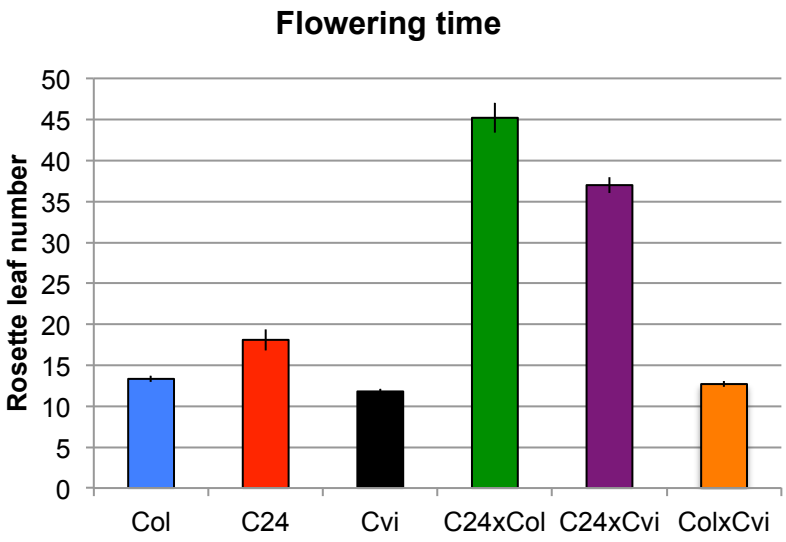

Figure S1. Flowering time in three F_1 hybrids and their parental lines as measured by leaf number at bolting. Data represent mean values ± standard error obtained from more than twenty plants.

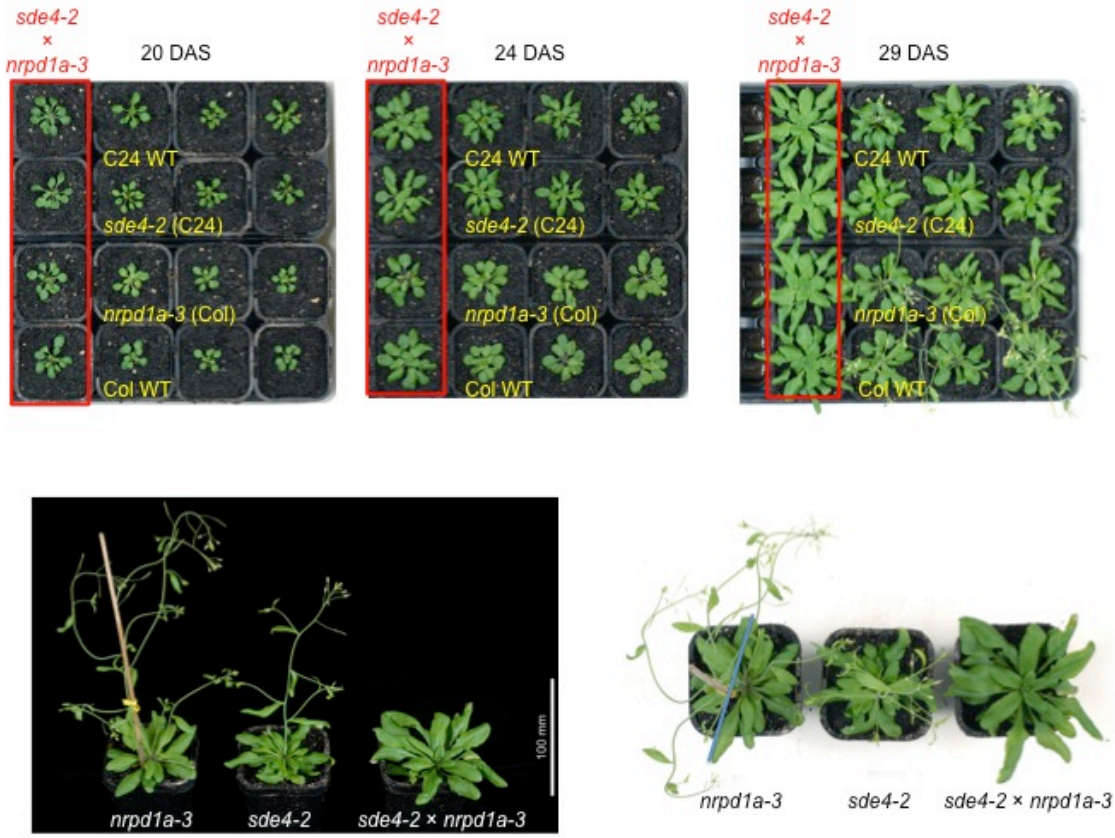

Figure S2. Phenotype of the *pol IV* mutant hybrid. Seedlings at 20 DAS (Upper Left), 24 DAS (Upper middle), and 29 DAS plants (Upper Right). *Pol IV* mutant hybrid showed late flowering time and greater biomass than its parents (Bottom).

