Supplementary Information

Rice APC/C^{TE} controls tillering through mediating the degradation of MONOCULM 1

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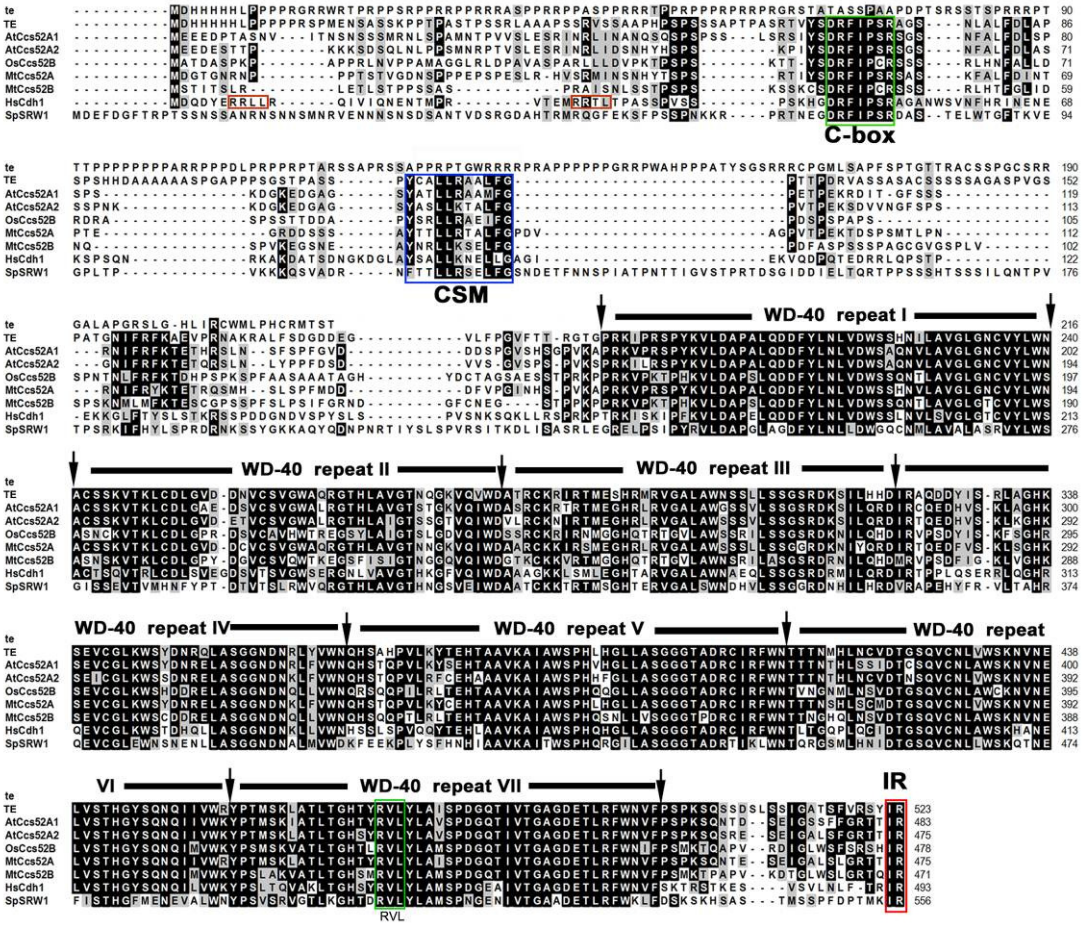
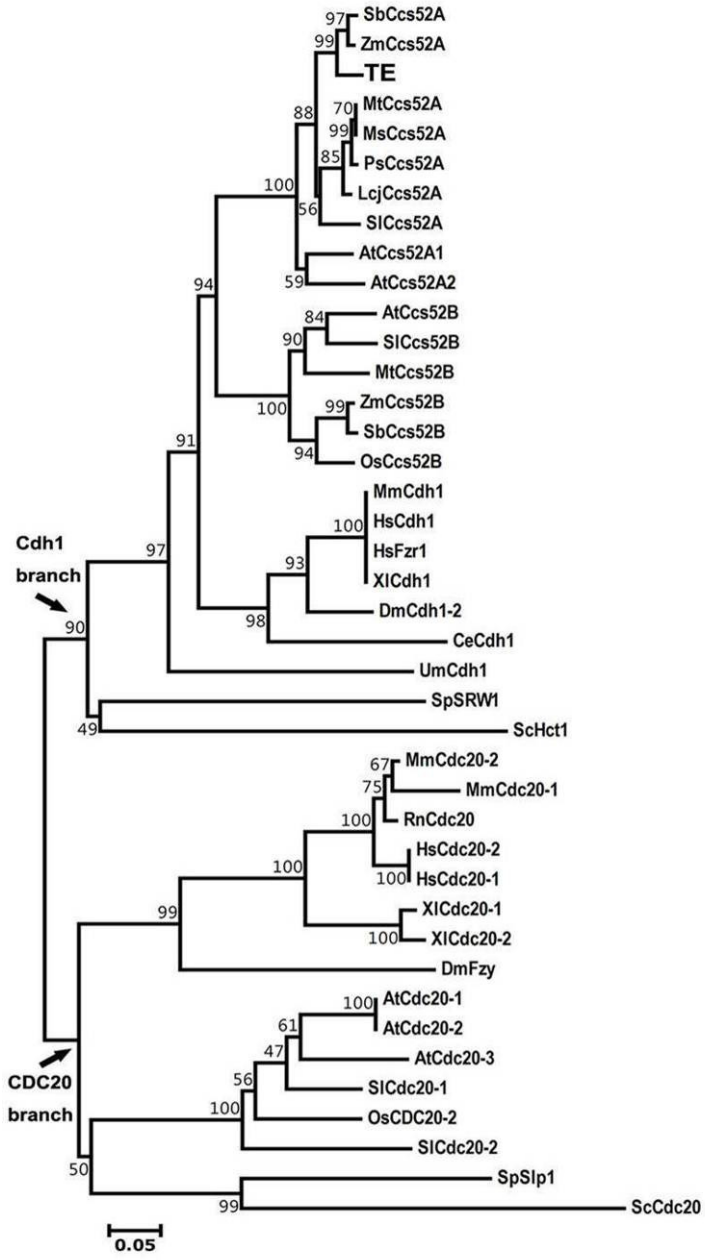
Supplementary Figures

