Supplementary Information

The interaction between OsMADS57 and OsTB1 modulates rice tillering via *DWARF14*

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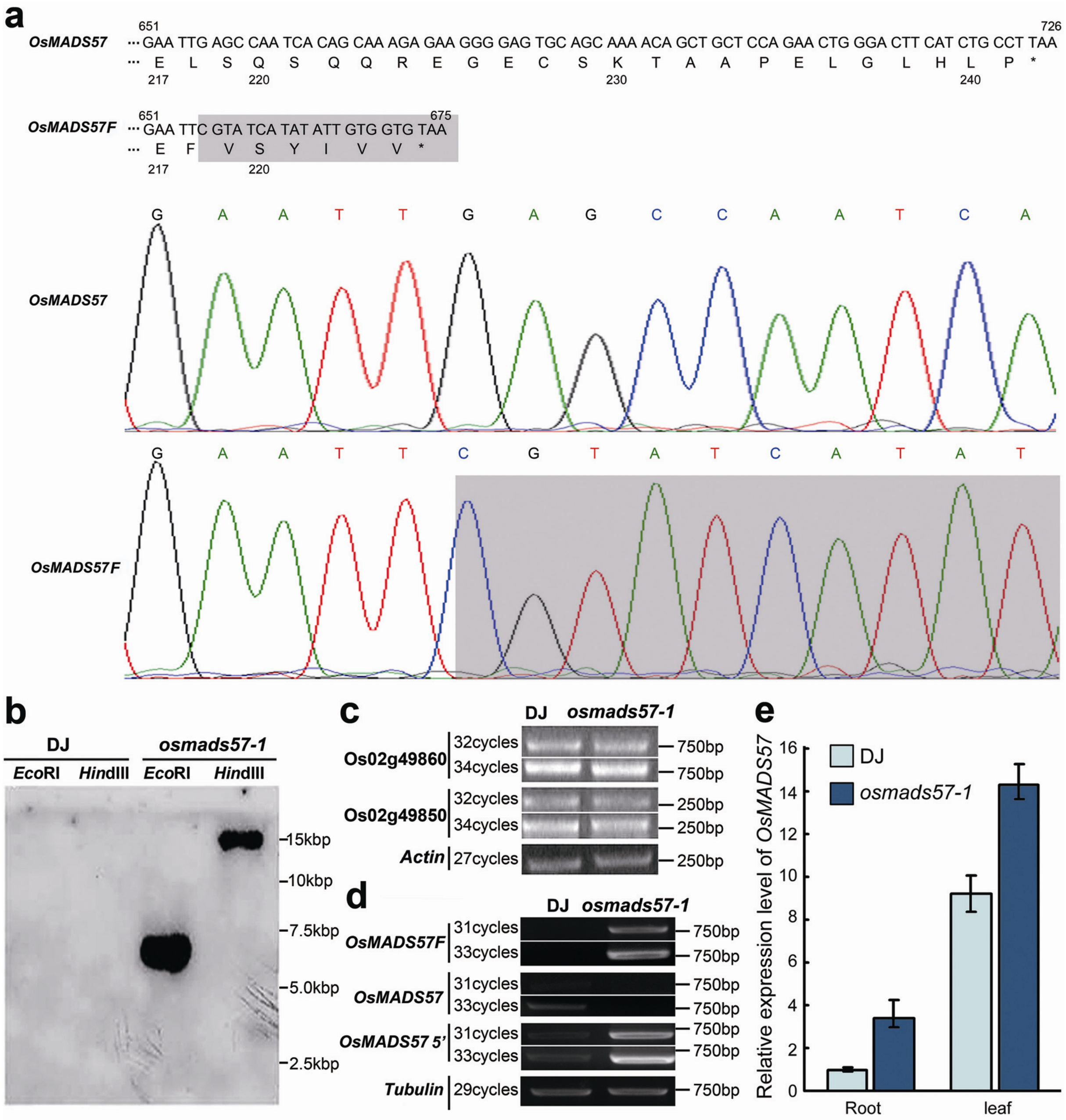
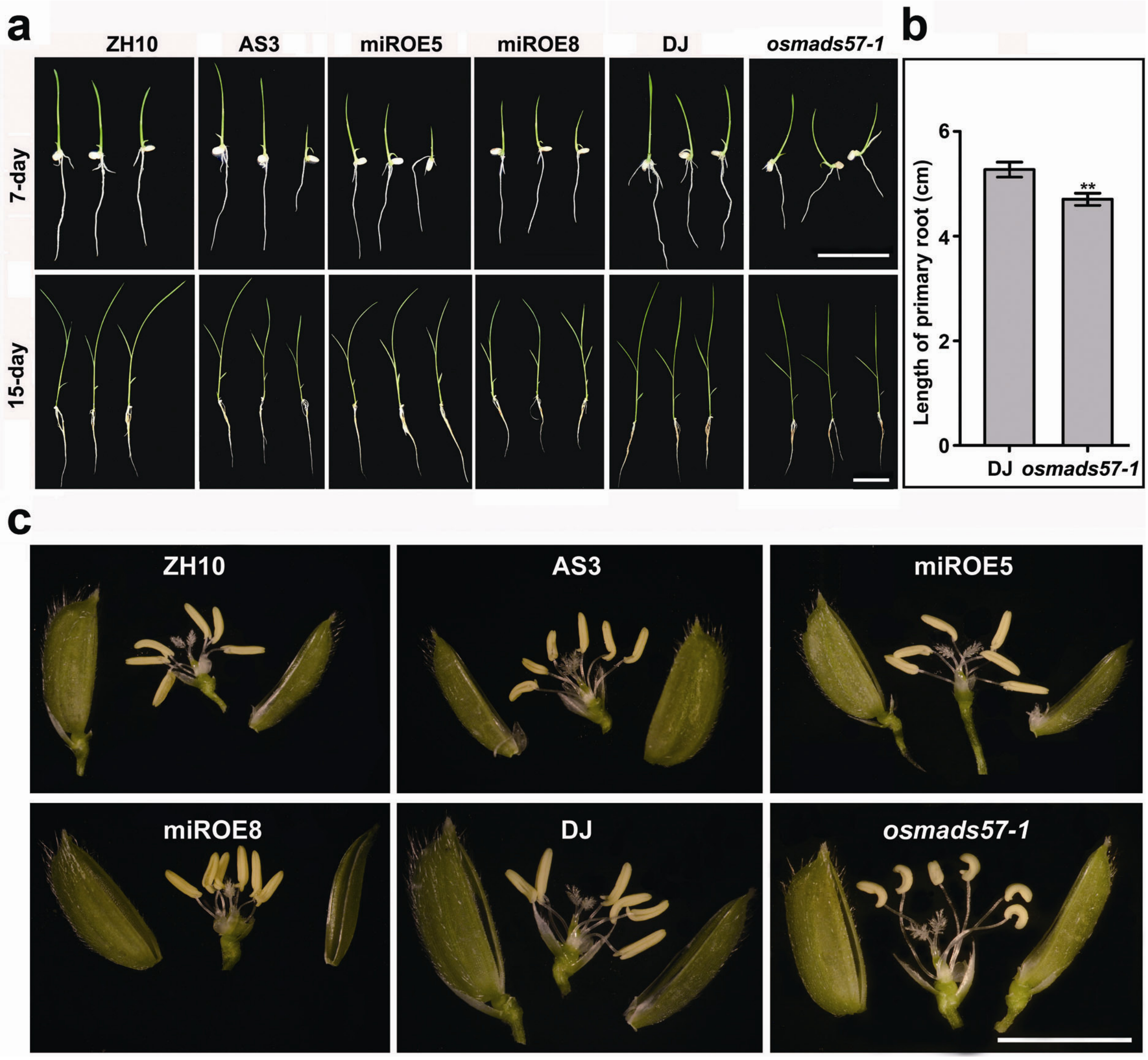
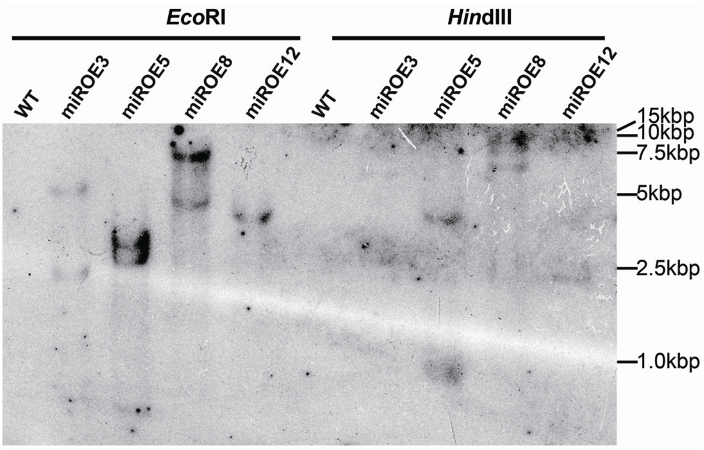


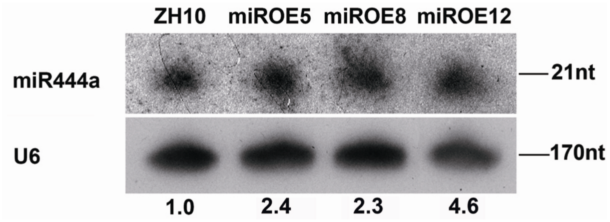
Supplementary Figure S1. Molecular identification of the *osmads57-1* mutant. (**a**) Sequencing result and the different amino acids of OsMADS57 and OsMADS57F. The shadow part indicated the sequence from T-DNA in *osmads57-1*. OsMADS57F, the fusion protein in which 7 amino acids encoded by the sequence from T-DNA fused to the C terminal 217-amino acids of OsMADS57. (**b**) Southern blot assay of *osmads57-1* mutant. Genomic DNA isolated from wild type DJ and *osmads57-1* mutant plants were digested with *Eco*R I or *Hin*d III. The blot was hybridized with the open reading frame of the *GUS* gene labeled with [α-^{32}P] dCTP. *GUS* was present in the T-DNA vector. (**c**) RT-PCR analysis of the neighboring genes Os02g49850 and Os02g49860 in DJ and *osmads57-1*. (**d**) RT-PCR analysis of different region of *OsMADS57*. *OsMADS57*, the full length of *OsMADS57* cDNA; *OsMADS57F*, the recombinant *OsMADS57* cDNA; *OsMADS57 5'*, the 5' -fragment upstream the T-DNA insertion position. (**e**) The transcriptional level of *OsMADS57* in DJ and *osmads57-1* detected by qRT-PCR.