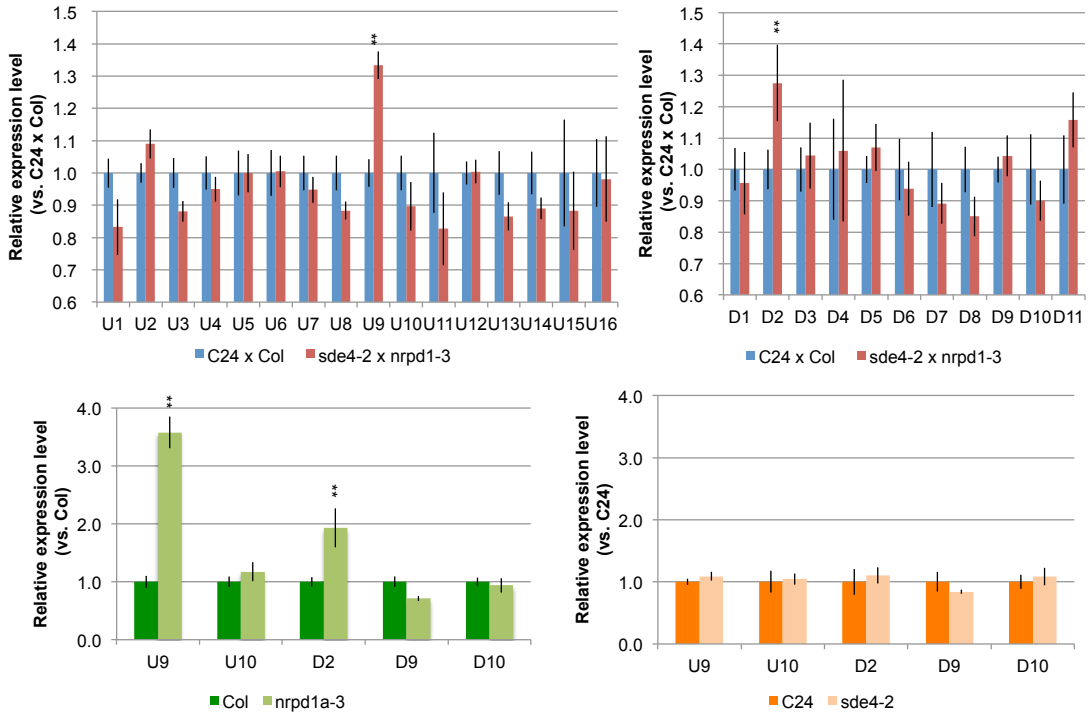

Figure S3. Expression analysis of non-additively expressed genes between C24 x Col hybrids and parental lines in *pol IV* mutant hybrids. Expression levels of up- (U1-U16, Upper left) and down-regulated (D1-D11, Upper right) genes in C24 x Col hybrids were compared between C24 x Col and *pol IV* mutant hybrids. Expression levels of U9, U10, D2, D9, and D10 genes were compared between Col-0 and *nrpd1a-3* (Bottom left) or between C24 and *sde4-2* (Bottom right). Data represent mean values ± standard error obtained from three biological and technical replications. **, $p<0.01$

