

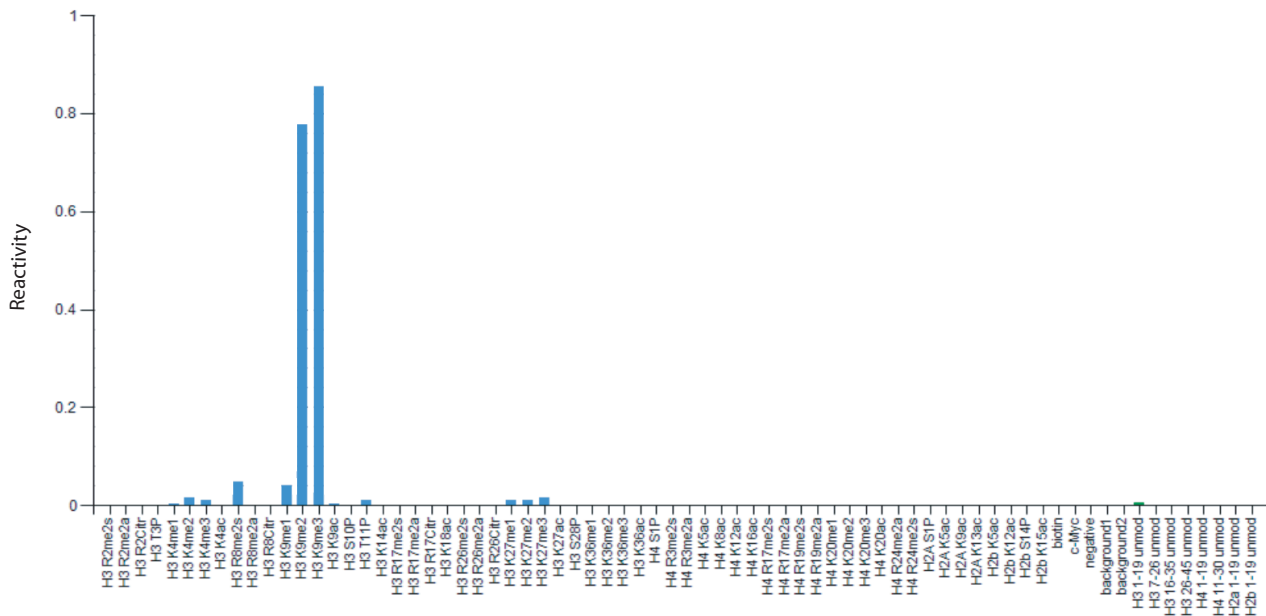
Supplementary Figure 1 CMT2 does not methylate CG sites in vitro and its activity is distinct from CMT3. (a) RT-PCR on CMT2 and ACTIN transcripts in wild type and *cmt2-7* mutants. A no RT control for the CMT2 amplification is also shown. Cartoon of T-DNA insertion site in the CMT2 gene (At4g19020) is also shown. Thick lines, exons; thin lines, introns. (b) CMT3 in vitro methyltransferase activity assay performed in parallel to the CMT2 assay. Error bars represent SD for two technical replicates. (c) CMT2 in vitro methyltransferase activity on CG sites. Error bars represent SD for two technical replicates.

