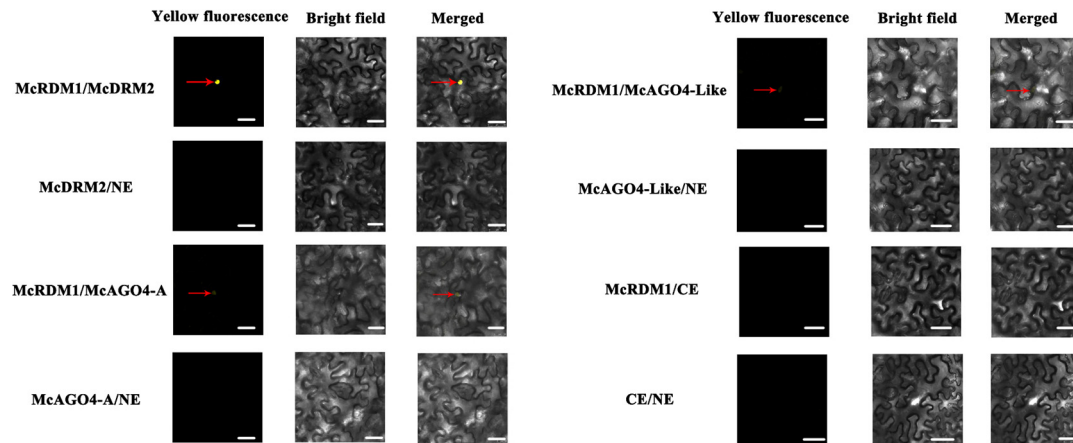
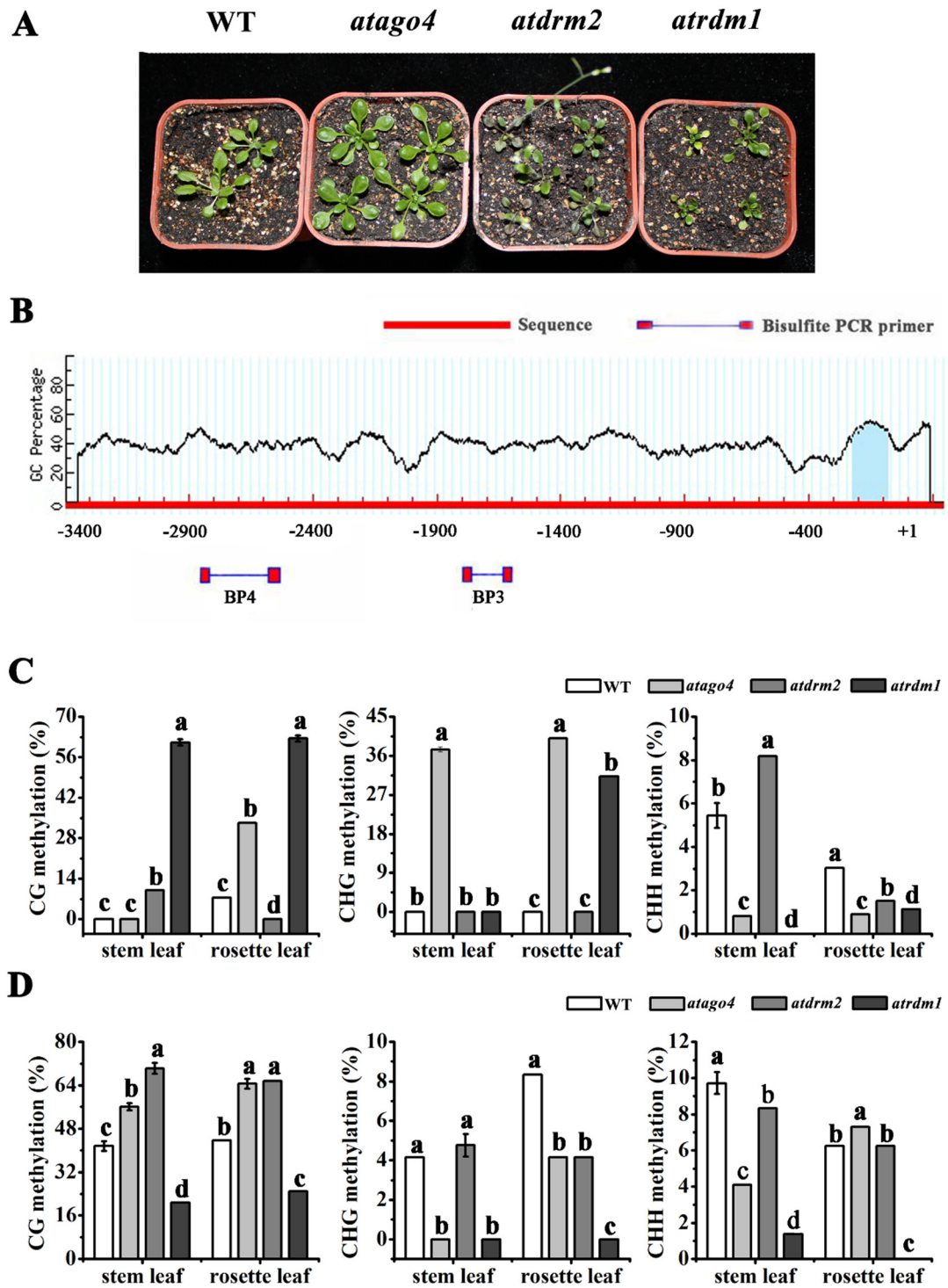


