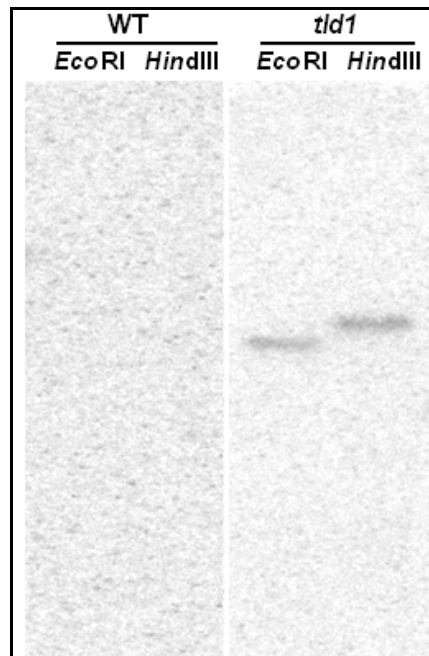
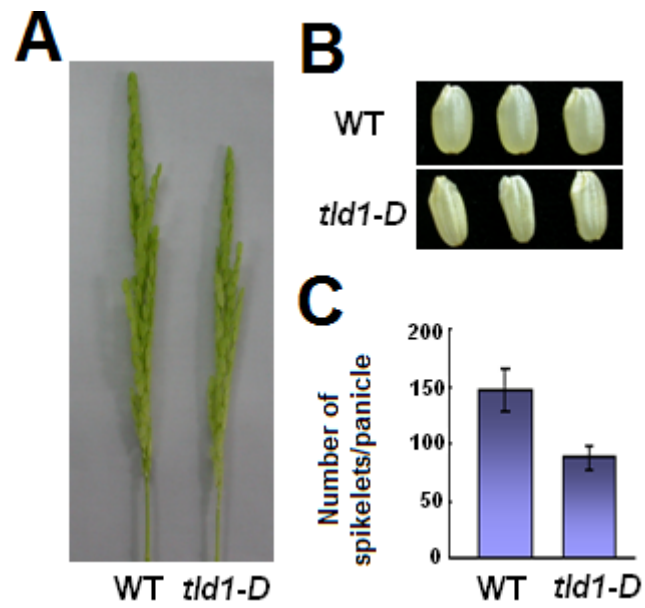


