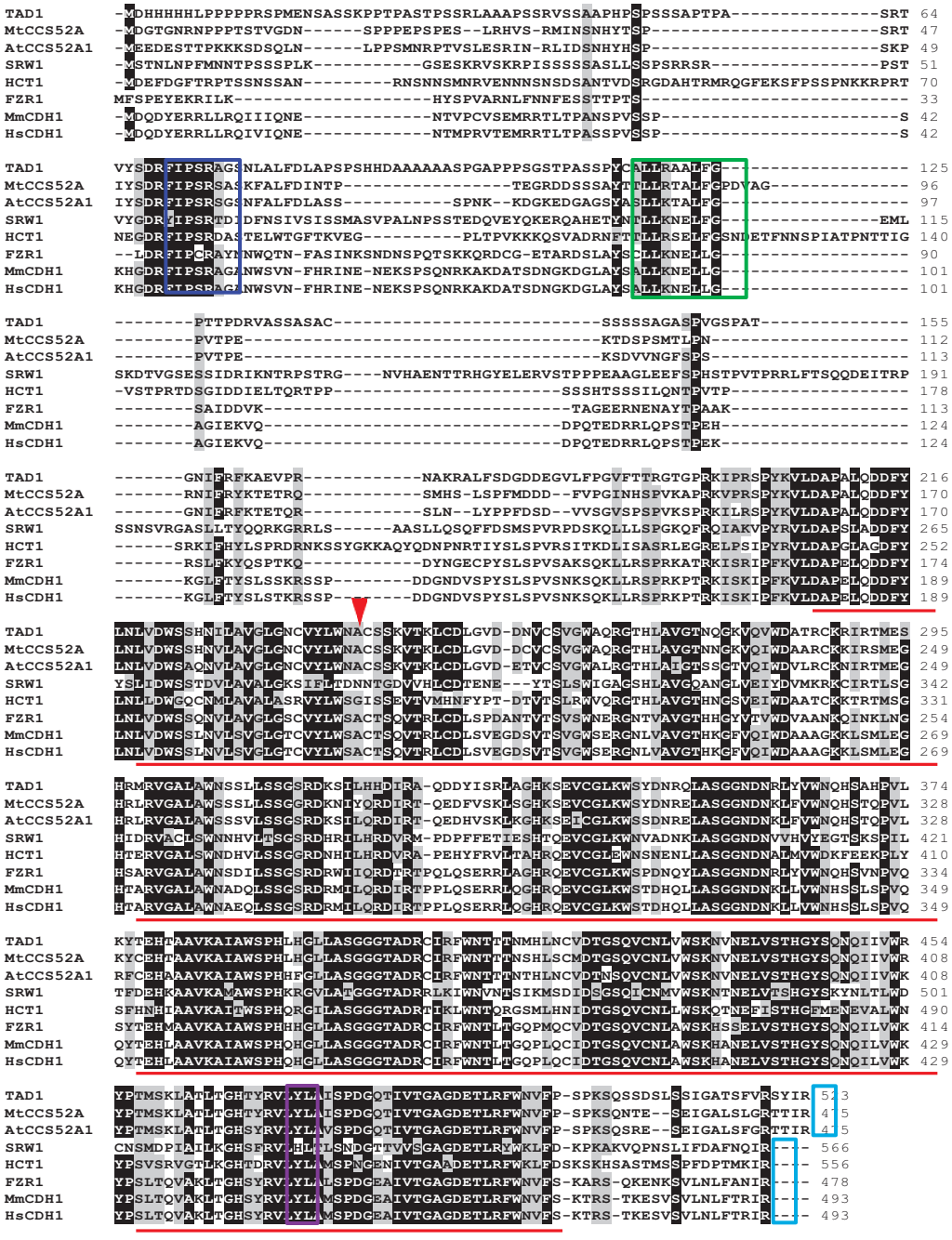
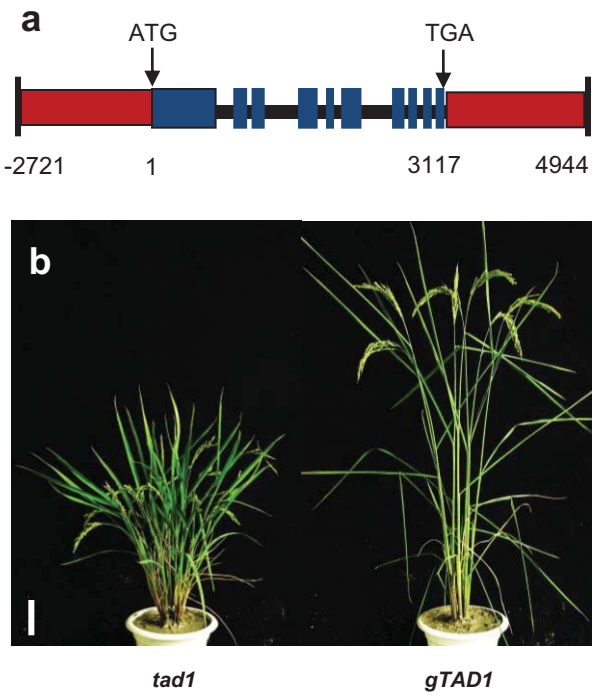
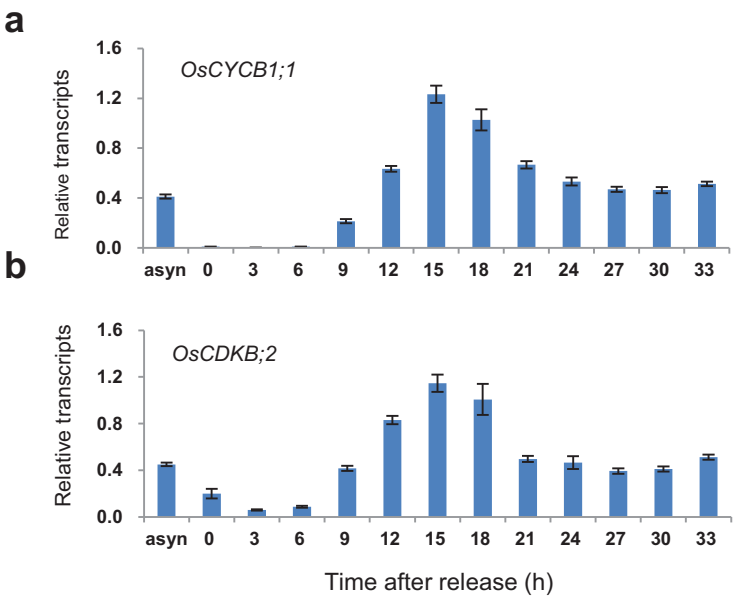


