Supplementary Table S1. Sequences used in the identification and phylogenetic analysis of DNMTs [30].

Protein name	Organism	Accession / annotation / location
MET1 family		
methyltransferase 1	***Arabidopsis thaliana***	NP_199727 (GenBank)
DNA methyltransferase 2	***A. thaliana***	NP_193150 (GenBank)
DNA methyltransferase type 1	***Nicotiana tabacum***	BAF36443 (GenBank)
cytosine-5 DNA methyltransferase	***Oryza sativa***	DAA01513 (GenBank)
DNA methyl transferase 1	***Zea mays***	NP_001105186 (GenBank)
putative methyltransferase 1, partial	***Pinus sylvestris***	AWH12136 (GenBank)
putative methyltransferase 1-2, partial	***P. sylvestris***	AWH12137 (GenBank)
putative methyltransferase 1-1	***Pinus taeda***	PITA_000005661 (ConGenIE)
putative methyltransferase 1-1	***Picea abies***	MA_88843g0010 (ConGenIE)
putative methyltransferase 1-2	***P. abies***	MA_10436985g0010 (ConGenIE)
putative methyltransferase 1-3	***P. abies***	MA_10433746g0010 (ConGenIE)
CMT family		
chromomethylase 1	***A. thaliana***	NP_565245 (GenBank)
chromomethylase CMT2	***A. thaliana***	AAK69757 (GenBank)
chromomethylase 3	***A. thaliana***	AAK71870 (GenBank)
chromomethylase-like protein	***N. tabacum***	BAC53936 (GenBank)
DNA cytosine methyltransferase MET2a	***Z. mays***	AAK11516 (GenBank)
DNA methyltransferase 105	***Z. mays***	AAM28227 (GenBank)
putative chromomethylase, partial	***P. sylvestris***	AWH12138 (GenBank)
putative chromomethylase	***P. taeda***	PITA_000002248 (ConGenIE)
putative chromomethylase	***P. abies***	MA_173651 (ConGenIE)
DRM family		
DRM 1	***A. thaliana***	NP_197042 (GenBank)
DRM 2	***A. thaliana***	NP_196966 (GenBank)
DNA methyltransferase	***N. tabacum***	BAC67060 (GenBank)
DNA methyltransferase DMT106	***Z. mays***	AAM93211 (GenBank)
DNA cytosine methyltransferase Zmet3	***Z. mays***	AAF68437 (GenBank)
putative DRM-1, partial	***P. sylvestris***	AWH12139 (GenBank)
putative DRM-2, partial	***P. sylvestris***	AWH12140 (GenBank)
putative DRM-3, partial	***P. sylvestris***	AWH12141 (GenBank)
putative DRM-2	***P. taeda***	PITA_000020976 (ConGenIE)
putative DRM-3	***P. taeda***	PITA_000079456 (ConGenIE)
putative DRM-1	***P. abies***	MA_10433243g0010 (ConGenIE)
putative DRM-2	***P. abies***	MA_55726g0010 (ConGenIE)
putative DRM-4	***P. abies***	MA_637235g0010 (ConGenIE)

putative DRM-5	***P. abies***	MA_60018g0010 (ConGenIE)
putative DRM-6	***P. abies***	MA_10426609g0010 (ConGenIE)

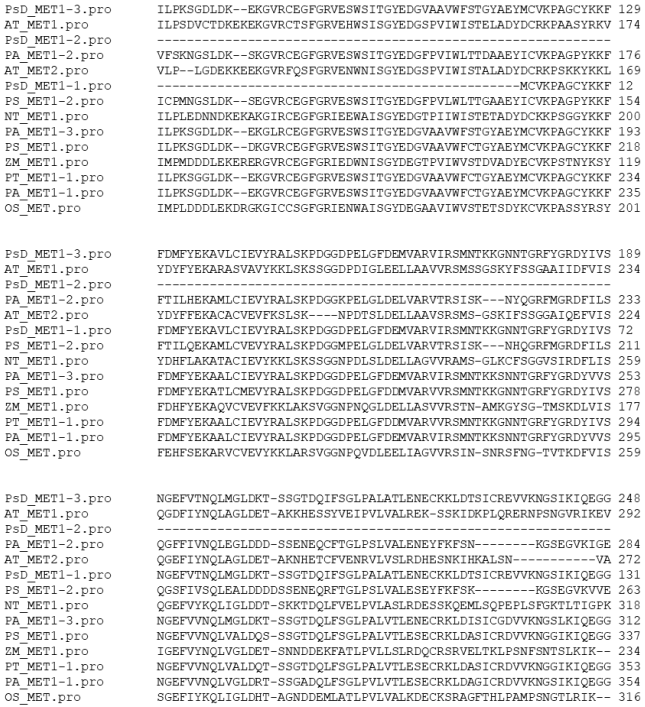
Supplementary Table S2. Primers for Sanger sequencing of *Pseudotsuga sinensis* DNMT genes.

