

Supplementary materials

Figure S1 PCR electrophoresis of *ZmPRMT1* genes.

- (A) *ZmPRMT1* gene clone electrophoresis diagram. M1:250-I Marker, A1-2: *ZmPRMT1* gene.
- (B) Recombinant plasmid bienzyme-cut electrophoresis diagram. M2:250-III Marker, B1-2: *ZmPRMT1* gene.

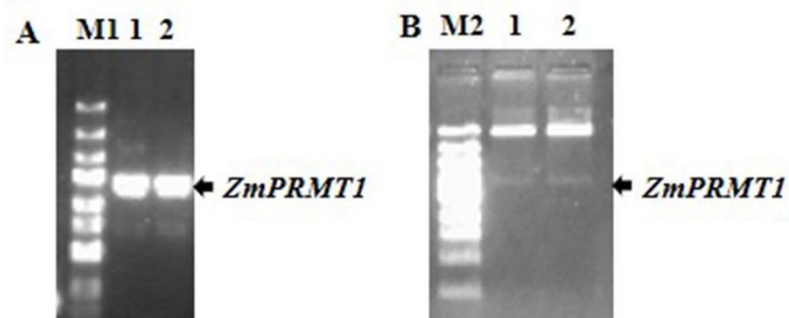


Figure S2 PCR electrophoresis of Hygromycin gene of 16 over-expression lines.

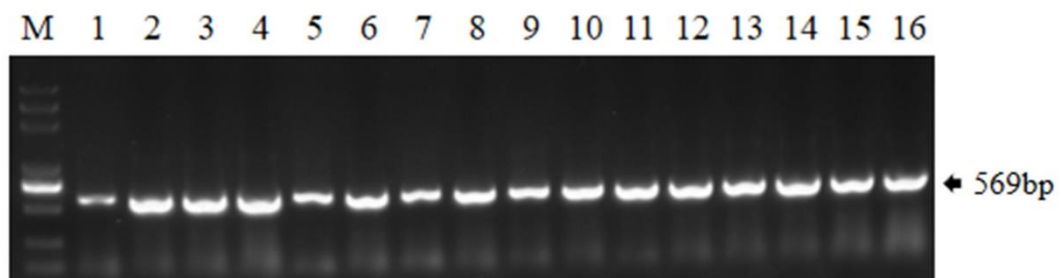


Figure S3 Alignment of the amino acid sequences of ZmPRMT1 protein and AtPRMT5 protein.

ZmPRMT1MILTLCAAEETGRKLEKYAVEKN	23
AtPRMT5	SELTITVLMVVGAGRGPLVRASLCAAEETDRKLEKYAVEKN	400
Consensus	lqaa eet rklkvyavekn	
ZmPRMT1	PNAVITLFSLIKLEGWESIVTVISSDMFCWDAPERADILV	63
AtPRMT5	PNAVITLHNIVKMEGWEDVVTIISCTMFEFNAPQCADILV	440
Consensus	pnav tlh l k egwe vt is dmr w ape adilv	
ZmPRMT1	SELIGSFGDNELSPECIDGAQRFLKPDGISIPSSYTSFIQ	103
AtPRMT5	SELIGSFGDNELSPECIDGAQRFLKPDGISIPSSYTSFIQ	480
Consensus	sellgsfgdnelspecldgaqrflkpdgisipssytsfiq	
ZmPRMT1	PITASKLHDDIKAHKDLAHFETAYVVKLHRIATLAEPCQV	143
AtPRMT5	PITASKLYNDVKAHKDLAHFETAYVVKLHSAKLAEPCSV	520
Consensus	pitaskl d kahkd ahfetayvvklh a lap q v	
ZmPRMT1	FTFTHPNFSFNASNQRYIKLQFEMLEIMGSCLVHGFAGYF	183
AtPRMT5	FTFTHPNFSIKVNNQRYIKLQFSLPSLAGSALVHGFAGYF	560
Consensus	ftfthpnfs nqry klqf d gs lvhgfagyf	
ZmPRMT1	DSVLYKDVHLGIEPTATPNMFSWFPIFFPLRKEIYVPEG	223
AtPRMT5	DSVLYKDVHLGIEPTATPNMFSWFPIFFPLRKEVEVHED	600
Consensus	dsvlykdvhlgiep tatpnmfswfpiffplrkp v	
ZmPRMT1	SPIEVHFWRCCAPTQVWYEWAVITPTFSEIHNSNGRSYWV	263
AtPRMT5	TPLEVHFWRCCGSSKVWYEWAVSSPTFSEPHNTNGRSYWV	640
Consensus	p evhfwrcc kvwyew v ptpsp hn ngrsywv	
ZmPRMT1	G	264
AtPRMT5	G	641
Consensus	g	

