

1 **SUPPLEMENTAL DATA**

2 Supplemental tables and figures were ordered according to their appearance in the text.

3

4 **Supplemental Table S1.** Time points of floral transition at short-day (SD) and long-day  
5 (LD) conditions. Days after sowing (DAS) and developmental stage (according to  
6 Abendroth *et al.*, 2011) at which floral transition occurred in the maize lines 4F-240 BX  
7 16, 4F-350 CN 2, B77 and E2558W are indicated. Plants were grown in a greenhouse  
8 under LD conditions and in a growth chamber with SD and LD conditions. Greenhouse  
9 data are given as mean values  $\pm$  standard deviation of 4 (4F-240 BX 16, 4F-350 CN 2)  
10 and 3 (B77, E2558W) independently grown populations, which were grown over a  
11 period of two years.

	long-day (greenhouse)		short-day (chamber)		long-day (chamber)	
	time (DAS)	dev. Stage	time (DAS)	dev. stage	time (DAS)	dev. stage
<b>4F-240 BX 16</b>	24.5 ( $\pm$ 1.29)	V5	24	V4	28	V4/V5
<b>4F-350 CN 2</b>	34.5 ( $\pm$ 1.29)	V7/V8	31	V5	35	V8
<b>B77</b>	24.7 ( $\pm$ 0.58)	V5	26	V4	26	V5
<b>E2558W</b>	35.0 ( $\pm$ 1.73)	V8	31	V5	33	V6

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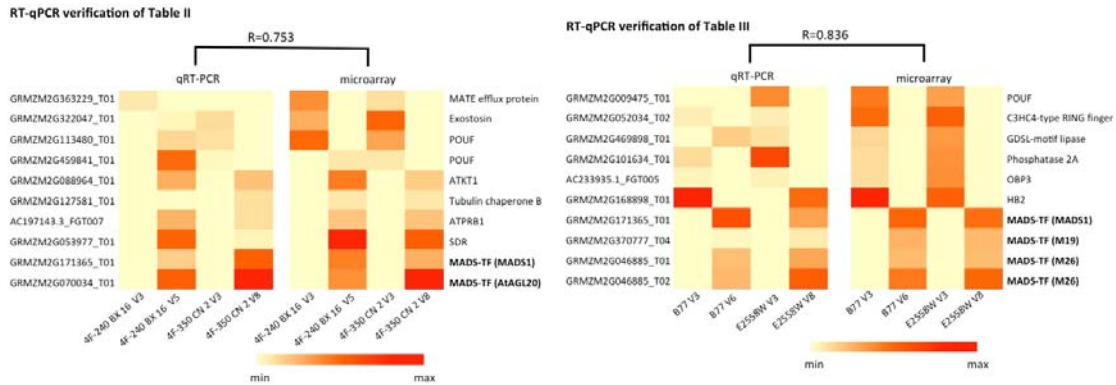
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22 **Supplemental Figure S1.** Validation of microarray results by RT-qPCR. Expression  
 23 levels of 10 selected genes from each microarray dataset were detected by RT-qPCR.  
 24 Heat map on the left was constructed with mean expression levels derived from three  
 25 biological replicates, while the right one showed expression level change in microarray  
 26 analysis. For each gene in one inbreed line, the minimum expression level at a certain  
 27 developmental stage was set to 1, and relative expression level in the other sample was  
 28 calculated according to the minimum expression level. Relative expression pattern is  
 29 shown by color scales as indicated in the bottom. R value on top represents the  
 30 correlation coefficient value between the two platforms.

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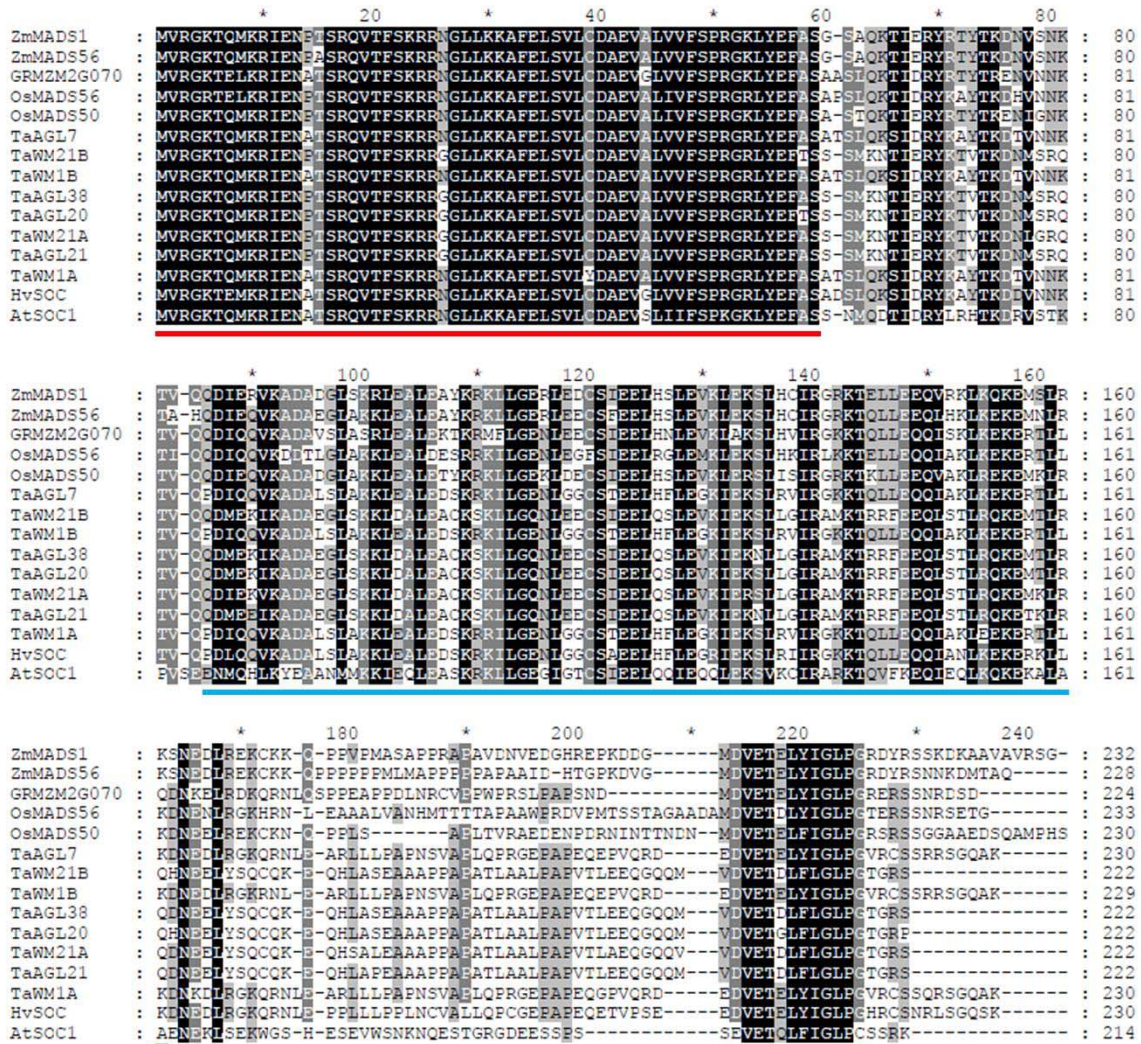
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33 **Supplemental Table S2.** Identifiers of proteins homologous to ZmMADS1 and ZMM26  
 34 in the plant species *Arabidopsis thaliana*, *Hordeum vulgare*, *Oryza sativa*, *Triticum*  
 35 *aestivum* and *Zea mays*.

