

## Supplementary Information for

**Title: DNA methylation-linked chromatin accessibility affects genomic architecture in Arabidopsis.**

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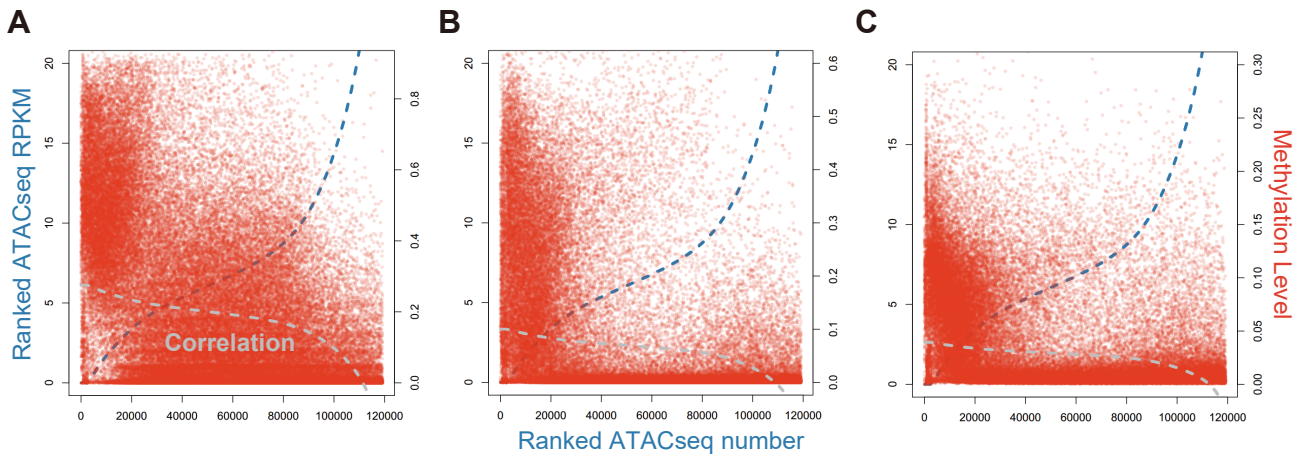
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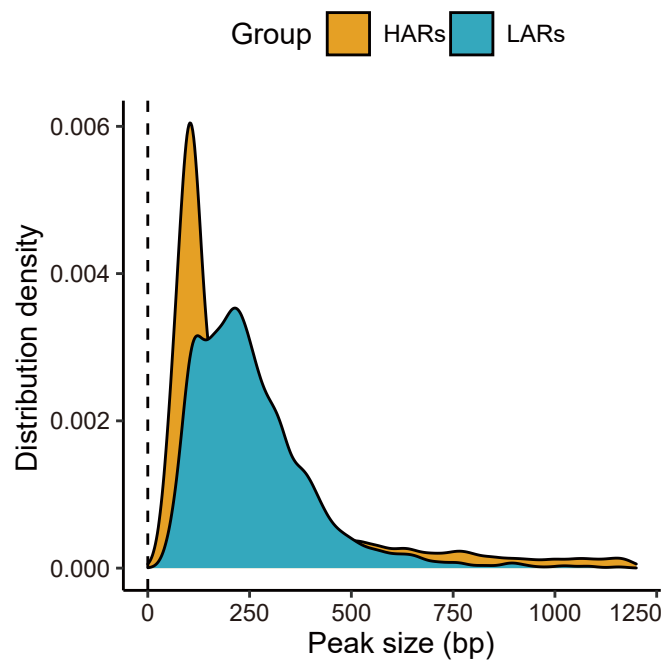
Figures S1 to S13  
Tables S1 to S3

## Supplementary Figures

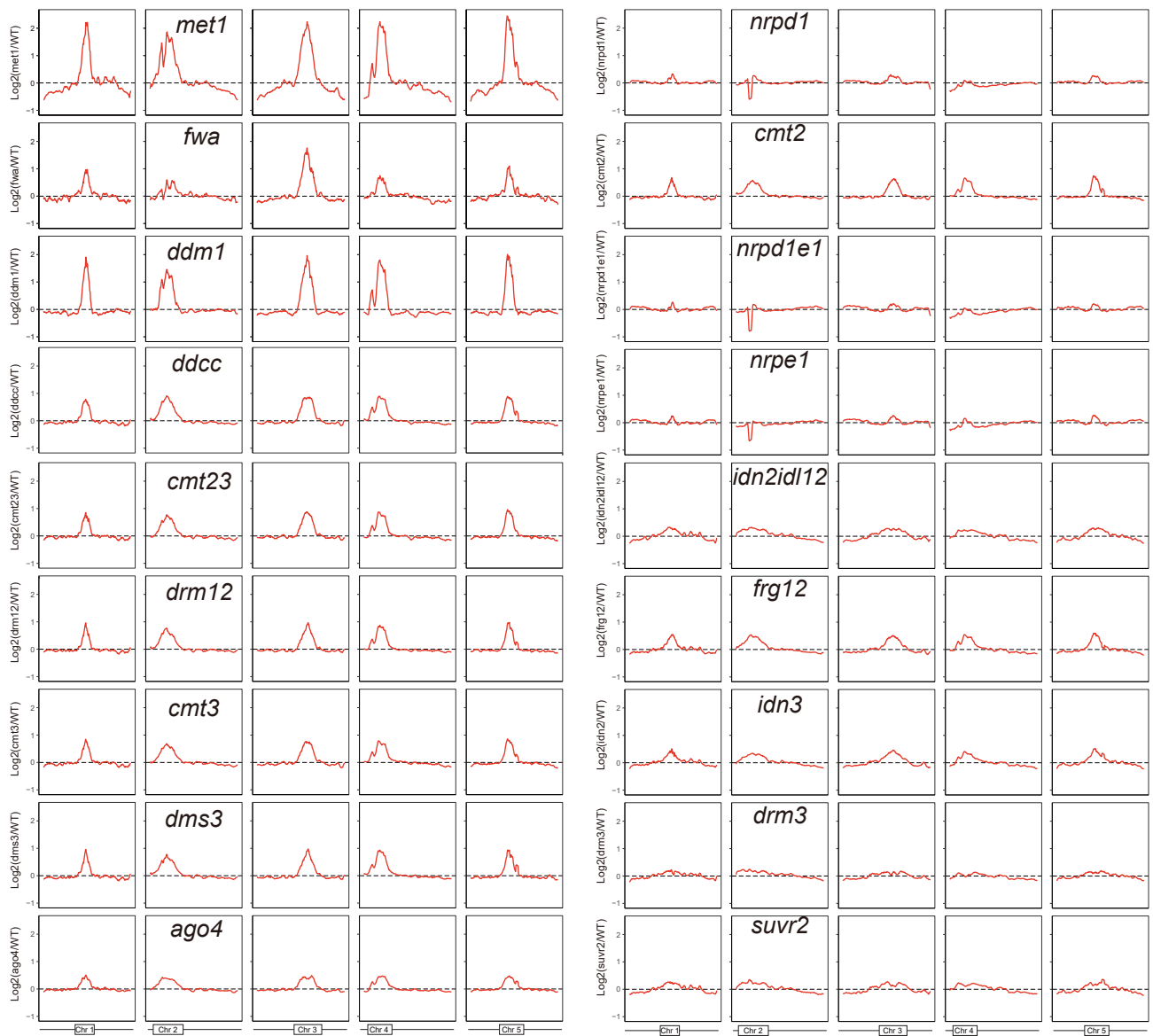


### Supplementary Fig. 1 Anti-correlation of DNA methylation and chromatin accessibility.

Scatter plot of anti-correlation of CG (A), CHG (B), and CHH (C) methylation with chromatin accessibility. Red dots represent 1 kb bins. Blue dotted line represents ranked ATAC-seq signals from low (left) to high (right). Grey dotted line represents correlation of ranked ATAC-seq and methylation level at 1 kb bins. X-axis indicates number of peaks ranked by ATAC-seq signal and y-axis indicates ATAC-seq signal (left) or methylation level (right).

