

AtDRM1 UBA-	1 MMILETLFNYSASTEASSSKSKVINHFIAMGFPEEHVIKAMQEHGDEDVGEITNALLT	148
AtDRM2 UBA-	2 SVIIDTISKYSSDCEAGSSKSKAIDHFLAMGFDEEKVVKAIQEHGEDNMEAIANALLS	149
PtDRM2 UBA-	1SSSAEASSSVGSSSGSKMIDHFVKMGFPEKMKMVAKAIKENGEGDADSVLETLLT	97
OsDRM2 UBA-	1LPQDANGKANGSG-ALVAEFMGMGFPKEMILKAIKEIGDTDTEQLLELLLT	90
AtDRM3 UBA-	1 SFHGLMEPKPEPDIEYET-DRIRIALLT-MKFPENLVDFALDRLGKDTPIDEMVDFIV	156
PtDRM3 UBA-	1 KYSTVTGVKEEPDVFDEVYDDKRVSLLK-MNFPAKEVELAMDKLGENAPINEIIDFII	173
OsDRM3 UBA-	1 HFAPRKEVIQDIKVEADSSSEKRSYLLSTMNFSQREVDLALNQLGEEASLEQLVDFIV	169

AtDRM1	UBA-2	LSSDDEEDELNNSSNEDRILQALIKMGYLREDAAIAIERCGEDASMEEVVDFICAAQ	232
AtDRM2	UBA-3	MLNSDDEKDPNSNENGSKIRSLVKMGFSELEASLAVERCGENVDIAELTDFLCAAQ	235
PtDRM2	UBA-2	FSDVDSADDEVITKTVSDEDNKLAFLRRMG Y KEADASIAITRCGTEATISELADFICAAQ	187
OsDRM2	UBA-2	TPHSDGSGDEDFFQEMSEKDEKMKSLVNMGFPEDEAKMAIDRC-LDAPVAVLVDSIYASQ	194
AtDRM3	UBA-2	PEVPNEQLFETMDKTLRLLEMGFSNDEISMAIEKIGTKGQISVLAESIVTGE	243
PtDRM3	UBA-2	SWHYDDYYQDVNDETLYGTMDKTLCLLNMGFSENEVSLAIDKFGSEVPVTELANAICAHQ	280
OsDRM3	UBA-2	EVKDESLFGVMDKTLHLLQMGFTEEEVSSVIDKAGPEATVLELADTIFARR	238



MEA-ISR Col



1-TTTAATGTAAATATGTATT	IGATGCATCTAA CATTTAC			AGAAAAAAGCTCTTTTAAAATCCC	SAAAGTAACTATTTCAAAAAATCTAAAT-118
119-TATAAACTTAAATGTTTGG2	AATCGCGAACGACTATTG	TAAATATAAATG⊂T	AAATATACATGAA	GATGTGAAAAACATGTTGGATTT	VGTGGAATCCTTAATGACCACGGTTAAAT-234
235-GCCGGGATCCAAAATCCGG	TTAGATTTCACAATGTCA	VATTACG-276			

MEA-ISR DRM2cat-Myc drm1 drm2

1 - TTTAATGTAAATATGTATTT	GATGCATCTAACATTTA	STATCTAAACAAATA		AGAAAAAAGCTCTTTTAAAATCCGAA	AGTAACTATTTC	AAAAAATCTAAAT-118
119-TATAAACTTAAATGTTTGGA	ATCCCGAACGACTATTG	TAAATATAAATGCI	FAAATATACATGAA	GATGTGAAAAACATGTTGGATTTGT	GGAATCGTTAATG/	ACCACGGTTAAAT-234
235-GGCGGGATCCAAAATCCGGT	TAGATITCACAATGT CA	TATTACG-276				

1-TTTAATGTAAATATGTATTT	GATGCATCTAACAT	TTAGTATCTAAA	Салатааа		AAGAAAAAAGCTCTTTTAAAATCCGAA	AGTAACTATI	TTTCAAAAAAATCTAAAT-118
119-TATAAACTTTAAATGTTTGGAJ	ATCGCGAACGACTA	ITTGCTAAATATAA	AATGCTAA	ATATACATGA	AGATGTGAAAAACATGTTGGATTTGT	GGAATCGTTZ	AATGACCACGGTTAAAT-234
235-GCCCGGATCCAAAATCCCGGT	TAGATTTCACAATG	TCATATTACG-2	76				

MEA-ISR DRM2uba-Myc drm1 drm2



MEA-ISR drm3-1



MEA-ISR drm1 drm2

FWA Col

1-	GCCCAT		TCCGTCGAGA	ATCTCAT	ATATTC	TTTATCGAAGC	CCATACZ		ETCGAC	GAATCTCATATAT			TTCA		CATA	ACGAGCGC		TAGG-12
124-GTTI	TTGCTI	TTCGCCA	TTGGTCCAAG	TGCTATT	IGGTTG	TTTAAGGTTG	TTTTAG		ГТТААЛ	TATTATTTTATG	TTTT		ACGA	TTTAI	ICGAI	TTGTGGG	ATACTC	GACAA-2
244-TCAG	ATTATT	GTTGTTT		AATATCA	SATCTT		TATCCCA	JTTCAACA'	TTCAT/		TACGG	TTTTTG		TCGA	PATTO	EGTCGAAG	TGCTAI	TTGG-3