Supplementary Figure S1 Alignment of TAD1 and its homologues.

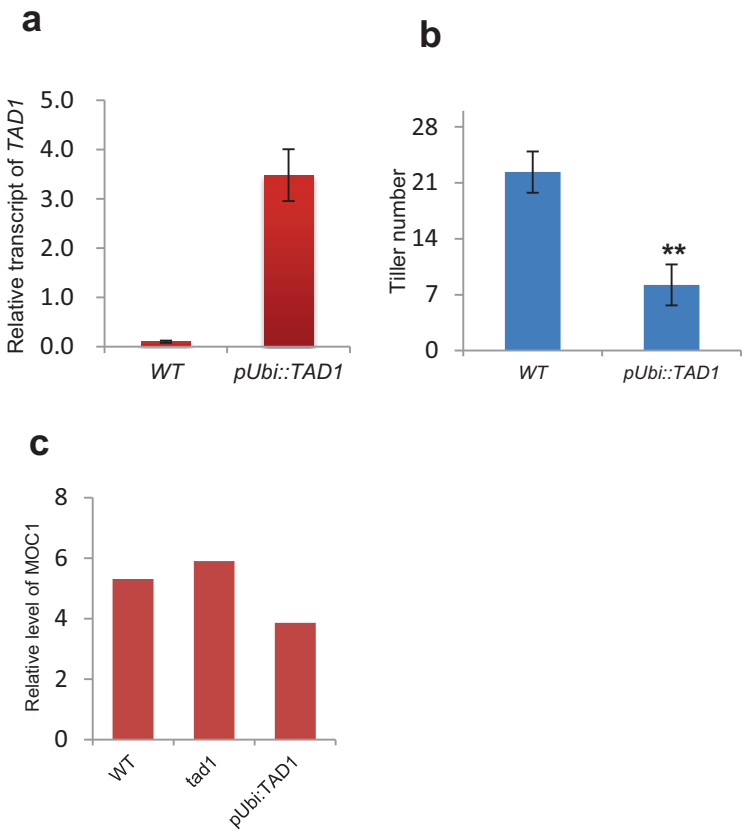
TAD1 and its homologous proteins contain different functional domains or motifs, including C-box (blue tangle), CSM (green tangle), WD repeats (red underlined), RVL (purple tangle), and IR (bright blue tangle). The red triangle indicates the mutation site in *tad1*. Accession numbers: TAD1, ABF93719; MtCcs52A, AF134835; AtCcs52A1, Q8L3Z8; SpSrw1,O13286; ScHct P53197. DmCdh1, NP_726941, MmCdh1, NP_062731; HsCdh1, NP_057347.