Supplementary Figure S1. Cloning and sequence characterization of *McCOP1-1* and *McCOP1-2*.

A. *McCOPI* nucleotide sequence alignment. B. Location of *McCOPI* coding sequences on chromosome 10. The sequence in the box is the 69-bp deletion in the *McCOPI-1* gene. Blue and green font represent the Real time (RT)-quantitative (q)PCR primers for *McCOPI-1* and *McCOPI-2*, respectively. Abbreviations: Md, *Malus x domestica* (AB668570.1); Rosa, *Rosa* spp. *hybrid cultivar* (AF394913.1).



Supplementary Figure S2. Interaction between McRDM1, McRDM2, and McAGO4. Bimolecular fluorescent complementation (BiFC) assay using *Nicotiana benthamiana*. Fusion constructs containing partial yellow fluorescent protein sequences and McRDM1/McDRM2, McRDM1/McAGO4-A and McRDM1/McAGO4-like were transiently co-expressed in *Nicotiana benthamiana* leaves. The yellow fluorescence represents protein interactions. **Scale bar=20 μ m.**



Supplementary Figure S3. *AtCOP1* promoter methylation level determined by bisulfite sequencing using different primers. A. The phenotype of WT, *atago4*, *atdrm2* and *atrdm1* seedlings. B. The position of BP3 and BP4 primers in the promoter sequence. C. *AtCOP1* promoter methylation level using BP3 primers. D. *AtCOP1* promoter methylation level using BP4 primers.

Error bars indicate the standard error of the mean \pm SE of three replicate measurements. Different letters above the bars indicate significantly different values ($p < 0.05$) calculated using one-way analysis of variance (ANOVA) followed by a Duncan's multiple range test.



Supplementary Figure S4. Sequence analysis of McAGO4-Like, McAGO4-A, McDRM2 and

McRDM1. A. Amino acid sequence alignment. B. Phylogenetic analysis of McCOP1 proteins from different plant species and functional domain analysis. The alignment was conducted with the **Mega10** program using ClustalX. The abbreviations used are as follows: Md, *Malus x domestica*; Pp, *Prunus persica*; Pm, *Prunus mume*; Fv, *Fragaria vesca* spp.; Vv, *Vitis vinifera*; At, *Arabidopsis thaliana*.

Supplementary Tables

Supplementary Table S1. Primer sequences used in this study

Primer	Oligonucleotide sequence 5' -> 3'
Cloning	
Q-McCOP1-F	GAAGTATTCGGATTTACGGTGGGGAC
Q-McCOP1-R	GACCTCCCAATTCTCGAAGGCCAAA
McCOP1-F	TCACGCACGCTTCACCCAGA
McCOP1-R	TGTAGCGATTCAAGACGGGGTT
McAGO4-A-F	GGCTTGTGGTTGAGCAGGTCTTAG
McAGO4-A-R	CGGCATCGAGGGATAAGAAACTGAAG
McAGO4-Like-F	CACGGCTGGATTTCAGAAGCGGTT
McAGO4-Like-R	GGTAACCATAGTAGGGCTCAAGGCTC
McDRM2-F	GGAGCTTGTAATCGCTGCGTGGGC
McDRM2-R	CCACAAGTAACCAGCCGACCGCAC
McRDM1-F	GTTTACAATGGATCCCACACG
McRDM1R	CCAAGCATCATAAAACAGTCC
Y1H	
YEMcAGO4-A-XhoI-F	AACTCGAGATGGAGCGCTTGAATCCCG
YEMcAGO4-A-NotI-R	TAGCGGCCGCTTAACAGAAGAACATGGAG
YEMcAGO4-Like-XhoI-F	CTCTCGAGATGGATTCGTTTGAGCCAGATG
YEMcAGO4-Like-NotI-R	TAGCGGCCGCTCAACAGAAGAACATG
YEMcDRM2-EcoRI-F	CGGAATTCATGGATGGTGAATACAGTAATG
YEMcDRM2-XhoI-R	TCTCGAGTCAATTGTTTCTTCCCATCATG
YEMcCOP1-EcoRI-F	ACGAATTCGACCTCCCAATTCTCG

