligo-C*, *4095*, *4156*). Coordinates are relative to the first nucleotide of the *ade6* start codon (see Figure 2); data are mean $\pm$ SD from three biological replicates using cells under the following conditions. **(A)** Asynchronous, vegetative population cultured in rich media. **(B)** Synchronized in G_0 (G_1) phase of the cell cycle by nitrogen starvation in defined minimal media (0 hours of meiosis). **(C)** At 3 hours of synchronous meiosis.

Table S1. Fission yeast strains used in study

Strain	Genotype ^a
WSP 0006	<i>h+ ade6-M375</i>
WSP 0016	<i>h- ade6-M210</i>
WSP 0020	<i>h+ ade6-M26 pat1-114</i>
WSP 2248	<i>h+ ade6-M375 pat1-114</i>
WSP 2388	<i>h+ ade6-M26 snf22::ura4F ura4-D18 his5-303</i>
WSP 2650	<i>h+ ade6-M26 atf1-D15::ura4F his3-D1 leu1-32 ura4-D18</i>
WSP 2651	<i>h- ade6-M210 atf1-D15::ura4F his3-D1 leu1-32 ura4-D18</i>
WSP 2654	<i>h+ ade6-M375 atf1-D15::ura4F his3-D1 leu1-32 ura4-D18</i>
WSP 2655	<i>h+ ade6-M26 pcr1-D1::his3F ura4-D18 his3-D1</i>
WSP 2657	<i>h- ade6-M210 pcr1-D1::his3F ura4-D18 his3-D1</i>
WSP 2659	<i>h+ ade6-M375 pcr1-D1::his3F ura4-D18 his3-D1</i>
WSP 4115	<i>h+ ade6-M26 ura4-D18 his3-D1</i>
WSP 5866	<i>h- ade6-M210 snf22::ura4F ura4-D18 leu1-32</i>
WSP 5867	<i>h+ ade6-M210 snf22::ura4F ura4-D18 leu1-32</i>
WSP 5887	<i>h- ade6-M210 mst2-D::kan^R</i>
WSP 5888	<i>h+ ade6-M210 mst2-D::kan^R</i>
WSP 5892	<i>h+ ade6-M375 mst2-D::kan^R</i>
WSP 5896	<i>h+ ade6-M26 mst2D::kan^R</i>
WSP 5930	<i>h+ ade6-M375 gcn5-D::ura4F ura4-D18</i>
WSP 5943	<i>h+ ade6-M26 gcn5-D::ura4F ura4-D18</i>
WSP 6140	<i>h+ ade6-M26 pat1-114 ura4-D18 his3-D1 pcr1-D1::his3F</i>
WSP 6540	<i>h+ ade6-4002 ura4-D18</i>
WSP 6546	<i>h+ ade6-4002 pat1-114 php2-D::kan^R</i>
WSP 6559	<i>h+ ade6-4095 ura4-D18</i>
WSP 6563	<i>h+ ade6-4099 pat1-114 rst2-D::ura4F ura4-D18</i>
WSP 6573	<i>h+ ade6-4099 ura4-D18</i>
WSP 6586	<i>h+ ade6-4156 ura4-D18</i>
WSP 6803	<i>h+ ade6-M375 rst2-D::ura4F ura4-D18</i>
WSP 6806	<i>h- ade6-M210 rst2-D::ura4F ura4-D18</i>
WSP 7086	<i>h+ ade6-4095 pat1-114</i>
WSP 7087	<i>h+ ade6-4099 pat1-114</i>
WSP 7090	<i>h+ ade6-4156 pat1-114</i>
WSP 7091	<i>h+ ade6-4002 pat1-114</i>
WSP 7489	<i>h+ ade6-4156 mst2-D::kan^R</i>
WSP 7492	<i>h+ ade6-4099 mst2-D::kan^R</i>
WSP 7494	<i>h+ ade6-4095 mst2-D::kan^R</i>
WSP 7495	<i>h+ ade6-4002 mst2D::kan^R ura4-D18</i>
WSP 7501	<i>h- ade6-M26 hrp3::kan^R leu1-32</i>
WSP 7511	<i>h-ade6-4002 php2-D::kan^R</i>
WSP 7519	<i>h+ ade6-M210 php2-D::kan^R</i>
WSP 7523	<i>h- ade6-M375 php2-D::kan^R</i>
WSP 7528	<i>h+ ade6-M375 php3-D::kan^R</i>
WSP 7531	<i>h+ ade6-M210 php3-D:: kan^R ura4-D18</i>
WSP 7533	<i>h- ade6-M210 php3-D::kan^R</i>
WSP 7543	<i>h- ade6-4002 php3-D::kan^R</i>
WSP 7560	<i>h+ ade6-4099 gcn5-D::ura4F ura4-D18</i>

