

## ***Supplementary Material***

**Supplementary Figure S1.** Locations of wheat dMTase genes on different chromosomes. Dotted lines indicate a homeologous relationship. The scale is in megabases (Mb).

**Supplementary Figure S2.** Multiple sequence alignment analysis of the 12 wheat dMTase protein sequences and an Arabidopsis dMTase protein sequence. The key conserved domains are highlighted by double lines (Domain A by green colour, HhH-GPD glycosylase domain by red colour and RRM\_DME domain by brown colour) and the domain names are shown at the top of the sequence. Names of genes are shown on the left.

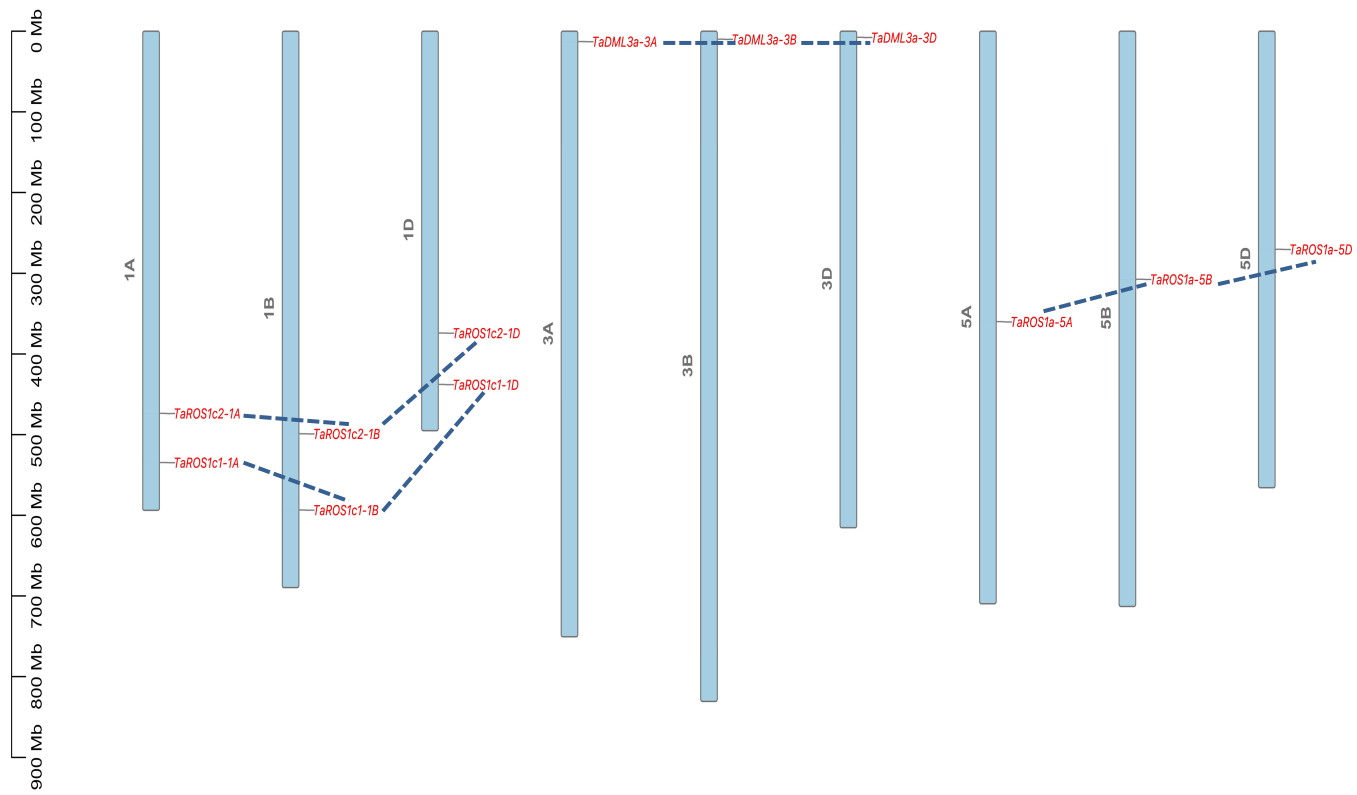
**Supplementary Figure S3.** Heatmap showing expression of 12 TadMTase genes in various tissues and developmental stages during hormonal stress (ABA and GA3). The "heatmap" colour represents relative expression values, calculated as log2 ratios between the signal intensities from hormonal treated genotypes vs. controls (C). The red colour indicates up-regulation and the green colour indicates down-regulation. ABA, abscisic acid; gibberellic acid, GA3.