YEMcCOP1-XhoI-R

ACCTCGAGGAAGTATTCGGATTTCAC

BiFC

McCOP1s-SalI-F

ACGC GTCGAC ATGGGAGAGAGCTCAATGG

McCOP1s-KpnI-R

CCGG GGTACC GGCTGCAAGTACGAGCAC

McMYB10-SalI-F

ACGC GTCGAC ATGGAGGGATATAACGAA

McMYB10-KpnI-R

CCGG GGTACC TTCTTCTTTTGAATGATTC

McAGO4-A-SalI-F

ACGC GTCGAC ATGGAGCGCTTGAATCCC

McAGO4-A-KpnI-R

CCGG GGTACC ACAGAAGAACATGGAGTTG

McAGO4-Like-SalI-F

ACGC GTCGAC ATGGATTTCGTTTGAGCCAG

McAGO4-Like-KpnI-R

CCGG GGTACC ACAGAAGAACATGGAACTG

McDRM2-SalI-F

ACGC GTCGAC ATGGATGGTGAATACAGT

McDRM2-KpnI-R

CCGG GGTACC ATTGTTTCTTCCCATCATGC

McRDM1-SalI-F

CCGC GGATCC ATGAAGAGGGCAGCTCCC

McRDM1-KpnI-R

CCGG GGTACC CGATTGCTTCGTAGCTGG

BPS

BP1-F

TTGTTTTTTTGATTGATGATTAAAT

BP1-R

TATACATATTTACTCTATTCCTAACTCCTC

BP2-F

TGTGTTTTTGATAAATGTTTTTTTT

BP2-R

AATCTACAATACCTTCACAATCTATTTAAA

BP3-F

ATAAGATTTATTTTGATATTTTGAAA

BP3-R

TACTATTAATCCTCTACCACAAAAC

BP4-F

ATTTTATTGAAAATTGGA AAA

BP4-R

CATATAAAAATTAAAACAACACACC

qRT-PCR

qMc/MdCOP1-1-F	ATTTCAACTCACCTCCGCATC
qMc/MdCOP1-1-R	TCAATTTCCGACTAAGAAGTTCAAA
qMc/MdCOP1-2-F	CTTGCTCGACAAGGGCTGCGAGATT
qMc/MdCOP1-2-R	GCCTCTCAACGGCAGTAATGTCCTCC
qMc/MdMYB10-F	GGACCAGCAGCAGGAAACTA
qMc/MdMYB10-R	ACAACCCTCCATTAATGCCGAC
qMc/MdAGO4-A-F	CTCCACCACCACCCATTATTCC
qMc/MdAGO4-A-R	TGCCCTTTAGTTCCATTCCCAC
qMc/MdAGO4-Like-F	CTATGATGGGGAGAAGAGCCTG
qMc/MdAGO4-Like-R	ACAGTTTCCATTGTTCTGCTTG
qMc/MdDRM2-F	TTTTTTGCGGTTGAAGAGAAGCC
qMc/MdDRM2-R	TGAACTGTCTCATCATCATCCCCT
qMc/MdRDM1-F	ACCTCACCAATCTTCTCCTAAAACA
qMc/MdRDM1-R	TGGCTTCGGCTTTACAAGGATG
qMc/MdCHS-F	GGAGACAACTGGAGAAGGACTGGAA
qMc/MdCHS-R	CGACATTGATACTGGTGTCTTCA
qMc/MdF3'H-F	ACGATGGCGGATGTTACGG
qMc/MdF3'H-R	GCTTTGACCCTGCACTTGCT
qMc/MdDFR-F	GATAGGGTTTGAGTTCAAGTA
qMc/MdDFR-R	TCTCCTCAGCAGCCTCAGTTTTCT
qMc/MdANS-F	GGAGAAGATCATCCTTAAGCCA
qMc/MdANS-R	CTAAGATATATCATACCAACTATGCC
qMc/MdUFGT-F	CCACCGCCCTTCCAAACACTCT
qMc/MdUFGT-R	CACCCTTATGTTACGCGGCATGT

