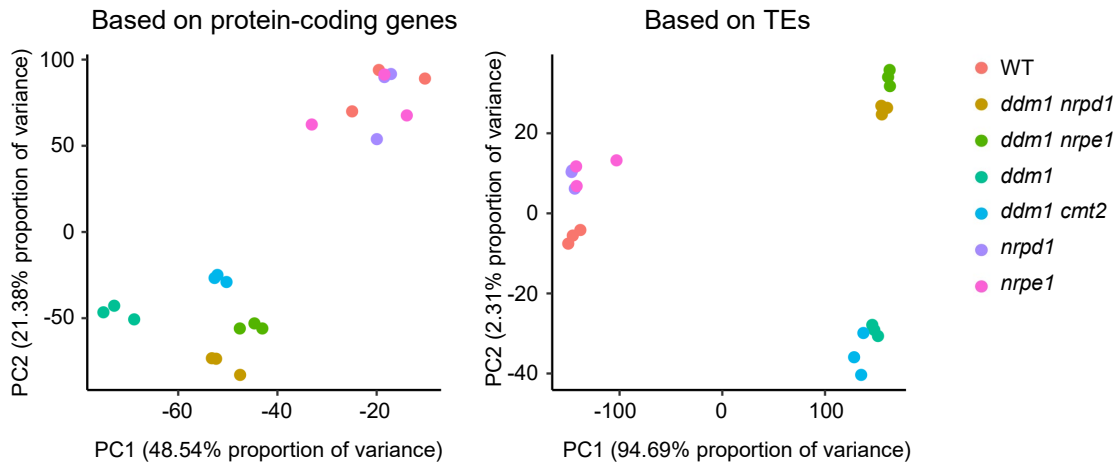


Supplementary Fig. 1. Classification of CHH hypo-DMRs into four major categories.

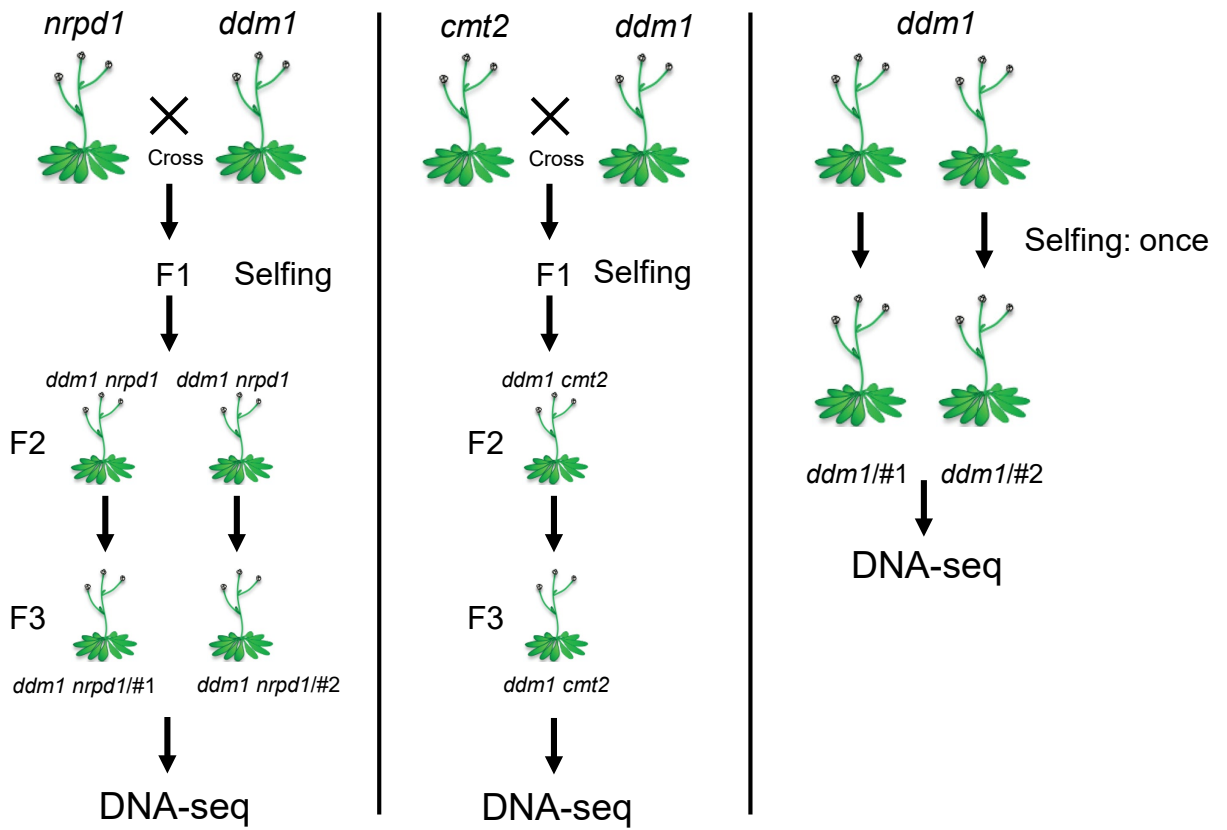
(A) Heatmap of CHH methylation levels in CMT2-only loci. Columns represent data for each indicated genotype; rows represent loci.

