



Supplementary Information for

The *mop1* (*mediator of paramutation1*) mutation affects the recombination landscape in maize

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Datasets S1 to S4

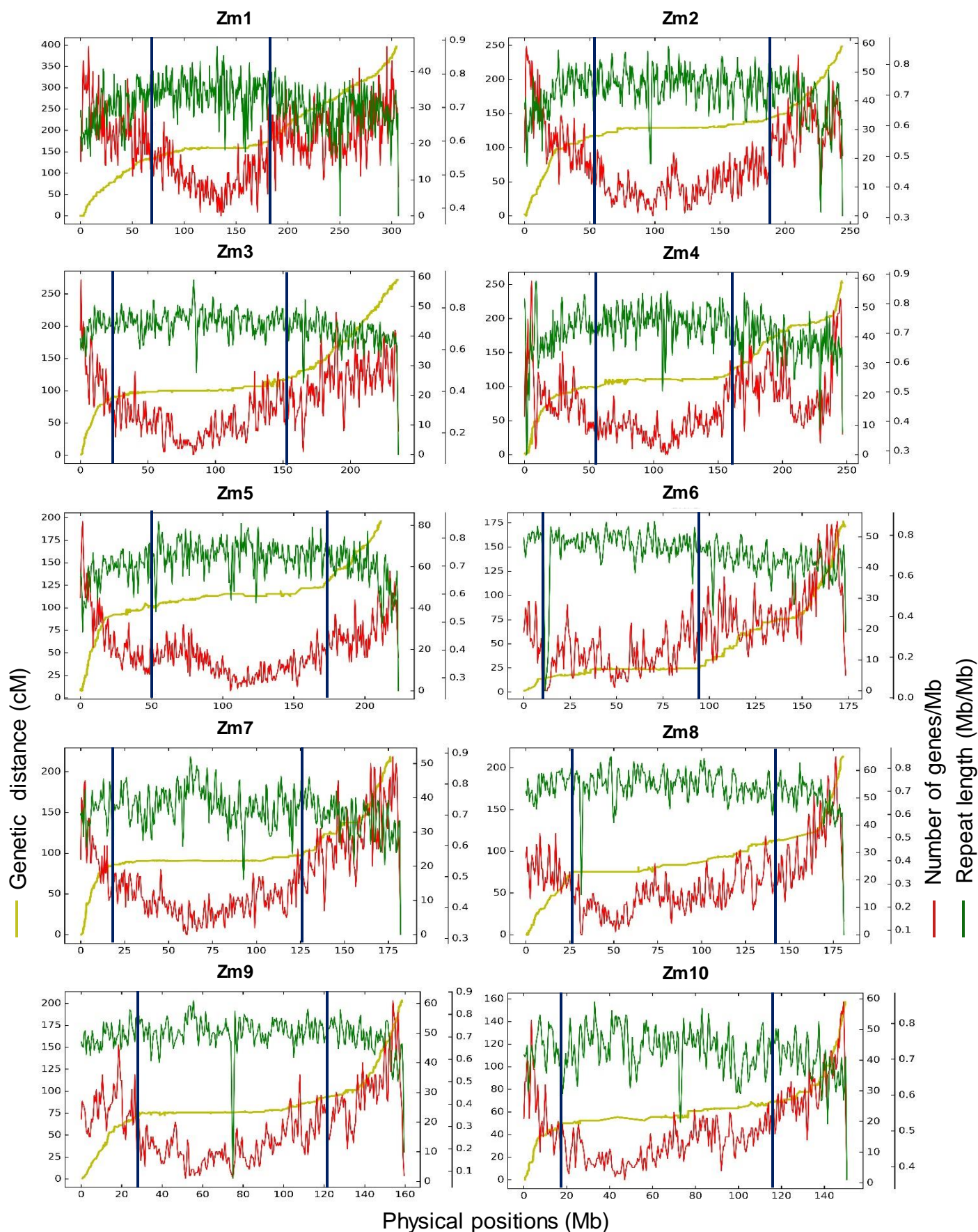


Fig. S1. Identification of pericentromeric regions and chromosomal arms of the ten maize chromosomes.

Red and green curves represent gene densities (no. of genes/Mb) and repeat length (Mb/Mb), which was measured in 1 Mb windows with 500 kb shifts. Yellow green curve demonstrates 6257 genetic markers in the integrated map previously described (1). Dark blue vertical bars indicate position of transition from chromosomal arms to pericentromeric regions. The region between two vertical bars for each chromosome was defined as pericentromeric regions. The regions outside of the vertical bars were defined as chromosomal arms.

