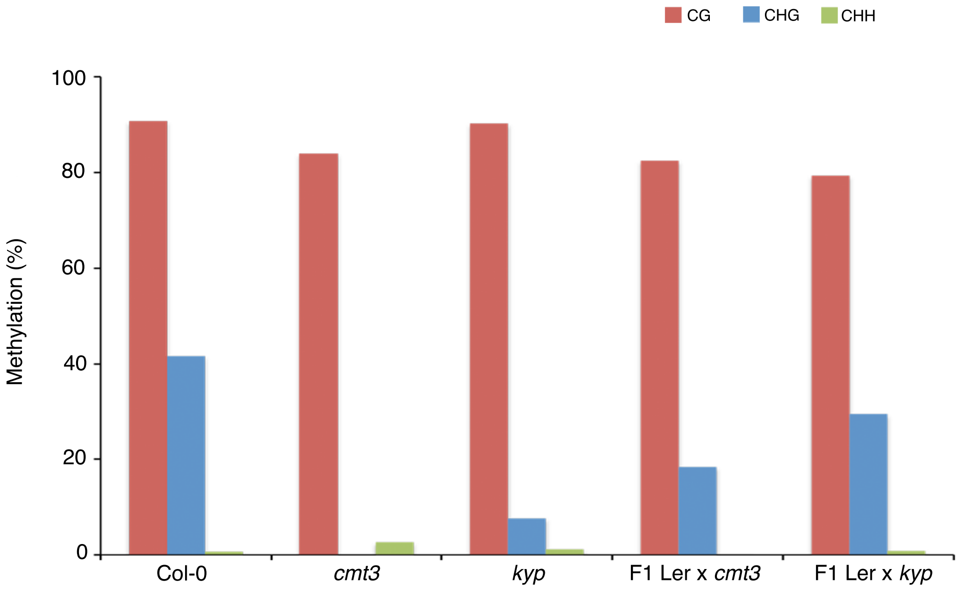
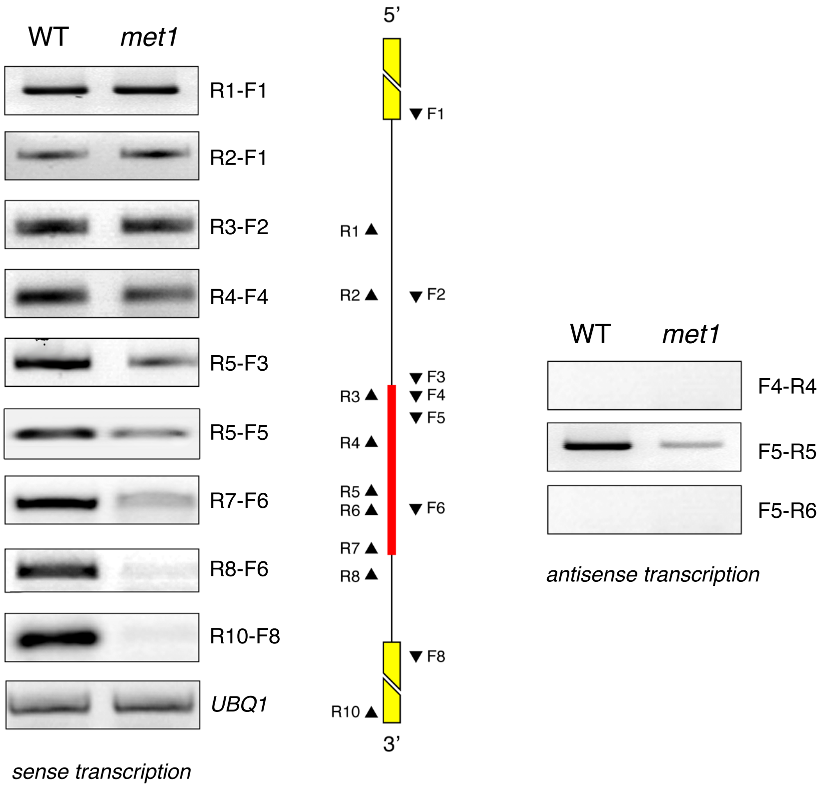
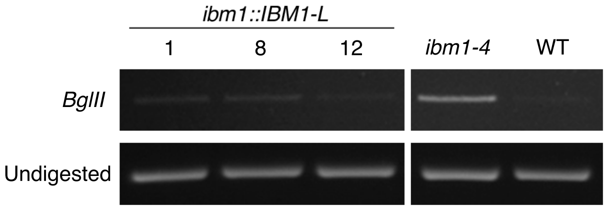


Supplementary Figure S1. Bisulfite sequencing analysis of cytosine methylation at the methylated zone of the large *IBM1* intron in wild-type, *cmt3* and *kyp* plants, and of the *cmt3*-derived and the *kyp*-derived alleles in Ler x *cmt3* and Ler x *kyp* F1 hybrids, respectively.