Supplementary Figure S2 Complementation test of *tad1*. (**a**) Schematic diagram of the complementation plasmid containing the entire *TAD1* (g*TAD1*). (**b**) Rescued phenotypes of *tad1* by transferring the complementation plasmid *gTAD1* into the *tad1* mutant plant. Scale bar, 10 cm.



Supplementary Figure S3 Expression patterns of G2/M phase maker genes during the cell cycle progression. (**a, b**) The relative transcript levels of *OsCYCB1;1* (**a**) and *OsCDKB;2* (**b**) in suspension cells at indicated time points released from synchronization. Transcript levels were analyzed by Real-time PCR using the rice *Actin* gene as the internal control. Values are means with SD of three independent experiments (n = 3).



Supplementary Figure S4 Overexpression of *TAD1* leads to the decreased tiller number in transgenic plants. (**a**) *TAD1* expression levels in wild-type and *TAD1*-overexpressing transgenic plants analyzed by Real-time PCR using rice *Actin* gene as the internal control. Values are means with SD of three independent experiments (n = 3). (**b**) Comparison of tiller number between the wild type and TAD1-overexpressing transgenic plants. Values are means with SE (n = 9 plants). The double asterisks indicate the significant difference determined by two-tailed t-test at $P < 0.01$. (**c**) Relative protein levels of MOC1 in the wild-type, *tad1* and *TAD1*-overexpressing transgenic plants. The immunoblot signals of MOC1 and Actin were quantified using Quantity One software (Bio-Rad). The relative protein levels of MOC1 were generated by normalization against the protein levels of Actin in the three samples mentioned above.

Supplementary Table S1. PCR-based molecular markers developed in this study

Name	BACs	Forward sequence (5'-3')	Reverse sequence(5'-3')
S7206	AC105733	CTTGTGACAATACAGAGACAAGC	TACCTCTCCCATCCGATTC
S7999	AC134236	GATGGGATTTGATTCCACAG	CACAGTTGGGAAATTTGTCC
S9681	AC119747	GACATCCGGTCAAATGTTCC	GTTCAAGCCGTAGCTCTTCC
S1396	AP000615	AGCTGGATACCAGCAGTGG	CATGTCCATGTTAAATAGTGCC
RM4683	AP008209	TACAGCAACAATCTTTAACC	TAGAGGGAGTATTGTGCTAG
S9110	AC105363	CCAGTGTGATTGCTGCTCC	GATTCGGATTCGAACTGGC
RM523	AC098695	AAGGCATTGCAGCTAGAAGC	GCACTTGGGAGGTTTGCTAG
S1273	AC098695	AGCATAACATCAAAGCCATG	ACTGCCTAGCTAGATAAGTTAGC
S3837	AC119747	GACACACAATTTGCTATGGACG	GGTCCGGGAGAACAATGC