Figure S4 Alignment of the amino acid sequences of PRMT proteins in maize.

ZmPRMT1	0
ZmPRMT2	0
ZmPRMT3	MASSPDLPFNVAFSVSAAP...AAEATAAFLGATTGAPRLCLVKSQKDEAEPTVDIDLADAVFKLGPMEWLCVCDE	77
ZmPRMT4	MASSPDLPFNVTFSVSEAAAGPAEGATAAFLGAATGAPRLSLVKA...EAEPTVEIDLADAVFKLGPTWLCVCDE	77
ZmPRMT5	0
ZmPRMT6	0
ZmPRMT7	0
ZmPRMT8	0
Consensus		
ZmPRMT1	0
ZmPRMT2	0
ZmPRMT3	SEAKAGVEE.....KSFSAIKVVLRTAEASKAFSLAQWKHQVISGKAGERLENGSIASKSKFDTKI	142
ZmPRMT4	SEAKDGVVEYVLNGYMLTLSSLRQKSFSAIKVVLRTAEASKAFSLAQWQHGVISGKAGERLENGSIASKSKFDTKI	157
ZmPRMT5MLPSHLNGHSALGR.RRPRLS.....AAAGESPAAAGVEAAAP	37
ZmPRMT6	0
ZmPRMT7MFTGAAGGIGNLPRPRRRLGGIGHGGVMVSPQGQVALGAHPHLAAPP	48
ZmPRMT8	0
Consensus		
ZmPRMT1	0
ZmPRMT2MLMAKCRTLQENEEIGTMASE	22
ZmPRMT3	EASSAKMYFHYYGQLLHQQNMQLQDFVRTGTYAAVMENRSDFEGRVVVDVGAGSGILSLFAAQAGARHVVAVEASEMAEN	222
ZmPRMT4	EASSAKMYFHYYGQLLHQQNMQLQDFVRTGTYAAVMENRSDFEGRVVVDVGAGSGILSLFAVQAGARHVVAVEASEMAPH	237
ZmPRMT5	LEEHDRIFYQAYSHLGIHETMIKDRVRTDAYHAAIMRHQKFIEGKVVLDVGCGTGILSVFCARAGAKRVYAVEACEIVVQ	117
ZmPRMT6MSLLCS.....QVYAVDASDIAPQ	19
ZmPRMT7	CTDYDVAIFYKAYSHIGVHEEMLKDHVRTSTYRNAIMHHKDLISGKVVLDVGCGTGVLISFCAFAGATRVYAVDASDIAPQ	128
ZmPRMT8MLKDVVRTKTYQNVITQSSFLIKNKVVLDVGAGTGILSLFCAKAGAKVYAEICSQMADM	60
Consensus		
ZmPRMT1MRCWDA.PEKADILVSELIGSFGDNE.ISPECIDGAORFLKPDGISTPSSYTSFTOPT	57
ZmPRMT2	G.KIHELGMKIAVLKSONNELRNQFDVLYKHMDGVTDNVERSNELVLS.IIQEELAKDLELTRLKEVLAQKGATQDAPVE	100
ZmPRMT3	AQRLMSGNPSLGQRITVIRGKVVEVEL.PEKADILISEPMGTLVNERMLESYVIARDRLAPDGKMFPTTGRHMAPFS	301
ZmPRMT4	AQRLISGNPSLGHRITVIRGKVVEEVL.PEKADILISEPMGTLVNERMLESYVIARDRLAPDGKMFPTTGRHMAPFS	316
ZmPRMT5	AREIVKAN.NLTDQIVVIHGRVEDVDL.EEKVDVISEWMGYMLLYESMLPSVLFARDKWLKPGGLILPSHASLYMAPVT	195