<b>Species</b>	<b>Protein</b>	<b>Protein identifier</b>
<b><i>Arabidopsis thaliana</i></b>	AtAGL24	AT4G24540
	AtSOC1	AT2G45660
	AtSVP	AT2G22540
<b><i>Hordeum vulgare</i></b>	HvBM1	emb CAB97349.1
	HvBM1-2	emb CAB97350.1
	HvBM10	gb ABM21529.1
	HvSOC	dbj BAK00484.1
	HvVRT-2	gb ABB13345.1
<b><i>Oryza sativa</i></b>	OsMADS22	LOC_Os02g52340
	OsMADS47	LOC_Os03g08754
	OsMADS50	LOC_Os03g03070
	OsMADS55	LOC_Os06g11330
	OsMADS56	LOC_Os10g39130
<b><i>Triticum aestivum</i></b>	TaAGL7	gb ABF57947.1
	TaAGL11	gb ABF57916.1
	TaAGL13	gb ABF57917.1
	TaAGL20	gb ABF57922.1
	TaAGL21	gb ABF57923.1
	TaAGL36	gb ABF57936.1
	TaAGL38	gb ABF57938.1
	TaMADS10	gb ABL11476.1
	TaVRT-2	gb AAY43789.1
	TaWM1A	gb CAM59039.1
	TaWM1B	gb CAM59040.1
	TaWM21A	gb CAM59065.1
	TaWM21B	gb CAM59066.1
	TaWM22A	gb CAM59067.1
	TaWM22B	gb CAM59068.1
	TaWM24A	gb CAM59069.1
	TaWM24B	gb CAM59070.1
	TaWM28A	gb CAM59074.1
TaWM28B	gb CAM59075.1	
<b><i>Zea mays</i></b>	GRMZM2G070034	GRMZM2G070034
	ZmMADS1	GRMZM2G171365
	ZmMADS47	GRMZM2G059102
	ZmMADS56	GRMZM2G026223
	ZMM19	GRMZM2G370777
	ZMM21	GRMZM5G814279
	ZMM26	GRMZM2G046885

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39 **Supplemental Figure S2.** Protein sequence alignment of ZmMADS1 and homologous  
 40 proteins from maize, rice, wheat, barley and *Arabidopsis*. Conserved amino acids  
 41 between the sequences are shaded in black. The red bar marks the MADS-domain, the  
 42 blue bar marks the K-domain and the green bar marks the SOC1 motif.

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*          20          40          60          80
ZmM26 : -----MARERRRIKRIEAAARQVTFKRRRGLFKKAEI SVLCDADVALVVFSSSTGKLSGFASSSMNIIIDKYN : 70
ZmM19 : -----MARERRRIKRIEAAARQVTFKRRRGLFKKAEI SVLCDADVALVVFSSSTGKLSGFASSSMNIIIDKYS : 70
ZmMADS47 : -----MVGTKRERIAIRRIDNLAARQVTFKRRRGLFKKAEI SVLCDADVALVVFSSSTGKLSGFASSSMKQVIDRMD : 74
ZmM21 : -----MARERRRIKRIEAAARQVTFKRRRGLFKKAEI SVLCDADVALVVFSSSTGKLSGFASSSMNIIIDKYS : 70
HvBM10 : -----MARERRRIKRIEAAARQVTFKRRRGLFKKAEI SVLCDADVALVVFSSSTGKLSGFASSSMNIIIDKYS : 70
HvVRT-2 : -----MARERRRIKRIEAAARQVTFKRRRGLFKKAEI SVLCDADVALVVFSSSTGKLSGFASSSMNIIIDKYS : 70
HvBM1-2 : -----MAGKRERIAIRRIDNLAARQVTFKRRRGLFKKAEI SVLCDADVALVVFSSSTGKLSGFASSSMNIIIDKYN : 72
HvBM1 : -----MAGKRERIAIRRIDNLAARQVTFKRRRGLFKKAEI SVLCDADVALVVFSSSTGKLSGFASSSMNIIIDKYN : 72
OsMADS22 : -----MARERRRIKRIEAAARQVTFKRRRGLFKKAEI SVLCDADVALVVFSSSTGKLSGFASSSMNIIIDKYN : 70
OsMADS55 : -----MARERRRIKRIEAAARQVTFKRRRGLFKKAEI SVLCDADVALVVFSSSTGKLSGFASSSMNIIIDKYT : 70
OsMADS47 : MAGGGGGGGRGEGERAATGKRERIAIRRIDNLAARQVTFKRRRGLFKKAEI SVLCDADVALVVFSSSTGKLSGFASSSMNIIIDKYN : 89
TaAGL11 : -----MARERRRIKRIEAAARQVTFKRRRGLFKKAEI SVLCDADVALVVFSSSTGKLSGFASSSMNIIIDKYS : 70
TaWM22A : -----MARERRRIKRIEAAARQVTFKRRRGLFKKAEI SVLCDADVALVVFSSSTGKLSGFASSSMNIIIDKYS : 70
TaWM22B : -----MARERRRIKRIEAAARQVTFKRRRGLFKKAEI SVLCDADVALVVFSSSTGKLSGFASSSMNIIIDKYS : 70
TaWM24B : -----MARERRRIKRIEAAARQVTFKRRRGLFKKAEI SVLCDADVALVVFSSSTGKLSGFASSSMNIIIDKYS : 70
TaWM24A : -----MARERRRIKRIEAAARQVTFKRRRGLFKKAEI SVLCDADVALVVFSSSTGKLSGFASSSMNIIIDKYS : 70
TaAGL36 : -----MARERRRIKRIEAAARQVTFKRRRGLFKKAEI SVLCDADVALVVFSSSTGKLSGFASSSMNIIIDKYS : 70
TaVRT-2 : -----MARERRRIKRIEAAARQVTFKRRRGLFKKAEI SVLCDADVALVVFSSSTGKLSGFASSSMNIIIDKYS : 70
TaWM28B : -----MAGKRERIAIRRIDNLAARQVTFKRRRGLFKKAEI SVLCDADVALVVFSSSTGKLSGFASSSMNIIIDKYN : 72
TaWM28A : -----MAGKRERIAIRRIDNLAARQVTFKRRRGLFKKAEI SVLCDADVALVVFSSSTGKLSGFASSSMNIIIDKYN : 72
TaAGL13 : -----MAGKRERIAIRRIDNLAARQVTFKRRRGLFKKAEI SVLCDADVALVVFSSSTGKLSGFASSSMNIIIDKYN : 72
TaMADS10 : -----MAGFRERIAIRRIDNLAARQVTFKRRRGLFKKAEI SVLCDADVALVVFSSSTGKLSGFASSSMNIIIDKYN : 72
AtSVP : -----MAREKIRIKRIDNLAARQVTFKRRRGLFKKAEI SVLCDADVALVVFSSSTGKLSGFASSSMKREIVLRHN : 70
AtAGL24 : -----MAREKIRIKRIDNLAARQVTFKRRRGLFKKAEI SVLCDADVALVVFSSSTGKLSGFASSSMRRIILERN : 70