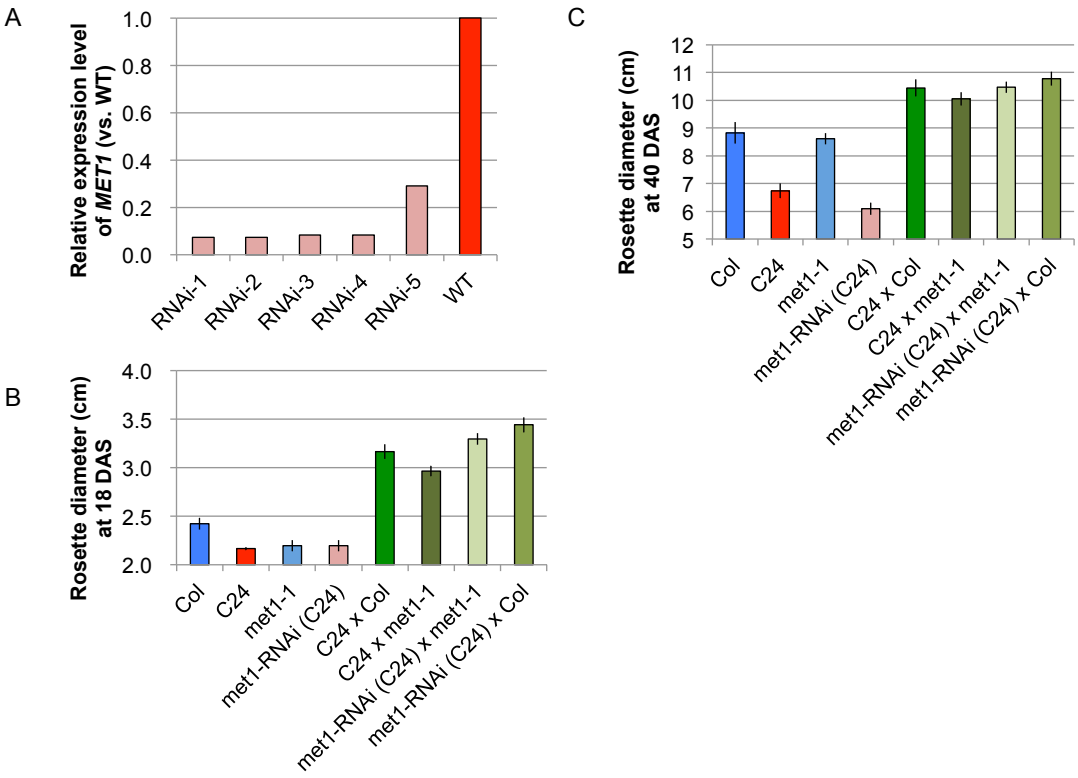

Figure S4. Rosette diameter in the hybrids between *met1*-RNAi plants and *met1-1*. (A) *MET1* expression levels in leaves of T_1 plants analyzed by RT-qPCR. Relative expression levels of *met1*-RNAi plants were calculated with a control of wild type plants C24 being given a value of 1.0. The *actin* gene was used as a standard of expression level. The rosette diameter at 18 DAS (B) and 40 DAS (C). Data represent mean values ± standard error obtained from more than twenty plants.