**Supplementary Table S1.** Primer pairs used for qRT-PCR analysis.

**Supplementary Table S2.** Sequence homology (BLASTP) of dMTase genes between wheat, Arabidopsis and rice

**Supplementary Table S3.** List of SSR markers along with the following details, type of repeat motif, repeat position, primer sequences, T<sub>m</sub> (°C) and product size(bp).

**Supplementary Table S4.** Details of Monopartite and bipartite nuclear localization signals (NLS) predicted in TadMTases (cut-off score = 5).



**Supplementary Figure S1.** Locations of wheat dMTase genes on different chromosomes. Dotted lines indicate a homeologous relationship. The scale is in mega bases (Mb).

[illegible]

TaDML3a-3A	-----EARDPI-----	-----PGLMPPATPDNGRRPPFDSSDSSCSAAAPASAD	GVFKRGGHIFLSPPIGECRSVP	70			
TaDML3a-3B	-----EARDPI-----	-----PGLMPPATPDNGRRPPFDSSDSSCSAAAPASAD	GVFKRGGHIFLSPPIGECRSVP	70			
TaDML3a-3C	-----EARDPI-----	-----PGLMPPATPDNGRRPPFDSSDSSCSAAAPASAD	GVFKRGGHIFLSPPIGECRSVP	70			
TaROS1c1-1A	RGADDAARSAAASVRRRLQSE	LCEGQVGGKSLA	NSCHLVEEILLIAKRSFCSCTATVTAQAGHLGLVD	ETSPGGCA	NSCIEMNNKLLDEYLHEMGT	380	
TaROS1c1-1A	RGADDAARSAAASVRRRLQSE	FCEGQVGGKSLA	NSCHLVEEILLIAKRSFCSCTATVTAQAGHLGLVD	ETSPGGCA	NSCIEMNNKLLDEYLHEMGT	380	
TaROS1c1-1B	MGADDAARSAAASVRRRLQSE	FCEGQVGGKSSA	NSCHLVEEILLIAKRSFCSCTATVTAQAGHLGLVD	ETSPGGCA	NSCIEMNNKLLDEYLHEMGT	384	
TaROS1c1-1B	RGADDAARSAAASVRRRLQSE	FCEGQVGGKSSA	NSCHLVEEILLIAKRSFCSCTATVTAQAGHLGLVD	ETSPGGCA	NSCIEMNNKLLDEYLHEMGT	384	
TaROS1c1-1D	RGADDAARSAAASVRRRLQSE	LCEGQVGGKSSA	NSCHLVEEILLIAKRSFCSCTATVTAQAGHLGLVD	ETSPGGCA	NSCIEMNNKLLDEYLHEMGT	367	
TaROS1c1-1D	RGADDAARSAAASVRRRLQSE	FCEGQVGGKSSA	NSCHLVEEILLIAKRSFCSCTATVTAQAGHLGLVD	ETSPGGCA	NSCIEMNNKLLDEYLHEMGT	367	
TaROS1a-5A	VTNVCICHGVSTGSPPIPPPK	IEGHSANENLIG	ITSDYLKFTTSPSPYRGTGALGLHGSHSSHVIAL	ALDRENNASNGAHPGLNMNLDQNRNGWAS	DACHAASP	SGSYFFETTKMRNTNYSKCLN	492
TaROS1a-5B	VTNVCICHGVSTGSPPIPPPK	IEGHSANENLIG	ITSDYLKFTTSPSPYRGTGALGLHGSHSSHVIAL	ALDRENNASNGAHPGLNMNLDQNRNGWAS	DACHAASP	SGSYFFETTKMRNTNYSKCLN	492
TaROS1a-5D	VTNVCICHGVSTGSPPIPPPK	IEGHSANENLIG	ITSDYLKFTTSPSPYRGTGALGLHGSHSSHVIAL	ALDRENNASNGAHPGLNMNLDQNRNGWAS	DACHAASP	SGSYFFETTKMRNTNYSKCLN	492
TaROS1a-5E	VTNVCICHGVSTGSPPIPPPK	IEGHSANENLIG	ITSDYLKFTTSPSPYRGTGALGLHGSHSSHVIAL	ALDRENNASNGAHPGLNMNLDQNRNGWAS	DACHAASP	SGSYFFETTKMRNTNYSKCLN	492
TaROS1a-5F	VTNVCICHGVSTGSPPIPPPK	IEGHSANENLIG	ITSDYLKFTTSPSPYRGTGALGLHGSHSSHVIAL	ALDRENNASNGAHPGLNMNLDQNRNGWAS	DACHAASP	SGSYFFETTKMRNTNYSKCLN	492
TaROS1a-5G	VTNVCICHGVSTGSPPIPPPK	IEGHSANENLIG	ITSDYLKFTTSPSPYRGTGALGLHGSHSSHVIAL	ALDRENNASNGAHPGLNMNLDQNRNGWAS	DACHAASP	SGSYFFETTKMRNTNYSKCLN	492
TaROS1a-5H	VTNVCICHGVSTGSPPIPPPK	IEGHSANENLIG	ITSDYLKFTTSPSPYRGTGALGLHGSHSSHVIAL	ALDRENNASNGAHPGLNMNLDQNRNGWAS	DACHAASP	SGSYFFETTKMRNTNYSKCLN	492
TaROS1a-5I	VTNVCICHGVSTGSPPIPPPK	IEGHSANENLIG	ITSDYLKFTTSPSPYRGTGALGLHGSHSSHVIAL	ALDRENNASNGAHPGLNMNLDQNRNGWAS	DACHAASP	SGSYFFETTKMRNTNYSKCLN	492