Supplemental data

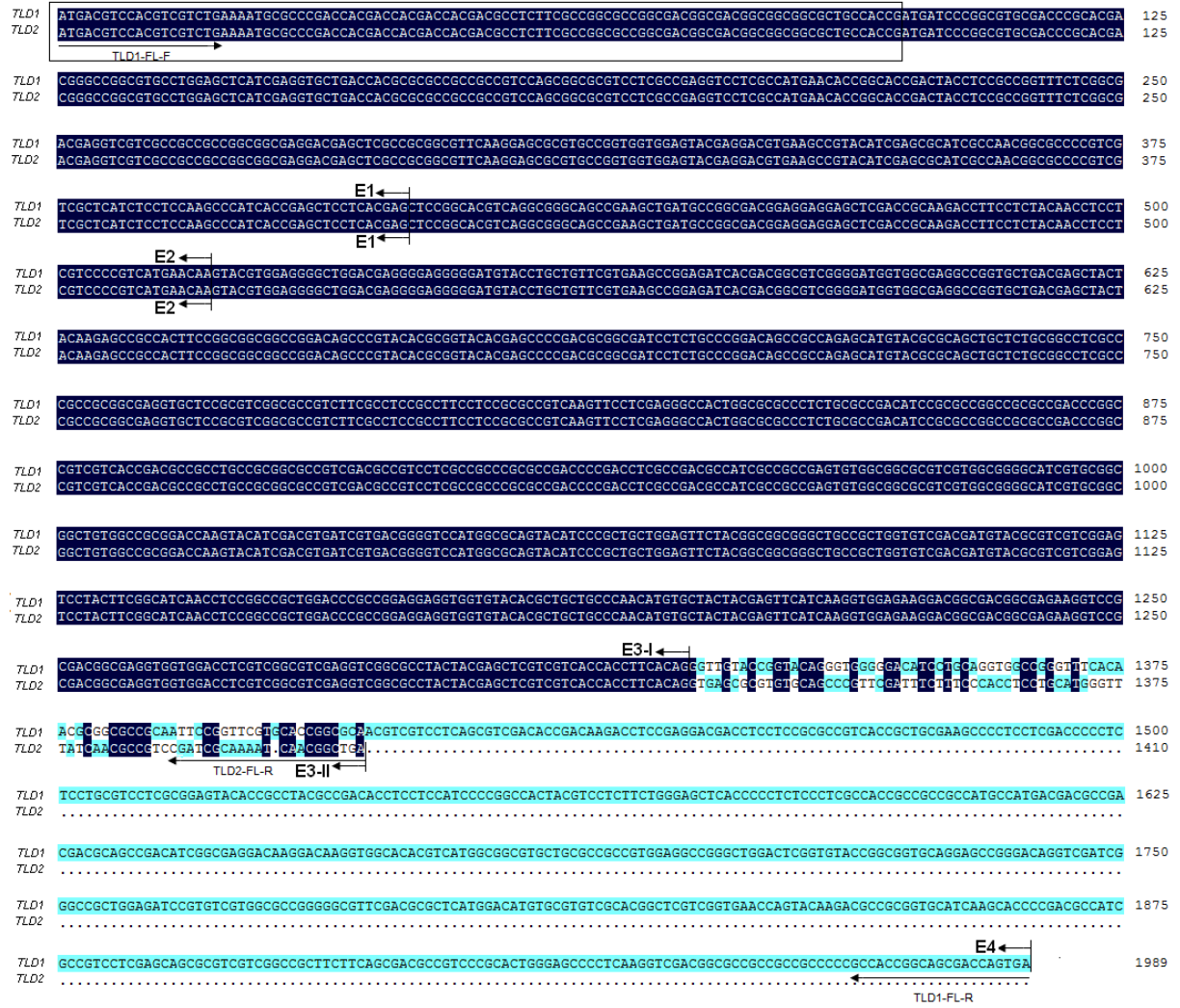
1. Supplemental Figures



Supplemental Figure S1 Determination of the number of T-DNA insertions in *tld1-D* by Southern blotting. Genomic DNA isolated from wild-type (WT) or homozygous *tld1* plants was digested with *EcoRI* or *HindIII*. The blot was probed with α -³²P-dCTP-hygromycin coding sequence. A single band was detected in the *tld1* mutant, while no band was detected in WT.



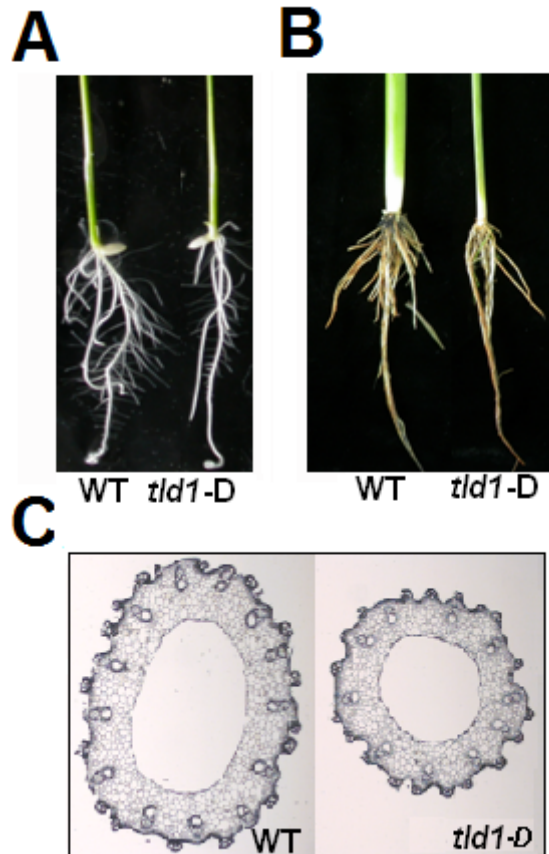
Supplemental Figure S2 Productivity of WT vs. *tld1-D*. (A) Representative panicles from WT and *tld1-D* plants. (B) Mature seeds from WT and *tld1-D* plants. (C) The number of spikelets per panicle (n=10).



Supplemental Figure S3 The coding sequences of the *TLD1* and *TLD2* splice variants. The four exons in *TLD1* are indicated by arrows along the upper edge, while the three exons in *TLD2* are indicated by arrows along the lower edge. The primers used to clone the open reading frames of *TLD1* and *TLD2* are underlined. Similarities are shown in black. The 99 extra base pairs described in the text are boxed.