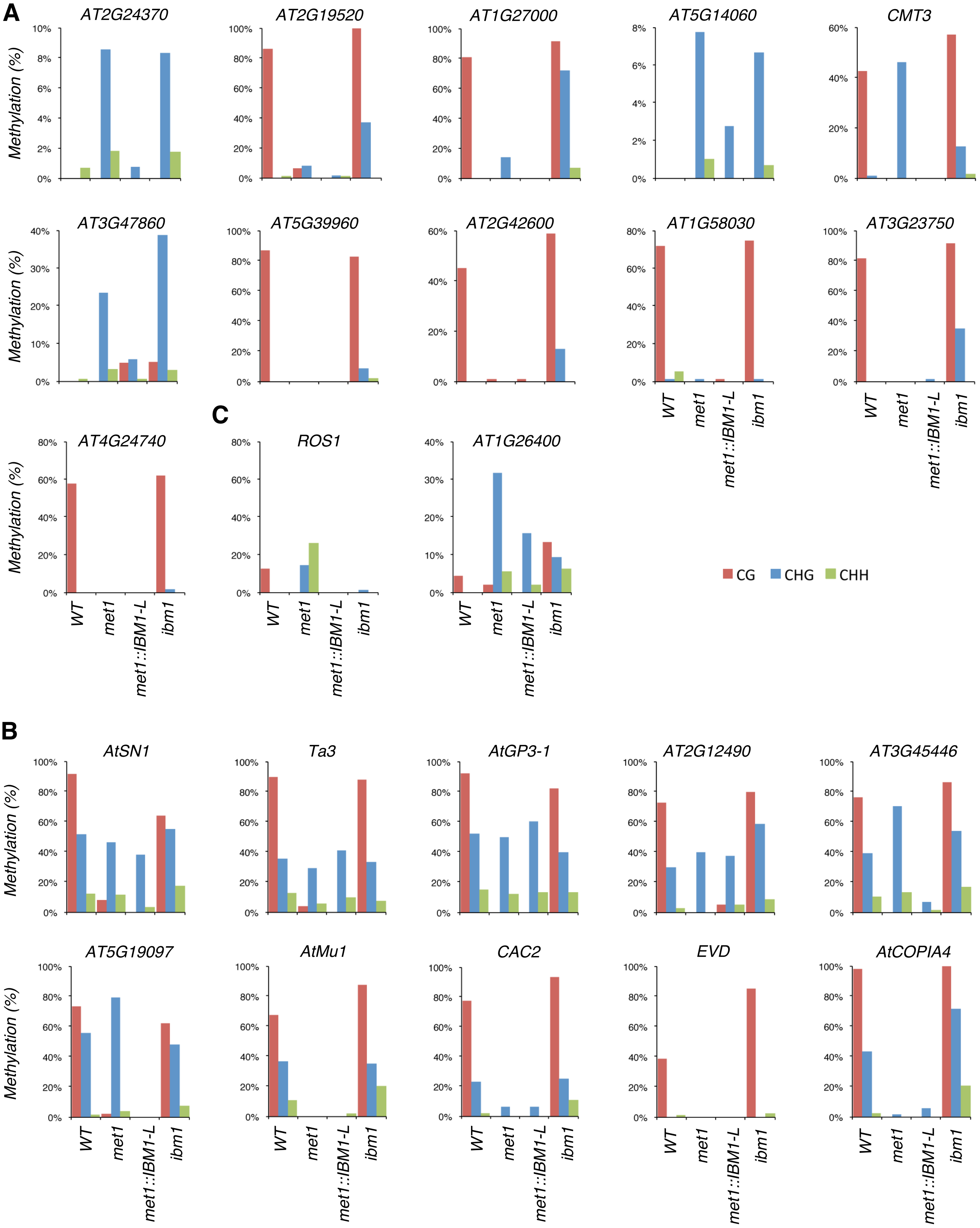
Proportions of methylated cytosines at CG (red), CHG (blue) and CHH (green) sites are indicated as percentages.