[illegible]



## Domain A

K

K

K

K

### HhH-GPD Glycosylase Domain

HhH motif

K

TaDML3a-3A : DEHRAFFVIVNRRIVRIQWVBI CCSS--EFPSGLYELMDCVGYLWPRICIDIKELV----ELICIMITFGKVICTRVDFNCNACFRGGGRVRSKILTRPLLPAEEHVRGGERKSNVTSERLLSNG : 711  
 TaDML3a-3B : DEHRAFFVIVNRRIVRIQWVBI CCSS--EFPSGLYELMDCVGYLWPRICIDIKELV----ELICIMITFGKVICTRVDFNCNACFRGGGRVRSKILTRPLLPAEEHVRGGERKSNVTSERLLSNG : 713  
 TaDML3a-3D : DEHRAFFVIVNRRIVRIQWVBI CCSS--EFPSGLYELMDCVGYLWPRICIDIKELV----ELICIMITFGKVICTRVDFNCNACFRGGGRVRSKILTRPLLPAEEHVRGGERKSNVTSERLLSNG : 713  
 TaROS1c1-1A : LHCIAFFVIVNVRICVRLGWVFIQIPLPESICLHLELYFVLIRIQYLYWPRICIKLDKRLV----ELIHMITFGKVICTRVDFNCNACFRGGGRVRSKILTRPLLPAEEHVRGGERKSNVTSERLLSNG : 1269  
 TaROS1c2-1A : LHCIAFFVIVNVRICVRLGWVFIQIPLPESICLHLELYFVLIRIQYLYWPRICIKLDKRLV----ELIHMITFGKVICTRVDFNCNACFRGGGRVRSKILTRPLLPAEEHVRGGERKSNVTSERLLSNG : 1440  
 TaROS1c1-1B : LHCIAFFVIVNVRICVRLGWVFIQIPLPESICLHLELYFVLIRIQYLYWPRICIKLDKRLV----ELIHMITFGKVICTRVDFNCNACFRGGGRVRSKILTRPLLPAEEHVRGGERKSNVTSERLLSNG : 1273  
 TaROS1c2-1B : LHCIAFFVIVNVRICVRLGWVFIQIPLPESICLHLELYFVLIRIQYLYWPRICIKLDKRLV----ELIHMITFGKVICTRVDFNCNACFRGGGRVRSKILTRPLLPAEEHVRGGERKSNVTSERLLSNG : 1280  
 TaROS1c1-1D : LHCIAFFVIVNVRICVRLGWVFIQIPLPESICLHLELYFVLIRIQYLYWPRICIKLDKRLV----ELIHMITFGKVICTRVDFNCNACFRGGGRVRSKILTRPLLPAEEHVRGGERKSNVTSERLLSNG : 1256  
 TaROS1c2-1D : LHCIAFFVIVNVRICVRLGWVFIQIPLPESICLHLELYFVLIRIQYLYWPRICIKLDKRLV----ELIHMITFGKVICTRVDFNCNACFRGGGRVRSKILTRPLLPAEEHVRGGERKSNVTSERLLSNG : 1444  
 TaROS1a-5A : LHCIAFFVIVNVRICVRLGWVFIQIPLPESICLHLELYFVLIRIQYLYWPRICIKLDKRLV----ELIHMITFGKVICTRVDFNCNACFRGGGRVRSKILTRPLLPAEEHVRGGERKSNVTSERLLSNG : 1656  
 TaROS1a-5B : LHCIAFFVIVNVRICVRLGWVFIQIPLPESICLHLELYFVLIRIQYLYWPRICIKLDKRLV----ELIHMITFGKVICTRVDFNCNACFRGGGRVRSKILTRPLLPAEEHVRGGERKSNVTSERLLSNG : 1611  
 TaROS1a-5D : LHCIAFFVIVNVRICVRLGWVFIQIPLPESICLHLELYFVLIRIQYLYWPRICIKLDKRLV----ELIHMITFGKVICTRVDFNCNACFRGGGRVRSKILTRPLLPAEEHVRGGERKSNVTSERLLSNG : 1610  
 ATSGO4560 : LHCIAFFVIVNVRICVRLGWVFIQIPLPESICLHLELYFVLIRIQYLYWPRICIKLDKRLV----ELIHMITFGKVICTRVDFNCNACFRGGGRVRSKILTRPLLPAEEHVRGGERKSNVTSERLLSNG : 1678