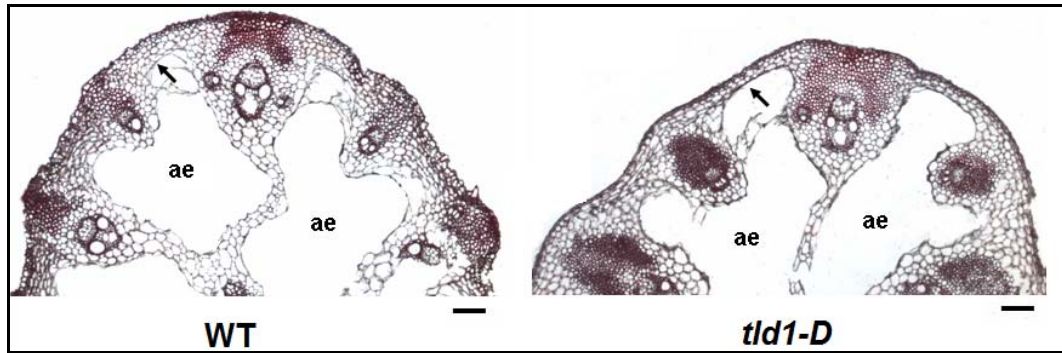
AtGH3.3HTVDSLRSPMMHSPST.KDVKARFIEEIRNVDFVOKKVIRESLHNSDTEYLKRFK.....LNGRTDR..KTRFRTMVFVLDLDRPEHCRILANGDRS	93
AtGH3.6MPEAPKIAALEVSDSESLAEKKNKQIFEDVITINADVQRVVLEELHLSRNADVVEYLKRHG.....LEGRTDR..ETFKRMVQVITHEIDIGPHNRIANGDRS	95
AtGH3.5MPEAPKKESEVFDLTDQKNKQKQLEELHLSRNADVQRVVLEELHLSRNADVVEYLKRHD.....LNGRTDR..ETFKRMVQVITHEIDIGPHNRIANGDRS	95
AtGH3.2MAVDSPLQSRMVSATTSEKDVAKKPFIEEIRNRPDPSVCEKVLGEHLTNSNTTEYLKRFD.....LDGVDDR..KTRFRTMVFVLDLDRPEHCRILANGDRS	94
AtGH3.17MIPSYDPMNDTEAGKLEEDLITINAEALCQQVLLHOLISQNSGTCLYLRAPL.....DGEADKVKQSFNKKVQVNVNDVVRPFIQRIADGESS	85
OsGH3.1MPEAPTAKTAPAYGYAPG.AHAEAELFIEHVITANAGVQRVVLEELHLSRNADVVEYLKRHYG.....IPGSPDVV.DAFRRLVQVITHEIDIGPHNRIANGDRS	95
OsGH3.8MAVMTDVSTTGTALRTPAAGAVKE.GDVEKRFIEEIRNVDFVOKKVIRESLHNSDTEYLKRFK.....LDGATDR..AAFRKRVVQVITHEIDIGPHNRIANGDRS	100
TLD1	MTSSTSENAPDHDHDDASSPAPATATAAALPPMIPACDPHDGPAC <u>ELIEVLITR</u> AAAVQRRVLAELVLANMTGTDLRRFLGDEVVAAAGCEDELAAAFKERVVVEEIVDVRPHERIANGAPS	125
TLD2	MTSSTSENAPDHDHDDASSPAPATATAAALPPMIPACDPHDGPAC <u>ELIEVLITR</u> AAAVQRRVLAELVLANMTGTDLRRFLGDEVVAAAGCEDELAAAFKERVVVEEIVDVRPHERIANGAPS	125
AtGH3.3	MILSSYITIDELTSSGTSAGEKRLMFTIEEELDRSLLSLLMFMMDQVWGLDCKGMLFLFKSESKTPGGLPARPVLTSYYSSEDFKRMFPDPVWVYTSNEALLGPDSSQSHYICMLCGLL	218
AtGH3.6	QVLCMNIISDELSSGTSAGEKRLMFTIEEELDRSLLSLLMFMMDQVWGLDCKGMLFLFKSESKTPGGLPARPVLTSYYSSEDFKRMFPDPVWVYTSNEALLGPDSSQSHYICMLCGLL	220
AtGH3.5	PILSSKIDDELSSGTSAGEKRLMFTIEEELDRSLLSLLMFMMDQVWGLDCKGMLFLFKSESKTPGGLPARPVLTSYYSSEDFKRMFPDPVWVYTSNEALLGPDSSQSHYICMLCGLL	220
AtGH3.2	PILSSSHITDELSSGTSAGEKRLMFTIEEELDRSLLSLLMFMMDQVWGLDCKGMLFLFKSESKTPGGLPARPVLTSYYSSEDFKRMFPDPVWVYTSNEALLGPDSSQSHYICMLCGLL	219
AtGH3.17	DIVSAQITIDELTSSGTSAGEKRLMFTIEEELDRSLLSLLMFMMDQVWGLDCKGMLFLFKSESKTPGGLPARPVLTSYYSSEDFKRMFPDPVWVYTSNEALLGPDSSQSHYICMLCGLL	210
OsGH3.1	PIFSGKIDDELSSGTSAGEKRLMFTIEEELDRSLLSLLMFMMDQVWGLDCKGMLFLFKSESKTPGGLPARPVLTSYYSSEDFKRMFPDPVWVYTSNEALLGPDSSQSHYICMLCGLL	220
OsGH3.8	PILSITHTVDELSSGTSAGEKRLMFTIEEELDRSLLSLLMFMMDQVWGLDCKGMLFLFKSESKTPGGLPARPVLTSYYSSEDFKRMFPDPVWVYTSNEALLGPDSSQSHYICMLCGLL	225
TLD1	SLISSKIDDELSSGTSAGEKRLMFTIEEELDRSLLSLLMFMMDQVWGLDCKGMLFLFKSESKTPGGLPARPVLTSYYSSEDFKRMFPDPVWVYTSNEALLGPDSSQSHYICMLCGLL	250