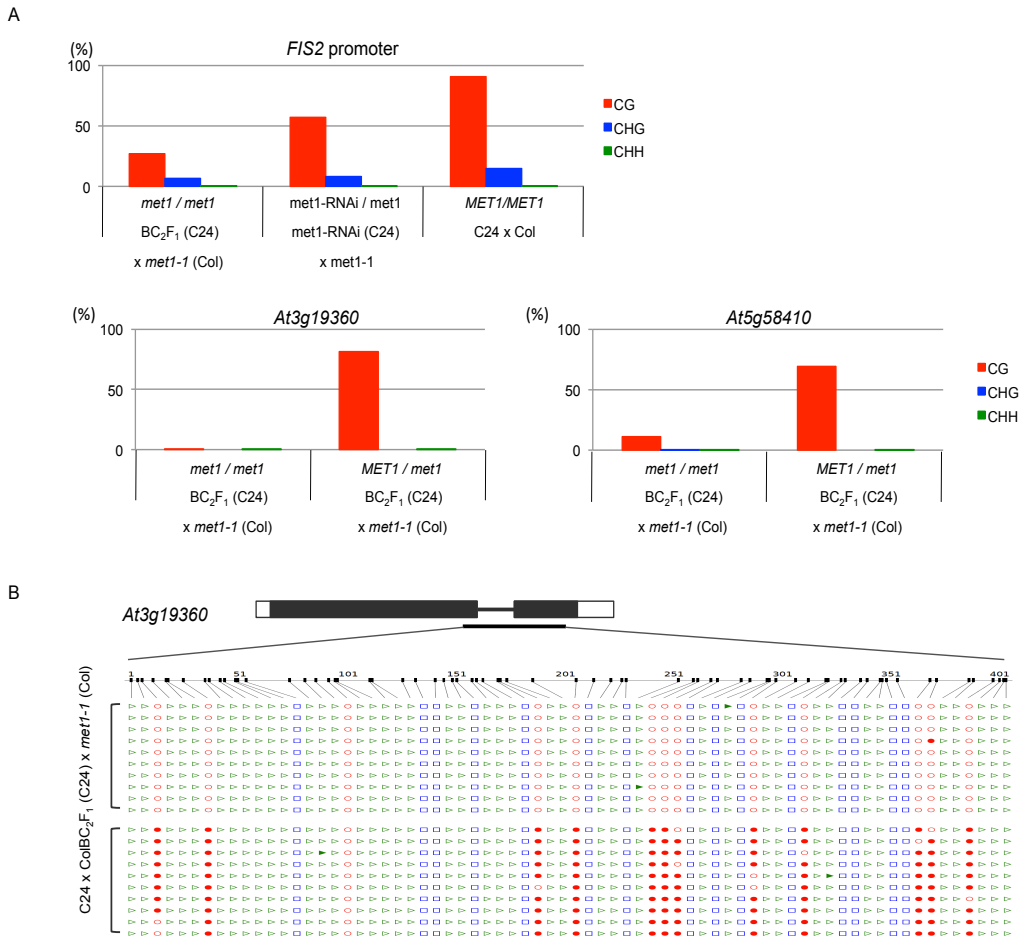

Figure S5. Validation of decrease in DNA methylation in *met1*-RNAi (C24) x *met1-1* or BC_2F_1 (C24) x *met1-1* hybrid by bisulfite-sequencing. (A) The percentage of DNA methylation in *FIS2* (Upper), At3g19630 (Bottom left), and At5g58410 (Bottom right) is shown in the bar graph. Ten clones from bisulfite-treated templates were sequenced. (B) DNA methylation pattern visualized by CyMATE (http://www.cymate.org/) in exon regions of At3g19630. Closed circles, triangles and squares represent methylated cytosine for CG, CHG, and CHH context, respectively. Open circles, triangles and squares represent non-methylated cytosine for CG, CHG, and CHH context, respectively.

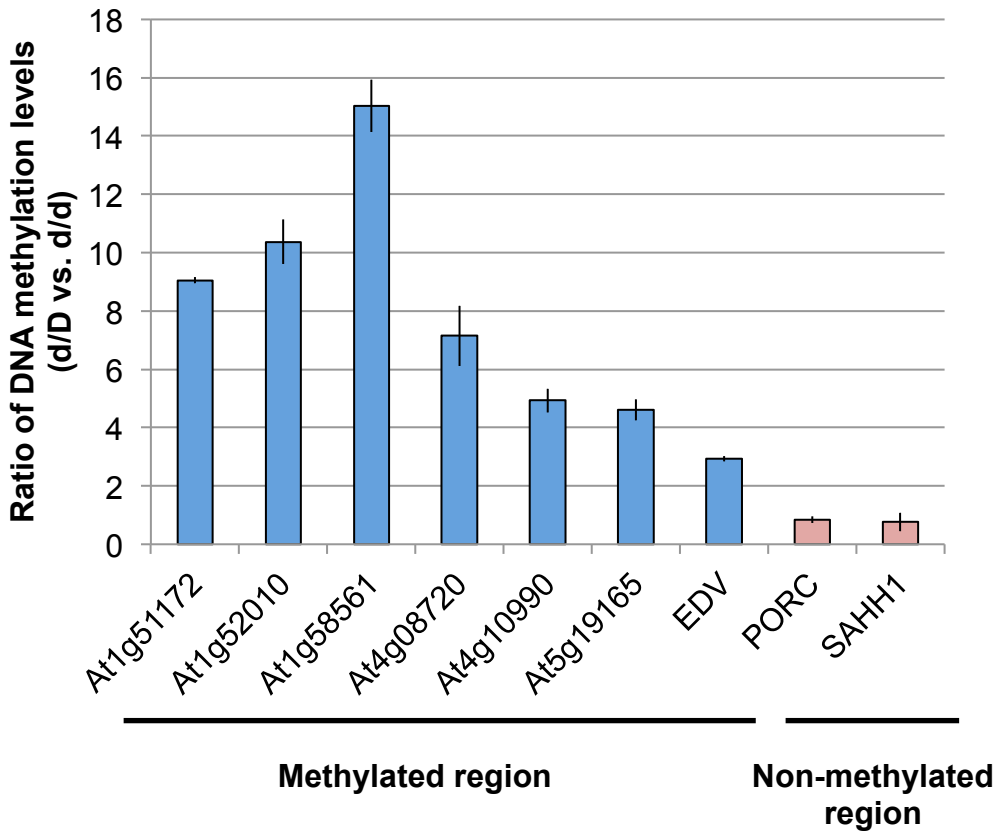

Figure S6. Ratio of DNA methylation levels in the heterozygous *ddm1* hybrids compared with the homozygous *ddm1* hybrids. At1g51172, At1g52010, At1g58561, At4g08720, At4g10990, At5g19165 and *EDV* are methylated in Col, and *PORC* and *SAHH1* have no DNA methylation.