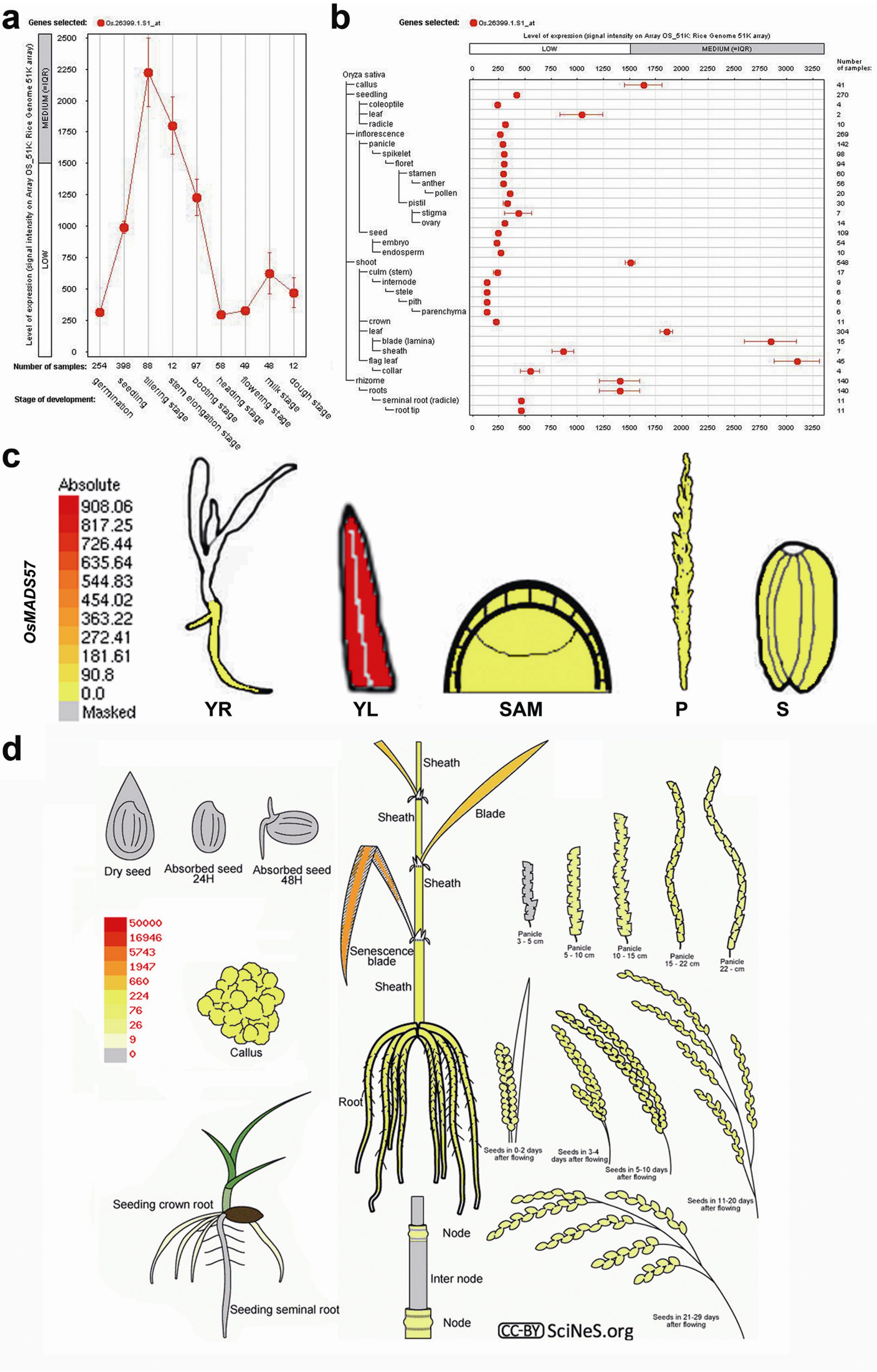
Supplementary Figure S2. Phenotype analysis of wild-type, mutant, and transgenic rice plants. (**a**) Phenotypes of 7-day-old and 15-day-old seedlings. Bars = 5cm. (**b**) Primary roots length analysis of DJ and *osmads57-1* (7-day-old). ** indicates P <0.01 by Student's *t*-test. (**c**) Flower phenotypes of wild-type and transgenic rice plants. ZH10, wild type Zhonghua10; DJ, wild type Dongjin; AS3, antisense *OsMADS57*-overexpressed line 3; miROE, *OsMIR444a*-overexpressed line. Bar = 1cm.



Supplementary Figure S3. Southern blot analysis of *OsMIR444a* transgenic rice plants. Genomic DNA isolated from wild-type and transgenic line 5 (miROE5), line 8 (miROE8) and line 12 (miROE12) was digested with *Eco*R I and *Hin*d III. The blot was hybridized with the open reading frame of the *GUS* gene labeled with [α-^{32}P] dCTP. *GUS* was present in the vector. Southern blot analysis with various insertions on the genome indicated that miROE5, miROE8 and miROE12 were independent lines.

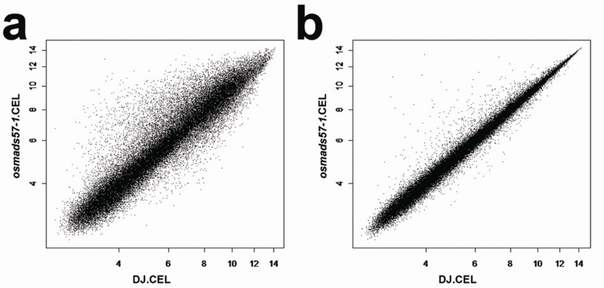


Supplementary Figure S4. Northern blot analysis of miR444a in the transgenic lines miROE5, miROE8, and miROE12. Numerals indicate the miR444a content of transgenic plants relative to that of ZH10 plants. U6 was used as loading control.

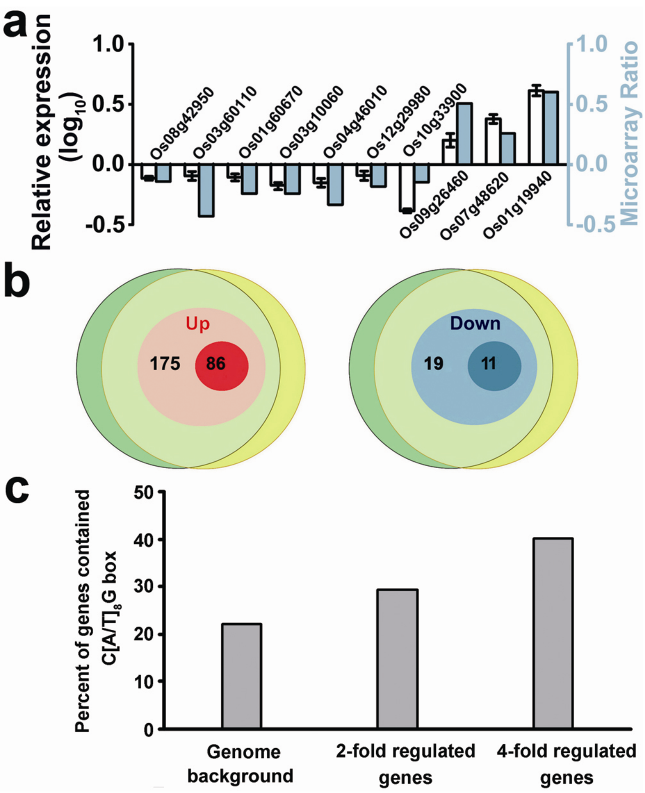


Supplementary Figure S5. Expression pattern of *OsMADS57*. (a) Expression pattern of

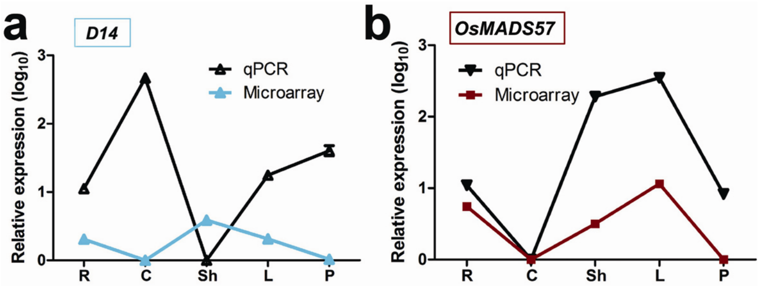
OsMADS57 in different developmental stages based on microarray data displayed in the Genvestigator (https://www.genevestigator.com/gv/). (**b**) Expression pattern of *OsMADS57* in different organs based on microarray data displayed in the Genvestigator (https://www.genevestigator.com/gv/). (**c**) Relative expression of *OsMADS57* in young seedling root (YR), young leaf (YL), shoot apical meristem (SAM), inflorescence (P) and seeds (S) based on microarray data displayed in the eFP browser (http://www.bar.utoronto.ca/efp/cgi-bin/efpWeb.cgi). Color scale shows microarray signal level. (**d**) Relative OsMADS57 expression in different rice tissues as determined by microarray analysis using the eFP browser (HANDB-OS). Color scale indicates microarray signal levels.



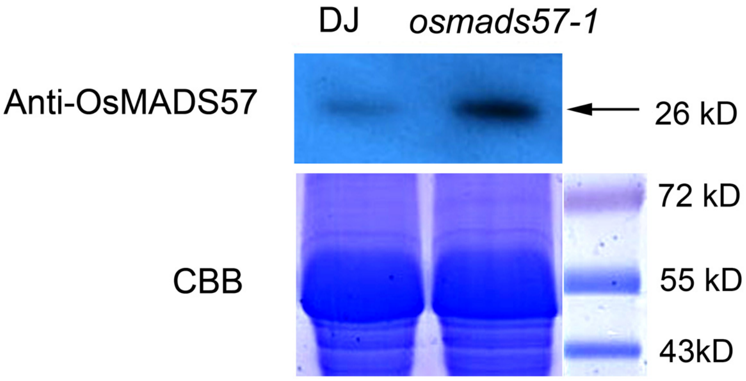
Supplementary Figure S6. Scatter plots of the two biologically replicated microarray data depicting global expression patterns of wild type DJ versus *osmads57-1*. (**a**) Microarray replicates 1. (**b**) Microarray analysis 2. In each scatterplot, the wild type DJ sample versus *osmads57-1* sample microarray expression data following normalization with RMA is shown. All 57,381 Log base 2 transformed probe (gene) signal intensities (range 0 - 14) for the DJ arrays are plotted on the x-axes and the corresponding value (range 0 - 14) for the *osmads57-1* arrays on the y-axes.