TLD2	SLISSKIDDELSSGTSAGEKRLMFTIEEELDRSLLSLLMFMMDQVWGLDCKGMLFLFKSESKTPGGLPARPVLTSYYSSEDFKRMFPDPVWVYTSNEALLGPDSSQSHYICMLCGLL	250
	Motif I	
AtGH3.3	MRHFVLRGAVFASGLRAIRGLQTNKKEADDISTG.TLSSRIIDPAIKESMSKILTK.PDOPADPITSVGQDNSEEGHILTRINENKLVIVITGAMAOYIPPLEYVSGGLPMAGTHYASS	341
AtGH3.6	QHKVLRGAVFASGFRARIRGLEKHWELARIDRTG.TLSSRIIDPSVREAVGETUK..PDPADPITSVGQDNSEEGHILTRINENKLVIVITGAMAOYIPPLEYVSGGLPMAGTHYASS	341
AtGH3.5	QKQVLRGAVFASGFRARIRGLEKHWELARIDRTG.TLSSRIIDPSVREAVAKTK..PDPADPITSVGQDNSEEGHILTRINENKLVIVITGAMAOYIPPLEYVSGGLPMAGTHYASS	341
AtGH3.2	MRHFVLRGAVFASGLRAIRGLQTNKKEADDISTG.TLSSRIIDPAIKESMSKILTK.PDOPADPITSVGQDNSEEGHILTRINENKLVIVITGAMAOYIPPLEYVSGGLPMAGTHYASS	341
AtGH3.17	QRSHVLRGAVFASGLRAIRGLEKHWELARIDRTG.TVTSWITDSSCRDVLSTLNG.PQGEADEIEESEAKRS.EGQILRRIRURKRTIDVIVITGAMAOYIPPLEYVSGGLPMAGTHYASS	332
OsGH3.1	HRADVLRGAVFASGLRAIRGLEKHWELARIDRTG.ELDPEIDRVVRDAGRVLR..ADPALADEIEESEAKRS.EGQILRRIRURKRTIDVIVITGAMAOYIPPLEYVSGGLPMAGTHYASS	341
OsGH3.8	QRNVLRGAVFASGLRAIRGLQTNKKEADDISTG.ELTPRVTDPSVREAVAAIIL..PDPADPITSVGQDNSEEGHILTRINENKLVIVITGAMAOYIPPLEYVSGGLPMAGTHYASS	346
TLD1	RRGVLRGAVFASGFRARIRGLEKHWELARIDRTG.DAACRGAVDAVLAARADPDLADATAAEGGAS.MRGIVRRLURRRTIDVIVITGAMAOYIPPLEYVSGGLPMAGTHYASS	374
TLD2	RRGVLRGAVFASGFRARIRGLEKHWELARIDRTG.DAACRGAVDAVLAARADPDLADATAAEGGAS.MRGIVRRLURRRTIDVIVITGAMAOYIPPLEYVSGGLPMAGTHYASS	374
	Motif II	
AtGH3.3	ESYFGNLRPLDPCPSESVYTLIPMAYEELPHE.....HEVPTKSELVLLADVEVKELELVITTYAGLNRYRVGILQVTFGYNAPQFVKFRRKRVLLSIESDKTDEAE	448
AtGH3.6	EQYFGNLRPLDPCPSESVYTLIPMAYEELPHE.....SLPKALTEKEQQLDDVDVVKLQEVLDVVITTYAGLYRYRVGVVLSVAGFRMNAPOFSFCRKNVLLSIDSDKTDEVE	462
AtGH3.5	EQYFGNLRPLDPCPSESVYTLIPMAYEELPHE.....NLPKALTEKEQQLDDVDVVKLQEVLDVVITTYAGLYRYRVGVVLSVAGFRMNAPOFSFCRKNVLLSIDSDKTDEVE	462
AtGH3.2	ESYFGNLRPLDPCPSESVYTLIPMAYEELPHE.....AEASLDESLVLLADVEVKELELVITTYAGLYRYRVGILQVTFGYNAPQFVKFRRKRVLLSIESDKTDEAE	455
AtGH3.17	EQYFGNLRPLDPCPSESVYTLIPMAYEELPHE.....ATAEASHRDLDVVDVVKLQEVLDVVITTYAGLYRYRVGVVLSVAGFRMNAPOFSFCRKNVLLSIDSDKTDEVE	457
OsGH3.1	EQYFGNLRPLDPCPSESVYTLIPMAYEELPHE.....AASGDATOLDDVLRVGEVRETELVITTYAGLNRYRVGVVLSVAGFRMNAPOFSFCRKNVLLSIDSDKTDEAE	456