Gene	Forward Primers (5'-3')	Reverse Primers (5'-3')
PsCMT	CGACAGTGTGTGATGAATCTGA	GGTTGGTAGAGGATATTGCGGA
	GTAGCTGGGTGTTATGGTCTAC	TAGGTCTGCTCTCCCACG
PsMET1-1	GAGCCAAACCATGACCAGT	GTATTCATCGACCTGACCACTC
	GGTTTGGGCGTGTTGAGTC	TATTCGTCCATCTCATCCTCGG
	TCACAAGAAAATCAATCCGGTG	CTGCCACAGTATCTCCATGTAT
	GAGAGACTTTATACAGGAGTGCT	TGCCTCTTGACATCACATTTTC
PsMET1-2	CCTCGGGAGCTAATACAGATGA	TTTATCGTGCTCTGTCAAAGCC
	GGCCTTGGTAATGGACAATGTC	CCACCACAGCCAGCAAAAATAT
	GGGGTTTCACAATCACGTAAAA	TCAGCACATTAATCTTTTGGCT
PsMET1-3	GAGCTGACCCAAAAAGCACG	AAGCAGGTGCCGAAATACCA
	CCGGAACTGGGGTTTGATGA	AAAAACCTCCACATCGGCCT
	CTCGCAGGATGCTCCATGAT	ACATCCCAACCCAGTTTGCT
	TTCGTACGGATGGAGCTTGG	TTCCATGGGCACAGAACCTC
	TGGGTGGTGGCGTTTTAGTT	CAGTCCCCAGGCCTAAAGTG
PsDRM-1	TACTCGTGAGCATGGAAATGTT	CTATGCCACCAAAATGACGAG
	AATAACTCGTCATTTTGGTG	CTATGCCACCAAAATGACGAG
PsDRM-2	ACTTGGTTTTGCGTTCACCA	CTTCTGCACCCCCAATTCCA
	TTATGCGAAAGACTGCGGAC	GGAATGCTTCCCATCCAGCC

Supplementary Table S3. qPCR primers for *Pseudotsuga sinensis* DNMT genes.

Gene	GenBank No.	Forward primer (5′-3′)	Reverse primer(5′-3′)
PsCMT	MZ447430	TGCATTGAGTCCCCTGGTTC	ATTTGGAACACCACCTCGCT
PsDRM-1	MZ447429	ATGGGCCTCCGTTCTTCTAC	ATAGACGGCAGAGGCAAGAC
PsDRM-2	MZ447428	TGGCCTGCTTGGGATTACAG	GGAGCCAACTGATCTGGACC
PsMET1-1	MZ447427	GGCCGGTTTTATGGAAGGGA	CACTCGTTTTCCAAGGTCGC
PsMET1-2	MZ447426	CTCGACATCAGAGGTGGCTG	TCTCCCATTGCACTTCGCTC
PsMET1-3	MZ447425	AGACCTTCCTCGCAGAATGC	TTGCCGTCCAGACAATACCC

Supplementary Figure S1. Alignment of MET1 amino acid sequences. The alignment of the amino acid sequences of *Pinus sylvestris* (PS), *Pinus taeda* (PT) and *Picea abies* (PA) MET1s with the amino acid sequences of *Arabidopsis thaliana* (AT) MET1 and MET2, *Zea mays* (ZM) MET1, *Nicotiana tabacum* (NT) MET1and *Oryza sativa* (OS) MET. PsD MET1-1, PsD MET1-2 and PsD MET1-3 represent PsMET1-1, PsMET1-2 and PsMET1-3, respectively. Alignment was done with Clustal X2 using default parameters. Identical residues are shown with a black star and similar residues with a black dot.



```
PsD_MET1-3.pro      ------------------------------------------------------------
AT_MET1.pro         ERGGFFSLPLSDIGRSSGFCTSCKIREDEEKRSTIKLNVSKTGFFINGIEYSVEDFVYVN 920
PsD_MET1-2.pro      -----------------------------------MLKNKDGFRYDGVDYHPFDFIYVD 24
PA_MET1-2.pro       ERGAFLSLPYDTLGLGNGQCLSCRLREDEKQSLALCMLKNKDGFRYEGVKYYLLDFVYVD 894
AT_MET2.pro         ERGGFFSLPRNDMGLGSGFCSSCKIRENEEERSKTKLNDSKTGFLSNGIEYHNGDFVYVL 900
PsD_MET1-1.pro      ------------------------------------------------------------