a

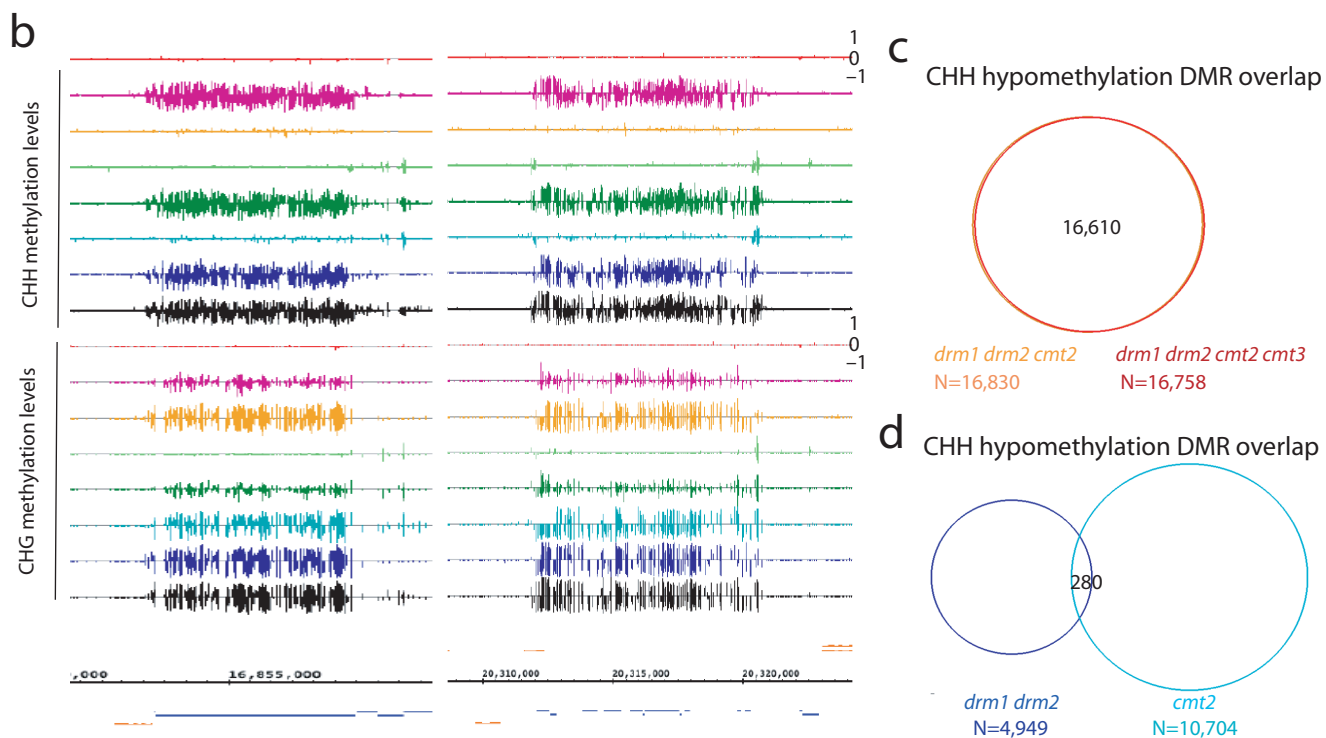
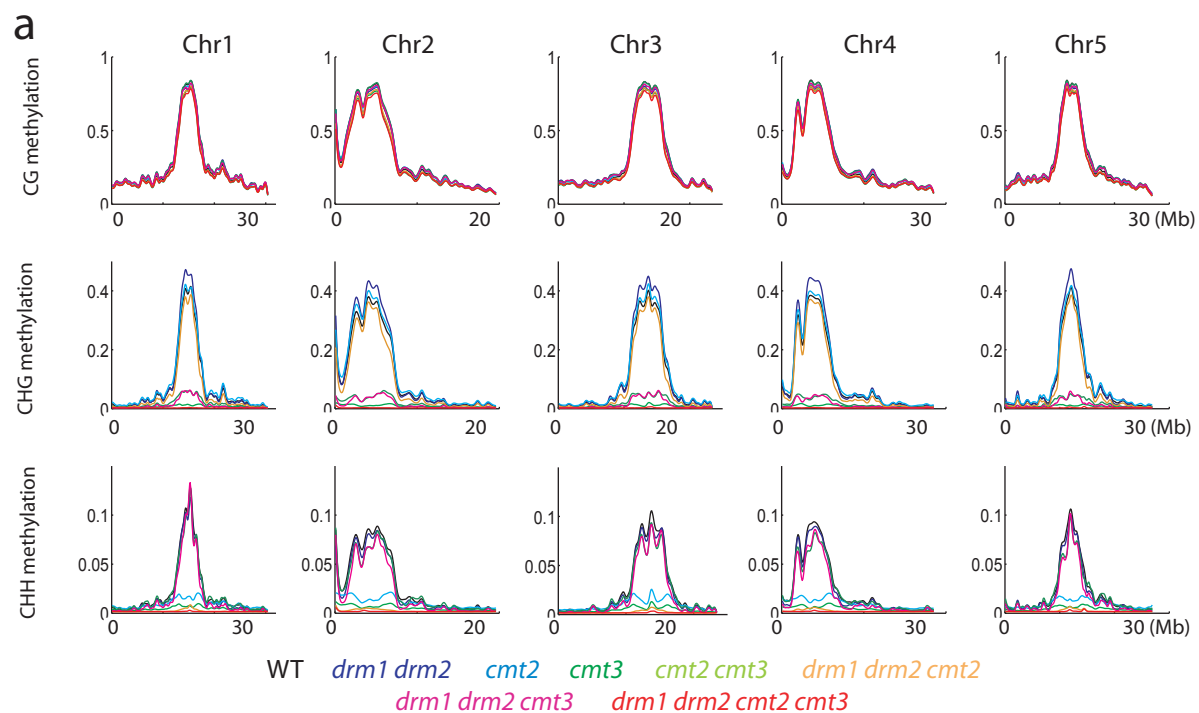
Sequence	Position	Protein	Sequence	Position	Protein
cmt2 cmt3 zmet2	60 0 0	cmt2 cmt3 zmet2	CEEAQERWRWRYELKERKSKS--RQQQSEDDDEDKIVANVECHYSQAKVDG-HTFSLGDFDA ESEAKSTWPDYKPIEVQPPKASSRKKTKDDEKVEIIRARCHYRRAIVDEPQIYELNDDA ADEARSNWPKRYGRSTAA-----KKPDEEELKARCHYRSKAKVDN-VVYCLGDDV *:*	586 116 192	BAH Domain
cmt2 cmt3 zmet2	120 0 0	cmt2 cmt3 zmet2	YIK-GEEETHVGVQIVEFFKTIIDGESYFRVQVFRATDTIMEERQ-----ATNHDKRRLF VYQSGEGKDPFKIKIEMFEGANGKLYFTARWYRPSDITVMKFEILLI-----KKKRVF VYKAGNEADYIGRIIEFFEGTDQCHYFTCRWFFRAEDIVNLSVSIVDGHKHDPRRVE *:	639 170 252	
cmt2 cmt3 zmet2	180 0 0	cmt2 cmt3 zmet2	YSTVMNDNFVDCILSKVIVLQVSPRVGLK---PNSIKSDYFDMEYCVVEYTFQILRNPK FSEIQDINELGLLEKLNILMIPLNENKTIIPATENCDFPCDMNVFLPYDTFEAIQRF LSEKKNNDVLDICIIKVKIVHVDENMDPKAKAQLIEESCDDLYFCCMSVYAYSTFANISSEN *:	696 230 312	
cmt2 cmt3 zmet2	240 0 0	cmt2 cmt3 zmet2	TSENKLE---CCADVVPTESTES-----ILKKSFSGELFVLDDLYSGCGGMSTGLSLGA MMAISESST-ISSDITDREGAAAIIEIGCESQETEGHKKATLLDLYSGCGAMSTGLCMGA GQSGSDTASGISSD-----DVLDTSSMPTRTATLLDLYSGCGGMSTGLCLGA *:	747 289 361	
cmt2 cmt3 zmet2	300 0 0	cmt2 cmt3 zmet2	KISGVVVIKAVAQNTAACKSLKLNHPNTQVRNDAAGDFLQLLKEWDLCKRYVFNNDQ QISGLNLVTKAVDMNAHACKSLQHNHPETNVRNMTAEDFFLLKKEWKLCHFSLRNRP ALSGKLETRAVDFNSFACQSLKYHPQTEVRNEKADEFLLAKKEWAVLCKRYVQDVDS *:	807 349 421	
cmt2 cmt3 zmet2	360 0 0	cmt2 cmt3 zmet2	RIDTLRSV---NSTKETSGSSSSDDSDSESEYVEKLVDCIPGDDHDKGNLGLKFKVHW NSEYANLHGLNNDVNEEDVSESENEEDDGEVFTVDKIVGISFGVPKLLKRGVLYLKVW NLAS-----SEDO-ADEDSPLDKKIEFVVEKLVGICVYGGSD--RENGIYFKVQW *:	864 409 466	CHROMO Domain
cmt2 cmt3 zmet2	420 0 0	cmt2 cmt3 zmet2	KGYRSDEDIWELAEELSNQDAIREFVTSGFKSKILPLPGRVGVICGGPFCQGISGYNRH LNYDDSHDIWEPFIEGLSNCRGKIEEFVKGKSGILPFGGVDVCGGPPCCQGISGHNRF EGYGPEDDIWEPIDNLSDCPCQKIREFVQEGHKRKLPLPFGVDVVICGGPFCQGISGYNRY *:	924 469 526	
cmt2 cmt3 zmet2	480 0 0	cmt2 cmt3 zmet2	RNVDSPLNDRNQIIVFMDIVEYLPKSVVLMENVVVDILRMDKGSIGRYALSRLVNMRYQ RNLLDPLEDKNKQLLVYMNIVEYLPKPFVLMENVVMDLMAKGYLARFAVGRLLQMYQ RNRDEPLKDEKNQMVTFMDIVAVLKPVKVLMENVVVDILKFDAGYLGKVALSCLVAMKYQ *:	984 529 586	
cmt2 cmt3 zmet2	540 0 51	cmt2 cmt3 zmet2	ARLGIMTAGCYGLSQFRSVFMWGA VPNKLPFPPLPHTDVIYRYGLPLEFERNVVAE VNRGMMAGAYGLAQFLRFLWGLAPSEIIPOFPLPHTDVIYRYGLPLEFERNVVAE ARLGMVWAGCYGLPQFRMRFVFLWGLSSMLVPLPYDVIYRYGGAPNAPFSCQMVAYDE *:	1044 589 646	
cmt2 cmt3 zmet2	600 469 96	cmt2 cmt3 zmet2	GQPRKLEKALVLKDAISDLPHVSNDEDEKRELPYESLPKTFDQRYIRSTRKRLDLSAIDN- GHTVKLADKLLKDVISDLPAVANSEKREITDYKDPITTFQFKFIRLRKDEASGQ--SK TQKPSLKKALLGDAISDLPKVQNHQPNVMEYGGSPKTEFQRYIRLSRKDMLDWSFGEG *:	1103 647 706	
cmt2 cmt3 zmet2	660 529 56	cmt2 cmt3 zmet2	CMKRTMLLHHRPFHINEDDYARVQIIPKRRKANFRDLPLGLVIRNN-IVCRDPSMEPVIL SKSKKHVLYDHPHPLNINDVERVQVPPKRRKANFRDFPGVIVGPGNVVKLEEGKERVKL AGPDEGKLLDHOPLRNNDDYERVQIIPVKKKANFRDLKGVYVGMANNIVWDEPEIERVKL *:	1162 707 766	
cmt2 cmt3 zmet2	720 143	cmt2 cmt3 zmet2	PSGKPLVPYVFTFQOQKSKRPFARLWDEIVPTVTLVPTCHSQALLHPEQDRVLTIRE ESGKTLVPDYALTYIVDGKSCKPFGRWLWDEIVPTVTRAEFHNQVLIHPEQNRVLSIREN SSGKPLVPDYAMSFIKGKSLKPFGRWLWDEIVPTVTRAEFHNQVLIHPTQARVLTIREN *:	1222 767 826	
cmt2 cmt3 zmet2	780 1281 827 886	cmt2 cmt3 zmet2	ARLQGFDDYKLFQFCGTIKERYCQIGNAVAVSVSRALGYSLGMFAFRGLARDE-HLIKLPQNF ARLQGFDDYKLFQFPKQKYIQVGNVAVPVAKALGYALGTAFQGLAVGKDPDLLLPEGF ARLQGFDDYRLLRFGPIKERYIQVGNVAVPVARALGYCLGQAYLGESEGSDFLYQLPPSF *****:	1281 827 886	
cmt2 cmt3 zmet2	840 1295 839 912	cmt2 cmt3 zmet2	SHSTYPOLQE--TIPH----- 1295 AFMKPTLPSELA----- 839 TSVGGRTAGQARASPVGTPEGEVVEQ 912 *:		