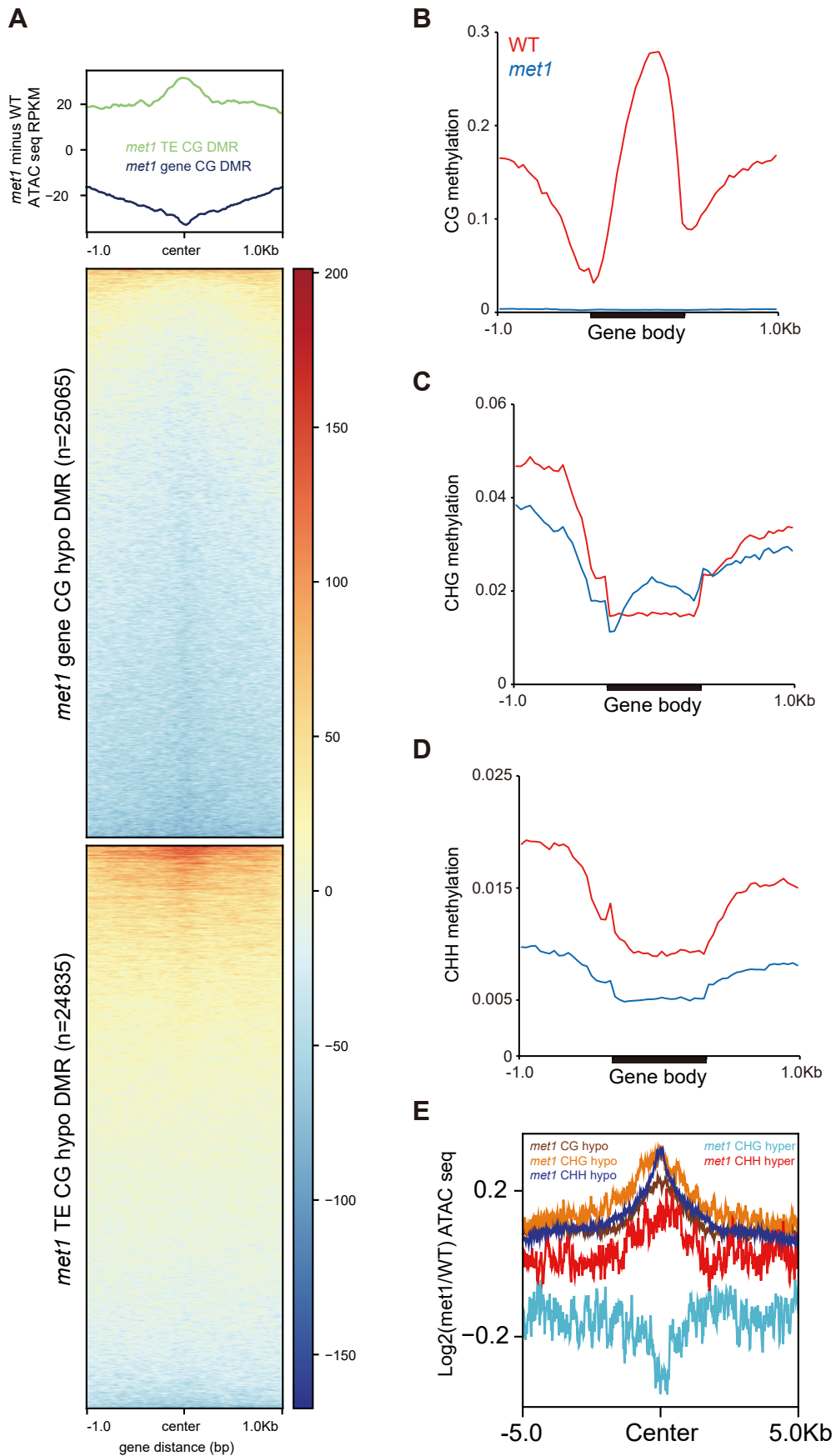


**Supplementary Fig. 2** Size distribution of HARs and LARs in mutants.

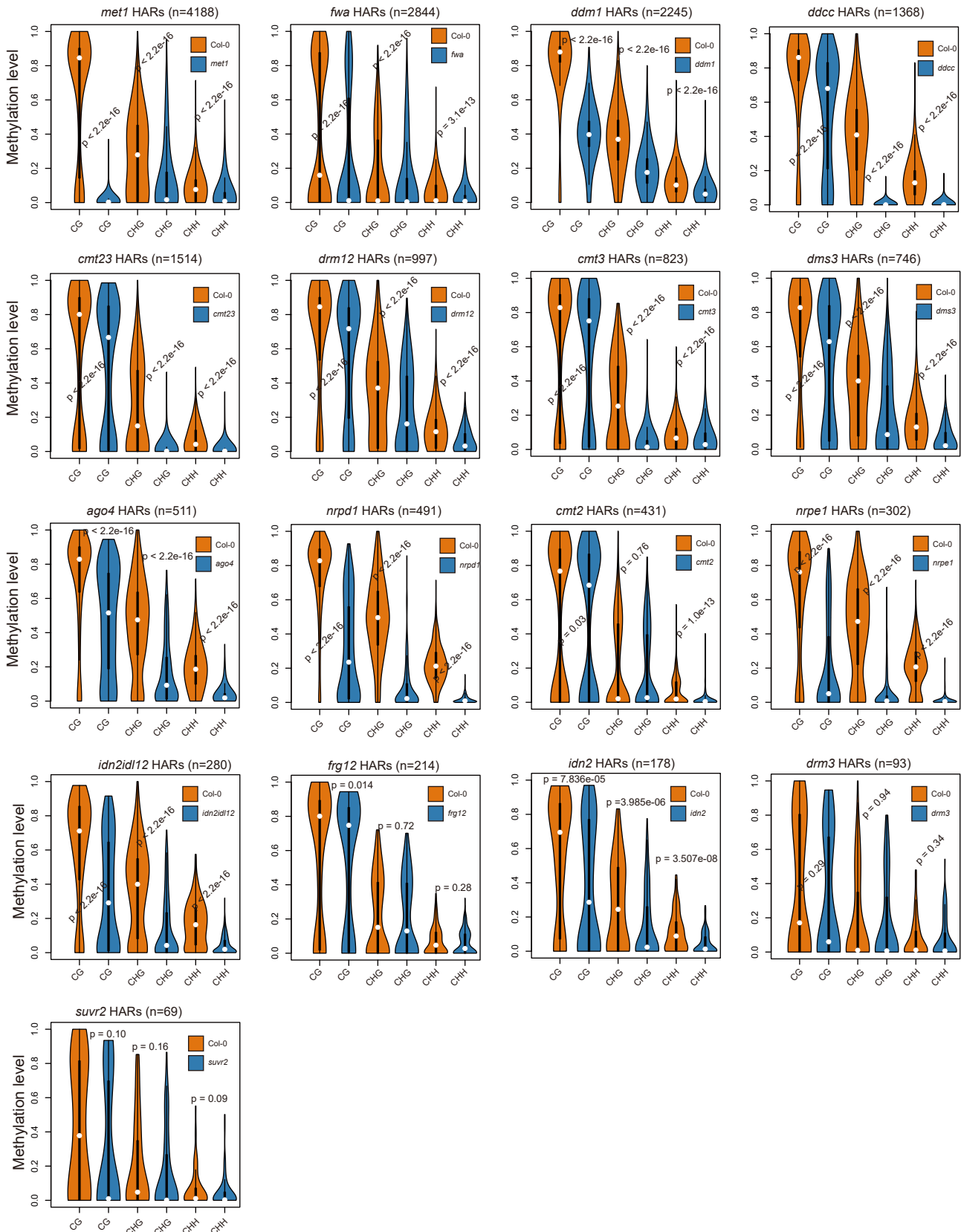


**Supplementary Fig. 3 Genome-wide patterns of chromatin accessibility variations in 18 mutants.**

Variation in accessibility is shown across chromosomes for *met1*, *ddm1*, *fwa*, *nrpe1*, *nrpd1*, *nrpd1e1*, *nrpe1*, *cmt2*, *cmt3*, *dms3*, *drm1*, *drm2*, *drm1*, *drm2*, *cmt2*, *cmt3*, *cmt2*, *cmt3*, *drm3*, *idn2*, *idn2*, *idl1*, *idl2*, *suvr2*, *ago4*, and *frg1*, *frg2*. Variation in accessibility (Log2 mutant vs Col-0) is depicted on the y-axis. Box in each chromosome represents pericentromeric heterochromatin region.