D RRM\_DME Domain C C C C

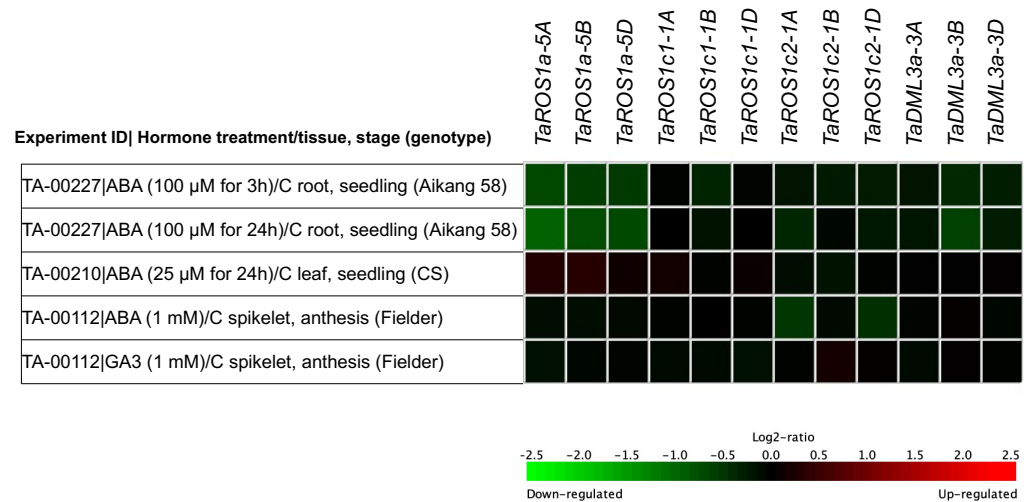
TaDML3a-3A : CMPSPTQVCH--HCEESRSAGROPFR--SCPTIIEFGSEYEVYBALDEQYVNGDLVIE-DIMSGHYDVEINLCSNKPVSNCSWTPNNGRD----VLNSQHTSSRLHGRIRTEHLAVLPDSEH : 837  
 TaDML3a-3B : SIPS-----HCEESRTAGROPFR--SCPTIIEFGSEYEVYBALDEQYVNGDLVIE-DIMSGHYDVEINLCSNKPVSNCSWTPNNGRD----VLNSQHTSSRLHGRIRTEHLAVLPDSEH : 834  
 TaDML3a-3D : CMPS-----HCEESRTAGROPFR--SCPTIIEFGSEYEVYBALDEQYVNGDLVIE-DIMSGHYDVEINLCSNKPVSNCSWTPNNGRD----VLNSQHTSSRLHGRIRTEHLAVLPDSEH : 834  
 TaROS1c1-1A : GSMPTFMSVLPDEESTRGKVFPHN--NSPTIIEFGSEYEVYBALDEQYVNGDLVIE-DIMSGHYDVEINLCSNKPVSNCSWTPNNGRD----VLNSQHTSSRLHGRIRTEHLAVLPDSEH : 1399  
 TaROS1c2-1A : GSMPTFMSVLPDEESTRGKVFPHN--NSPTIIEFGSEYEVYBALDEQYVNGDLVIE-DIMSGHYDVEINLCSNKPVSNCSWTPNNGRD----VLNSQHTSSRLHGRIRTEHLAVLPDSEH : 1572  
 TaROS1c1-1B : GSMPTFMSVLPDEESTRGKVFPHN--NSPTIIEFGSEYEVYBALDEQYVNGDLVIE-DIMSGHYDVEINLCSNKPVSNCSWTPNNGRD----VLNSQHTSSRLHGRIRTEHLAVLPDSEH : 1403  
 TaROS1c2-1B : GSMPTFMSVLPDEESTRGKVFPHN--NSPTIIEFGSEYEVYBALDEQYVNGDLVIE-DIMSGHYDVEINLCSNKPVSNCSWTPNNGRD----VLNSQHTSSRLHGRIRTEHLAVLPDSEH : 1420  
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 TaROS1a-5A : CQCVYISMRNCHDWNANAHHIL--NSPTIIEFGSEYEVYBALDEQYVNGDLVIE-DIMSGHYDVEINLCSNKPVSNCSWTPNNGRD----VLNSQHTSSRLHGRIRTEHLAVLPDSEH : 1790  
 TaROS1a-5B : CQCVYISMRNCHDWNANAHHIL--NSPTIIEFGSEYEVYBALDEQYVNGDLVIE-DIMSGHYDVEINLCSNKPVSNCSWTPNNGRD----VLNSQHTSSRLHGRIRTEHLAVLPDSEH : 1745  
 TaROS1a-5D : CQCVYISMRNCHDWNANAHHIL--NSPTIIEFGSEYEVYBALDEQYVNGDLVIE-DIMSGHYDVEINLCSNKPVSNCSWTPNNGRD----VLNSQHTSSRLHGRIRTEHLAVLPDSEH : 1744  
 ATSGO4560 : YPPVAIPMIEPLPLEKSLASGAPNRE--SCPTIIEFGSEYEVYBALDEQYVNGDLVIE-DIMSGHYDVEINLCSNKPVSNCSWTPNNGRD----VLNSQHTSSRLHGRIRTEHLAVLPDSEH : 1812