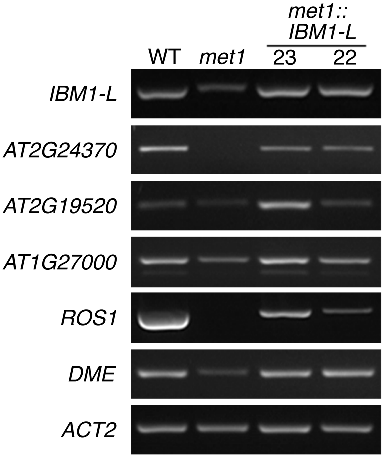
Supplementary Figure S2. RT-PCR analysis of sense (left panel) and antisense (right) *IBM1-L* transcription in wild-type and *met1-3* plants, using primer sets designed along the length of the large intron of the *IBM1* gene (middle). Primer positions, intron, exons and the methylated intronic region are indicated by black triangles, a black line, yellow boxes and a red bar, respectively. The amplification of *UBQ1* was used to normalize the RNA template levels.



Supplementary Figure S3. CHG methylation at the *BNS* locus in 3 independent *ibm1::IBM1-L* lines and in *ibm1* and wild-type plants. DNA methylation was analyzed by restriction digestion with the methylation-sensitive enzyme *BglII* followed by PCR with BNS-F2/R3 primers (Supplementary Table 1).