Supplementary Table S2. Predicted genes/ORFs between markers RM523 and S1273

Accession number	Annotation
LOC_Os03g03130	ubiquitin-conjugating enzyme
LOC_Os03g03140	RNA recognition motif containing protein
LOC_Os03g03150	WD40 repeat-containing protein
LOC_Os03g03164	homeobox protein knotted-1

Supplementary Table S3. Primer sequences for generating DNA constructs

Construct	Primer name	Sequence (5'-3')
gTAD1	gTAD1F1-F	CTACAGCGACCGCTTCATC
	gTAD1F1-R	GTAGCTCCTAACAAATGATGTGG
	gTAD1F2-F	TGTTTCCATCTCCCAAGTCC
	gTAD1F2-R	GGGGTACCCACTTCTCTGAGTGAGACCATCC
REP5N-TAD1	5NTAD1-F	CTCGAGATGGATCACCACCACCACC
	5NTAD1-R	GCGGCCGCTTACCGGATGTAGCTCCTAAC
REP2-TAD1	REPTAD-F	CATATGATGGCGGGGGGGCTC
	REPTAD-R	GGATCCCCGTATGTGGCTTCTCGAG
pUbi::TAD1	TAD1OE-F	GGGGTACCATGGATCACCACCACCACCAC
	TAD1OE-R	CGACTAGTTCACCGGATGTAGCTCCTAA
TAD1-*in situ*	SKTAD1-F	GCGAATTCTCCCAAGTCCCAGAGTTCTG
	SKTAD1-R	ACGGATCCCCAGCTCCAAGTTGACTCAG
SCN-TAD1	SCNTAD1-F	CAACTAGTATGGATCACCACCACCACCAC
	SCNTAD1-R	CCGGTACCCCGGATGTAGCTCCTAACAAAT
SCNTAD1-N203	SCNTAD1-F	CAACTAGTATGGATCACCACCACCACCAC
	N203R	GGGGTACCATAAGGTGACCTAGGGATCT
SCNTAD1-WD	WD-F	GCGCGGATCCAAGGTGCTGGATGCTCCCGCATTG
	WD-R	GGGGTACCGTTCCAAAACCGAAGCGTTTC
SCNTAD1-C398	C398-F	CAACTAGTATGACGCCCGACCGGGTGGCGT
	SCNTAD1-R	CCGGTACCCCGGATGTAGCTCCTAACAAAT
SCNTAD1-C410	C410-F	GCGCGGATCCCCCTACTGCGCGCTCCTC
	SCNTAD1-R	CCGGTACCCCGGATGTAGCTCCTAACAAAT
SCNTAD1-C456	C456-F	CTAGTCTAGAGACCGCTTCATCCCCAGCC
	SCNTAD1-R	CCGGTACCCCGGATGTAGCTCCTAACAAAT
SCNTAD1-N460	SCNTAD1-F	CAACTAGTATGGATCACCACCACCACCAC
	N460-R	CCGGTACCCTTTGACATTGTTGGGTATC
pActin::MOC1-GFP	MOC1GFP-F	GGACCCGGGATGCTCCGGTCACTCCACTCC
	MOC1GFP-R	CGGTCTAGACGACGACGACGGCTGCCAC
SCC-MOC1	SCCMOC1-F	CGGGATCCATGCTCCGGTCACTCCACTCC
	SCCMOC1-R	CCGGTACCCGACGACGACGGCTGCCAC
SCC-mMOC1	mMOC1-F	CGGCGCCGTCGACGGCGGACTTGGCGCTGGCGTGCGCG
	mMOC1-R	CGCGCACGCCAGCGCCAAGTCCGCCGTCGACGGCGCCG
SF-OsAPC10	OsAPC10-F	CGGGGGATCCATGGAATCCGACGGCGAGGAG
	OsAPC10-R	GGGGTACCCCTAACAGTAGAGTAGGTGAC

Supplementary Table S4. Primer sequences for real-time PCR analyses

Primer name	Sequence (5'-3')
QTAD1-F	GCAGTCGTGACAAGAGCATCCT
QTAD1-R	AGCCCACAGACCTCCGATTTATG
QActin-F	CTTCATAGGAATGGAAGCTGCGGGTA
QActin-R	CGACCACCTTGATCTTCATGCTGCTA