TaDML3a-3A : DEF--EYVPEDEPSYILVRHGN-----PGAVNMCVRCITLLPCRTASGCFELMCTYFCDEVFADSSSRVDDELFTGCFQVYFGSSHSIGLQGRVD : 930  
 TaDML3a-3B : DEF--EYVPEDEPSYILVRHGN-----PGAVNMCVRCITLLPCRTASGCFELMCTYFCDEVFADSSSRVDDELFTGCFQVYFGSSHSIGLQGRVD : 941  
 TaDML3a-3D : DEF--EYVPEDEPSYILVRHGN-----PGAVNMCVRCITLLPCRTASGCFELMCTYFCDEVFADSSSRVDDELFTGCFQVYFGSSHSIGLQGRVD : 941  
 TaROS1c1-1A : COLGLDRREDGDPSPYILVIMQDINAMIKAKPCSSFMEDGFSNNEKQYVLEBENGSRVVRATLLVPCRTAKGSEFELMCTYFCQVNEVFADSSSRVDDELFTGCFQVYFGSSHSIGLQGRVD : 1536  
 TaROS1c2-1A : COLGLDRREDGDPSPYILVIMQDINAMIKAKPCSSFMEDGFSNNEKQYVLEBENGSRVVRATLLVPCRTAKGSEFELMCTYFCQVNEVFADSSSRVDDELFTGCFQVYFGSSHSIGLQGRVD : 1709  
 TaROS1c1-1B : COLGLDRREDGDPSPYILVIMQDINAMIKAKPCSSFMEDGFSNNEKQYVLEBENGSRVVRATLLVPCRTAKGSEFELMCTYFCQVNEVFADSSSRVDDELFTGCFQVYFGSSHSIGLQGRVD : 1540  
 TaROS1c2-1B : COLGLDRREDGDPSPYILVIMQDINAMIKAKPCSSFMEDGFSNNEKQYVLEBENGSRVVRATLLVPCRTAKGSEFELMCTYFCQVNEVFADSSSRVDDELFTGCFQVYFGSSHSIGLQGRVD : 1557  
 TaROS1c1-1D : COLGLDRREDGDPSPYILVIMQDINAMIKAKPCSSFMEDGFSNNEKQYVLEBENGSRVVRATLLVPCRTAKGSEFELMCTYFCQVNEVFADSSSRVDDELFTGCFQVYFGSSHSIGLQGRVD : 1523  
 TaROS1c2-1D : COLGLDRREDGDPSPYILVIMQDINAMIKAKPCSSFMEDGFSNNEKQYVLEBENGSRVVRATLLVPCRTAKGSEFELMCTYFCQVNEVFADSSSRVDDELFTGCFQVYFGSSHSIGLQGRVD : 1711  
 TaROS1a-5A : GCV--DREPDIDGYYLITPGGTASQIDATACNSNESGKLSSA--FSNSMBAQAQVRCITLLVPCRTAKGSEFELMCTYFCQVNEVFADSSSRVDDELFTGCFQVYFGSSHSIGLQGRVD : 1925  
 TaROS1a-5B : GCV--DREPDIDGYYLITPGGTASQIDATACNSNESGKLSSA--FSNSMBAQAQVRCITLLVPCRTAKGSEFELMCTYFCQVNEVFADSSSRVDDELFTGCFQVYFGSSHSIGLQGRVD : 1880  
 TaROS1a-5D : GCV--DREPDIDGYYLITPGGTASQIDATACNSNESGKLSSA--FSNSMBAQAQVRCITLLVPCRTAKGSEFELMCTYFCQVNEVFADSSSRVDDELFTGCFQVYFGSSHSIGLQGRVD : 1879  
 ATSGO4560 : DGMD--RREPDIDGYYLITPGGTASQIDATACNSNESGKLSSA--FSNSMBAQAQVRCITLLVPCRTAKGSEFELMCTYFCQVNEVFADSSSRVDDELFTGCFQVYFGSSHSIGLQGRVD : 1947

