DNA methylation epigenetically silences crossover hotspots and controls chromosomal domains of meiotic recombination in Arabidopsis

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SUPPLEMENTAL FIGURE LEGENDS

Supplemental Figure S1. Crossovers numbers in wild type and *met1* backcross populations. Histograms showing the numbers of crossovers identified by low coverage sequencing in wild type (Col/Ler) or *met1* (Col/Ler) male backcross populations. Mean values are indicated by the vertical dotted red lines. Histograms for individual chromosomes are also shown. Artefactual *met1* crossovers are identified on chromosome 5, due to the presence of a Col/Col region on the south arm of chromosome 5, remaining from introgression of *met1-3* (Col) into Ler.

Supplemental Figure S2. Meiotic DNA double strand break foci in proximity to chromocenters in wild type and *met1*. (A-H) Localization of γ-H2A.X (red) in wild-type Col (A-D) and *met1-3* (E-H) leptotene stage nuclei. Images show blow-ups of densely DAPI-stained centromeric regions marked with white arrowheads. Yellow arrowheads indicate γ-H2A.X foci localized within the DAPI-dense regions. Images (A) and (B) are blow-ups of the nuclei shown in Fig. 6A-6C. Images (E) and (F) are blow-ups of the nuclei shown in Fig. 6D-6F. Scale bars =1 μM.

SUPPLEMENTAL TABLES

Supplemental Table 1. Crossover distributions within the *3a* hotspot in wild type and methylated *HP3* hairpin lines. Shading indicates positions overlapping hairpin targeted regions.

Supplemental Table 2. Crossover distributions within the *3a* hotspot in wild type and methylated hairpin *HP4* lines.

Supplemental Table 3. Crossover distributions within the *3b* hotspot in wild type and methylated hairpin lines. Shading indicates positions overlapping hairpin targeted regions.

Supplemental Table 4. Coordinates of *3a* and *3b* hotspot RdDM target regions and those analysed by sodium bisulphite sequencing, chromatin immunprecipitation (ChIP) or *Mcr*BC.

Supplemental Table 5. DNA methylation in wild type and *HP* lines assayed by sodium-bisulphite sequencing.

Supplemental Table 6. Sodium bisulphite sequencing analysis of DNA methylation in the 5' proximal interval of *HP3*.

Supplemental Table 7. Sodium bisulphite sequencing analysis of DNA methylation in the central interval of *HP3*.

Supplemental Table 8. Sodium bisulphite sequencing analysis of DNA methylation in the 3' proximal interval of *HP3*.

Supplemental Table 9. Sodium bisulphite sequencing analysis of DNA methylation in the 5' proximal interval of *HP4*.

Supplemental Table 10. Sodium bisulphite sequencing analysis of DNA methylation in the central interval of *HP4*.

Supplemental Table 11. Sodium bisulphite sequencing analysis of DNA methylation in the 3' proximal interval of *HP4*.

Supplemental Table 12. Sodium bisulphite sequencing analysis of DNA methylation in the 5' proximal interval of *HP5*.

Supplemental Table 13. Sodium bisulphite sequencing analysis of DNA methylation in the central interval of *HP5*.

Supplemental Table 14. Sodium bisulphite sequencing analysis of DNA methylation in the 3' proximal interval of *HP5*.

Supplemental Table 15. Aligning read pairs for barcoded libraries generated from wild type or *met1* Col/Ler backcross individuals.

Supplemental Table 16. Crossover and double crossover numbers identified by low coverage sequencing of wild type (n=187) and *met1* (n=192) Col/Ler backcross populations.

Supplemental Table 17. *I1b* genetic distance in wild type, meiotic recombination and DNA methylation mutants.

Supplemental Table 18. *CEN3* genetic distance in wild type, meiotic recombination and DNA methylation mutants.

Supplemental Table 19. Tetrad analysis of genetic distance and crossover interference in wild type and *met1*.

Supplemental Table 20. Genetic distances of *CEN3* and *420* in wild type naïve and *met1* backgrounds.

Supplemental Table 21. *CEN3* recombination data in wild type and *met1* backgrounds.

Supplemental Table 22. *420* recombination data in wild type and *met1* backgrounds.

Supplemental Table 23. Coverage of cytosines in CG, CHG and CHH contexts for each individual bisulfite sequenced.

Supplemental Table 24. Analysis of sodium bisulphite conversion based on chloroplast genomic DNA.

Supplemental Table 25. Methylation levels in *420-CEN3* naïve Col-0 and *met1/+* individuals.

Supplemental Table 26. Correlations between crossover frequency and DNA methylation levels between chromosomal regions.

Supplemental Table 27. γ-H2AX foci count in wild type and *met1* leptotene stage meiocytes.

Supplemental Table 28. Fertility of *met1 spo11* mutant backgrounds.

Supplemental Table 29. Oligonucleotides.

Supplemental Table 1. Crossover distributions within the *3a* hotspot in wild type and methylated *HP3* hairpin lines. Shading indicates positions overlapping hairpin targeted regions.

Coordinates (bp)	Interval length (bp)	Crossovers (Col/Ler)	cM/Mb (Col/Ler)	Crossovers (*HP3*/Ler)	cM/Mb (*HP3*/Ler)
634,109	829	14	15.53	22	17.44
634,938	1,181	5	3.89	9	5.01
636,119	80	3	34.49	0	0
636,199	1,084	22	18.67	8	4.85
637,283	94	5	48.93	0	0
637,377	377	14	34.16	0	0
637,754	220	15	62.71	1	2.99
637,974	509	35	63.25	1	1.29
638,483	31	0	0	0	0
638,514	11	0	0	0	0
638,525	78	0	0	0	0
638,603	30	0	0	0	0
638,633	6	0	0	0	0
638,639	32	0	0	0	0
638,671	6	0	0	0	0
638,677	2	0	0	0	0
638,679	2	0	0	0	0
638,681	6	0	0	0	0
638,687	92	3	29.99	1	7.14
638,779	885	80	83.15	54	40.10
639,664	210	12	52.56	7	21.90
639,874	60	4	61.32	2	21.90
639,934	0	0	0	0	0
Total	5,825	212	34.68	105	11.85

Supplemental Table 2. Crossover distributions within the *3a* hotspot in wild type and methylated hairpin *HP4* lines. Shading indicates positions overlapping hairpin targeted regions.

Coordinates (bp)	Interval length (bp)	Crossovers (Col/Ler)	cM/Mb (Col/Ler)	Crossovers (*HP4*/Ler)	cM/Mb (*HP4*/Ler)
634,109	829	14	15.53	18	19.16
634,938	1,181	5	3.89	5	3.74
636,119	80	3	34.49	1	11.03
636,199	1,084	22	18.67	25	20.35
637,283	94	5	48.93	4	37.55
637,377	377	14	34.16	10	23.40
637,754	220	15	62.71	9	36.10
637,974	509	35	63.25	8	13.87
638,483	31	0	0	0	0
638,514	11	0	0	0	0
638,525	78	0	0	0	0
638,603	30	0	0	0	0
638,633	6	0	0	0	0
638,639	32	0	0	0	0
638,671	6	0	0	0	0
638,677	2	0	0	0	0
638,679	2	0	0	0	0
638,681	6	0	0	0	0
638,687	92	3	29.99	1	9.59
638,779	885	80	83.15	15	14.96
639,664	210	12	52.56	5	21.01
639,874	60	4	61.32	1	14.71
639,934	0	0	0	0	0
Total	5,825	212	34.68	102	15.62

Supplemental Table 3. Crossover distributions within the *3b* hotspot in wild type and methylated hairpin lines. Shading indicates positions overlapping hairpin targeted regions.

Coordinates (bp)	Interval length (bp)	Crossovers (Col/Ler)	cM/Mb (Col/Ler)	Crossovers (*HP5*/Ler)	cM/Mb (*HP5*/Ler)
647,266	200	0	0	0	0
647,466	55	3	58.0	2	5.4
647,521	270	12	47.2	21	11.6
647,791	316	1	3.4	4	1.9
648,107	222	11	52.7	13	8.7
648,329	322	11	36.3	6	2.8
648,651	376	17	48.1	13	5.2
649,027	191	11	61.2	12	9.4
649,218	200	13	69.1	9	6.7
649,418	788	21	28.3	13	2.5
650,206	362	7	20.6	6	2.5
650,568	8	0	0	0	0
650,576	50	0	0	0	0
650,626	4	0	0	0	0
650,630	5	0	0	0	0
650,635	123	0	0	1	1.2
650,758	41	0	0	0	0
650,799	90	0	0	0	0
650,889	1	0	0	0	0
650,890	4	0	0	0	0
650,894	14	0	0	1	10.7
650,908	24	0	0	0	0
650,933	138	0	0	0	0
651,071	4	0	0	0	0
651,075	11	0	0	0	0
651,086	2	0	0	0	0
651,088	8	0	0	0	0
651,096	16	0	0	0	0
651,112	10	0	0	0	0
651,122	8	0	0	0	0
651,130	15	0	0	0	0
651,145	7	0	0	0	0
651,152	2	0	0	0	0
651,154	25	0	0	0	0
651,179	11	0	0	17	230.7
651,190	34	0	0	0	0
651,224	24	0	0	0	0
651,248	7	0	0	0	0

651,255	2	0	0	0	0
651,257	3	0	0	0	0
651,260	14	0	0	0	0
651,274	5	0	0	0	0
651,279	8	0	0	0	0
651,287	17	0	0	0	0
651,304	6	0	0	0	0
651,310	18	0	0	0	0
651,328	5	0	0	0	0
651,333	2	0	0	0	0
651,335	4	0	0	0	0
651,339	18	0	0	0	0
651,357	1	0	0	0	0
651,358	5	0	0	0	0
651,363	4	0	0	0	0
651,367	4	0	0	0	0
651,371	28	0	0	0	0
651,399	25	0	0	0	0
651,424	2	0	0	0	0
651,426	7	0	0	0	0
651,433	2	0	0	0	0
651,435	8	0	0	0	0
651,443	1	0	0	0	0
651,444	9	0	0	0	0
651,453	1	0	0	0	0
651,454	30	0	0	0	0
651,484	24	0	0	0	0
651,508	10	0	0	1	14.9
651,518	16	0	0	0	0
651,534	125	0	0	0	0
651,659	54	4	78.7	8	22.1
651,713	525	0	0	0	0
652,238	191	0	0	7	5.5
652,429	583	0	0	0	0
653,012	0	0	0	0	0
Total	5,746	111	21.41	134	3.5

Supplemental Table 4. Coordinates of *3a* and *3b* hotspot RdDM target regions and those analysed by sodium bisulphite sequencing, chromatin immunprecipitation (ChIP) or *Mcr*BC.