Supplementary Figure S7. Whole-genome microarray analysis of *osmads57-1* and cis-element CArG box screening. (**a**) Comparison of qRT-PCR analysis of transcript levels and the microarray ratio for the 10 randomly chosen genes. qRT-PCR expression was normalized to *ACTIN* expression, which was defined as 0. Values represent means ± SE of three technical replicates. (**b**) Genes up- or down-regulated in *osmads57-1* in the microarray data. The biggest cakes with green and yellow represent the number of gene signals in *osmads57-1* and wild-type DJ, respectively. The pink cake represents the genes up-regulated at least 2-fold in *osmads57-1*. The red cake represents the predicted target genes. The azury cake represents genes down-regulated at least 2-fold in *osmads57-1*. The blue cake represents the predicted target genes. (**c**) The proportion of genes contained the CArG-box sequence C[A/T]$_8$G in whole genome, genes with more than 2-fold and woth more than 4-fold.



Supplementary Figure S8. Expression pattern comparing of Affymatric chip and qPCR. (**a**) *D14* gene expression showed inconsistent pattern between Microarray and qPCR. (**b**) The consistent patterns on *OsMADS57* were the positive controls. It hints the biased probes of *D14* appeared on the Affymetrix GenChip. Expression pattern of *D14* and *OsMADS57* in different organs based on microarray data displayed in the Genvestigator (https://www.genevestigator.com/gv/). R, root; C, colm; Sh, sheath; L, leaf; P, panicle.



Supplementary Figure S9. Specifical verification of the OsMADS57 polyclonal antibody. Western blot analysis of the expression level of OsMADS57 protein in WT Dongjin (DJ) and mutant *osmads57-1* seedlings shows that the purified anti-MADS57 polyclonal antibody is specific and can be used in the chromatin immunoprecipitation assays. The Rubisco small subunit was stained by coomassie brilliant blue (CBB) and used as the loading control for total protein.

Supplementary Table S1. The up- or down-regulated genes in mutant *osmads57-1* from the microarray data (up- and down-regulated genes with │$\log_2$ ratio│≧1).

No.	Probe ID	Locus ID	Change ($\log_2$ ratio)	Putative function
1	Os.43929.1.S1_s_at	LOC_Os03g02470	7.32	expressed protein
2	Os.10266.1.S1_at	LOC_Os03g43100	5.47	expressed protein
3	Os.10660.1.S1_at	LOC_Os07g06834	5.21	expressed protein
4	OsAffx.22999.1.S1_at	LOC_Os07g32710	5.16	retrotransposon protein, putative, unclassified, expressed
5	Os.44418.1.S1_at	LOC_Os07g11150	4.87	expressed protein
6	Os.15171.1.S1_s_at	LOC_Os12g37260	4.50	lipoxygenase 2.1, chloroplast precursor, putative, expressed
7	OsAffx.21743.1.S1_s_at	LOC_Os12g35470	4.35	expressed protein
8	Os.6863.1.S1_s_at	LOC_Os12g14440	4.09	Jacalin-like lectin domain containing protein, putative, expressed
9	Os.20614.3.S1_x_at	LOC_Os01g36064	3.81	hAT dimerisation domain-containing protein, putative, expressed
10	Os.30000.1.S1_at	LOC_Os07g36560	3.70	transferase family protein, putative, expressed
11	OsAffx.21616.1.S1_s_at	LOC_Os01g54890	3.67	ethylene-responsive transcription factor 2, putative, expressed
12	Os.11812.1.S1_at	LOC_Os02g48770	3.64	SAM dependent carboxyl methyltransferase, putative, expressed
13	Os.48216.1.S1_at	LOC_Os09g34250	3.58	UDP-glucoronosyl and UDP-glucosyl transferase domain containing protein, expressed
14	Os.32194.1.S1_at	LOC_Os03g39960	3.56	expressed protein

15	Os.20154.1.S1_at	LOC_Os02g56700	3.51	dehydrogenase, putative, expressed
16	Os.9739.1.S1_at	LOC_Os04g05650	3.47	expressed protein
17	Os.11851.1.S1_at	LOC_Os03g11900	3.35	transporter family protein, putative, expressed
18	Os.14616.1.S1_at	LOC_Os07g34260	3.32	chalcone and stilbene synthases, putative, expressed
19	Os.21524.1.S1_at	LOC_Os10g05820	3.31	POEI5 - Pollen Ole e I allergen and extensin family protein precursor, expressed
20	Os.20420.1.S1_at	LOC_Os01g18120	3.23	cinnamoyl CoA reductase, putative, expressed
21	Os.23207.1.S1_at	LOC_Os08g04340	3.15	plastocyanin-like domain containing protein, putative, expressed
22	Os.7095.1.S1_at	LOC_Os04g49210	3.13	naringenin,2-oxoglutarate 3-dioxygenase, putative, expressed
23	OsAffx.28294.3.S1_x_at	LOC_Os05g36240	3.06	expressed protein
24	Os.10659.1.S1_at	LOC_Os07g26100	3.03	expressed protein
25	**Os.26399.1.S1_at**	**LOC_Os02g49840**	**2.99**	**OsMADS57 - MADS-box family gene with MIKC^c type-box, expressed**
26	Os.10908.1.S1_a_at	LOC_Os08g36910	2.98	alpha-amylase precursor, putative, expressed
27	Os.55611.1.S1_s_at	LOC_Os11g05660	2.96	OsFBX396 - F-box domain containing protein, expressed
28	Os.53604.1.S1_at	LOC_Os03g52860	2.91	lipoxygenase, putative, expressed
29	Os.29987.2.S1_at	LOC_Os05g50610	2.87	WRKY8, expressed
30	Os.46604.1.S1_s_at	LOC_Os01g35330	2.83	circumsporozoite protein precursor, putative, expressed
31	Os.54232.1.S1_at	LOC_Os05g37190	2.78	ZOS5-08 - C2H2 zinc finger protein, expressed

32	Os.50399.1.S1_at	LOC_Os06g05420	2.78	expressed protein
33	Os.8545.1.S1_s_at	LOC_Os01g19940	2.76	expressed protein
34	Os.55682.1.S1_at	LOC_Os03g22820	2.75	expressed protein
35	Os.57052.1.S1_at	LOC_Os03g04760	2.74	expressed protein
36	Os.22935.1.S1_at	LOC_Os05g12040	2.73	cytochrome P450 51, putative, expressed
37	Os.50449.1.S1_at	LOC_Os03g10640	2.71	calcium-transporting ATPase, plasma membrane-type, putative, expressed
38	Os.10579.1.S1_at	LOC_Os08g02700	2.69	fructose-bisphospate aldolase isozyme, putative, expressed
39	Os.44475.1.S1_x_at	LOC_Os07g37730	2.69	NADH-ubiquinone oxidoreductase, mitochondrial precursor, putative, expressed
40	Os.32459.1.S1_at	LOC_Os01g03310	2.68	BBTI1 - Bowman-Birk type bran trypsin inhibitor precursor, expressed
41	OsAffx.30784.1.S1_at	LOC_Os11g02540	2.67	WRKY50, expressed
42	Os.33184.1.S1_at	LOC_Os01g51870	2.65	methyltransferase, putative, expressed
43	Os.487.1.S1_at	LOC_Os01g15340	2.61	flowering promoting factor-like 1, putative, expressed
44	Os.55961.1.S1_at	LOC_Os07g34280	2.60	CXE carboxylesterase, putative, expressed
45	Os.48082.1.S1_at	LOC_Os09g25070	2.58	WRKY62, expressed
46	Os.54936.1.S1_at	LOC_Os03g57640	2.57	gibberellin receptor GID1L2, putative, expressed
47	Os.32889.1.S1_at	LOC_Os07g03040	2.56	expressed protein
48	Os.54934.1.S1_at	LOC_Os05g37060	2.55	MYB family transcription factor, putative, expressed

49	Os.49838.1.S1_at	LOC_Os04g47720	2.55	cis-zeatin O-glucosyltransferase, putative, expressed
50	Os.49527.1.S1_at	LOC_Os03g03790	2.51	AMP-binding domain containing protein, expressed
51	Os.8778.1.S1_a_at	LOC_Os06g11290	2.48	12-oxophytodienoate reductase, putative, expressed
52	Os.27247.1.S1_at	LOC_Os06g50950	2.47	GDSL-like lipase/acylhydrolase, putative, expressed
53	Os.6776.1.S1_at	LOC_Os07g35480	2.45	glucan endo-1,3-beta-glucosidase precursor, putative, expressed
54	OsAffx.16037.1.S1_at	LOC_Os07g01960	2.45	hypothetical protein
55	Os.11417.1.S1_at	LOC_Os02g26810	2.45	cytochrome P450, putative, expressed
56	Os.26932.1.S1_at	LOC_Os07g37320	2.44	transporter family protein, putative, expressed
57	Os.26511.1.S1_at	LOC_Os04g49370	2.44	expressed protein
58	Os.50413.1.S1_at	LOC_Os04g01690	2.43	pyridoxal-dependent decarboxylase protein, putative, expressed
59	Os.7935.2.S1_x_at	LOC_Os07g46852	2.43	sex determination protein tasselseed-2, putative, expressed
60	Os.16099.1.S1_at	LOC_Os01g18860	2.42	S-adenosylmethionine synthetase, putative, expressed
61	Os.467.1.S1_a_at	LOC_Os01g42380	2.36	pleiotropic drug resistance protein, putative, expressed
62	Os.5049.1.S1_at	LOC_Os10g20470	2.32	MATE efflux family protein, putative, expressed
63	Os.9067.1.S1_at	LOC_Os07g44140	2.32	cytochrome P450 72A1, putative, expressed
64	Os.56966.1.S1_at	LOC_Os05g50390	2.32	expressed protein
65	Os.21524.2.S1_x_at	LOC_Os10g05840	2.30	POEI6 - Pollen Ole e I allergen and extensin family protein precursor,