b

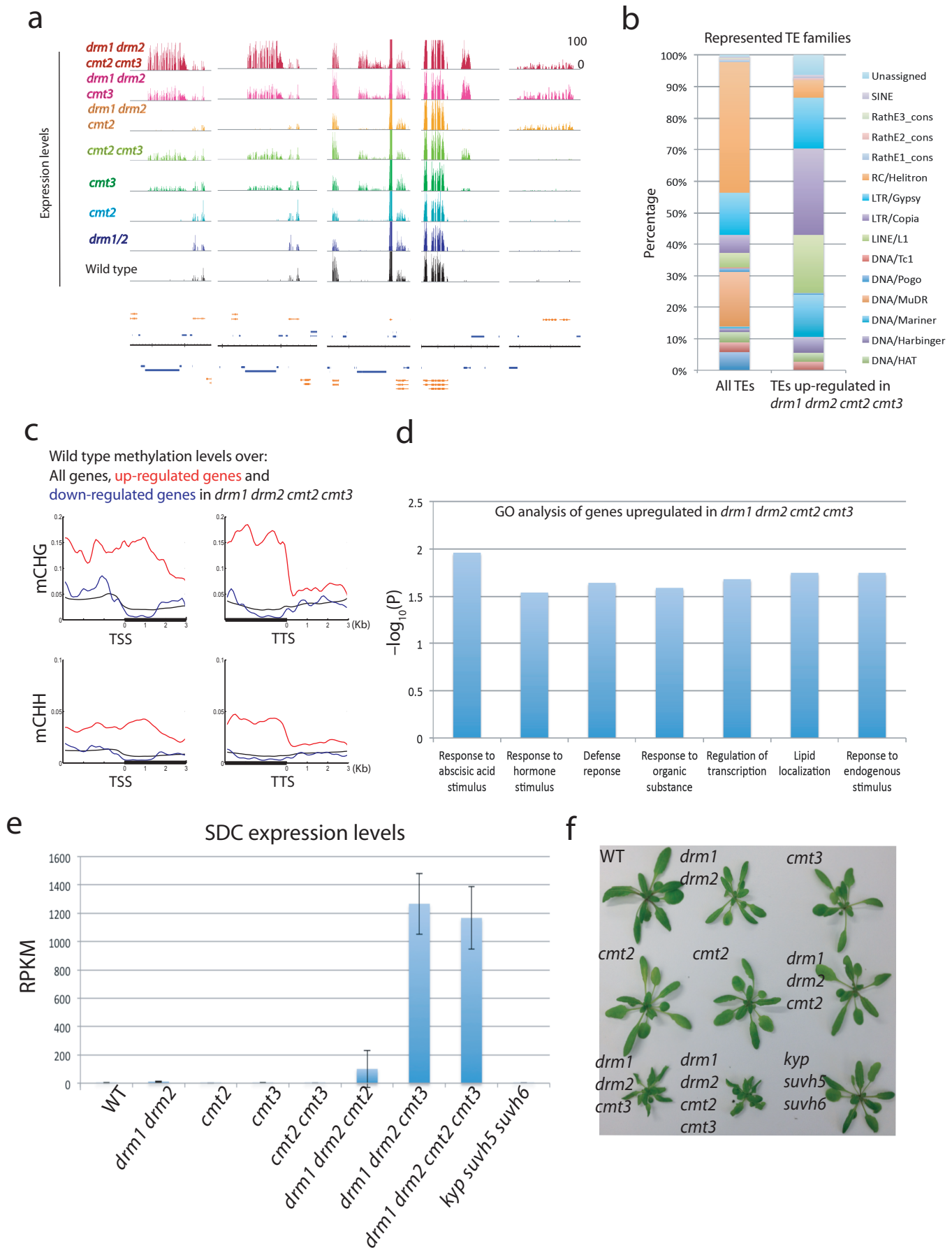
Single Modification Peptide Reactivity



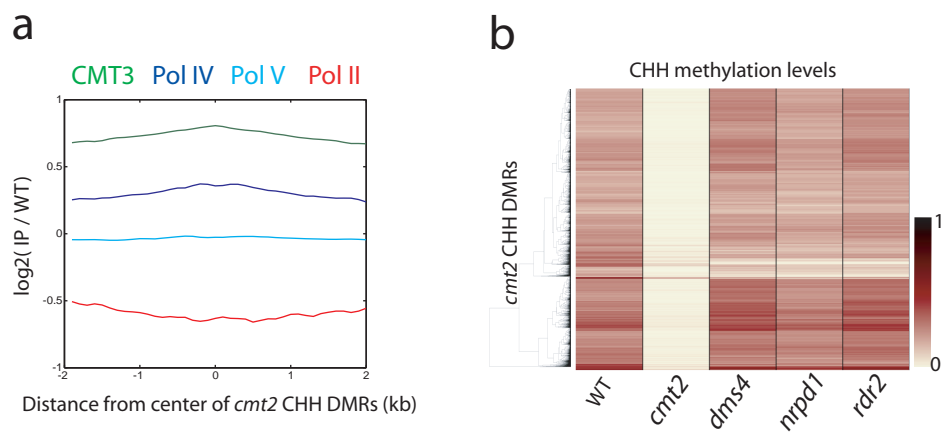
Supplementary Figure 2 CMT2 preferentially binds H3K9 di- and trimethylated peptides in vitro. (a) Sequence comparison between CMT2, CMT3, and ZMET2 (the maize CMT3 homolog) by ClustalW (<http://www.genome.jp/tools/clustalw/>). BAH and CHROMO domains are shaded. (b) Single modification peptide reactivity from the peptide array generated by the manufacturer software (Active Motif).