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*          100          120          140          160          180
ZmM26 : THSKNLKTE-QPSIDIN-LEHSKYANINEQLAEASIRLRMRGEELEGLNVELOCLEKNLESLGHFVICTKQQQLEQINIDLEPKST : 157
ZmM19 : THSKNLKAE-QPSIDIN-LEHSKYANINEQLAEASIRLRMRGEELEGLNVELOCLEKNLESLGHFVICTKQQQLEQISDLQKST : 157
ZmMADS47 : SHSKNLRSPEQSSQLQSHMDGTCARLKEELAEASIRLRMRGEELEGLNVELOCLEKNLESLGHFVICTKRSCKILLDEISLQPKRT : 163
ZmM21 : THSKNLKSHQPSIDIN-VEOSKYSGNEQLAEASIRLRMRGEELEGLNVELOCLEKNLESLGHFVICTKQDLLEMOQIGELLQKGT : 158
HvBM10 : THSKNLKTD-OPTADIN-LEHSKYANINDOLAEASIRLRMRGEELEGLNVELOCLEKNLETLGHFVICTKQQQLEQINIDLEPKST : 157
HvVRT-2 : THSKNLKSDQPPADIN-LEHCKYDSINEQLAEASIRLRMRGEELEGLNVELOCLEKNLETLGHFVICTKQRQEMQOISDLQKGT : 158
HvBM1-2 : SHSKLKKVDEPSQDTH--EDSNCARLDELAEASIRLRMRGEELEGLNVELOCLEKNLESLGHFVICTKRSCKIMQOISLEPKRV : 159
HvBM1 : SHSKLKKVDEPSQDTH--EDSNCARLDELAEASIRLRMRGEELEGLNVELOCLEKNLESLGHFVICTKRSCKIMQOISLEPKRV : 159
OsMADS22 : THSKNLKAE-QPSIDIN-LEHSKYANINEQLAEASIRLRMRGEELEGLNVELOCLEKNLESLGHFVICTKQQQEMQOISLEPKST : 157
OsMADS55 : THSKNLKTDKQPSIDIN--MRGEELEGLNVELOCLEKNLESLGHFVICTKQQQEMQOISLEPKST : 136
OsMADS47 : SHSKTLQRAE-PSQDLQGEDSTCARLKEELAEASIRLRMRGEELEGLNVELOCLEKNLESLGHFVICTKRSCKILLDEISLQPKRT : 177
TaAGL11 : THSKNLKTD-OPTADIN-LEHSKYANINDOLAEASIRLRMRGEELEGLNVELOCLEKNLETLGHFVICTKQQQLEQINIDLEPKST : 157
TaWM22A : THSKNLKTD-REPADIN-LEHSKYANINDOLAEASIRLRMRGEELEGLNVELOCLEKNLETLGHFVICTKQQQLEQINIDLEPKST : 157
TaWM22B : THSKNLKTD-OPTADIN-LEHSKYANINDOLAEASIRLRMRGEELEGLNVELOCLEKNLETLGHFVICTKQQQLEQINIDLEPKST : 157
TaWM24B : THSKNLKSDQPPADIN-LEHCKYDSINEQLAEASIRLRMRGEELEGLNVELOCLEKNLETLGHFVICTKQRQEMQOISDLQKGT : 158
TaWM24A : THSKNLKSDQPPADIN-LEHCKYDSINEQLAEASIRLRMRGEELEGLNVELOCLEKNLETLGHFVICTKQRQEMQOISDLQKGT : 158
TaAGL36 : THSKNLKSDQPPADIN-LEHCKYDSINEQLAEASIRLRMRGEELEGLNVELOCLEKNLETLGHFVICTKQRQEMQOISDLQKGT : 158
TaVRT-2 : THSKNLKSDQPPADIN-LEHCKYDSINEQLAEASIRLRMRGEELEGLNVELOCLEKNLETLGHFVICTKQRQEMQOISDLQKGT : 158
TaWM28B : SHSKLKKADEPSQDTH--EDSNCARLDELAEASIRLRMRGEELEGLNVELOCLEKNLESLGHFVICTKRSCKIMQOISLEPKRV : 159
TaWM28A : SHSKLKKADEPSQDTH--EDSNCARLDELAEASIRLRMRGEELEGLNVELOCLEKNLESLGHFVICTKRSCKIMQOISLEPKRV : 159
TaAGL13 : SHSKLKKADEPSQDTH--EDSNCARLDELAEASIRLRMRGEELEGLNVELOCLEKNLESLGHFVICTKRSCKIMQOISLEPKRV : 159
TaMADS10 : SHSKLKKADEPSQDTH--EDSNCARLDELAEASIRLRMRGEELEGLNVELOCLEKNLESLGHFVICTKRSCKIMQOISLEPKRV : 159
AtSVP : LQSKNLEKLD-QPSHETQLVENSNDHRSKIDAKSHIRLRMRGEELEGLNVELOCLEKNLESLGHFVICTKRSCKIMQOISLEPKRV : 158
AtAGL24 : LEASINIKLMDPPSTHTR--LQSKNLEKLD-QPSHETQLVENSNDHRSKIDAKSHIRLRMRGEELEGLNVELOCLEKNLESLGHFVICTKRSCKIMQOISLEPKRV : 158