PS_MET1-2.pro       ERGAFISLPYDTLGLGNGQCLSCGLREDEKQSLELCLVKNKDGFRYEGVKYSLLDFVYVD 873
NT_MET1.pro         DRGAFFRLPFDKMGLGNGLCYSCELQRIDQEKESFKLDMSNSSFVYLGTEYSIDDFVYIH 946
PA_MET1-3.pro       EKGAFFSLPFDTLGLGTGQCHACKARENETK-KEFELFPRKDGFTYKGVEYFVHDFVYID 930
PS_MET1.pro         EKGAFFSVPFDTLGLGTGQCHGCNVREKETK-KEFELFPSKDGFTYNGVDYFVHDFIYID 961
ZM_MET1.pro         EKGAFFALSRDKMGLGSGLCSSCDNIEPDSDE--LKI-FSKTSFVYRKVTYNVNEFLYIS 842
PT_MET1-1.pro       EKGAFFSVPFDTLGLGTGQCHGCNAREKETK-KEFELFPSKDGFTYNGVDYFVHDFVYID 977
PA_MET1-1.pro       EKGAFLNLPIDTLGLGTGQCHACKMRENETK-KEFELLPSKDGFTYKGVDYFVHDFVYID 847
OS_MET.pro          EKGGFFSLPYDKIGNGTGICSSCE-RKPVGNE--FKL-LSESSFVFENITYNIHDFLYIR 921

PsD_MET1-3.pro      ------------------------------------------------------------
AT_MET1.pro         PDSIG--GLKEGSK-TSFKSGRNIGLRAYVVCQLLEIVPKE-SRKADLGSFDVKVRRFYR 976
PsD_MET1-2.pro      PEQFPP-FGEEKEPIERFKSSRNRGLRAYIVCQILEIRSSRSLNKGELKPTEIIVRRFYR 83
PA_MET1-2.pro       PEQFPP-LGDEKEPIERFKASRNRGLRAYTVCQILEIRSSSSLNKGELKPTQIIVRRFFR 953
AT_MET2.pro         PNYITKDGLKKGSRRTTLKCGRNVGLKAFVVCQLLDVIVLEESRKASKASFQVKLTRFYR 960
PsD_MET1-1.pro      ------------------------------------------------------------
PS_MET1-2.pro       PGQFPP-LGDDKEPIERFKASRNRGLRAYIVCQILEIKSSSSLNKGESKPTQIILRRFFR 932
NT_MET1.pro         PDHFA----VERGGSGTFKAGRNVGLMAYVVCQLLEIFGPKGSKQAKVDSTNVKVRRFFR 1002
PA_MET1-3.pro       PLQLPS-LGEEKE-IEKFKAGRNKGLRAYAICQILEIKIANGLKKADLKSVKVTVKRFFR 988
PS_MET1.pro         PLQLPS-FGEEKE-IEKFKAGRNKGLSAYVICQILEIKIANGSKKGDLKSAKVTVRRFFR 1019
ZM_MET1.pro         PDFFA----EDED-RATFKAGRNVGLKPYAVCQILSIPEGAGSKKLNPASANISARRFYR 897
PT_MET1-1.pro       PLQLPS-FREEKE-IEKFKAGRNKGLSAYVICQILEIKIPNGSKKGDLKSAKVTVRRFFR 1035
PA_MET1-1.pro       PLQLPS-FGEEKE-VEKFKAGRNKGLSAYSICQILEIKIINGSKKADLKSAKVTIRRFFR 905
OS_MET.pro          PEFFS----QGEG-HETYKAGRNVGLKPYAVCHLLSVHGPAGSRKANPESTKVKVRRFYR 976

PsD_MET1-3.pro      ------------------------------------------------------------
AT_MET1.pro         PEDVSAEKAYASDIQELYFSQDTVVLPPGALEGKCEVRKKSDMPLSREYPISDHIFFCDL 1036
PsD_MET1-2.pro      PEDIGTEKAYTADIREVYYSDETATIEVSALKGKCEVRRHQYLSLVPGNAIFDHIFFCSC 143
PA_MET1-2.pro       PEDIGNEKAYTADIREVYYSDETATIEVSAIKGKCEVRRHQHLSLVPGNVIFDHIFFCSC 1013
AT_MET2.pro         PEDISEEKAYASDIQELYYSQDTYILPPEAIQGKCEVRKKSDMPLCREYPILDHIFFCEV 1020
PsD_MET1-1.pro      ------------------------------------------------------------
PS_MET1-2.pro       PEDIGTEKAYTADIREVYYSNETATVEVTAIKGKCEVRRHQHLSLTPGNAIFDHIFFCSC 992
NT_MET1.pro         PEDISSDKAYSSDIREIYYSEEIHTVPVETIEGKCEVRKKYDIPSEDVPATFDHVFFCEY 1062