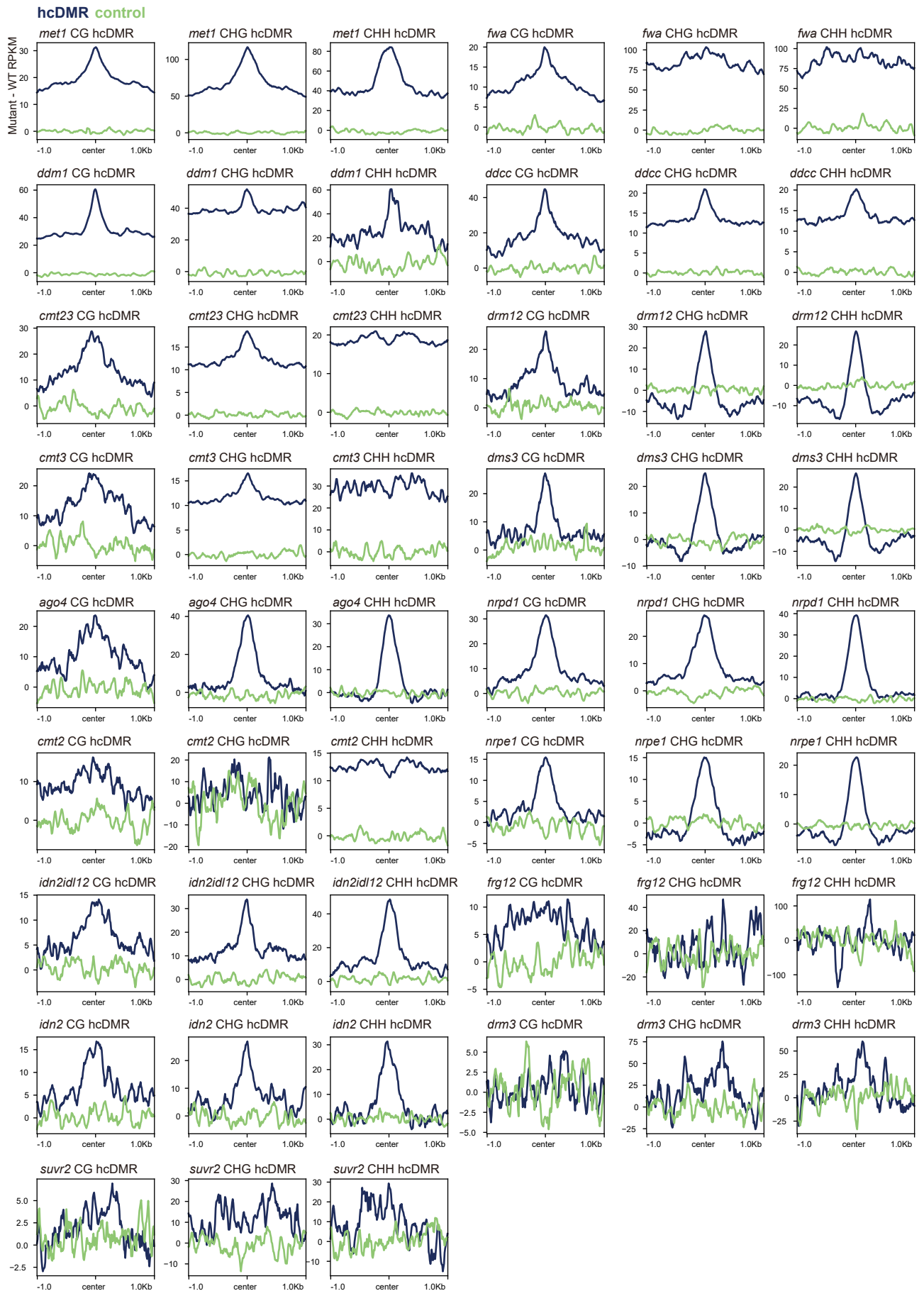


**Supplementary Fig. 4 ATAC-seq and DNA methylation profile of *met1* DMRs.**  
**(A)** Chromatin accessibility changes in *met1* CG hypo DMRs distributed at genic or TE regions. Metaplot of CG **(B)**, CHG **(C)**, and CHH **(D)** methylation over protein encoding genes in *met1* and Col-0. **(E)** Metaplot of ATAC-seq signal over *met1* hypo/hyper CG, CHG and CHH DMRs.



**Supplementary Fig. 5 Violin plot shows CG, CHG, and CHH methylation level of MARs in mutants.**

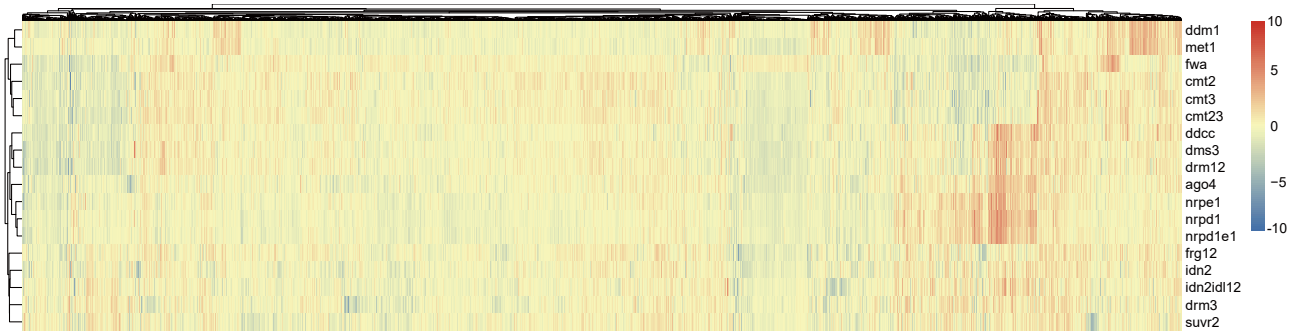
CG, CHG, and CHH methylation level of MARs were calculated in *met1*, *ddm1*, *fwa*, *nrpd1*, *nrpe1*, *cmt2* *cmt3* (*cmt23*), *dms3*, *drm1* *drm2* (*drm12*), *drm1* *drm2* *cmt2* *cmt3* (*ddcc*), *cmt2*, *cmt3*, *drm3*, *idn2*, *idn2* *idl1* *idl2* (*idn2idl12*), *svvr2*, *ago4*, and *frg1* *frg2* (*frg12*). The p value was calculated with Student's t-test.



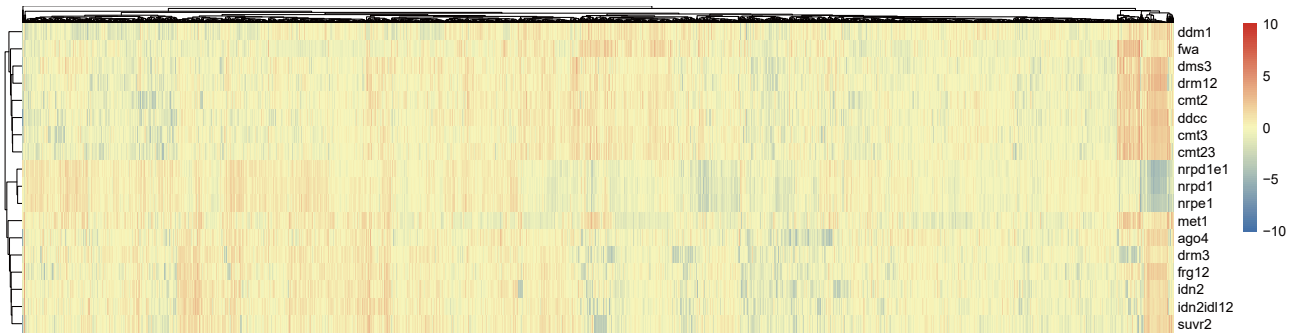
**Supplementary Fig. 6 Metaplot plot of ATAC-seq over CG, CHG, and CHH hcDMRs in mutants.**

Metaplot plot of ATAC-seq data over CG, CHG, and CHH DMRs of *met1*, *ddm1*, *fwa*, *nrpd1*, *nrpe1*, *cmt2*, *cmt3*, *dms3*, *drm1* *drm2*, *drm1* *drm2* *cmt2* *cmt3*, *cmt2*, *cmt3*, *drm3*, *idn2*, *idn2 idl1 idl2*, *suvr2*, *ago4*, and *frg2*. A random, equal size, shuffle region was used as control.