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80          *          200          *          220          *          240          *          260
ZmM26 : QIAGENMRLRNOVSCIPVAGKQ-----AVAD--TE-NVIAFEGQSSSVMTALHSGS--SQDNDGSDVSLKLEGLFCVAVK : 228
ZmM19 : QIAGENMRLRNOVSHIPVAGKQ-----SVAD--AE-NVIAFEGQSSSVMTALHSGS--SQDNDGSDVSLKLEGLFCVAVK : 228
ZmMADS47 : QIAGENMRLRNOVTRVSRMETQ-----LGAD--PE-FVVEEGQSSSVTNTSYPRP--PLDTESSDTSRLRGLFLFSK : 233
ZmM21 : QIADENRRLKKECK-----ISSLKTGS-----RNI----- : 183
HvBM10 : QIAGENMRLRNOVACVPTAGKL-----VVVD--TE-NVIAFEGQSSSVMTALHSGS--SQDNDGSDVSLKLEGLFCVAVK : 225
HvVRT-2 : QIAGENMRLRNOVACVPTAGKL-----VVVD--TE-NVIAFEGQSSSVMTALHSGS--SQDNDGSDVSLKLEGLFCVAVK : 223
HvBM1-2 : QIAGENMRLRNOVACVPTAGKL-----EM-----QVAA--DPLVVVYDEGQSSSVTNTSYPRP--PLDTESSDTSRLRGLFLFSK : 227
HvBM1 : QIAGENMRLRNOVACVPTAGKL-----EM-----QVAA--DPLVVVYDEGQSSSVTNTSYPRP--PLDTESSDTSRLRGLFLFSK : 229
OsMADS22 : QIAGENMRLRNOVSCIPVAGKQ-----AVAD--TE-NVIAFEGQSSSVMTALHSGS--SQDNDGSDVSLKLEGLFCVAVK : 228
OsMADS55 : QIAGENMRLRNOVTRVSRMETQ-----LGAD--PE-FVVEEGQSSSVTNTSYPRP--PLDTESSDTSRLRGLFLFSK : 199
OsMADS47 : QIAGENMRLRNOVTRVSRMETQ-----QPGP--DS-EIVVEEGQSSSVTNTSYPRP--PPDNDYSSDTSRLRGLFLFSK : 248
TaAGL11 : QIAGENMRLRNOVACVPTAGKL-----VVVD--TE-NVIAFEGQSSSVMTALHSGS--SQDNDGSDVSLKLEGLFCVAVK : 228
TaWM22A : QIAGENMRLRNOVACVPTAGKL-----VVVD--TE-NVIAFEGQSSSVMTALHSGS--SQDNDGSDVSLKLEGLFCVAVK : 228
TaWM22B : QIAGENMRLRNOVACVPTAGKL-----VVVD--TE-NVIAFEGQSSSVMTALHSGS--SQDNDGSDVSLKLEGLFCVAVK : 228
TaWM24B : QIAGENMRLRNOVACVPTAGKL-----AVAE--AE-NVVEPDAHSSDSVMTAVHSGS--SQDNDGSDVSLKLEGLFCVAVK : 226
TaWM24A : QIAGENMRLRNOVACVPTAGKL-----AVAE--AE-NVVEPDAHSSDSVMTAVHSGS--SQDNDGSDVSLKLEGLFCVAVK : 226
TaAGL36 : QIAGENMRLRNOVACVPTAGKL-----AVADAE--NVVDDVHSSDSVMTAVHSGS--SQDNDGSDVSLKLEGLFCVAVK : 228
TaVRT-2 : QIAGENMRLRNOVACVPTAGKL-----AVAE--AE-NVVEPDAHSSDSVMTAVHSGS--SQDNDGSDVSLKLEGLFCVAVK : 226
TaWM28B : QIAGENMRLRNOVACVPTAGKL-----EM-----QVAA--DS-PAVVEEGQSSSVTNTSYPRP--PLDTESSDTSRLRGLFLFSK : 226
TaWM28A : QIAGENMRLRNOVACVPTAGKL-----EM-----QVAA--DS-PAVVEEGQSSSVTNTSYPRP--PLDTESSDTSRLRGLFLFSK : 226
TaAGL13 : QIAGENMRLRNOVACVPTAGKL-----EM-----QVAA--DS-PAVVEEGQSSSVTNTSYPRP--PLDTESSDTSRLRGLFLFSK : 226
TaMADS10 : QIAGENMRLRNOVACVPTAGKL-----EM-----QVAA--DS-PAVVEEGQSSSVTNTSYPRP--PLDTESSDTSRLRGLFLFSK : 226
AtSVP : QIADENRRLKKECK-----ISSLKTGS-----RNI----- : 240
AtAGL24 : QIADENRRLKKECK-----ISSLKTGS-----RNI----- : 220

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45 **Supplemental Figure S3.** Protein sequence alignment of ZMM26 and its homologs from  
46 maize, barley, rice, wheat and *Arabidopsis*. Conserved amino acids between the  
47 sequences are shaded in black. The red bar marks the MADS-domain and the blue bar  
48 marks the K-domain.