				expressed
66	Os.1606.1.S1_at	LOC_Os04g56430	2.25	cysteine-rich receptor-like protein kinase, putative, expressed
67	Os.12038.1.S1_at	LOC_Os01g65700	2.17	expressed protein
68	Os.10546.1.S1_s_at	LOC_Os09g34230	2.16	UDP-glucoronosyl/UDP-glucosyl transferase, putative, expressed
69	Os.55392.1.S1_at	LOC_Os02g57350	2.16	expressed protein
70	Os.4766.1.S1_at	LOC_Os10g28350	2.14	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase protein, putative, expressed
71	Os.15633.1.S2_at	LOC_Os10g35460	2.14	COBRA, putative, expressed
72	Os.53407.1.S1_at	LOC_Os08g06210	2.13	expressed protein
73	Os.52536.1.S1_at	LOC_Os04g43800	2.13	phenylalanine ammonia-lyase, putative, expressed
74	Os.7938.1.S1_at	LOC_Os04g59190	2.13	peroxidase precursor, putative, expressed
75	Os.17182.1.S1_at	LOC_Os03g04570	2.13	peptide transporter PTR3-A, putative, expressed
76	Os.6075.1.S2_at	LOC_Os04g06520	2.12	expressed protein
77	Os.54358.1.S1_at	LOC_Os11g17954	2.12	transposon protein, putative, Pong sub-class, expressed
78	Os.44418.2.S1_at	LOC_Os02g03640	2.08	expressed protein
79	Os.11952.1.S1_at	LOC_Os02g11070	2.07	3-ketoacyl-CoA synthase, putative, expressed
80	Os.10356.1.S1_at	LOC_Os03g08320	2.07	ZIM domain containing protein, putative, expressed
81	Os.50985.1.S1_at	LOC_Os05g36260	2.07	soluble inorganic pyrophosphatase, putative, expressed
82	Os.10930.1.S1_at	LOC_Os02g41670	2.06	phenylalanine ammonia-lyase, putative, expressed

83	Os.46956.1.S1_at	LOC_Os01g50940	2.06	helix-loop-helix DNA-binding domain containing protein, expressed
84	Os.10505.1.S1_a_at	LOC_Os10g39010	2.05	TKL_IRAK_CrRLK1L-1.16 - The CrRLK1L-1 subfamily has homology to the CrRLK1L homolog, expressed
85	OsAffx.29770.1.S1_at	LOC_Os09g08720	1.98	cinnamoyl CoA reductase, putative, expressed
86	Os.26698.1.S1_a_at	LOC_Os01g19820	1.98	universal stress protein domain containing protein, putative, expressed
87	Os.15917.1.S1_at	LOC_Os04g41960	1.98	NADP-dependent oxidoreductase, putative, expressed
88	Os.55674.1.S1_at	LOC_Os05g46830	1.97	proline-rich protein, putative, expressed
89	Os.55253.1.S1_at	LOC_Os05g11610	1.96	expressed protein
90	Os.4618.1.S1_at	LOC_Os01g32670	1.95	expressed protein
91	Os.57191.1.S1_at	LOC_Os06g05470	1.94	expressed protein
92	Os.4184.1.S1_at	LOC_Os02g15350	1.93	dof zinc finger domain containing protein, putative, expressed
93	OsAffx.26230.2.S1_at	LOC_Os02g42450	1.93	RIPER1 - Ripening-related family protein precursor, expressed
94	Os.27292.1.A1_at	LOC_Os04g44354	1.92	UDP-glucoronosyl and UDP-glucosyl transferase domain containing protein, expressed
95	OsAffx.13360.1.S1_at	LOC_Os03g45280	1.88	dehydrin, putative, expressed
96	Os.49410.1.A1_at	LOC_Os04g33240	1.86	sex determination protein tasselseed-2, putative, expressed
97	Os.11193.1.S1_at	LOC_Os03g55240	1.85	cytochrome P450, putative, expressed
98	Os.6244.1.S1_x_at	LOC_Os03g13740	1.85	immediate-early fungal elicitor

				protein CMPG1, putative, expressed
99	Os.7206.1.S1_at	LOC_Os01g45250	1.84	DUF1645 domain containing protein, putative, expressed
100	Os.12948.1.S1_at	LOC_Os02g08420	1.84	cinnamoyl CoA reductase, putative, expressed
101	Os.12535.1.S1_at	LOC_Os01g52230	1.80	phosphoethanolamine/phosphocholine phosphatase, putative, expressed
102	Os.8920.1.S1_at	LOC_Os07g47790	1.80	AP2 domain containing protein, expressed
103	OsAffx.8070.1.S1_x_at	LOC_Os01g60590	1.79	transposon protein, putative, Pong sub-class, expressed
104	Os.11195.1.S1_at	LOC_Os07g17330	1.77	B12D protein, putative, expressed
105	Os.45887.1.S1_at	LOC_Os01g12750	1.76	cytochrome P450, putative, expressed
106	Os.15281.1.S1_x_at	LOC_Os07g46920	1.76	sex determination protein tasselseed-2, putative, expressed
107	Os.12498.2.S1_at	LOC_Os01g72360	1.76	expressed protein
108	Os.34139.1.S1_at	LOC_Os08g04630	1.75	external NADH-ubiquinone oxidoreductase 1, mitochondrial precursor, putative, expressed
109	Os.47761.1.S1_at	LOC_Os03g13300	1.74	glutamate decarboxylase, putative, expressed
110	Os.14631.1.S1_at	LOC_Os07g13770	1.74	UDP-glucoronosyl and UDP-glucosyl transferase domain containing protein, expressed
111	Os.30608.2.S1_x_at	LOC_Os02g41954	1.73	gibberellin 2-beta-dioxygenase 7, putative, expressed
112	OsAffx.23744.1.S1_s_at	LOC_Os01g51310	1.73	expressed protein
113	Os.34199.1.S1_at	LOC_Os01g72630	1.72	expressed protein
114	Os.18041.1.S1_at	LOC_Os02g51730	1.72	dnaJ homolog subfamily C member 7, putative, expressed

115	Os.7770.1.S1_at	LOC_Os05g05030	1.70	expressed protein
116	Os.16540.1.S1_at	LOC_Os07g06830	1.70	gibberellin receptor GID1L2, putative, expressed
117	Os.24471.1.S1_at	LOC_Os07g30760	1.70	UDP-glucoronosyl and UDP-glucosyl transferase domain containing protein, expressed
118	Os.9116.1.S1_at	LOC_Os01g28680	1.70	WD domain, G-beta repeat domain containing protein, expressed
119	Os.8629.1.S1_x_at	LOC_Os12g02320	1.68	LTPL12 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
120	OsAffx.26673.1.S1_at	LOC_Os05g01010	1.66	expressed protein
121	Os.35013.1.S1_at	LOC_Os03g16170	1.66	protein phosphatase 2C, putative, expressed
122	Os.27170.1.S1_at	LOC_Os01g50400	1.66	STE_MEKK_ste11_MAP3K.5 - STE kinases include homologs to sterile 7, sterile 11 and sterile 20 from yeast, expressed
123	Os.48711.1.A1_at	LOC_Os11g45990	1.65	von Willebrand factor type A domain containing protein, putative, expressed
124	Os.18570.1.S1_at	LOC_Os07g02970	1.65	expressed protein
125	Os.52661.1.S1_at	LOC_Os11g44680	1.64	calmodulin binding protein, putative, expressed
126	Os.49479.1.S1_at	LOC_Os05g05020	1.64	expressed protein
127	OsAffx.9584.1.S1_x_at	LOC_Os01g60600	1.64	WRKY108, expressed
128	OsAffx.28294.2.S1_at	LOC_Os07g05840	1.60	expressed protein
129	Os.26430.1.A1_at	LOC_Os12g07180	1.58	transposon protein, putative, Pong sub-class, expressed
130	Os.22783.1.S1_s_at	LOC_Os05g31750	1.58	annexin, putative, expressed
131	Os.53217.1.S1_x_at	LOC_Os03g03034	1.57	flavonol synthase/flavanone

				3-hydroxylase, putative, expressed
132	OsAffx.24369.13.S1_s_at	LOC_Os01g49370	1.55	expressed protein
133	OsAffx.26540.1.S1_s_at	LOC_Os04g49550	1.54	RING-H2 finger protein ATL2A, putative, expressed
134	Os.57108.1.S1_at	LOC_Os12g24330	1.53	expressed protein
135	Os.27251.1.S1_at	LOC_Os04g10350	1.52	1-aminocyclopropane-1-carboxylate oxidase homolog 2, putative, expressed
136	Os.55583.1.S1_at	LOC_Os09g38110	1.50	RING-H2 finger protein, putative, expressed
137	Os.45928.1.S1_at	LOC_Os01g32460	1.50	expressed protein
138	Os.648.1.S1_at	LOC_Os01g43480	1.49	AAA-type ATPase family protein, putative, expressed
139	Os.4385.1.S1_at	LOC_Os11g08210	1.48	no apical meristem protein, putative, expressed
140	Os.11575.3.S1_x_at	LOC_Os03g46440	1.48	BTBA4 - Bric-a-Brac,Tramtrack, Broad Complex BTB domain with Ankyrin repeat region, expressed
141	Os.49627.1.S1_at	LOC_Os06g37150	1.47	L-ascorbate oxidase precursor, putative, expressed
142	Os.1191.1.S1_at	LOC_Os03g04060	1.47	CHIT16 - Chitinase family protein precursor, expressed
143	Os.50104.1.S1_at	LOC_Os06g40180	1.47	phospholipase D, putative, expressed
144	Os.19375.1.S1_at	LOC_Os08g34790	1.43	AMP-binding domain containing protein, expressed
145	Os.21801.1.S1_at	LOC_Os01g04620	1.42	transposon protein, putative, unclassified, expressed
146	Os.5045.1.S1_at	LOC_Os01g03680	1.40	BBTI8 - Bowman-Birk type bran trypsin inhibitor precursor, expressed