ZmPRMT6	AMEIVREN.ELSDKVVVLHGRIEDVDI.EEKVDVISEWMGYMLLYESMLGSVIFARDKWLKPGGLILPSHASLYMAPVT	97
ZmPRMT7	AMEIVREN.ELSDKVVVLHGRIEDVDI.EEKVDVISEWMGYMLLYESMLGSVIFARDKWLKPGGLILPSHASLYMAPVT	206
ZmPRMT8	AEQIVKSN.GYSDVITVIRGKVVEIELEVPKVDVISEWMGYFLIFENMLNTVLYARDKWLADGGVVLPRDTSRLRLTAIE	139
Consensusd.....1.....	
ZmPRMT1	ASKLHDDIK.....AHKDTIAHFETAYVVKIHRITATAPF.....QQVRDLICVCFIGSDQIYLCHEIWLS	118
ZmPRMT2	TSDDAGNGQ.....EADSDTLQVKAES.....	122
ZmPRMT3	DEYLYVEIANKALFWQQHNEFFGVDLTPLHGSAFQGYFSQFVVDAFDPR.LLISFPITYHTLDFTSMKEEELYEINIPLSFV	380
ZmPRMT4	DEYLYVEMANKALFWQQHNEFFGVDLTPLHGSAFQGYFSQFVVDAFDPR.LLISFPITYHTLDFTSMKEEELYEINIPLSFV	395
ZmPRMT5	NRERYEDSV.....DFWRDVYGINMSALVPLAKKFTSEETSETIGGENVISWFSVKRFDCYNFTAEEFKSITSKYKVS	270
ZmPRMT6	NSQRYHDSI.....YFWRDVYGIKMSSMMPLAKLCAFMESVETISGENVLTWPAVVAQVDCYTIQAQKLETITAAFKFT	172
ZmPRMT7	NSQRYHDSI.....YFWRDVYGIKMSSMMPLAKLCAFMESVETISGENVLTWPAVVAQVDCYTIQAQKLETITAAFKFT	281
ZmPRMT8	DAEYK.....	144
Consensus		
ZmPRMT1	PLLV.....	122
ZmPRMT2	122
ZmPRMT3	ASVGTRVHGLACWFDVLFNGSTVQRWLTAPGSPTTHWYQLRCVLSQPLYVMAGQEITGRHLHVAHSAQSYTIYLTMSAK	460
ZmPRMT4	ASVGTRVHGLACWFDVLFNGSTVQRWLTAPGSPTTHWYQLRCVLSQPLYVMAGQEITGRHLHVAHSAQSYTIYLTMSAK	475
ZmPRMT5	SMMLGELCYSNHNLPLVF.....	288
ZmPRMT6	SMLQGVV.....	179
ZmPRMT7	SMLQAPLHGFAFWDFVEFNGPVRQKSKKQPSQSLDENTQNASPSNRKRKPDVSIVLSTAPEDAPTHWQQTLLYLFEPFIEL	361
ZmPRMT8	144
Consensus		
ZmPRMT1	122
ZmPRMT2	122
ZmPRMT3	MWGVGAEGGGILQTSTGKLELKEPYRISQPQSYMLPQDQQQQQQLSSLQPHGSEQQMGEGLSPGITIDQVDKDYGL	537
ZmPRMT4	MWGVGAEGGGILQTSTGKLELKEPYRISQPQSCVLPQDQQQQQQL.LPSLQAQGEQQMGEGLSPAFTIDQDCLN...	548
ZmPRMT5	288
ZmPRMT6	179
ZmPRMT7	NKDQIIIEGSVTISQSQ.....	377
ZmPRMT8	144
Consensus		