OsGH3.8	ESYFGNLRPLDPCPSESVYTLIPMAYEELPHE.....DGDGKVRDGEVDDVGEVEGAYTELVITTYAGLYRYRVGILQVTFGYNAPQFVKFRRKRVLLSIESDKTDEAE	485
TLD1	ESYFGNLRPLDPCPSESVYTLIPMAYEELPHE.....DGDGKVRDGEVDDVGEVEGAYTELVITTYAGLYRYRVGILQVTFGYNAPQFVKFRRKRVLLSIESDKTDEAE	485
TLD2	ESYFGNLRPLDPCPSESVYTLIPMAYEELPHE.....DGDGKVRDGEVDDVGEVEGAYTELVITTYAGLYRYRVGILQVTFGYNAPQFVKFRRKRVLLSIESDKTDEAE	469
	Motif III	
AtGH3.3	LQSAVENASL..LLGEGQTRVIEYTSYAEKTIIPGHYVLYWELLVKDQTNPPN.DEVMA.....RCCLMEESLNSVYRQSVADKSIGPLEIRVVNKGTFEELMDYAIRGSA	553
AtGH3.6	LQNAVKNVAT..HLVFPDASLSEYTSYADTSSIPGHYVLYWELCLNG..NTPIPPSVFE.....DCLTIEESLNSVYRQSVADKSIGPLEIRVVNKGTFEELMDYAIRGSA	566
AtGH3.5	LQNAVKNVAT..HLVFPDASLSEYTSYADTSSIPGHYVLYWELCLDG..NTPIPPSVFE.....DCLAVEESLNSVYRQSVADKSIGPLEIRVVNKGTFEELMDYAIRGSA	566
AtGH3.2	LQSAVENASR..HLFAEQGTRVIEYTSYAEKTIIPGHYVLYWELLGQNSALMSEVEMA.....RCCLMEESLNSVYRQSVADKSIGPLEIRVVNKGTFEELMDYAIRGSA	561
AtGH3.17	LLNAVTOAKMLHMQHPSLLLTYEYTSYADTSSIPGHYVLYWELPKRHSNDPKLDDKT.....MEDCCSEVEDCLDLYVVRCKRNRDKSIGPLEIRVVNKGTFEELMDYAIRGSA	566
OsGH3.1	LHAVSGAVQ..HLAPFGASLVEYTSYADAATIPGHYVLYWELIRAGS...TVAPSAVFE.....ECCLSVREALNSVYRQSVADKSIGPLEIRVVNKGTFEELMDYAIRGSA	555
OsGH3.8	LQRAVERASA..LLRPHGASVVEYTSYAEKTIIPGHYVLYWELTKGAGATVVDADTLG.....RCCLMEESLNSVYRQSVADKSIGPLEIRVVNKGTFEELMDYAIRGSA	562
TLD1	LLRAVTAARP..LLDPLSCVLAETAYADTSSIPGHYVLYWELTPSPSPPPPCHDDADDAADGEGDKKHVHVMAACAAVEAGLDSVTRCRSRDRSIGPLEIRVVNKGTFEELMDYAIRGSA	608
TLD2	LLRAVTAARP..LLDPLSCVLAETAYADTSSIPGHYVLYWELTPSPSPPPPCHDDADDAADGEGDKKHVHVMAACAAVEAGLDSVTRCRSRDRSIGPLEIRVVNKGTFEELMDYAIRGSA	469
AtGH3.3	SINQYKTPRCVVSFTPEMELLSRVVSTHFSPALPHVSPERRR.....	595
AtGH3.6	SINQYKTPRCVVFAPITIELLSRVVDSYFSPKCPKVSFGHKQWGSN.....	612
AtGH3.5	SINQYKTPRCVVFAPITIELLSRVVDSYFSPKCPKVSFGHKQWGSN.....	612
AtGH3.2	SINQYKTPRCVVSFTPEMELLSRVVSAHFSPALPHVSPERRR.....	603
AtGH3.17	SINQYKTPRCVKSQGALEILDSRVVIGRFSSKRVPOWEPLGLDLS.....	609
OsGH3.1	SINQYKAPRCVVRPQVVELLDARVQVQKYSFKPCPKVSPGNQKNKSRLVGGKD.....	609
OsGH3.8	SINQYKTPRCVFTPRIVELLSRVVSSHFSPALPHVTPARRSE.....	605
TLD1	SVNQYKTPRCIKHPDAIVLEQRVVGRFSDAVPHHEPLKVDGAAAPATGSDC.....	662
TLD2	SVNQYKTPRCIKHPDAIVLEQRVVGRFSDAVPHHEPLKVDGAAAPATGSDC.....	469