WSP 7561	<i>h+ ade6-4002 gcn5-D::ura4F ura4-D18</i>
WSP 7565	<i>h+ ade6-4156 gcn5-D::ura4F ura4-D18</i>
WSP 7566	<i>h- ade6-4095 gcn5-D::ura4F ura4-D18</i>
WSP 7570	<i>h+ ade6-M210 gcn5-D::ura4F ura4-D18</i>
WSP 7571	<i>h- ade6-M210 gcn5-D::ura4F ura4-D18</i>
WSP 7574	<i>h+ ade6-M210 hrp3::kan^R</i>
WSP 7576	<i>h- ade6-M210 hrp3::kan^R</i>
WSP 7577	<i>h+ ade6-M26 hrp3::kan^R ura4-D18</i>
WSP 7580	<i>h+ ade6-M26 hrp3::kan^R</i>
WSP 7583	<i>h+ ade6-4156 hrp3::kan^R</i>
WSP 7586	<i>h- ade6-4095 hrp3::kan^R</i>
WSP 7670	<i>h+ ade6-4156 snf22::ura4F ura4-D18</i>
WSP 7673	<i>h+ ade6-4095 snf22::ura4F ura4-D18 leu1-32</i>
WSP 7677	<i>h+ ade6-4156 snf22::ura4F ura4-D18</i>
WSP 7678	<i>h+ ade6-4002 pat1-114 php3-D::kan^R</i>
WSP 7704	<i>h+ ade6-4002 php5::kan^R ura4-D18</i>
WSP 7713	<i>h- ade6-M210 php5::kan^R</i>
WSP 7715	<i>h- ade6-M375 php5:: kan^R ura4-D18</i>
WSP 7720	<i>h+ ade6-M26 php5::kan^R</i>
WSP 7725	<i>h+ ade6-M375 snf22::ura4F ura4-D18</i>
WSP 7763	<i>h- ade6-M375 hrp3::kan^R</i>

^a Fission yeast nomenclature (Kohli 1987) uses a “D” to designate deletion. These are referred to as “Δ” in the text and figures for the sake of clarity. Genotypes *ade6-M26*, *ade6-4095* and *ade6-4156* correspond to their type of DNA sequence motif (*M26*, *4095* or *4156*). The *ade6-4002* allele contains the CCAAT DNA sequence motif; the *ade6-4099* allele contains the *Oligo-C* DNA sequence motif. See Table S2 for the DNA sequences and locations of the *ade6* alleles.

Table S2. DNA sequences and locations of *ade6* alleles used in this study

<i>ade6</i> allele	Relevant sequence		
	121		1461
<i>ade6</i> (wt)	...AAACAAATTG	A.TGGAGGAC	GTGAGCACAT...AGATGCCTCG...
<i>ade6-M26</i>	...AAACAAATTG	A.TGGAtGAC	GTGAGCACAT...AGATGCCTCG...
<i>ade6-CCAAT</i> ^a	...AAACAAATTG	AtTGGAGGAC	GTGAGCACAT...AGATGCCTCG...
<i>ade6-Oligo-C</i>	...tAACAAATTG	A. accccGca	cTGAGCACAT...AGATGCCTCG...
<i>ade6-4095</i> ^b	...tAACAAATTG	g.TctgGacC	GTGAGCACAT...AGATGCCTCG...
<i>ade6-4156</i>	...tAACAAATTc	g.gccgaGAC	GTGAGCACAT...AGATGCCTCG...
<i>ade6-M375</i>	...AAACAAATTG	A.TtGAGGAC	GTGAGCACAT...AGATGCCTCG...
<i>ade6-M210</i>	...AAACAAATTG	A.TGGAGGAC	GTGAGCACAT...AGATGcTTCG...

The *ade6* ORF is 1,659 bp in length and all coordinates described in this study are numbered relative to the first nucleotide of the start codon. The hotspot (*M26*, *CCAAT*, *Oligo-C*, *4095*, *4156*), basal recombination control (*M375*), and test-cross (*M210*) alleles differ from wild-type (wt) only by the indicated bp substitutions (bold lower case). The bp substitutions of the hotspot alleles create DNA binding sites (grey shading) for sequence-specific, hotspot-activating binding proteins (see Table 1). Each mutant allele also renders cells auxotrophic for adenine, allowing one to score for the frequency of adenine prototrophic recombinants (*ade6*⁺) from heteroallelic crosses that contain a 5' allele (*M375*, *M26*, *CCAAT*, *Oligo-C*, *4095* or *4156*) and the 3' test-cross allele (*M210*).

^a The consensus motif 5'-CCAATCA-3' is on the complementary strand.

^b The consensus motif is 5'-GGTCTRGACC-3' where R = A or G.

Table S3. DNA sequences and locations of PCR primers used in this study.