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50 **Supplemental Table S3.** Log<sub>2</sub> transformed relative expression values of *ZmGIGZ1a* in  
 51 leaves of the maize lines 4F-350 CN 2, 4F-240 BX 16, E2558W and B77. Samples were  
 52 taken in 4 hour intervals over a period of 2 days. Plants were grown under SD  
 53 conditions. Mean values of biological triplicates and standard deviations (st dev) are  
 54 indicated.

SD <i>GIGZ1a</i> time (h)	4F-350 CN2		4F-240 BX16		E2558W		B77	
	mean	st dev	mean	st dev	mean	st dev	mean	st dev
0	0,30	0,46	0,49	0,60	0,36	0,13	0,13	0,18
4	3,11	0,56	4,53	1,05	3,04	0,58	1,76	0,90
8	5,42	0,07	6,56	1,33	5,69	0,88	3,53	0,84
12	4,62	0,67	7,38	0,20	5,27	0,76	3,30	0,40
16	3,86	0,07	3,03	0,73	4,47	0,39	3,22	0,61
20	2,27	0,67	2,56	1,72	2,44	0,63	1,46	0,61
24	0,73	0,32	1,70	1,33	0,21	0,30	0,43	0,24
28	3,03	0,34	4,50	1,11	3,25	0,62	1,68	0,73
32	5,28	0,14	5,92	0,93	5,69	0,63	3,87	0,70
36	5,01	0,30	5,87	1,02	5,10	0,47	3,66	0,49
40	4,20	0,23	4,34	1,49	3,98	0,98	3,40	0,85
44	1,62	0,35	0,76	0,81	2,35	0,40	1,25	0,60
48	0,03	0,04	0,43	0,55	0,45	0,42	0,02	0,03

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57 **Supplemental Table S4.** Log<sub>2</sub> transformed relative expression values of *ZmGIGZ1a* in  
 58 leaves of the maize lines 4F-350 CN 2, 4F-240 BX 16, E2558W and B77. Samples were  
 59 taken in 4 hour intervals over a period of 2 days. Plants were grown under LD  
 60 conditions. Mean values of biological triplicates and standard deviations (st dev) are  
 61 indicated.

LD <i>GIGZ1a</i> time (h)	4F-350 CN2		4F-240 BX16		E2558W		B77	
	mean	st dev	mean	st dev	mean	st dev	mean	st dev
0	0,93	0,31	0,00	0,00	0,88	0,35	0,77	0,55
4	2,54	0,11	4,10	0,59	3,87	0,34	1,93	0,63
8	4,35	0,40	8,14	0,79	5,45	0,64	3,76	0,24
12	4,83	0,28	6,38	0,45	5,32	0,29	4,56	0,66
16	2,78	0,15	4,08	0,76	3,70	0,21	3,30	0,58
20	2,45	0,06	1,57	0,67	1,61	0,47	1,76	0,57
24	0,42	0,23	0,35	0,26	0,00	0,00	0,31	0,27
28	2,49	0,34	5,51	1,03	4,01	0,42	1,82	0,68
32	4,26	0,18	6,40	0,28	6,42	0,29	4,22	0,62
36	4,72	0,51	6,59	0,88	6,23	0,27	4,56	0,27
40	2,90	0,28	4,68	0,57	4,15	0,46	3,41	0,47
44	2,40	0,47	3,08	1,92	2,92	0,69	1,43	0,33
48	0,00	0,00	1,98	2,17	1,13	0,12	0,33	0,33

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65 **Supplemental Table S5.** Log2 transformed relative expression values of *ZmMADS1* in  
 66 leaves of the maize lines 4F-350 CN 2, 4F-240 BX 16, E2558W and B77. Samples were  
 67 taken in 4 hour intervals over a period of 2 days. Plants were grown under SD  
 68 conditions. Mean values of biological triplicates and standard deviations (st dev) are  
 69 indicated.

SD <i>MADS1</i> time (h)	4F-350 CN2		4F-240 BX16		E2558W		B77	
	mean	st dev	mean	st dev	mean	st dev	mean	st dev
0	3,70	0,03	3,55	0,66	2,90	0,30	4,04	0,35
4	0,15	0,14	1,92	2,43	0,99	0,32	1,55	0,63
8	0,18	0,13	0,52	0,69	0,31	0,44	0,22	0,31
12	0,66	0,47	2,06	1,46	1,24	0,23	0,24	0,30
16	2,77	0,21	2,63	1,92	2,95	0,58	2,01	0,52
20	2,05	0,48	3,38	1,59	2,80	0,17	2,58	0,68
24	2,75	0,15	4,41	0,30	2,49	0,32	3,52	0,55
28	0,91	0,70	3,10	1,05	0,66	0,33	1,34	0,33
32	0,67	0,31	0,81	0,42	1,01	0,72	0,90	0,39
36	1,07	0,31	2,32	0,67	0,90	0,29	0,60	0,31
40	2,25	0,57	3,02	1,40	2,09	0,57	1,47	0,98
44	1,91	0,43	2,20	0,48	2,51	0,17	3,23	0,53
48	2,70	0,44	2,33	0,60	3,11	0,82	3,47	0,89

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72 **Supplemental Table S6.** Log2 transformed relative expression values of *ZmMADS1* in  
 73 leaves of the maize lines 4F-350 CN 2, 4F-240 BX 16, E2558W and B77. Samples were  
 74 taken in 4 hour intervals over a period of 2 days. Plants were grown under LD conditions.  
 75 Mean values of biological triplicates and standard deviations (st dev) are indicated.

LD <i>MADS1</i> time (h)	4F-350 CN2		4F-240 BX16		E2558W		B77	
	mean	st dev	mean	st dev	mean	st dev	mean	st dev
0	2,33	0,29	1,94	1,06	1,86	0,23	3,03	0,35
4	0,80	0,12	0,62	0,25	0,57	0,42	1,43	0,43
8	0,03	0,04	0,83	0,58	0,24	0,34	0,13	0,16
12	0,55	0,09	0,23	0,17	0,18	0,06	0,06	0,08
16	0,73	0,16	1,29	0,91	0,92	0,40	1,06	0,34
20	2,36	0,16	1,66	0,67	1,03	0,19	1,72	0,48
24	3,13	0,54	1,19	0,34	1,48	0,32	3,06	0,20
28	0,92	0,05	1,50	0,19	0,46	0,07	1,22	0,44
32	0,61	0,16	0,40	0,32	0,57	0,48	0,95	0,31
36	0,74	0,63	0,85	0,61	0,83	0,28	1,24	0,11
40	1,30	0,40	0,91	0,64	0,50	0,17	1,35	0,38
44	2,26	0,36	1,19	0,64	1,13	0,70	2,08	0,50
48	2,62	0,22	2,06	0,27	2,32	0,14	2,87	0,56

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79 **Supplemental Table S7.** Log2 transformed relative expression values of *ZMM19* in  
 80 leaves of the maize lines 4F-350 CN 2, 4F-240 BX 16, E2558W and B77. Samples were  
 81 taken in 4 hour intervals over a period of 2 days. Plants were grown under SD  
 82 conditions. Mean values of biological triplicates and standard deviations (st dev) are  
 83 indicated.