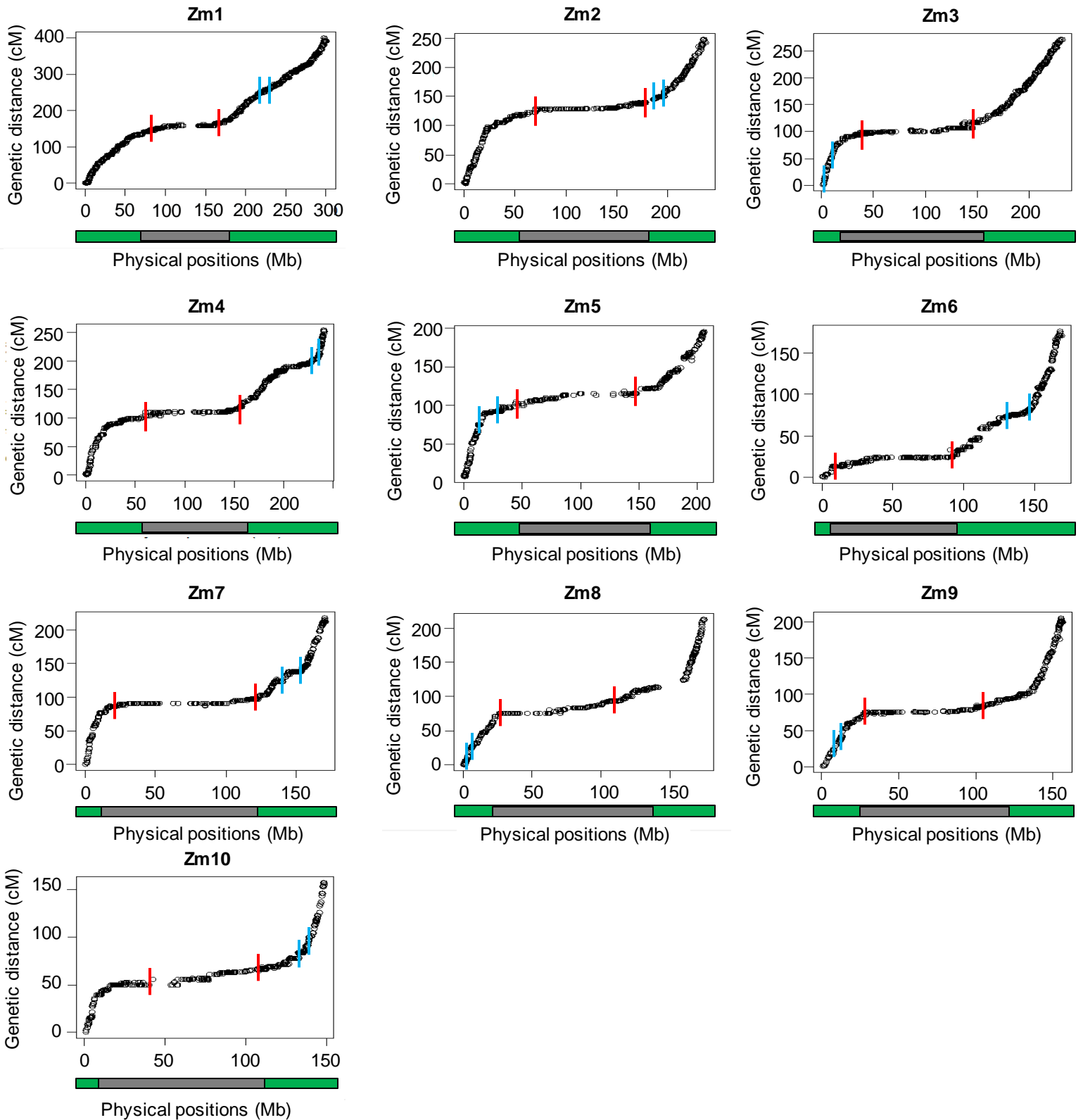


Fig. S2. Locations of marker pairs of the ten maize chromosomes selected to compare the recombination frequencies between *mop1* mutant and its heterozygous sibling. Each panel was generated by MaryMap using the available markers in the reference B73 genome (black dots) (2). The vertical bars represent polymorphic InDel markers between B73 and Mo17. Red and blue bars represent marker pairs located in pericentromeric regions and chromosomal arms, respectively. Within each panel, the slope of the line indicates gene density; a greater slope corresponds to chromosomal arms that have a high gene density. Green and grey bars indicate the chromosomal arms and pericentromeric regions of each chromosome, respectively.

