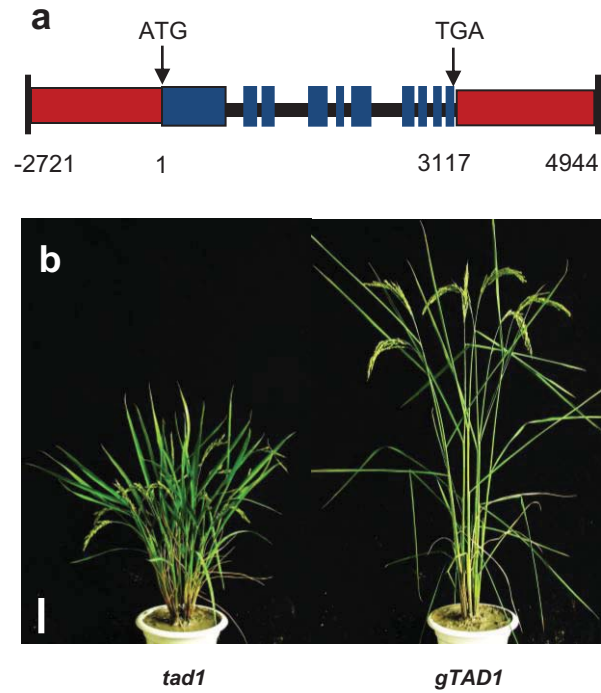


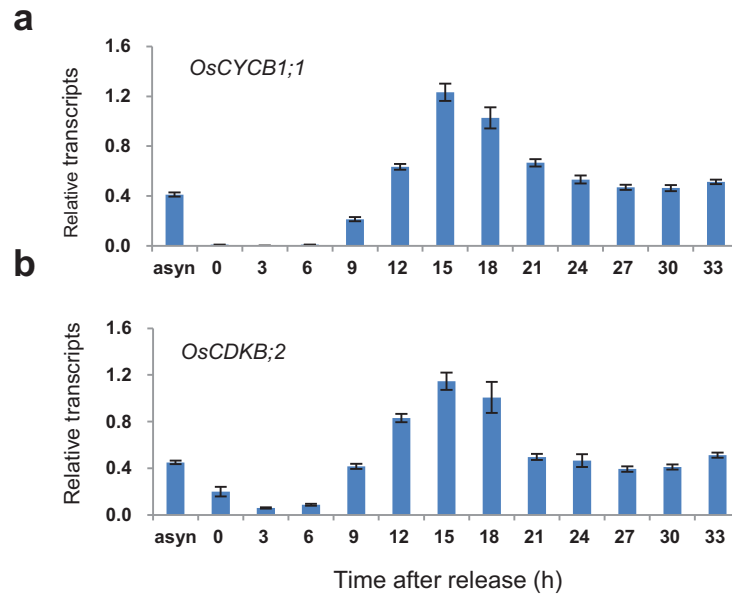
TAD1	-MDHHHHLLPPPPRSPMENSASSKPTTASTPSSRLAAAPSSRVSSAAPHSPSSSAPTFA-----SRT	64
MtCCS52A	-MDGTGNRRNPPPTSTVGDN-----SPPPEPSPE--LRHVS-RMINSNHYS-SP-----SRT	47
AtCCS52A1	-MEDEESTPKKKSDSQLN-----LPPSMNRPTVLESERIN-RLIDSNHYHSP-----SKP	49
SRW1	-MSTNLNPFMNNTPSSSPLK-----GSEKRVKRPISSSSSASLLSSPSRRSR-----PST	51
HCT1	-MDEFDGFTRPTSSSSAN-----RNSNNSMNRVNNNSNSDSANTVDSRGDAHTRMRQGFEKSPSSPNKKRPT	70
FZR1	MFSPEYEKRILK-----HYSFVARNLFNNFESSTTPTS-----	33
MmCDH1	-MQDDYERRLLRQIIQNE-----NTVPCVSEMRRTLTPANSFVSSP-----S	42
HsCDH1	-MQDDYERRLLRQIVIQNE-----NTMPRVTEMRRTLTPASSFVSSP-----S	42
TAD1	VYSDR FIPSRAGNLALFDLAPSPSHHDAAAAAASPGAPPSPGSGTPASSPVCALLRAALFG-----	125
MtCCS52A	IYSDR FIPSRSAK FALFDINTP-----TEGRDSSSAITPLLRALFGPDVAG-----	96
AtCCS52A1	IYSDR FIPSRSGNFALFDLASS-----SPNK--KDGKEDGAGSAYALLKALFG-----	97
SRW1	VYQDR FIPSRIDDFNSIVSISSMASVPALNPSSTEDQVEYQKERQAHETNLLKNEELFG-----	115
HCT1	NEGDR FIPSRDASTELWTGFTKVEG-----PLTPVKKQSVADRNETLLRSEELFGSNIEFFNNSPTATPNTTG	140
FZR1	--LDR FIPGRAYINWQTN-FASINKSNDNSPQTSKKQRDCG-ETARDSLAVSLLKNEELFG-----	90
MmCDH1	KHGDR FIPSRAGNWSVN-FHRINE-NEKSPSQNRKAKDATSDNGKDGLANSAALLKNEELFG-----	101
HsCDH1	KHGDR FIPSRAGNWSVN-FHRINE-NEKSPSQNRKAKDATSDNGKDGLANSAALLKNEELFG-----	101
TAD1	-----PTTPDRVASSASAC-----SSSSSAGASPVGSPAT-----	155
MtCCS52A	-----FVTPE-----KTDSFSMTLPN-----	112
AtCCS52A1	-----FVTPE-----KSDVVGNSPSS-----	113
SRW1	SKDTVGSSESIDRIKTRPSTRG---NVHAENTTRHGYELERVSTPPPEAAGLEEFSPHSTVTPRRLFTSQQDEITRP	191
HCT1	-VSTPRTDSGIDDIELTQRTTP-----SSSHTSSILQNTVTP-----	178