147	Os.12642.1.S1_at	LOC_Os08g42750	1.40	CAMK_CAMK_like.37 - CAMK includes calcium/calmodulin depedent protein kinases, expressed
148	Os.52344.1.S1_at	LOC_Os08g26840	1.40	plant protein of unknown function domain containing protein, expressed
149	Os.26626.1.S1_at	LOC_Os05g33400	1.38	basic 7S globulin precursor, putative, expressed
150	Os.12199.1.S1_at	LOC_Os01g66120	1.36	No apical meristem protein, putative, expressed
151	Os.11552.1.S1_at	LOC_Os04g59150	1.36	peroxidase precursor, putative, expressed
152	Os.1438.1.S1_at	LOC_Os01g06590	1.35	zinc finger, C3HC4 type domain containing protein, expressed
153	Os.46872.1.S1_at	LOC_Os10g37160	1.35	transposon protein, putative, unclassified, expressed
154	OsAffx.24166.1.S1_at	LOC_Os02g08440	1.35	WRKY71, expressed
155	Os.50455.1.S1_at	LOC_Os06g40170	1.34	phospholipase D, putative, expressed
156	Os.22706.1.S1_at	LOC_Os02g54760	1.32	cyclic nucleotide-gated ion channel 14, putative, expressed
157	Os.12063.1.S1_at	LOC_Os02g11859	1.31	expressed protein
158	Os.5711.1.S1_at	LOC_Os01g32610	1.31	expressed protein
159	Os.34174.1.S1_at	LOC_Os04g38790	1.30	expressed protein
160	OsAffx.3357.1.S1_s_at	LOC_Os03g28990	1.30	zinc finger family protein, putative, expressed
161	Os.6452.2.A1_a_at	LOC_Os01g43710	1.27	cytochrome P450 72A1, putative, expressed
162	Os.7985.1.S1_at	LOC_Os03g18070	1.25	omega-3 fatty acid desaturase, chloroplast precursor, putative, expressed

163	Os.11575.4.S1_x_at	LOC_Os01g08500	1.25	transposon protein, putative, Pong sub-class, expressed
164	Os.21260.1.S1_at	LOC_Os03g08580	1.22	expressed protein
165	OsAffx.19515.1.S1_s_at	LOC_Os12g06080	1.22	expressed protein
166	Os.10172.1.S1_at	LOC_Os02g41510	1.22	MYB family transcription factor, putative, expressed
167	Os.48076.1.S1_at	LOC_Os12g36750	1.21	expressed protein
168	OsAffx.19635.1.S1_at	LOC_Os12g12720	1.18	jasmonate-induced protein, putative, expressed
169	Os.36901.1.S1_at	LOC_Os01g58150	1.17	expressed protein
170	Os.33722.1.S1_at	LOC_Os01g53430	1.14	anthocyanidin 5,3-O-glucosyltransferase, putative, expressed
171	OsAffx.24356.1.S1_at	LOC_Os02g20950	1.12	expressed protein
172	Os.10339.1.S1_at	LOC_Os03g04770	1.11	beta-amylase, putative, expressed
173	Os.11617.1.S1_at	LOC_Os05g49140	1.10	CGMC_MAPKCMGC_2.8 - CGMC includes CDA, MAPK, GSK3, and CLKC kinases, expressed
174	OsAffx.30647.1.S1_x_at	LOC_Os10g32940	1.09	expressed protein
175	Os.19952.1.S1_at	LOC_Os01g09450	1.06	OsIAA2 - Auxin-responsive Aux/IAA gene family member, expressed
176	Os.27486.1.S1_x_at	LOC_Os11g01074	-1.05	RNase P subunit p30, putative, expressed
177	OsAffx.6610.1.A1_at	LOC_Os10g08879	-1.10	nucleotide-sensitive chloride conductance regulator containing protein, expressed
178	Os.9194.1.S1_at	LOC_Os02g52040	-1.10	phosphate-induced protein 1 conserved region domain containing protein, expressed

179	OsAffx.24040.1.S1_s_at	LOC_Os01g74340	-1.12	RNA recognition motif containing protein, putative, expressed
180	Os.50487.1.S1_at	LOC_Os03g21960	-1.15	aminotransferase, putative, expressed
181	Os.50502.1.S1_at	LOC_Os11g27329	-1.15	OsSCP62 - Putative Serine Carboxypeptidase homologue, expressed
182	Os.27509.1.S1_at	LOC_Os01g53790	-1.17	stress-induced protein, putative, expressed
183	Os.5213.1.S1_at	LOC_Os02g44720	-1.19	expressed protein
184	Os.50578.1.S1_x_at	LOC_Os11g20239	-1.39	expressed protein
185	Os.35216.1.S1_at	LOC_Os02g34760	-1.40	retrotransposon protein, putative, unclassified, expressed
186	Os.9661.1.S1_at	LOC_Os03g04620	-1.42	CCT motif family protein, expressed
187	Os.17826.1.A1_at	LOC_Os02g04690	-1.42	cycloartenol synthase, putative, expressed
188	Os.23790.1.S1_at	LOC_Os10g29650	-1.43	retrotransposon protein, putative, unclassified, expressed
189	Os.20355.1.S1_at	LOC_Os01g72100	-1.49	OsCML10 - Calmodulin-related calcium sensor protein, expressed
190	Os.9311.1.S1_at	LOC_Os03g19420	-1.57	nicotianamine synthase, putative, expressed
191	Os.14101.3.S1_at	LOC_Os01g61200	-1.59	GDSL-like lipase/acylhydrolase, putative, expressed
192	Os.12783.1.S1_at	LOC_Os07g46210	-1.66	LTPL2 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
193	Os.5816.1.S1_at	LOC_Os09g35010	-1.68	dehydration-responsive element-binding protein, putative, expressed
194	Os.50472.2.S1_s_at	LOC_Os02g29774	-2.16	expressed protein

Supplementary Table S2. Functional classification of the up- and down-regulated genes in *osmads57-1*.

Probe ID	Locus ID	Change (Log_2 ratio)	Putative function
Transcription factor			
Os.10172.1.S1_at	LOC_Os02g41510	1.22	MYB family transcription factor, putative, expressed
Os.1438.1.S1_at	LOC_Os01g06590	1.35	zinc finger, C3HC4 type domain containing protein, expressed
Os.26399.1.S1_at	LOC_Os02g49840	2.99	OsMADS57 - MADS-box family gene with MIKC^c type-box, expressed
Os.29987.2.S1_at	LOC_Os05g50610	2.87	WRKY8, expressed
Os.4184.1.S1_at	LOC_Os02g15350	1.93	dof zinc finger domain containing protein, putative, expressed
Os.46956.1.S1_at	LOC_Os01g50940	2.06	helix-loop-helix DNA-binding domain containing protein, expressed
Os.48082.1.S1_at	LOC_Os09g25070	2.58	WRKY62, expressed
Os.54232.1.S1_at	LOC_Os05g37190	2.78	ZOS5-08 - C2H2 zinc finger protein, expressed
Os.54934.1.S1_at	LOC_Os05g37060	2.55	MYB family transcription factor, putative, expressed
Os.55583.1.S1_at	LOC_Os09g38110	1.50	RING-H2 finger protein, putative, expressed
Os.8920.1.S1_at	LOC_Os07g47790	1.80	AP2 domain containing protein, expressed
OsAffx.24166.1.S1_at	LOC_Os02g08440	1.35	WRKY71, expressed
OsAffx.26540.1.S1_s_at	LOC_Os04g49550	1.54	RING-H2 finger protein ATL2A, putative, expressed
OsAffx.30784.1.S1_at	LOC_Os11g02540	2.67	WRKY50, expressed
OsAffx.3357.1.S1_s_at	LOC_Os03g28990	1.30	zinc finger family protein, putative, expressed
OsAffx.9584.1.S1_x_at	LOC_Os01g60600	1.64	WRKY108, expressed

Hormone			
Os.10339.1.S1_at	LOC_Os03g04770	1.11	beta-amylase, putative, expressed
Os.10908.1.S1_a_at	LOC_Os08g36910	2.98	alpha-amylase precursor, putative, expressed
Os.16540.1.S1_at	LOC_Os07g06830	1.70	gibberellin receptor GID1L2, putative, expressed
Os.19952.1.S1_at	LOC_Os01g09450	1.06	OsIAA2 - Auxin-responsive Aux/IAA gene family member, expressed
Os.30608.2.S1_x_at	LOC_Os02g41954	1.73	gibberellin 2-beta-dioxygenase 7, putative, expressed
Os.54936.1.S1_at	LOC_Os03g57640	2.57	gibberellin receptor GID1L2, putative, expressed
OsAffx.19635.1.S1_at	LOC_Os12g12720	1.18	jasmonate-induced protein, putative, expressed
OsAffx.21616.1.S1_s_at	LOC_Os01g54890	3.67	ethylene-responsive transcription factor 2, putative, expressed
OsAffx.24166.1.S1_at	LOC_Os02g08440	1.35	WRKY71, expressed
Cell division			
Os.648.1.S1_at	LOC_Os01g43480	1.49	AAA-type ATPase family protein, putative, expressed
Cell wall			
Os.1191.1.S1_at	LOC_Os03g04060	1.47	CHIT16 - Chitinase family protein precursor, expressed
Metabolism			
Os.10546.1.S1_s_at	LOC_Os09g34230	2.16	UDP-glucoronosyl/UDP-glucosyl transferase, putative, expressed
Os.10579.1.S1_at	LOC_Os08g02700	2.69	fructose-bisphospate aldolase isozyme, putative, expressed
Os.11552.1.S1_at	LOC_Os04g59150	1.36	peroxidase precursor, putative, expressed
Os.11952.1.S1_at	LOC_Os02g11070	2.07	3-ketoacyl-CoA synthase, putative, expressed