Start (bp)	End (bp)	Size	Fragment	Hotspot	Description
634,082	634,934	852	*HP1*	*3a*	Hairpin arm
635,048	636,794	1,746	*HP2*	*3a*	Hairpin arm
637,091	638,234	1,143	*HP3*	*3a*	Hairpin arm
638,334	639,011	677	*HP4*	*3a*	Hairpin arm
647,649	650,049	2,400	*HP5*	*3b*	Hairpin arm
636,962	637,304	342	*HP3*_left	*3a*	Bisulphite sequencing
637,324	637,711	387	*HP3*_middle	*3a*	Bisulphite sequencing
637,980	638,341	361	*HP3*_right	*3a*	Bisulphite sequencing
638,235	638,519	284	*HP4*_left	*3a*	Bisulphite sequencing
638,522	638,871	349	*HP4*_middle	*3a*	Bisulphite sequencing
638,935	639,265	330	*HP4*_right	*3a*	Bisulphite sequencing
647,567	647,888	321	*HP5*_left	*3b*	Bisulphite sequencing
648,148	648,492	344	*HP5*_middle	*3b*	Bisulphite sequencing
650,009	650,153	144	*HP5*_right	*3b*	Bisulphite sequencing
637,715	637,944	229	*HP3-1*	*3a*	ChIP-qPCR
637,106	637,324	218	*HP3-2*	*3a*	ChIP-qPCR
638,741	638,956	215	*HP4-1*	*3a*	ChIP-qPCR
638,338	638,489	151	*HP4-2*	*3a*	ChIP-qPCR
647,821	647,990	169	*HP5-1*	*3b*	ChIP-qPCR
648,790	648,980	190	*HP5-2*	*3b*	ChIP-qPCR
634,050	634,357	307	*HP1a*	*3a*	*Mcr*BC
634,627	634,969	342	*HP1b*	*3a*	*Mcr*BC
636,320	636,835	515	*HP2a*	*3a*	*Mcr*BC
635,018	635,562	544	*HP2b*	*3a*	*Mcr*BC
637,078	637,324	246	*HP3a*	*3a*	*Mcr*BC
637,995	638,261	266	*HP3b*	*3a*	*Mcr*BC
638,584	639,038	454	*HP4a*	*3a*	*Mcr*BC
638,237	638,584	347	*HP4b*	*3a*	*Mcr*BC
647,612	647,999	387	*HP5a*	*3b*	*Mcr*BC
649,755	650,059	304	*HP5b*	*3b*	*Mcr*BC

Supplemental Table 5. DNA methylation in wild type and *HP* lines assayed by sodium-bisulphite sequencing. Methylation levels are averaged across three intervals within each of the loci. The top row indicates the genotype with the targeted sequence analysed indicated in parentheses.

Sequence Context	Col/Ler [*HP3*]	Col/Ler [*HP4*]	Col/Ler [*HP5*]	*HP3/*Ler [*HP3*]	*HP4/*Ler [*HP4*]	*HP5/*Ler [*HP5*]
CG	0.84	0	0.16	42.32	61.74	23.48
CHG	0	0.64	0.98	50.93	59.64	19.15
CHH	0.65	0.49	0.56	12.71	15.05	6.10
Total	0.61	0.47	0.53	20.34	24.88	11.16

Supplemental Table 6. Sodium bisulphite sequencing analysis of DNA methylation in the 5' proximal interval of *HP3*.

		Col/Ler		*HP3*/Ler	
Position	Context	Fraction methylated	Number of clones	Fraction methylated	Number of clones
636,962	CHH	0.055	18	0	22
636,963	CHH	0	18	0	22
636,968	CHH	0	18	0	22
636,995	CHH	0	18	0.045	22
637,027	CHH	0	18	0	22
637,034	CHH	0	18	0	22
637,040	CHH	0	18	0	22
637,055	CHH	0	18	0	22
637,056	CHH	0	18	0	22
637,057	CHH	0	18	0	22
637,058	CHH	0	18	0	22
637,060	CHH	0	18	0	22
637,063	CHH	0	18	0	22
637,067	CHH	0	18	0	22
637,068	CHH	0	18	0	22
637,075	CHH	0	17	0.045	22
637,078	CHH	0.055	18	0.045	22
637,081	CHH	0	15	0.09	22
637,084	CHH	0	17	0.142	21
637,087	CHH	0.055	18	0.09	22
637,094	CHH	0	18	0.181	22
637,100	CHH	0	18	0.272	22
637,118	CHH	0	18	0.227	22
637,124	CHH	0	18	0.363	22
637,125	CHH	0	18	0.409	22
637,127	CHH	0	18	0.318	22
637,142	CHH	0	18	0.38	21
637,143	CHH	0	18	0.285	21
637,153	CHH	0	18	0.363	22
637,161	CHH	0	16	0.363	22
637,165	CHH	0	16	0.318	22
637,169	CHH	0.055	18	0.272	22
637,172	CHH	0.055	18	0.227	22
637,177	CHH	0	18	0.181	22
637,185	CHH	0	18	0.045	22
637,186	CHH	0	18	0.045	22
637,203	CHH	0.055	18	0.09	22
637,211	CHH	0	18	0.045	22
637,217	CHH	0	18	0.045	22
637,223	CHH	0	18	0	22
637,279	CHH	0	17	0.1	20
637,282	CHH	0	18	0.142	21
637,287	CHH	0	18	0.047	21

637,289	CHH	0	18	0.142	21
637,292	CHH	0	18	0.047	21
637,297	CHH	0	16	0	20
637,298	CHH	0	16	0.05	20
636,976	CG	0.111	18	0.045	22
637,052	CG	0	18	0	22
637,065	CG	0	18	0	22
637,110	CG	0	16	0.181	22
637,253	CG	0	18	0.5	22
636,969	CHG	0	18	0	22
636,975	CHG	0	18	0	22
636,979	CHG	0	18	0	22
637,064	CHG	0	18	0	22
637,147	CHG	0	16	0.476	21
637,299	CHG	0	16	0.3	20

Supplemental Table 7. Sodium bisulphite sequencing analysis of DNA methylation in the central interval of *HP3*.

		Col/Ler		*HP3*/Ler	
Position	Context	Fraction methylated	Number of clones	Fraction methylated	Number of clones
637,311	CHH	0	19	0.076	26
637,322	CHH	0	19	0	26
637,323	CHH	0	19	0.076	26
637,330	CHH	0	19	0	26
637,336	CHH	0	19	0	26
637,362	CHH	0	19	0	26
637,363	CHH	0	19	0	26
637,375	CHH	0	19	0.038	26
637,376	CHH	0	19	0.038	26
637,382	CHH	0	16	0.038	26
637,388	CHH	0	19	0.038	26
637,394	CHH	0	17	0.076	26
637,404	CHH	0	19	0.076	26
637,416	CHH	0	19	0.115	26
637,418	CHH	0	19	0.076	26
637,431	CHH	0.058	17	0.076	26
637,437	CHH	0	19	0.076	26
637,440	CHH	0	19	0.076	26
637,484	CHH	0	19	0.153	26
637,485	CHH	0.052	19	0.23	26
637,487	CHH	0	19	0.23	26
637,491	CHH	0	19	0.192	26
637,498	CHH	0	19	0	26
637,499	CHH	0	19	0	26
637,500	CHH	0	19	0.153	26
637,503	CHH	0	19	0.153	26
637,506	CHH	0	19	0.153	26
637,524	CHH	0	19	0.153	26
637,543	CHH	0	19	0.192	26
637,546	CHH	0	19	0.269	26
637,552	CHH	0	19	0.192	26
637,553	CHH	0	19	0.23	26
637,572	CHH	0.052	19	0.115	26
637,598	CHH	0	19	0.307	26
637,612	CHH	0	19	0.346	26
637,622	CHH	0	19	0.24	25
637,626	CHH	0.052	19	0.23	26
637,673	CHH	0	17	0.076	26
637,689	CHH	0	18	0.153	26
637,701	CHH	0	18	0.038	26
637,314	CG	0	19	0.153	26
637,339	CG	0	19	0.192	26
637,356	CG	0	19	0.461	26

637,359	CG	0	19	0.153	26
637,391	CG	0	18	0.384	26
637,413	CG	0	18	0.423	26
637,420	CG	0	19	0.346	26
637,442	CG	0	19	0.346	26
637,639	CG	0	19	0.961	26
637,655	CG	0	19	0.961	26
637,319	CHG	0	19	0	26
637,358	CHG	0	19	0.038	26
637,427	CHG	0	19	0.423	26
637,508	CHG	0	19	0.576	26
637,554	CHG	0	19	0.923	26
637,604	CHG	0	19	1	26
637,684	CHG	0	19	0.884	26

Supplemental Table 8. Sodium bisulphite sequencing analysis of DNA methylation in the 3' proximal interval of *HP3*.

		Col/Ler		*HP3*/Ler	
Position	Context	Fraction methylated	Number of clones	Fraction methylated	Number of clones
637,981	CHH	0	16	0	16
637,985	CHH	0	16	0.25	16
637,989	CHH	0	16	0	16
637,992	CHH	0.062	16	0	16
637,995	CHH	0	16	0.187	16
637,998	CHH	0	16	0.062	16
638,000	CHH	0	16	0.375	16
638,012	CHH	0	16	0	16
638,028	CHH	0	16	0.187	16
638,051	CHH	0	16	0.187	16
638,057	CHH	0	16	0.187	16
638,060	CHH	0	16	0.125	16
638,069	CHH	0	16	0.187	16
638,077	CHH	0	16	0.133	15
638,080	CHH	0	16	0.062	16
638,092	CHH	0	16	0	16
638,094	CHH	0	16	0.133	15
638,099	CHH	0	16	0	16
638,114	CHH	0	16	0	16
638,115	CHH	0	16	0.187	16
638,116	CHH	0	16	0.187	16
638,121	CHH	0	16	0.187	16
638,134	CHH	0	16	0.187	16
638,135	CHH	0	16	0.25	16
638,149	CHH	0	16	0.25	16
638,150	CHH	0.062	16	0.25	16
638,155	CHH	0	16	0.25	16
638,157	CHH	0.062	16	0.187	16
638,168	CHH	0	16	0.187	16
638,172	CHH	0.062	16	0.125	16
638,181	CHH	0	16	0.312	16
638,185	CHH	0	16	0.375	16
638,187	CHH	0	16	0.375	16
638,200	CHH	0	16	0.312	16
638,207	CHH	0	16	0.375	16
638,209	CHH	0	16	0.437	16
638,226	CHH	0	16	0.25	16
638,233	CHH	0	16	0.062	16
638,234	CHH	0	16	0.25	16
638,237	CHH	0	16	0.062	16
638,280	CHH	0	16	0	16
638,281	CHH	0	16	0.062	16
638,286	CHH	0	16	0	16

638,301	CHH	0.062	16	0	16
638,310	CHH	0	15	0	16
638,330	CHH	0	16	0	16
638,146	CG	0	16	0.937	16
638,164	CG	0	16	0.937	16
638,174	CG	0	16	1	16
638,231	CG	0.062	16	0.812	16
638,339	CG	0	16	0.066	15
638,039	CHG	0	16	0.687	16
638,190	CHG	0	16	0.937	16
638,247	CHG	0	16	0.812	16
638,257	CHG	0	16	0.875	16

Supplemental Table 9. Sodium bisulphite sequencing analysis of DNA methylation in the 5' proximal interval of *HP4*.