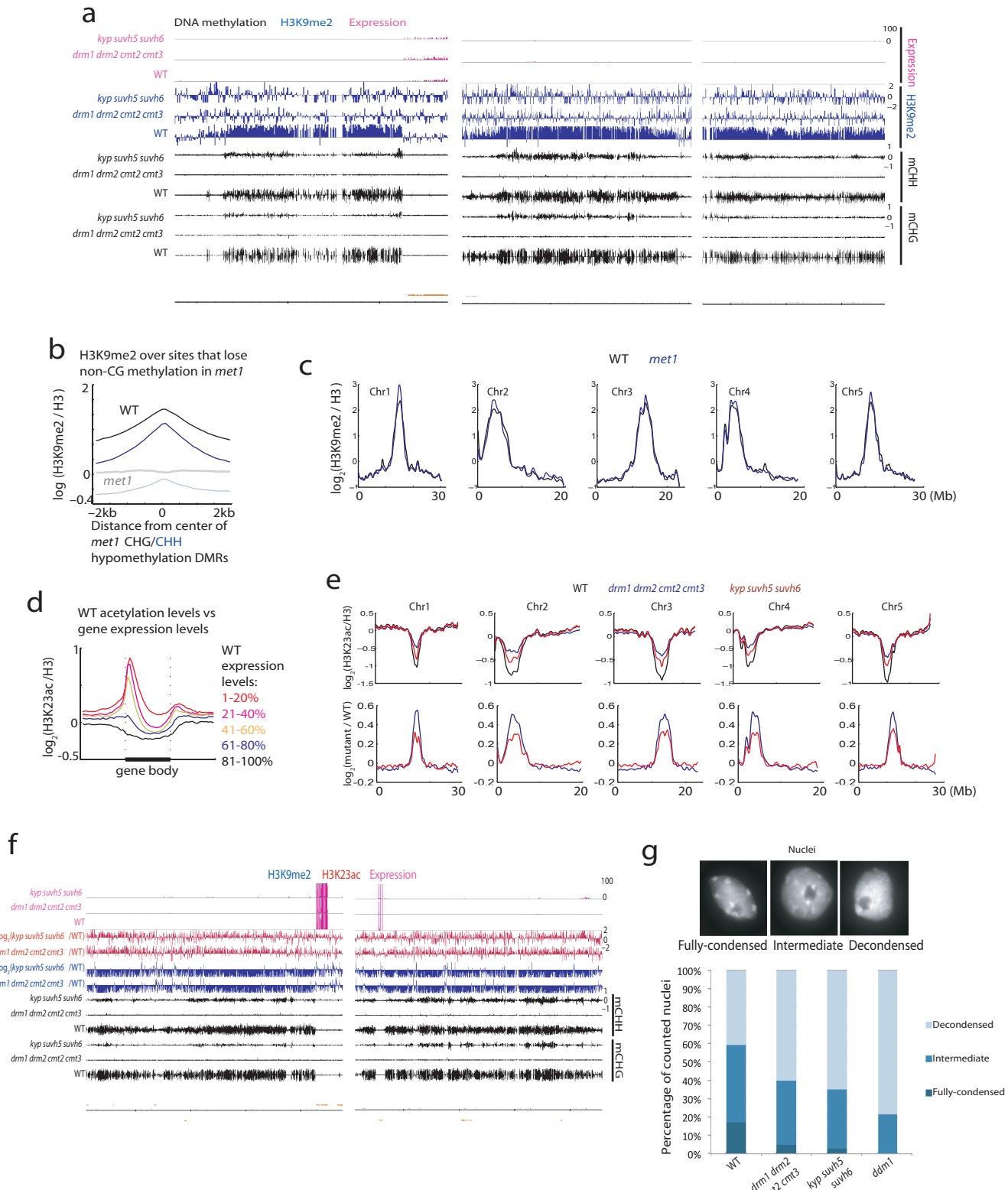
Supplementary Figure 3 Contributions of non-CG methyltransferases in DNA methylation patterning. (a) CG, CHG, and CHH methylation levels across chromosomes. (b) Genome browser views of CHG and CHH methylation in chromosome 1. Blue bars, TEs; Yellow bars, genes. (c) Overlap between *drm1 drm2 cmt2* and *drm1 drm2 cmt2 cmt3* CHH DMRs. (d) Overlap between *drm1 drm2* and *cmt2* CHH DMRs.



Supplementary Figure 4 Roles of non-CG methyltransferases in gene silencing. (a) Genome browser views of RNA-seq data. Blue bars, TEs; Yellow bars, genes. (b) Types of TEs upregulated in *drm1 drm2 cmt2 cmt3* mutants. (c) Wild-type CHG and CHH methylation levels over genes. (d) Gene ontology analysis of genes upregulated in *drm1 drm2 cmt2 cmt3* mutants using DAVID (<http://david.abcc.ncifcrf.gov/>). (e) Expression levels of SDC. Error bars represent SD from two biological replicates. (f) Photo of plants of indicated genotypes.



Supplementary Figure 5 24nt-siRNAs produced at CMT2 sites do not guide DNA methylation in cis. (a) Average distribution of Pol IV over CMT2 target sites. ChIP-seq data on epitope-tagged CMT3₁, Pol IV₂, Pol V₃ relative to the respective controls, as well as Pol II relative to input genomic DNA was plotted over CMT2 target sites. (b) Heatmaps of CHH methylation levels⁴ within *cmt2* CHH DMRs.



Supplementary Figure 6 Non-CG methylation shapes the histone modification landscape. (a) Genome browser views of DNA methylation, expression levels, and H3K9me2 in wild type, *drm1 drm2 cmt2 cmt3*, and *kyp suvh5 suvh6* mutants in chromosome 1. Yellow bars, genes. (b) Average distribution of H3K9me2 over previously defined *met1* CHG hypomethylation DMRs (black) and CHH hypomethylation DMRs (blue). Wild-type data is plotted in solid lines, and *met1* data is plotted in faded lines. (c) Distribution of H3K9me2 over chromosomes in wild type and *met1* mutants. (d) Average distribution of wild-type H3K23ac levels over genes categorized by indicated wild-type expression levels. (e) Distribution of H3K23ac relative to H3 across chromosomes. (f) Genome browser views of DNA methylation, expression levels, H3K23ac, and H3K9me2 in wild type, *drm1 drm2 cmt2 cmt3*, and *kyp suvh5 suvh6* mutants in chromosome 1. Yellow bars, genes. (g) Chromocenter decondensation assay in indicated genotypes. >100 nuclei were assayed per genotype.