PA_MET1-3.pro       PEDVGFEKAYTADIREVYYSEETATLSVGTIHGKCDVRRQHHFSAVSGNVILDHTFWCSC 1048
PS_MET1.pro         PEDVGPEKAYTADIREVYYSEEMATLSVGTIHGKCDVKRQHHFSAVSGSVVLDHTFWCSC 1079
ZM_MET1.pro         PDDISSAKAYASDIREVYYSEDVIDVPVDMIEGKCEVRKKNDLASSDLPVMFEHVFFCEL 957
PT_MET1-1.pro       PEDVGPEKAYTADIREVYYSEEMATLSVGTIHGKCDVKRQHHFSAVSGSVILDHTFWCSC 1095
PA_MET1-1.pro       PEDVGSEKAYTADIREVYYSEETATLSVGTIHGKCDVKRQHHFSSVSGNVILDHTFWCSC 965
OS_MET.pro          PDDISSTKAYSSDIREVYYSEDIISVPVVMIEGKCEVRLKDDLPNSDLPAVVEHVFCCEY 1036

PsD_MET1-3.pro      ------------------------------------------------------------
AT_MET1.pro         FFDTSKGSLKQLPANMKPKFS-------TIKDDTLLRKKKGKGVESEIES-EIVKPVEPP 1088
PsD_MET1-2.pro      IYNPKKGTLMQLPLNVKLSSS-KSMVGKKNKRFVDETASAKRKGKTISVEQSAEEMLEAS 202
PA_MET1-2.pro       IYNPKKGTLKQLPANVKLSSS-KTIVGKKGKRHVDETASAKRKGKTISVEQSAEEMLEAS 1072
AT_MET2.pro         FYDSSTGYLKQFPANMKLKFS-------TIKDETLLREKKGKGVETGTSSGMLMKPDEVP 1073
PsD_MET1-1.pro      ------------------------------------------------------------
PS_MET1-2.pro       IYNPKKGTLEQLPANIKLSSSSKSIVGKKGKHHVDETASAKRKGKTISVEQAAEEMLEAT 1052
NT_MET1.pro         LYDPLNGSLKQLPAQVKLRFS-------RVKLDDAASRKRKGKGKEGEDELRVGQLNVAS 1115
PA_MET1-3.pro       IFDPSKGTVKQLPANVKLSSS-KSMADAKGKSHVDREDVKMK-GKAIVGEHPSEDKMESS 1106
PS_MET1.pro         IFDPSKGTVKQLPANVKLSSS-KGMADAKGKSPVDR-DVKMK-GKSIVEELPAQDKMDNS 1136
ZM_MET1.pro         IYDRASGALKQLPP--NVRFM-------SMVQRTSALKKNKGKQICEPDQIDSGKWLDVP 1008
PT_MET1-1.pro       IFDPSKGTVKQLPANVKLSSS-KGMADAKGKSPVDR-DVKMK-GKSIVEELPAQDKMDSS 1152
PA_MET1-1.pro       IFDPSKGTVKQLPANVKLGSS-KSMADAKGKSHVDRGDVKMK-GKAIVGELPAQDKMESL 1023
OS_MET.pro          LYDPANGALKQLPP--NVRLV-------TLTRKVPASKKNKGKQICDIELGGSDKPKDGQ 1087

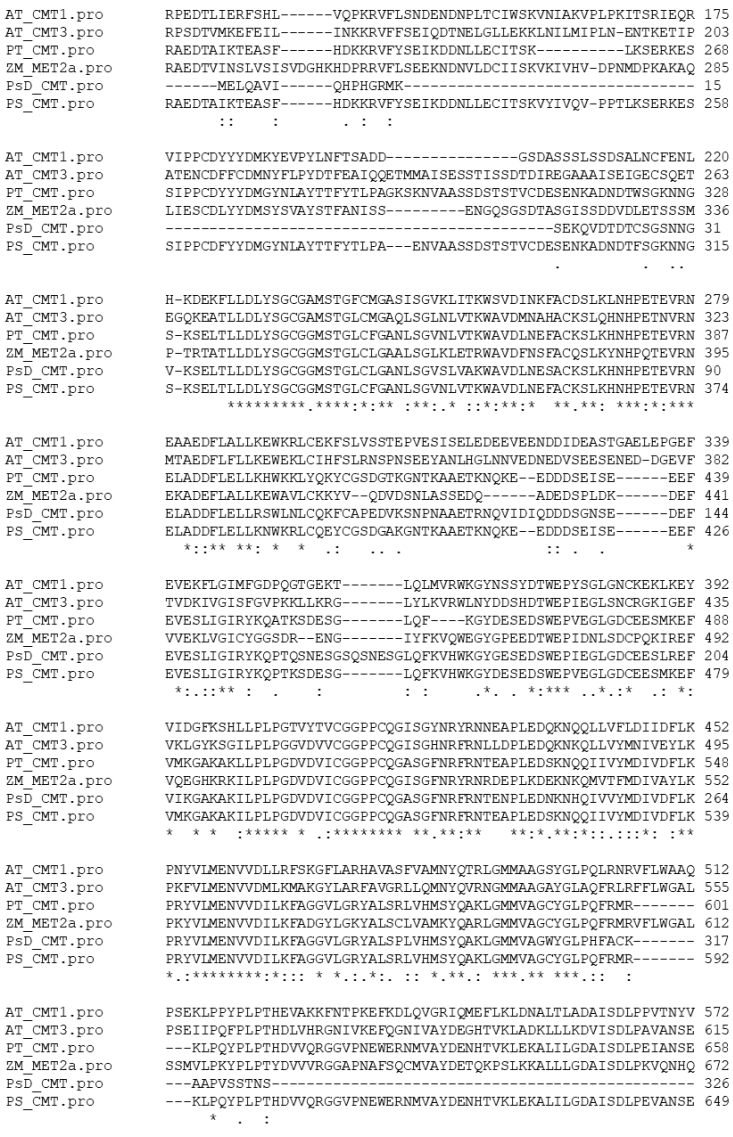
PsD_MET1-3.pro      ------------------------------------------------------------
AT_MET1.pro         KEIRLATLDIFAGCGGLSHGLKKA------------GVSDAKWAIEYEEPAGQAFKQNHP 1136
PsD_MET1-2.pro      HDCRLSTLDIFAGCGGRSNGLQKS------------GVSFTKWAIEYDQAAAESFKLNHP 250
PA_MET1-2.pro       HDCRLSTLDIFAGCGGLSKGLQKS------------GVSFTKWAIEYDQAAAEAFKLNHP 1120
AT_MET2.pro         KEKPLATLDIFAGCGGLSHGLENA------------GVSTTKWAIEYEEPAGHAFKQNHP 1121
PsD_MET1-1.pro      ------------------------------------------------------------
PS_MET1-2.pro       HRCCLSTLDIFAGCGGLSHGLQKS------------GASFTKWAIEYDQAAAEAFKLNHP 1100
NT_MET1.pro         QQNRLATLDIFAGCGGLSEGLQRS------------GVSDTKWAIEYEEPAGDAFKLNHP 1163
PA_MET1-3.pro       CQNCLVTLDIFAGCGGLSHGLQQS------------GVTLTKWAIEYEEPAAEAFKLNHP 1154