(B) Heatmap of CHH methylation levels in RdDM-and-CMT2 loci.

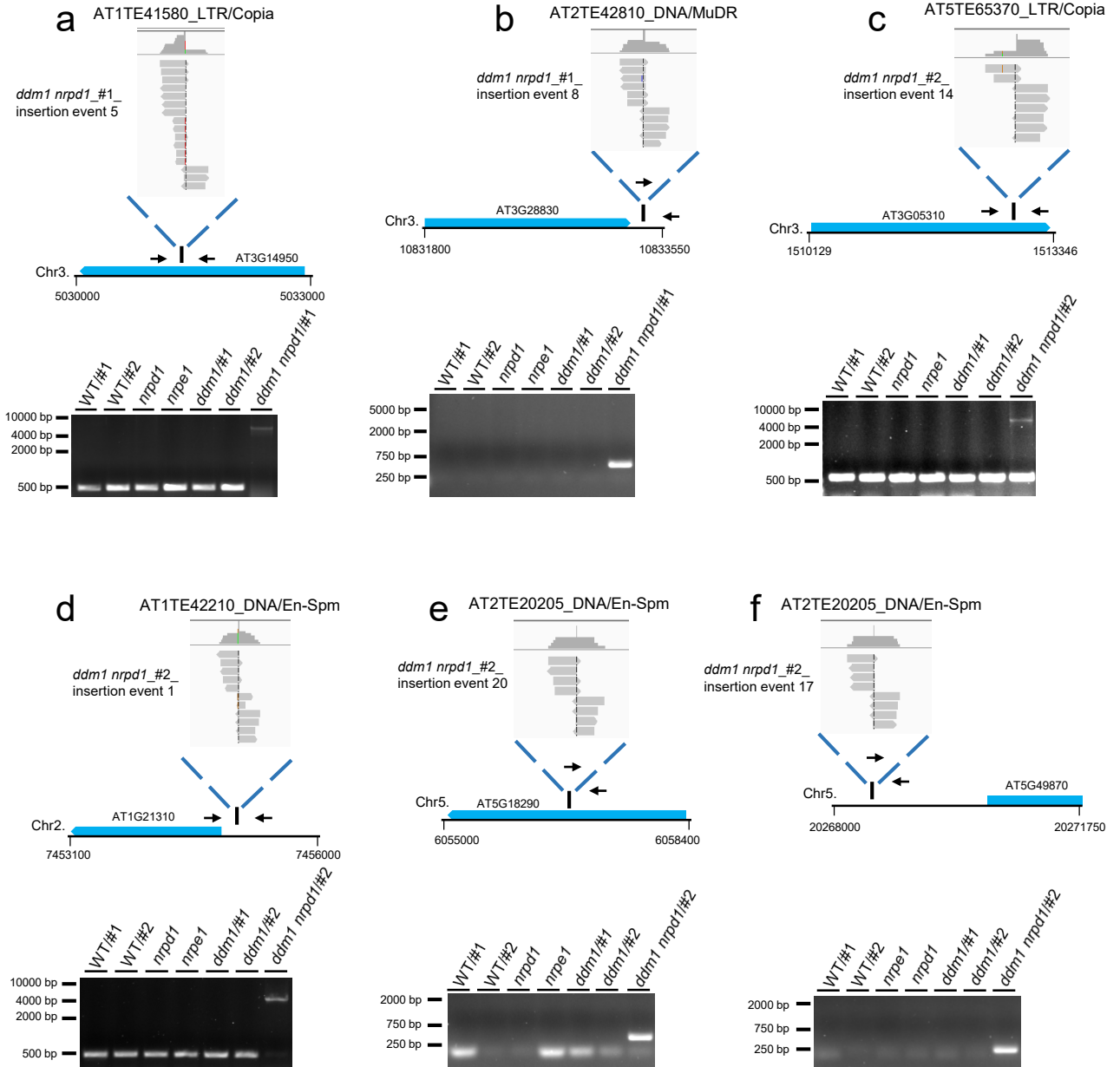
(C) Metaplot and heatmap of NRPD1 ChIP-seq signals in RdDM-and-CMT2 loci.