		Col/Ler		*HP4*/Ler	
Position	Context	Fraction methylated	Number of clones	Fraction methylated	Number of clones
638,237	CHH	0	29	0	26
638,280	CHH	0	29	0	26
638,281	CHH	0.034	29	0	26
638,286	CHH	0	29	0	25
638,301	CHH	0	29	0	26
638,310	CHH	0	29	0.038	26
638,330	CHH	0	29	0	26
638,342	CHH	0	29	0.076	26
638,343	CHH	0	29	0.115	26
638,346	CHH	0	29	0.153	26
638,353	CHH	0	29	0.115	26
638,356	CHH	0	29	0.115	26
638,369	CHH	0	29	0.08	25
638,375	CHH	0	29	0.269	26
638,399	CHH	0	29	0.23	26
638,409	CHH	0	29	0.192	26
638,411	CHH	0	29	0.307	26
638,417	CHH	0	29	0.192	26
638,426	CHH	0.034	29	0.384	26
638,429	CHH	0	29	0.346	26
638,431	CHH	0	29	0.384	26
638,438	CHH	0	29	0.346	26
638,446	CHH	0	29	0.23	26
638,450	CHH	0	29	0.307	26
638,455	CHH	0	29	0.192	26
638,458	CHH	0	29	0.23	26
638,477	CHH	0	29	0.153	26
638,486	CHH	0	29	0.23	26
638,489	CHH	0	29	0.269	26
638,491	CHH	0	29	0.192	26
638,501	CHH	0	29	0.269	26
638,503	CHH	0.034	29	0.153	26
638,505	CHH	0	29	0.269	26
638,508	CHH	0	29	0.153	26
638,339	CG	0	29	0.576	26
638,391	CG	0	29	0.884	26
638,480	CG	0	28	0.807	26
638,247	CHG	0	29	0.038	26
638,257	CHG	0	29	0.04	25
638,357	CHG	0	29	0.884	26
638,390	CHG	0	28	0.576	26
638,400	CHG	0.034	29	0.884	26
638,472	CHG	0	29	0.653	26

Supplemental Table 10. Sodium bisulphite sequencing analysis of DNA methylation in the central interval of *HP4*.

		Col/Ler		*HP4*/Ler	
Position	Context	Fraction methylated	Number of clones	Fraction methylated	Number of clones
638,524	CHH	0	23	0.14	22
638,532	CHH	0	23	0.18	22
638,537	CHH	0	23	0.18	22
638,539	CHH	0.045	22	0.41	22
638,542	CHH	0	23	0.09	22
638,546	CHH	0	23	0.27	22
638,550	CHH	0	23	0.32	22
638,557	CHH	0	23	0.27	22
638,562	CHH	0	23	0.32	22
638,571	CHH	0	23	0.32	22
638,580	CHH	0	23	0.41	22
638,584	CHH	0	23	0.36	22
638,593	CHH	0	23	0.38	21
638,598	CHH	0.043	23	0.27	22
638,609	CHH	0	23	0.45	22
638,621	CHH	0	23	0.09	22
638,626	CHH	0	23	0.18	22
638,628	CHH	0	23	0.09	22
638,637	CHH	0	23	0.09	22
638,639	CHH	0	23	0.14	22
638,640	CHH	0	23	0.23	22
638,651	CHH	0	23	0.27	22
638,668	CHH	0.043	23	0.14	22
638,671	CHH	0	23	0.18	22
638,677	CHH	0	23	0.14	22
638,708	CHH	0	23	0.05	22
638,717	CHH	0	23	0.18	22
638,720	CHH	0	23	0.14	22
638,757	CHH	0	23	0.05	22
638,758	CHH	0	23	0.14	22
638,760	CHH	0	23	0.05	22
638,761	CHH	0.043	23	0.14	22
638,763	CHH	0	23	0.18	22
638,764	CHH	0	23	0.27	22
638,773	CHH	0	23	0.18	22
638,778	CHH	0	23	0.1	21
638,793	CHH	0	23	0.18	22
638,796	CHH	0	23	0.23	22
638,809	CHH	0	23	0.14	21
638,816	CHH	0.043	23	0.09	22
638,817	CHH	0.086	23	0.05	22
638,842	CHH	0	22	0	22
638,843	CHH	0	22	0.09	22

638,850	CHH	0	22	0.05	22
638,858	CHH	0	23	0	22
638,859	CHH	0	23	0.09	22
638,861	CHH	0	23	0.09	22
638,862	CHH	0	23	0.05	22
638,735	CG	0	23	0.91	22
638,739	CG	0	23	0.82	22
638,766	CG	0	23	0.95	22
638,864	CG	0	23	0.95	22
638,595	CHG	0	23	0.82	22
638,602	CHG	0	23	0.95	22
638,617	CHG	0	23	0.73	22
638,734	CHG	0	23	0.82	22
638,770	CHG	0	23	0.77	22
638,774	CHG	0	23	0.95	22
638,802	CHG	0	23	0.82	22
638,868	CHG	0.09	22	0.41	22

Supplemental Table 11. Sodium bisulphite sequencing analysis of DNA methylation in the 3' proximal interval of *HP4*.

		Col/Ler		*HP4*/Ler	
Position	Context	Fraction methylated	Number of clones	Fraction methylated	Number of clones
638,955	CHH	0	23	0.59	22
638,973	CHH	0	23	0.636	22
638,987	CHH	0	23	0.181	22
638,992	CHH	0	22	0.181	22
639,001	CHH	0	22	0.318	22
639,008	CHH	0	23	0.09	22
639,009	CHH	0	23	0.09	22
639,029	CHH	0	23	0	22
639,037	CHH	0	22	0	22
639,038	CHH	0	23	0	22
639,050	CHH	0	23	0	22
639,059	CHH	0	23	0	22
639,109	CHH	0	23	0	22
639,110	CHH	0	22	0	20
639,113	CHH	0	23	0.318	22
639,123	CHH	0	23	0.227	22
639,140	CHH	0	23	0	22
639,141	CHH	0	23	0.045	22
639,148	CHH	0	23	0	22
639,174	CHH	0	23	0	22
639,185	CHH	0	23	0	22
639,196	CHH	0	22	0	22
639,197	CHH	0.043	23	0.045	22
639,199	CHH	0.086	23	0.047	21
639,201	CHH	0	23	0	22
639,215	CHH	0	23	0	21
639,217	CHH	0	23	0	22
639,223	CHH	0	23	0	21
639,229	CHH	0	23	0	22
639,235	CHH	0	23	0.045	22
639,237	CHH	0	23	0	22
639,252	CHH	0.043	23	0	22
639,257	CHH	0	23	0	22
639,259	CHH	0	23	0	22
638,939	CG	0	23	1	22
639,006	CG	0	23	0.954	22
639,067	CG	0	23	0.045	22
639,153	CG	0	23	0.045	22
639,192	CG	0	23	0	22
639,206	CG	0	23	0	22
638,951	CHG	0	23	1	22
638,995	CHG	0	23	0.863	22
639,152	CHG	0	23	0	22

639,160	CHG	0	23	0.181	22
639,240	CHG	0	23	0	22

Supplemental Table 12. Sodium bisulphite sequencing analysis of DNA methylation in the 5' proximal interval of *HP5*.

		Col/Ler		*HP5*/Ler	
Position	Context	Fraction methylated	Number of clones	Fraction methylated	Number of clones
647,581	CHH	0	24	0.041	24
647,592	CHH	0	24	0	24
647,593	CHH	0	24	0	24
647,598	CHH	0.041	24	0	24
647,603	CHH	0	24	0	24
647,607	CHH	0	24	0	24
647,612	CHH	0	24	0	24
647,621	CHH	0	24	0	24
647,634	CHH	0	24	0	24
647,640	CHH	0	24	0	24
647,644	CHH	0	24	0	24
647,659	CHH	0	24	0	24
647,673	CHH	0	24	0	24
647,679	CHH	0	24	0	24
647,685	CHH	0	24	0.041	24
647,702	CHH	0	24	0	24
647,722	CHH	0.041	24	0.041	24
647,731	CHH	0	24	0	24
647,751	CHH	0.041	24	0.083	24
647,755	CHH	0	24	0	24
647,772	CHH	0	24	0	24
647,774	CHH	0	24	0	23
647,777	CHH	0	24	0	24
647,781	CHH	0	24	0	24
647,793	CHH	0	24	0	24
647,797	CHH	0	24	0	24
647,803	CHH	0	24	0	24
647,817	CHH	0	24	0	24
647,823	CHH	0	24	0	24
647,825	CHH	0.041	24	0	24
647,836	CHH	0	24	0	24
647,843	CHH	0	24	0	24
647,856	CHH	0	24	0	24
647,868	CHH	0	24	0	24
647,879	CHH	0	24	0	24
647,881	CHH	0	22	0.043	23
647,570	CG	0	24	0	24
647,573	CG	0	24	0	24
647,583	CG	0	24	0	24
647,588	CG	0	24	0	24
647,623	CG	0	24	0	24
647,628	CG	0	24	0	24
647,689	CG	0	23	0.125	24

647,734	CG	0	24	0.083	24
647,742	CG	0	24	0.041	24
647,765	CG	0	24	0	24
647,785	CG	0	24	0.083	24
647,829	CG	0	24	0	24
647,859	CG	0	24	0.041	24
647,866	CG	0	24	0.083	24
647,874	CG	0	24	0.083	24
647,587	CHG	0	24	0	24
647,741	CHG	0	24	0.083	24
647,757	CHG	0	24	0	24
647,764	CHG	0	24	0	24
647,810	CHG	0	24	0.041	24
647,828	CHG	0	24	0	24
647,848	CHG	0	24	0.083	24
647,858	CHG	0	24	0	24
647,873	CHG	0.083	24	0	24

Supplemental Table 13. Sodium bisulphite sequencing analysis of DNA methylation in the central interval of *HP5*.