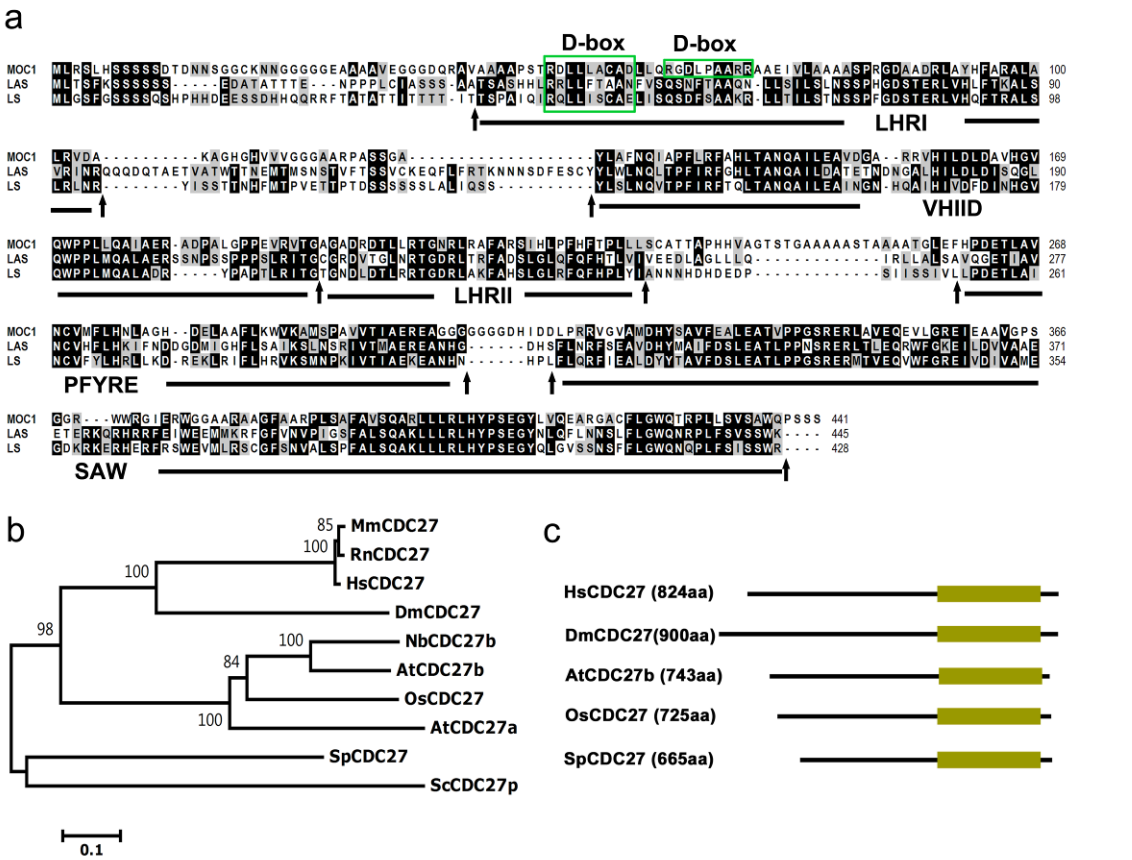


Supplementary Figure S1 | Protein sequence alignment of Cdh1-like proteins of *S. pombe* (SpSRW1), *H. sapiens* (HsCdh1), *A. thaliana* (AtCcs52A1, AtCcs52A2), *M. truncatula* (MtCcs52A, MtCcs52B), *O. sativa* (TE, OsCcs52B) and the truncated te protein. The conserved domains (seven WD-40 repeats) and motifs (C-box, CSM, IR, and RVL) are marked. In addition, the two degradation signals are also marked by two red boxes in the N-terminal region of HsCdh1.

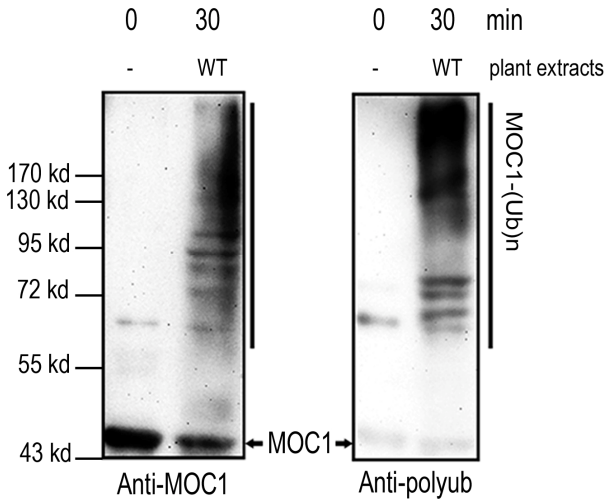


Supplementary Figure S2 | Phylogenetic analysis of TE protein. Protein sequences were aligned with CLUSTAL W in MEGA4.0[49] and the phylogenetic tree was analyzed by MEGA4.0[49]. Accession numbers presented here are the following: SpSlp1, P78972; ScCdc20, P26309; SlCdc20-1, CBH19893; OsCDC20-2, BAF15668.1; SlCdc20-2, CBH19894; MmCdc20-1, XP 139652; HsCdc20-1, NP 001246; HsCdc20-2, A56021; MmCdc20-2, NP 075712; RnCdc20, NP 741990; XlCdc20-1, AAH42288; XlCdc20-2, AAC41376; DmFzy, NP 477501; AtCdc20-1, At4g33260; AtCdc20-2, At4g33270; AtCdc20-3, At5g27570; ScHct1, P53197; UmCdh1, AY118173; SpSRW1, O13286.1;