Amplicon number ^a	Primer name ^b	Primer sequence
1	<i>ade6</i> -537-F	5'-CTTCGATAATGTCGAGTTCCTCTT-3'
	<i>ade6</i> -451-R	5'-CTGAAACTAAACCCAGGGAGTC-3'
2	<i>ade6</i> -460-F	5'-TTTAGTTTCAGGTATGTTTTGGTCA-3'
	<i>ade6</i> -361-R	5'-TACGGTCTATTA AAAAGTCGTCCAT-3'
3	<i>ade6</i> -370-F	5'-ATAGACCGTATTCTGCACTTGG-3'
	<i>ade6</i> -260-R	5'-AGCAACGTTTTGTTGTCGTTATA-3'
4	<i>ade6</i> -276-F	5'-CGACAACAACGTTGCTTTATAT-3'
	<i>ade6</i> -175-R	5'-CAACTTAAAGCAGCATACGCTAA-3'
5	<i>ade6</i> -221-F	5'-AAAATAGCAAAGCTATATTGATTTTAGCG-3'
	<i>ade6</i> -127-R	5'-GCATCGTATTAATTCTGTCAATCGTTAC-3'
6	<i>ade6</i> -145-F	5'-GACAGAATTAATACGATGCAAACCTC-3'
	<i>ade6</i> -41-R	5'-TGAGATGGTAAATGTTGAAAAAACG-3'
7	<i>ade6</i> -57-F	5'-CAACATTTACCATCTCATTAAAGCTGAG-3'
	<i>ade6</i> +36-R	5'-ACCTCCAAGGATCCCTACAA-3'
8	<i>ade6</i> +24-F	5'-GATCCTTGGAGGTGGTCAAT-3'
	<i>ade6</i> +118-R	5'-CAGGAGAATTTGCTGCATCC-3'
9	<i>ade6</i> +104-F	5'-CAGCAAATTCTCCTGCCAAAC-3'
	<i>ade6</i> +190-R	5'-GACAGTTCAACAATTGCATCGG-3'
10	<i>ade6</i> +200-F	5'-GCACGTTATTAACAAGTAAATTGAGC-3'
	<i>ade6</i> +298-R	5'-ATCGCAGAGTTGCAGGAGAG-3'
11	<i>ade6</i> +275-F	5'-AACCCCTCCTGCAACTCT-3'
	<i>ade6</i> +379-R	5'-GGTCAGGTGCATCGCAA-3'
12	<i>ade6</i> +372-F	5'-ACCTGACCAGGAAAGTGTG-3'
	<i>ade6</i> +457-R	5'-GACCGTCGTAAGCCAATGT-3'
13	<i>ade6</i> +438-F	5'-AACATTGGCTTACGACGG-3'
	<i>ade6</i> +522-R	5'-ACGATCACCAAGTGCTTTGA-3'
14	<i>ade6</i> +514-F	5'-GGTGATCGTCCGCTTTATGT-3'
	<i>ade6</i> +629-R	5'-TGAATGGTCTCAGTTGTAGGATAAG-3'
15	<i>ade6</i> +602-F	5'-ATGCTTATCCTACAAGT-3'
	<i>ade6</i> +699-R	5'-TTGAGCACGCTGTTGAATTG-3'
smc5 ^c	<i>smc5</i> -F	5'-GGATTACTTTTTCTTCGTTTCGAAGG-3'
	<i>smc5</i> -R	5'-CTCCTAGTTGACTGAAATCCTCCTTA-3'

^a The amplicon numbers correspond to those depicted schematically in Figure 2.

^b The number after *ade6* indicates position of the 5' end of the primer, relative to (+ or -) the first nucleotide in the start codon of *ade6*; F, forward primer; R, reverse primer.

^c The *smc5* primers amplify a nucleosome-protected region of chromosome I (coordinates 5,229,713 to 5,229,787) near the 5' end of the *smc5* gene that serves as an internal reference.

Table S4. Discrete data for DNA sequence-dependent, binding protein-dependent activation of meiotic recombination hotspots

