Supporting Information

Tamaki et al. 10.1073/pnas.1417623112

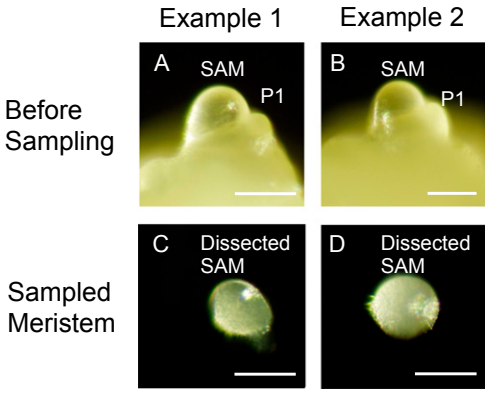


Fig. S1. Dissection of SAMs of rice. Sampling of SAM from rice. Two examples of sampling are shown (*A* and *C* for example 1 and *B* and *D* for example 2). (*A* and *B*) Plants at 28 DAG were dissected under a microscope to expose the SAM. (*C* and *D*) The dome-shaped structure of the SAM was further dissected for sampling. P1, leaf primodia at plastochron 1 (P1) stage. (Scale bars, 50 μm.)

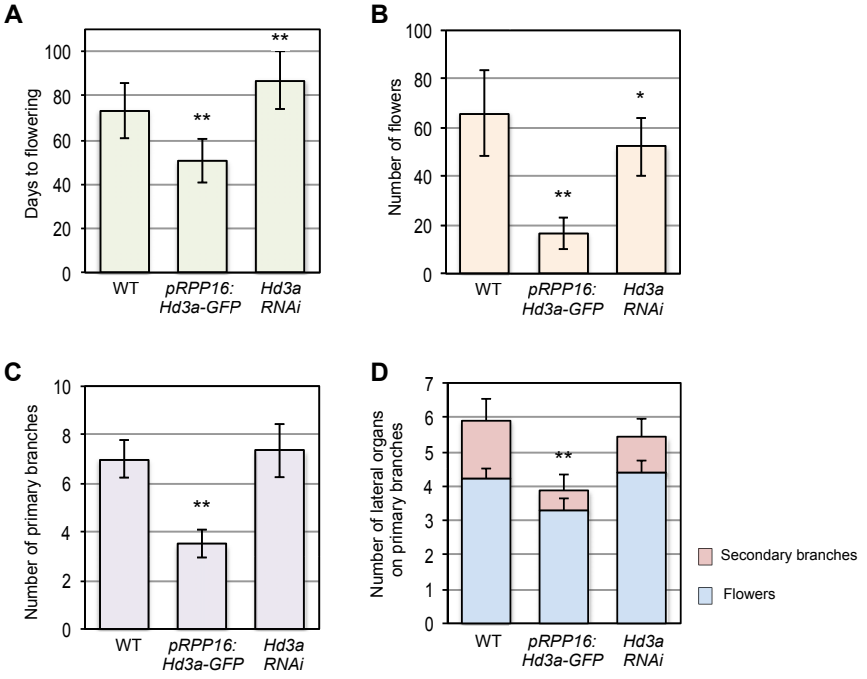
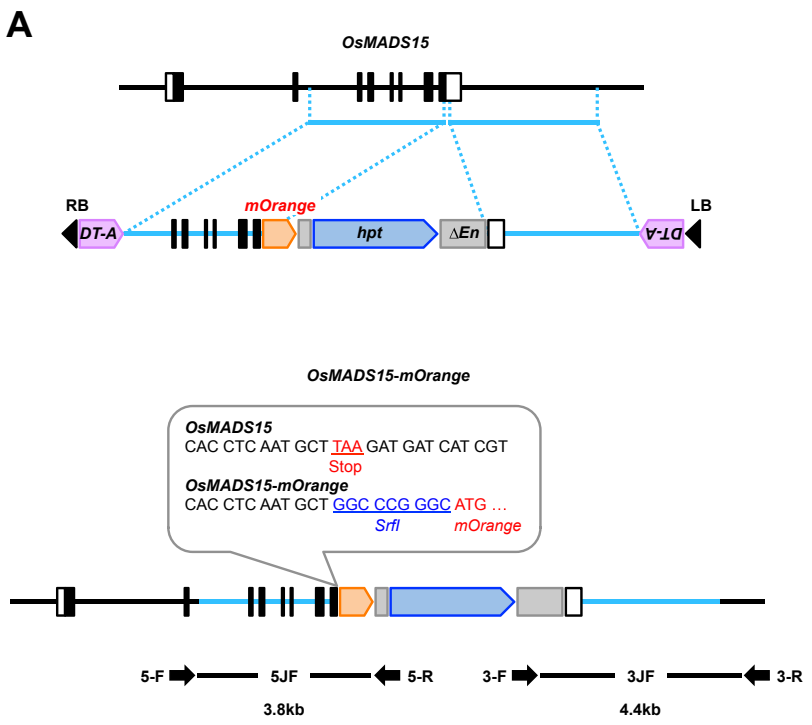
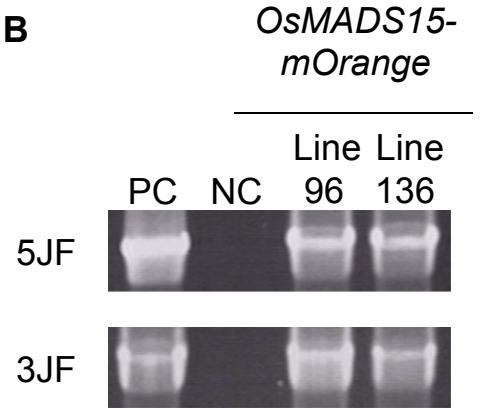