Table S1 The information of PRMT genes in plants

Name	Gene ID
<i>ZmPRMT1</i>	Zm00001d015228_T003
<i>ZmPRMT2</i>	Zm00001d054001_T001
<i>ZmPRMT3</i>	Zm00001d022469_T005
<i>ZmPRMT4</i>	Zm00001d007133_T002
<i>ZmPRMT5</i>	Zm00001d026614_T002
<i>ZmPRMT6</i>	Zm00001d032633_T001
<i>ZmPRMT7</i>	Zm00001d036131_T001
<i>ZmPRMT8</i>	Zm00001d020188_T004
<i>AtPRMT1A</i>	AT2G19670.1
<i>AtPRMT3</i>	AT3G12270.1
<i>AtPRMT4A</i>	AT5G49020.2
<i>AtPRMT4B</i>	AT3G06930.2
<i>AtPRMT5</i>	AT4G31120.1
<i>AtPRMT6</i>	AT3G20020.1
<i>AtPRMT10</i>	AT1G04870.2
<i>AtPRMT11</i>	AT4G29510.1
<i>OsPRMT5</i>	LOC_Os02g04660
<i>OsPRMT10</i>	LOC_Os06g05090
<i>SbPRMT5</i>	SORBI_3004G036700
<i>SbPRMT10</i>	SORBI_3010G032700

Table S2 The signal values for maize PRMT genes in the 60 tissues

Gene Name Tissues	ZmPR MT1	ZmPR MT2	ZmPR MT3	ZmPR MT4	ZmPR MT5	ZmPR MT6	ZmPR MT7	ZmPR MT8
24H_Germinating								
Seed	10.64	11.63	10.52	12.73	11.57	12.1	11.52	12.23
6DAS_GH_Coleop								
tile	12.79	13.32	10.24	12.75	12.32	12.22	12.52	12.73
6DAS_GH_Primary								
Root	12.52	13.25	10.13	12.6	11.78	12	12.29	12.61
V1_GH_Primary								
Root	11.71	12.72	9.89	12.38	10.94	11.56	11.48	11.88
VE_Whole								
Seedling	12.43	11.62	10.32	12.12	11.33	11.89	11.76	11.64
VE_Primary Root	12.23	12.25	10.2	13.07	11.83	12.75	12.41	12.85
V1_Pooled Leaves	11.65	11.01	10.59	11.38	8.63	11.52	9.96	9.35
V1_Stem and								
SAM	13.07	12.44	9.96	13.17	12.27	12.53	12.96	13.18
V4_Stem and								
SAM_R3	12.32	11.71	10.16	12.41	11.76	12.12	11.52	12.18
V3_Stem and	12.84	12.39	10.24	12.99	12.02	12.43	12.57	12.75

SAM**V3_First Leaf and**

Sheath	10.88	11.48	9.95	11.94	10.1	11.82	10.96	11.59
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V3_Topmost Leaf	11.93	11.42	9.85	11.73	9.59	11.79	10.82	10.97
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V5_Shoot Tip	12.66	12.32	10.62	12.7	12.24	12.55	12.76	12.57
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V5_First

Internode	12.5	12.1	9.86	12.34	12.01	12.36	12.21	12.05
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V5_Tip of stage-2

Leaf	11.58	11.43	10.27	11.58	10.67	11.58	10.84	10.84
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V5_Base of stage-2

Leaf	12.52	11.47	10.6	11.93	11.5	11.78	11.91	11.56
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V7_First

Internode	11.83	11.42	10.21	12.32	11.13	12.1	10.84	11.47
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V7_Tip of stage-2

Leaf	10.92	10.9	10.81	11.98	7.62	11.6	9.44	10.97
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V7_Base of stage-2

Leaf	12.81	12.01	10.01	12.64	12.16	12.07	11.91	12.14
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V9_Fourth