Cross ^a	Relevant genotype ^b	Replicate	<i>ade6⁺</i> recombinant		Total		Rec. freq. per 10 ⁴ cells
			Colonies counted	Titer per ml	Colonies counted	Titer per ml	
1	<i>ade6-M375</i>	A	353	35300	110	110 × 10 ⁶	3.21
		B	312	31200	89	89 × 10 ⁶	3.50
		C	487	48700	155	155 × 10 ⁶	3.14
2	<i>ade6-M26</i>	A	180	180000	235	235 × 10 ⁵	76.6
		B	399	399000	685	685 × 10 ⁵	58.2
		C	189	189000	320	320 × 10 ⁵	59.1
3	<i>ade6-M26 atf1Δ</i>	A	440	44000	113	113 × 10 ⁶	3.89
		B	690	69000	142	142 × 10 ⁶	4.86
		C	370	37000	130	130 × 10 ⁶	2.85
4	<i>ade6-M26 pcr1Δ</i>	A	120	1200	385	385 × 10 ⁵	3.12
		B	95	950	415	415 × 10 ⁵	2.29
		C	166	1660	560	560 × 10 ⁵	2.96
5	<i>ade6-4002</i>	A	123	123000	211	211 × 10 ⁵	58.3
		B	87	87000	129	129 × 10 ⁵	67.4
		C	200	200000	410	410 × 10 ⁵	48.8
6	<i>ade6-4002 php2Δ</i>	A	163	1630	313	313 × 10 ⁴	5.21
		B	230	2300	401	401 × 10 ⁴	5.74
		C	310	3100	650	650 × 10 ⁴	4.77
7	<i>ade6-4002 php3Δ</i>	A	112	11200	256	256 × 10 ⁵	4.38
		B	167	16700	260	260 × 10 ⁵	6.42
		C	103	10300	58	58 × 10 ⁵	17.8
8	<i>ade6-4002 php5Δ</i>	A	60	600	299	299 × 10 ⁴	2.01
		B	350	3500	268	268 × 10 ⁵	1.31
		C	82	820	960	960 × 10 ⁴	0.854
9	<i>ade6-4099</i>	A	150	1500000	162	162 × 10 ⁶	92.6
		B	140	1400000	117	117 × 10 ⁶	120
		C	498	4980000	298	298 × 10 ⁶	167
10	<i>ade6-4099 rst2Δ</i>	A	96	960	239	239 × 10 ⁴	4.02
		B	273	2730	641	641 × 10 ⁴	4.26
		C	500	5000	270	270 × 10 ⁴	18.5
11	<i>ade6-4095</i>	A	692	69200	130	130 × 10 ⁵	53.2
		B	833	83300	125	125 × 10 ⁵	66.6
		C	282	28200	112	112 × 10 ⁵	25.2
12	<i>ade6-4156</i>	A	233	233000	455	455 × 10 ⁵	51.2
		B	341	341000	575	575 × 10 ⁵	59.3
		C	120	120000	270	270 × 10 ⁵	44.4
13	<i>ade6-M375</i>	A	353	35300	110	110 × 10 ⁶	3.21
		B	312	31200	89	89 × 10 ⁶	3.50
		C	487	48700	155	155 × 10 ⁶	3.14
14	<i>ade6-M375 atf1Δ</i>	A	232	2320	432	432 × 10 ⁴	5.37

		B	157	1570	344	344×10^4	4.56
		C	133	1330	543	543×10^4	2.44
15	<i>ade6-M375 pcr1Δ</i>	A	358	35800	185	185×10^5	1.94
		B	429	42900	70	70×10^5	6.13
		C	333	33300	215	215×10^5	1.55
16	<i>ade6-M375 php2Δ</i>	A	428	42800	447	447×10^5	9.57
		B	360	36000	444	444×10^5	8.11
		C	378	37800	380	380×10^5	9.95
17	<i>ade6-M375 php3Δ</i>	A	86	8600	100	100×10^5	8.60
		B	153	15300	195	195×10^5	7.85
		C	85	8500	111	111×10^5	7.66
18	<i>ade6-M375 php5Δ</i>	A	160	16000	270	270×10^5	5.93
		B	80	8000	150	150×10^5	5.33
		C	217	21700	234	234×10^5	9.27
19	<i>ade6-M375 rst2Δ</i>	A	98	980	358	358×10^5	0.27
		B	520	5200	340	340×10^5	1.53
		C	433	4330	187	187×10^5	2.32

^a Cross number corresponds to lane number listed in Figure 1.

^b See Table S1 for complete genotypes. Frequencies were determined by test crosses to a corresponding strain with the *M210* test cross allele. See primary text for additional details.

Table S5. Discrete data for impact of chromatin remodeling enzymes on the activation of meiotic recombination hotspots

Cross ^a	Relevant genotype ^b	Replicate	<i>ade6⁺</i> recombinant		Total		Rec. freq. per 10 ⁴ cells
			Colonies counted	Titer per ml	Colonies counted	Titer per ml	
1	<i>ade6-M375</i>	A	403	40300	84	84 × 10 ⁶	4.80
		B	310	3100	102	102 × 10 ⁶	3.04
		C	290	29000	61	61 × 10 ⁶	4.75
2	<i>ade6-M375 snf22Δ</i>	A	470	4700	188	188 × 10 ⁵	2.50
		B	650	6500	199	199 × 10 ⁵	3.27
		C	380	3800	107	107 × 10 ⁵	3.55
3	<i>ade6-M375 hrp3Δ</i>	A	500	50000	720	720 × 10 ⁵	6.94
		B	140	14000	620	620 × 10 ⁵	2.26
		C	300	30000	343	343 × 10 ⁵	8.75
4	<i>ade6-M375</i>	A	353	35300	110	110 × 10 ⁶	3.21
		B	312	31200	89	89 × 10 ⁶	3.51
		C	487	48700	155	155 × 10 ⁶	3.14
5	<i>ade6-M375 gcn5Δ</i>	A	171	17100	721	721 × 10 ⁵	2.37
		B	140	14000	800	800 × 10 ⁵	1.75
		C	269	26900	512	512 × 10 ⁵	5.25
6	<i>ade6-M375 mst2Δ</i>	A	123	12300	466	466 × 10 ⁵	2.64
		B	196	19600	267	267 × 10 ⁵	7.34
		C	129	12900	370	370 × 10 ⁵	3.49
7	<i>ade6-M26</i>	A	180	180000	235	235 × 10 ⁵	76.6
		B	399	399000	685	685 × 10 ⁵	58.3
		C	189	189000	320	320 × 10 ⁵	59.1
8	<i>ade6-M26 snf22Δ</i>	A	223	22300	340	340 × 10 ⁵	6.56
		B	194	19400	70	70 × 10 ⁵	27.7
		C	123	12300	98	98 × 10 ⁵	12.6
9	<i>ade6-M26 hrp3Δ</i>	A	187	187000	128	128 × 10 ⁶	14.6
		B	262	262000	93	93 × 10 ⁶	28.2
		C	224	224000	75	75 × 10 ⁶	29.9
10	<i>ade6-M26 gcn5Δ</i>	A	156	156000	73	73 × 10 ⁶	21.4
		B	229	229000	104	104 × 10 ⁶	22.0
		C	158	158000	350	350 × 10 ⁵	45.1
11	<i>ade6-M26 mst2Δ</i>	A	186	186000	392	392 × 10 ⁵	47.5
		B	150	150000	391	391 × 10 ⁵	38.4
		C	92	92000	498	498 × 10 ⁵	18.5
12	<i>ade6-4002</i>	A	224	224000	360	360 × 10 ⁵	62.2
		B	120	120000	140	140 × 10 ⁵	85.7
		C	222	222000	378	378 × 10 ⁵	58.7
13	<i>ade6-4002 snf22Δ</i>	A	128	12800	99	99 × 10 ⁶	12.9
		B	450	4500	104	104 × 10 ⁶	4.33
		C	80	800	130	130 × 10 ⁶	0.620
14	<i>ade6-4002 hrp3Δ</i>	A	250	25000	420	420 × 10 ⁴	59.5