A

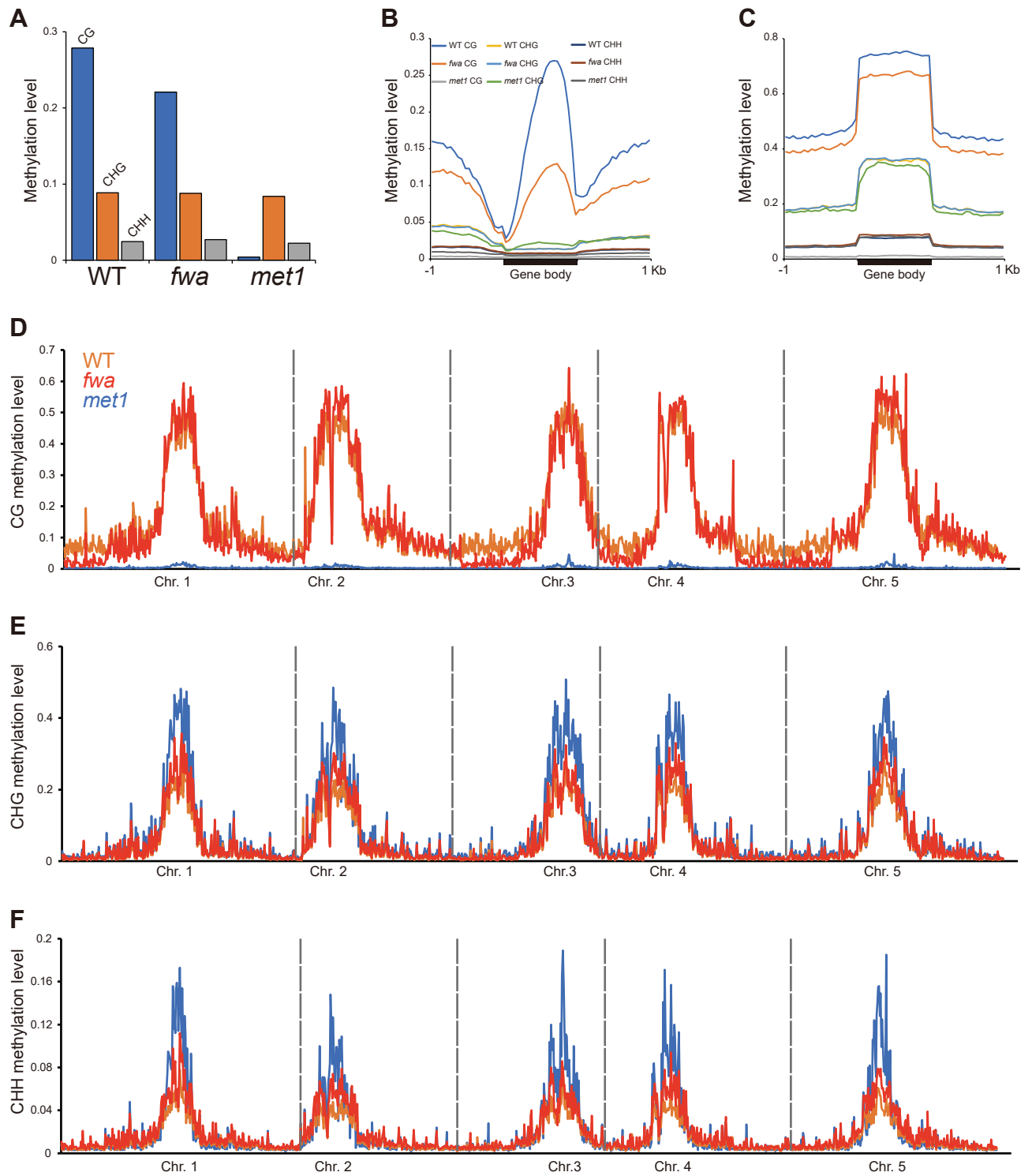


B



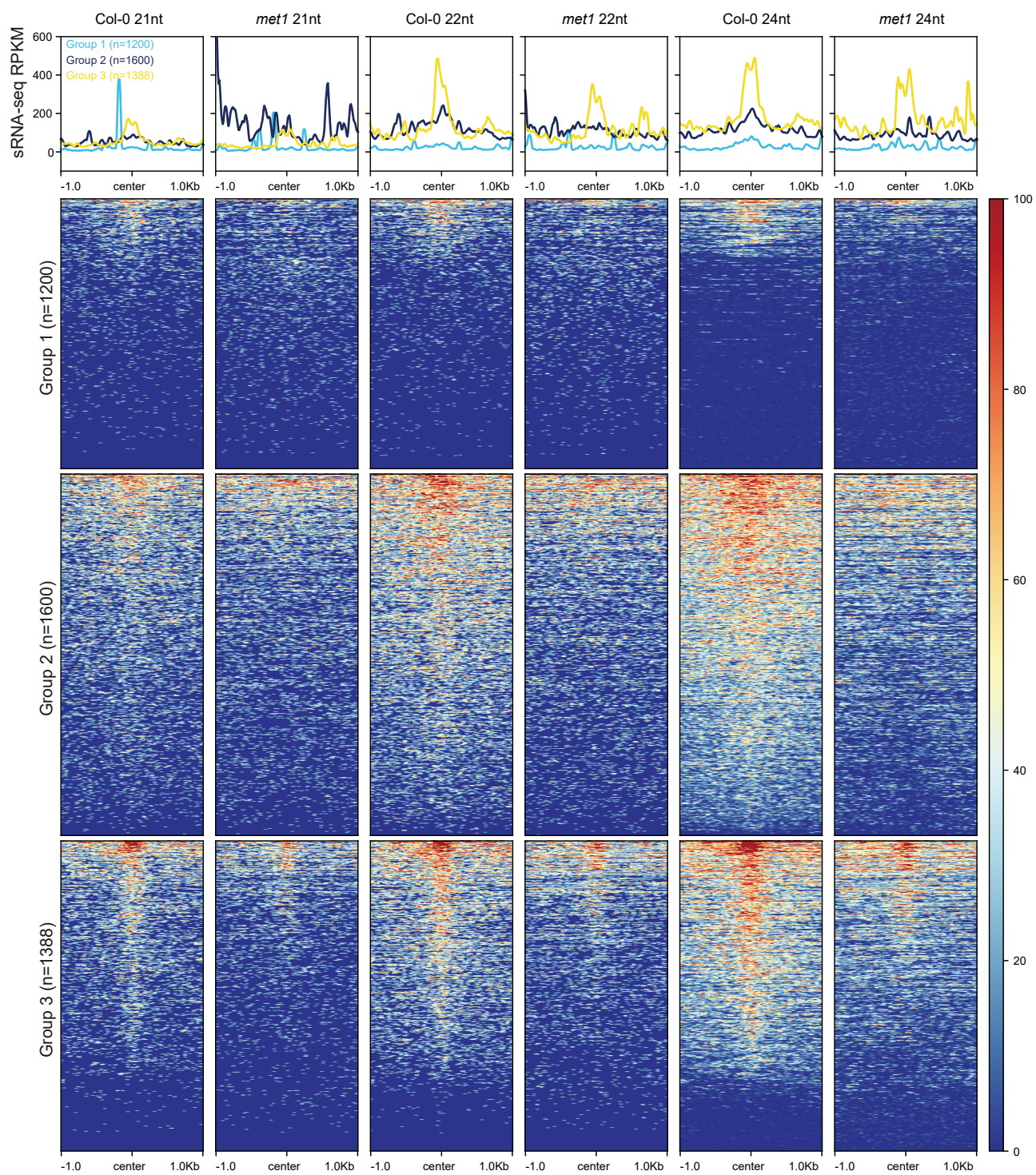
**Supplementary Fig. 7 Overlap of HARs and LARs.** Clustering of HARs (A) and LARs (B) of *met1*, *ddm1*, *fwa*, *nrpd1*, *nrpe1*, *cmt2 cmt3 (cmt23)*, *dms3*, *drm1 drm2 (drm12)*, *drm1 drm2 cmt2 cmt3 (ddcc)*, *cmt2*, *cmt3*, *drm3*, *idn2*, *idn2 idl1 idl2 (idn2idl12)*, *suvr2*, *ago4*, and *frg1 frg2 (frg12)*.