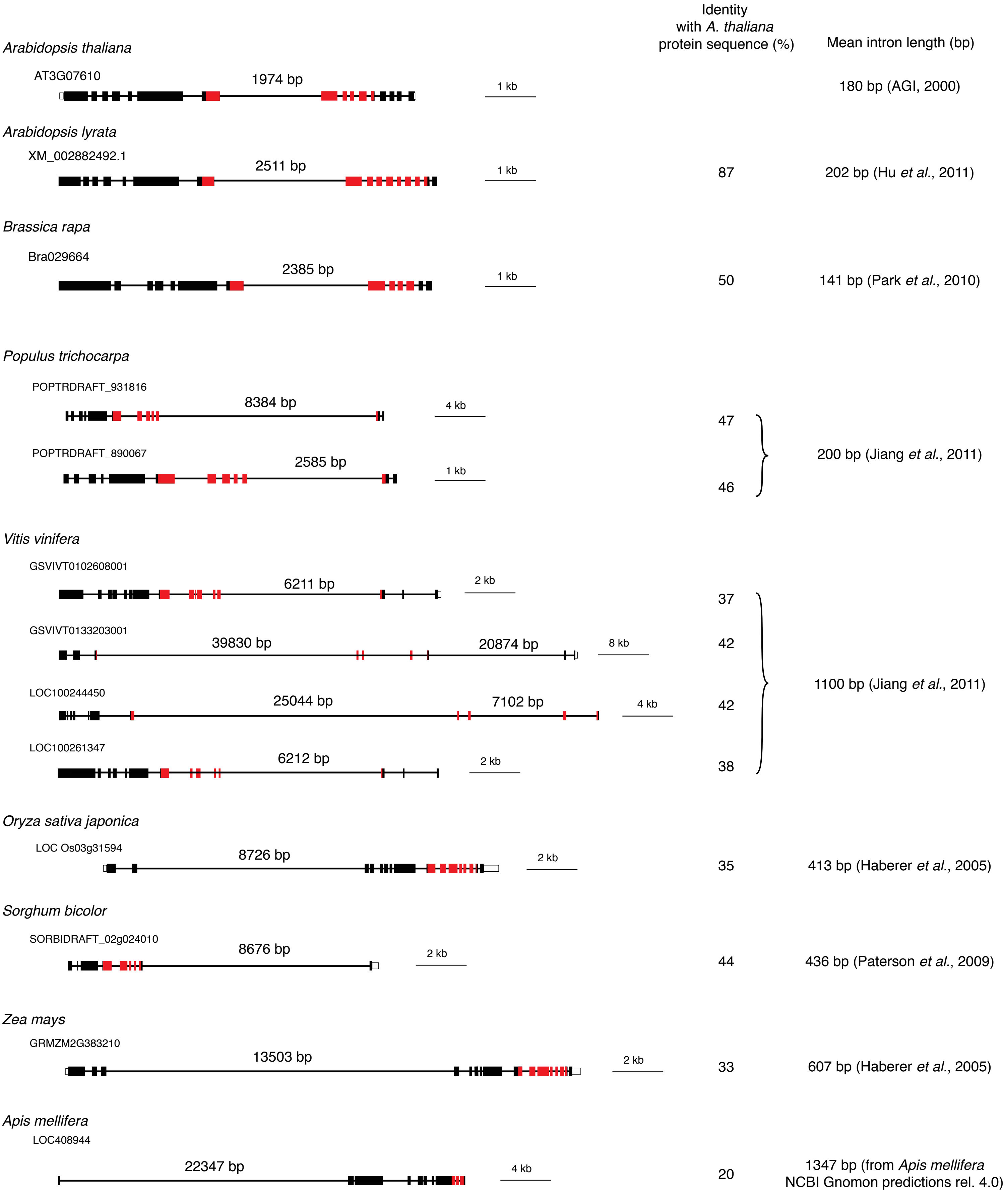


Supplementary Figure S4. Bisulfite sequencing analysis of the DNA methylation patterns at eleven genes (**A**), ten transposable elements (**B**) and at the *ROS1* gene and the *AT1G26400* ROS1 target locus (**C**), in wild-type, *met1*, *met1::IBM1-L* and *ibm1* plants. Proportions of methylated cytosines at CG (red), CHG (blue) and CHH (green) sites are indicated as percentages.