		Col/Ler		*HP5*/Ler	
Position	Context	Fraction methylated	Number of clones	Fraction methylated	Number of clones
648,150	CHH	0	24	0.344	29
648,159	CHH	0	24	0.068	29
648,162	CHH	0	24	0.31	29
648,165	CHH	0	24	0.068	29
648,166	CHH	0.041	24	0.068	29
648,189	CHH	0	23	0.103	29
648,192	CHH	0	24	0.172	29
648,204	CHH	0	24	0.275	29
648,208	CHH	0	24	0.172	29
648,211	CHH	0	24	0.241	29
648,213	CHH	0	24	0.275	29
648,249	CHH	0	24	0.275	29
648,260	CHH	0	24	0.034	29
648,274	CHH	0.041	24	0.103	29
648,288	CHH	0	24	0.137	29
648,293	CHH	0	24	0.034	29
648,294	CHH	0.041	24	0.068	29
648,313	CHH	0	24	0.206	29
648,338	CHH	0	24	0.068	29
648,345	CHH	0	24	0.137	29
648,346	CHH	0	23	0.137	29
648,354	CHH	0	24	0.068	29
648,355	CHH	0	24	0.103	29
648,395	CHH	0	24	0.206	29
648,449	CHH	0	24	0.137	29
648,456	CHH	0	24	0.103	29
648,462	CHH	0	22	0.034	29
648,465	CHH	0	23	0.103	29
648,478	CHH	0	24	0.137	29
648,484	CHH	0	24	0.206	29
648,486	CHH	0	22	0.137	29
648,245	CG	0	24	0.931	29
648,252	CG	0	24	0.965	29
648,276	CG	0	24	0.965	29
648,481	CG	0	24	0.931	29
648,490	CG	0	20	0.931	29
648,169	CHG	0	24	0.827	29
648,251	CHG	0.041	24	0.758	29
648,348	CHG	0	24	0.931	29

Supplemental Table 14. Sodium bisulphite sequencing analysis of DNA methylation in the 3' proximal interval of *HP5*.

		Col/Ler		*HP5*/Ler	
Position	Context	Fraction methylated	Number of clones	Fraction methylated	Number of clones
650,011	CHH	0	24	0	24
650,014	CHH	0	24	0	24
650,017	CHH	0	24	0	24
650,022	CHH	0	24	0	24
650,030	CHH	0	24	0	24
650,041	CHH	0	24	0	24
650,043	CHH	0.045	22	0.041	24
650,057	CHH	0	24	0	24
650,059	CHH	0	24	0	24
650,064	CHH	0	24	0	24
650,069	CHH	0	24	0	24
650,076	CHH	0.041	24	0	24
650,101	CHH	0	24	0	23
650,104	CHH	0	24	0.041	24
650,108	CHH	0	24	0	23
650,120	CHH	0.041	24	0	24
650,121	CHH	0.041	24	0	24
650,125	CHH	0	24	0.041	24
650,127	CHH	0.043	23	0	24
650,132	CHH	0	24	0	23
650,139	CHH	0	24	0	24
650,140	CHH	0	24	0	24
650,142	CHH	0	24	0	24
650,020	CG	0	20	0.083	24
650,024	CG	0	20	0.083	24
650,032	CG	0.041	24	0	24
650,036	CG	0	24	0.125	24
650,088	CG	0	24	0.041	24
650,099	CG	0	24	0	24
650,144	CG	0	24	0	24
650,070	CHG	0	24	0	24
650,082	CHG	0.041	24	0.083	24
650,087	CHG	0	24	0	24
650,092	CHG	0	24	0.041	24
650,147	CHG	0	24	0	24

Supplemental Table 15. Aligning read pairs for barcoded libraries generated from wild type or *met1* Col/Ler backcross individuals. The L lane indicates lane number. The barcode numbers correspond to adapter sequences described in (Rowan et al. 2015).

Barcode	Genotype	L	Matching reads	Genotype	L	Matching reads	Genotype	L	Matching reads	Genotype	L	Matching reads
1	Wild type	1	2164637	Wild type	2	2060772	*met1*	1	3170175	*met1*	2	3002529
2	Wild type	1	2588529	Wild type	2	1555203	*met1*	1	2159598	*met1*	2	2477162
3	Wild type	1	1987316	Wild type	2	545028	*met1*	1	2707544	*met1*	2	2147938
4	Wild type	1	4204637	Wild type	2	1282210	*met1*	1	2250254	*met1*	2	2351340
5	Wild type	1	3116924	Wild type	2	1790925	*met1*	1	3593043	*met1*	2	2428440
6	Wild type	1	1989204	Wild type	2	1484266	*met1*	1	2049669	*met1*	2	1218619
7	Wild type	1	1918624	Wild type	2	1683554	*met1*	1	2535472	*met1*	2	5095730
8	Wild type	1	1446392	Wild type	2	785844	*met1*	1	1810268	*met1*	2	1175290
9	Wild type	1	1870901	Wild type	2	1301743	*met1*	1	2441510	*met1*	2	3038972
10	Wild type	1	1758096	Wild type	2	1902689	*met1*	1	2877161	*met1*	2	2706809
11	Wild type	1	2035284	Wild type	2	1496943	*met1*	1	2417339	*met1*	2	2031320
12	Wild type	1	nd	Wild type	2	2896349	*met1*	1	2307554	*met1*	2	835646
13	Wild type	1	2560436	Wild type	2	2201788	*met1*	1	2708047	*met1*	2	3307178
14	Wild type	1	2922566	Wild type	2	2421638	*met1*	1	2645630	*met1*	2	2660823
15	Wild type	1	2891425	Wild type	2	879846	*met1*	1	2609484	*met1*	2	2251453
16	Wild type	1	1391410	Wild type	2	1656797	*met1*	1	2562448	*met1*	2	2089285
17	Wild type	1	1114564	Wild type	2	1384512	*met1*	1	1923146	*met1*	2	2345895
18	Wild type	1	2241842	Wild type	2	1204877	*met1*	1	1658224	*met1*	2	2023943
19	Wild type	1	2973766	Wild type	2	1068931	*met1*	1	1825071	*met1*	2	1056208
20	Wild type	1	1932439	Wild type	2	977777	*met1*	1	1816791	*met1*	2	2518009
21	Wild type	1	2090298	Wild type	2	844022	*met1*	1	1700792	*met1*	2	841221
22	Wild type	1	4492692	Wild type	2	1705999	*met1*	1	2235759	*met1*	2	2541795
23	Wild type	1	2191266	Wild type	2	2570535	*met1*	1	2261000	*met1*	2	1023723
24	Wild type	1	1155891	Wild type	2	1416504	*met1*	1	2526867	*met1*	2	2432502
25	Wild type	1	1428147	Wild type	2	1199289	*met1*	1	2158171	*met1*	2	2409352
26	Wild type	1	1985226	Wild type	2	1664774	*met1*	1	2451657	*met1*	2	2178667
27	Wild type	1	na	Wild type	2	1488090	*met1*	1	2004866	*met1*	2	2619111
28	Wild type	1	2088609	Wild type	1	na	*met1*	1	1699933	*met1*	2	2473398
29	Wild type	1	2611747	Wild type	2	1471263	*met1*	1	1940718	*met1*	2	1062757
30	Wild type	1	3340676	Wild type	2	2322220	*met1*	1	2190171	*met1*	2	1540056
31	Wild type	1	3338992	Wild type	2	2060935	*met1*	1	1860339	*met1*	2	1479292
32	Wild type	1	2686601	Wild type	2	2827665	*met1*	1	2800659	*met1*	2	1133247
33	Wild type	1	2682974	Wild type	2	2061516	*met1*	1	2266828	*met1*	2	2525547
34	Wild type	1	1389622	Wild type	2	1540792	*met1*	1	2776131	*met1*	2	1662479
35	Wild type	1	3705969	Wild type	2	2086016	*met1*	1	2873682	*met1*	2	2420455
36	Wild type	1	1887717	Wild type	2	2015764	*met1*	1	2500332	*met1*	2	2999133
37	Wild type	1	1483233	Wild type	2	2361585	*met1*	1	2740322	*met1*	2	3844824
38	Wild type	1	na	Wild type	2	1312722	*met1*	1	2254464	*met1*	2	2215029
39	Wild type	1	1446717	Wild type	2	1269300	*met1*	1	1832327	*met1*	2	3024979
40	Wild type	1	2543107	Wild type	2	1594646	*met1*	1	2759495	*met1*	2	3088129

41	Wild type	1	3387336	Wild type	2	1976858	*met1*	1	1655797	*met1*	2	2251467
42	Wild type	1	2493455	Wild type	2	1422031	*met1*	1	2319989	*met1*	2	4418994
43	Wild type	1	1748579	Wild type	2	1462074	*met1*	1	2210316	*met1*	2	1085295
44	Wild type	1	3650649	Wild type	2	1998601	*met1*	1	1974589	*met1*	2	950514
45	Wild type	1	1821110	Wild type	2	1812669	*met1*	1	2753440	*met1*	2	1493787
46	Wild type	1	1821216	Wild type	2	878097	*met1*	1	2512225	*met1*	2	2232698
47	Wild type	1	2908437	Wild type	2	2350713	*met1*	1	1903959	*met1*	2	1616465
48	Wild type	1	2416552	Wild type	2	1384248	*met1*	1	2275150	*met1*	2	3774435
49	Wild type	1	1719335	Wild type	2	2172122	*met1*	1	2941977	*met1*	2	2426584
50	Wild type	1	2156315	Wild type	2	4537428	*met1*	1	3503934	*met1*	2	2496702
51	Wild type	1	1416440	Wild type	2	2140396	*met1*	1	2427146	*met1*	2	1605232
52	Wild type	1	2196961	Wild type	2	3425900	*met1*	1	2558544	*met1*	2	4060503
53	Wild type	1	1135996	Wild type	2	2530094	*met1*	1	3253013	*met1*	2	2225060
54	Wild type	1	1833930	Wild type	2	1927897	*met1*	1	3158198	*met1*	2	2041660
55	Wild type	1	1647142	Wild type	2	1492700	*met1*	1	1812581	*met1*	2	1777913
56	Wild type	1	1220085	Wild type	2	1856733	*met1*	1	2181542	*met1*	2	2510668
57	Wild type	1	1605413	Wild type	2	679399	*met1*	1	1941123	*met1*	2	692640
58	Wild type	1	1584600	Wild type	2	1512446	*met1*	1	2206609	*met1*	2	2508772
59	Wild type	1	4152993	Wild type	2	1029584	*met1*	1	2340018	*met1*	2	1498548
60	Wild type	1	2103623	Wild type	2	1697146	*met1*	1	2414886	*met1*	2	1305916
61	Wild type	1	2015782	Wild type	2	1925896	*met1*	1	2140175	*met1*	2	1540847
62	Wild type	1	2134326	Wild type	2	2858875	*met1*	1	2024616	*met1*	2	1735993
63	Wild type	1	na	Wild type	2	2201584	*met1*	1	2217303	*met1*	2	2058730
64	Wild type	1	2407315	Wild type	2	1212943	*met1*	1	1934972	*met1*	2	1228237
65	Wild type	1	1772251	Wild type	2	1235452	*met1*	1	1799592	*met1*	2	1128288
66	Wild type	1	1560607	Wild type	2	1497192	*met1*	1	2135377	*met1*	2	1624373
67	Wild type	1	1898420	Wild type	2	1621869	*met1*	1	1382135	*met1*	2	907931
68	Wild type	1	2028896	Wild type	2	1888781	*met1*	1	1939222	*met1*	2	1689935
69	Wild type	1	1069605	Wild type	2	1172276	*met1*	1	1050290	*met1*	2	990786
70	Wild type	1	1313988	Wild type	2	576153	*met1*	1	891333	*met1*	2	1280779
71	Wild type	1	1141458	Wild type	2	1206109	*met1*	1	2175817	*met1*	2	1905720
72	Wild type	1	3293448	Wild type	2	1928217	*met1*	1	1920273	*met1*	2	1144275
73	Wild type	1	1972291	Wild type	2	1381342	*met1*	1	1838425	*met1*	2	914306
74	Wild type	1	2308834	Wild type	2	1044164	*met1*	1	1750047	*met1*	2	821499
75	Wild type	1	3098189	Wild type	2	1326670	*met1*	1	2139737	*met1*	2	475906
76	Wild type	1	3050744	Wild type	2	1612668	*met1*	1	1492199	*met1*	2	1532256
77	Wild type	1	2522386	Wild type	2	1228615	*met1*	1	1614714	*met1*	2	1082204
78	Wild type	1	1484280	Wild type	2	1153877	*met1*	1	1864176	*met1*	2	1035493
79	Wild type	1	2742049	Wild type	2	2110032	*met1*	1	1736637	*met1*	2	1156204
80	Wild type	1	2019910	Wild type	2	2002620	*met1*	1	2076568	*met1*	2	1427362
81	Wild type	1	1663779	Wild type	2	1317288	*met1*	1	1567852	*met1*	2	775735
82	Wild type	1	1772355	Wild type	2	1235414	*met1*	1	1800542	*met1*	2	1469182
83	Wild type	1	2604686	Wild type	2	1230285	*met1*	1	2379990	*met1*	2	1037338
84	Wild type	1	880122	Wild type	2	2508013	*met1*	1	1896345	*met1*	2	2302021