Internode	13.07	12.2	10.55	12.46	12.34	12.4	12.36	12.34
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V9_Eighth Leaf	11.07	11.61	10.58	11.87	9.6	11.49	10.35	10.89
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V9_Eleventh Leaf	11.9	11.72	10.42	11.92	10.17	11.76	10.75	10.66
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V9_Thirteenth

Leaf	12.2	11.77	10.11	12.09	10.88	11.83	10.71	10.99
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V9_Immature

Leaves	12.47	11.32	10.91	12.09	11.2	11.81	11.35	10.93
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V13_Immature

Tassel	12.82	12.45	11.01	12.91	12.68	12.7	12.37	12.74
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V18_Meiotic

Tassel	11.31	11.17	9.91	11.94	10.87	11.81	10.52	11.26
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V18_Immature

Cob	12.67	12.59	11.14	13.06	13.16	12.49	12.06	12.33
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VT_Thirteenth

Leaf	11.49	11.23	10.64	11.51	10.31	11.76	9.96	9.99
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R1_Pre-pollinatio

n Cob	12.64	12.28	10.6	12.19	12.43	12.33	12.43	11.97
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R1_Silks	12.52	10.74	11.17	12.04	12.35	12.45	12.18	11.45
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R1_Anthers	11.25	11.47	10.13	11.4	10.71	12.26	9.89	10.85
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R1_Innermost

Husk	11.82	11.48	9.88	12.23	11.4	11.94	11.37	11.07
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R2_Thirteenth

Leaf	11.67	11.4	10.11	11.88	10.81	12.02	10.17	10.79
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R2_Outer Husk	11.63	11.88	10.04	12.32	11.49	11.87	11.39	11.35
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R2_Innermost

Husk	11.56	11.89	10.09	12.39	11.51	11.72	11.02	11.38
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2DAP_Whole								
Seed	12.42	12.18	10.34	12.23	12.29	12.42	12.27	12.05
4DAP_Whole								
Seed	12.42	12.07	10.12	12.08	12.37	12.2	11.74	11.67
6DAP_Whole								
Seed	12.13	12.02	10.15	12.44	12.34	12.63	11.38	11.72
8DAP_Whole								
Seed	12.37	12.13	10.21	12.46	12.22	12.46	11.84	11.64
10DAP_Whole								
Seed	12.41	11.95	10.76	12.71	12.17	12.57	12.22	12.23
12DAP_Whole								
Seed	13.17	12.07	10.42	12.93	12.45	12.88	12.73	12.77
12DAP_Endosperm	13.57	12.66	10.76	12.8	12.73	13.31	13.38	13.33
14DAP_Whole								
Seed	13.33	12.04	10.37	12.27	12.07	12.71	12.93	12.91
14DAP_Endosperm	13.35	12.5	10.51	12.22	12.16	12.94	13.19	13.16
16DAP_Whole								
Seed	13.47	12.34	10.73	12.19	12.33	12.55	12.66	12.5
16DAP_Endosperm	13.71	12.65	10.75	12.22	11.91	12.89	12.99	13.18
16DAP_Embryo	12.74	12.57	11.01	13.1	13.15	12.66	12.74	12.71
18DAP_Whole								
Seed	13.19	12.19	10.23	11.99	11.54	12.27	12.28	12.55
18DAP_Endosperm	13.52	12.27	10.61	12.07	11.61	12.68	12.64	12.92
18DAP_Embryo	12.56	12.55	10.83	13.1	13.14	12.85	12.76	12.81
18DAP_Pericarp	11.94	11.56	10.64	12.3	12.01	12.33	11.29	11.25
20DAP_Whole								
Seed	13.14	12.36	10.53	12.08	11.68	12.69	12.17	12.53
20DAP_Endosperm	13.37	12.52	10.52	12.06	11.08	12.94	12.38	12.79
20DAP_Embryo	12.69	12.56	10.73	13.03	12.94	12.59	12.22	12.55
22DAP_Whole								
Seed	13.19	12.33	10.28	12.16	11.61	12.87	11.58	12.17
22DAP_Endosperm	13.36	12.47	10.51	12.4	10.94	13.03	11.88	12.68
22DAP_Embryo	12.99	12.76	11.15	12.75	13.1	12.83	11.86	12.12
24DAP_Whole								
Seed	13	12.25	10.14	12.21	11.61	12.65	11.78	12.22
24DAP_Endosperm	13.12	12.14	10.31	12.09	10.27	12.58	11.79	12.29
24DAP_Embryo	13.02	12.69	10.48	12.69	12.94	12.75	11.5	12.34