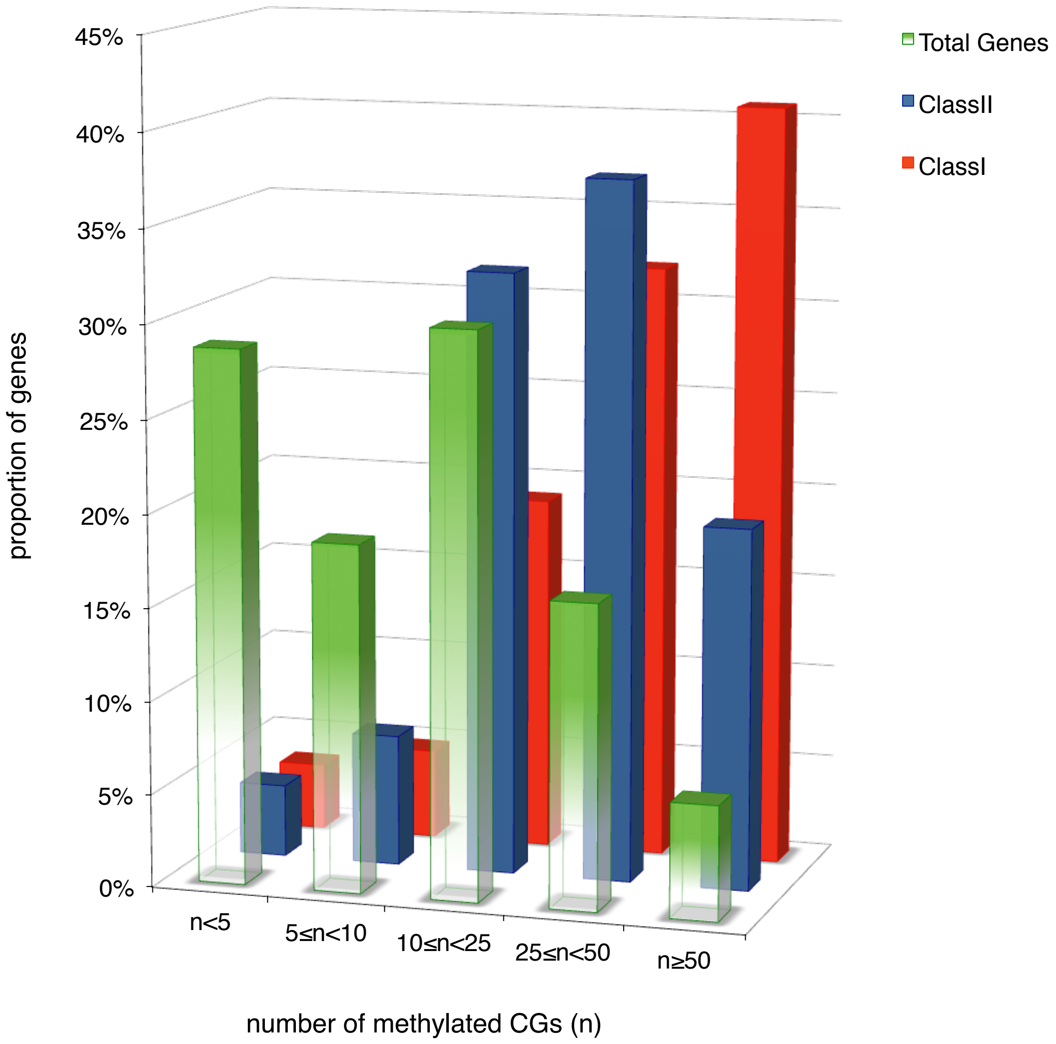


Supplementary Figure S5. Transcription analysis in 2 independent *met1::IBM1-L* lines. Representative images of RT-PCR analyses at *IBM1-L, AT2G24370*, *AT2G19520* and *AT1G27000, ROS1* and *DME* genes*.*

Supplementary Figure S6. Abnormal flower phenotypes observed in some *met1-3* lines. Images of a whole inflorescence shoot (A) and magnification of two abnormal siliques (B & C).