FWA

drm3-1

1-	GCCCAI		TTCCGTCGAGA	ATCTCAT	ATATT(TTTATCGAA	GCCCA	TACATCI	TCGZ	AGAA			PATCCC	ATTCP	ACAT		ACGAG	TAGG-1.	23
124-67777					TGGTT	ደጥጥ አልርርጥ ጥ			ጣጣ አ	ላ ጥል ጥ	ተን ጥጥጥን ልጥር	շփութութ			ጥጥጥ አ		۰		243
	7.00.11																		243
244 - TCAG	TTAAG	TTGT	TTTTCCAGCCA	CTTTAAT	SATCT'	ΓGCGCCGCTC		TTACGAT	GATT	PTGT.			TOAGAT	GCTTT	TCGA	CATT		TTTGG-:	494





Table S1. Sodium bisulfite sequencing analysis of MEA-ISR.

	Number of	Total	Mathulated CC	0/ CC	05% confidence	D voluo
Constine				70 CG	95% connuence	r-value
Genotype	ciones	CG	Siles	methylation	Interval	
		siles				
Col	18	162	155	95.7	91.4-97.9	-
DRM2-Myc drm1 drm2	22	198	167	84.3	78.6-88.8	9.3x10 ⁻⁴
DRM2cat-Myc drm1 drm2	21	189	154	81.5	75.3-86.4	8.8x10⁻⁵
DRM2uba-Myc drm1 drm2	26	234	164	70.1	63.9-75.6	5.7x10 ⁻¹⁰
drm3-1	22	198	159	80.3	74.2-85.2	2.8x10⁻⁵
drm1 drm2	18	162	138	85.2	78.9-89.8	2.5x10 ⁻³
	Number of	Total	Methylated	% CHG		
Genotype	clones	CHG	CHG sites	methylation		
		sites		-		
Cal	10	26	10	27.0	15 0 44 0	
	18	30	10	27.8	15.9-44.0	-
DRM2-Myc arm1 arm2	22	44	11	25.0	14.6-39.4	9.7X10
DRM2cat-Myc drm1 drm2	21	42	0	0.0	0.0-8.4	9.1x10
DRM2uba-Myc drm1 drm2	26	52	3	5.8	2.0-15.6	1.1x10 ⁻
drm3-1	22	44	3	6.8	2.4-18.2	2.6x10 ⁻²
drm1 drm2	18	36	0	0.0	0.0-9.6	2.2x10 ⁻³
	Number of	Total	Methylated	% CHH		
Genotype	clones	CHH	CHH sites	methylation		
		sites		-		
Col	18	432	80	18.5	15 1-22 5	
DRM2-Myc drm1 drm2	22	528	104	10.5	16 5-23 3	7.0×10^{-1}
DRM2cot Mvc drm1 drm2	21	504	104	0.9	0320	0.3×10^{-21}
	21	604	4	0.0	0.3-2.0	9.5×10 4.0×10 ⁻²¹
	20	024	11	1.8	1.0-3.1	4.2X IU
arm3-1	22	528	23	4.4	2.9-6.5	3.7X10
drm1 drm2	18	432	0	0.0	0.0-0.9	1.8x10 ⁻²⁰

Table S2. Sodium bisulfite sequencing analysis of FWA.

Genotype	Number of clones	Total CG sites	Methylated CG sites	% CG methylation	95% confidence interval	<i>P</i> -value
Col drm3-1 drm1 drm2	28 30 7	336 360 84	262 292 79	78.0 81.1 94.0	73.2-82.1 76.8-84.8 86.8-97.4	3.5x10 ⁻¹ 1.3x10 ⁻³
Genotype	Number of clones	Total CHG sites	Methylated CHG sites	% CHG methylation		
Col drm3-1 drm1 drm2	28 30 7	280 300 70	51 19 2	18.2 6.3 2.9	14.1-23.2 4.1-9.7 0.8-9.8	2.0x10 ⁻⁵ 2.5x10 ⁻³
Genotype	Number of clones	Total CHH sites	Methylated CHH sites	% CHH methylation		
Col drm3-1 drm1 drm2	28 30 7	1148 1230 287	223 46 0	19.4 3.7 0	17.2-21.8 2.8-5.0 0-1.3	3.5x10 ⁻³³ 9.5x10 ⁻¹⁶