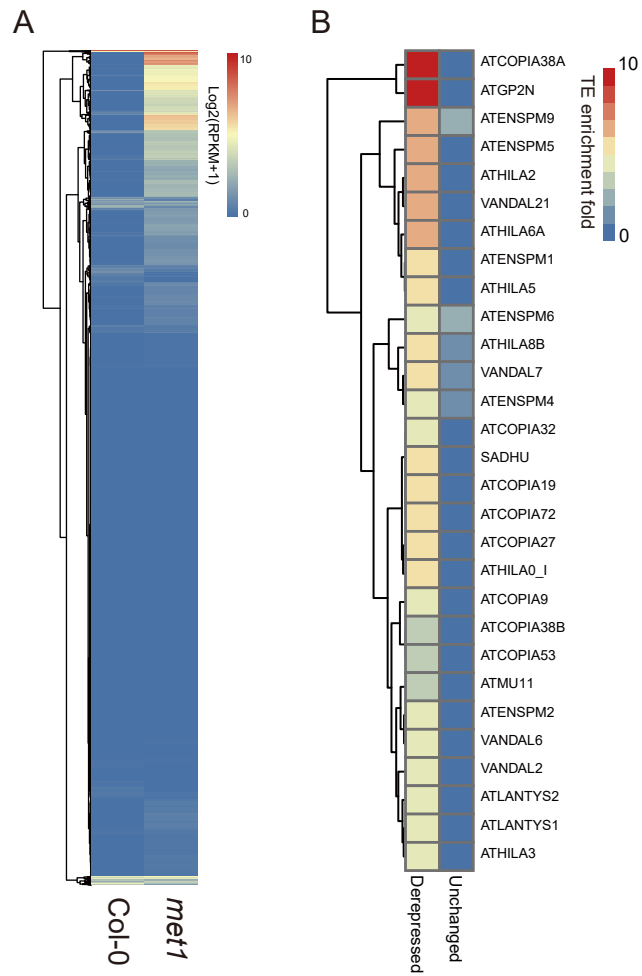
**Supplementary Fig. 8 DNA methylation in *met1* and *fwa*.**

(A) Whole genome methylation level in Col-0, *fwa*, and *met1*. Metaplot of DNA methylation over gene (B) and TE (C). Chromosome view of CG (D), CHG (E), and CHH (F) methylation. Methylation levels were calculated with Arabidopsis chromosomes divided into 100 kb bins.



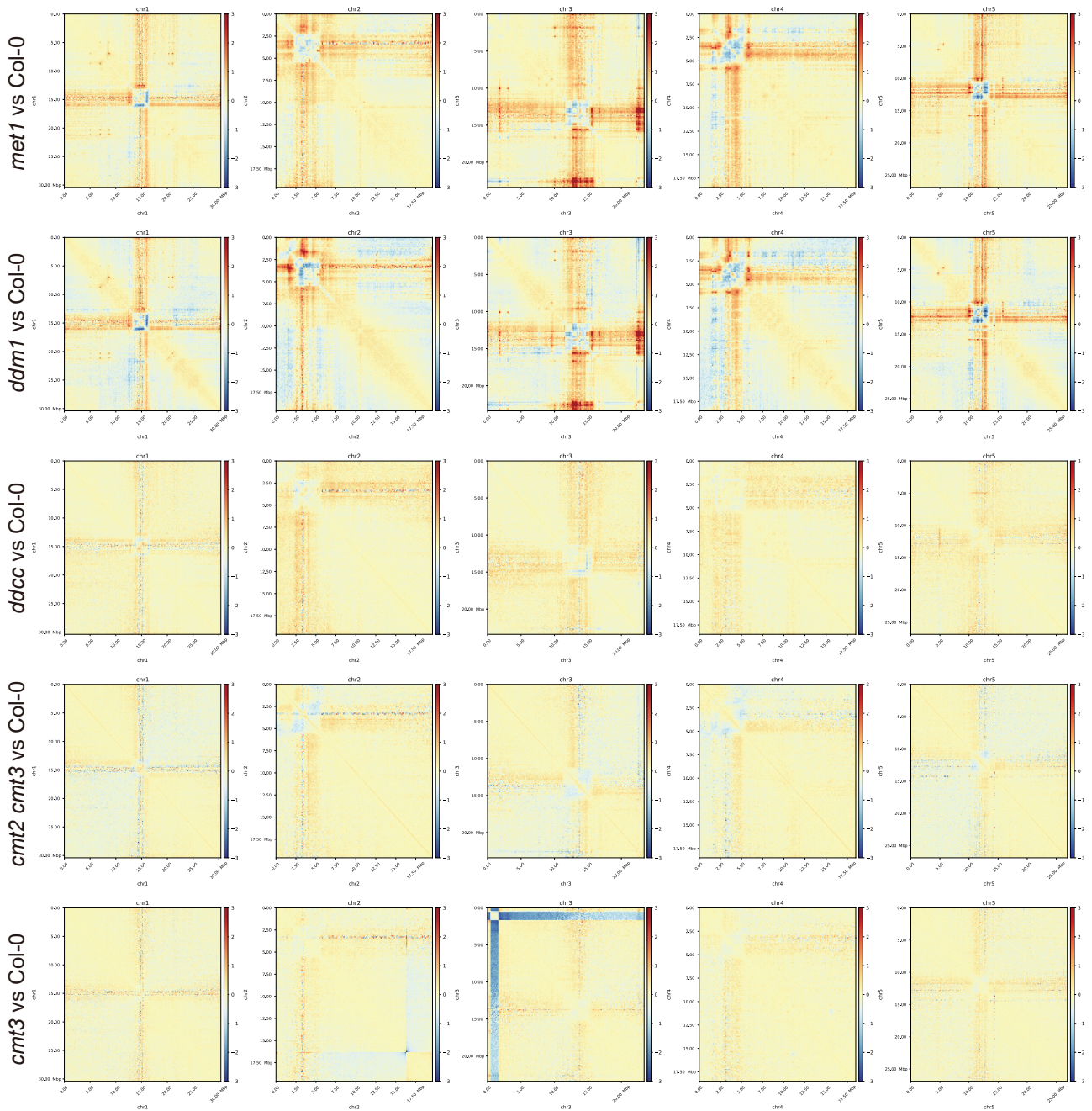
**Supplementary Fig. 9 sRNA heatmap of HARs.**

21 nt, 22 nt, and 24 nt siRNA over 3 groups of *met1* HARs in Col-0 and *met1*.



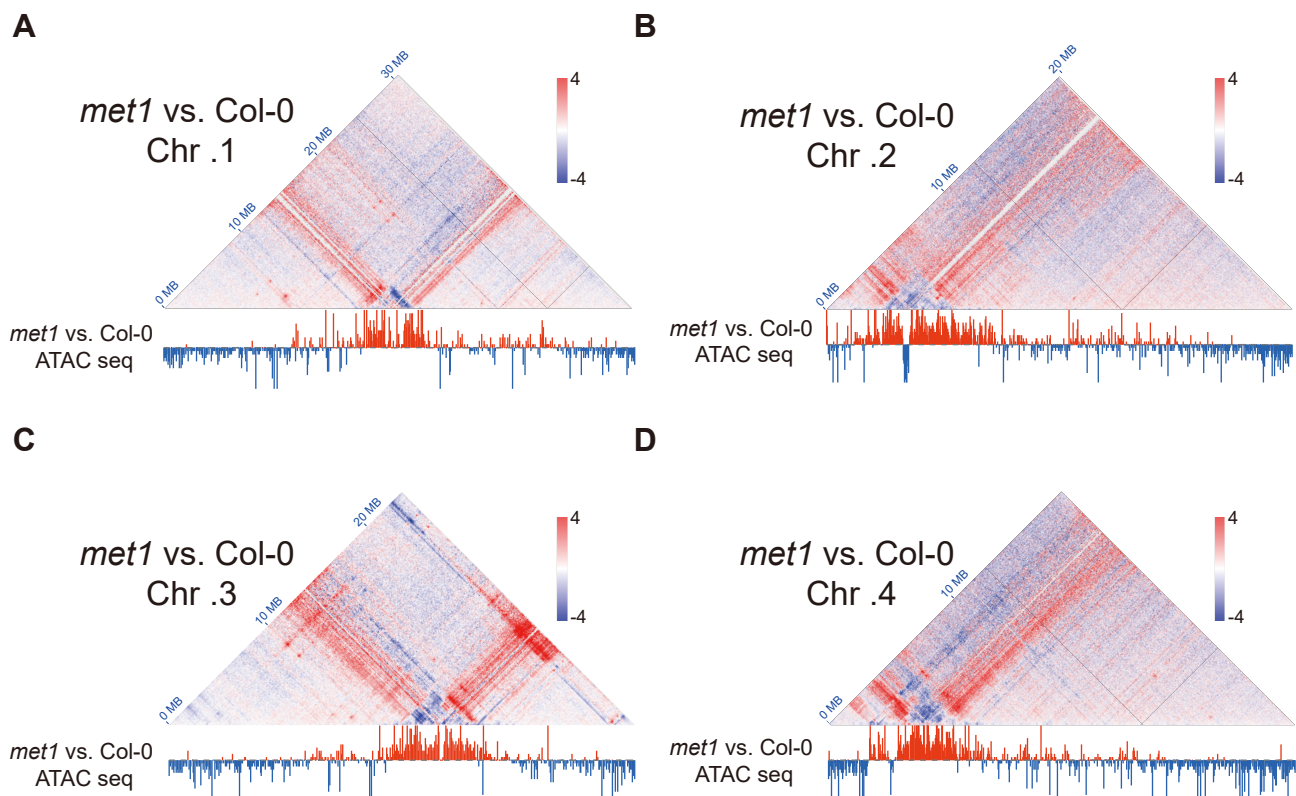
**Supplementary Fig. 10 TE transcription in *met1*.**

**(A)** Expression level of TEs with HARs in Col-0 and *met1* (n=6302). **(B)** Heatmap showing type enrichment of TEs in peaks of more accessibility in *met1*.