PS_MET1.pro         RQNSLATLDIFAGCGGLSHGLGQS------------GVSFTKWAIEYEEPAAEAFKLNHP 1184
ZM_MET1.pro         KENRLATLDIFAGCGGLSEGLQQA------------GVSFTKWAIEYEEPAGEAFNKNHP 1056
PT_MET1-1.pro       RQNSLATLDIFAGCGGLSHGLGQSGTYPEFLLFDFVGVSFTKWAIEYEESAAEAFKLNHP 1212
PA_MET1-1.pro       CQNSLVTLDIFAGCGGLSHGLEQS------------GASFPKWAIEYDEPAAEAFKLNHP 1071
OS_MET.pro          SENCLATLDIFAGCGGLSEGLQRS------------GLSLTKWAIEYEEPAGDAFGENHP 1135

PsD_MET1-3.pro      ------------------------------------------------------------
AT_MET1.pro         ESTVFVDNCNVILRAIMEKGGDQDDCVSTTEANELAAKLTEEQKSTLPLPGQVDFINGGP 1196
PsD_MET1-2.pro      EAEVFCQNCNVILRSIMEKGGDIDDCISTSEVAELCLELTDEQKSKLPLPGQVDFIDGGP 310
PA_MET1-2.pro       EAEVFCQNCNVILRSIMEKGGDIDECISTSEAAELSLELTDEQKTKLPLPGQVDFIEGGP 1180
AT_MET2.pro         EATVFVDNCNVILRAIMEKCGDVDDCVSTVEAAELAAKLDENQKSTLPLPGQVDFINGGP 1181
PsD_MET1-1.pro      ------------------------------------------------------------
PS_MET1-2.pro       EAEVFCQNCNVILRSIMEKGGDIDDCISTQEAVELSLELTDEQKSKLPLPGQVDFINGGP 1160
NT_MET1.pro         EAKVFIQNCNVILRAVMQKCGDAEDCISTSEASELAAAMDENELNSLPLPGQVDFINGGP 1223
PA_MET1-3.pro       EAEIFCDNCNVILRSIMEKGGDEEDCISTTEAVELSAKLTDEQRKNLPMPGQVDFINGGP 1214
PS_MET1.pro         EAEVFCDNCNVILRSIMEKGGDEEDCISTTEATELAAKLTDEQRRNLPMPGQVDFINGGP 1244
ZM_MET1.pro         EAVVFVDNCNVILKAIMDKCGDTDDCVSTSEAAEQAAKLPEVNINNLPVPGEVEFINGGP 1116
PT_MET1-1.pro       EAEVFCDNCNVILRSIMEKGGDEEDCISTTEAAELAAKLTDEQKRNLPMPGQVDFINGGP 1272
PA_MET1-1.pro       EAEVFCNNCNVILRSIMYKGGDEEDCISTPEAAELSAKLTDEQRRNLPMPGQVDFINGGP 1131
OS_MET.pro          EAAVFVENCNVILKAIMDKCGDSDDCISTSEAAERAAKLSEDKIKNLPVPGEVEFINGGP 1195

PsD_MET1-3.pro      ------------------------------------------------------------
AT_MET1.pro         PCQGFSGMNRFNQSSWSKVQCEMILAFLSFADYFRPRYFLLENVRTFVSFNKGQTFQLTL 1256
PsD_MET1-2.pro      PCQVFSGINRFNQRTWSEVQWEMILAFLSYADYFRPRFILLENVRNFVSFNKSQTFCLML 370
PA_MET1-2.pro       PCQGFSGMNRFNQRTWSKVQCEMILAFLSYADYFRPRFFLLENVRNFVSFKKGQTFCLML 1240
AT_MET2.pro         PCQGFSGMNRFSHGSWSKVQCEMILAFLSFADYFRPKYFLLENVKKFVTYNKGRTFQLTM 1241
PsD_MET1-1.pro      ------------------------------------------------------------
PS_MET1-2.pro       PCQVFSGMNRFNQRTWSKVRCEMILTFLSYADYFRPRFLLLENVRNFLSFNKGQTFRLML 1220
NT_MET1.pro         PCQGFSGMNRFNQSTWSKVQCEMILAFLSFADYYRPKFFLLENVRNFVSFNQKQTFRLTV 1283
PA_MET1-3.pro       PCQ-------------------------------------------------------- 1217
PS_MET1.pro         PCQGFSGMNRFNQRAWSKVQCEMILAFLSYADYFRPRFFLLENVRNFVAYNKGQTFRLTL 1304