Fig. S2. Inflorescence phenotypes of *pRPP16:Hd3a–GFP* and *Hd3a* RNAi. Days to flowering (*A*), number of flowers (*B*), number of primary branches (*C*), and number of lateral organs on primary branches (*D*). In *D*, blue and pink bars indicate number of flowers and number of secondary branches, respectively. Results from WT and pRPP16:Hd3a–GFP are the same as those in Fig. 2. $*P < 0.05$; $**P < 0.01$ (significant difference relative to WT by *t* test).





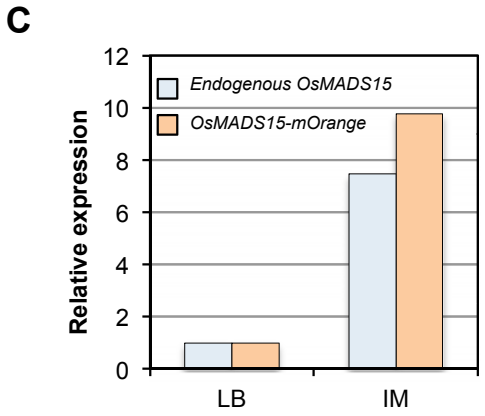


Fig. S3. *mOrange* knock-in modification of the *OsMADS15* locus by gene targeting. (*A*, *Upper*) Schematic diagrams of the *OsMADS15* gene and the T-DNA region of the knock-in targeting vector p15Or. Black and white boxes indicate exons and UTRs, respectively. Blue lines represent the sequence corresponding to the homologous regions carried by p15Or. RB, right border; *DT-A*, *diphtheria toxin A* gene; *hpt*, *hygromycin phosphotransferase* gene for positive selection; *ΔEn*, functional transcriptional stop sequence from *En/Spm* transposon; LB, left border. (*A*, *Lower*) Structure of resultant *OsMADS15–mOrange* gene. Lines 5JF and 3JF indicate the 5′ and 3′ junction fragments generated by homologous recombination. Flanking black arrows 5-F/5-R and 3-F/3-R represent primers used for PCR screening of targeted callus lines. (*B*) Confirmation of gene targeting by PCR screening. The regions amplified are indicated in *A*. As a positive control of PCR (PC), we constructed a plasmid containing the same *OsMADS15–mOrange* DNA sequence predicted to arise from successful gene targeting and used this plasmid as a template. NC, negative control without template. (*C*) Expression patterns of the endogenous *OsMADS15* gene and the *OsMADS15–mOrange* gene in heterozygous plants. Endogenous *OsMADS15* expression was quantified by qPCR using primers that anneal within the 3′ UTR of *OsMADS15*, and *OsMADS15–mOrange* expression was quantified by using primers annealing in the *mOrange* coding region. Relative expression was calculated by normalizing the level in the leaf blade (LB) to 1. IM, inflorescence meristem at stage 3.