Supplementary Fig. 2. Principal component analysis (PCA) of the indicated transcriptomes.

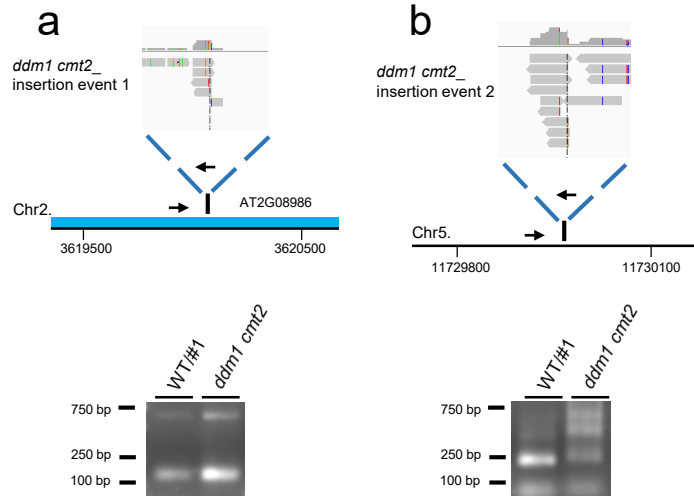


Supplementary Fig. 3. Flow diagram showing the generation of materials for DNA-seq.

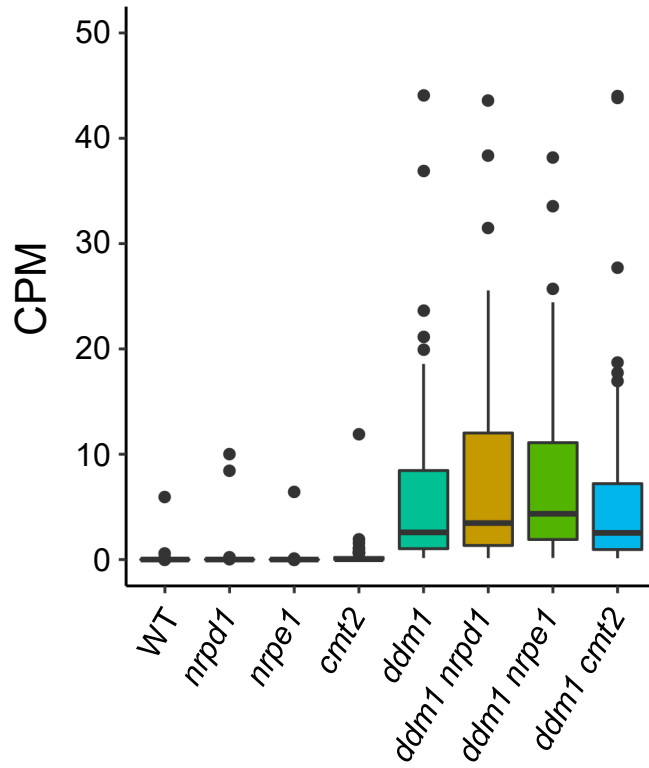


Supplementary Fig. 4. New TE insertions identified in *ddm1 nrpd1* and confirmed by PCR.

Primer positions are indicated (black arrows). Upper panel, IGV screenshots showing split-reads at the TE insertion sites.



Supplementary Fig. 5. The putative TE insertions in *ddm1 cmt2* could not be confirmed.
 Primer positions are indicated (black arrows). Upper panel, IGV screenshots showing split-reads at the TE insertion sites.