ZM_MET1.pro         PCQGFSGMNRFNQSPWSKVQCEMILAFLSFAEYFRPRFFLLENVRNFVSFNKGQTFRLAV 1176
PT_MET1-1.pro       PCQGFSGMNRFNQRAWSKVQCEMILAFLSYADYFRPRFFLLENVRNFVAYNKGQTFRLTL 1332
PA_MET1-1.pro       PCQGFSGMNRFNQRTWSKVQCEMILAFLSYADYFRPRFFLLENVRNFVSYNKGQTFRLTL 1191
OS_MET.pro          PCQGFSGMNRFNQSPWSKVQCEMILAFLSFAEYFRPRFFLLENVRNFVSFNKGQTFRLTL 1255

PsD_MET1-3.pro      ------------------------------------------------------------
AT_MET1.pro         ASLLEMGYQVRFGILEAGAYGVSQSRKRAFIWAAAPEEVLPEWPEPEMHVFGVPKLKISLS 1316
PsD_MET1-2.pro      ASLLEMGYQVQFGVLQAGNYGVSQSRKRAFIWAASPEEFLPEWPDPM------------ 417
PA_MET1-2.pro       ASLLEMGYQVRFGVLQAGNYGVSQSRKRAFIWAASPEEFLPEWPDPMHVFAGSQLKISLP 1300
AT_MET2.pro         ASLLEMGYQVRFGILEAGTYGVSQPRKRVIIWAASPEEVLPEWPEPMHVFDNPGSKISLP 1301
PsD_MET1-1.pro      ------------------------------------------------------------
PS_MET1-2.pro       ASLLEMGYQVRFGVLQAGNYGVSQSRKRVFIWAASPEEFLPEWPEPMHVFASSQLKISLP 1280
NT_MET1.pro         ASLLEMGYQVRFGILEAGAFGVPQSRKRAFIWAASPEEILPEWPEPMHVFGVPELKITLS 1343
PA_MET1-3.pro       ---------VRFGVLQAGNYGVSQSRKRAFIWAASPKESLPEWPEPMHVFGSSQLKISLP 1268
PS_MET1.pro         ASLLEMGYQVRFGVLQAGNYGVSQSRKRAFIWAASPQESLPEWPEPMHVFGSSQIKISLP 1364
ZM_MET1.pro         ASLLEMGYQVRFGILEAGAFGVAQSRKRAFIWAAAPGEMLPDWPEPMHVFASPELKITLP 1236
PT_MET1-1.pro       ASLLEMGYQVRFGVLQAGNYGVSQSRKRAFIWAASPQESLPEWPEPMHVFGSSQIKISLP 1392
PA_MET1-1.pro       ASLLEMGYQVRFGVLQAGNY-------------ASPQESLPEWPEPMHVFGTSQIKISMP 1238
OS_MET.pro          ASLLEMGYQVRFGILEAGAYGVAQSRKRAFIWAAAPGETLPEWPEPMHVFASPELKITLP 1315
```

Supplementary Figure S2. Alignment of CMT amino acid sequences. The alignment of the amino acid sequences of *Pinus sylvestris* (PS) and *Pinus taeda* (PT) CMTs with the amino acid sequences of *Arabidopsis thaliana* (AT) CMT1 and CMT3 and *Zea mays* (ZM) MET2a (ZMET2). PsD CMT represents PsCMT. Alignment was done with Clustal X2 using default parameters. Identical residues are shown with a black star and similar residues with a black dot.



Supplementary Figure S3. Alignment of DRM amino acid sequences. The alignment of the amino acid sequences of *Pinus sylvestris* (PS), *Pinus taeda* (PT) and *Picea abies* (PA) DRMs with the amino acid sequences of *Arabidopsis thaliana* (AT) DRM-1 and DRM-2, *Zea mays* (ZM) Zmet3, *Nicotiana tabacum* (NT) DRM. PsD DRM-1 and PsD DRM-2 represent PsDRM-1 and PsDRM-2, respectively. Alignment was done with Clustal X2 using default parameters. Identical residues are shown with a black star and similar residues with a black dot.