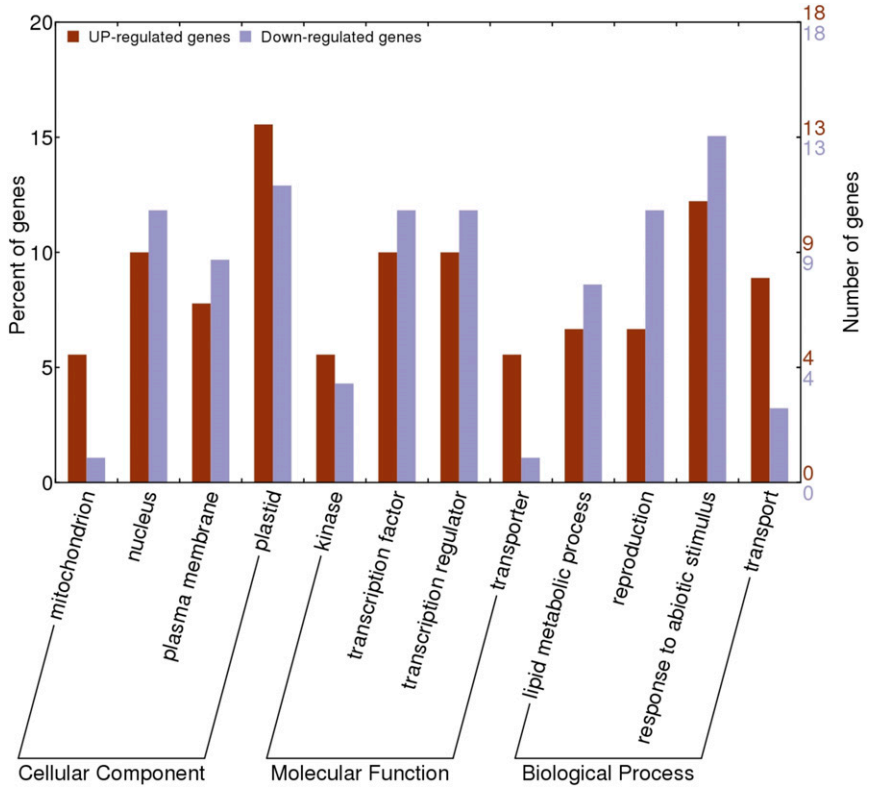


Fig. S4. Comparison of enriched GO terms between Hd3a–up-regulated and –down-regulated genes. Enrichment in GO terms between up- and down-regulated genes was analyzed by WEGO (1). GO terms that were represented by more than five genes were considered for the analysis.

1. Ye J, et al. (2006) WEGO: A web tool for plotting GO annotations. Nucleic Acids Res 34(web server issue):W293–W297.

Table S1. Summary of read numbers based on RNA-seq data from rice meristems

	WT 1	WT 2	WT 3	RNAi 1	RNAi 2	RNAi 3
Used reads	50,777,755	51,563,430	50,188,150	52,894,765	51,017,354	51,926,998
Mapped reads (percentage of total, %)	43,738,292 (86.1)	44,398,235 (86.1)	43,325,565 (86.3)	36,453,629 (68.9)	34,520,738 (67.7)	35,777,143 (68.9)
Unmapped reads (percentage of total, %)	7,039,463 (13.9)	7,165,195 (13.9)	6,862,585 (13.7)	16,44,1136 (31.1)	16,496,616 (32.3)	16,149,855 (31.1)