		B	247	24700	305	305×10^4	81.0
		C	280	28000	730	730×10^4	38.4
15	<i>ade6-4002</i>	A	123	123000	211	211×10^5	58.3
		B	87	87000	129	129×10^5	67.4
		C	200	200000	410	410×10^5	48.8
16	<i>ade6-4002 gcn5Δ</i>	A	590	59000	189	189×10^5	31.2
		B	121	121000	420	420×10^5	28.8
		C	549	54900	232	232×10^5	23.7
17	<i>ade6-4002 mst2Δ</i>	A	340	34000	725	725×10^4	46.9
		B	407	40700	100	100×10^5	40.7
		C	323	32300	739	739×10^4	43.7
18	<i>ade6-4099</i>	A	150	15000	162	162×10^4	92.6
		B	140	14000	117	117×10^4	120
		C	498	49800	298	298×10^4	167
19	<i>ade6-4099 snf22Δ</i>	A	180	1800	175	175×10^4	10.3
		B	96	960	75	75×10^4	12.8
		C	102	1020	167	167×10^4	6.11
20	<i>ade6-4099</i>	A	111	1110000	81	81×10^6	137
		B	320	3200000	299	299×10^6	107
		C	135	135×10^4	108	108×10^6	125
21	<i>ade6-4099 hrp3Δ</i>	A	139	139000	122	122×10^5	114
		B	428	428000	400	400×10^5	107
		C	499	499000	621	621×10^5	80.4
22	<i>ade6-4099 mst2Δ</i>	A	371	371000	300	300×10^5	124
		B	609	609000	298	298×10^5	204
		C	168	168000	103	103×10^5	163
23	<i>ade6-4099</i>	A	450	450000	360	360×10^5	125
		B	391	391000	291	291×10^5	134
		C	664	664000	700	700×10^5	94.9
24	<i>ade6-4099 gcn5Δ</i>	A	146	146000	154	154×10^5	94.8
		B	243	243000	193	193×10^5	126
		C	139	139000	142	142×10^5	97.9
25	<i>ade6-4095</i>	A	351	35100	110	110×10^5	31.9
		B	186	18600	79	79×10^5	23.5
		C	503	50300	187	187×10^5	26.9
26	<i>ade6-4095 snf22Δ</i>	A	540	54000	270	270×10^5	20.0
		B	235	23500	143	143×10^5	16.4
		C	295	29500	296	296×10^5	9.97
27	<i>ade6-4095</i>	A	240	24000	331	331×10^4	72.5
		B	698	69800	839	839×10^4	83.2
		C	323	32300	370	370×10^4	87.3
28	<i>ade6-4095 mst2</i>	A	370	370000	266	266×10^5	139
		B	337	337000	363	363×10^5	92.8
		C	365	365000	321	321×10^5	113
29	<i>ade6-4095</i>	A	692	69200	130	130×10^5	53.2
		B	833	83300	125	125×10^5	66.6
		C	282	28200	112	112×10^5	25.2