Supplementary Figure S7. Orthologs of the *A. thaliana IBM1* gene containing a large intron.
Boxes represent exons, with coding regions in black and untranslated regions in white. The region encoding the jmjC domain is shown in red (Saze *et al*, 2008). Length of the large introns and scale bars are indicated for each gene. The mean length of introns in each organism and the percentage of identity of each orthologous protein with Arabidopsis IBM1 protein are indicated.
Orthologous genes were identified by blastp of the Arabidopsis IBM1 protein sequence against non-redundant protein sequences of the NCBI database (http://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE=Proteins). Additional genes annotated as orthologs of the *IBM1* gene in the Gramene database were selected (http://www.gramene.org/).
The percentage of identity of each orthologous protein with the Arabidopsis IBM1 protein sequence were determined by alignment of orthologous protein sequences using the ClustalW2 program (http://www.ebi.ac.uk/Tools/msa/clustalw2/).



Supplementary Figure S8. Proportion of genes with the indicated number of methylated CG dinucleotides (n). Shown are Class I and Class II genes displaying DNA hypermethylation in the *ibm1-4* mutant (Miura et al, 2009) and total genes. The number of methylated CG dinucleotides was extracted from previously published datasets (Lister et al, 2008).

Locus	Primer	Sequence (5'-3')	Methods
18S rRNA	18S-F2	TCCTATTGTGTTGGCTTCGG	RT-PCR
	18S-R	CACGTAGCTAGTTAGCAGGCTG	
ACT2 (AT3G18780)	ACT2-F[1]	CTAAGCTCTCAAGATCAAAGGC	RT-PCR
	ACT2-R[1]	AACATTGCAAAGAGTTTCAAGG	
AT1G26400	At1g26400-RT-F1	GATCTTAGCTTCATCCACGTTCAA	RT-PCR, ChIP
	At1g26400-RT-R1	CGTCGACTCCAGGAGAATTT	
	At1g26400-BS-F	CTTAAACTACRCTTTTAATACTTAACTAAT	Bisulfite sequencing
	At1g26400-BS-R	GGGGAATTTAAAGAGATTGATGGATGTTAAAG	
AT1G27000	At1g27000-F	TGTGAATTCTGCTGTTTTGTTG	RT-PCR
	At1g27000-R	ACAACCACATCACGTTCCAA	
	AT1G27000-BS-F	CAAATTATRCAATRATTCCAAATCCATCTCAAA	Bisulfite sequencing, ChIP (with AT1G27000-BS-Fbis/R)
	AT1G27000-BS-Fbis	CATAACCACAACCACATCACRTTCCAAAAC	
	AT1G27000-BS-R	TTGAAAAGAGATTTYAGTGTTGTAAGGGAAT	
AT1G58030	AT1G58030-F	ATTTACAAAGGCCGTGGACA	RT-PCR, ChIP
	AT1G58030-R	TGTATCGGTGTGGCTGCTTA	
	AT1G58030-BS-F	CCCRTTTRTTCCCCTCCTACCTATCATCT	Bisulfite sequencing
	AT1G58030-BS-R	GATTTGTGTTAYATATATAAYAAAAGAGATG	
	AT1G58030-BS-Fbis	CCTACCTATCATCTRCATTCTCATCAACAT	
AT2G12490	copia66_F	GTGCCCCTGTACCCCTGGAT	RT-PCR
	copia66_R	CTGATTTGACTAGAACCGAAGAA	
	AT2G12490-BS-F	CAACACAACTCRATCAARCTTCAATTC	Bisulfite sequencing
	AT2G12490-BS-Fbis	ATCRATCAARAACATAATCAAACAAAA	
	AT2G12490-BS-R	TGAAGGTGATYAAAYGGAAGTAAGT	
AT2G19520	At2g19520-F	AAACAAGGGAACTTAGAAGCAA	RT-PCR
	At2g19520-R	TCTCTTAACCCACTGACACTATCTTG	
	AT2G19520-BS-F	TATRAARTATATCTCTTAACCCACT	Bisulfite sequencing
	AT2G19520-BS-Fbis	CTCTTAACCCACTRACACTATCTTA	
	AT2G19520-BS-R	GGGAAYTTAGAAGYAAGTAAAATGAGAAAGT	
AT2G24370	AT2G24370_F1	TGCGGATGTTTAGTCTACGAGTTC	RT-PCR, ChIP
	AT2G24370_R1	CATTGGTGGTTTTGCTGTTATCA	
	AT2G24370-F	ATTTRTACAATTTTAACACTTTCTCCACAA	Bisulfite sequencing
	AT2G24370-Fbis	ACACTCTATTRCATCTCCTTATACTAC	
	AT2G24370-R	ACTAGAGAAAGGAACTTTGGTTGATTTA	
AT2G42600	AT2G42600-F	AAAACCGAAGAGGTTGCAGA	RT-PCR, ChIP
	AT2G42600-R	ACCCGATCATGACTTCTTGC	
	AT2G42600-BS-F	CCTCRTCCAACRRTCCCACCTCTTCC	Bisulfite sequencing
	AT2G42600-BS-R	GAATGGTYGGAGGATAAAAGAYAGGAATGG	
	AT2G42600-BS-Fbis	CTCCRTATTCTTTTRCCACCTTCAC	
AT3G23750	AT3G23750-F	TGGATGTGTATGCATTTGGTG	RT-PCR, ChIP
	AT3G23750-R	ATGTCGGGTCTTTGTTGAGG	
	AT3G23750-BS-F	TTCACATCRATTCCRAAACTCTCTTC	Bisulfite sequencing
	AT3G23750-BS-R	ATTGGTTGYAYTGGATATTGATGTTATA	
	AT3G23750-BS-Rbis	GGAAGAGTAAYGAYGAAAGTGGATGTGTATG	
AT3G45446	AT3G45446-F	CCATTGTACTCCCAACACCA	RT-PCR, ChIP
	AT3G45446-R	TGAGAATTATGGCAACAAGGTG	
	AT3G45446-BS-F	TACTCCCAACACCATATCAATACCTT	Bisulfite sequencing
	AT3G45446-BS-R	GTGGATYAGAAAGGTGAGAATTATGG	
	AT3G45446-BS-Fbis	CCATCCACATTAATTTTTCTCCCATC	
AT3G47860	AT3G47860-F	TCAGAAGAGTGTTTTGATTCTGGA	RT-PCR, ChIP
	AT3G47860-R	TTGGCACAATTTGGCTATGA	
	AT3G47860-BS-F	CTCTTRCACTRATCTCTTATATAAACCTAAT	Bisulfite sequencing
	AT3G47860-BS-R	AYTTAAGATYYGATGTGGGATAAAAT	
	AT3G47860-BS-Rbis	GTAYTTTTGGTTTYTYTGTGGAGTGTATG	
AT4G24740	AT4G24740-F	TGGTCAAGTGCTAGAATGTTGG	RT-PCR, ChIP
	AT4G24740-R	ATGGTTACGATAGTCAAACCAGTTC	
	AT4G24740-BS-F	ACTACACACATRCTACACATTCCAA	Bisulfite sequencing
	AT4G24740-BS-R	GTTGGGATAGGGAGAGGAAGGAAATGGTGG	
	AT4G24740-BS-Rbis	GTGAGGYTGYTATGATTGAAATTGAAATG	