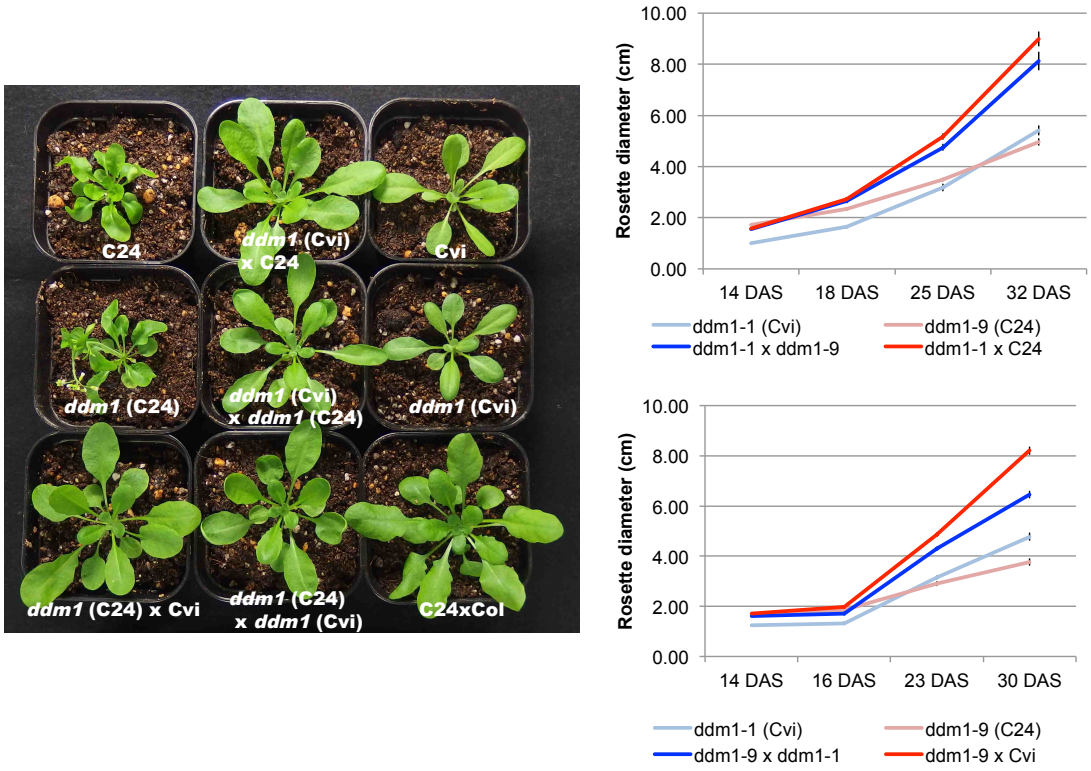

Figure S7. Phenotype of the *ddm1* mutant hybrid between C24 and Cvi background lines. Time course of rosette diameter is shown in right panel. Data represent mean values ± standard error obtained from more than twenty plants.