Os.14616.1.S1_at	LOC_Os07g34260	3.32	chalcone and stilbene synthases, putative, expressed
Os.14631.1.S1_at	LOC_Os07g13770	1.74	UDP-glucoronosyl and UDP-glucosyl transferase domain containing protein, expressed
Os.24471.1.S1_at	LOC_Os07g30760	1.70	UDP-glucoronosyl and UDP-glucosyl transferase domain containing protein, expressed
Os.26626.1.S1_at	LOC_Os05g33400	1.38	basic 7S globulin precursor, putative, expressed
Os.27292.1.A1_at	LOC_Os04g44354	1.92	UDP-glucoronosyl and UDP-glucosyl transferase domain containing protein, expressed
Os.33722.1.S1_at	LOC_Os01g53430	1.14	anthocyanidin 5,3-O-glucosyltransferase, putative, expressed
Os.48216.1.S1_at	LOC_Os09g34250	3.58	UDP-glucoronosyl and UDP-glucosyl transferase domain containing protein, expressed
Os.49838.1.S1_at	LOC_Os04g47720	2.55	cis-zeatin O-glucosyltransferase, putative, expressed
Os.6776.1.S1_at	LOC_Os07g35480	2.45	glucan endo-1,3-beta-glucosidase precursor, putative, expressed
Os.7985.1.S1_at	LOC_Os03g18070	1.25	omega-3 fatty acid desaturase, chloroplast precursor, putative, expressed
OsAffx.26230.2.S1_at	LOC_Os02g42450	1.93	RIPER1 - Ripening-related family protein precursor, expressed
OsAffx.29770.1.S1_at	LOC_Os09g08720	1.98	cinnamoyl CoA reductase, putative, expressed
Os.12783.1.S1_at	LOC_Os07g46210	-1.66	LTPL2 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
Os.17826.1.A1_at	LOC_Os02g04690	-1.42	cycloartenol synthase, putative, expressed
Os.9311.1.S1_at	LOC_Os03g19420	-1.57	nicotianamine synthase, putative, expressed
Os.50502.1.S1_at	LOC_Os11g27329	-1.15	OsSCP62 - Putative Serine

			Carboxypeptidase homologue, expressed
Os.5049.1.S1_at	LOC_Os10g20470	2.32	MATE efflux family protein, putative, expressed
Member related protein			
Os.11851.1.S1_at	LOC_Os03g11900	3.35	transporter family protein, putative, expressed
Os.17182.1.S1_at	LOC_Os03g04570	2.13	peptide transporter PTR3-A, putative, expressed
Os.22706.1.S1_at	LOC_Os02g54760	1.32	cyclic nucleotide-gated ion channel 14, putative, expressed
Os.26932.1.S1_at	LOC_Os07g37320	2.44	transporter family protein, putative, expressed

Supplementary Table S3. Genes containing CArG box *cis*-elements in the promoter region that were up- or down-regulated in *osmads57-1* mutant plants.

No.	Probe ID	Locus ID	Change (Log2 ratio)	Putative function
1	OsAffx.22999.1.S1_at	LOC_Os07g32710	5.16	retrotransposon protein, putative, unclassified, expressed
2	Os.15171.1.S1_s_at	LOC_Os12g37260	4.50	lipoxygenase 2.1, chloroplast precursor, putative, expressed
3	Os.6863.1.S1_s_at	LOC_Os12g14440	4.09	Jacalin-like lectin domain containing protein, putative, expressed
4	Os.30000.1.S1_at	LOC_Os07g36560	3.70	transferase family protein, putative, expressed
5	Os.11812.1.S1_at	LOC_Os02g48770	3.64	SAM dependent carboxyl methyltransferase, putative, expressed
6	Os.20154.1.S1_at	LOC_Os02g56700	3.51	dehydrogenase, putative, expressed
7	Os.11851.1.S1_at	LOC_Os03g11900	3.35	transporter family protein, putative, expressed
8	Os.14616.1.S1_at	LOC_Os07g34260	3.32	chalcone and stilbene synthases, putative, expressed
9	Os.20420.1.S1_at	LOC_Os01g18120	3.23	cinnamoyl CoA reductase, putative, expressed
10	Os.7095.1.S1_at	LOC_Os04g49210	3.13	naringenin,2-oxoglutarate 3-dioxygenase, putative, expressed
11	Os.26399.1.S1_at	LOC_Os02g49840	2.99	OsMADS57 - MADS-box family gene with MIKC^c type-box, expressed
12	Os.55611.1.S1_s_at	LOC_Os11g05660	2.96	OsFBX396 - F-box domain containing protein, expressed
13	Os.53604.1.S1_at	LOC_Os03g52860	2.91	lipoxygenase, putative, expressed
14	Os.29987.2.S1_at	LOC_Os05g50610	2.87	WRKY8, expressed
15	Os.46604.1.S1_s_at	LOC_Os01g35330	2.83	circumsporozoite protein precursor, putative, expressed
16	Os.22935.1.S1_at	LOC_Os05g12040	2.73	cytochrome P450 51, putative, expressed
17	Os.10579.1.S1_at	LOC_Os08g02700	2.69	fructose-bisphospate aldolase isozyme, putative, expressed
18	Os.44475.1.S1_x_at	LOC_Os07g37730	2.69	NADH-ubiquinone oxidoreductase,

				mitochondrial precursor, putative, expressed
19	OsAffx.30784.1.S1_at	LOC_Os11g02540	2.67	WRKY50, expressed
20	Os.487.1.S1_at	LOC_Os01g15340	2.61	flowering promoting factor-like 1, putative, expressed
21	Os.55961.1.S1_at	LOC_Os07g34280	2.60	CXE carboxylesterase, putative, expressed
22	Os.48082.1.S1_at	LOC_Os09g25070	2.58	WRKY62, expressed
23	Os.54936.1.S1_at	LOC_Os03g57640	2.57	gibberellin receptor GID1L2, putative, expressed
24	Os.49838.1.S1_at	LOC_Os04g47720	2.55	cis-zeatin O-glucosyltransferase, putative, expressed
25	Os.8778.1.S1_a_at	LOC_Os06g11290	2.48	12-oxophytodienoate reductase, putative, expressed
26	Os.27247.1.S1_at	LOC_Os06g50950	2.47	GDSL-like lipase/acylhydrolase, putative, expressed
27	Os.11417.1.S1_at	LOC_Os02g26810	2.45	cytochrome P450, putative, expressed
28	Os.6776.1.S1_at	LOC_Os07g35480	2.45	glucan endo-1,3-beta-glucosidase precursor, putative, expressed
29	Os.50413.1.S1_at	LOC_Os04g01690	2.43	pyridoxal-dependent decarboxylase protein, putative, expressed
30	Os.16099.1.S1_at	LOC_Os01g18860	2.42	S-adenosylmethionine synthetase, putative, expressed
31	Os.467.1.S1_a_at	LOC_Os01g42380	2.36	pleiotropic drug resistance protein, putative, expressed
32	Os.5049.1.S1_at	LOC_Os10g20470	2.32	MATE efflux family protein, putative, expressed
33	Os.9067.1.S1_at	LOC_Os07g44140	2.32	cytochrome P450 72A1, putative, expressed
34	Os.21524.2.S1_x_at	LOC_Os10g05840	2.30	POEI6 - Pollen Ole e I allergen and extensin family protein precursor, expressed
35	Os.10546.1.S1_s_at	LOC_Os09g34230	2.16	UDP-glucoronosyl/UDP-glucosyl transferase, putative, expressed
36	Os.4766.1.S1_at	LOC_Os10g28350	2.14	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase protein, putative, expressed

37	Os.7938.1.S1_at	LOC_Os04g59190	2.13	peroxidase precursor, putative, expressed
38	Os.54358.1.S1_at	LOC_Os11g17954	2.12	transposon protein, putative, Pong sub-class, expressed
39	Os.10356.1.S1_at	LOC_Os03g08320	2.07	ZIM domain containing protein, putative, expressed
40	Os.11952.1.S1_at	LOC_Os02g11070	2.07	3-ketoacyl-CoA synthase, putative, expressed
41	Os.50985.1.S1_at	LOC_Os05g36260	2.07	soluble inorganic pyrophosphatase, putative, expressed
42	Os.46956.1.S1_at	LOC_Os01g50940	2.06	helix-loop-helix DNA-binding domain containing protein, expressed
43	Os.10505.1.S1_a_at	LOC_Os10g39010	2.05	TKL_IRAK_CrRLK1L-1.16 - The CrRLK1L-1 subfamily has homology to the CrRLK1L homolog, expressed
44	Os.15917.1.S1_at	LOC_Os04g41960	1.98	NADP-dependent oxidoreductase, putative, expressed
45	Os.26698.1.S1_a_at	LOC_Os01g19820	1.98	universal stress protein domain containing protein, putative, expressed
46	OsAffx.29770.1.S1_at	LOC_Os09g08720	1.98	cinnamoyl CoA reductase, putative, expressed
47	Os.4184.1.S1_at	LOC_Os02g15350	1.93	dof zinc finger domain containing protein, putative, expressed
48	OsAffx.26230.2.S1_at	LOC_Os02g42450	1.93	RIPER1 - Ripening-related family protein precursor, expressed
49	Os.27292.1.A1_at	LOC_Os04g44354	1.92	UDP-glucoronosyl and UDP-glucosyl transferase domain containing protein, expressed
50	Os.6244.1.S1_x_at	LOC_Os03g13740	1.85	immediate-early fungal elicitor protein CMPG1, putative, expressed
51	Os.12948.1.S1_at	LOC_Os02g08420	1.84	cinnamoyl CoA reductase, putative, expressed
52	Os.15281.1.S1_x_at	LOC_Os07g46920	1.76	sex determination protein tasselseed-2, putative, expressed
53	Os.14631.1.S1_at	LOC_Os07g13770	1.74	UDP-glucoronosyl and UDP-glucosyl transferase domain containing protein, expressed
54	Os.47761.1.S1_at	LOC_Os03g13300	1.74	glutamate decarboxylase, putative, expressed