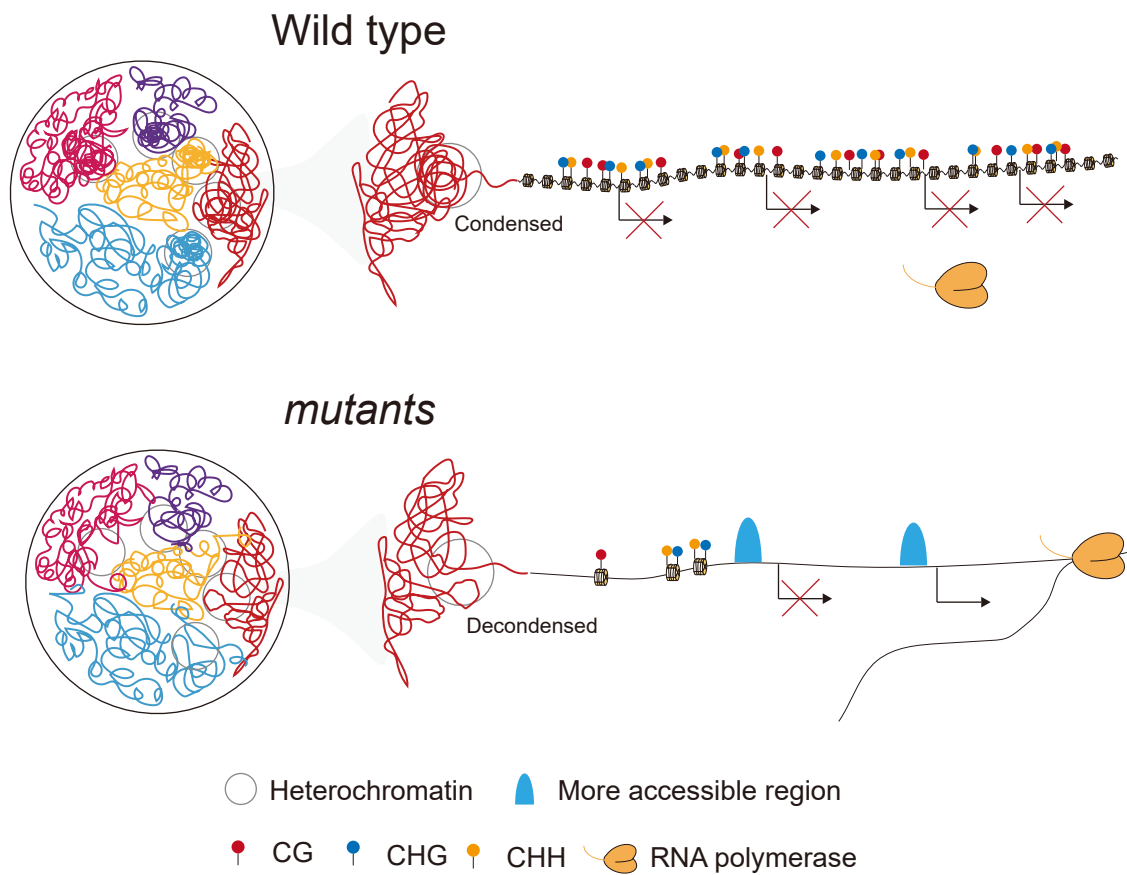
**Supplementary Fig. 11 Chromosome conformation variations in *met1*, *ddm1*, *ddcc*, *cmt2 cmt3*, and *cmt3*.**

Chromosome conformation variations of *met1*, *ddm1*, *ddcc*, *cmt2 cmt3*, and *cmt3* are presented by comparing Hi-C matrix with Col-0 in 100 kb resolution.



**Supplementary Fig. 12 Re-distribution of chromosome conformation in *met1* related to chromatin accessibility variation.**

Chromosome conformation and chromatin accessibility variations across chromosome 1 (A), chromosome 2 (B), chromosome 3 (C) and chromosome 4 (D). Red indicates level of Hi-C or ATAC-seq is higher in *met1*. Blue indicates level of Hi-C or ATAC-seq is lower in *met1*.



**Supplementary Fig. 13 Proposed model for the connection of DNA methylation with genome architecture.**

Genomic 3D structures are well maintained by three contexts of DNA methylation and other factors. In genomic regions where CG, CHG, and CHH methylation is lost simultaneously, nucleosomes become disassembled. Transcription further enhances the accessibility of heterochromatin and leads to long-range interactions between previously inaccessible heterochromatin regions and euchromatin regions. In some cases, DNA methylation may be solely responsible for chromatin accessibility increases.

**Supplementary Table 1 TE type enrichment of FC = 0 group.**

Type	Copy number	Enrichment Fold
TA1-2	2	6.854743697
VANDAL20	18	4.838629294
ATCOPIA2	2	4.569805377
ATREP17	11	4.435410186
VANDAL22	14	3.998590097
VANDAL18	4	3.916987672
VANDAL13	10	3.607750957
VANDAL9	11	3.507069267
ATCOPIA60	1	3.427371848
ATHATN9	3	3.42736294
VANDAL10	3	3.163716475
ATCOPIA65A	2	3.046547475
ATMU4	3	2.937740754
VANDALNX1	3	2.937740754
VANDAL18NB	4	2.886200766
ATMU1	12	2.78836221
ATCOPIA97	2	2.741888927
ATCOPIA84	2	2.741888927
VANDAL12	7	2.593679152
ATENSPM6	27	2.45135846
VANDAL2N1	9	2.419314647
ATMU5	4	2.284908627
ATMUN2	1	2.284902688
ATCOPIA40	1	2.284902688
ATENSPM9	16	2.261352565
ATDNA2T9B	4	2.109146847
ARNOLD1	6	2.109146003
ATCOPIA64	2	2.109144316
BRODYAGA1	38	2.075534379
ATHAT7	3	2.056416695
ATDNA12T3_2	98	2.035645675
ATCOPIA65	5	2.016095539
ATDNA2T9A	7	1.999295049
ATCOPIA15	2	1.958493836
ATCOPIA91	1	1.958493836
ATCOPIA10	1	1.958493836
ATCOPIA82	1	1.958493836
ATHAT10	5	1.958492091

ATCOPIA42	5	1.958492091
ATMU2	9	1.927891028
ATENSPM4	7	1.919323446
VANDAL7	5	1.904090522
ATHAT1	14	1.827926494
TNAT2A	5	1.803875479
BOMZH2	6	1.750142101
TAT1_ATH	11	1.733378803
ATCOPIA17	2	1.713682584
VANDAL18NA	3	1.71368147
ATCOPIA28	10	1.692525072
ATMUNX1	19	1.680513244
ATREP8	9	1.64513404
VANDAL14	3	1.645133356
ATENSPM1A	9	1.602403399
ATCOPIA25	1	1.523273738
ATMU8	1	1.523273738
ATCOPIA71	1	1.523273738
ATCOPIA95	8	1.523272418
ATREP10	7	1.523272229
ATHPOGON2	3	1.523271978
ATCOPIA58	2	1.523271098
ATCOPIA54	2	1.523271098
ATREP6	20	1.514856439
ATHATN2	5	1.490157632
ATENSPM7	8	1.482102997
VANDALNX2	4	1.482102373
TAG1	3	1.468870377
ATCOPIA29	2	1.443100383
ATHAT2	2	1.443100383
ATCOPIA26	2	1.443100383
TNAT1A	17	1.438646034
ARNOLDY2	30	1.428067737
BRODYAGA1A	61	1.427093013
ATREP13	11	1.422678887
ATREP7	17	1.421101617
SIMPLEGUY1	12	1.418219021
HELITRONY1A	28	1.416474571
ATHILA8B	8	1.406097335
ATCOPIA41	4	1.406097335
ATHPOGON3	12	1.394181474
ATCOPIA66	2	1.370944464