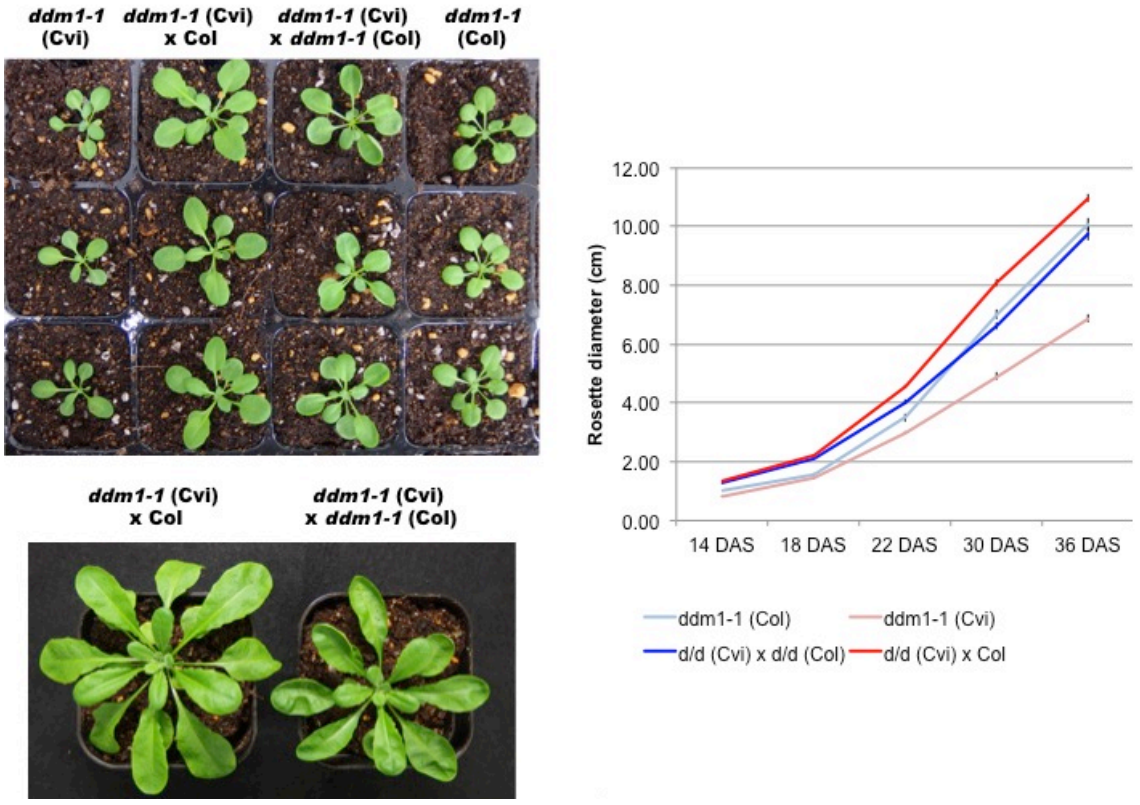

Figure S8. Phenotype of the *ddm1* mutant hybrid between Cvi and Col background lines at 21 DAS (Upper left) and 36 DAS (Bottom left). Time course of rosette diameter is shown in right panel. Data represent mean values ± standard error obtained from more than twenty plants.

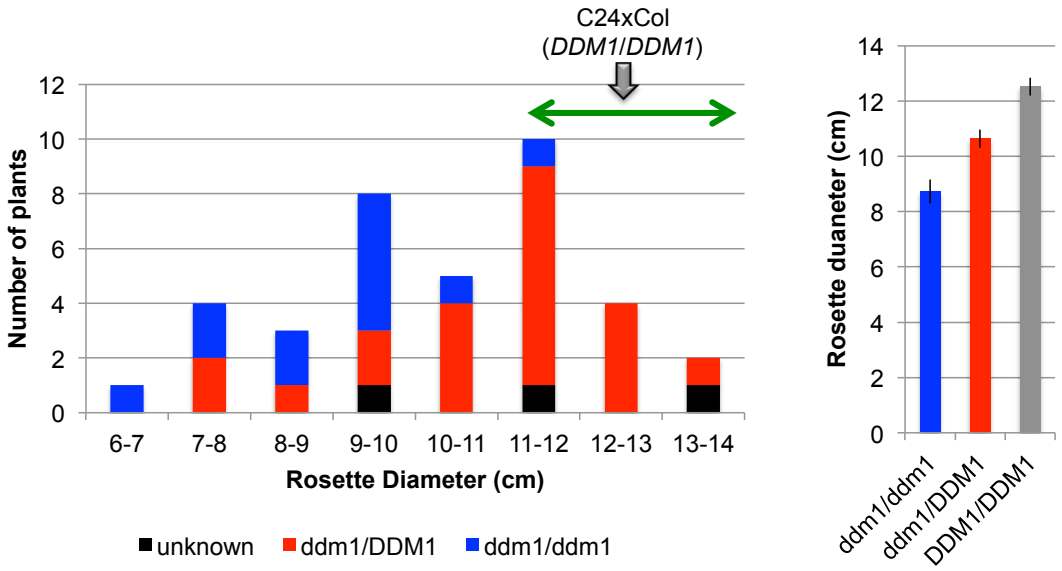

Figure S9. Rosette diameter (RD) in the hybrid between C24 (*ddm1*/*ddm1*) x Col (*DDM1*/*ddm1*) at 28 DAS. Frequency distribution of the RD for C24 (*ddm1*/*ddm1*) x Col (*DDM1*/*ddm1*) hybrids (Left panel). Rosette diameter of heterozygous and homozygous *ddm1* hybrids and C24 x Col wild type hybrid (*DDM1*/*DDM1*) at 28 DAS (Right panel). Unknown represents plants genotypes has not been determined.