85	Wild type	1	775070	Wild type	2	1765791	*met1*	1	1917383	*met1*	2	1265965
86	Wild type	1	1711858	Wild type	2	2168744	*met1*	1	2324899	*met1*	2	856834
87	Wild type	1	1412918	Wild type	2	1438599	*met1*	1	1894324	*met1*	2	1575882
88	Wild type	1	1102423	Wild type	2	1388655	*met1*	1	2152417	*met1*	2	3432713
89	Wild type	1	1001510	Wild type	2	1714441	*met1*	1	2296608	*met1*	2	1711693
90	Wild type	1	3457096	Wild type	2	578887	*met1*	1	1177297	*met1*	2	1454286
91	Wild type	1	2540367	Wild type	2	1495746	*met1*	1	3193507	*met1*	2	928627
92	Wild type	1	3677498	Wild type	2	3091065	*met1*	1	2420734	*met1*	2	1968210
93	Wild type	1	4640036	Wild type	2	796801	*met1*	1	1378933	*met1*	2	2462571
94	Wild type	1	3143689	Wild type	2	1143858	*met1*	1	1816058	*met1*	2	1362111
95	Wild type	1	2999715	Wild type	2	718774	*met1*	1	1386873	*met1*	2	555990
96	Wild type	1	5417394	Wild type	2	3196324	*met1*	1	2097022	*met1*	2	999601

Supplemental Table 16. Crossover and double crossover numbers identified by low coverage sequencing of wild type (n=187) and *met1* (n=192) Col/Ler backcross populations. Total crossovers (COs) and double crossovers (DCOs) are listed, and by chromosome. As *met1-3* was backcrossed from Col into Ler, in order to generate the *met1* Col/Ler F_1 line used for genetic mapping, there is an approximately 5.15 Mb Col/Col introgressed region surrounding *met1* on the south arm of chromosome 5. For this reason artefactual crossovers are identified on chromosome 5 in *met1* and therefore were excluded from subsequent analysis. To test whether wild type and *met1* crossovers were significantly different we used a general linear model (GLM) assuming a negative binomial distribution and *P* values for each comparison are listed.

	COs		DCOs		GLM *P*	
	Wild type	*met1*	Wild type	*met1*	COs	DCOs
Chr1	253	217	105	66	0.966	0.566
Chr2	184	163	44	35	0.972	0.798
Chr3	174	188	45	57	0.962	0.567
Chr4	177	137	45	25	0.971	0.647
Chr5	218	378	77	212	0.748	0.792
All	1,006	1,083	316	395	0.877	0.601

Supplemental Table 17. *I1b* genetic distance in wild type, meiotic recombination and DNA methylation mutants. Genetic distances (cM) were calculated as 2x(100x(eYFP alone/adjusted total)) (Yelina et al. 2012, 2013).

Genotype	Pollen (total)	Pollen (adjusted total)	eYFP alone	cM
Col	10,000	8,167	309	7.6
Col	10,000	7,900	279	7.1
Col	10,000	8,087	326	8.1
zip4-2	9,746	4,109	47	2.3
zip4-2	8,602	2,943	35	2.4
zip4-2	7,872	2,975	24	1.6
met1-3/+	10,000	6,324	379	12
met1-3/+	10,000	6,342	343	10.8
met1-3/+	10,000	6,546	360	11
met1-3/+	10,000	6,166	356	11.5
met1-3/+	10,000	3,881	205	10.6
met1-3/+ zip4-2	10,000	4,104	55	2.7
met1-3/+ zip4-2	10,000	4,180	65	3.1
met1-3/+ zip4-2	10,000	4,313	52	2.4
fancm-1	10,190	7,327	681	18.6
fancm-1	10,000	7,976	559	14
fancm-1	10,000	8,848	725	16.4
fancm-1 zip4-2	10,000	7,283	590	16.2
fancm-1 zip4-2	10,000	7,142	554	15.5
fancm-1 zip4-2	10,000	7,986	677	17
fancm-1 met1-3/+	10,000	6,900	695	20.1
fancm-1 met1-3/+	10,000	6,367	607	19.1
fancm-1 met1-3/+	4,067	2,439	197	16.2
fancm-1 met1-3/+	7,051	5,320	489	18.4
fancm-1 met1-3/+	4,695	3,111	298	19.2
fancm-1 met1-3/+ zip4-2	10,000	7,126	554	15.5
fancm-1 met1-3/+ zip4-2	10,000	4,709	342	14.5
fancm-1 met1-3/+ zip4-2	5,664	3,392	206	12.1
fancm-1 met1-3/+ zip4-2	5,293	3,466	220	12.7
fancm-1 met1-3/+ zip4-2	10,000	5,546	281	10.1

Supplemental Table 18. *CEN3* genetic distance in wild type, meiotic recombination and DNA methylation mutants. Genetic distances, in cM, were calculated as 2x(100x(eYFP alone/adjusted total)) (Yelina et al. 2012, 2013).

Genotype	Pollen (total)	Pollen (adjusted total)	eYFP alone	cM
Col	10,000	7,556	445	11.8
Col	10,000	7,372	384	10.4
Col	10,000	7,192	402	11.2
zip4-2	22,330	9,977	74	1.5
zip4-2	17,301	6,109	41	1.3
zip4-2	29,044	11,964	88	1.5
met1-3/+	10,000	7,244	53	1.5
met1-3/+	10,000	8,619	70	1.6
met1-3/+	10,000	9,240	76	1.6
met1-3/+	10,000	7,557	58	1.5
met1-3/+	10,000	6,445	66	2
met1-3/+ zip4-2	10,000	4,741	29	1.2
met1-3/+ zip4-2	10,000	4,589	30	1.3
met1-3/+ zip4-2	10,000	4,731	28	1.2
fancm-1	10,000	5,859	474	16.2
fancm-1	10,000	7,315	481	13.2
fancm-1	10,000	7,519	459	12.2
fancm-1 zip4-2	10,000	6,899	257	7.5
fancm-1 zip4-2	10,000	6,673	263	7.9
fancm-1 zip4-2	10,000	6,946	259	7.5
fancm-1 met1-3/+	10,000	5,744	215	7.5
fancm-1 met1-3/+	10,000	6,680	264	7.9
fancm-1 met1-3/+	10,000	6,542	248	7.6
fancm-1 met1-3/+	10,000	6,953	271	7.8
fancm-1 met1-3/+	10,000	6,925	294	8.5
fancm-1 met1-3/+	10,000	7,199	307	8.5
fancm-1 met1-3/+ zip4-2	10,000	6,142	180	5.9
fancm-1 met1-3/+ zip4-2	10,000	6,592	201	6.1
fancm-1 met1-3/+ zip4-2	10,000	5,396	145	5.4
fancm-1 met1-3/+ zip4-2	10,000	7,615	234	6.1
fancm-1 met1-3/+ zip4-2	10,000	5,221	156	6
fancm-1 met1-3/+ zip4-2	10,000	7,036	187	5.3
fancm-1 met1-3/+ zip4-2	10,000	5,170	121	4.7
fancm-1 met1-3/+ zip4-2	10,000	6,674	207	6.2

Supplemental Table 19. Tetrad analysis of genetic distance and crossover interference in wild type and *met1*. A-L indicate tetrads with different numbers of crossovers between FTLs: non-crossover (NCO; A), single crossover interval 1 (SCO-I1; B), single crossover interval 2 (SCO-I2; C), two strand double crossover (2st DCO; D), three strand double crossover a (3st DCOa; E), three strand double crossover b (3st DCOb; F), four strand double strand crossover (4st DCO; G), non-parental ditype interval 1, non-crossover interval 2 (NPD-I1 NCO-I2; H), non-crossover interval 1, non-parental ditype interval 2 (NCO-I1 NPD-I2; I), non-parental ditype interval 1, single crossover interval 2 (NPD-I1 SCO-I2; J), single crossover interval 1, non-parental ditype interval 2 (SCO-I1 NPD-I2; K) and non-parental ditype interval 1, non-parental ditype interval 2 (NPD-I1 NPD-I2; L) as in (Berchowitz and Copenhaver 2008).

Tetrad class	*I1bc* Wild type	*I1bc* *met1*	*I5ab* Wild type	*I5ab* *met1/+*
A NCO	8,384	5,394	3,196	2,385
B SCO-I1	1,711	1,715	4,296	4,718
C SCO-I2	4,255	3,663	2,490	2,401
D 2st DCO	74	91	181	256
E 3st DCOa	67	95	145	285
F 3st DCOb	73	97	161	280
G 4st DCO	63	111	142	255
H NPD-I1 NCO-I2	9	11	84	138
I NCO-I1 NPD-I2	64	80	25	29
J NPD-I1 SCO-I2	1	0	11	13
K SCO-I1 NPD-I2	0	2	2	14
L NPD-I1 NPD-I2	0	0	0	0
Total	14,701	11,259	10.733	10,774
Genetic distance/Interference	*I1bc* Wild type	*I1bc* *met1*	*I5ab* Wild type	*I5ab* *met1/+*
I1b cM	6.97	9.67	25.61	31.16
I1c cM	16.72	20.20	15.34	17.39
I1b w/o adjacent CO, cM	8.73	12.51	31.68	38.30
I1b with adjacent CO, cM	3.08	4.78	11.04	16.53
Interference ratio	0.35	0.38	0.35	0.43

Supplemental Table 20. Genetic distances of *CEN3* and *420* in wild type naïve and *met1* backgrounds. Genotype indicates that of the female parent crossed to *420-CEN3*.