Supplementary Fig. 6. Boxplots of the expression levels of transposed TE subfamilies from *ddm1 nrpd1* in the indicated genotypes. CPM (Counts per million) were averaged from biological replicates. The horizontal line within the box represents the median; the whiskers extend to 1.5 times the interquartile range; and the lower and upper boundaries of the box represent the first and third quartiles, respectively.

Supplementary Table 1. Summary of whole-genome bisulfite sequencing data

Samples	Raw reads	Clean reads	Unique mapped rates	Multiple mapped rates	Coverage	Conversion rates
WT_rep 1	36,264,579	32,559,941	77.5%	90.3%	16.91	99.86%
WT_rep 2	36,267,633	32,197,538	76.9%	89.4%	16.77	99.83%
<i>nrpd1</i> _rep 1	29,336,271	26,163,948	77.1%	91.1%	13.48	99.84%
<i>nrpd1</i> _rep 2	36,262,399	32,870,411	77.2%	90.7%	16.89	99.85%
<i>nrpe1</i> _rep 1	39,677,251	35,308,859	76.9%	90.8%	18.12	99.87%
<i>nrpe1</i> _rep 2	34,845,602	31,371,293	77.5%	90.9%	15.82	99.86%
<i>ddm1</i> _rep 1	32,475,420	29,265,663	75.6%	91.0%	14.70	99.86%
<i>ddm1</i> _rep 2	36,645,583	32,887,312	75.2%	90.9%	16.00	99.86%
<i>ddm1 nrpd1</i> _rep 1	37,391,733	31,324,280	83.7%	92.6%	13.71	99.92%
<i>ddm1 nrpd1</i> _rep 2	33,159,491	28,052,780	83.4%	92.6%	12.01	99.93%
<i>ddm1 nrpe1</i> _rep 1	34,299,641	28,984,929	81.1%	91.3%	11.49	99.91%
<i>ddm1 nrpe1</i> _rep 2	54,575,907	46,418,075	83.5%	93.5%	17.36	99.70%
<i>cmt2</i>	32,703,998	29,165,447	78.0%	88.3%	17.35	99.04%
<i>ddm1 cmt2</i>	32,621,092	29,740,205	76.3%	87.9%	16.31	99.59%

Supplementary Table 2. Summary of ChIP sequencing data

Samples	Raw reads	Clean reads	Mutiple mapped rates	Unique mapped rates
WT_rep1	15,933,198	10,701,417	76.9%	56.1%
WT_rep2	15,731,918	11,235,065	58.9%	37.9%
<i>nrdp1</i> /NRPD1-Flag_rep1	16,400,098	11,219,757	83.3%	55.5%
<i>nrdp1</i> /NRPD1-Flag_rep2	12,280,039	8,118,607	85.3%	55.7%
<i>ddm1</i> _rep1	16,235,710	12,414,327	58.1%	33.7%
<i>ddm1</i> _rep2	11,074,701	7,971,309	68.4%	39.5%
<i>ddm1 nrdp1</i> /NRPD1-Flag_rep1	20,073,114	15,578,487	91.1%	54.3%
<i>ddm1 nrdp1</i> /NRPD1-Flag_rep2	13,968,551	9,581,040	81.8%	49.3%