30	<i>ade6-4095 hrp3Δ</i>	A	105	105000	186	186×10^5	56.5
		B	100	100000	266	266×10^5	37.6
		C	129	129000	267	267×10^5	48.3
31	<i>ade6-4095 gcn5Δ</i>	A	105	105000	244	244×10^5	43.0
		B	106	106000	265	265×10^5	40.0
		C	90	90000	300	300×10^5	30.0
32	<i>ade6-4156</i>	A	233	233000	455	455×10^5	51.2
		B	341	341000	575	575×10^5	59.3
		C	120	120000	270	270×10^5	44.4
33	<i>ade6-4156 snf22Δ</i>	A	535	53500	985	985×10^5	5.43
		B	350	35000	479	479×10^5	7.31
		C	370	37000	347	347×10^5	10.7
34	<i>ade6-4156 hrp3Δ</i>	A	142	142000	348	348×10^5	40.8
		B	177	177000	426	426×10^5	41.6
		C	312	312000	438	438×10^5	71.2
35	<i>ade6-4156 gcn5Δ</i>	A	281	281000	290	290×10^5	96.9
		B	311	311000	667	667×10^5	46.6
		C	229	229000	590	590×10^5	38.8
36	<i>ade6-4156 mst2Δ</i>	A	167	167000	272	272×10^5	61.4
		B	245	245000	401	401×10^5	61.1
37	<i>ade6-4156</i>	A	479	479000	304	304×10^5	158
		B	110	110000	185	185×10^5	59.5
		C	214	214000	267	267×10^5	80.2
38	<i>ade6-4156 mst2Δ</i>	A	101	101000	137	137×10^5	73.7
		B	236	236000	315	315×10^5	74.9
		C	159	159000	219	219×10^5	72.6

^a Data plotted in Figure 5 involved pairwise comparisons between wild-type and deletion mutant crosses conducted on the same day using the same batches of reagents. These matched groups are crosses 1-3, 4-6, 7-11, 12-14, 15-17, 18-19; 20-22, 23-24, 25-26, 27-28, 29-31, 32-36 and 37-38.

^b See Table S1 for complete genotypes and the primary text for additional details.

Table S6. Discrete data for DNA sequence-specific, binding protein-dependent remodeling of chromatin structure at meiotic recombination hotspots

Relevant genotype ^a	PCR primer pair ^b	Mononucleosomal DNA enrichment ^c		
		Vegetative (mean+/- SD) ^d	Pre-meiosis (mean+/- SD)	3 hr meiosis (mean+/- SD)
<i>ade6-M375 pat1-114</i>	1	0.144 +/- 0.014	0.144 +/- 0.007	0.230 +/- 0.077
	2	1.076 +/- 0.114	1.076 +/- 0.057	0.868 +/- 0.148
	3	0.066 +/- 0.013	0.068 +/- 0.015	0.044 +/- 0.026
	4	0.092 +/- 0.020	0.160 +/- 0.038	0.062 +/- 0.035
	5	0.137 +/- 0.027	0.279 +/- 0.063	0.105 +/- 0.056
	6	0.086 +/- 0.020	0.151 +/- 0.028	0.120 +/- 0.059
	7	1.681 +/- 0.273	2.725 +/- 0.438	2.347 +/- 0.933
	8	0.144 +/- 0.020	0.319 +/- 0.014	0.388 +/- 0.172
	9	1.122 +/- 0.165	1.621 +/- 0.205	1.743 +/- 0.364
	10	0.089 +/- 0.024	0.124 +/- 0.012	0.200 +/- 0.089
	11	0.596 +/- 0.106	1.170 +/- 0.083	2.023 +/- 0.350
	12	0.100 +/- 0.028	0.249 +/- 0.016	0.555 +/- 0.091
	13	0.430 +/- 0.011	0.842 +/- 0.054	0.859 +/- 0.181
	14	0.039 +/- 0.006	0.122 +/- 0.003	0.039 +/- 0.036
	15	0.685 +/- 0.102	0.393 +/- 0.051	0.685 +/- 0.056
<i>ade6-M26 pat1-114</i>	1	0.197 +/- 0.030	0.156 +/- 0.009	0.115 +/- 0.054
	2	1.194 +/- 0.133	0.732 +/- 0.107	0.845 +/- 0.028
	3	0.068 +/- 0.022	0.010 +/- 0.001	0.021 +/- 0.002
	4	0.080 +/- 0.024	0.015 +/- 0.003	0.027 +/- 0.003
	5	0.183 +/- 0.047	0.028 +/- 0.003	0.042 +/- 0.006
	6	0.136 +/- 0.040	0.033 +/- 0.002	0.041 +/- 0.013
	7	1.758 +/- 0.209	1.102 +/- 0.094	1.183 +/- 0.112
	8	0.245 +/- 0.036	0.163 +/- 0.030	0.259 +/- 0.031
	9	0.869 +/- 0.087	0.770 +/- 0.027	0.332 +/- 0.044
	10	0.255 +/- 0.020	0.070 +/- 0.043	0.429 +/- 0.023
	11	0.566 +/- 0.047	0.747 +/- 0.037	0.314 +/- 0.098
	12	0.150 +/- 0.047	0.158 +/- 0.039	0.463 +/- 0.026
	13	0.433 +/- 0.161	0.623 +/- 0.032	0.365 +/- 0.051
	14	0.119 +/- 0.037	0.092 +/- 0.029	0.317 +/- 0.021
	15	0.519 +/- 0.197	0.565 +/- 0.028	0.329 +/- 0.091
<i>ade6-M26 pat1-114 pcr1Δ</i>	1	n.a.	0.148 +/- 0.051	0.121 +/- 0.006
	2	n.a.	0.242 +/- 0.018	0.784 +/- 0.098
	3	n.a.	0.002 +/- 0.001	0.007 +/- 0.003
	4	n.a.	0.002 +/- 0.000	0.009 +/- 0.002
	5	n.a.	0.007 +/- 0.002	0.016 +/- 0.004
	6	n.a.	0.003 +/- 0.000	0.015 +/- 0.002
	7	n.a.	0.440 +/- 0.056	1.164 +/- 0.032
	8	n.a.	0.094 +/- 0.033	0.294 +/- 0.028
	9	n.a.	0.774 +/- 0.067	0.641 +/- 0.029
	10	n.a.	0.064 +/- 0.029	0.189 +/- 0.012
	11	n.a.	0.649 +/- 0.131	0.595 +/- 0.070
	12	n.a.	0.178 +/- 0.053	0.165 +/- 0.022
	13	n.a.	0.731 +/- 0.068	0.619 +/- 0.035
	14	n.a.	0.046 +/- 0.023	0.098 +/- 0.009
	15	n.a.	0.323 +/- 0.046	0.475 +/- 0.060
<i>ade6-4002 pat1-114</i>	1	0.238 +/- 0.032	0.133 +/- 0.011	0.133 +/- 0.006
	2	1.735 +/- 0.129	0.998 +/- 0.083	0.894 +/- 0.216
	3	0.108 +/- 0.030	0.027 +/- 0.001	0.025 +/- 0.010