CEN3 (cM)	*420* (cM)	Genotype	BS-seq	*CEN3* cM Group
10.6	21.2	Col-0 naive	no	n/a
12.3	21.8	Col-0 naive	no	n/a
11.9	20.0	Col-0 naive	no	n/a
11.3	19.4	Col-0 naive	no	n/a
11.1	n/a	Col-0 naive	no	n/a
11.0	19.8	Col-0 naive	yes	n/a
10.9	n/a	Col-0 naive	no	n/a
8.6	28.3	*met1-3 -/+*	yes	1
8.2	26.8	*met1-3 -/+*	yes	1
8.1	28.0	*met1-3 -/+*	yes	1
5.7	26.5	*met1-3 -/+*	yes	2
5.7	31.2	*met1-3 -/+*	no	n/a
5.4	29.2	*met1-3 -/+*	yes	2
5.2	29.5	*met1-3 -/+*	yes	2
4.6	27.1	*met1-3 -/+*	no	n/a
4.5	29.0	*met1-3 -/+*	no	n/a
4.4	30.8	*met1-3 -/+*	yes	3
4.3	30.6	*met1-3 -/+*	yes	3
4.1	27.6	*met1-3 -/+*	no	n/a
4.0	28.3	*met1-3 -/+*	yes	3
3.8	n/a	*met1-3 -/+*	no	n/a
3.7	33.1	*met1-3 -/+*	yes	4
3.1	27.8	*met1-3 -/+*	yes	4
2.5	28.7	*met1-3 -/+*	no	n/a
2.4	28.3	*met1-3 -/-*	no	n/a
2.2	29.8	*met1-3 -/+*	yes	5
2.1	26.7	*met1-3 -/-*	no	n/a
2.1	29.9	*met1-3 -/-*	no	n/a
2.0	32.6	*met1-3 -/+*	yes	5
1.9	32.4	*met1-3 -/+*	yes	5
1.3	31.1	*met1-3 -/-*	no	n/a

Supplemental Table 21. *CEN3* recombination data in wild type and *met1* backgrounds. For wild type samples a mixture of flow cytometry (rows 1-4) and tetrad (rows 5-7) are shown. Flow cytometry data was used to calculate genetic distance as 2x(100x(eYFP alone/adjusted total)) (Yelina et al. 2012, 2013). *CEN3* cM was calculated from tetrad data as: (½PD + 3NPD)/Total.

Genotype	Total tetrads	PD	NPD	Pollen (adjusted total)	YFP	CEN3 (cM)
Wild type	1,000	225	0			11.3
Wild type	1,014	208	3			11.1
Wild type	1,004	221	0			11.0
Wild type	1,085	236	0			10.9
Wild type				8,333	441	10.6
Wild type				8,363	514	12.3
Wild type				7,884	469	11.9
met1/+	1,163	201	0			8.6
met1/+	1,018	167	0			8.2
met1/+	1,039	162	1			8.1
met1/+	1,087	119	1			5.7
met1/+	965	110	0			5.7
met1/+	1,026	111	0			5.4
met1/+	1,299	136	0			5.2
met1/+	1,045	97	0			4.6
met1/+	1,001	85	1			4.5
met1/+	809	53	3			4.4
met1/+	1,066	91	0			4.3
met1/+	1,014	78	1			4.1
met1/+	923	73	0			4.0
met1/+	907	69	0			3.8
met1/+	900	66	0			3.7
met1/+	1,191	74	0			3.1
met1/+	1,095	49	1			2.5
met1/+	906	43	0			2.4
met1/+	1,000	43	0			2.2
met1-/-	876	36	0			2.1
met1-/-	750	31	0			2.1
met1/+	1,032	41	0			2.0
met1-/-	864	26	1			1.9
met1-/-	818	21	0			1.3

Supplemental Table 22. *420* recombination data in wild type and *met1* backgrounds. *420* cM were calculated using the formula: $100 \times (1 - [1-2(N_G+N_R)/N_T]^{\frac{1}{2}})$, where N_G is a number of green-alone fluorescent seeds, N_R is a number of red-alone fluorescent seed and N_T is the total number of seeds counted.

Genotype	Green-alone	Red-alone	Both red and green	Neither red or green	Total	*420* cM
Wild type	280	253	2,014	496	3,043	19.4
Wild type	244	252	1,845	446	2,787	19.8
Wild type	245	239	1,651	418	2,553	21.2
Wild type	272	215	1,637	388	2,512	21.8
Wild type	221	222	1,584	435	2,462	20.0
met1/+	330	313	1,637	368	2,648	28.3
met1/+	317	360	1,830	414	2,921	26.8
met1/+	311	380	1,781	401	2,873	28.0
met1/+	316	299	1,693	369	2,677	26.5
met1/+	344	339	1,585	325	2,593	31.2
met1/+	337	329	1,664	343	2,673	29.2
met1/+	327	347	1,672	333	2,679	29.5
met1/+	317	310	1,697	353	2,677	27.1
met1/+	300	324	1,576	319	2,519	29.0
met1/+	298	299	1,413	284	2,294	30.8
met1/+	328	336	1,579	316	2,559	30.6
met1/+	362	339	1,855	391	2,947	27.6
met1/+	349	349	1,795	380	2,873	28.3
met1/+	365	348	1,576	292	2,581	33.1
met1/+	280	311	1,488	393	2,472	27.8
met1/+	349	337	1,733	368	2,787	28.7
met1-/-	317	364	1,750	369	2,800	28.3
met1/+	340	372	1,766	326	2,804	29.8
met1-/-	317	323	1,748	377	2,765	26.7
met1-/-	352	333	1,669	338	2,692	29.9
met1/+	343	338	1,517	297	2,495	32.6
met1/+	364	368	1,650	313	2,695	32.4
met1-/-	361	394	1,757	363	2,875	31.1

Supplemental Table 23. Coverage of cytosines in CG, CHG and CHH contexts for each individual bisulfite sequenced.

Genotype	CG read number	CG coverage	CHG read number	CHG coverage	CHH read number	CHH coverage
420-CEN3, naïve	67,989,599	12.21	70,844,535	11.63	379,159,928	12.15
met1/+	100,645,548	18.08	106,300,353	17.44	572,857,484	18.36
420-CEN3 met1/+ 1	58,358,586	10.48	60,662,034	9.95	334,707,521	10.73
420-CEN3 met1/+ 2	115,238,981	20.70	120,324,368	19.75	657,789,802	21.08
420-CEN3 met1/+ 3	91,805,992	16.49	96,132,919	15.78	522,766,903	16.76
420-CEN3 met1/+ 4	98,958,507	17.77	104,362,480	17.13	556,289,421	17.83
420-CEN3 met1/+ 5	106,877,268	19.20	110,983,196	18.21	606,873,835	19.45
420-CEN3 met1/+ 6	75,748,912	13.61	79,443,683	13.04	425,283,636	13.63
420-CEN3 met1/+ 7	55,370,857	9.94	57,592,023	9.45	318,107,079	10.20
420-CEN3 met1/+ 8	65,347,854	11.74	68,474,126	11.24	365,048,599	11.70
420-CEN3 met1/+ 9	78,756,470	14.15	81,882,645	13.44	443,145,370	14.20
420-CEN3 met1/+ 10	54,748,630	9.83	68,474,126	11.24	312,062,139	10.00
420-CEN3 met1/+ 11	73,802,870	13.26	77,006,790	12.64	418,560,009	13.42
420-CEN3 met1/+ 12	60,483,494	10.86	63,152,124	10.36	339,995,012	10.90
420-CEN3 met1/+ 13	65,987,906	11.85	69,007,502	11.32	373,161,158	11.96
420-CEN3 met1/+ 14	8,2071,448	14.74	85,440,245	14.02	472,324,578	15.14

Supplemental Table 24. Analysis of sodium bisulphite conversion based on chloroplast genomic DNA. Numbers in indicate the % of unmethylated cytosines.

Genotype	CG	CHG	CHH
420-CEN3, naïve	99.69	99.65	99.63
met1/+	99.70	99.68	99.65
420-CEN3 met1/+ 1	99.71	99.67	99.65
420-CEN3 met1/+ 2	99.65	99.62	99.60
420-CEN3 met1/+ 3	99.69	99.66	99.64
420-CEN3 met1/+ 4	99.69	99.66	99.64
420-CEN3 met1/+ 5	99.65	99.61	99.60
420-CEN3 met1/+ 6	99.70	99.67	99.65
420-CEN3 met1/+ 7	99.70	99.67	99.64
420-CEN3 met1/+ 8	99.70	99.67	99.65
420-CEN3 met1/+ 9	99.65	99.64	99.61
420-CEN3 met1/+ 10	99.70	99.66	99.64
420-CEN3 met1/+ 11	99.70	99.67	99.65
420-CEN3 met1/+ 12	99.71	99.69	99.66
420-CEN3 met1/+ 13	99.71	99.68	99.66
420-CEN3 met1/+ 14	99.72	99.68	99.66

Supplemental Table 25. Methylation levels in *420-CEN3* naïve Col-0 and *met1/+* individuals. CG, CHG and CHH levels were calculated within *CEN3* or *420*. CG levels within genes, TEs or random sequences are also shown. Random sequences are 5 Mb total of randomly selected 1 kb probes throughout the genome.