C C C C

TaDML3a-3A : DDYKRGVYVIRGSDRRRSRRICAAHSINERKEDSSKQKEGVGLGSNEQKAPSN----- : 989  
 TaDML3a-3B : DDYKRGVYVIRGSDRRRSRRICAAHSINERKEDGSKHKESGLGKSNEQKAPSN----- : 1000  
 TaDML3a-3D : DDYKRGVYVIRGSDRRRSRRICAAHSINERKEDNSKNKEGGLGKSNEQKAPLN----- : 1000  
 TaROS1c1-1A : CCFKRGFVYVIRGSDRRRSRRICAAHSINERKEDNSKNKEGGLGKSNEQKAPLN----- : 1595  
 TaROS1c2-1A : CCFKRGFVYVIRGSDRRRSRRICAAHSINERKEDNSKNKEGGLGKSNEQKAPLN----- : 1765  
 TaROS1c1-1B : CCFKRGFVYVIRGSDRRRSRRICAAHSINERKEDNSKNKEGGLGKSNEQKAPLN----- : 1600  
 TaROS1c2-1B : CCFKRGFVYVIRGSDRRRSRRICAAHSINERKEDNSKNKEGGLGKSNEQKAPLN----- : 1613  
 TaROS1c1-1D : CCFKRGFVYVIRGSDRRRSRRICAAHSINERKEDNSKNKEGGLGKSNEQKAPLN----- : 1586  
 TaROS1c2-1D : HHCRQ-----IICNYQQLLES--FCRSNN----- : 1734  
 TaROS1a-5A : CCFKRGFVYVIRGSDRRRSRRICAAHSINERKEDNSKNKEGGLGKSNEQKAPLN----- : 1975  
 TaROS1a-5B : CCFKRGFVYVIRGSDRRRSRRICAAHSINERKEDNSKNKEGGLGKSNEQKAPLN----- : 1930  
 TaROS1a-5D : CCFKRGFVYVIRGSDRRRSRRICAAHSINERKEDNSKNKEGGLGKSNEQKAPLN----- : 1929  
 ATSGO4560 : CCFKRGFVYVIRGSDRRRSRRICAAHSINERKEDNSKNKEGGLGKSNEQKAPLN----- : 1987

**Supplementary Figure S2.** Multiple sequence alignment analysis of the 12 wheat dMTase protein sequences and an Arabidopsis dMTase protein sequence. The key conserved domains are highlighted by double lines (Domain A by green colour, HhH-GPD glycosylase domain by red colour and RRM\_DME domain by brown colour) and the domain names are shown at the top of the sequence. Names of genes are shown on the left.



**Supplementary Figure S3.** Heatmap showing expression of 12 TadMTase genes in various tissues and developmental stages during hormonal stress (ABA and GA3). The "heatmap" colour represents relative expression values, calculated as log2 ratios between the signal intensities from hormonal treated genotypes vs. controls (C). The red colour indicates up-regulation and the green colour indicates down-regulation. ABA, abscisic acid; gibberellic acid, GA3.



**Supplementary Table S1.** Primer pairs used for qRT-PCR analysis.

Gene	Forward sequence (5'-3')	Reverse sequence (5'-3')
<i>TaROS1a-5A</i>	ATTGCTCGCATGCATCTAGTTC	AAACACCCACTACTGAATCCACAA
<i>TaROS1c1-1B</i>	TTGCATCAGGGCTGAAATATCTT	GGATGTGGTCACAGATGGATACA
<i>TaROS1c2-1A</i>	GGCCATCCGGGAACGA	CCATGATCTCTAACCAAGCGATT
<i>TaDML3a-3B</i>	TGAAGAGCGAGTTCCAGAAGATC	CAGCACCAGGAGGAGGATTG
<i>TaDML3a-3D</i>	TTTGAAGAGCGAGTTCCAGAAGA	GCACCAGGAGGAGGATTGTC
Wheat GADPH	GGTGCCAAGAAGGTCATCAT	TGGTCATCAAACCCTCAACA