	4	0.156 +/- 0.030	0.050 +/- 0.001	0.028 +/- 0.010
	5	0.193 +/- 0.034	0.093 +/- 0.015	0.055 +/- 0.015
	6	0.173 +/- 0.032	0.095 +/- 0.005	0.112 +/- 0.025
	7	2.420 +/- 0.112	1.388 +/- 0.086	1.530 +/- 0.235
	8	0.399 +/- 0.031	0.277 +/- 0.046	0.283 +/- 0.049
	9	1.158 +/- 0.099	0.616 +/- 0.067	0.372 +/- 0.046
	10	0.426 +/- 0.031	0.302 +/- 0.010	0.372 +/- 0.052
	11	0.757 +/- 0.041	0.660 +/- 0.057	0.721 +/- 0.058
	12	0.326 +/- 0.027	0.268 +/- 0.007	0.369 +/- 0.010
	13	0.663 +/- 0.060	0.650 +/- 0.036	0.880 +/- 0.060
	14	0.193 +/- 0.009	0.181 +/- 0.004	0.176 +/- 0.007
	15	0.766 +/- 0.040	0.695 +/- 0.051	0.592 +/- 0.003
<i>ade6-4002 pat1-114 php3Δ</i>	1	n.a.	0.158 +/- 0.019	0.144 +/- 0.036
	2	n.a.	0.537 +/- 0.119	0.655 +/- 0.126
	3	n.a.	0.033 +/- 0.009	0.020 +/- 0.004
	4	n.a.	0.032 +/- 0.007	0.019 +/- 0.002
	5	n.a.	0.044 +/- 0.006	0.038 +/- 0.005
	6	n.a.	0.032 +/- 0.005	0.020 +/- 0.004
	7	n.a.	0.801 +/- 0.157	1.508 +/- 0.155
	8	n.a.	0.185 +/- 0.013	0.207 +/- 0.035
	9	n.a.	0.778 +/- 0.040	0.958 +/- 0.223
	10	n.a.	0.163 +/- 0.013	0.106 +/- 0.021
	11	n.a.	1.007 +/- 0.089	0.560 +/- 0.080
	12	n.a.	0.181 +/- 0.020	0.080 +/- 0.013
	13	n.a.	0.881 +/- 0.035	0.857 +/- 0.088
	14	n.a.	0.058 +/- 0.002	0.053 +/- 0.005
	15	n.a.	0.607 +/- 0.060	0.609 +/- 0.062
<i>ade6-4099 pat1-114</i>	1	n.a.	0.259 +/- 0.054	0.289 +/- 0.094
	2	n.a.	0.995 +/- 0.003	0.995 +/- 0.127
	3	n.a.	0.008 +/- 0.001	0.015 +/- 0.003
	4	n.a.	0.012 +/- 0.002	0.034 +/- 0.016
	5	n.a.	0.020 +/- 0.004	0.016 +/- 0.003
	6	n.a.	0.018 +/- 0.004	0.021 +/- 0.004
	7	n.a.	1.460 +/- 0.052	1.233 +/- 0.043
	8	n.a.	0.266 +/- 0.030	0.467 +/- 0.083
	9	n.a.	0.705 +/- 0.067	0.482 +/- 0.077
	10	n.a.	0.312 +/- 0.039	0.545 +/- 0.109
	11	n.a.	1.014 +/- 0.181	1.008 +/- 0.300
	12	n.a.	0.324 +/- 0.070	0.574 +/- 0.142
	13	n.a.	0.757 +/- 0.101	0.916 +/- 0.170
	14	n.a.	0.185 +/- 0.028	0.347 +/- 0.079
	15	n.a.	0.971 +/- 0.157	0.977 +/- 0.238
<i>ade6-4099 pat1-114 rst2Δ</i>	1	n.a.	0.114 +/- 0.010	0.154 +/- 0.016
	2	n.a.	0.608 +/- 0.019	0.965 +/- 0.013
	3	n.a.	0.012 +/- 0.004	0.015 +/- 0.002
	4	n.a.	0.025 +/- 0.010	0.023 +/- 0.005
	5	n.a.	0.025 +/- 0.007	0.031 +/- 0.006
	6	n.a.	0.021 +/- 0.006	0.028 +/- 0.005
	7	n.a.	1.218 +/- 0.004	1.366 +/- 0.065
	8	n.a.	0.251 +/- 0.042	0.293 +/- 0.021
	9	n.a.	0.671 +/- 0.022	0.681 +/- 0.063
	10	n.a.	0.121 +/- 0.015	0.170 +/- 0.032
	11	n.a.	0.619 +/- 0.063	0.721 +/- 0.031
	12	n.a.	0.104 +/- 0.013	0.128 +/- 0.020
	13	n.a.	0.719 +/- 0.039	0.682 +/- 0.004
	14	n.a.	0.061 +/- 0.009	0.092 +/- 0.013
	15	n.a.	0.650 +/- 0.053	0.692 +/- 0.005
<i>ade6-4095 pat1-114</i>	1	0.135 +/- 0.004	0.131 +/- 0.023	0.176 +/- 0.007
	2	1.167 +/- 0.067	0.935 +/- 0.137	1.037 +/- 0.099