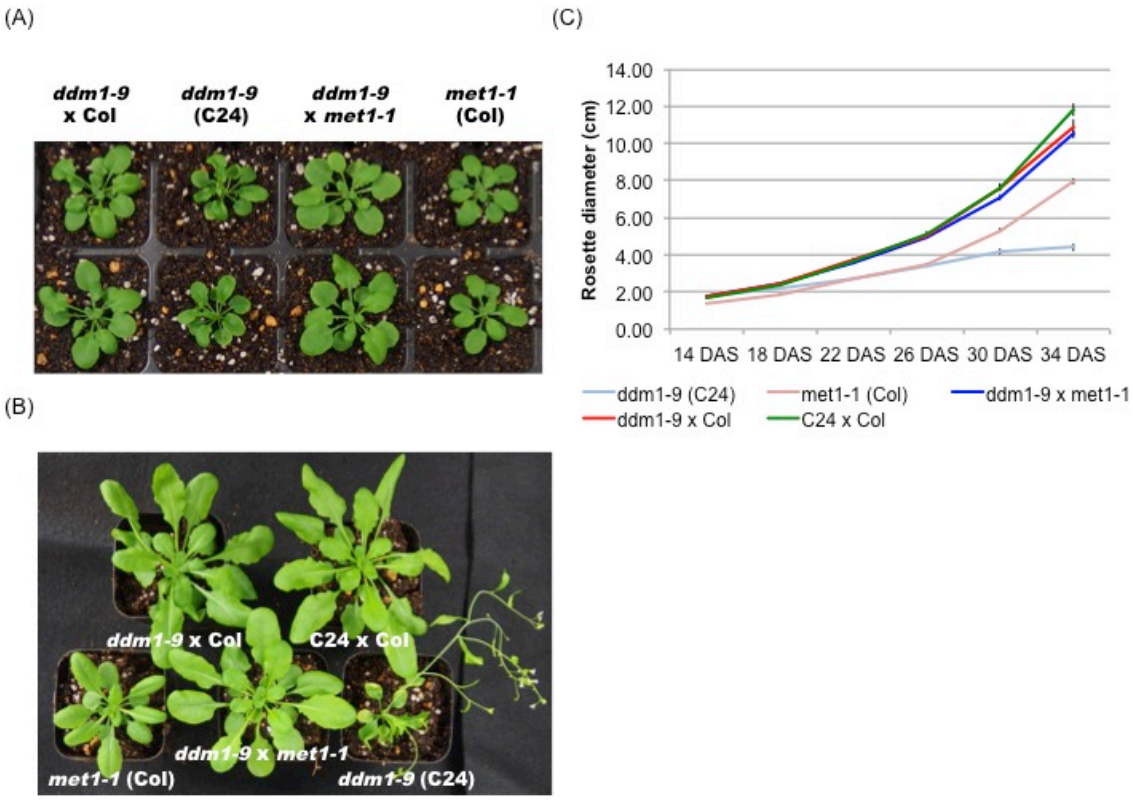

Figure S10. Phenotype of the hybrids between *ddm1-9* (C24) and *met1-1* (Col) mutant. Seedling of *ddm1-9* (C24) x *met1-1* (Col) hybrids at 21 (A) and 34 (B) DAS. (C) Time course of rosette diameter. Data represent mean values ± standard error obtained from more than twenty plants.

Table S1 Primer sequences for genotyping of mutants

Target	Primer sequences (5'-3')		
ddm1-1	ATTTGCTGATGACCAGGTCCT	CATAAACCAATCTCATGAGGC	CAPS: *Nsi* I
ddm1-9	AGATTTCAGTGATGAGAAGAGCAGC	GACCCTTCACTGGAAAAGCTTCAGC	Direct sequencing
met1-1	ACTTTGGCTTCCCTTCTCGA	CAGCCCCAGGCCTAGTTGGG	CAPS: *Hae* III