Table S2. Primers used in this study

Name	Sequence	Note
MADS15 5′-F	AGTCAAGCTTAACTTCAAACCTCGTGTCTTTTGCACTCTGGC	PCRs for cloning of 5′-homologous region of p15Or
MADS15 5′-R	TGACGCCCGGGCCAGCATTGAGGTGGCTCAGCATCCATGG	PCRs for cloning of 5′-homologous region of p15Or
MADS15 3′-F	AGTCGTTTAAACGATGATCATCGTCGTCGTCGTCGGCCAAAC	PCRs for cloning of 3′-homologous region of p15Or
MADS15 3′-R	TGACACTAGTGCCGACTTCGTGCTGTACAAGCTCAAGGAG	PCRs for cloning of 3′-homologous region of p15Or
5-F	TCCTTTTCTATTGCATTAGCATTTC	Detection of 5JF generated by GT with p15Or
5-R	TCCACGATGGTGTAGTCCTCGTTGT	Detection of 5JF generated by GT with p15Or
3-F	CATGCTAGTCCGCCTCCGGATCAGAGCACG	Detection of 3JF generated by GT with p15Or
3-R	GCGCCATGGAGATGAACAAGGTGAGGTACA	Detection of 3JF generated by GT with p15Or
mOr-qF2	CGGCGAGTTCATCTACAAGG	qPCR of mOrange
mOr-qR2	TGGTCTTCTTCTGCATTACGG	qPCR of mOrange
OsMADS15-F	CGTCGTCGGCCAAACAG	qPCR and In situ hybridization of OsMADS15
OsMADS15-R	TGACTTCAATTCATTCAAGGTTGCT	qPCR and In situ hybridization of OsMADS15
Ubq-Real-F	AACCAGCTGAGGCCCAAGA	qPCR of Ubiquitin
Ubq-Real-R	ACGATTGATTTAACCAGTCCATGA	qPCR of Ubiquitin
OsFD1-F	CAAAGCTAGCTAATCCAGG	qPCR and in situ hybridization of OsFD1
OsFD1-R	GCCACAGCTAAGCTTCCTCCTAG	qPCR and In situ hybridization of OsFD1
GF14b-F	GCGGAAGAGATCAGGGAAG	qPCR and In situ hybridization of GF14b
GF14b-R	CGACAACAATCACAGCCACA	qPCR and In situ hybridization of GF14b
Hd3a-F	GCTCACTATCATCATCCAGCATG	qPCR of Hd3a
Hd3a-R	CCTTGCTCAGCTATTTAATTGCATAA	qPCR of Hd3a
RFT1-F	TGGGTTAGCTGACCTAGATTCAAA	qPCR of RFT1
RFT1-R	GCCAACCACAAGAGGATCG	qPCR of RFT1
IAA19-F	TGCCAAGGCACAAGTTGTTG	qPCR of IAA19
IAA19-R	CACTGGCGGCCAATGTATT	qPCR of IAA19
OsAUR1 -F	ACCTTTTGTCTCAGCCCACTAGA	qPCR of Aurora Kinase OsAUR1
OsAUR1 -R	GATACTGGGCCGAGAGATTGC	qPCR of Aurora Kinase OsAUR1
PCNA -F	CACCTCGGCATCCCTGACT	qPCR of PCNA
PCNA -R	CCTTGCAGATCCTGGAAAACTC	qPCR of PCNA
CycB2,2 - F	GCATGCGCCCGAGATG	qPCR of CycB2,2
CycB2,2 - R	GGTGCTCCGATGATGTTCTTG	qPCR of CycB2,2
proline oxidase - F	CTGGTCGTGTTTCCGTTTGTT	qPCR of proline oxidase
proline oxidase - R	AGAAGACTCGCGACAATTGACA	qPCR of proline oxidase
LOC_Os01g15180 -F	TAACGAGACAGTGGAGCAGC	qPCR of LOC_Os01g15180
LOC_Os01g15180 -R	TACTTCACGATCCCAGTCGG	qPCR of LOC_Os01g15180
LOC_Os07g05750 -F	GGAGGGTCCCATGAAACAGG	qPCR of LOC_Os07g05750
LOC_Os07g05750 -R	GTGGTAGATGGATCGGCACA	qPCR of LOC_Os07g05750
LOC_Os08g12460 -F	GATAGGAGGCAGCTTGACCA	qPCR of LOC_Os08g12460
LOC_Os08g12460 -R	TGCAATCATTCATCAGAGGAAGA	qPCR of LOC_Os08g12460
LOC_Os05g23389 -F	TGGTGGTATTGAGGCACATGTG	qPCR of LOC_Os05g23389
LOC_Os05g23389 -R	GACATTGTTAGACCCGCCCATAA	qPCR of LOC_Os05g23389
LOC_Os12g04830 -F	TACAGTTGTACACCTCTGATCAG	qPCR of LOC_Os12g04830
LOC_Os12g04830 -R	ACTGAGTACTACCCATTGTGAATCT	qPCR of LOC_Os12g04830
LOC_Os12g26830 -F	TTTGTCCCTCGCTACCAATTG	qPCR of LOC_Os12g26830
LOC_Os12g26830 -R	CATGGGCAGGGCACAAG	qPCR of LOC_Os12g26830
LOC_Os07g33180 -F	AGACGGCTCCACTCCACA	qPCR of LOC_Os07g33180
LOC_Os07g33180 -R	CTGATGGTGTGGAGGATTAGGTGTA	qPCR of LOC_Os07g33180
LOC_Os01g11720 -F	CAAGTGCTAGTCCAGAGGCC	qPCR of LOC_Os01g11720
LOC_Os01g11720 -R	GTCTTCACGGTGGAGCTTATC	qPCR of LOC_Os01g11720
LOC_Os02g30960 -F	CAAGGGCAAGCAACCTCTTG	qPCR of LOC_Os02g30960
LOC_Os02g30960 -R	CCTCCACAATGGCTTGTTTTC	qPCR of LOC_Os02g30960

Other Supporting Information Files

Dataset S1 (XLSX)