FZR1	-----SAIDDVK-----TAGEERNENAYTPAAK-----	113
MmCDH1	-----AGIEKVQ-----DPQTEDRRLLQPSLPEH-----	124
HsCDH1	-----AGIEKVQ-----DPQTEDRRLLQPSLPEK-----	124
TAD1	-----GNIFRFKAEVPR-----NAKRALFSDGDDEGLVFPVFTTRGTGPRKIPRSPEYKVLDAPELQDDFY	216
MtCCS52A	-----RNIERFKTETRO-----SMHS--LSPFMDDD--FVPGINHSFPVKAPRKYKVLDAPELQDDFY	170
AtCCS52A1	-----GNIERFKTETOR-----SLN--LYPPFSD--VVGVSFSPVSPKILRSPEYKVLDAPELQDDFY	170
SRW1	SSNSVRGASLLTYQQRKRRLLS-----AASLLQSQFFDSMSFVRPDSKQLLLSPGQFROIAKVYRVLDAPELQDDFY	265
HCT1	-----SRKIFHYLSPDRNKSSYGKKAQYQDNPNRTIYSLSPVRSITKDLISASRLEGRELPSIPYRVLDAPELQDDFY	252
FZR1	-----RSLFKYQSPTKQ-----DYNCEPCYSLSPVSAKSQKLLRSRPRKATRKISRIPIPKVLDAPELQDDFY	174
MmCDH1	-----KGLFTYSLSSKRSSP-----DDGNDVSPYSLSPVSNKSQKLLRSRPRKPTRKISKIPIPKVLDAPELQDDFY	189
HsCDH1	-----KGLFTYSLSTRSSP-----DDGNDVSPYSLSPVSNKSQKLLRSRPRKPTRKISKIPIPKVLDAPELQDDFY	189
TAD1	LNLVDWSSHNILAVCLGNCVYLWACSSKVTKLCDLGVD-DNYCSVGNARQGHVAVGTNQGKVVWDATRCRIRRTMES	295
MtCCS52A	LNLVDWSSHNVLAVCLGNCVYLWACSSKVTKLCDLGVD-DGVCVGNARQGHVAVGTNNGKVVWDAAARCKIRSMEG	249
AtCCS52A1	LNLVDWSSAQNVLAVCLGNCVYLWACSSKVTKLCDLGVD-ETVCSVGNALRGTHLAVGTSSGTVQTDVLRCKNIRTMEG	249
SRW1	YSLIDWSSTDVAVLALGKSIETLDDNNTGCVVHLCDFENE---YTSLSVIGAGSHLAVGQANGVETVDVMKRCIRTLSG	342
HCT1	LNLLDWGQCNMLAVLALASRVYLVSGISSEVTVMHNFYPT-DTIVTSLRNVQRGTHLAVGTNNGSVEIWDAAATCKRTRTMSG	331
FZR1	LNLVDWSSONVAVLAVCLGNCVYLWACSSKVTKLCDLSPDANTVTSVSNBERGNTVAVGTHHGCVTVDVAANKQINKLNG	254
MmCDH1	LNLVDWSSINVLAVCLGNCVYLWACSSKVTKLCDLVSGGDSVTVSVGNBERGNLVAVGTTHKGFVQIWDAAAGKKLMSLEG	269
HsCDH1	LNLVDWSSINVLAVCLGNCVYLWACSSKVTKLCDLVSGGDSVTVSVGNBERGNLVAVGTTHKGFVQIWDAAAGKKLMSLEG	269