55	Os.30608.2.S1_x_at	LOC_Os02g41954	1.73	gibberellin 2-beta-dioxygenase 7, putative, expressed
56	Os.16540.1.S1_at	LOC_Os07g06830	1.70	gibberellin receptor GID1L2, putative, expressed
57	Os.24471.1.S1_at	LOC_Os07g30760	1.70	UDP-glucoronosyl and UDP-glucosyl transferase domain containing protein, expressed
58	Os.8629.1.S1_x_at	LOC_Os12g02320	1.68	LTPL12 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
59	Os.27170.1.S1_at	LOC_Os01g50400	1.66	STE_MEKK_ste11_MAP3K.5 - STE kinases include homologs to sterile 7, sterile 11 and sterile 20 from yeast, expressed
60	Os.48711.1.A1_at	LOC_Os11g45990	1.65	von Willebrand factor type A domain containing protein, putative, expressed
61	Os.22783.1.S1_s_at	LOC_Os05g31750	1.58	annexin, putative, expressed
62	Os.26430.1.A1_at	LOC_Os12g07180	1.58	transposon protein, putative, Pong sub-class, expressed
63	Os.53217.1.S1_x_at	LOC_Os03g03034	1.57	flavonol synthase/flavanone 3-hydroxylase, putative, expressed
64	OsAffx.26540.1.S1_s_at	LOC_Os04g49550	1.54	RING-H2 finger protein ATL2A, putative, expressed
65	Os.27251.1.S1_at	LOC_Os04g10350	1.52	1-aminocyclopropane-1-carboxylate oxidase homolog 2, putative, expressed
66	Os.55583.1.S1_at	LOC_Os09g38110	1.50	RING-H2 finger protein, putative, expressed
67	Os.648.1.S1_at	LOC_Os01g43480	1.49	AAA-type ATPase family protein, putative, expressed
68	Os.4385.1.S1_at	LOC_Os11g08210	1.48	no apical meristem protein, putative, expressed
69	Os.1191.1.S1_at	LOC_Os03g04060	1.47	CHIT16 - Chitinase family protein precursor, expressed
70	Os.50104.1.S1_at	LOC_Os06g40180	1.47	phospholipase D, putative, expressed
71	Os.19375.1.S1_at	LOC_Os08g34790	1.43	AMP-binding domain containing protein, expressed
72	Os.12642.1.S1_at	LOC_Os08g42750	1.40	CAMK_CAMK_like.37 - CAMK includes calcium/calmodulin depedent protein kinases, expressed

73	Os.5045.1.S1_at	LOC_Os01g03680	1.40	BBTI8 - Bowman-Birk type bran trypsin inhibitor precursor, expressed
74	Os.52344.1.S1_at	LOC_Os08g26840	1.40	plant protein of unknown function domain containing protein, expressed
75	Os.26626.1.S1_at	LOC_Os05g33400	1.38	basic 7S globulin precursor, putative, expressed
76	Os.11552.1.S1_at	LOC_Os04g59150	1.36	peroxidase precursor, putative, expressed
77	Os.12199.1.S1_at	LOC_Os01g66120	1.36	No apical meristem protein, putative, expressed
78	Os.46872.1.S1_at	LOC_Os10g37160	1.35	transposon protein, putative, unclassified, expressed
79	OsAffx.24166.1.S1_at	LOC_Os02g08440	1.35	WRKY71, expressed
80	Os.22706.1.S1_at	LOC_Os02g54760	1.32	cyclic nucleotide-gated ion channel 14, putative, expressed
81	OsAffx.3357.1.S1_s_at	LOC_Os03g28990	1.30	zinc finger family protein, putative, expressed
82	Os.6452.2.A1_a_at	LOC_Os01g43710	1.27	cytochrome P450 72A1, putative, expressed
83	Os.11575.4.S1_x_at	LOC_Os01g08500	1.25	transposon protein, putative, Pong sub-class, expressed
84	Os.7985.1.S1_at	LOC_Os03g18070	1.25	omega-3 fatty acid desaturase, chloroplast precursor, putative, expressed
85	Os.10172.1.S1_at	LOC_Os02g41510	1.22	MYB family transcription factor, putative, expressed
86	OsAffx.19635.1.S1_at	LOC_Os12g12720	1.18	jasmonate-induced protein, putative, expressed
87	Os.27486.1.S1_x_at	LOC_Os11g01074	-1.05	RNase P subunit p30, putative, expressed
88	Os.9194.1.S1_at	LOC_Os02g52040	-1.10	phosphate-induced protein 1 conserved region domain containing protein, expressed
89	OsAffx.6610.1.A1_at	LOC_Os10g08879	-1.10	nucleotide-sensitive chloride conductance regulator containing protein, expressed
90	Os.50487.1.S1_at	LOC_Os03g21960	-1.15	aminotransferase, putative, expressed
91	Os.50502.1.S1_at	LOC_Os11g27329	-1.15	OsSCP62 - Putative Serine Carboxypeptidase homologue, expressed
92	Os.35216.1.S1_at	LOC_Os02g34760	-1.40	retrotransposon protein, putative,

				unclassified, expressed
93	Os.9661.1.S1_at	LOC_Os03g04620	-1.42	CCT motif family protein, expressed
94	Os.23790.1.S1_at	LOC_Os10g29650	-1.43	retrotransposon protein, putative, unclassified, expressed
95	Os.20355.1.S1_at	LOC_Os01g72100	-1.49	OsCML10 - Calmodulin-related calcium sensor protein, expressed
96	Os.9311.1.S1_at	LOC_Os03g19420	-1.57	nicotianamine synthase, putative, expressed
97	Os.14101.3.S1_at	LOC_Os01g61200	-1.59	GDSL-like lipase/acylhydrolase, putative, expressed

Supplementary Table S4. F2 generation phenotype analysis of the double mutant (*d14osmads57-1*).

Phenotype (Tiller numbers)	Wild type (10-14)	*osmads57-1* (26-28)	*d14* (43-46)
Plant numbers of Genotype	38 (Dongjin, 26; Shiokari, 12)#	13 (*OsMADS57*$^{-/-}$*D14*$^{+/+}$) and (*OsMADS57*$^{-/-}$*D14*$^{+/-}$)	17 (*OsMADS57* $^{+/+}$*D14*$^{-/-}$), (*OsMADS57* $^{+/-}$*D14* $^{-/-}$) and (*OsMADS57* $^{-/-}$*D14* $^{-/-}$)

#The tiller numbers between the parents (Dongjin, 10.3±2.3; Shiokari 12.5±1.4) at the Sanya field, Hainan province, China, were no significant difference in the statistics.

Supplementary Table S5. Primer sequences used in this study.

Experiment	Primer name	Sequence
RT-PCR analysis	qMSF	5’GCACCAACATGAAAACTGTGA3’
	qMSR	5’CTCCCTCTGCCAAATCTTAATT3’
	qMS1F	5’TTGAGCCAATCACAGCAAAGAG3’
	qMS1R	5’TCGTCCAGCTTGTACGGCATAG3’
	qD14F	5’CGCCTTCGTCGGCCACTC3’
	qD14R	5’TCGAACCCGCCGTGGTAGTC3’
	qD27F	5'-TCTGGGCTAAAGAATGAAAAGGA-3'
	qD27R	5'-AGAGCTTGGGTCACAATCTCG-3'
	qUbiF	5'-GCCCAAGAAGAAGATCAAGAAC-3'
	qUbiR	5'-AGATAACAACGGAAGCATAAAAGTC-3'
	qACTF	5’CGTATGAGCAAGGAGATCAC3’
	qACTR	5’CACATCTGTTGGAAGGTGCT3’
	Os02g49850F	5' TGATCGTCGGGTTCCTCGTG 3'
	Os02g49850R	5' CAGATGAAGTAGTGCGTGCC 3'
	Os02g49860F	5' ACTCCTGTGCGTCAACCTCG 3'
	Os02g49860R	5' GGCTGGCTTCTTGTTCGTGT 3'
	OsMADS57 5’F	5' ATGGGGAGGGGGAAGATAG 3'
	OsMADS57 5’R	5' AATTTAGGCTTCTAGAAAGTTCG 3'
	MSTF	5’ATGGGGAGGGGGAAGATA3’
	MSTR	5’ ATTCAAGACTAGGAGGCATAT3’
	MSF	5' ATGGGGAGGGGGAAGATAGT 3'
	MSR	5' TTAAGGCAGATGAAGTCCCAGT 3'
	ACTINF	5'GAACTGGTATGGTCAAGGCTG3'
	ACTINR	5'ACACGGAGCTCGTTGTAGAAG3'
	TubulinF	5‘TCAGATGCCCAGTGACAGGA3’
	TubulinR	5‘TTGGTGATCTCGGCAACAGA3’
Mutant identify	2715-L2-LB	5’ACGTCCGCAATGTGTTATTAA3’
	Ngus-RB	5’AACGCTGATCAATTCCACAG3’
	M3A50432sense	5’TGGGACTTCTTGAACTGCTGA3’
	3A05432antisense1	5’CTGAAAGGCTTTGTGCTTGTTT3’
Vector construct	OsMADS57OEF	5’ CGGGATCCATGGGGAGGGGGAAGATAGT3’
	OsMADS57OER	5’GGGGTACCTTAAGGCAGATGAAGTCCCAGT3’
	OsMADS57ASF	5’GGGGTACCATGGGGAGGGGGAAGATAGT3’
	OsMADS57ASR	5' CGGGATCCTTAAGGCAGATGAAGTCCCAGT 3'
	miR444aOEBglIIF	5’GAAGATCTGCAATTGGGGGCAGCAAGC3’
	miR444aOESacIR	5’ CGAGCTCTGGCAACAGGAGGCAGCAAG3’