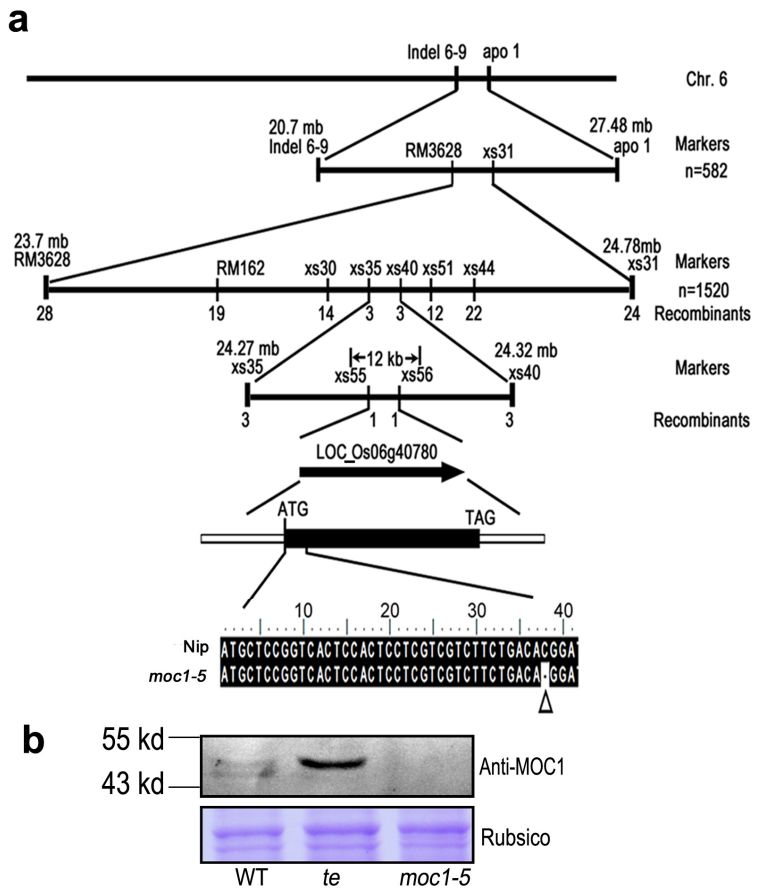
CeCdh1, NP 496075; XlCdh1, CAA74576; HsCdh1, NP 057347; HsFzr1, Q9UM11.2; MmCdh1, NP 062731; DmCdh1-2, NP 726941; OsCcs52B, LOC_Os01g74146; AtCcs52A2, At4g11920; AtCcs52A1, At4g22910; SlCcs52A, CBH19891; MtCcs52A, AF134835; TE, LOC_Os03g03150; ZmCcs52A, ACN36196; ZmCcs52B, ACG33710; AtCcs52B, At5g13840; MtCcs52B, AY357299; SpSrw1, O13286; SlCcs52B, CBH19892; LcjCcs52A, DQ059035.1; PsCcs52A, DQ059036; MsCcs52A, AF079404; SbCcs52A, XP_002468612.1; and SbCcs52B, XP_002457025.1. *Sp, S. pombe*; *Sc, S. cerevisiae*; *Sl, Solanum lycopersicum*; *Mm, Mus musculus*; *Hs, Homo sapiens*; *Rn, Rattus norvegicus*; *Xl, Xenopus laevis*; *Dm, D. melanogaster*; *At, A. thaliana*; *Um, Ustilago maydis*; *Ce, Caenorhabditis elegans*; *Os, Oryza sativa*; *Mt, M. truncatula*; *Zm, Zea mays*; *Lcj*, *Lotus corniculatus var. Japonicus*; *Ps, Pisum sativum*; *Ms, Medicago sativa*; *Sb, Sorghum bicolor*.



Supplementary Figure S3 | Phylogenetic and protein sequence analysis of MOC1 and OsCDC27. (**a**) Sequence alignment of MOC1, LAS and LS proteins. The conserved domains (LHRI, VHIID, LHRII, PFYRE and SAW) were marked. The typical degradation box (D-box) is marked by a green box in the N-terminal region of MOC1, LAS and LS. (**b**) Phylogenetic analysis showing that OsCDC27 is the rice homolog of HsCDC27, DmCDC27, AtCDC27a, AtCDC27b, and SpCDC27. Protein sequences were aligned with CLUSTAL W in MEGA4.0[49] and the phylogenetic tree was constructed by MEGA4.0[49]. Accession numbers presented here are the following: HsCDC27, NP_001247.3; MmCDC27, NP_663411.2; RnCDC27, NP_001019964.1; DmCDC27, NP_648093.2; SpCDC27, NP_594604.2; ScCDC27p, NP_009469.1; AtCDC27b, NP_849994.1; AtCDC27a, NP_188253.3; OsCDC27, NP_001058099.1; NbCDC27b, BAF64845.1. (**c**) OsCDC27 has the same conserved TPR domain (indicated as green boxes) as HsCDC27, DmCDC27, AtCDC27b, and SpCDC27 in their C-terminal region.



Supplementary Figure S4 | Ubiquitination analysis of MOC1. *In vitro* ubiquitination assay showing that MOC1 is poly-ubiquitinated (represented by multiple up-shifted bands) by WT plant extracts and can be detected by antibodies against MOC1 or polyub antibodies on Western blots.



Supplementary Figure S5 | Mapping of the *moc1-5* allele. (**a**) Mapping of *moc1-5*. (**b**) Western blot analysis showing the absence of MOC1 proteins in *moc1-5* plants (top). Rubisco staining showing a roughly equal loading of proteins (bottom).