Supplementary Table 1. List of TEs upregulated in *drm1 drm2 cmt2 cmt3* mutants.

TE ID	strand	start	end	Family	Superfamily
AT1TE14085	+	4329877	4334393	ATMU4	DNA/MuDR
AT1TE18410	+	5691740	5696671	ATCOPIA89	LTR/Copia
AT1TE19130	+	5911725	5916535	ATMU3	DNA/MuDR
AT1TE28830	-	8927732	8933058	Unassigned	Unassigned
AT1TE29570	+	9175323	9177761	HARBINGER	DNA/Harbinger
AT1TE33490	+	10357357	10363358	TA11	LINE/L1
AT1TE34580	+	10696714	10701584	ATCOPIA73	LTR/Copia
AT1TE36570	-	11302246	11310368	ATENSPM3	DNA/En-Spm
AT1TE38530	+	11887152	11901703	ARNOLD2	DNA/MuDR
AT1TE39375	+	12139300	12139652	VANDAL12	DNA/MuDR
AT1TE39380	-	12140695	12141659	ATMU10	DNA/MuDR
AT1TE39515	-	12172517	12177219	ATENSPM10	DNA/En-Spm
AT1TE40355	+	12406709	12410000	ATCOPIA60	LTR/Copia
AT1TE42875	-	13127113	13128014	ATSINE2A	SINE
AT1TE43225	-	13230993	13235723	ROMANIAT5	LTR/Copia
AT1TE43880	-	13417658	13421489	ATMU11	DNA/MuDR
AT1TE44380	+	13559846	13564825	ATCOPIA89	LTR/Copia
AT1TE45510	+	13871158	13871383	ATENSPM6	DNA/En-Spm
AT1TE46065	+	14021370	14024147	ATGP3	LTR/Gypsy
AT1TE46405	-	14129761	14134840	ATCOPIA66	LTR/Copia
AT1TE56390	-	17023916	17029257	ATCOPIA79	LTR/Copia
AT1TE56395	-	17029261	17029605	TA12	LINE/L1
AT1TE56400	+	17029606	17030400	ATLINE1_1	LINE/L1
AT1TE57530	+	17360726	17365910	ATCOPIA49	LTR/Copia
AT1TE58075	+	17520595	17525126	ATCOPIA38A	LTR/Copia
AT1TE58700	-	17676786	17681203	ATCOPIA51	LTR/Copia
AT1TE58825	+	17713520	17714780	ATGP1	LTR/Gypsy
AT1TE59745	-	18002177	18007370	ATCOPIA49	LTR/Copia
AT1TE66380	+	20085179	20090143	ATCOPIA48	LTR/Copia
AT1TE71770	-	21746740	21747327	ATHATN3	DNA/HAT
AT1TE71775	+	21748194	21753388	ATCOPIA8B	LTR/Copia
AT1TE72615	-	21991449	21992506	ATHAT1	DNA/HAT
AT1TE74860	-	22693955	22699336	HARBINGER	DNA/Harbinger
AT1TE82600	+	25159043	25163500	ATMU2	DNA/MuDR
AT1TE86360	+	26366603	26371673	ATCOPIA11	LTR/Copia
AT1TE93275	+	28515062	28516118	HELITRON1	RC/Helitron
AT2TE01560	-	376596	377257	TA11	LINE/L1
AT2TE02290	-	532333	537391	TA11	LINE/L1
AT2TE06885	-	1485441	1490713	ATLINE1_6	LINE/L1
AT2TE07145	-	1547661	1552033	ATCOPIA95	LTR/Copia
AT2TE07550	-	1629644	1637481	ATGP1	LTR/Gypsy
AT2TE08110	+	1741426	1757083	ARNOLD2	DNA/MuDR
AT2TE08225	+	1781546	1786791	ATGP3	LTR/Gypsy
AT2TE08785	-	1906835	1912111	ATCOPIA66	LTR/Copia
AT2TE09340	+	2034071	2034139	BRODYAGA1A	DNA/MuDR
AT2TE10595	+	2297816	2298721	Unassigned	Unassigned
AT2TE11560	-	2576249	2578241	ATHILA6A	LTR/Gypsy
AT2TE12310	+	2791702	2800659	ATHILA4A	LTR/Gypsy
AT2TE12315	+	2793396	2799755	ATGP5	LTR/Gypsy

AT2TE13060	+	2995751	2996370	ATCOPIA32	LTR/Copia
AT2TE16710	+	3919162	3922206	ATHILA	LTR/Gypsy
AT2TE16715	+	3922207	3922448	ATHILA	LTR/Gypsy
AT2TE16725	+	3922475	3925831	ATLINE1_6	LINE/L1
AT2TE17165	+	4061046	4065458	ATCOPIA66	LTR/Copia
AT2TE17205	-	4071511	4074675	ATHILA4A	LTR/Gypsy
AT2TE17405	-	4122248	4126434	ATHILA2	LTR/Gypsy
AT2TE18240	+	4336398	4337750	ATIS112A	DNA/Harbinger
AT2TE20735	+	5040995	5048412	ATLANTYS1	LTR/Gypsy
AT2TE22315	-	5517609	5520081	ATLINE1_6	LINE/L1
AT2TE22555	+	5585394	5585503	ATREP4	RC/Helitron
AT2TE22635	-	5600343	5605594	TA11	LINE/L1
AT2TE23240	+	5736801	5737912	ATIS112A	DNA/Harbinger
AT2TE23670	-	5808801	5814890	ATGP1	LTR/Gypsy
AT2TE25295	-	6215135	6215240	ATHILA2	LTR/Gypsy
AT2TE25320	-	6217199	6217671	ARNOLD2	DNA/MuDR
AT2TE25875	-	6351159	6353252	Unassigned	Unassigned
AT2TE26275	+	6433987	6439754	ATLINE1_6	LINE/L1
AT2TE26680	-	6524256	6533075	ATENSPM10	DNA/En-Spm
AT2TE26685	-	6527043	6528197	ATHILA4A	LTR/Gypsy
AT2TE27390	+	6700893	6706745	ATLINE1_6	LINE/L1
AT2TE27645	-	6766438	6772521	TA11	LINE/L1
AT2TE27870	+	6837289	6843328	ATCOPIA37	LTR/Copia
AT2TE28015	+	6880749	6880917	ATDNAI27T9C	DNA/MuDR
AT2TE28020	+	6881261	6884610	ATMU1	DNA/MuDR
AT2TE28025	-	6884611	6885154	ATGP10	LTR/Gypsy
AT2TE28030	-	6885155	6885238	ATGP10	LTR/Gypsy
AT2TE28035	+	6886557	6887874	ATMU2	DNA/MuDR
AT2TE28180	-	6918536	6918694	VANDAL1	DNA/MuDR
AT2TE28325	+	6953995	6958817	ATCOPIA38B	LTR/Copia
AT2TE29460	-	7232311	7237513	TA11	LINE/L1
AT2TE30555	-	7448762	7454292	ATCOPIA71	LTR/Copia
AT2TE35840	-	8561844	8567009	ATCOPIA69	LTR/Copia
AT2TE37050	-	8816056	8820891	ATCOPIA72	LTR/Copia
AT2TE37435	-	8893463	8895164	ATREP12	RC/Helitron
AT2TE41170	+	9653805	9654719	ATIS112A	DNA/Harbinger
AT2TE58010	-	13223059	13227048	Unassigned	Unassigned
AT2TE69490	+	15566814	15568070	ATREP12	RC/Helitron
AT2TE78210	+	17337767	17342489	TA11	LINE/L1
AT2TE82000	+	18106654	18107024	RathE2_cons	RathE2_cons
AT2TE84695	-	18652626	18655464	ATLINE1_4	LINE/L1
AT3TE20780	-	4929015	4932433	VANDAL21	DNA/MuDR
AT3TE35825	+	8537355	8543559	ATGP7	LTR/Gypsy
AT3TE37690	-	9011213	9017190	TA11	LINE/L1
AT3TE40125	-	9608086	9610451	ATDNAI27T9A	DNA/MuDR
AT3TE40420	-	9692214	9697529	ATCOPIA82	LTR/Copia
AT3TE44395	-	10687034	10687244	VANDAL21	DNA/MuDR
AT3TE45330	+	10902528	10902659	ATSINE2A	SINE
AT3TE45385	-	10917704	10922777	ATLINE1_6	LINE/L1
AT3TE45390	-	10922914	10923082	ATLINE1_4	LINE/L1
AT3TE45620	-	10970102	10976062	TA11	LINE/L1
AT3TE46000	-	11066661	11067771	ATLINEIII	LINE/L1