SD <i>ZmM19</i> time (h)	4F-350 CN2		4F-240 BX16		E2558W		B77	
	mean	st dev	mean	st dev	mean	st dev	mean	st dev
0	0,86	0,16	1,10	1,01	0,44	0,16	1,29	0,31
4	1,60	0,53	2,01	1,35	1,53	0,36	2,25	0,63
8	2,59	0,12	2,32	0,83	1,90	0,35	2,34	0,19
12	1,28	0,55	3,08	0,62	1,53	0,65	1,51	0,06
16	1,11	0,23	0,85	0,63	1,27	0,44	1,86	0,34
20	0,34	0,48	0,31	0,44	0,28	0,22	0,35	0,25
24	1,49	0,46	2,11	1,18	0,15	0,19	0,80	0,38
28	1,60	0,24	1,82	1,05	1,20	0,31	1,98	0,34
32	2,37	0,25	2,33	1,22	2,60	0,37	2,39	0,35
36	1,78	0,30	2,24	0,77	1,48	0,29	2,14	0,08
40	1,16	0,19	3,19	1,06	0,86	0,53	1,95	0,51
44	0,07	0,09	0,56	0,64	0,05	0,05	0,07	0,10
48	1,21	0,04	1,00	0,51	0,40	0,66	0,25	0,22

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86 **Supplemental Table S8.** Log2 transformed relative expression values of *ZMM19* in  
 87 leaves of the maize lines 4F-350 CN 2, 4F-240 BX 16, E2558W and B77. Samples were  
 88 taken in 4 hour intervals over a period of 2 days. Plants were grown under LD  
 89 conditions. Mean values of biological triplicates and standard deviations (st dev) are  
 90 indicated.

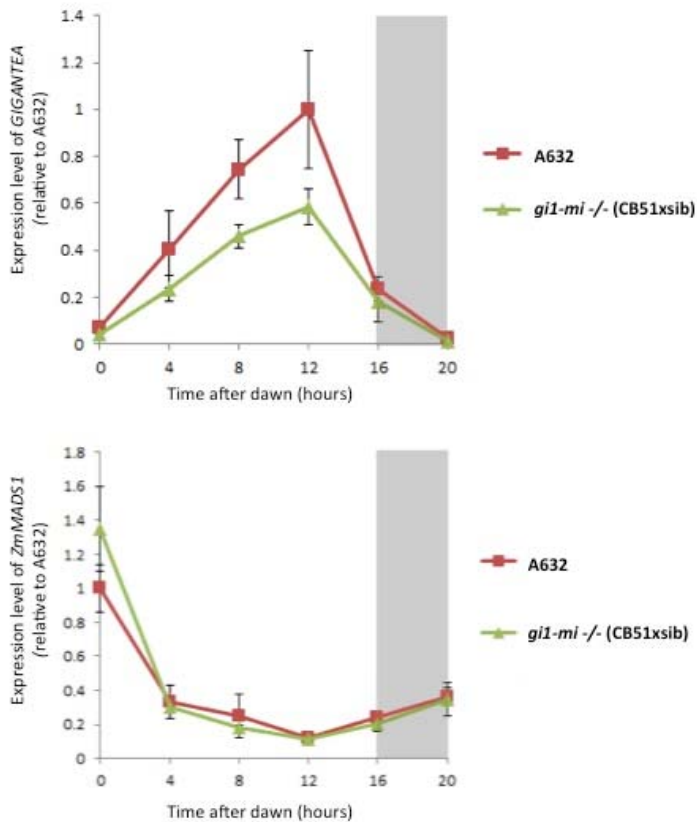
LD <i>ZmM19</i> time (h)	4F-350 CN2		4F-240 BX16		E2558W		B77	
	mean	st dev	mean	st dev	mean	st dev	mean	st dev
0	0,74	0,51	0,39	0,38	0,54	0,27	1,03	0,37
4	1,08	0,36	1,82	0,34	1,11	0,33	1,75	0,19
8	1,20	0,71	2,18	0,58	0,99	0,32	1,88	0,11
12	1,31	0,48	2,29	0,50	1,14	0,30	2,29	0,60
16	0,00	0,00	1,33	0,32	0,49	0,39	1,34	0,41
20	0,93	0,52	0,74	0,82	0,14	0,10	0,96	0,78
24	0,97	0,14	0,76	0,67	0,22	0,18	1,11	0,79
28	1,65	0,61	1,24	0,23	1,69	0,38	1,83	0,33
32	1,51	0,37	2,42	0,25	2,35	0,42	2,30	0,57
36	1,67	0,90	2,08	0,48	2,19	0,06	2,46	0,25
40	0,59	0,34	1,90	0,83	0,70	0,22	1,59	0,19
44	1,14	0,68	0,93	0,81	0,57	0,42	0,68	0,59
48	0,65	0,35	0,78	0,66	0,61	0,30	0,64	0,46