Supplementary Tables

Supplementary Table S1 | Molecular markers used for mapping of the *TE* gene

Marker	Type	Primer sequences (5' → 3')	
		Forward primer	Reverse primer
g41	SSR	CGCTCTGAAATCCGATATTTGC	GGCTCTCTCCTCCTCGTTGC
RM22	SSR	GGTTTGGGAGCCCATAATCT	CTGGGCTTCTTTCACTCGTC
RM523	SSR	AAGGCATTGCAGCTAGAAGC	AAGGCATTGCAGCTAGAAGC
g62	InDel	GCATAACATCAAAGCCATGCTA	GCTCCAATTCGATCTTCGTC
g105	InDel	GCCCTTCTCATTGCCTCG	CTCTTCTCGCTTCTTCTTTTCG
g118	InDel	ATGTACAATAGTATTCCCACGTC	AAAACAAGGTTTAATGGTAGTG

Supplementary Table S2 | Molecular markers developed in this study for mapping of the *moc1-5* allele

Marker	Type	Primer sequences (5' → 3')	
		Forward primer	Reverse primer
Indel 6-9	InDel	GTGCGAATTCCTCCACCTC	CGACATGGCTGGTCTCTCTC
xs31	InDel	TGCCAATTAGCTCGATTCTG	TGGTCAAAATTTGTTCAAACTCA
apo1	InDel	CCGGTTTTGGTTTGTCTCAG	ATTCCTTTGTGGGCTCCTTT
RM3628	SSR	GCCCTAGACACACCCGTACC	TGCCAGATCAGAAATCATGC
RM162	SSR	GTGGTAGGGCGAAATGATCTGC	ATCACGCGCTCCTACCTCACC
xs30	InDel	CAGCCGATTGGACTCGAT	AACACCTTGCCGAACACC
xs35	InDel	TAAAAGAAAGGTTACTCATGGATTTTT	TAATGCCTGCTGCATCTTAGG
xs40	InDel	TCCTCACACACAAGCACACA	TCAAATTGGCATGCATTGAT
xs51	InDel	AAGTTCGCCGGAGAGAGAAG	CAGCGTCATGGTTTCTGAAAGCCA
xs44	InDel	TTAATTAATCACCAATGCAATCTATGA	CCAGCAACTTTTGCTTTGTG
xs55	InDel	CTTAGATTTGACACAACCTGCAC	ATTCTGCAGTGCACGAGCTA
xs56	InDel	AACTATAGATCGGGATCGCTCA	TTCAAAGAAACGAAAATCAACG

Supplementary Table S3 Primers used for construction of protein expression plasmids

Fragment or plasmid	Forward primer (5' → 3')	Reverse primer(5' → 3')
TE	CTAGGAAGATCTATGGATCACCACCACCACCAC	CTAGATCTCGAGTCACCGGATGTAGCTCCTAACAAATG
MOC1	CGCGGATCCATGCTCCGGTCACTCCACTCC	CGCAAGCTTCTACGACGACGACGGCTGCCA
pMAL-c2x::MBP-MOC1-m	GCGGACTTGGCGCTGGCGTGCGCGGACCTG	CGTCGACGGCGCCGCCGCCGCAACGGCAC

Supplementary Table S4 Primers used for construction of yeast two-hybrid assay plasmids

Fragment	Forward primer (5'→3')	Reverse primer (5'→3')
OsCDC27	AGTGAATTCATGGAAACCCTAATGGTGGAC	ATAGGATCCTTAAATCTCATCATCATCATCATCATCATCC
MOC1	AGTGAATTCATGCTCCGGTCACTCCACTCCTC	AATGGATCCCTACGACGACGACGGCTGC
MOC1-m	AGTGAATTCATGCTCCGGTCACTCCACTCCTC	AATGGATCCCTACGACGACGACGGCTGC
MOC1d	AGTGAATTCGGCCATGGCCACGTCGTC	AATGGATCCCTACGACGACGACGGCTGC
TE	GGAATTCCATATGATGGATCACCACCACCACCACCTG	CTAGGAAGATCTTCACCGGATGTAGCTCCTAACAAATG

Supplementary Table S5 Primers used in Real time Quantitative RT-PCR

Gene Name	Type	Primer sequences (5' → 3')	
		Forward primer	Reverse primer
Actin	qRT-PCR	TCGTCTGCGATAATGGAACTG	CCGACAATGCTGGGGAAG
TE	qRT-PCR	TGGTCTTCGCATAATATCCTTG	TGTCCCTACAGCAAGGTGAGT
OsTB1	qRT-PCR	CCTACCATGAGAGAAGAGACCA	GTAGTGGGCTATGATCAGATGTG
OSH1	qRT-PCR	CTCAACACGCTCTCCATCTC	GCTTGAGCTCCTGATCCAC

Supplementary Reference:

49. Tamura, K., Dudley, J., Nei, M. & Kumar, S. MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. *Mol. Biol. Evol.* **24**, 1596-1599 (2007).