AT3TE47360	-	11369855	11370572	ATGP1	LTR/Gypsy
AT3TE49090	+	11793559	11798454	ATMU5	DNA/MuDR
AT3TE50125	-	12025064	12040032	ATCOPIA43	LTR/Copia
AT3TE51670	-	12539771	12540250	ATHILA3	LTR/Gypsy
AT3TE51675	-	12540252	12547951	ATCOPIA43	LTR/Copia
AT3TE51895	-	12603266	12606828	ROMANIAT5	LTR/Copia
AT3TE51900	-	12607223	12608295	ATCOPIA28	LTR/Copia
AT3TE52120	+	12669318	12670623	LIMPET1	DNA/MuDR
AT3TE52420	+	12739591	12741997	ATIS112A	DNA/Harbinger
AT3TE54330	-	13282293	13287570	ATLINE1_6	LINE/L1
AT3TE59985	+	14656779	14662773	ATLINE1_6	LINE/L1
AT3TE60310	-	14749400	14750294	SADHU	Unassigned
AT3TE60460	+	14795320	14804954	ATHILA6A	LTR/Gypsy
AT3TE62100	+	15280256	15289099	HELITRON2	RC/Helitron
AT3TE62395	+	15361697	15365347	Unassigned	Unassigned
AT3TE62685	-	15455636	15468075	ATHILA0_1	LTR/Gypsy
AT3TE62785	-	15493534	15499327	ATLINE1_6	LINE/L1
AT3TE63540	-	15711476	15722693	ATHILA2	LTR/Gypsy
AT3TE63900	+	15808431	15810650	Unassigned	Unassigned
AT3TE63950	+	15814611	15818285	META1	LTR/Copia
AT3TE64435	-	15919028	15924078	ATCOPIA11	LTR/Copia
AT3TE67325	-	16600733	16604312	ATHAT2	DNA/HAT
AT3TE67635	-	16691859	16697596	ATCOPIA32	LTR/Copia
AT3TE68730	-	16957465	16962731	ATCOPIA79	LTR/Copia
AT3TE70590	-	17402796	17417981	ARNOLD3	DNA/MuDR
AT3TE76225	+	18791152	18796089	ATCOPIA52	LTR/Copia
AT3TE76405	+	18843490	18844703	ATREP12	RC/Helitron
AT3TE82555	-	20304981	20309967	ATGP3	LTR/Gypsy
AT3TE86800	+	21322657	21327537	TA11	LINE/L1
AT3TE90530	+	22232308	22236743	ATCOPIA23	LTR/Copia
AT3TE94580	-	23203577	23207484	ATLINEIII	LINE/L1
AT4TE09315	+	1919524	1925047	ATLINE1_6	LINE/L1
AT4TE09800	-	2064099	2068831	ATCOPIA59	LTR/Copia
AT4TE09825	-	2072130	2075641	HELITRONY3	RC/Helitron
AT4TE09845	+	2076982	2077353	ATIS112A	DNA/Harbinger
AT4TE10490	+	2245569	2256834	VANDAL18	DNA/MuDR
AT4TE10600	-	2286691	2288784	ATCOPIA57	LTR/Copia
AT4TE22970	-	5485146	5494752	VANDAL8	DNA/MuDR
AT4TE25100	+	5965693	5970901	ATCOPIA69	LTR/Copia
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AT4TE27915	-	6529315	6537160	ATGP1	LTR/Gypsy
AT4TE28870	+	6723347	6728790	ATCOPIA17	LTR/Copia
AT4TE29830	-	6914662	6919511	ATCOPIA22	LTR/Copia
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AT5TE25535	-	7056105	7057389	ATREP12	RC/Helitron
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AT5TE31645	+	8746717	8746891	ATREP1	RC/Helitron
AT5TE32880	-	9092669	9094772	ATHAT1	DNA/HAT
AT5TE33455	+	9249018	9253968	ATMU1	DNA/MuDR
AT5TE34980	-	9641505	9643917	Unassigned	Unassigned
AT5TE35950	+	9871829	9872479	HELITRONY1D	RC/Helitron
AT5TE36230	+	9949205	9954436	ATCOPIA86	LTR/Copia
AT5TE36235	-	9956859	9957640	SADHU	Unassigned
AT5TE36620	+	10050547	10056385	ATLINE1_6	LINE/L1
AT5TE37660	-	10308656	10309446	ATGP3	LTR/Gypsy
AT5TE37665	-	10309447	10311540	ATGP7	LTR/Gypsy
AT5TE37825	+	10365545	10368534	ATLANTYS2	LTR/Gypsy
AT5TE39275	-	10802072	10802878	ATLINE1_6	LINE/L1
AT5TE39630	-	10901851	10903017	ATIS112A	DNA/Harbinger
AT5TE47750	-	13467425	13471354	ATLINEIII	LINE/L1
AT5TE47755	-	13471681	13472449	ATIS112A	DNA/Harbinger
AT5TE50380	-	14113154	14118424	ATCOPIA91	LTR/Copia
AT5TE50490	+	14146158	14147779	ATLINE1_5	LINE/L1
AT5TE61735	-	17090876	17095159	ATCOPIA15	LTR/Copia
AT5TE63010	+	17439696	17440858	ATLINE1_6	LINE/L1
AT5TE63020	+	17441792	17445927	ATLINE1_6	LINE/L1
AT5TE63610	+	17596759	17605846	ENDOVIR1	LTR/Copia
AT5TE69650	+	19358618	19363928	Unassigned	Unassigned
AT5TE74020	+	20543499	20543652	ATHILA4C	LTR/Gypsy
AT5TE76490	-	21242985	21243125	ATENSPM2	DNA/En-Spm
AT5TE77610	+	21542894	21546691	ATCOPIA85	LTR/Copia
AT5TE83215	-	23134881	23139981	ATCOPIA49	LTR/Copia

Supplementary Table 2. List of genes upregulated in *drm1 drm2 cmt2 cmt3* mutants.