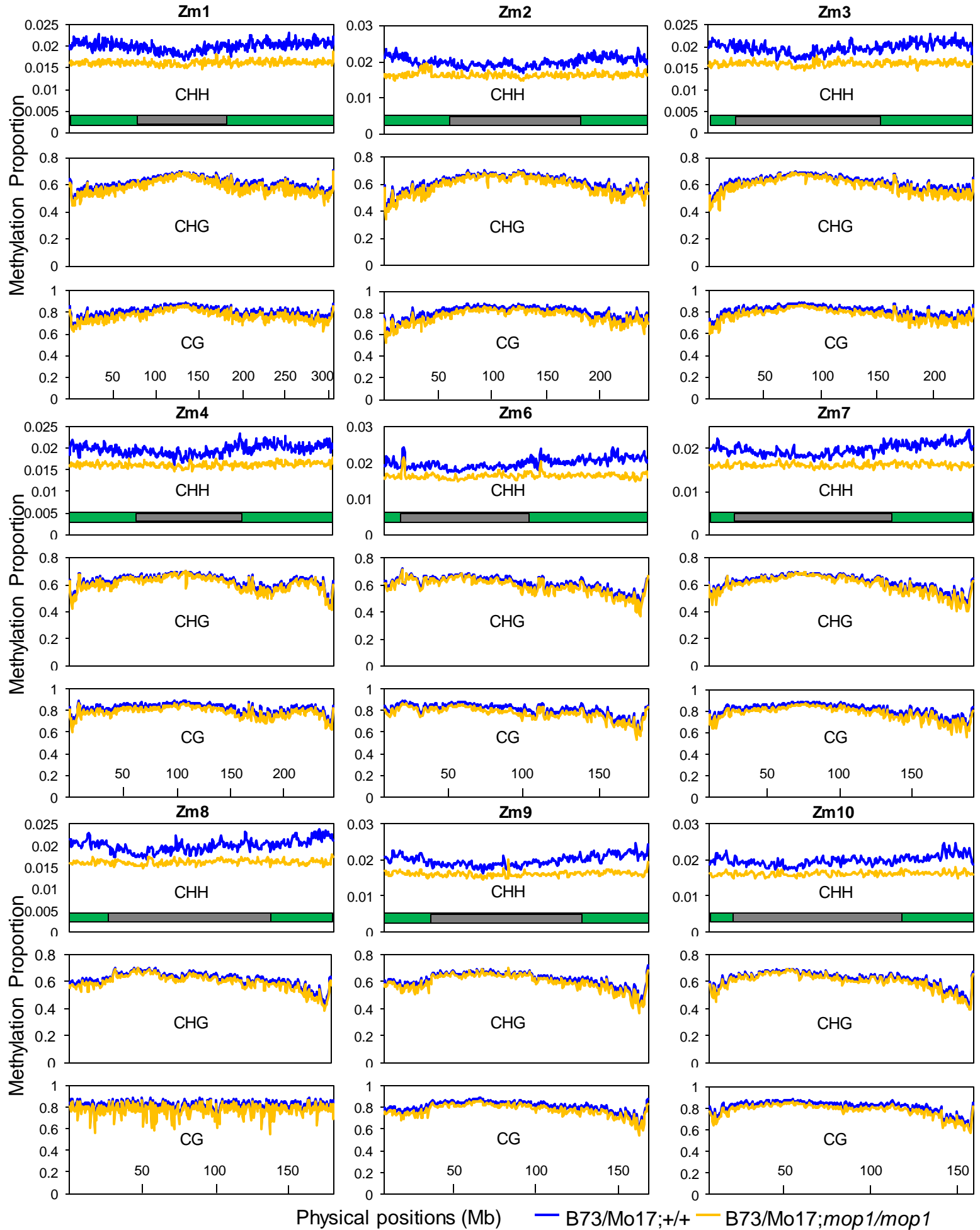


Fig. S3. Patterns of DNA methylation along the nine chromosomes in immature anthers.

Methylation for each sample was calculated as the proportion of methylated C over total C in each sequence context (CG, CHG, and CHH) averaged for each 1Mb windows with 500 kb shifts. The average methylation levels were determined by combining the biological replicates for each genotype.