	Total leaf number	
Genotype and line number	T ₁ leaf number	T ₂ progeny
Wild type Col4-3	32	13.8 +/- 0.65
Col5-1	27	11.7 +/- 0.62
Col1-3	22	13.7 +/- 0.34
Col3-1	27	12.4 +/- 0.64
Col2-5	26	11.0 +/- 0.21
Col1-1	21	12.4 +/- 0.68
Col3-8	19	22.4 +/- 0.55
Col2-6	20	17.9 +/- 0.61
Col4-8	26	17.6 +/- 0.71
Col4-4	24	16.5 +/- 0.65
drm3 7-9	35	11.1 +/- 0.34
drm3 12-19	39	32.4 +/- 1.64
drm3 5-1	32	11.2 +/- 0.27
drm3 11-1	39	12.9 +/- 0.81
drm3 9-6	31	23.7 +/- 1.84
drm3 1-5	32	10.4 +/- 0.15
drm3 2-1	36	22.9 +/- 1.16
drm3 5-1	38	17.0 +/- 1.01
drm3 1-4	36	14.0 +/- 0.69
drm3 2-4	30	16.8 +/- 0.7
<i>drm1 drm2</i> 2-9	42	41.3 +/- 1.45
<i>drm1 drm2</i> 2-1	47	46.8 +/- 1.63
drm1 drm2 3-8	42	48.4 +/- 1.08
drm1 drm2 5-5	42	44.5 +/- 0.81
drm1 drm2 2-9	42	51.0 +/- 1.24
drm1 drm2 2-9	49	45.8 +/- 0.85

Table S3. Average flowering-time of T_2 *FWA* transformant lines.

Table S4. Oligonucleotide sequences

Name	Sequence
JP980	5'-AAACCTTTCGTAAGCTACAGCCACTTTGTT-3'
JP981	5'-TCGGATTGGTTCTTCCTACCTCTTTACCTT-3'
JP1026	5'-AAAGTGGTTGTAGTTTATGAAAGGTTTTAT-3'
JP1027	5'-CTTAAAAAATTTTCAACTCATTTTTTAAAAAA-3'
JP2027	5'- TAG CATCTGAATTTCATAACCAATCTCGATACAC-3'
JP2603	5'-CTTGTAATTGGAGGAAGTCCTGCTAACAATCTGGCAGGCGGTAATAGG-3'
JP2604	5'-CCTATTACCGCCTGCCAGATTGTTAGCAGGACTTCCTCCAATTACAAG-3'
JP2631	5'-GTTTTTGCTACATTGTTTGACATGGGAGCTCCTGTTGAGATGATTTCTAGAGCGATC-3'
JP2632	5'-GATCGCTCTAGAAATCATCTCAACAGGAGCTCCCATGTCAAACAATGTAGCAAAAAC-3'
JP2633	5'-GCTATTGATCATTTCCTTGCTATGGGAGCTGATGAAGAAAAAGTTGTCAAAGCCATTC-3'
JP2634	5'-GAATGGCTTTGACAACTTTTCTTCATCAGCTCCCATAGCAAGGAAATGATCAATAGC-3'
JP2635	5'-GCAAAATACGGTCTTTGGTGAAGATGGGTGCTTCAGAGCTTGAAGCTTCTTTAGCTGTC-3'
JP2636	5'-GACAGCTAAAGAAGCTTCAAGCTCTGAAGCACCCATCTTCACCAAAGACCGTATTTTGC-3'
JP3192	5'-AGAGATCAAGTGGTGTTGATGGG-3'
JP3193	5'-TCCAGAAGAATACACTGGCTACG-3'
JP3477	5'-GTCGACATCCTGATAGAATAGTTATATCTCAAGTTTATCACTGC-3'
JP3479	5'-GTCGACATAACTTAAAACCTTATAATTAGATCAGATGTAAAACTTGTTCG-3'
JP3483	5'-GATCTTTGCCGGAAAACAATTGGAGG-3'
JP3484	5'-CGACTTGTCATTAGAAAGAAAGAGAGAT-3'
JP3510	5'- TTAACATTAATAAACAACAGC-3'
JP4549	5'-CGGGATCCATGGCTGATATGCGTAGACGAAATGG-3'
JP4550	5'-CGGGATCCCTACGAACTTGAGTCACCCATATCTTCGG-3'
JP4551	5'-CGGGATCCATGGAAACCCCATGGATGCAAGATGAG-3'
JP4552	5'-CGGGATCCCTACATCATATCTCTGACACGTTTCG-3'
JP6063	5'-CGGGATCCATGTACCCATACGACGTACCAGACTACGCAGTGATTTGGAATAACGATGATGATG
JP6065	5'-CATGCCATGGTCAAGATCCTCTCATCCTCGCACG-3'
JP6067	5'-
	AGGCGCGCCATGGAACAAAAACTAATATCAGAAGAAGACCTAGCTGATATGCGTAGACGAAATGGAAG-
	3'
JP6068	5'-GAAGGCCTCTACATCATATCTCTGACACGTTTCG-3'
JP6069	5'- CCCACCTGAGTTTGTGGACT-3'
JP6070	5'-TTTTACCCACCCAAACCAAA-3'
JP6699	5'-ACTTAATTAGCACTCAAATTAAACAAAATAAGT-3'
JP6700	5'-TTTAAACATAAGAAGAAGTTCCTTTTTCATCTAC-3'
JP2004	5'-GGTTTTATATTAATATTAAAGAGTTATGGGTYGAAGTTT-3'
JP2005	5'-CAAAATACTTTACACATAAACRAAAAAAAAAAAAAAAAA
JP4423	5'-AACCAAAATCATTCTCTAAACAAAATATAAAAAAATC-3'