Gene ID	strand	start	end	Description
AT1G02220	-	428814	430647	NAC domain containing protein 3
AT1G02230	-	435174	436776	NAC domain containing protein 4
AT1G02340	-	465718	467844	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT1G02450	-	497976	498516	NIM1-interacting 1
AT1G02850	+	630505	633259	beta glucosidase 11
AT1G03850	-	976097	977761	Glutaredoxin family protein
AT1G07430	-	2280835	2282828	highly ABA-induced PP2C gene 2
AT1G07900	+	2442622	2443632	LOB domain-containing protein 1
AT1G10070	+	3288087	3290471	branched-chain amino acid transaminase 2
AT1G11210	-	3755677	3756998	Protein of unknown function (DUF761)
AT1G13470	-	4620228	4621580	Protein of unknown function (DUF1262)
AT1G18830	+	6489309	6494218	Transducin/WD40 repeat-like superfamily protein
AT1G19250	-	6650529	6653078	flavin-dependent monooxygenase 1
AT1G21550	-	7553101	7553876	Calcium-binding EF-hand family protein
AT1G23050	+	8168443	8169267	hydroxyproline-rich glycoprotein family protein
AT1G26390	-	9130017	9131779	FAD-binding Berberine family protein
AT1G28000	-	9756674	9757963	Pentatricopeptide repeat (PPR) superfamily protein
AT1G28330	-	9933922	9935271	dormancy-associated protein-like 1
AT1G30190	+	10618966	10619802	
AT1G31820	-	11416451	11418279	Amino acid permease family protein
AT1G32560	+	11774484	11775279	Late embryogenesis abundant protein, group 1 protein
AT1G33055	-	11971308	11972578	
AT1G33840	-	12283862	12285306	Protein of unknown function (DUF567)
AT1G33960	+	12346232	12348513	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT1G34060	-	12396420	12398369	Pyridoxal phosphate (PLP)-dependent transferases superfamily protein
AT1G34310	-	12508548	12511520	auxin response factor 12
AT1G35730	-	13227324	13229796	pumilio 9
AT1G36060	-	13454496	13456331	Integrase-type DNA-binding superfamily protein
AT1G36675	+	13867568	13869490	glycine-rich protein
AT1G36920	+	13983512	13984424	
AT1G36922	+	13984576	13985290	
AT1G47265	+	17324318	17324911	
AT1G47890	+	17643976	17647035	receptor like protein 7
AT1G47980	-	17691834	17693867	
AT1G48000	-	17704179	17706460	myb domain protein 112
AT1G54575	+	20387060	20387710	
AT1G55390	-	20680876	20683043	Cysteine/Histidine-rich C1 domain family protein
AT1G55430	-	20697649	20699622	Cysteine/Histidine-rich C1 domain family protein
AT1G56600	+	21207537	21209596	galactinol synthase 2
AT1G63540	+	23566958	23569495	hydroxyproline-rich glycoprotein family protein

AT1G64110	-	23796719	23801725	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT1G67980	+	25487714	25489231	caffeoyl-CoA 3-O-methyltransferase
AT1G68050	+	25508676	25510889	flavin-binding, kelch repeat, f box 1
AT1G68620	+	25765947	25767240	alpha/beta-Hydrolases superfamily protein
AT1G71920	+	27067128	27069166	HISTIDINE BIOSYNTHESIS 6B
AT1G76590	+	28740691	28742207	PLATZ transcription factor family protein
AT1G76930	-	28895301	28896883	extensin 4
AT1G79900	-	30052297	30053936	Mitochondrial substrate carrier family protein
AT2G02103	-	530241	531636	
AT2G03570	-	1085560	1085988	
AT2G05380	+	1966816	1968037	glycine-rich protein 3 short isoform
AT2G05540	+	2033156	2034217	Glycine-rich protein family
AT2G06555	-	2604148	2604927	
AT2G07215	-	2996776	2997889	
AT2G10975	+	4335137	4335909	
AT2G13430	+	5590052	5591422	
AT2G13450	-	5598421	5599923	
AT2G13770	+	5736570	5737847	
AT2G15790	-	6877774	6880898	peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYP40) / rotamase
AT2G16676	-	7230346	7232223	
AT2G17050	-	7410835	7415610	disease resistance protein (TIR-NBS-LRR class), putative
AT2G17060	+	7422411	7426877	Disease resistance protein (TIR-NBS-LRR class) family
AT2G17690	+	7682383	7684083	F-box family protein with a domain of unknown function (DUF295)
AT2G18050	+	7846050	7846884	histone H1-3
AT2G19190	-	8326049	8329944	FLG22-induced receptor-like kinase 1
AT2G20880	+	8985973	8987263	Integrase-type DNA-binding superfamily protein
AT2G21850	+	9315218	9318238	Cysteine/Histidine-rich C1 domain family protein
AT2G21910	+	9341498	9343030	cytochrome P450, family 96, subfamily A, polypeptide 5
AT2G24340	-	10355430	10359546	sequence-specific DNA binding transcription factors
AT2G25625	+	10906428	10907288	
AT2G26010	+	11087348	11087944	plant defensin 1.3
AT2G33080	+	14032015	14034237	receptor like protein 28
AT2G33175	-	14062754	14063275	
AT2G33830	-	14309484	14310351	Dormancy/auxin associated family protein
AT2G34655	+	14596631	14597540	
AT2G35070	+	14783291	14784710	
AT2G35950	+	15104761	15106088	embryo sac development arrest 12
AT2G37130	-	15597921	15600077	Peroxidase superfamily protein
AT2G37770	+	15834867	15836881	NAD(P)-linked oxidoreductase superfamily protein
AT2G38530	+	16128378	16129158	lipid transfer protein 2
AT2G40955	+	17093093	17095132	
AT2G41590	+	17343360	17345005	