```
PS_DRM-1.pro       CMRPRGYVHNLPIDGRSRVLPLPPMTIHEAFPHTKKFWPPWDNREKLNCMCPGRVSDVLC 402
AT_DRM-2.pro       AARKRGYIHNLPINNRRFQIQPPPKYTIHDAFPLSKRWWPEWDKRTKLNCILTCTGSAQLT 404
PA_DRM-5.pro       SMRPRGYVHNLPIDGRFQVLPLPPMTIHEALPQTKKYWPPWDGRKKLNCICGARGSDILC 222
PsD_DRM-1.pro      SMRPRGYVHNLPIDGRFQVLPLPSMTIHEALPQTKKYWPPWDGRKKLNCICPGRGSDVLC 132
PA_DRM-2.pro       SRRPRGYVHNLPIDGRFQVLPLPPMTIHEALPQTKKYWPTWDGRKKLNCICSGRFSDVLC 375
PA_DRM-1.pro       SRRPRGYVHNLPIDGRLQVLPLPPMTIHEALPQTKKYWPTWDGRKKLNCIGTGRCNDVLC 258
PS_DRM-3.pro       SSRKRGYVHNLPIENRYQISPLPPMTIQEAFPDMQKYWPSWDYRTKLNCINTAVGSAPLC 97
NT_DRM.pro         AARKRGYIHNLPVENRFPLFPLAPRTIHEALPLSKKWWPSWDPRTKLNCLQTAIGSAQLT 386
ZM_Zmet3.pro       AARKRGYIHNLPLENRSPLLPIPPKTISEAFPRTKRWWPSWDPRRQFNCLQTCVSSAKLL 386
PA_DRM-6.pro       SRRQRGYVHNLPIDGRFQVLPLPPMTIHEAFPQTEEYWPPWDDREKLNCICTGRGSDVLC 132
PT_DRM-3.pro       SSRKRGYVHNLPIENRYQISPLPPMTIQEAFPDMQKYWPSWDYRTKLNCINTAVGSAPLC 123
AT_DRM-1.pro       AARKRGYIHNLPIQNRFQIQPPQHNTIQEAFPLTKRWWPSWDGRTKLNCLLTCIASSRLT 402
PA_DRM-4.pro       SSRKRGYVHNLPIENRFRVFPLPPMTIQEAFPDTQKYWPSWDYRTKLNCINTVVGSAPLC 170
PS_DRM-2.pro       SSRKRGYVHNLPIENRFQILPLPPMTIEEAFPDTQKYWPAWDYRKKLNCINTGWASAPLC 129
PsD_DRM-2.pro      -------------------MPLPPMTIEEAFPETQKYWPAWDYRKKLNCINTGWASAPLC 41
PT_DRM-2.pro       SSRKRGYVHNLPIENRFQILPLPPMTIEEAFPDTQKYWPAWDYRKKLNCINTGWASAPLC 143
                                      *    ** :*:*  :.:** ** * ::**:     .  *

PS_DRM-1.pro       QALRSILTTSEG--NPTLHEQSHILENCKKWDLVWVGPDQMAPLEPNEIELILGFDKDHT 460
AT_DRM-2.pro       NRIRVALEPYNEEPEPPKHVQRYVIDQCKKWNLVWVGKNKAAPLEPDEMESILGFPKNHT 464
PA_DRM-5.pro       QELRSIMTNSNG--NPALPDQAYILENCKKWNLVWVGPDQMAPLEPNEIELLLGFDKDHS 280
PsD_DRM-1.pro      QELRSIMINSHG--HPTLPDHAYILENCKKWNLVWVGPDQMAPLEPNEIELILGFNKDHT 190
PA_DRM-2.pro       QELRSIMRNSNG--NPALADQAYILKKCKKWNLVWVGPDQMAPLEPHEIELILGYEKDHT 433
PA_DRM-1.pro       QELRSIMRNSDG--NPKLSDQAYILENCKKWNLVWVGPDQMAPLEPNEIELILGFDKDHT 316
PS_DRM-3.pro       DRMRSIIKCSNG--NPSIQDQARILHYCKKWNLVWVGPDQLAPLEPHEMEIALGFDVGHT 155
NT_DRM.pro         NRIRKAVEDFDG--EPPMRVQKFVLDQCRKWNLVWVGRNKVAPLEPDEVEMLLGFPKNHT 444
ZM_Zmet3.pro       ERIRVALTNSSD--PPPPRVQKYVLEECRKWNLAWVGLNKVAPLEPDEMEFLLGFPKDHT 444
PA_DRM-6.pro       QELRTIMRTSNG--NPTLADQSYILENCKKWNLIWVGPGQMAPLEPHEIELILGFEKDHT 190
PT_DRM-3.pro       DRMRSIIKCSNG--NPSIQEQARILHYCKKWNLVWVGPDQLAPLEPHEMEIALGFDVGHT 181
AT_DRM-1.pro       EKIREALERYDG--ETPLDVQKWVMYECKKWNLVWVGKNKLAPLDADEMEKLLGFPRDHT 460
PA_DRM-4.pro       ERMRSIIKSSPG--KPSIKDQARLLHHCKKWNLVWVGPDQLAPLEPHEIELALGFDVGHT 228
PS_DRM-2.pro       ERLRAIVLRSHG--NPSINDQALVLHHCKKWNLVWVGPDQLAPLEPHEIEVALGFDVGHT 187
PsD_DRM-2.pro      ERLRSIVLRSHE--EPSIKDQALVLHHCKKWNLVWVGPDQLAPLEPHEIELALGFDIGHT 99
PT_DRM-2.pro       ERLRTIVLRSHG--NPSINDQALVLDHCKKWNLVWVGPDQLAPLEPQEIEVALGFDVGHT 201