	OsMADSXhoIF	5’CCCTCGAGATGGGGAGGGGGAAGATAGT3’
	OsMADSKpnIR	5’GGGGTACCAGGCAGATGAAGTCCCAGTTC3’
In situ hybridization	MS1sensePF	5’TAATACGACTCACTATAGGGAGCCAATCACAGCAAAGAGAAG3’
	MS1sensePR	5’AAGCAATAGAGAGTAAGCAGGGTT3’
	MS1antisensePF	5’AGCCAATCACAGCAAAGAGAAG3’
	MS1antisensePR	5’TAATACGACTCACTATAGGGAAGCAATAGAGAGTAAGCAGGGTT3’
	D14T7F	5’TAATACGACTCACTATAGGGGTGCTGTCGCATGGCTTC’3
	D14R	5’GGCAGGTCGTCGACGTAGG’3
	D14F	5’GGTGCTGTCGCATGGCTTC’3
	D14T7R	5’TAATACGACTCACTATAGGGGCAGGTCGTCGACGTAGG’3
	ACTINT7F	5'TAATACGACTCACTATAGGGGAACTGGTATGGTCAAGGCTG3'
	ACTINR	5'ACACGGAGCTCGTTGTAGAAG3'
	ACTINF	5'GAACTGGTATGGTCAAGGCTG3'
	ACTT7R	5'TAATACGACTCACTATAGGGACACGGAGCTCGTTGTAGAAG3'
Yeast one hybrid	MSEcoRIsense	5’GGAATTCATGGGGAGGGGGAAGATAGT3’
	MSBamHIantisense	5’CGGATCCTTAAGGCAGATGAAGTCCCAGT3’
	MSNKEcoRIF	5’GAATTCATGGGGAGGGGGAAGATAG3’
	MSNKBamHIR	5’GGATCCTTAATTTAGGCTTCTAGAAAGTTCG3’
	D14pEcoRIF	5’CGGAATTCGAGCCACCACAGAAGATAAAG3’
	D14pXhoIR	5’CCTCGAGCTTCAGTTATTTAGGGGGGTG3’
miR444a Northern blotting	miR444a1 probe	5’GCAGCAAGCTTGAGGCAGCAA3’
	U6 probe	5’TGTATCGTTCCAATTTTATCGGATGT3’
EMSA	D14site1F	5’CAATAATAGCATTAAAAAGGAAGGG3’
	D14site1R	5’CCCTTCCTTT TTAATGCTAT TATTG3’
	D14site2F	5’AATTC AGCATTAAAA AGGAAAGCAT TAAAAAGGAA AGCATTAAAA AGGAAG3’
	D14site2R	5’CTTCCTTTTTA ATGCTTTCCT TTTTAATGCT TTCCTTTTTA ATGCTG3’
	MSEcoRIF	5’GAATTCATGGGGAGGGGGAAGATAG3’
	MSXhoIR	5’CCTCGAGTTAAGGCAGATGAAGTCCCAGT3’
Subcellular localization	MSXhoIF	5’CCGCTCGAGATGGGGAGGGGGAAGATAGT3’
	MSBamHIR	5’CGGGATCCAGGCAGATGAAGTCCCAGT3’
Luciferase assay	TB1BiFCBamHIsense	5’ GGATCCATGCTTCCTTTCTTCGATT3’
	TB1BiFCKantisense	5’GGTACCGCAGTAGTGCCGCGAA3’
	D14pPstIF	5’AACTGCAGCCCTTGTCTAAGACCTTTATGCGTTTG3’
	D14pBamHIR	5’CGGGATCCTCACACCAGCGCGGCGGATT3’
	MSNKXhoIF	5’CCTCGAGATGGGGAGGGGGAAGATAG3’

	MSNKKpnIR	5’GGTACCATTTAGGCTTCTAGAAAGTTCG3’
	MADS3XbaIF	5’GCTCTAGA ATGATGAACATGATGACCGATC3’
	MADS3KpnIR	5’GGGGTACC ACGTACGTGTGTACGTACGGT3’
	del494-503	5’AAGAGAGTATAAAGGCAAAGTATCATTATGAAATTATCTAATAAGTCACATTTTATGACATTC3’
	del494-503-antisense	5’GAATGTCATAAAATGTGACTTATTAGATAATTTCATAATGATACTTTGCCTTTATACTCTCTT3’
	del1455-1465	5’CGGAGACATAACCCATCAATAATAGAATGGCCATCTATCATCA3’
	del1455-1465-antisense	5’TGATGATAGATGGCCATTCTATTATTGATGGGTTATGTCTCCG3’
CoIP assay	MSNCFBamHI	5’CGGATCCATGGTCATGTCGCAACAA3’
	MSNCRKpnI	5’GGGTACCTTAAGGCAGATGAAGTCCCAGT3’
	OsMADS57BamHIF	5’CGGGATCCATGGGGAGGGGGAAGATAGT3’
	OsMADS57KpnIR	5’GGGGTACCTTAAGGCAGATGAAGTCCCAGT3’
	OsTBBamHIsense	5’GGATCCATGCTTCCTTTCTTCGATT 3’
	OsTBKpnIantisense	5’GGTACCTCAG CAGTAGTGCC GCGAA3’
Y2H assay	TB1Esense	5’ GAATTCATGCTTCCTTTCTTCGATTCC 3’
	TB1Bantisense	5’GGATCCTCAGCAGTAGTGCCGCGA3’
	MSNEcoRIF	5’GAATTCATGGGGAGGGGGAAGATAG3’
	MSNBamHIR	5’GGATCCTTAATTTAGGCTTCTAGAAAGTTCG3’
	MADSEcoRIsense	5’CGGAATTCATGGGGAGGGGGAAGATAGTGAT3’
	MADSXhoIantisense	5’CCCTCGAGTTAAGGCAGATGAAGTCCCAGTTCTG3’
RT-PCR analysis	Os08g42950.1HF	5’ACTGTTGAAGCACGAGATCTGC3’
	Os08g42950.1HR	5’ACCTTATCAGGCTTCCCCAT3’
	Os03g60110KHF	5’AGCCAAGAAATTATGCGGGT3’
	Os03g60110KHR	5’TTTGGCGAAGACATAGGGCTAG3’
	Os01g60670RKF	5’TGCATTGGATTTGTCACACA3’
	Os01g60670RKR	5’GTAAGGTCCCATTCAGCTTGTT
	Os03g10060S2F	5’TTGAGATCAGAACGCACCAGCGAT3’
	Os03g10060S2R	5’AGCTGGAGCTGCATCAAGGAATCT3’
	Os04g46010.1PPRF	5’CCAGGTGTATGATTGGATGACA3’
	Os04g46010.1PPRR	5’CCACGTACTTTTGCAATCAGAT3’
	Os10g33900GRF7F	5’GCTGGGCTATTCTGGGAGTG3’
	Os10g33900GRF7R	5’TCTCTCGAGCACCGCCAT3’
	LOC_Os10g33900F	5’GGTCATTCCCAAGACTCTCATG3’
	LOC_Os10g33900R	5’AGGGCTATGAAGGCATCAGA3’
	qD14F	5’CGCCTTCGTCGGCCACTC3’
	qD14R	5’TCGAACCCGCCGTGGTAGTC3’

	Os09g26460F	5’AAGCGCATGACATGCAGAT3’
	Os09g26460R	5’TGAAGATTTGCGAGGAGTACAC3’
	Os07g48620F	5’ AGACGTGTAATCCTGTCGAGCCAA3’
	Os07g48620F	5’ TATGGAGATGGAGCCGCTGCAATA3’
	Os01g19940F	5’TCATTAATAAGGACCATGAGCG3’
	Os01g19940R	5’TTACTCCCTGAAAAACATGTGC3’
ChIP	D14p (-2200) F	5’AAGAGAGTATAAAGGCAAAGTATC3’
	D14p (-2200) R	5’CCAAATGGAACATAACAAAGC3’
	D14p (-1300) F	5’CACTAAATTGTTTGCCCAAGTAAA3’
	D14p (-1300) R	5’CGTAGCCCTGATGAAAAGAAT3’
	D14p (-600--500) F	5’CGCTACATTACAGACACTAACAGCGACG3’
	D14p (-600--500) R	5’CTTCACAATCCCAACCAGAGATGC3’
	D14p(-300--1) F	5’GAAGCAATCACACACCTTCTCTGC3’
	D14p (-300--1) R	5’ATGGTCTTGACTCTTGCCTCGCTT3’
	UBQ F	5’TATCCAACATGAATGCCACA3’
	UBQ R	5’CAGCACGAGATGAGTAAAACAA3’

Supplementary Materials and Methods

Yeast two-hybrid assays

Yeast two-hybrid assays were performed as described previously (Han et al, 2008). cDNA of full-length *OsMADS57* was inserted into pGBKT7 and pGADT7. Vectors encoding the N-terminus (1-168aa) and the C terminus (169-241aa) of OsMADS57 were constructed into pGBKT7 and pGADT7. The cDNA encoding full-length OsTB1 was inserted into the GAL4 activation domain vector pGADT7. pGBKT7-OsMADS57 and pGADT7-OsMADS57, pGBKT7-OsMADS57 and pGADT7-OsMADS57N, pGBKT7-OsMADS57 and pGADT7-OsMADS57C, pGBKT7-OsMADS57N and pGADT7-OsMADS57N, pGBKT7-OsMADS57C and pGADT7-OsMADS57C, pGBKT7-OsMADS57 and pGADT7-OsTB1, and pGBKT7-OsMADS57 and pGADT7 were transformed into the yeast strain AH109. pGBKT7-OsMADS57 and pGADT7, and pGBKT7 and pGADT7-OsTB1 were used as negative controls. Positive colonies were firstly screened on synthetic dropout medium (SD/-Trp/-Leu/-His/-Ade). Then interactions were further examined by β-Galactosidase Assay on lift and confirmed after 3 h.

Affymetrix GeneChip analyses

The developing axillary buds from *OsMADS57* and wild-type DJ were obtained at the 30-day stage. Total RNA was isolated using a mirVana miRNA Isolation Kit (Ambion) and purified using a Qiagen kit. For microarray assays, 8 μg of total RNA were used to synthesize biotin-labeled cRNA probes. Affymetrix GeneChip assays followed the GeneChip Standard Protocol (Eukaryotic Target Preparation, Affymetrix).

To identify genes with differential expression between *OsMADS57* and wild-type DJ, a $\log_2$-transformed signal ratio for each gene was calculated using the R package affy, which is a part of Bioconductor project (http://www.bioconductor.org) and normalized using the RMA algorithm with $\log_2$ ratio ≥ 1 (2-fold change) as a cut-off. The functional annotation added to the regulated genes was derived from the Institute for Genomic Research (TIGR) database and functional classification was performed using the GOEAST Affymetrix tool (http://omicslab.genetics.ac.cn/GOEAST/) and AgriGO (http://bioinfo.cau.edu.cn/agriGO/).

To identify OsMADS57 targets, the reported C-A/T-A/T-A/T-A/T-A/T-A/T-A/T-A/T-G boxes (MADS protein binding *cis*-element) were used as our primary binding motif to screen using MochiView for the favorite CArG box in the region -1,500 bp from the initial translation code in all regulated genes(Homann & Johnson, 2010; Tang & Perry, 2003). The promoter sequence datasets for all regulated genes were developed using database queries according to the rice annotations in TIGR. The MEME suite was employed to identify a probable OsMADS57 binding motif from the corresponding CArG boxes of all target gene promoters (Bailey et al, 2009).

Northern blot analysis of small RNAs

Small RNAs were extracted from 10-day-old rice seedlings using a mirVana miRNA Isolation Kit (Ambion) following the manufacturer's protocol and treated with RNase-free DNase I (MBI Fermentas) as described online. The enriched small RNAs were treated, separated in 15% polyacrylamide-urea gels, electro-transferred to Zeta-Probe membranes (Bio-Rad), and hybridized with an antisense oligonucleotide probe as described previously (Xie et al, 2003). The U6 antisense oligonucleotide probe was used as a control (Supplementary Table 4 online).

Supplementary References

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