Supplementary Table 3. The CMT2-to-RdDM loci that overlap with *Athila6A* TEs

Category of loci	Chromosome	Start	End	TE ID	TE subfamily	TE Superfamily
CMT2-to-RdDM loci	Chr1	13794006	13794194	AT1TE45175	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr1	13794953	13795247	AT1TE45175	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr1	13794953	13795247	AT1TE45180	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr1	13863406	13863647	AT1TE45475	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr1	15638626	15638795	AT1TE51475	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr2	2401808	2402297	AT2TE10985	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr2	3637251	3637499	AT2TE15880	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr2	4184002	4184599	AT2TE17640	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr2	4202903	4203342	AT2TE17730	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr2	4504506	4504697	AT2TE18860	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr2	4521459	4521890	AT2TE18895	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr2	4989333	4990081	AT2TE20440	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr2	5995417	5995650	AT2TE24385	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr2	5996237	5996398	AT2TE24385	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr3	13585851	13586032	AT3TE55255	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr3	13654460	13654641	AT3TE55395	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr3	13662652	13663043	AT3TE55425	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr3	13823358	13823594	AT3TE56710	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr3	13969355	13969541	AT3TE57345	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr3	14099403	14099698	AT3TE57785	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr3	14410306	14410475	AT3TE59105	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr3	14410552	14410799	AT3TE59105	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr3	14551064	14551292	AT3TE59610	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr3	14804203	14804399	AT3TE60460	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr3	14804455	14804846	AT3TE60460	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr4	2885701	2885894	AT4TE13480	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr4	3284803	3284999	AT4TE15030	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr4	3484424	3484575	AT4TE15755	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr4	3629901	3630094	AT4TE16175	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr4	3916552	3916733	AT4TE17115	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr4	4176602	4176800	AT4TE18060	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr4	4414306	4414536	AT4TE18705	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr5	10581909	10582246	AT5TE38625	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr5	11809472	11809700	AT5TE42435	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr5	12139801	12140045	AT5TE43260	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr5	12140256	12140446	AT5TE43260	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr5	12410709	12410938	AT5TE43980	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr5	12611707	12611947	AT5TE44690	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr5	12747051	12747299	AT5TE45065	ATHILA6A	LTR/Gypsy
CMT2-to-RdDM loci	Chr5	13011851	13012100	AT5TE46215	ATHILA6A	LTR/Gypsy

Supplementary Table 4. Summary of RNA sequencing data

Samples	Raw reads	Clean reads	Mutiple mapped rates	Unique mapped rates
<i>ddm1_rep 1</i>	15,450,933	8,393,308	95.1%	93%
<i>ddm1_rep 2</i>	14,302,536	7,566,163	94.8%	93%
<i>ddm1_rep 3</i>	19,031,784	9,739,562	94.8%	92.5%
<i>ddm1 nrpd1_rep 1</i>	19,827,888	15,532,920	96.1%	94%
<i>ddm1 nrpd1_rep 2</i>	29,980,975	23,949,867	96.7%	94.8%
<i>ddm1 nrpd1_rep 3</i>	18,114,078	14,413,851	96.2%	94.1%
<i>ddm1 nrpe1_rep 1</i>	19,985,707	15,653,033	95.7%	93.3%
<i>ddm1 nrpe1_rep 2</i>	21,719,250	17,284,010	96.3%	94%
<i>ddm1 nrpe1_rep 3</i>	22,013,606	17,849,217	96.5%	94.5%
<i>ddm1 cmt2_rep 1</i>	14,700,829	10,363,894	96.7%	95.3%
<i>ddm1 cmt2_rep 2</i>	25,254,592	17,238,531	97%	95.6%
<i>ddm1 cmt2_rep 3</i>	16,556,494	11,139,750	94.8%	93.4%

Supplementary Table 5. Summary of DNA sequencing data

Samples	Raw reads	Clean reads	Mutiple mapped rates	Unique mapped rates
WT/#1	21,669,780	19,792,467	96.1%	67.3%
WT/#2	21,302,454	19,481,752	95.3%	64%
<i>nrpd1</i>	19,330,958	17,763,119	94.8%	62.2%
<i>ddm1</i> #1	18,779,262	17,205,352	94.9%	65.5%
<i>ddm1</i> #2	19,241,410	17,599,640	94.9%	65%
<i>ddm1-1 nrpd1</i> #1	19,495,655	17,866,798	86.8%	60.7%
<i>ddm1-1 nrpd1</i> #2	18,261,733	16,708,944	90.2%	63.5%
<i>ddm1 cmt2</i>	18,345,052	17,502,246	86.5%	61.3%

Supplementary Table 6. Summary of putative TE transposition events identified in *ddm1 nrp1* and *ddm1 cmt2*

