***eLife’s* transparent reporting form**

We encourage authors to provide detailed information *within their submission* to facilitate the interpretation and replication of experiments. Authors can upload supporting documentation to indicate the use of appropriate reporting guidelines for health-related research (see [EQUATOR Network](http://www.equator-network.org/%20)), life science research (see the [BioSharing Information Resource](https://biosharing.org/" \t "_blank)), or the [ARRIVE guidelines](http://www.plosbiology.org/article/info:doi/10.1371/journal.pbio.1000412) for reporting work involving animal research. Where applicable, authors should refer to any relevant reporting standards documents in this form.

If you have any questions, please consult our Journal Policies and/or contact us: [editorial@elifesciences.org](mailto:editorial@elifesciences.org).

**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
* You should state the statistical method of sample size computation and any required assumptions
* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

We investigated DNA methylation and sRNA expression at thousands of transposons in *Arabidopsis* genome.

The association between nonCG methylation and sRNA expression is supported by the tight correlation between these two elements in various genetic backgrounds where nonCG methylation and H3K9 methylation level is uncoupled.

**Replicates**

* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
* The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
* If you encountered any outliers, you should describe how these were handled
* Criteria for exclusion/inclusion of data should be clearly stated
* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

Bisulfite sequencing was performed on one or two biological replicates of each genotype, typical for genome-wide DNA methylation analysis. To evaluate the association between histone modification and DNA methylation/sRNA expression across hundreds to thousands of loci, we sequenced one or two biological replicates of ChIP-sequencing libraries in *wild-type, h1, cmt2cmt3, h1cmt2cmt3, ddm1*, and *h1ddm1* plants. For sRNA expression analysis, we sequenced sRNAs from three biological replicates (except for *met1* and *h1met1* (one biological replicate)).

The detailed analysis approach is described in the methods section. All data generated for this research are available in GEO with accession number GSE179796.

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE179796>

**Statistical reporting**

* Statistical analysis methods should be described and justified
* Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
* For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
* Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

*P* values were calculated by Student’s *t*-test otherwise indicated.

Pearson correlation coefficient is shown for correlation analysis (Figure S1, Figure7, and Figure 8).

(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

**Group allocation**

* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
* Indicate if masking was used during group allocation, data collection and/or data analysis

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

The data was grouped by genotype (*wild-type, h1, cmt2, h1cmt2, h1cmt2shh1, cmt2cmt3, h1cmt2cmt3, ddm1, h1ddm1, met1,* and *h1met1*). We did not attempt randomization or masking during data collection and analysis.

**Additional data files (“source data”)**

* We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
* Include model definition files including the full list of parameters used
* Include code used for data analysis (e.g., R, MatLab)
* Avoid stating that data files are “available upon request”

Please indicate the figures or tables for which source data files have been provided:

Source data 1 provide the lists of CMT, DRM, and intermediate transposons (TEs). Among TEs with more than 2% mCHH methylation in wild type plants, CMT TEs were demethylated in *cmt2* plants and DRM TEs were demethylated in *drm2* plants (mCHH in the mutants <0.02, Fisher's exact test *p* <0.01, TEs longer than 200 bp). Intermediate TEs have more than 2% mCHH in *cmt2* and *drm2* plants.