Genotype	*CEN3* CG	*CEN3* CHG	*CEN3* CHH	*420* CG	*420* CHG	*420* CHH	Gene CG	TEs CG	Random CG
420-CEN3, naïve	70.32	31.68	7.93	12.19	1.47	0.91	12.89	53.77	28.27
420-CEN3 met1/+ 1	46.05	31.6	8.58	6.53	1.59	0.88	7.11	38.24	18.36
420-CEN3 met1/+ 2	53.55	32	7.76	8.58	1.6	0.89	8.17	43.23	20.87
420-CEN3 met1/+ 3	48.50	30.18	7.91	7.01	1.4	0.82	8.00	41.83	20.28
420-CEN3 met1/+ 4	48.97	31.17	7.93	6.96	1.34	0.79	7.40	38.97	18.71
420-CEN3 met1/+ 5	53.63	34.22	8.85	8.47	1.68	0.92	7.89	40.49	19.62
420-CEN3 met1/+ 6	50.30	30.72	8.21	6.81	1.39	0.85	7.74	43.97	20.61
420-CEN3 met1/+ 7	49.67	30.92	8.17	6.53	1.51	0.87	7.25	40.00	18.95
420-CEN3 met1/+ 8	57.11	31.29	7.58	7.94	1.48	0.85	7.68	44.11	20.44
420-CEN3 met1/+ 9	58.76	33.04	8.43	6.81	1.43	0.87	8.30	43.97	20.98
420-CEN3 met1/+ 10	46.70	30.08	7.89	6.66	1.55	0.86	8.15	41.24	20.74
420-CEN3 met1/+ 11	48.95	30.27	7.61	6.93	1.43	0.81	7.47	40.92	19.14
420-CEN3 met1/+ 12	51.05	30.72	7.39	7.28	1.52	0.84	7.27	40.15	19.17
420-CEN3 met1/+ 13	54.23	28.86	6.97	6.67	1.38	0.81	7.43	43.64	20.13
420-CEN3 met1/+ 14	48.23	29.55	7.85	6.91	1.39	0.8	7.56	40.54	19.34
met1/+	41.68	27.19	6.05	6.69	1.36	0.71	4.20	38.13	16.35

Supplemental Table 26. Correlations between crossover frequency and DNA methylation levels between chromosomal regions. The left flank within *CEN3* was from 11,115,724-12,782,751 bp, the core centromere was from 12,782,751-14,750,881 bp and the right flank was from 14,750,881-16,520,560 bp. Random sequences are 5 Mb total of randomly selected 1 kb probes throughout the genome. The centromeric regions analysed for each chromosome were between the following coordinates: *CEN1* was from 12-17.5 Mb, *CEN2* was from 1-7.5 Mb, *CEN4* was from 2-5.5 Mb and *CEN5* from 9.5-16 Mb. The chromosome 1 north sub-telomere region analysed was from 256,516-5,361,637 bp and the south sub-telomere was from 25-30 Mb. We also include two additional columns for the significant correlations, where we exclude the wild type (Col/Col) sample and repeat analysis.

Region 1 / Parameter	Region 2 / Parameter	Spearman's *r* wt included	*P* value wt included	Spearman's *r* wt excluded	*P* value wt excluded
CEN3 / cM	*CEN3* / CG	0.768	0.0013	0.714	0.0056
CEN3 / cM	*CEN3* / CHG	0.179	0.524		
CEN3 / cM	*CEN3* / CHH	-0.384	0.158		
CEN3 / cM	*CEN3* / All contexts	0.349	0.203		
CEN3 / cM	*CEN3* / CG left flank	0.729	0.0029	0.666	0.0115
CEN3 / cM	*CEN3* / CG right flank	0.745	0.0014	0.686	0.0067
CEN3 / cM	*CEN3* / CG core	0.786	0.0008	0.736	0.0038
CEN3 / CG	*CEN3* / CG left flank	0.975	< 2.2e^{-16}	0.969	< 2.2e^{-16}
CEN3 / CG	*CEN3* / CG right flank	0.974	9.005e^{-10}	0.968	1.421e-^{08}
CEN3 / CG	*CEN3* / CG core	0.989	< 2.2e^{-16}	0.987	< 2.2e^{-16}
CEN3 / CG left flank	*CEN3* / CG right flank	0.928	6.383e^{-07}	0.911	5.951e-^{06}
CEN3 / cM	*CEN1* / CG	0.146	0.602		
CEN3 / cM	*CEN2* / CG	0.314	0.254		
CEN3 / cM	*CEN4* / CG	0.190	0.498		
CEN3 / cM	*CEN5* / CG	-0.086	0.763		
CEN3 / cM	Random1 / CG	0.307	0.265		
CEN3 / cM	Random2 / CG	0.207	0.458		
420 / cM	*420* / CG	-0.319	0.247		
420 / cM	*420* / CHG	0.542	0.037	0.592	0.0257
420 / cM	*420* / CHH	0.202	0.471		
420 / cM	*420* / all contexts	-0.084	0.767		
420 / cM	North sub-telomere Chr1 / CG	-0.175	0.532		
420 / cM	South sub-telomere Chr1 / CG	-0.410	0.129		
420 / cM	*CEN3* / cM	-0.708	0.0031	-0.640	0.0136
420 / cM	*CEN3* / CG	-0.683	0.0050	-0.609	0.0207
CEN3 / cM	*420* / CG	0.515	0.049	0.403	0.153
420 / CG	*CEN3* / CG	0.519	0.048	0.407	0.148

Supplemental Table 27. γ-H2AX foci count in wild type and *met1* leptotene stage meiocytes.

Total number of γ-H2AX foci		Total number of γ-H2AX foci on DAPI-dense regions	
Wild-type	*met1-3*	Wild-type	*met1-3*
156	133	2	3
155	193	3	5
150	233	6	12
227	177	5	3
148	128	5	7
181	154	4	4
209	227	4	1
134	167	6	7
151		10	
158		7	
155		2	
206		18	
153		6	
145		4	
186		2	
211		4	
154		14	
196		4	
197		3	
152		10	
194		3	

Supplemental Table 28. Fertility of *met1 spo11* mutant backgrounds.

Genotype	No of seeds	No of siliques	Seeds per silique
spo11-1	25	50	0.5
met1-3+/+ spo11-1	12	50	0.2
met1-3+/+ spo11-1	24	50	0.5
met1-3+/- spo11-1	0	50	0.0
met1-3+/- spo11-1	25	50	0.5
met1-3+/- spo11-1	0	50	0.0
met1-3-/- spo11-1	4	55	0.1
met1-3-/- spo11-1	1	50	0.0
met1-3-/- spo11-1	5	50	0.1
met1-3-/-	360	12	30.0
met1-3-/-	285	10	28.5
met1-3-/-	211	10	21.1
met1-3-/-	207	12	17.3
met1-3-/-	253	10	25.3
met1-3-/-	147	9	16.3
met1-3-/-	214	10	21.4
Col wild type	512	13	39.4

Supplemental Table 29. Oligonucleotides.

Name	Sequence (5′-3′)	Application
bis7-3a-F2	tggtttttaaatygtggaagtaaatagaatatgattttt	*3a*, BS-seq *HP3*_right
bis7-3a-R2	aacaaacttatccatattacaacaactaaaaaactaaaaaaaa	*3a*, BS-seq *HP3*_right
bis-3a-hp7-F9	ttttttatatattttattttagaattttagttaaygatttagtt	*3a*, BS-seq *HP3*_middle
bis7-3a-R4	acataaaataaaattataacaactacccataactcratataaataa	*3a*, BS-seq *HP3*_middle
bis7-3a-F6	tataatagttaagagtaaaagatataaaaaaagtgtagagataaatygtt	*3a*, BS-seq *HP4*_left
bis7-3a-R6	tctcaataatttattttttatttatttattataatatactttttttaataa	*3a*, BS-seq *HP4*_left
bis-3a-hp7-F7	gaagttattagatttattgaggaggtttttatttatttggtttt	*3a*, BS-seq *HP3*_left
bis-3a-hp7-R7	aactcrttaacattatttttttaactaaatcrttaactaaa	*3a*, BS-seq *HP3*_left
bis-2885-F1	aataatggaagttatattttgagttgtattttataattgaagttttt	*3a*, BS-seq *HP4*_middle
bis-2885-R1	aacaaattcaatttattaaaatctaatattaaaattttatatattacaaa	*3a*, BS-seq *HP4*_middle
bis-2885-F2	attttaatattagattttaataaattgaatttgttttgagtggtttatt	*3a*, BS-seq *HP4*_right
bis-2885-R2	ccaaaacaaaattttaatcttttaattctctatacrtaaa	*3a*, BS-seq *HP4*_right
3b-bis-F1	tttaggggttttttgatttttagatattgaaagaaaaagat	*3a*, BS-seq *HP5*_left
3b-bis-R1	aaaataaaacaataatatcttcccraatttcraatcaataa	*3b*, BS-seq *HP5*_left
3b-bis-F3	attaatttatgggttatatatttagagtagatattaaagtgaaat	*3b*, BS-seq *HP5*_middle
3b-bis-R3	aaaaacaaaacataacatataaaaacttttaaacacattcaataa	*3b*, BS-seq *HP5*_middle
3b-bis-F6	ygtttaatttttttttgtttaattatgggataygaaataatgaygtt	*3b*, BS-seq *HP5*_right
3b-bis-R5	aataacccratccaaatttattaaaaaaaaaaaaaaactcrataaaa	*3b*, BS-seq *HP5*_right
At3g02880-upstream-F	caccttaccttcctttcaaattgatac	*3a HP1* cloning
At3g02880-upstream-R	ctgttacgaacagcgagtaa	*3a HP1* cloning & siRNA probe
At3g02880-HindIII-F	aagcttgagagaagaaagacagagctg	*3a HP1* hairpin cloning
At3g02880-HindIII-R	ctttcttctctcaagcttgccggctaagagagagaa	*3a HP1* cloning
3a-intergenic1-F	caccgttcttgttctagtttgttcg	*3a HP3* cloning and siRNA probe
3a-intergenic1-R	ggcgatttgtctctacactt	*3a HP3* cloning and siRNA probe
3a-intergenic1-EcoRI-F	gaattcctagtcaacgaattcagccaaaaaac	*3a HP3* cloning
3a-intergenic2-EcoRI-R	gaattcgttgactaggaattctgggataagatgtg	*3a HP3* cloning