Table S1. Comparisons of the pericentromeric regions and chromosomal arms of the ten chromosomes of the maize genome

Features	Pericentromeric regions		Chromosomal arms		<i>P</i> Values ^a	Ratio
	Total	Average ± SD	Total	Average ± SD		
Sizes (Mb)	1060.89	106.09 ± 13.67	1045.45	104.55 ± 44.60	0.9142	1.01
LTR-RTs (Mb) ^b	1141.86	114.19 ± 15.17	1014.99	101.50 ± 42.57	0.3486	1.13
DNA TEs (Mb) ^b	4.29	0.43 ± 0.08	6.28	0.63 ± 0.25	0.0310	0.68
Helitrons (Mb) ^b	186.14	18.61 ± 2.11	199.81	19.98 ± 8.41	0.6168	0.93
No. of genes	11,961	1,196 ± 207	27,044	2,704 ± 966	0.0010	0.44
Gene densities (no./Mb)	-	11.29 ± 1.33	-	26.54 ± 2.4	<0.0001	0.43
Recombination rates (cM/Mb)	-	0.20 ± 0.07	-	2.17 ± 0.47	<0.0001	0.09
Recombination frequencies (cM/gene)	-	0.017 ± 0.006	-	0.081 ± 0.01	<0.0001	0.21

^a Student's paired *t* test

^b The overall contribution of the transposable elements are only approximations due to difficulties in annotation.

Table S2. Comparison of recombination frequency in the second biological replicate comparing B73/Mo17;*mop1/mop1* and B73/Mo17;+/+

Chromosome	Marker pairs	Marker position (version 2)	Marker position (version 4)	Marker location	B73/Mo17;+/+			B73/Mo17; <i>mop1/mop1</i>			Recombinants in <i>mop1/mop1</i> vs. +/+ (%)	P value of χ^2 test
					Parental	Recombinants	Genetic distance (cM)	Parental	Recombinants	Genetic distance (cM)		
1	DEL.17179	217,420,353	220,618,790	Arms	135	17	11.18	115	15	11.54	3.1	0.8980
1	DEL.18364	231,506,640	235,100,067	Arms	138	17	10.97	124	9	6.77	-62.1	0.1211
2	INS.39880	186,567,278	192,152,725	Arms	97	38	28.15	115	11	8.73	-222.4	<0.0001
2	DEL.50069	196,147,461	202,422,924	Arms	126	22	14.86	113	15	11.72	-26.8	0.3170
4	DEL.87712	236,702,644	241,951,472	Arms	106	42	28.38	86	40	31.75	10.6	0.4018
4	DEL.88225	241,232,962	246,774,777	Arms	127	26	16.99	114	17	12.98	-30.9	0.2210
5	INS.72736	15,139,215	15,682,111	Arms	131	18	12.08	106	20	15.87	23.9	0.1915
5	INS.74132	31,823,952	32,947,841	Arms	133	15	10.14	115	18	13.53	25.1	0.1940
5	DEL.101474	201,464,758	206,962,581	Arms	138	14	9.21	120	11	8.40	-9.7	0.7474
5	INS.82912	215,984,724	221,868,273	Arms	150	13	7.98	128	4	3.03	-163.2	0.0360
7	DEL.127155	140,576,071	145,310,108	Arms	131	13	9.03	113	5	4.24	-113.1	0.0694
7	INS.103353	154,057,203	159,368,007	Arms	125	21	14.38	106	17	13.82	-4.1	0.8589
7	DEL.116777	1,520,755	1,624,194	Arms	131	18	12.08	106	20	15.87	23.9	0.1915
7	DEL.117010	3,194,424	3,343,108	Arms	133	15	10.14	115	18	13.53	25.1	0.1940
10	INS.29294	144,934,439	145,650,284	Arms	138	14	9.21	120	11	8.40	-9.7	0.7474
10	INS.29644	148,410,425	149,178,420	Arms	150	13	7.98	128	4	3.03	-163.2	0.0360
1	INS.6094	76,569,094	78,066,611	Peri.	131	13	9.03	113	5	4.24	-113.1	0.0694
1	INS.10411	170,185,497	172,063,830	Peri.	125	21	14.38	106	17	13.82	-4.1	0.8589
2	DEL.42973	69,833,090	71,702,178	Peri.	150	13	7.98	128	4	3.03	-163.2	0.0360
2	DEL.48980	178,134,254	183,563,424	Peri.	131	13	9.03	113	5	4.24	-113.1	0.0694
5	DEL.92285	43,094,158	44,371,298	Peri.	131	13	9.03	113	5	4.24	-113.1	0.0694
5	DEL.96846	147,538,205	151,042,601	Peri.	131	13	9.03	113	5	4.24	-113.1	0.0694
7	INS.95452	19,624,345	20,468,482	Peri.	125	21	14.38	106	17	13.82	-4.1	0.8589
7	INS.100248	121,191,052	125,104,915	Peri.	125	21	14.38	106	17	13.82	-4.1	0.8589

Arms, chromosomal arms; Peri., pericentromeric regions.