ATCOPIA93	1	1.370944464
ATCOPIA32B	1	1.370944464
ATENSPM10	8	1.354020057
ATREP10B	48	1.340231402
ATREP10C	12	1.337507404
ATHATN5	4	1.305661588
ATTIRTA1	9	1.298789918
ATTIR16T3A	10	1.293344442
ATMU7	3	1.285260685
ATIS112A	16	1.267926155
AT9TSD1	5	1.246313855
ATTIRX1B	4	1.246313502
ATCOPIA35	2	1.246313502
ATRE1	2	1.246313502
ATHATN4	5	1.224057966
VANDAL5A	5	1.224057966
HELITRONY1D	67	1.214990995
ATHATN1	6	1.192126375
ATDNA2T9C	21	1.189663042
HELITRONY2	17	1.177074048
ATREP9	17	1.159505735
ATMUN1	9	1.153131261
ATHATN10	4	1.142454313
ATCOPIA44	1	1.142454313
ATREP11	70	1.141095764
VANDAL5	7	1.129013502
HELITRONY3A	4	1.119138623
ATGP5	7	1.115885676
RathE2_cons	6	1.111577248
ARNOLDY1	19	1.099069864
RathE1_cons	17	1.094181476
ATREP19	15	1.088051592
VANDAL3	14	1.084363273
VANDAL4	8	1.075250954
VANDAL1N1	4	1.054573423
ATN9_1	5	1.05457317
RathE3_cons	8	1.054573107
ATMU6N1	3	1.054573002
HELITRONY1E	34	1.042777001
ATREP4	63	1.038095402
ATHILA4D_LTR	8	1.034675554
HELITRONY1C	9	1.028208882

ATHILA7	10	1.023093217
DT1	9	1.003130553
HELITRONY3	102	0.999545359
ATREP1	36	0.991044613
ATHILA8A	7	0.989341747
ATENSPM5	8	0.988068526
BOMZH1	2	0.979246918
ATDNATA1	2	0.979246918
VANDAL2	3	0.956473437
SIMPLEHAT2	5	0.939003378
ATREP10A	19	0.933618448
HELITRONY1B	28	0.927209193
HELITRON2	13	0.91867448
ARNOLD3	3	0.913963609
ATGP3	4	0.913963451
HARBINGER	6	0.913963292
ATCOPIA48	1	0.913962976
ATHATN8	1	0.913962976
ATREP5	41	0.900781196
ATREP10D	85	0.899848107
VANDAL8	8	0.891671603
BRODYAGA2	34	0.887850117
ATHILA7A	2	0.884480833
ATENSPM11	3	0.87507105
ATREP16	3	0.87507105
ATTIRX1A	4	0.870441274
ATHILA4B LTR	9	0.862832519
ATREP3	90	0.85743611
ATMU9	1	0.856841292
ATCOPIA96	1	0.856841292
ATCOPIA34	1	0.856841292
ATLINE1_3A	10	0.856840624
VANDAL1	5	0.856840624
Unassigned	7	0.849258054
VANDAL17	11	0.847213286
ATREP2	10	0.835942128
ATCOPIA50	1	0.806438216
TAG2	5	0.797061197
ATLINE2	8	0.794750737
ATHPOGON1	10	0.787899456
ATHATN3	4	0.783397185
ATLINEIII	11	0.769407925

ATHILA4	14	0.767729187
ATREP15	56	0.76543293
ATGP10	9	0.747788172
HELITRON1	7	0.738201219
ATLINE1A	15	0.711563208
ATCOPIA94	2	0.703048668
META1	7	0.695406895
ATHATN3A	1	0.685472232
ATCOPIA75	1	0.685472232
ATMU11	1	0.685472232
ATCOPIA59	1	0.685472232
ATLINE1_4	5	0.672031846
ATLINE1_2	2	0.668753702
VANDAL16	2	0.652830794
RP1_AT	4	0.630319565
ATMU10	4	0.630319565
HELITRON4	9	0.620025367
VANDAL6	4	0.616155117
ATHILA6B	6	0.61385593
ATHILA6A	11	0.610542315
AT9NMU1	2	0.609309073
ATLINE1_5	4	0.602613281
ATENSPM2	5	0.601291662
ARNOLD4	1	0.596063457
ATGP7	2	0.5833807
ATREP14	2	0.5833807
ATREP11A	4	0.577239964
ATCOPIA57	2	0.571227157
TAG3N1	4	0.565338141
ATHILA3	10	0.564174952
ATENSPM3	4	0.559569489
ATGP6	1	0.548377785
ATHPOGO	1	0.548377785
ATCOPIA69	1	0.548377785
ATDNAI26T9	1	0.548377785
ATHILA4A	12	0.530688393
ATMU6	1	0.527286712
ATCOPIA11	1	0.527286712
HELITRON3	2	0.517337777
ATCOPIA24	1	0.507757326
ATTIRX1D	1	0.489623459
SIMPLEHAT1	2	0.489623186

ATENSPM1	1	0.456981488
ATLINE1_1	2	0.449490126
ATLANTYS1	5	0.448021231
ATGP8	3	0.44704729
ATCOPIA37	1	0.428420228
ATLINE1_6	4	0.425099202
ATHILA5	4	0.418609156
ATCOPIA30	1	0.41543803
ATHILA4C	6	0.39930437
ATCOPIA13	1	0.391698418
ATLANTYS3	4	0.386181726
ATLANTYS2	5	0.382945541
ATDNAI27T9C	3	0.380818104
ATDNA1T9A	1	0.380818104
ATDNAI27T9A	3	0.354554755
ATREP2A	3	0.354554755
ATREP18	10	0.350625339
TA11	4	0.349285366
ATHILA	5	0.34619825
TSCL	2	0.338505014
ATDNAI27T9B	1	0.318824479
ATCOPIA68	1	0.318824479
ATHATN6	1	0.318824479
ROMANIAT5	1	0.279784656
LIMPET1	2	0.236369837
VANDAL21	1	0.214210114
ATHILA0_I	2	0.198687684
ATHATN7	1	0.19309082
ATSINE4	1	0.139892372
ATHILA2	4	0.132779183
ATGP1	1	0.095204526

**Supplementary Table 2 TE type enrichment of FC > 2 groups.**

Type	Copy number	Enrichment Fold
ATCOPIA38A	1	10.53681978
ATGP2N	25	9.756316864
ATENSPM9	33	7.169385296
ATHILA2	133	6.786429271
VANDAL21	20	6.585513645
ATHILA6A	77	6.56951782
ATENSPM5	34	6.454991595
ATENSPM1	9	6.322091867
ATHILA5	39	6.273834014
ATCOPIA27	5	5.545698262
ATHILA0_I	36	5.497473425
ATHILA8B	20	5.403499051
ATCOPIA19	1	5.268426321
ATCOPIA72	1	5.268426321
SADHU	4	5.268416051
VANDAL7	9	5.268412628
ATCOPIA32	2	5.268405781
ATENSPM4	12	5.057676649
ATLANTYS1	36	4.958505245
VANDAL2	10	4.900849252
ATHILA3	56	4.856478974
ATLANTYS2	40	4.709195166
ATCOPIA9	2	4.683037504
ATENSPM2	25	4.621413954
VANDAL6	19	4.498869079
ATENSPM6	32	4.465938336
ATMU11	4	4.214727911
ATCOPIA38B	1	4.214727911
ATCOPIA53	1	4.214727911
VANDAL12	7	3.986905453
ATMU9	3	3.951312038
ATGP2	9	3.951309471
ATHILA	37	3.938005089
ATHILA8A	18	3.910573798
ATGP10	30	3.831572277
ATENSPM11	8	3.587002954
ATCOPIA44	2	3.512275085
ATGP5	14	3.430594477
ATGP6	4	3.371782329
ATENSPM1A	12	3.284205164

ATGP3	9	3.161047577
ATHAT7	3	3.161045934
VANDAL8	18	3.08394866
VANDAL18	2	3.01052262
ATCOPIA22	2	3.01052262
ATMU4	2	3.01052262
ATLANTYS3	20	2.968119682
ARNOLD3	6	2.809820555
ATMU3	2	2.809818608
ENDOVIR1	2	2.809818608
ATHAT3	3	2.748738576
ATGP7	6	2.690252215
ATMU5	3	2.634206314
ATENSPM7	9	2.563011729
ATSINE2A	4	2.554382484
VANDAL14	3	2.528836747
VANDAL3	21	2.50026329
ARNOLD2	8	2.479252622
VANDAL9	5	2.450424626
TAT1_ATH	10	2.422258462
ATHAT1	12	2.408416665
ATENSPM3	11	2.365409877
ATCOPIA55	1	2.341518752
ATMU8	1	2.341518752
ATLINE1_6	14	2.287062432
ATHAT2	2	2.218279305
ATCOPIA41	4	2.16139962
ATCOPIA32B	1	2.107363956
ATHILA6B	13	2.044458235
ATHILA7A	3	2.039385704
VANDAL1	7	1.84394418
ATMU1	5	1.785902035
ATCOPIA95	6	1.756137543
ATCOPIA8A	1	1.756137543
ATCOPIA89	1	1.756137543
ATIS112A	14	1.705382097
ATDNAI26T9	2	1.685891165
ATCOPIA69	2	1.685891165
VANDAL20	4	1.652835082
ARNOLD1	3	1.621049715
ATGP9B	2	1.561010698
ATCOPIA15	1	1.50526131