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PS_DRM-1.pro       R-GASSRTDRIQCLGNAFQIDTVAYHLSALKLFYPDGLNVLSLFSGIGGAEVALHRLGIH 519
AT_DRM-2.pro       RGGGMSRTERFKSLGNSFQVDTVAYHLSVLKPIFPHGINVLSLFTGIGGGEVALHRLQIK 524
PA_DRM-5.pro       R-GASARTDRLQCLGNAFQIDTVAYHLSVLKPFYPYGLNVLSLFSGIGGAEVALHRIGIH 339
PsD_DRM-1.pro      R-GASSRTDRIQCLANAFQIDTVAYHLSVLKPLYPDGLKVLSLFSGIGGAEVALHRIGIH 249
PA_DRM-2.pro       R-GASSRTDRLQRLGNAFQTDTVAYHLSALKPFYPDGLKVLSLFSGIGGAEVALHHIGIH 492
PA_DRM-1.pro       R-GASSRTDRIQCLGNAFQIDTVGYHLSVLKPFYPDGLNVLSLFSGIGGAEVALHRIGIH 375
PS_DRM-3.pro       R-GASTRTERVRSLGNAFQVDTVGYHLSVLKCLYPDGLNVLSLFSGIGGAEVALDRLGIT 214
NT_DRM.pro         RGGGISRTDRYKSLGNSFQVDTVAYHLSVLKDLFPGGINVLSLFSGIGGGEVALYRLGIP 504
ZM_Zmet3.pro       R-GIS-RTERYRSLGNSFQVDTVAYHLSVLKDLFPQGMNVLSLFSGIGGAEVALHRLGIR 502
PA_DRM-6.pro       R-GANSRTDRLQCLGNAFQTDTVAYHLSVLKPFYPDGLNVLSLFSGIGGAEVALYRIGIH 249
PT_DRM-3.pro       R-GASTRTERVRSLGNAFQVDTVGYHLSVLKCLYPDGLSVLSLFSGIGGAEVALDRLGIT 240
AT_DRM-1.pro       RGGGISTTDRYKSLGNSFQVDTVAYHLSVLKPLFPNGINVLSLFTGIGGGEVALHRLQIK 520
PA_DRM-4.pro       R-GSSTRTERVRSLGNAFQTDTVAYHLSVLKHLYPNGINVLSLFSGIGGAEVALHRLGIT 287
PS_DRM-2.pro       R-GSSSRTERIRSLGNAFQTDTVGYHLSVLKHLFPGGINVLSLFSGIGGAEVALHRLGIT 246
PsD_DRM-2.pro      R-GSSTRTERIRSLGNAFQTDTVGYHLSVLKHLFPGGINVLSLFSGIGGAEVALHRLGIT 158
PT_DRM-2.pro       R-GSSNRTERIRSLGNAFQTDTVGYHLSVLKHLFTGGINVLSLFSGIGGAEVALHRLGIA 260
                   * *    *:* : *.*:** ***.****.** ::. *:.*****:****.**** :: *

PS_DRM-1.pro       LKCVVSVEICPKNRLILSSWWIKTNQTGRLIQKEDVQHLTRDVLQELVDMVGGFDLVIGG 579
AT_DRM-2.pro       MKLVVSVEISKVNRNILKDFWEQTNQTGELIEFSDIQHLTNDTIEGLMEKYGGFDLVIGG 584
PA_DRM-5.pro       LKCVVSVEICPKNRLILSSWWTKTRQTGRLIEKEDVQHLTRDVLEELVDTVGGFDLIIGG 399
PsD_DRM-1.pro      LKYVVAVEISPNNMLI-------------------------------------------- 265
PA_DRM-2.pro       LKCIVSVEICPKNRLILSSWWMKTCQTGRLIEKEDVRHLTRDVLEELIDTVGGFDLVIGG 552
PA_DRM-1.pro       LKCVVSVELCPKNRLILSSWWMKTGQTGRLILKEDIQYLSRDVLEELVDTVGGFDLVIGG 435
PS_DRM-3.pro       LKYVVSAEICKENRLILKSWWEKTEQKGKLIELEDVQNLAEDELENLIDTVGGFDLIIGG 274
NT_DRM.pro         LNTVVSVEKSEVNRDIVRSWWEQTNQRGNLIHFNDVQQLNGDRLEQLIESFGGFDLVIGG 564
ZM_Zmet3.pro       MNTVISVEKSEVNRTILKSWWDQT-QTGTLIEITDVQTLSSERIEAYIRRIGGFDLVIGG 561
PA_DRM-6.pro       LKCVVAVETCPKNRFILRSWWRKTSQTGRLIEKEEVQHLNRDVLEELIDTVGGFDLVIGG 309
PT_DRM-3.pro       LKYVVSAEICKVNRLILKSWWEKTEQKGKLIELEDVQNLAEDELENLIDTVGGFDLIIGG 300
AT_DRM-1.pro       MNVVVSVEISDANRNILRSFWEQTNQKGILREFKDVQKLDDNTIERLMDEYGGFDLVIGG 580
PA_DRM-4.pro       LKYVISAEICKENRLILRSWWEKTRQTGELIELEDVQNLTDKKLEDLIDIVGGFDLIIGG 347
PS_DRM-2.pro       LKYVVSAEIGKENRLILGSWWEKTQQKGKLIEVEDVQNLAEKELRDLIDLVGGFDLIIGG 306
PsD_DRM-2.pro      LKCVVSAEICKENRLILKSWWEKTQQNGKLIEVEDVQNLADKELENLIDLVGGF------ 212
PT_DRM-2.pro       LKYVVSAEICKENRLILRSWWEKTQQKGKLIEVEDVQNLAEKELTDLIDLVGGFDLIIGG 320
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