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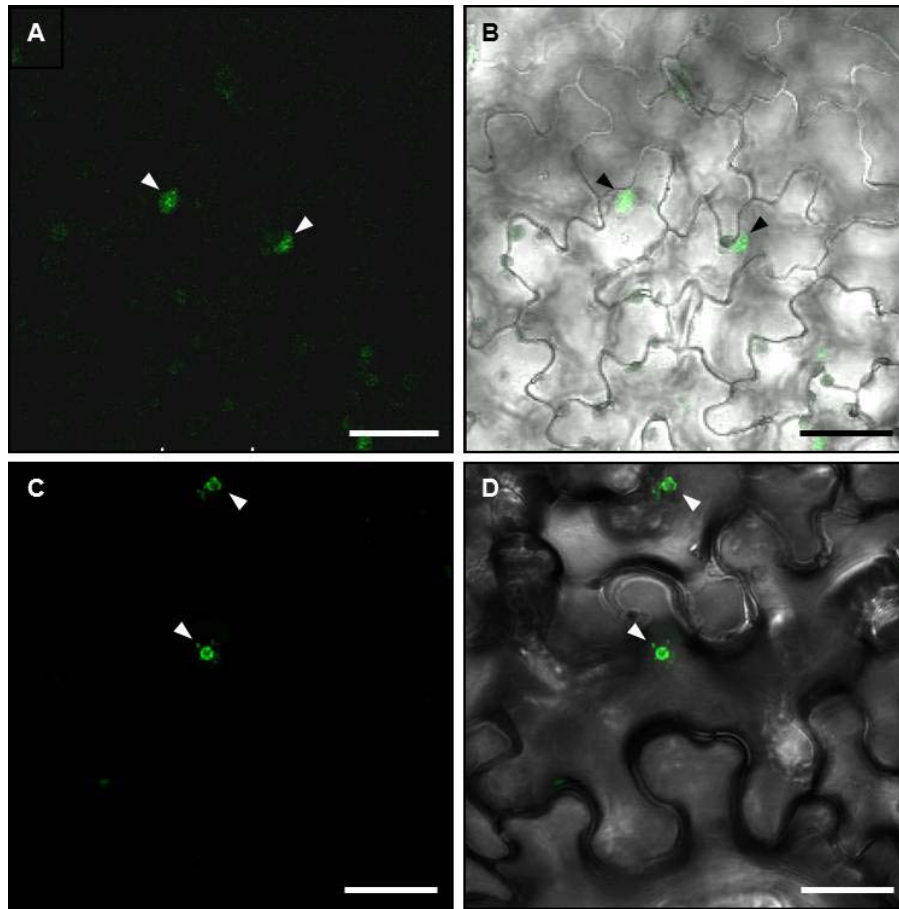


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95 **Supplemental Figure S4.** Diurnal expression of *ZmMADS1* is not dependent on  
96 *GIGANTEA*. Experiment was performed according to Bendix et al. (2013). Above:  
97 Expression level of *GIGANTEA* was reduced in the *gi1-mi-/- (CB51xsib)* mutant allele  
98 under LD conditions compared with inbreed line A632 containing the same genetic  
99 background. Plants were grown under LD condition in the greenhouse. Samples from  
100 the uppermost leaf of V8 stage were taken. Diurnal regulation of *ZmMADS1* was not  
101 altered in the *gi1-mi-/- (CB51xsib)* mutant allele. Sampling was done as described above.  
102 Mean of three biological replicates are shown and error bars are standard deviation of  
103 the mean. Relative expression levels are shown with red and green lines, respectively.  
104 Grey areas indicate dark periods. The highest expression level of the control was set to 1  
105 in each experiment and relative gene expression levels calculated accordingly.

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111 **Supplemental Figure S5.** Subcellular localization of ZmMADS1-GFP. A and B, Confocal  
 112 laser scanning microscopy (CLSM) image of *Arabidopsis soc1-2* leaf epidermis cells (A)  
 113 and *Nicotiana benthamiana* leaf epidermis (C) cells transiently transformed with  
 114 p35S:ZmMADS1-GFP. Fluorescence signal was detected in the nucleus (arrow heads). B  
 115 and D, Merge of fluorescence and bright field image of *Arabidopsis soc1-2* leaf (B) and  
 116 tobacco leaf (D). The scale bar represents 25  $\mu\text{m}$ .

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122 **Supplemental Table S9.** Flowering time in *pUBI:MADS1* plants given as days after  
 123 emergence of plants until reaching VT, anthesis and R1 (silking). The height from the  
 124 bottom to the lowest branch of the tassels is indicated in cm. Numbers of plants (n),  
 125 mean values and  $\pm$  standard deviation are indicated. Asterisks indicate highly significant  
 126 differences ( $p \leq 0.01$ ) to the control plants.

	Days to VT	Days to anthesis	Days to R1	Height in cm
<b><i>pUBI:MADS1</i> group 1</b>	66.7 $\pm$ 4.45 (n = 9)	68.7 $\pm$ 4.55 (n = 9) *	79.3 $\pm$ 10.39 (n = 9)	243.2 $\pm$ 16.70 (n = 9) *
<b><i>pUBI:MADS1</i> group 2</b>	62.6 $\pm$ 11.53 (n = 12)	66.2 $\pm$ 5.27 (n = 12)	77.2 $\pm$ 8.28 (n = 11)	221.3 $\pm$ 13.21 (n = 12)
<b><i>pUBI:MADS1</i> group 3</b>	56.7 $\pm$ 2.05 (n = 7) *	57.7 $\pm$ 2.31 (n = 7) *	62.9 $\pm$ 4.91 (n = 8) *	160.6 $\pm$ 47.71 (n = 8) *
<b>Control</b>	63.1 $\pm$ 5.28 (n = 59)	64.3 $\pm$ 4.73 (n = 57)	78,7.7 $\pm$ 9.96 (n = 48)	224.7 $\pm$ 18.89 (n = 58)

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130 **Supplemental Table S10.** Flowering time in *pUBI:MADS1-RNAi* plants given as days  
 131 after emergence of plants until reaching anthesis and R1 (silking), respectively. The  
 132 height from the bottom to the lowest branch of the tassels is indicated in cm. Numbers of  
 133 plants (n), mean values and  $\pm$  standard deviation are indicated. Asterisks mark  
 134 significant differences ( $p \leq 0.05$ ), while two asterisks mark highly significant differences  
 135 ( $p \leq 0.01$ ) to control plants.