Table S3. Comparison of the numbers of HEI10 foci between B73/Mo17;+/+ and B73/Mo17;mop1/mop1

B73/Mo17;+/+ (WT)		B73/Mo17;mop1/mop1 (mutant)	
Meiocyte	HEI10 foci	Meiocyte	HEI10 foci
WT-1	21	mt-2	18
WT-2	20	mt-3	21
WT-3	21	mt-4	17
WT-4	18	mt-5	20
WT-5	20	mt-7	17
WT-6	18	mt-8	19
WT-7	19	mt-9	19
WT-8	21	mt-10	18
WT-9	20	mt-11	19
WT-10	22	mt-12	17
WT-11	21	mt-14	21
WT-12	21	mt-15	19
WT-13	21	mt-16	21
WT-14	22	mt-17	21
WT-15	21	mt-18	18
WT-17	21	mt-19	17
WT-18	18	mt-20	22
WT-19	20	mt-22	19
WT-20	22	mt-23	16
WT-21	21	mt-26	21
WT-23	22	mt-28	24
WT-24	19		
WT-26	21		
WT-27	21		

Table S4. Summary of the whole genome bisulfite sequencing data

Sample name	Genotype	Clean reads	Bisulfite conversion rate (%)	Replicate
1982-6	B73/Mo17;+/+	76,153,365	99.2	Replicate 1
1982-5	B73/Mo17; <i>mop1/mop1</i>	75,214,817	99.2	
1983-16	B73/Mo17;+/+	81,377,469	99.0	Replicate 2
1983-26	B73/Mo17; <i>mop1/mop1</i>	68,479,889	99.2	

Table S5. Meiotic recombination rates between B73/Mo17;+/+ and B73/Mo17;lb11/lb11 along chromosome 5 in maize

Chromosomes	Markers	Marker position v2	Marker position v4	B73/Mo17;+/+			B73/Mo17;lb11/lb11			Recombinants in lb11/lb11 vs. +/+ (%)	P value of χ^2 test
				Parental	Recombinants	Genetic distance (CM)	Parental	Recombinants	Genetic distance (CM)		
	DEL.88310	899,349	935,600								
	DEL.88604	2,762,137	2,844,642	234	17	6.77	206	8	3.74	-44.8	0.0773
	INS.72301	10,086,976	10,492,066	187	63	25.20	164	50	23.36	-7.3	0.5363
	INS.72736	15,139,215	15,682,110	215	29	11.89	176	30	14.56	22.5	0.2350
	INS.74132	31,823,952	32,947,840	184	30	14.02	172	29	14.43	2.9	0.8673
Zm5	DEL.92285	43,094,158	44,371,297	198	14	6.60	185	14	7.04	6.5	0.8064
	DEL.96846	147,538,205	151,042,600	209	32	13.28	173	35	16.83	26.7	0.1315
	DEL.99134	175,449,608	179,470,138	211	31	12.81	177	35	16.51	28.9	0.1070
	DEL.100248	188,858,032	193,893,000	205	33	13.87	188	22	10.48	-24.4	0.1552
	DEL.101474	201,464,758	206,962,580	210	30	12.50	184	26	12.38	-1.0	0.9584
	INS.82912	215,984,724	221,868,272	156	90	36.59	137	77	35.98	-1.7	0.8544

Dataset S1 (separate file). Primer sequences of the InDel markers used in this study.

Dataset S2 (separate file). Comparison of recombination frequency in the backcross populations derived from B73/Mo17;*mop1/mop1* and B73/Mo17;*mop1/+*.

Dataset S3 (separate file). Meiotic recombination rates between B73/Mo17;*mop1/mop1* and B73/Mo17;*mop1/+* along six entire maize chromosomes.

Dataset S4 (separate file). Comparison of recombination frequency in the backcross populations of two biological replicates derived from B73/Mo17;*+/+* and B73/Mo17;*lbf1/lbf1*.

SI References

1. S. Liu et al., Mu transposon insertion sites and meiotic recombination events co-localize with epigenetic marks for open chromatin across the maize genome. *PLoS Genet* 5, e1000733 (2009).
2. C. Rezvoy, D. Charif, L. Gueguen, G. A. Marais, MareyMap: an R-based tool with graphical interface for estimating recombination rates. *Bioinformatics* 23, 2188-2189 (2007).