**Supplementary Table S2.** Sequence homology (BLASTP) of dMTase genes between wheat, Arabidopsis and rice

Wheat		Arabidopsis		E-Value	Identities (%)	Rice		E-Value	Identities (%)
Gene Name	Gene ID	Gene Name	Gene ID			Gene Name	Gene ID		
<i>TaROS1a-5A</i>	TraesCS5A02G169000	<i>AtROS1</i>	AT2G36490	0	65.2	<i>OsROS1a</i>	Os01t0218032	3.90E-164	87.5
<i>TaROS1a-5B</i>	TraesCS5B02G165800	<i>AtROS1</i>	AT2G36490	0	62.9	<i>OsROS1a</i>	Os01t0218032	3.90E-164	87.5
<i>TaROS1a-5D</i>	TraesCS5D02G173300	<i>AtROS1</i>	AT2G36490	0	61.0	<i>OsROS1a</i>	Os01t0218032	5.30E-164	87.1
<i>TaROS1c1-1A</i>	TraesCS1A02G349600	-	-	-	-	<i>OsROS1c</i>	Os05t0445900	2.30E-137	82.7
<i>TaROS1c1-1B</i>	TraesCS1B02G364100	-	-	-	-	<i>OsROS1c</i>	Os05t0445900	2.30E-137	82.5
<i>TaROS1c1-1D</i>	TraesCS1D02G352500	-	-	-	-	<i>OsROS1c</i>	Os05t0445900	3.60E-135	81.4
<i>TaROS1c2-1A</i>	TraesCS1A02G278000	-	-	-	-	<i>OsROS1c</i>	Os05t0445900	8.60E-144	85.7
<i>TaROS1c2-1B</i>	TraesCS1B02G286900	-	-	-	-	<i>OsROS1c</i>	Os05t0445900	1.20E-143	83.8
<i>TaROS1c2-1D</i>	TraesCS1D02G277100	-	-	-	-	<i>OsROS1c</i>	Os05t0445900	1.00E-145	84.2
<i>TaDML3a-3A</i>	TraesCS3A02G022500	<i>AtDML3</i>	AT4G34060	3.70E-27	52.0	<i>OsDML3a</i>	Os02t0496500	1.30E-56	59.6
<i>TaDML3a-3B</i>	TraesCS3B02G023200	<i>AtDML3</i>	AT4G34060	9.50E-27	52.0	<i>OsDML3a</i>	Os02t0496500	4.50E-59	62.1
<i>TaDML3a-3D</i>	TraesCS3D02G024100	<i>AtDML3</i>	AT4G34060	6.90E-27	52.0	<i>OsDML3a</i>	Os02t0496500	1.10E-54	59.6

**Supplementary Table S3.** List of SSR markers along with the following details, type of repeat motif, repeat position, primer sequences, T<sub>m</sub> (°C) and product size(bp).

Gene Name	(Motif) repeats	Position	Primer details			
			Forward Primer (5'-3')	Reverse Primer (5'-3')	T <sub>m</sub> (°C)	Product size (bp)
<i>TaROS1a-5A</i>	(AAAT)3	12464-75	AAGGAAAACGTGGGAATTGG	GCCTTGCATAGAGTGGTCTTG	60.05	288
<i>TaROS1a-5B</i>	(ATTT)3	8045-56	CCGTTCACTCGGGAAGTTT	TCCCAGCCTCACACAAATC	59.55	361
	(TA)19	13536-73	ACAGCTCCCAAGAGGATAAACA	CTACCCCATTATAGCTCCCTCC	60.15	198
<i>TaROS1a-5D</i>	NA	-	-	-	-	-
<i>TaROS1c1-1A</i>	(CAG)4	1051-62	GCCAAATGGTTTAGATGCAGA	GGCTCTATGTTTCTTCCTCCG	60.15	322
	(CAG)6	11575-92	TTCCCTGACAAAGAGTGTGATG	TCTAAAATCAGCCCCAAACAAC	60.24	342
<i>TaROS1c1-1B</i>	(GAAA)3	4392-404	ATCACTGGTGGAACGGTAGC	GATTGCTCTGCCAAAACAT	60.11	351
	(AAAT)3	7305-17	TTGGATATTCTGGCTCAATGC	CAAACACAGGCCAACACAAAT	60.44	329
	(CAG)8	12326-49	TTGCTTCCAGACTTATTTGGGT	AACTAACTAATACGGCCCATGC	59.72	321
<i>TaROS1c1-1D</i>	(CAG)6	110111-28	ACAAAGAGTGTGACGCGATG	CTGAGAACGTGAAAACGCTG	59.76	390
<i>TaROS1c2-1A</i>	(TCA)4	1163-74	TCTGAACATCCACCAATACAGC	CAGTGAGGCCAATTCATCAGTA	60.06	174
<i>TaROS1c2-1B</i>	(TCA)4	1113-24	ATGCAGAAGCACCCACAAC	AGGAAGCAGTGAGGCCAAT	59.75	140
	(AATAA)3	8032-46	AACCATGTTCTGACTCTCCGAT	ATCATGCAACAAACACAGGCTA	60.25	386
<i>TaROS1c2-1D</i>	(TCA)4	1112-23	TCTTCCGAGGTTGTATGTTGG	CAGTGAGGCCAATTCATCAGT	60.05	393
<i>TaDML3a-3A</i>	(CCCGC)3	106-20	TATCCCATGTGCCCTGCTG	ATCCGTGGAGGAATCGAAC	59.60	282
	(AG)8	5857-73	TCCTTATCTCCTGGTTCGTCAT	AGTTGCATACCTCAATGCTCCT	60.06	217
	(ATT)5	6298-311	CGTGCATCAACCATCTCATACT	GTTGTAAGAAGTGACCGTGCAG	59.92	241
<i>TaDML3a-3B</i>	(GCC)4	95-107	ATTGTCACTGCTGCTGCCT	CAGATTTCGATCAAGAAGAAGGG	59.89	147
<i>TaDML3a-3D</i>	NA	-	-	-	-	-