Supplemental Figure S4 Alignment of the deduced primary sequences of TLD1 and TLD2, together with members of the GH3 families in rice (*Oryza sativa*) and *Arabidopsis*. The gene accession numbers for each homolog are as follows: AtGH3.3 (At2g23170), AtGH3.6 (At5g54510), AtGH3.5 (At4g27260), AtGH3.2 (At4g37390), AtGH3.17 (At1g28130), OsGH3.1 (Os01g57610), and OsGH3.8 (Os07g40290). Three conserved motifs are underlined.

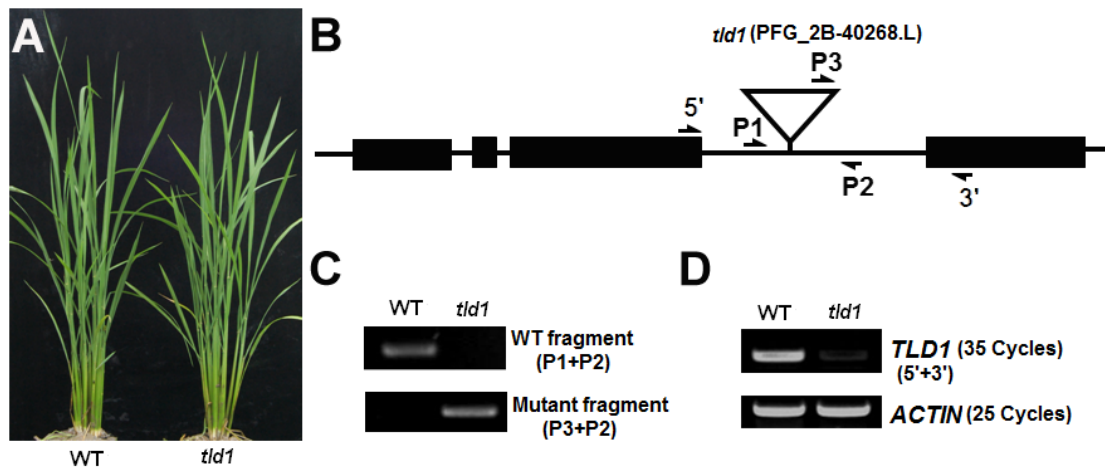


Supplemental Figure S5 Comparison of culm and root from WT and *tld1-D* plants.

One-week-old *tld1-D* seedlings grown on 0.5X MS agar medium (A) and soil-grown *tld1-D* plants at the tillering stage (B) display fewer lateral roots and adventitious roots compared to WT seedlings. (C) Comparison of culm cross-sections prepared in (B).

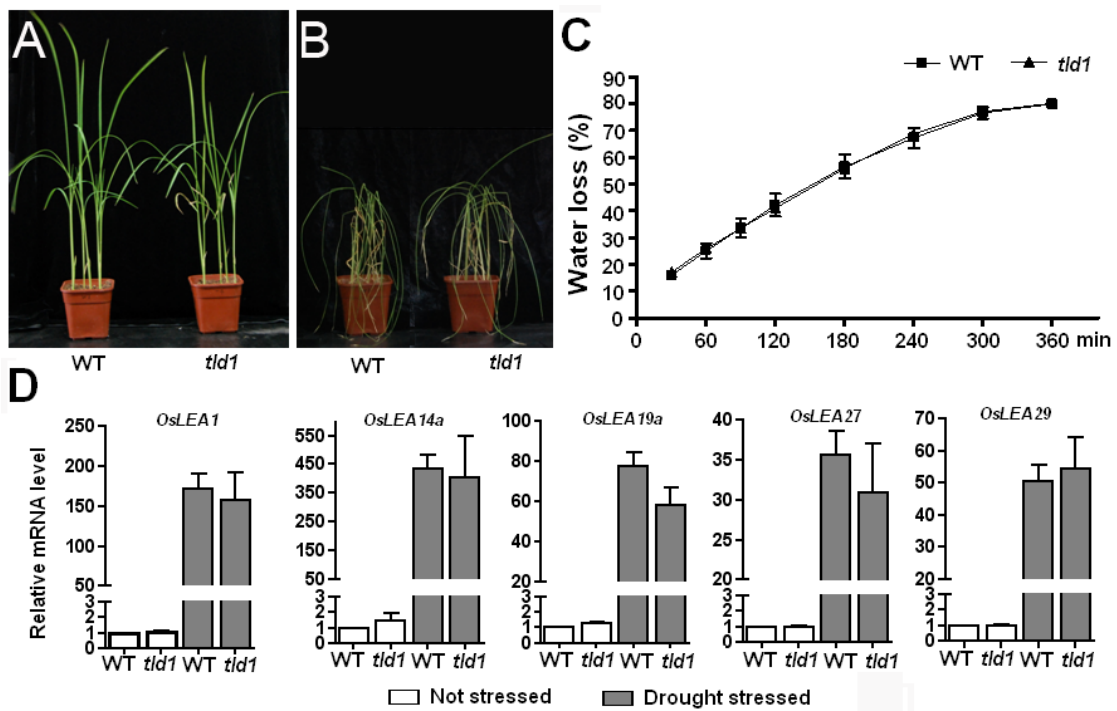


Supplemental Figure S6 Comparison of the lamina joint in cross-section between WT and *tld1-D*. The reduced sclerenchymatous cell layers in *tld1-D* (arrow) are shown. ae: lysigenous aerenchyma. Bar, 10 μ m.