<i>ade6-4156 pat1-114</i>	3	0.076 +/- 0.014	0.016 +/- 0.003	0.023 +/- 0.003
	4	0.063 +/- 0.003	0.025 +/- 0.005	0.025 +/- 0.001
	5	0.117 +/- 0.039	0.038 +/- 0.006	0.041 +/- 0.006
	6	0.107 +/- 0.018	0.036 +/- 0.010	0.052 +/- 0.001
	7	1.853 +/- 0.381	1.980 +/- 0.246	1.727 +/- 0.051
	8	0.272 +/- 0.025	0.238 +/- 0.037	0.414 +/- 0.008
	9	0.242 +/- 0.046	0.310 +/- 0.032	0.236 +/- 0.012
	10	0.687 +/- 0.021	0.627 +/- 0.036	0.632 +/- 0.008
	11	0.232 +/- 0.036	0.285 +/- 0.001	0.351 +/- 0.019
	12	0.437 +/- 0.049	0.405 +/- 0.022	0.479 +/- 0.030
	13	0.363 +/- 0.036	0.409 +/- 0.019	0.425 +/- 0.018
	14	0.349 +/- 0.026	0.318 +/- 0.034	0.343 +/- 0.014
	15	0.501 +/- 0.067	0.514 +/- 0.033	0.377 +/- 0.013
	1	0.152 +/- 0.016	0.095 +/- 0.036	0.074 +/- 0.009
	2	1.191 +/- 0.122	0.433 +/- 0.099	0.578 +/- 0.055
	3	0.101 +/- 0.005	0.026 +/- 0.011	0.009 +/- 0.002
	4	0.114 +/- 0.017	0.035 +/- 0.016	0.010 +/- 0.002
	5	0.245 +/- 0.011	0.058 +/- 0.023	0.020 +/- 0.003
	6	0.115 +/- 0.012	0.037 +/- 0.016	0.011 +/- 0.002
	7	2.336 +/- 0.248	1.161 +/- 0.241	1.177 +/- 0.133
	8	0.361 +/- 0.048	0.227 +/- 0.066	0.166 +/- 0.015
	9	0.192 +/- 0.002	0.124 +/- 0.036	0.189 +/- 0.005
	10	0.786 +/- 0.040	0.606 +/- 0.125	0.563 +/- 0.003
	11	0.108 +/- 0.019	0.120 +/- 0.036	0.172 +/- 0.004
	12	0.276 +/- 0.020	0.264 +/- 0.041	0.300 +/- 0.019
	13	0.341 +/- 0.020	0.242 +/- 0.054	0.413 +/- 0.004
	14	0.282 +/- 0.033	0.233 +/- 0.051	0.201 +/- 0.002
	15	0.648 +/- 0.040	0.306 +/- 0.063	0.374 +/- 0.004

^a See Table S1 for complete genotypes.

^b PCR amplicon numbers correspond to those shown in Figure 2; see Figure S3 for primer sequences and amplicon coordinates.

^c Data are mean $\pm$ SD from three independent biological replicates.

^d n.a., not applicable. The impacts of protein deletions upon sequence-specific chromatin remodeling were determined only for cells in meiosis.