**Supplementary Table S4.** Details of Monopartite and bipartite nuclear localization signals (NLS) predicted in TadMTases (cut-off score = 5).

Protein name	Position (aa)	NLS sequence	Score	Monopartite/bipartite
TaROS1a-5A	90	PPKAKRKKHRP	9.0	monopartite
	498	PETYKRMRTDNY	7.0	monopartite
	749	PSEKRKAGRP	5.0	monopartite
TaROS1a-5B	68	PPKAKRKKHRP	9.0	monopartite
	476	PETYKRMRTDNY	7.0	monopartite
	106	RKYVRKNMPAGQPPSEQIAESHRKATLKPAKRS	7.0	bipartite
	128	RKATLKPAKRSLNFEGEVPQENTHPSQAQVVSCDP	5.2	bipartite
TaROS1a-5D	68	PPKAKRKKHRP	9.0	monopartite
	102	PSGKRKYVRK	5.0	monopartite
	476	PETYKRMRTDNY	7.0	monopartite
	697	PSEKRKAGRP	5.0	monopartite
	128	RKATVKPAKRSLNFEGEVPQENTHPSQAQVVSCDP	5.2	bipartite
TaROS1c1-1A	215	LKPRRKKHRAK	7.5	monopartite
	550	FTKKRSRRVRCHYRRSEGNFQPPNNKNFYHD	6.0	bipartite
	1029	RTTRKEKTENFDWDKLRRQACADGHMKERKSE	5.5	bipartite
TaROS1c1-1B	219	VKPRRKKHRAK	7.5	monopartite
	1033	RTTRKEKTENFDWDKLRRQACADGHMKERKSE	5.5	bipartite
TaROS1c1-1D	202	VNPRRKKHRAK	7.5	monopartite
	536	FTKKRSRRVRRHYGRSEGIFQPPNNRKFYHD	5.0	bipartite
	1017	TTRKEKTENFDWDKLRRQACADGHMKERKSE	5.3	bipartite
TaROS1c2-1A	259	PRRKKHRAK	6.5	monopartite
	1200	RTPRKKNTENFDWDKFRRQACADGHMKERKSE	5.4	bipartite
TaROS1c2-1B	96	VKPRRKKHRAK	7.5	monopartite
	1042	RTTRKKNTENFDWDKFRRQAFADGHMKERKSE	5.4	bipartite
TaROS1c2-1D	260	PRRKKHRAK	6.5	monopartite
	1204	RTTRKKNTENFDWDKFRRQACADGHMKERKSE	5.2	bipartite
TaDML3a-3A	169	DKLSKRKLDFD	5.0	monopartite
	358	PMNKRKGNAE	6.0	monopartite
	118	RPRKKSTKGVPRCLKVMKDKHPKPARTTPAKPHKTP	5.5	bipartite
TaDML3a-3B	172	KLSKRKLDFD	6.0	monopartite
	360	PMNKRKGNAE	6.0	monopartite
	144	RTPAKPHKTPVAKKDGGAGSVGDGTDNKLSKRK	6.7	bipartite
TaDML3a-3D	172	KLSKRKLDFD	6.0	monopartite
	360	PLNKRKGNAE		monopartite
	144	RTPAKPHKTPAKTKDGGAGSVGDGTDNKLSKRK	7.5	bipartite