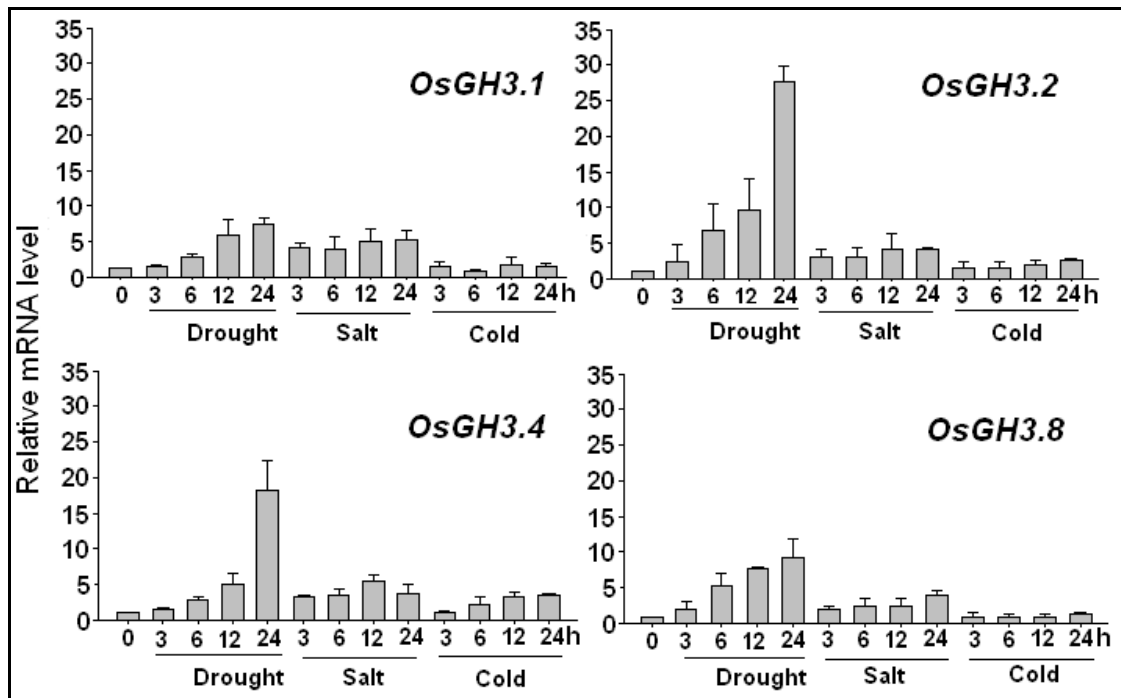


Supplemental Figure S 7 Characterization of *TLD1* loss-of-function mutant.

(A) No obvious difference between the wild-type (*Hwayoung*, left) *tld1* mutant (right) at tillering stage. *tld1* (PFG_2B-40268.L) is in *Hwayoung* background. (B) Schematic representation of the T-DNA insertion site of *tld1*. P1, P2, and P3 are primers used for DNA identification, 5' and 3' are primers used for RNA identification (for primer sequence see Supplemental Table S5). (C) Genotyping of *tld1* homozygous. (D) Identification of *TLD1* transcripts in *tld1* mutant by RT-PCR, RNA was isolated from roots of WT and *tld1* homozygous. *OsACTIN* was used as an internal control.



Supplemental Figure S 8 No difference between WT and *tld1* under drought stress. Three-week-old WT and *tld1* seedlings were grown in soil before (A) and after (B) drought stress for 7 days. (C) Water loss from three-week-old *tld1* and WT seedlings. (D) *LEA* expression in WT and *tld1* mutant before and after 6 hours drought stress by qRT-PCR.



Supplemental Figure S9 Differential expression of several *OsGH3* members under salt, cold, and drought stress. Total RNA was extracted from 14-day-old WT rice seedlings; the fold-changes in mRNA expression were determined by qRT-PCR.

2. Supplemental Tables

Supplemental Table S1 Optimal parameters for the MRM detection of plant hormones by LC-MS/MS.

Compound	Transition (<i>m/z</i>)	Retention time (min)	Collision energy (eV)
IAA	176.00/130.47	6.15	13
D₂-IAA	182.05/135.92	6.15	18
IAA-Ala	247.09/130.17	5.70	29
IAA-Asp	291.10/130.10	4.99	30
IAA-Leu	289.10/130.10	7.53	30
IAA-Phe	323.14/130.86	7.60	33
IAA-Glu	305.10/130.10	4.96	32
ABA	263.08/153.06	6.81	14

Supplemental Table S2 Primers used for gene cloning.

Primer name	5'→3'
TLD1 promoter-F	gtcgacGAAGCTAGTAGAGAAATGCTAG
TLD1 promoter-R	gaattcGTTAGATGATCCATGCATGCATG
Used to clone the <i>TLD1</i> promoter	
TLD1-FL-F/P1f	tctagaAATGACGTCCACGTCGTCTG
TLD1-FL-R/P1r	ggatccCTGGTCGCTGCCGGTGCC
TLD2-FL-R/P2r	ggatccGCCGTTGATTTTGCGATCGG
TLD1-FL-F/P1f and TLD1-FL-R/P1r were used to clone <i>TLD1</i> . TLD1-FL-F/P1f and TLD2-FL-R/P2r were used to clone <i>TLD2</i> .	
GST-TLD1,2-F	cgggatccATGACGTCCACGTCGTCTG
GST-TLD1-R	cggaattcCTGGTCGCTGCCGGTGCC
GST-TLD2-R	cggaattcGCCGTTGATTTTGCGATCG
Used for expression of TLD1 and TLD2	

Supplemental Table S3 Primers used for the RT-PCR.