	Days to anthesis	Days to R1	Height in cm
<b><i>pUBI:MADS1-RNAi</i> group 1</b>	67.6 $\pm$ 1.71 (n = 10)	74.3 $\pm$ 4.32 (n = 10)	149.1 $\pm$ 11.73 (n = 10)
<b><i>pUBI:MADS1-RNAi</i> group 2</b>	73.3 $\pm$ 2.45 (n = 10) **	78.8 $\pm$ 0.92 (n = 10) **	158.8 $\pm$ 15.62 (n = 10) *
<b>Control</b>	68.9 $\pm$ 2.61 (n = 12)	74.3 $\pm$ 3.31 (n = 12)	143.5 $\pm$ 14.69 (n = 12)

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Name	Sequence
ZmGAPDH-fwd	AGGGTCCACTCAAGGGTATCAT
ZmGAPDH-rev	ACGAGCTTGACGAAGTGGTC
ZmMADS1-fwd	ACGTGGAGGACGGTCACCGG
ZmMADS1-rev	GACCTGACCGCCACTGCAGC
ZmMADS56-fwd	TGCAAGCCAAGCCCAAGCCA
ZmMADS56-rev	TGAGCAGGCCGGAGCAGCTA
GRMZM2G070034-fwd	GACCCTGCTCCAAGACAACA
GRMZM2G070034-rev	TCCCTGCCGGGTAATCCTAT
ZMM26-fwd	GGCAGATGAGAGGTGAAGA
ZMM26-rev	GACAAGGAGCCTCATTTCTG
ZMM19-fwd	TGATCTGGGTGGAGCTGCGG
ZMM19-rev	CTACGCTCAGTTGTATGCAGACTC
ZmGIGZ1a-fwd	AGCCCGTCCTACCGGTGCC
ZmGIGZ1a-rev	TTGGAAGCCGATGTCAGATCCAGGA
GRMZM2G053977_T01-fwd	AACTTCTTGAAGGCCCGATT
GRMZM2G053977_T01-rev	ATCACATGCTTTGTGCCGTA
GRMZM2G070034_T01-fwd	GCCGTAAGCTTGGCAAGTAG
GRMZM2G070034_T01-rev	AGCAGGGTCCTCTCCTTCTC
GRMZM2G171365_T01-fwd	GGCAGAGACTACCGCTCAAG
GRMZM2G171365_T01-rev	CTTGCATCTCGATCTCCACA
GRMZM2G363229_T01-fwd	TGCTGATGATGCTGATAGGC
GRMZM2G363229_T01-rev	AGAGCTGGAGGACGACTACG
GRMZM2G322047_T01-fwd	GCATCCGAATCCTGTCAAGT
GRMZM2G322047_T01-rev	CTCAGACGAGCACACCAAAA
GRMZM2G459841_T01-fwd	ATGGAGACCTCTGAGCGGAA
GRMZM2G459841_T01-rev	GCGATACGTCCACACCTCAT
GRMZM2G113480_T01-fwd	GAAACGAAGCTGACCAGGAG
GRMZM2G113480_T01-rev	CCACCATCTTGCTCTTCCAC
GRMZM2G088964_T01-fwd	CTGCGAATGAAGCTGCACAA
GRMZM2G088964_T01-rev	TGCATGCGAACTGTTCTATTTTGA
GRMZM2G127581_T01-fwd	AAAGGCATTGCTTCTTTGA

GRMZM2G127581_T01-rev	ATGATTGCCCAAGAAGATGC
AC197143.3_FGT007-fwd	CCAGCAGCAGCATAGCAGTA
AC197143.3_FGT007-rev	CCTGCTCCTTCTCCTTCTCC
GRMZM2G046885_T01-fwd	GAGGCTCCTTGTCGATTCTG
GRMZM2G046885_T01-rev	AACGGTACAAGCGGAACATC
GRMZM2G046885_T02-fwd	GGAAAACAGAACAGCCTTCG
GRMZM2G046885_T02-rev	GCACCCTATGCAGACCAGAT
GRMZM2G168898_T01-fwd	ACGGGGAACACACAAAACAT
GRMZM2G168898_T01-rev	GCAGGAAGGAGAACATCTGC
GRMZM2G370777_T04-fwd	AACTGGCAGAGGAGAACAGG
GRMZM2G370777_T04-rev	TGTGAACTCCCAGAATGCAA
GRMZM2G009475_T01-fwd	ACGCCTTCATCACCAAGTTC
GRMZM2G009475_T01-rev	TATTTATAGGCCCCCGTGCT
GRMZM2G052034_T02-fwd	CTGCTACTCGACGACCCTTC
GRMZM2G052034_T02-rev	ATATGGGGCACGAGAACTTG
GRMZM2G469898_T01-fwd	CACACCCACACCTCATCCTGA
GRMZM2G469898_T01-rev	CGCATGTGCGGTAAGAGACG
GRMZM2G101634_T01-fwd	GAGAGGAGGCAGGAGATGTG
GRMZM2G101634_T01-rev	ATCCTTGGCTCGGAGAAGAT
AC233935.1_FGT005-fwd	GCAGGAAGGGTCATCAAAGA
AC233935.1_FGT005-rev	CGAAGAATGGAATCCAGGAA
GIGANTEA-fwd	CCATTCTGGATCTGACATCG
GIGANTEA-rev	ATTAGAGCCGTCCTACTCGC
GRMZM5G816228-fwd	CGAGACCAGGAGAACCAAAAG
GRMZM5G816228-rev	TGAGGAGTTTGTCCATAACCAC
GRMZM2G393334_T01-fwd	ATCTCGTTGGGGATGTCTTG
GRMZM2G393334_T01-rev	AGCACCGTTCAAATGTCTCC

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150 **Supplemental Table S12.** Primers used in this study for cloning.

<b>Name</b>	<b>Sequence</b>
CDS MADS1 5' pENTR	CACCATGGTGCGGGGCAAGACGCAGATG
CDS MADS1 3'	CTAGCCTGACCTGACCGCCACTG
CDS MADS1 3' degenBamHI	GGATCMGCCTGACCTGACCGCCACTG
M5RNAi-s-BSRGI	GACACATGTACAAAGCAGAAGGAGATGAGTCT
M5RNAi-s-MluI	GACACAACGCGTTCTCCACGTCCATCCCGTCG
M5RNAi-a-BamH	GACACAGGATCCTCTCCACGTCCATCCCGTCG
M5RNAi-a-EcoRI	GACACAGAATTCAAGCAGAAGGAGATGAGTCT
M5RNAi1-XmaI-f	GACACACCCGGGCTGCAGTGCAGCGTGACCCG
M5RNAi1-HindIII-r	GACACAAAGCTTTAAATTGAACGGAGAATATT

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