TAD1	HRMRVGAIAWSSSLSSGSRDKSLHHDIRA-QDDYISRLACHKSEVCGLKWSYDNRQLASGGNDNRLYVWNQHSIAHPVL	374
MtCCS52A	HRIRVGAIAWSSSLSSGSRDKNRYORDIRT-QEDFVSKLSCHKSEVCGLKWSYDNRRELASGGNDNKLFWVWNQHSIQPVL	328
AtCCS52A1	HRIRVGAIAWSSSLSSGSRDKSLORDIRT-QEDHVSKLCHKSEVCGLKWSYDNRRELASGGNDNKLFWVWNQHSIQPVL	328
SRW1	HIDRVACLSWNNHVLSSGSRDHRILHRDVRM-PDPFFETIESHTQEVCGLKWVADNKLASGGNDNVVHVYEGTSSKSPIL	421
HCT1	HTIRVGAIAWSSSLSSGSRDHRILHRDVRM-PEHYFRVLTAFHROEVCGLEWNSNENLLASGGNDNKLFWVWNQHSIAHPVL	410
FZR1	HSARVGAIAWSSSLSSGSRDHRILORDIRPPLQSERLQCHROEVCGLKWSYDNRQLASGGNDNRLYVWNQHSVNPVQ	334
MmCDH1	HTARVGAIAWSSSLSSGSRDHRILORDIRPPLQSERLQCHROEVCGLKWSYDNRQLASGGNDNKLFWVWNQHSVNPVQ	349
HsCDH1	HTARVGAIAWSSSLSSGSRDHRILORDIRPPLQSERLQCHROEVCGLKWSYDNRQLASGGNDNKLFWVWNQHSVNPVQ	349
TAD1	KYTEHAAVKAIAWSPHHLHGHLASGGGTADRCLRFWNTLTFNMHLNCDVDTGSQVCNVLVSKNVNVELVSTHGYSOQIIVWR	454
MtCCS52A	KYCEHAAVKAIAWSPHHLHGHLASGGGTADRCLRFWNTLTFNSHLSLSCMDTGSQVCNVLVSKNVNVELVSTHGYSOQIIVWR	408
AtCCS52A1	RFEHAAVKAIAWSPHHLHGHLASGGGTADRCLRFWNTLTFNTHLNCVDVDTGSQVCNVLVSKNVNVELVSTHGYSOQIIVWR	408
SRW1	TFDEHAAVKAIAWSPHRRGGLASGGGTADRRLKINWNTSKMSDLDSSGQICNMVWSKNTNELVSHHGYSKYNLTFWD	501
HCT1	SEHNHAAVKAIAWSPHQRGLASGGGTADRTEKLWNTORGSMHLNIDTGSQVCNVLVSKNVNVELVSTHGEMENEVALWN	490
FZR1	SYTEHAAVKAIAWSPHHLHGHLASGGGTADRCLRFWNTLTFGQPMQCVDTGSQVCNVLVSKNVNVELVSTHGYSOQIIVWR	414
MmCDH1	QYTEHAAVKAIAWSPHHLHGHLASGGGTADRCLRFWNTLTFGQPLQCIDTGSQVCNVLVSKNVNVELVSTHGYSOQIIVWR	429
HsCDH1	QYTEHAAVKAIAWSPHHLHGHLASGGGTADRCLRFWNTLTFGQPLQCIDTGSQVCNVLVSKNVNVELVSTHGYSOQIIVWR	429
TAD1	YPTMSKLAALTLGHTYRV.YLALHSPDQOTIVTGAGDETLRFWNVFP-SPKSQSSDSLSEIGATSFVRSYIR	513