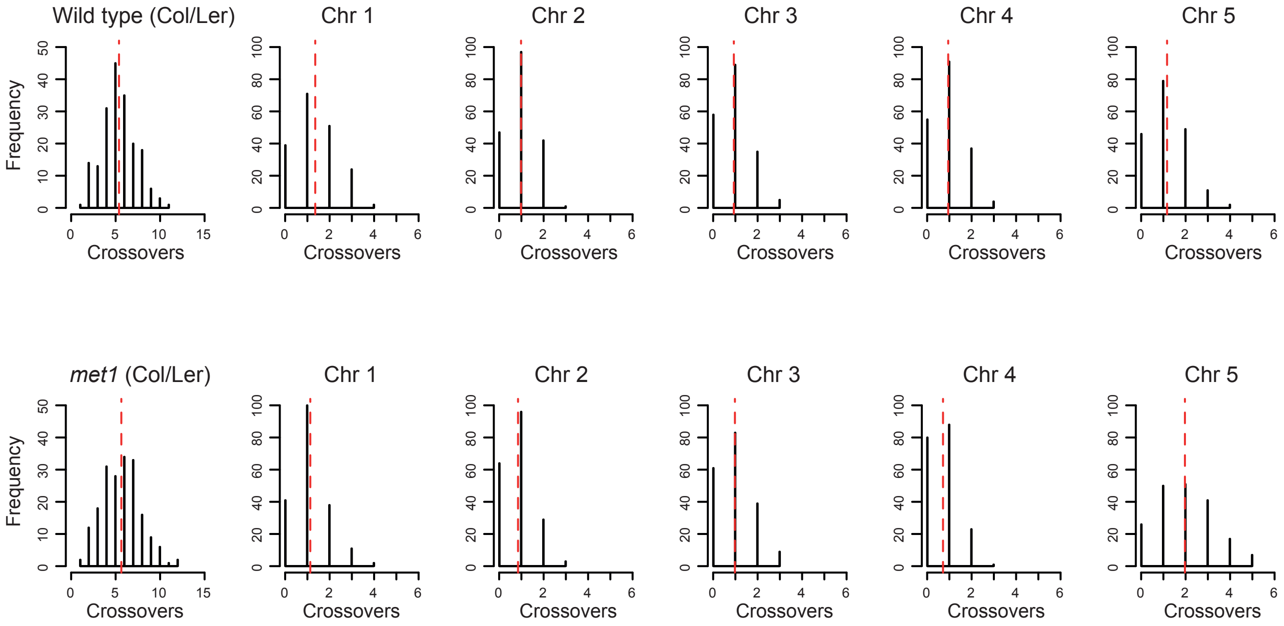
At3g02885-gbm-F	caccttggacggccttctttag	*3a HP4* cloning and siRNA probe
At3g02885-gbm-R	atggcgaattgtatcagaag	*3a HP4* cloning and siRNA probe
At3g02885-gbm-HindIII-F	aagcttcaatatcagaaaactaatagcc	*3a HP4* cloning
At3g02885-gbm-HindIII-R	gttttctgatattgaagctttatatatatatgacag	*3a HP4* cloning
At3g02880-gbm- F	cacctattcggttctttaccaatcg	*3a HP2* cloning
At3g02880-gbm- R	acggtgtttgttgctcgg	*3a HP2* cloning
At3g02880-EcoRV-F	gatatcgatttggatggattgttg	*3a HP2* cloning & siRNA probe
At3g02880-EcoRV-R	ccatccaaatcgatatccccgaaagatttcac	*3a HP2* cloning
At3g02880-gbm-mid-R	aatgtttccatgagaagttgtc	*3a HP2* cloning & siRNA probe
Upstr-At3g02880-MCRBC-F1	ccacttcttaagttctctgttgacc	*3a*, *Mcr*BC analysis
upstr-At3g02880-MCRBC-R1	aacgacctctgtttttcctttc	*3a*, *Mcr*BC analysis
upstr-At3g02880-MCRBC-F2	gagagagaagaaagacagagctg	*3a*, *Mcr*BC analysis
upstr-At3g02880-MCRBC-R2	cactcatgttccatagcaaagg	*3a*, *Mcr*BC analysis
Intergenic 1-MCRBC-F1	cttccacatacaaacatcatc	*3a*, *Mcr*BC analysis
Intergenic 1-MCRBC-R1	ctctgttttaatctgtttctacaag	*3a*, *Mcr*BC analysis
Intergenic 1-MCRBC-F2	acttcccgcctttttctac	*3a*, *Mcr*BC analysis
Intergenic 1-MCRBC-R2	tggctgaatcgttgactagg	*3a*, *Mcr*BC analysis
gbm-At3g02885-MCRBC-F1	cattgagatctttatgttcatgc	*3a*, *Mcr*BC analysis
gbm-At3g02885-MCRBC-R1	ggcaatcaagatttttaacc	*3a*, *Mcr*BC analysis
gbm-At3g02885-MCRBC-F2	cttgtagaaacagattaaaacagag	*3a*, *Mcr*BC analysis
gbm-At3g02885-MCRBC-R2	gcatgaacataaagatctcaatg	*3a*, *Mcr*BC analysis
gbm-At3g02880-MCRBC-F1	ccgttgaactgggaaacc	*3a*, *Mcr*BC analysis
gbm-At3g02880-MCRBC-R1	ctcaggttggtaccttgtgag	*3a*, *Mcr*BC analysis
gbm-At3g02880-MCRBC-F2	tcacggctctccgattac	*3a*, *Mcr*BC analysis

gbm-At3g02880-MCRBC-R2	cttgtcgctatctttcttctcc	*3a*, *Mcr*BC analysis
3b-dir-Fupstream	caccttgataatgtcaataagataaatgc	*3b HP5* cloning
3b-R	tctttagagttccgtacgtg	*3b HP5* cloning
3b-EcoRI-F	gaattccaaccatctgtgttgtgg	*3b HP5* cloning & siRNA probe
3b-EcoRI-R	aacacagatggttggaattcttattgttgtttcactttgatgtc	*3b HP5* cloning & siRNA probe
siRNA-1-3b-F	gaacctttaaaattacaacttgg	*3b HP5* siRNA probe,
siRNA-2-3b-R	tgaagcacattcaatggtgg	*3b HP5* siRNA probe
3b-long-5MCRBC-F	ctaagagaacacgatacgaaatc	*3b*, *Mcr*BC
3b-long-5MCRBC-R	gctgttatatcgtcgaatgg	*3b*, *Mcr*BC
3b-3MCRBC-F	gcagagcagaggaaatcaag	*3b*, *Mcr*BC
3b-3MCRBC-R	ttgcatcaggacatgatttg	*3b*, *Mcr*BC
At5g13440-F	acaagccaatttttgctgagc	*Mcr*BC analysis, unmethylated control
At5g13440-R	acaacagtccgagtgtcatggt	*Mcr*BC analysis, unmethylated control
LTR-Ta3-F	tttgctctcaaactctcaattgaagttt	*Mcr*BC analysis, methylated control
LTR-Ta3-R	tagggttcttagttgatcttgtattgagctc	*Mcr*BC analysis, methylated control
met1-3-F	gattgtgtctctactacagaggc	Genotyping met1-3
met1-3-R	gttaagctcattcatagccttgc	Genotyping *met1-3*
met1-3-T	tggacgtgaatgtagacacgtcg	Genotyping *met1-3*
fancm-F	acaatatatgtttcgtgcaggtaagacattggaag	Genotyping *fancm-1*
fancm-R	caccaatagatgttgcgacaat	Genotyping *fancm-1*
zip4-F	gctggatcgagctcttgaat	Genotyping *zip4-2*
zip4-R	attctgttctcgctttccag	Genotyping *zip4-2*
SALK-LB	caaaccagcgtggaccgcttgctg	Genotyping *zip4-2*
PE-top adapter	acactctttccctacacgacgctcttccgatct	BS-seq NGS library construction
PE-bottom adapter	gatcggaagagcggttcagcaggaatgccgag	BS-seq NGS library construction
PE1.0	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttccgatct	BS-seq NGS library construction
iCPRtag1	caagcagaagacggcatacgagataacgtgatgagatcggtctcggcattcctgctgaaccgctcttccgatc	BS-seq NGS library construction

iCPRtag2	caagcagaagacggcatacgagataaacatcggagatcggtctcggcattcctgctgaaccgctcttccgatc	BS-seq NGS library construction
iCPRtag3	caagcagaagacggcatacgagatatgcctaagagatcggtctcggcattcctgctgaaccgctcttccgatc	BS-seq NGS library construction
iCPRtag4	caagcagaagacggcatacgagatagtggtcagagatcggtctcggcattcctgctgaaccgctcttccgatc	BS-seq NGS library construction
iCPRtag5	caagcagaagacggcatacgagataccactgtgagatcggtctcggcattcctgctgaaccgctcttccgatc	BS-seq NGS library construction
iCPRtag6	caagcagaagacggcatacgagatacattggcgagatcggtctcggcattcctgctgaaccgctcttccgatc	BS-seq NGS library construction
iCPRtag7	caagcagaagacggcatacgagatcagatctggagatcggtctcggcattcctgctgaaccgctcttccgatc	BS-seq NGS library construction
iCPRtag8	caagcagaagacggcatacgagatcatcaagtgagatcggtctcggcattcctgctgaaccgctcttccgatc	BS-seq NGS library construction
iCPRtag9	caagcagaagacggcatacgagatcgctgatcgagatcggtctcggcattcctgctgaaccgctcttccgatc	BS-seq NGS library construction
iCPRtag10	caagcagaagacggcatacgagatacaagctagagatcggtctcggcattcctgctgaaccgctcttccgatc	BS-seq NGS library construction
iCPRtag11	caagcagaagacggcatacgagatctgtagccgagatcggtctcggcattcctgctgaaccgctcttccgatc	BS-seq NGS library construction
iCPRtag12	caagcagaagacggcatacgagatagtacaaggagatcggtctcggcattcctgctgaaccgctcttccgatc	BS-seq NGS library construction
iCPRtag13	caagcagaagacggcatacgagataacaaccagagatcggtctcggcattcctgctgaaccgctcttccgatc	BS-seq NGS library construction
iCPRtag14	caagcagaagacggcatacgagataaccgagagagatcggtctcggcattcctgctgaaccgctcttccgatc	BS-seq NGS library construction
iCPRtag15	caagcagaagacggcatacgagataacgcttagagatcggtctcggcattcctgctgaaccgctcttccgatc	BS-seq NGS library construction
iCPRtag16	caagcagaagacggcatacgagataagacggagagatcggtctcggcattcctgctgaaccgctcttccgatc	BS-seq NGS library construction
iCPRtag17	caagcagaagacggcatacgagataaggtacagagatcggtctcggcattcctgctgaaccgctcttccgatc	BS-seq NGS library construction
Ta2-JP1725	aaacgatgcgttgggataggtc	ChIP-qPCR
Ta2-JP1726	atactctccacttcccgtttttctttttta	ChIP-qPCR

ACTIN 2/7-JP1595	cgtttcgctttccttagtgttagct	ChIP-qPCR
ACTIN 2/7-JP1596	agcgaacggatctagagactcaccttg	ChIP-qPCR
HP3-ChiP-F1	tttacaccgagtcatgggca	ChIP-qPCR
HP3-ChiP-R1	accatcaacttgctaaggtca	ChIP-qPCR
HP3-ChiP-F2	tgttcgttaattcttgagcctca	ChIP-qPCR
HP3-ChiP-R2	tggctgaatcgttgactagga	ChIP-qPCR
HP4-ChiP-F1	ttggggtttgagtttgccac	ChIP-qPCR
HP4-ChiP-R1	tgtcagtctccaacctcgtt	ChIP-qPCR
HP4-ChiP-F2	acggccttctttagtcttcca	ChIP-qPCR
HP4-ChiP-R2	gtagcttccgttgttcagca	ChIP-qPCR
HP5-ChiP-F1	aacacaaccgatgagcaagg	ChIP-qPCR
HP5-ChiP-R1	tcgtcgaatggggtagacat	ChIP-qPCR
HP5-ChiP-F2	actaggctgcgtcgtgtaaa	ChIP-qPCR
HP5-ChiP-R2	ggagttttgttccgtggctc	ChIP-qPCR

Yelina_Fig_S1



Yelina_Fig_S2