ATDNAI27T9B	3	1.470254776
ATHILA4C	14	1.43218966
ATCOPIA67	1	1.404909304
ATCOPIA48	1	1.404909304
ATHILA4B_LTR	9	1.3263135
ATCOPIA5	1	1.317104013
ATCOPIA34	1	1.317104013
ATCOPIA96	1	1.317104013
ATGP1	9	1.317103157
HELITRON1	8	1.29683998
ATCOPIA49	2	1.239626311
TAG2	5	1.225212313
ATMU10	5	1.211129231
ATDNAI27T9C	6	1.170758362
ATCOPIA58	1	1.170757347
HELITRON5	3	1.128945354
SIMPLEHAT1	3	1.128945354
VANDAL13	2	1.109139652
ATDNAI27T9A	6	1.090016308
ATCOPIA94	2	1.08069981
ATCOPIA59	1	1.053681978
ATHATN6	2	0.98016985
ATDNA12T3A	1	0.957892979
ATREP12	1	0.957892979
ATHILA4A	14	0.951713137
ATHILA7	6	0.943596109
LIMPET1	5	0.908346923
VANDAL4	4	0.826417541
ATCOPIA11	1	0.810525182
ATDNA2T9B	1	0.810525182
ATENSPM10	3	0.78050565
ATCOPIA24	1	0.780505349
AT9TSD1	2	0.7663146
VANDAL5A	2	0.752630236
ATCOPIA43	1	0.726677539
HARBINGER	3	0.702454895
ATMU2	2	0.658551365
ATCOPIA37	1	0.658551365
ATMU7	1	0.658551365
ATCOPIA42	1	0.602103987
ATDNA1T9A	1	0.585379181
SIMPLEHAT2	2	0.577360185

TA11	4	0.536908249
TACL	2	0.5203371
ATHILA4	6	0.505767539
ATHATN5	1	0.501753397
VANDAL16	1	0.501753397
ATCOPIA68	1	0.490084925
VANDAL17	4	0.473565166
ATLINE2	3	0.458122785
BOMZH2	1	0.448375369
ATREP16	1	0.448375369
VANDAL22	1	0.439034386
ATSINE4	2	0.430074523
ROMANIAT5	1	0.430074386
ATLINE1_4	2	0.41320877
HELITRON3	1	0.397616028
RathE1_cons	3	0.296811946
VANDAL5	1	0.247925262
ATHPOGON1	2	0.242225846
ATLINE1_5	1	0.231578584
ATGP8	1	0.229061393
ATTIRTA1	1	0.221827858
ATREP11A	1	0.221827858
HELITRON4	2	0.211795452
ATHILA4D_LTR	1	0.198808014
ATREP2A	1	0.181669385
ARNOLDY1	2	0.177836696
HELITRONY1C	1	0.175613754
TNAT1A	1	0.13008425
ATREP15	6	0.126063701
ATREP19	1	0.111500783
HELITRON2	1	0.10862705
ATLINEIII	1	0.107518614
HELITRONY2	1	0.10643257
ATDNA12T3_2	3	0.095789311
HELITRONY1E	2	0.094289256
ATREP10B	2	0.085839708
BRODYAGA1	1	0.083958761
BRODYAGA2	2	0.080280565
HELITRONY1A	1	0.07776254
ATREP4	3	0.075986713
ATREP10A	1	0.075532787
ATREP11	3	0.075173538



ATREP3	5	0.073223241
ARNOLDY2	1	0.07317239
ATLINE1A	1	0.072919203
BRODYAGA1A	2	0.071923717
ATREP5	2	0.067543745
HELITRONY3	4	0.060253463
HELITRONY1D	2	0.055750394
ATREP18	1	0.0538968
HELITRONY1B	1	0.050902532

**Supplementary Table 3 WGBS data used in this study.**

Name	SRR ID	WT control	Description	Reference
<i>frg12</i>	SRR1533696	SRR534193	SNF2 family chromatin modifiers. Defects in methylation at specific RdDM targeted loci.	18
<i>ago4</i>	SRR534197	SRR534193	AGO4 form a AGO4/sRNA complex with the 24 nt sRNAs produced by DCL3. <i>ago4</i> mutant shows loss of methylation at DRM1/2-dependent RdDM sites.	25
<i>nrpe1</i>	SRR534182	SRR534193	Largest subunit of plant-specific RNA polymerase V. Responsible for transcribing non-coding RNAs as scaffold for other RdDM components. Eliminates methylation at RdDM sites.	25
<i>nrpd1</i>	SRR534181	SRR534193	Largest subunit of plant-specific RNA polymerase IV. Responsible for transcribing single-stranded RNAs precursors of the sRNAs. Eliminate methylation at RdDM sites.	25
<i>nrpd1e1</i>	NA	NA	Cross of <i>nrpd1</i> and <i>nrpe1</i> .	NA
<i>drm3</i>	SRR534225	SRR534193	Encodes a DNA methyltransferase-like gene, which is homologous to DRM2. Loss of DRM3 results in moderate effects on RdDM and small RNA abundance.	19
<i>idn2</i>	SRR534235	SRR534193	Encodes a double-stranded RNA-binding protein with zinc finger domain, involved in de novo methylation of some RdDM sites.	20
<i>idn2idn12</i>	SRR534236	SRR534193	Cross of <i>idn2</i> and <i>idn1 idn12</i> . IDN2, IDNL1, IDNL2 form a complex involved in RdDM. Loss of IDN2, IDNL1, IDNL2 complex affect DNA methylation at RdDM sites.	21
<i>suvr2</i>	SRR534259	SRR534193	Arabidopsis homolog of Su(var)3-9, required for RdDM at some sites	25
<i>dms3</i>	SRR534216	SRR534193	DMS3 encodes a structural maintenance of chromosomes (SMC) hinge domain-containing protein. Loss of DMS3 eliminate methylation at RdDM sites.	25
<i>cmt3</i>	SRR534209	SRR534193	CMT3 encodes the main CHG specific DNA methyltransferase. <i>cmt3</i> mutant shows strong depletion of CHG methylation except at some DRM1/2 dependent CHG sites. CMT3 is also required for small proportion of CHH methylation.	25

<i>cmt23</i>	SRR1005413	SRR1005412	Cross of <i>cmt2</i> and <i>cmt3</i> .	6
<i>drm12</i>	SRR534222	SRR534193	Cross of <i>drm1</i> and <i>drm2</i> . DRM2 is the main DNA methyltransferases of the RdDM pathway. DRM1 is a close homolog with no known function.	25
<i>cmt2</i>	SRR869314	SRR534193	CMT2 is a DNA methyltransferase. CMT2 loss results in global loss of CHH methylation with CG and CHG methylation largely undisturbed, especially in the bodies of long transposons and in pericentromeric heterochromatin.	6
Col-0	SRR534193	NA	The wild type Arabidopsis ecotype Columbia-0.	NA
<i>ddm1</i>	SRR1609353	SRR1609352	Heterochromatic DNA methylation is severely reduced in <i>ddm1</i> , but genic methylation remained largely intact.	25
<i>met1</i>	SRR534239	SRR534193	The main enzyme that maintains preexisting CG methylation is MET1, a homolog of mammalian DNMT1. Loss of MET1 lead to elimination of CG methylation throughout the genome, and loss of CHG, CHH methylation at certain sites.	25
<i>fwa</i>	SRR6466273	SRR6466272	The <i>fwa</i> line was derived from crossing a <i>met1</i> homozygous mutant with wild type and selecting for a plant homozygous for wild type MET1 alleles in the F2 population. This line has a chimeric genomic methylation pattern showing methylation losses at FWA and many other loci.	15
<i>ddcc</i>	SRR1005415	SRR1005412	Quadruple mutant of <i>drm1 drm2 cmt2 cmt3</i> . All of non-CG methylation in the genome is eliminated in this mutant.	6

NA: Not available