AT5G14060	AT5G14060-F	GCAATGGAGTGAATGTGCAG	RT-PCR
	AT5G14060-R	CAACAACAACAACAACAATGGA	
	AT5G14060-BS-F	TCTTRACACATTCTTARCATTAAACTAC	Bisulfite sequencing, ChIP (with AT5G14060-BS-F/Rbis)
	AT5G14060-BS-R	TTTGATAGATTGTTTYTTTTGTGAGGGT	
	AT5G14060-BS-Rbis	GGGTYATATGTGGTATTGGTTAAAGGG	
AT5G19097	AT5G19097-F	CGAAGCCACAACATTTCCTT	RT-PCR, ChIP
	AT5G19097-R	CAGCCACTGCGTCTTTTACA	
	AT5G19097-BS-F	CTRAARCATCAATCCACAAATCATTCAT	Bisulfite sequencing
	AT5G19097-BS-R	GAAAGAATYTTTTAAAYTGAGAGATTTAGG	
	AT5G19097-BS-Fbis	CTTTCRAARCCACAACATTTCCTT	
AT5G39960	AT5G39960-F	GAGGGAAGAGGACGTATGGA	RT-PCR, ChIP
	AT5G39960-R	TAGGAGTCCCGCCTAAATCA	
	AT5G39960-BS-F	CTRTTTCCRCTTCCACCACCACCT	Bisulfite sequencing
	AT5G39960-BS-R	GGAAGAGGAYGTATGGAAGTAATGAAAGAAG	
	AT5G39960-BS-Fbis	TCCCRCCTAAATCAAAATCTTCCTTCAAT	
AtCOPIA4 (AT4G16870)	AtCOPIA4-F[2] (JP3067)	CTTGTTTGTCTTCCCCGTGT	RT-PCR, ChIP
	AtCOPIA4-R[2] (JP3087)	TGACGAAGAGCGTACCTGTG	
	AtCOPIA4-BS-R[3] (JP3100)	GGTTGTYTGTGTTTTTTATGGTTYAGATTTTATA	Bisulfite sequencing
	AtCOPIA4-BS-F[3] (JP3101)	ATAACTRAACCACARATTCARACCCATTTTCATTT	
AtGP3-1 (AT3G11970)	AtGP3-1-F	AAGCATTAATAGTACAAAGTTCCCC	RT-PCR
	AtGP3-1-R	TTCTCTTGGAAGTTGCAGAC	
	AtGP3-1_BS-F[4]	ATGYTAGTGTATYTTAAATAGTGTATYTTG	Bisulfite sequencing, ChIP (with AtGP3-1_BS-Fbis/R)
	AtGP3-1_BS-R[4]	AACRTTTACTTTCTTTACCTTTTTATATAA	
	AtGP3-1_BS-Fbis	GGTTYAGGATAGATTATTAAYGGGGGAA	
AtMu1 (AT4G08680)	AtMu1-F[5]	CCGAGAACTGGTTGTGGTTT	RT-PCR
	AtMu1-R[5]	GCTCTTGCTTTGGTGATGGT	
	AtMu1-BS-F1[6]	AATTTTATGGAATGAAGTTATATG	Bisulfite sequencing, ChIP (with AtMu1-BS-F1/Rbis)
	AtMu1-BS-R	AAATTTRAARCCTCTTTCTCATACA	
	AtMu1-BS-Rbis[6]	TTCTCATACARTRRCTTCAATTT	
AtSN1 (AT3G44000-AT3G44005)	ATS15[7]	ACCAACGTGTTGTTGGCCCAGTGGTAAATC	RT-PCR, ChIP
	ATSN1-F4[7]	AAAATAAGTGGTGGTTGTACAAGC	
	AtSN1-BS-F	CTCTCAAAACAAACCCCTTAAAC	Bisulfite sequencing
	AtSN1-BS-R	GTTGAGATGGTGTRTTGGAAAGG	
	AtSN1-BS-R1	GGAAGTTTGTATAGTTTAAARATAAG	
BNS (AT1G73177)	BNS-F2[8]	GCTAGAGGTTTTTAGTTCTCTG	*BNS* methylation analysis
	BNS-R3[8]	TTCCTTATGACATTTCAAGGTC	
CAC2 (AT1G35270 -AT1G35280)	CACTA2-RT-F	TTGGTCCGATAAGAGTTTCGT	RT-PCR
	CACTA2-RT-R	CGCAGGTTTCTTTCTTCAGC	
	CAC2-F	GCCTAAGTGTTGGCGGACTA	ChIP (with CAC2-bsR2)
	CAC2-bsF2[9]	CATATAAACCCCAAAATCAAATC	Bisulfite sequencing
	CAC2-bsR2[9]	ATGGAAAAGGAGAAGGAGGTAT	
	CAC2-bsR2bis	TYATTGATAGYAGTAGAGGATAG	
CMT3 (AT1G69770)	CMT3-MseI-F	ATGCCAAGGAATCAGTGGTC	RT-PCR
	CMT3-MseI-R	AACTTTTGAAATGGCGTTGTG	
	CMT3-R2	TAATTCCGCAGTTCCCACTT	ChIP (with CMT3-BS-Fbis)
	CMT3-BS-F	CCTAATTTTARTCAAAATTTRCTAAAAACATC	Bisulfite sequencing
	CMT3-BS-Fbis	TCAAAATTTRCTAAAAACATCAATACTTA	
	CMT3-BS-R	GGTGTATATGAAYATTGTAGAATATTTGAAG	
DME (AT5G04560)	DME-F	TGAGAGGAAGTTTTCCGCTC	RT-PCR
	DME-R	GTGTCGCTTCTGCTCTATGA	
EVD (AT5G17125)	EVD_RT_F[10]	GACCTGACATTTGTTTTGCG	RT-PCR
	EVD_RT_R[10]	GGTGAAGATATCCGCCAAC	
	EVD_TD	ACTCGTGAGTCCTCTTCAACGG	ChIP (with EVD-BS-R)
	EVD-BS-F[10]	ACATRATCTTATRCTCTRATACCAT	Bisulfite sequencing
	EVD-BS-R1[10]	GTAGAGGAYAAATGTTAATTYGTTGTTGG	
	EVD-BS-R2[10]	GTGYGAYAAGATYGATGTAGGTTATTG	