AT2G45220	-	18644084	18646447	Plant invertase/pectin methylesterase inhibitor superfamily
AT2G45360	+	18698592	18699514	Protein of unknown function (DUF1442)
AT2G46680	-	19165403	19166949	homeobox 7
AT2G47270	-	19411560	19412151	sequence-specific DNA binding transcription factors
AT2G47770	+	19568464	19569507	TSPO(outer membrane tryptophan-rich sensory protein)-related
AT3G01345	+	129138	130749	Expressed protein
AT3G01970	-	326397	327412	WRKY DNA-binding protein 45
AT3G04060	-	1053366	1055163	NAC domain containing protein 46
AT3G04070	-	1061526	1063103	NAC domain containing protein 47
AT3G08860	-	2696559	2699158	PYRIMIDINE 4
AT3G10815	-	3384807	3386327	RING/U-box superfamily protein
AT3G14280	-	4761432	4762395	
AT3G18250	-	6258067	6258417	Putative membrane lipoprotein
AT3G21710	+	7648359	7649799	
AT3G22460	+	7963537	7965907	O-acetylserine (thiol) lyase (OAS-TL) isoform A2
AT3G22620	+	8008534	8009590	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AT3G28510	+	10685524	10687364	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT3G28770	+	10796716	10803237	Protein of unknown function (DUF1216)
AT3G28899	+	10902327	10902515	
AT3G29035	+	11033665	11035308	NAC domain containing protein 3
AT3G29080	+	11069352	11071376	
AT3G29250	-	11193659	11194993	NAD(P)-binding Rossmann-fold superfamily protein
AT3G29639	-	11478732	11479749	
AT3G30770	+	12445493	12448085	Eukaryotic aspartyl protease family protein
AT3G30842	-	12593959	12600432	pleiotropic drug resistance 10
AT3G33528	-	14082795	14084346	
AT3G42800	+	14905230	14907035	
AT3G46280	-	17005483	17008424	protein kinase-related
AT3G48020	+	17724590	17725198	
AT3G48131	-	17775456	17775587	
AT3G50770	+	18873958	18874780	calmodulin-like 41
AT3G50840	-	18896175	18898621	Phototropic-responsive NPH3 family protein
AT3G53150	-	19697736	19699259	UDP-glucosyl transferase 73D1
AT3G54730	+	20259259	20260422	
AT3G59930	-	22139551	22140320	
AT4G00870	-	362169	363691	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT4G03156	-	1396002	1396784	small GTPase-related
AT4G05100	+	2618454	2619887	myb domain protein 74
AT4G10920	-	6697674	6699199	transcriptional coactivator p15 (PC4) family protein (KELP)
AT4G11910	+	7156252	7158042	
AT4G12470	-	7401109	7401907	azelaic acid induced 1
AT4G12490	-	7409621	7410406	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein

AT4G13660	+	7946155	7948376	pinorexinol reductase 2
AT4G14140	+	8146345	8152131	DNA methyltransferase 2
AT4G18150	+	10050211	10054031	Kinase-related protein of unknown function (DUF1296)
AT4G21440	-	11418246	11419760	MYB-like 102
AT4G23680	-	12336186	12337482	Polyketide cyclase/dehydrase and lipid transport superfamily protein
AT4G25480	-	13018214	13019121	dehydration response element B1A
AT4G28140	-	13974691	13975908	Integrase-type DNA-binding superfamily protein
AT4G29200	-	14398054	14400198	Beta-galactosidase related protein
AT4G33980	-	16282696	16285059	
AT5G01550	-	214517	216583	lectin receptor kinase a4.1
AT5G02020	-	386018	388123	
AT5G07550	-	2388310	2389249	glycine-rich protein 19
AT5G07560	-	2390207	2391075	glycine-rich protein 20
AT5G07570	+	2391722	2396329	glycine/proline-rich protein
AT5G09440	+	2938347	2939461	EXORDIUM like 4
AT5G12050	+	3890104	3891513	
AT5G13330	+	4272060	4274660	related to AP2 6I
AT5G15500	-	5031676	5033465	Ankyrin repeat family protein
AT5G22570	-	7495539	7496784	WRKY DNA-binding protein 38
AT5G23240	-	7826732	7828724	DNAJ heat shock N-terminal domain-containing protein
AT5G23950	+	8082744	8083604	Calcium-dependent lipid-binding (CaLB domain) family protein
AT5G24200	+	8203003	8205793	alpha/beta-Hydrolases superfamily protein
AT5G24240	-	8230942	8234150	Phosphatidylinositol 3- and 4-kinase
AT5G24250	-	8233696	8234652	
AT5G26270	+	9206508	9207512	
AT5G26340	-	9243511	9247066	Major facilitator superfamily protein
AT5G27850	+	9873152	9874598	Ribosomal protein L18e/L15 superfamily protein
AT5G35375	+	13592255	13593149	
AT5G39610	-	15858400	15859788	NAC domain containing protein 6
AT5G39770	-	15919241	15927549	Restriction endonuclease, type II-like superfamily protein
AT5G41830	-	16743762	16745334	RNI-like superfamily protein
AT5G44430	-	17908945	17909507	plant defensin 1.2C
AT5G44572	+	17968152	17969563	
AT5G46050	-	18675035	18679146	peptide transporter 3
AT5G47260	+	19189411	19192516	ATP binding
AT5G47280	+	19193157	19195559	ADR1-like 3
AT5G52070	+	21161311	21165025	Agenet domain-containing protein
AT5G52730	+	21380174	21380865	Copper transport protein family
AT5G54585	+	22175539	22176691	
AT5G59220	-	23894404	23896619	highly ABA-induced PP2C gene 1
AT5G59320	+	23928971	23929745	lipid transfer protein 3
AT5G64190	+	25679432	25681265	

Supplementary Table 3. List of oligos used for methyltransferase activity assays.

Primer number	Sequence (M=methylated cytosine)	Methylation status
3010	AACGCAGCATGCGCTGCTAGCGCAGCTAGCGCTGCATG	Unmethylated
3011	AACATGCAGCGCTAGCTGCGCTAGCAGCGCATGCTGCG	Unmethylated
3012	AAMGCAGCATGMGCTGCTAGMGCAGCTAGMGCTGCATG	CG methylated
3013	AACATGCAGMGCTAGCTGMGCTAGCAGMGCATGCTGMG	CG methylated
3014	AACGMAGCATGCGMTGCTAGCGMAGCTAGCGMTGCATG	CNG methylated
3015	AACATGMAGCGCTAGMTGCGCTAGMAGCGCATGMTGCG	CNG methylated
3016	AACGCAGMATGCGCTGMTAGCGCAGMTAGCGCTGMATG	CNN methylated
3017	AAMATGCAGCGMTAGCTGCGMTAGCAGCGMATGCTGCG	CNN methylated
3018	AAMGMAGMATGMGMTGMTAGMGMAGMTAGMGMTGMATG	All Cs methylated
3019	AAMATGMAGMGMTAGMTGMGMTAGMAGMGMATGMTGMG	All Cs methylated
3524	CGCGACGACGCACGACGACGACGACGCGAACGCGCGAA	CG unmethylated
3525	TTCGCGCGTTCGCGTCGTGCGTCGTGCGTCGTGCGCG	CG unmethylated

SUPPLEMENTARY REFERENCES

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- 4 Stroud, H., Greenberg, M. V., Feng, S., Bernatavichute, Y. V. & Jacobsen, S. E. Comprehensive Analysis of Silencing Mutants Reveals Complex Regulation of the Arabidopsis Methylome. *Cell* (2013).