qMc18S-F	ACACGGGGAGGTAGTGACAA
qMc18S-R	CCTCCAATGGATCCTCGTTA
qAtCHS-F	GCCGAGAACAATCGTGGAGCA
qAtCHS-R	AGTCAAGGTGGGTGTCAGAGG
qAtF3'H -F	TGGTAAAAAAGGAGGATTCAT
qAtF3'H-R	CCGTGAGTAGTCTCTGTTTCT
qAtDFR-F	TGGTGTCGGTCCATTCAT
qAtDFR-R	GAGAGAGCGCGGTGATAAGG
qAtUFGT-F	TGGAGGTGGCGGTTGAA
qAtUFGT-R	CTTTGCCGCGAGAACCA
qAtANS-F	AATGGAGCGTGTCAAGAAAGC
qAtANS-R	TTGAATCTTTCCAGTGGCTTG
qAtAGO4-F	ATTGTTACTCAATGCATGGCTC
qAtAGO4-R	GTGTCCGAACAGATGCTCTATA
qAtDRM2-F	ATGGTGATTTGGAATAACGA
qAtDRM2-R	TCAAGATCCTCTCATCCTCG
qAtRDM1-F	CAATGACAATGGAACTACGACC
qAtRDM1-R	ATACATCTCTGCTCTTCTCAGC
qAtCOP1-F	GTTGCTTGAGTTGGAATAAGCA
qAtCOP1-R	AAACTTTAACCTTGCAGTCGTC
qAtMYB75-F	TTCCTGTAAGAGCTGGGCTA
qAtMYB75-R	TTAAAGACCACCTATTCCCT
qAtACTIN-F	CTCTCCCGCTATGTATGTGCGCCA
qAtACTIN-R	GTGAGACACACCATCACCAG

Supplementary Table S2. Correlation analysis between the *McCOP1* promoter methylation level and *McCOP1* RNA expression profiles in ‘Radiant’ leaves.

Correlation coefficient values		McCOP1 expression levels		CG methylation			CHG methylation			CHH methylation		
		McCOP 1-1	McCOP 1-2	BP1	BP2	BP1+ BP2	BP1	BP2	BP1+ BP2	BP1	BP2	BP1+ BP2
McCOP1s expression level	McCOP1-1	1	0.95**	-0.24	-0.48**	-0.48**	0.11	-0.43*	-0.31	0.27	-0.70**	-0.72**
	McCOP1-2	0.95**	1	-0.27	-0.48**	0.49**	0.11	-0.42*	-0.31	0.21	-0.70**	-0.72**
CG methylation	BP1	-0.24	-0.27	1	0.26	0.29	-0.63**	-0.23	-0.48**	0.48**	0.23	0.31
	BP2	-0.48**	-0.48**	0.26	1	1.00**	-0.18	0.47**	0.32	-0.53**	0.88**	0.87**
	BP1+BP2	-0.48**	-0.49**	0.29	1.00**	1	-0.2	0.46**	0.3	-0.51**	0.88**	0.88**
CHG methylation	BP1	0.11	0.11	-0.63**	-0.18	-0.2	1	0.09	0.53**	-0.1	-0.21	-0.24
	BP2	-0.43*	-0.42*	-0.23	0.47**	0.46**	0.09	1	0.89**	-0.78**	0.73**	0.69**
	BP1+BP2	-0.31	-0.31	-0.48**	0.32	0.3	0.53**	0.89**	1	-0.71**	0.53**	0.48**
CHH methylation	BP1	0.27	0.21	0.48**	0.53**	-0.51**	-0.1	-0.78**	-0.71**	1	-0.59**	-0.51**
	BP2	-0.70**	-0.70**	0.23	0.88**	0.88**	-0.21	0.73**	0.53**	-0.59**	1	1.00**
	BP1+BP2	-0.72**	-0.72**	0.31	0.87**	0.88**	-0.24	0.69**	0.48**	-0.51**	1.00**	1

* p<0.05 ** p<0.01