Table S3 Primer sequences for qRT-PCR

Gene name	Forward primer sequence(5' →3')	Reverse primer sequence(5' →3')
<i>ZmPRMT1</i>	AATCTCTGGGAGATCGAATCAC	ACATCCTTCTCAAAAGTCTCGT
<i>ZmPRMT2</i>	GAAGGGTCTCCTATAGAAGTGC	TTCTCTGTTACAACACAAAGCG
<i>ZmPRMT3</i>	ATTAGTGGAAGCTGGTGAGA	TTGCTGATGTAATAATTGCCCG
<i>ZmPRMT4</i>	CCAGAGAAAGCTGACATACTGA	GTATTTCGTCAGAAAATGGAGCC
<i>ZmPRMT5</i>	CAAGCGCTTCGATTGCTATAAT	GGATCCGGGAAATACAAAATGG
<i>ZmPRMT6</i>	GCTCATTCAATTGTAACGCTTCT	ATGCATTCTACTTGTCCAGACA
<i>ZmPRMT7</i>	CATCCAAACCAAGTTATCGGTC	TTCTGATTGGCAATGTGACTTG
<i>ZmPRMT8</i>	TCCAGTCCCAAAAGTAGATGTC	CAAGCCATTTATCACGTGCATA
<i>ZmActin1</i>	CCTCACCGACCACCTAATG	CCATCAGGCATCTCGTAGC
<i>AtP5CS1</i>	AGAGTCAATGGTGGCTCGCTTAGT	ACACGGCCGATTGGATCTTCCATA
<i>AtP5CR</i>	AAGATTCTGGTTTCTGTTGC	AACGGTCTGTGAAGCTAAA
<i>AtPDH</i>	ATTTGGCAGTACAAAATGCT	AGGACAATGCATCTGACATA
<i>AtP5CDH</i>	CTCAAAGCTACTCTTTGGTG	TCGTAGATGACTTCTCTGTG
<i>AtFLC</i>	CCTAATTTGATCCTCAGGTTTGGG	CCGACGAAGAAAAAGTAGATAGGCAC
<i>AtFT</i>	GAGACCCTCTTATAGTAAGCAGAGTTG	GGGAGTTCAAGTGAAAGAACCAAAGT
<i>AtSOC1</i>	GCTCTCAGTGCTTTGTGATGC	AAGAACGTACTTGGAGCTGGC
<i>AtMAF1</i>	GGAAAGAATACGTTGCTGGCAACA	CCGTTGATGATGGTGGCTAATTGA
<i>AtMAF2</i>	GGCTCCGGAAAACCTCTACAA	TTCTGCAAGATCTAAGGCTTCA
<i>AtMAF3</i>	ACAGAACTAATGATGGAGGATATGAA	CTTCTTCCCCACCTGGCT
<i>AtMAF4</i>	GAGCAATGTCACCGGAAAGTAG	CAGTCGTTGGTGATGGTGGTTA
<i>AtMAF5</i>	AAGAGCAGTAATGTCACCGGAA	ACTTGAGAAGCGGGAGAGTC
<i>AtActin1</i>	CTTGACCAAGCAGCATGAA	CCGATCCAGACACTGTACTTCCTT

Table S4 Primer sequences for clone-PCR

Gene name	Forward primer sequence(5' →3')	Reverse primer sequence(5' →3')
<i>ZmPRMT1</i>	CCCAAGCTTATGATTTTGACATTGC	TGCTCTAGATTATAGACCAACCCAATAG G