IBM1	IBM1-F8	ACAACAAGTCCAAAATGTTG	RT-PCR (*IBM1-L*)
(AT3G07610)	IBM1-R10	TAAACACTCGCTGACATTTTCAGG	
	IBM1-F9	TATGTAGTTTGCCTTTGAAG	RT-PCR (*IBM1-S*)
	IBM1-R11	GTTCTGAAATCATTATAGATGTGC	
	IBM1-F10	TGAGATCCGCAATGGAAAG	probe for Northern blot analysis
	IBM1-R12	CCAAACAATCAACAGCAAC	
	IBM1-F1	TCTGATGCGGTTAGTACCC	RT-PCR along the length of *IBM1* gene, ChIP (with IBM1-F5/R6)
	IBM1-R1	CCAAAAACCGAATGCCAGGCC	
	IBM1-R2	TAAGCAGAATGGATGAAGGC	
	IBM1-F2	AGCCTTCATCCATTCTGCTT	
	IBM1-R3	GCGTAATCTTTGCATTCAATGTG	
	IBM1-F3	CAGCATTTTATAAATGTTTGATTG	
	IBM1-F4	ACATTGAATGCAAAGATTACGC	
	IBM1-F5	TAAAGTGTTTGTGATTGTTCGA	
	IBM1-F6	ACTTCTTGATATTGTTCGGAATG	
	IBM1-R4	CATTATTGATACGACAGACG	
	IBM1-R5	GCGAAATTGATGTTGGTCATT	
	IBM1-R6	ATCATTCCGAACAATATCAAGA	
	IBM1-R7	TGGAAAGAGTCATTGAGGTAG	
	IBM1-R8	CACAAAACCAAAATCTACTAAATTAACTATT	
	IBM1_polyR1	TTAGTACTACTCTGTTTAACTTAGAGGTA	dCAPS analysis
	IBM1-BS-F	GTTAATYGTYGATATAAYTGGTGTAGTT	Bisulfite sequencing, methylation analysis by restriction digestion
	IBM1-BS-R	CACAAAACCAAAATCTACTAAATTAACTATT	
	IBM1-BS-Fbis	TAGATTTTATATGTTGYTGTTA	
ROS1	ROS1-F	AGAAGAAATTCCTACCATCA	RT-PCR
(AT2G36490)	ROS1-R	ACCGTTCTTCGAGGTAATTC	
	ROS1-R2	AGAGGATGCTCGTCTGGAAG	ChIP (with ROS1-F)
	ROS1_BS_F[11]	TAGAGGAGGYGTTTTTTG	Bisulfite sequencing
	ROS1_BS_Fbis[11]	GAGGYGTTTTTTGAGGAT	
	ROS1_BS_R[11]	CATTTTTAACCTAAAAACRAAAAAA	
Ta3	Ta3-middle-F[2] (JP1565)	GATTCTTACTGTAAAGAACATGGCATTGAGAGA	RT-PCR
(AT1G37110)	Ta3-middle-R[2] (JP1566)	TCCAAATTTCCTGAGGTGCTTGTAACC	
	Ta3-LTR-F[2] (JP1617)	TAGGGTTCTTAGTTGATCTTGTATTGAGCTC	ChIP
	Ta3-LTR-R[2] (JP1618)	TTTGCTCTCAAACTCTCAATTGAAGTTT	
	Ta3-BS-F (JP1615)[3]	GGTTTAATGTTGGTTTAGTGATATTYGGTTTAGT	Bisulfite sequencing
	Ta3-BS-Rbis (JP1616)[3]	AATCAAAAAACRAATAAACCTCRCTCTRATACCACTTATT	
	Ta3-BS-R	CCATTAAACACCTTTATCTCAACTCTA	
TUB8	TUB8-F[12]	ATAACCGTTTCAAATTCTCTCTCTC	ChIP
(AT5G23860)	TUB8-R[12]	TGCAAATCGTTCTCTCCTTG	
UBQ1	UBQ-FWD (U1)[13]	ACCGGCAAGACCATCACTCT	RT-PCR
(AT3G52590)	UBQ-Rev (U2)[13]	AGGCCTCAACTGGTTGCTGT	

Supplementary Table 1. List of primers.

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