Samples	Insertion events	Chromosome	Start	End	TE family	TE	Validation of PCR
<i>ddm1 nrp1</i> #1	1	Chr1	15543127	15543136	ATCOPIA93	AT1TE41580	-
	2	Chr1	25709672	25709680	ATCOPIA93	AT1TE41580	-
	3	Chr2	11195486	11195492	ATCOPIA93	AT1TE41580	-
	4	Chr2	5858678	5858687	ATCOPIA93	AT1TE41580	-
	5	Chr3	5031388	5031394	ATCOPIA93	AT1TE41580	True
	6	Chr4	13975703	13975708	ATCOPIA93	AT1TE41580	-
	7	Chr1	13939816	13939826	VANDAL21	AT2TE42810	-
	8	Chr3	10833383	10833392	VANDAL21	AT2TE42810	True
	9	Chr3	5627951	5627960	ATCOPIA93	AT1TE41580	-
	10	Chr4	16492663	16492671	ATCOPIA21	AT5TE65370	-
	11	Chr5	18766909	18766918	ATCOPIA93	AT5TE20395	True
<i>ddm1 nrp1</i> #2	1	Chr1	7455158	7455167	ATENSPM3	AT1TE42210	Ture
	2	Chr3	14202166	14202173	ATGPN2	AT2TE00120	-
	3	Chr4	2688712	2688717	ATENSPM3	AT1TE42210	-
	4	Chr2	14784634	14784638	ATENSPM3	AT1TE42210	-
	5	Chr2	5055616	5055621	ATENSPM3	AT2TE18415	-
	6	Chr3	14991078	14991083	ATENSPM3	AT2TE18415	-
	7	Chr4	1190326	1190330	ATENSPM3	AT2TE18415	-
	8	Chr5	19987920	19987928	ATCOPIA93	AT1TE41580	-
	9	Chr5	26130632	26130638	ATENSPM3	AT1TE42210	-
	10	Chr5	5877092	5877095	ATENSPM3	AT2TE18415	-
	11	Chr1	20347534	20347537	ATENSPM3	AT2TE20205	-
	12	Chr1	29450386	29450390	ATENSPM3	AT2TE20205	-
	13	Chr1	30246543	30246549	ATCOPIA21	AT5TE65370	-
	14	Chr3	1512728	1512733	ATCOPIA21	AT5TE65370	True
	15	Chr3	4956195	4956199	ATENSPM3	AT2TE20205	True
	16	Chr4	9758568	9758572	ATENSPM3	AT2TE20205	-
	17	Chr5	20268875	20268878	ATENSPM3	AT2TE20205	True
	18	Chr5	20758651	20758656	ATENSPM3	AT2TE20205	-
	19	Chr5	23922941	23922944	ATENSPM3	AT2TE20205	-
	20	Chr5	6056700	6056703	ATENSPM3	AT2TE20205	Ture
	21	Chr5	6058222	6058225	ATENSPM3	AT2TE20205	-
	22	Chr5	9358929	9358932	ATENSPM3	AT2TE20205	-
<i>ddm1 cmt2</i>	1	Chr2	3620073	3620076	ATREP18	AT4TE14735	False
	2	Chr5	11730474	11730478	ATREP18	AT4TE14735	False

Supplementary Table 7. Primers used in this study

Primers for new TE insertion identify		
Insertion events	Forward (5' > 3')	Reverse (5' > 3')
<i>ddm1 nrpd1/#1_5</i>	CGTTACCACGATCACGCGCT	TGCAGCCATTGCGTCTGGAGC
<i>ddm1 nrpd1/#1_8</i>	GGGACTGGCCAGACGATTAT	TTTCGGGATATTACTATTTCACT
<i>ddm1 nrpd1/#1_11</i>	CTCTCTTAATCTTTAATACAATTCCGC	GGGTTGTGTGGAGATGCACCG
<i>ddm1 nrpd1/#2_1</i>	AAGAGGCCATTGGAGACCCCAT	CCGGAAAAAGAAAACTCAAGAGGCCA
<i>ddm1 nrpd1/#2_14</i>	GTGTTTGGTCCCAAGAATGCTGGA	GGGGATTCTCTGCCGCGGTT
<i>ddm1 nrpd1/#2_15</i>	TGGCTCGTGATCTCATCAAACCTTCT	TCCTCCAATTCCACAAGGCTTCC
<i>ddm1 nrpd1/#2_17</i>	AGCGCTTTTCACTGGCTAATAATG	TCTTAGATCCCGTAAATCGGCAAGACA
<i>ddm1 nrpd1/#2_20</i>	CTGGCTAATAATGTTGATATTTGT	CCCAAGAGGGGTCTTGGCCT
<i>ddm1 cmt2_1</i>	GGACTCATATGGACTTTGGGCTACACC	TGTCATGTGTATGATTGAGTATA
<i>ddm1 cmt2_2</i>	TGAAGCTTGGTTAGTGTTTTGGAGTGA	GACATCAAGTCATAACTGACTCCAA