MtCCS52A	YPTMSKLAALTLGHTYRV.YLALHSPDQOTIVTGAGDETLRFWNVFP-SPKSQNTSE--SEIGALSLGRITTR	415
AtCCS52A1	YPTMSKLAALTLGHTYRV.YLALHSPDQOTIVTGAGDETLRFWNVFP-SPKSQSRSE--SEIGALSFGRITTR	415
SRW1	CNSMDPIALTKGHSYRV.HLHLSNDGTIVVSGAGDETLRFWVWLEF-KPKAKVQPNSLIFDAFNQIR	566
HCT1	YPSVSRVGTLLKGHTRV.YLALHSPDQOTIVTGAGDETLRFWVWLEFDSKSKHSASTMSFPDPTMKIR	556
FZR1	YPSLTQVAKLTGHSYRV.YLALHSPDQEAIVTGAGDETLRFWNVFS-KARS-QKENKSVLNLNFANIR	478
MmCDH1	YPSLTQVAKLTGHSYRV.YLALHSPDQEAIVTGAGDETLRFWNVFS-KTRS-TKESVSVLNLNFTRIR	493
HsCDH1	YPSLTQVAKLTGHSYRV.YLALHSPDQEAIVTGAGDETLRFWNVFS-KTRS-TKESVSVLNLNFTRIR	493

## Supplementary Figure S1 Alignment of TAD1 and its homologues.

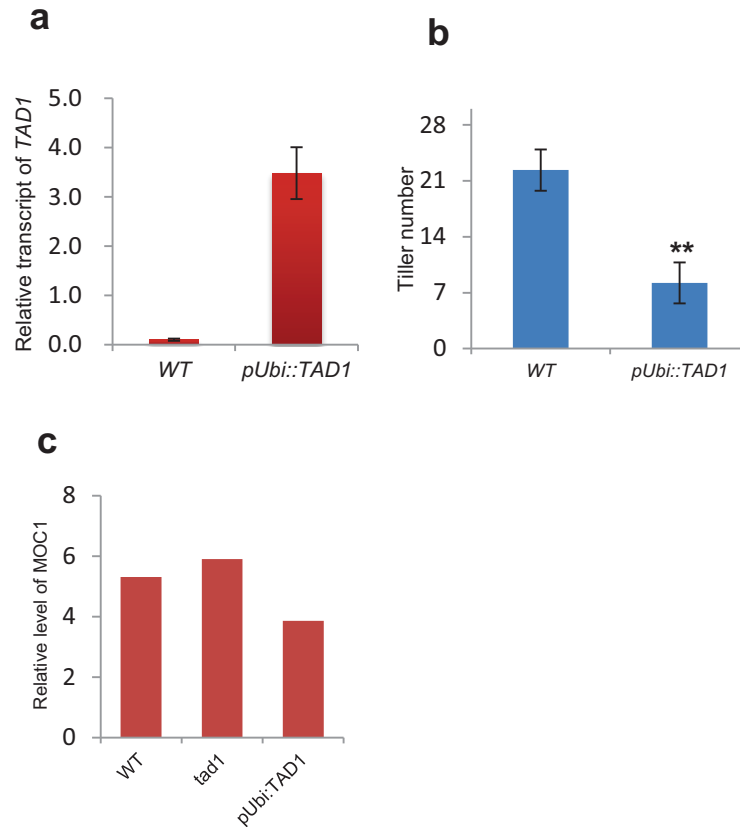
TAD1 and its homologous proteins contain different functional domains or motifs, including C-box (blue tangle), CSM (green tangle), WD repeats (red underlined), RVL (purple tangle), and IR (bright blue tangle). The red triangle indicates the mutation site in *tad1*. Accession numbers: TAD1, ABF93719; 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* (*gTAD1*). (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**

<b>Accession number</b>	<b>Annotation</b>
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**

<b>Construct</b>	<b>Primer name</b>	<b>Sequence (5'-3')</b>
<i>gTAD1</i>	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- <i>in situ</i>	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**

<b>Primer name</b>	<b>Sequence (5'-3')</b>
QTAD1-F	GCAGTCGTGACAAGAGCATCCT
QTAD1-R	AGCCACAGACCTCCGATTTATG
QActin-F	CTTCATAGGAATGGAAGCTGCGGGTA
QActin-R	CGACCACCTTGATCTTCATGCTGCTA