Table S2 Primer sequences for expression analysis

Target		Primer sequences (5'-3')	
RT-PCR			
MET1		TGCCAATGATTATCCTCTCCCATCG	TGTTTCATCGGTAGAAGTTCCAGTG
soloLTR		ATCAATTATTATGTCATGTTAAAACCGATTG	TGTTTCGAGTTTTATTCTCTCTAGTCTTCATT
AtSN1		AACGTGCTGTTGGCCCAGT	CTGGAAGTTCAAGCCCAAAG
GAP		CACTTGAAGGGTGGTGCCAAG	CCTGTTGTCGCCAACGAAGTC
RT-qPCR			
U1	At1g27730	TTCTCGCTCGCGACAACCGTCAGCC	CCCGCACCTTCGGAGTTGGACACGC
U2	At1g54040	AACTGTATCCTGCTTAGGCGTGCGC	ATTGCACAGCATTAGACTCATAGTC
U3	At4g03060	TGAATCATAATAATCTCTCCGAGAG	ATTATCATTAACACCGGTATCAGCG
U4	At4g29200	GCTCTTTGGACAGATTCGTGCTCGG	TCTCTATCAAATGGTGTCCATGGCC
U5	At4g16860	AAGCTTCAGTGGGGTAGATGTTCGC	TTCTGATCCTCTGGTTTGTCCTCGC
U6	At1g61500	CTCGTATTTATCGTTCATAATCGTG	ATGACCTTAAGATTTCCGCTATCTG
U7	At3g14210	ATGACCTTAAGATTTCCGCTATCTG	GGTATTAACCATCTTCCATAATCCG
U8	At5g56030	AGATCTTCCTCCGTGAACTCATCAG	AGACTCCCACACGTACTGCTCATCG
U9	At2g30790	GAGAAGGATTCAAAATCCAGATCCC	CCTAGCTCCTTTGAACCACCTCTTG
U11	At1g28370	ATGGCACCGA CAGTTAAAAC GGCGG	AGTTGGTTTT GGCTTTAGCT CCACG
U12	At2g26530	ATGGAAGTGA TGAGCTTGAC TGCCC	GTGATCTTCC TAGGCGTGCC TGGAG
U13	At4g20480	TGATGAGGGT GATGGAGCCT CCGCC	TTAAGGATGT CACGAGGGAC CTCTG
U14	At5g26030	GCAGGCAACG GCTTTATCAT CTGGG	GTTTCATCAT AAGAACAGTC TCCAG
U15	At1g31580	TGGCATCTTC TATAGTCTCT TCCAT	AACAGAAAGG GCACCTTCTG GGACG
U16	At5g15360	ATGATCAGTT GGAATTTTGA AGTGA	CAGATGCTGT CCACGAGCAA TCTAG
U17	At5g48540	TGGCTCTTGT ATGTAGCTGC AGAGC	TGCTGATATC TCCTCTACAT TGAGC
D1	At2g43570	CGCCTCTCAAAACTGTGGCTGCGCC	CCCTGTTTCTTGGGCTACGTGAGCG
D2	At3g57260	ACGGGATGCTAGGCGATACCTTGCC	ACCTTGACTTCAAGCCCTGCTCCAG
D3	At5g10760	CCATTCAAGTCAGCTCTCTGTTCCC	TCACTTCCGGTGTCGAAGACCAGCG
D4	At5g54610	TATTCTCTTATTCAAGCGGCTCCCG	CTCGTATTTATCGTTCATAATCGTG
D5	At2g24850	CCTCCGCCCATTCCAACTTCAGGAC	TCTCGGGGAGAAGATCGTATTTGCG
D6	At4g20110	GTCGAAGCACGACGGCTCGATAGCC	CCAAATGATTTATCGATTAACACCG
D7	At1g02340	CCAAATGATTTATCGATTAACACCG	ACTTGCTGTGAAAGATCAGGGCATG
D8	At2g14610	GTCTTTGTAGCTCTTGTAGGTGCTC	ACTTTGGCACATCCGAGTCTCACTG
D9	At2g45660	AGAATGCAACAAGCAGACAAGTGAC	TTGCTCAATCTGTTGCAGCTCCTCG
D10	At1g45145	ATGGCCGGTG AAGGAGAAGT GATTG	TTTGAATTCC TGAGCAACAG CTTGC
D11	At3g50770	GGCAACTCAA AAAGAGAAAC CTTCC	GATCTTACCG TCGCCGTCGC TGTCG

Table S3 Sequences of DNA oligo used for Northern blotting.

Target	Sequence (5'-3')
siRNA02	ATC GGC TGG CGG ACT GGT CAA C
siRNA1003	ATG CCA AGT TTG GCC TCA CGG TCT
miR171	GAT ATT GGC GCG GCT CAA TCA

Table S4 Primer sequences for DNA methylation analysis

Target	Primer sequences (5'-3')	
Chop-PCR		
AtSN1	AGGATTTATTTCAATCCACGAACCT	CGACTCCCATAAGTAACGAGTTG
actin	CTCATGAAGATTCTCACTGAG	ACAACAGATAGTTCAATTCCCA
Bisulfite sequencing		
FIS2	AYAATAATTAAGGTYYAATYGYATA	AAAAARAAATCATRRAAACAACAAR
At3g19630	GAGGTTGTGYATGAAGTTTGA	TCRATCCARTCTCCATATATTC
At5g58410	GTTGGTYTTGATATATAGAGGG	TTCTAACACTTCRRTCATCCTT
MeDIP-qPCR		
At1g51172	GAATCTGAAGCTCGCAGGTC	GCGAAGCGAAGGTAGTTGTC
At1g52010	ATGGTGAGACCGATGCTTCT	GAGAGGTTTCGCTCAAGGTG
At1g58561	ATCCAACAAAGGCAGAGGTG	GCAGCTAAGGCAAGTGGAAG
At4g08720	TCAAACCGATACCGTCTTCC	ATTGGACGGACAAGGAACAG
At4g10990	AGAAGGTGGCTCAAGTTGGA	GTTCCATGGCGAAATGAGTT
At5g19165	CGAAGCCATTTAAGCATATATCTGG	CGTGAGATAATTGGGAGGTTATTGT
EDV	TGGCATGCTAGGCTAGGYCATCCTC	GTGTATTCTCCTCCATTRTCGGTCC
PORC	GGCTTAGCGTCAGGATTGAATGGGC	TTTGCCAGCTTCCTCTTCAGATACG
SAHH1	GCTACTCTTTTGATTCATGAGGGTG	AGGGAACAAAAGAGTTCCATTTTGC

Table S5 Primer sequences for RNAi construct

Target	Primer sequences (5'-3')	
MET1	TCTGAACACCTGCCTCACAG	CCCATGGACGACCAAATATC