Gene name	Primer name	5'→3'
Os11g32510	RT-Os11g32510-F	GGTTGTACCGGTACAGGGTG
	RT-Os11g32510-R	GTGTGCCACCTTGTCCTTGTC
Os11g32520	RT-Os11g32520-F	AATGACGTCCACGTCGTCTG
	RT-Os11g32520-R	GCCGTTGATTTTGCGATCGG
Os11g32530	RT-Os11g32530-F	ATGCCAACTCATCACCTTAC
	RT-Os11g32530-R	TTACGCATCGCGCTGACG
Os11g32540	RT-Os11g32540-F	TTCAGTGCAGCGCACGTGAT
	RT-Os11g32540-R	AGTAACATCGTCTCGATGGAG
ACTIN	RT-ACTIN-F	CCTCGTCTCGACCTTGCTGGG
	RT-ACTIN-R	GAGAACAAGCAGGAGGACGGC
18S	RT-18S-F	CCACAT CCA AGG AAG GCA GC
	RT-18S-R	CAC CAG ACT TGC CCT CCA ATG

Supplemental Table S4 Primers used for qRT-PCR.

Gene name (Accession No)	Primer name	5'→3'
TLD1/OsGH3.13	q TLD1-F	TGTGTAATGTCAAACGTTGCTCAT
	q TLD1-R	TGATTCATAAAGAACACTGCTCGTATT
OsGH3.1	q-GH3.1-F	CGGGAACAAGCAATGGAACA
	q-GH3.1-R	CAGATCATCACCCCTCTAGCTTCAA
OsGH3.2	q-GH3.2-F	TCATGCCCGTCATGAACTTG
	q-GH3.2-R	TCGTCTCCGACTTGATGAACAG
OsGH3.4	q-GH3.4-F	CGCCTCCTCCGAGTGCTA
	q-GH3.4-R	ACATTGTTGGGATGAGGGTGTAG
OsGH3.8	q-GH3.8-F	TTGGACCGTGTCCAAGAATCT
	q-GH3.8-R	TCTTGCCACTAACTGACAGAGTTGA
OsIAA1	q-IAA1-F	GCCGCTCAATGAGGCATT
	q-IAA1-R	GCTTCCACTTTCTTTCAATCCAA
OsIAA9	q-IAA9-F	AAGAAAATGGCCAATGATGATCA
	q-IAA9-R	CCCATCACCATCCTCGTAGGT
OsIAA20	q-IAA20-F	TTGTACGTGAACGGGATTATTTTG
	q-IAA20-R	CATGCTTATGAAATTGCTGAAACA
OsLEA14a	q-OsLEA14a-F	TCGGGATGTCAGGCGATAA
	q-OsLEA14a-R	GCTTGTAGGTGCTGGTGTCTT
OsLEA1	q-OsLEA1-F	GTCGCAAGTCGAAGCACAAA
	q-OsLEA1-R	TGCGTTGCGTATCAGTGTGA
OsLEA19a	q-OsLEA19a-F	TGTTTTTGTGTCTTTTTGAGTCTGT
	q-OsLEA19a-R	CCACACCCGTCAGAAATCCT
OsLEA8a	q-OsLEA8a-F	GCTTGATGGACAAGGCGAAA
	q-OsLEA8a-R	GGCTCATCCCCTTGAACGA
OsLEA18	q-OsLEA18-F	CGGTTTCAGTTCTTTTGGTTGAAT
	q-OsLEA18-R	AAGTTCCTTTCCATTACAGTTACAGTCTT
OsLEA27	q-OsLEA27-F	CCCGGCCAGCACTAAATAAG
	q-OsLEA27-R	AAACTGCACGTACATCACGACAT
OsLEA28	q-OsLEA28-F	GTGTATAGCGTCCTCGAAGAGAATAGT
	q-OsLEA28-R	CACAAGCTATAGGTACAACCCAACA
OsLEA29	q-OsLEA29-F	CGAGCGCAATAAAAGGAAAAA
	q-OsLEA29-R	AGACACGGTCCGTAAGGAGAA
OsLEA23	q-OsLEA23-F	ACAAGAGCAGCGCTTAATTGG
	q-OsLEA23-R	GCTGCAGTGCAGAAAAAGCA
OsLEA24	q-OsLEA24-F	ATGCAGTGATCTGTCTCATGCAT
	q-OsLEA24-R	GCACCGTGCAGCCATTATTA
OsACTIN 1	q-ACTIN-F	TGGCATCTCTCAGCACATTCC
	q-ACTIN-R	TGCACAATGGATGGGTCAGA

Supplemental Table S5 Primers used for *tld1* identification

Primer name	5'→3'
tld1-K.out-P1	AGCTAACTGCAAGTCGATTGG
tld1-K.out-P3	CTTCCTTCATTTTACAATGTAAG
tld1-K.out-P2	GTAGGGAATCCCAAGCTATAAC
DNA level identification	
TLD1-RNA-5'	TCGTCGTCACCACCTTCACAG
TLD1-RNA-3'	GTGTGCCACCTTGTCCTTGT
RNA level identification	

3. Supplemental Methods

Quantification of IAA, its conjugates, and ABA by LC-MS/MS

The mobile phase was composed of 0.1% acetic acid in deionized water as solvent A and methanol as solvent B. A linear gradient was run at 200 $\mu\text{L}/\text{min}$, consisting of 20% solvent B at the start ($t=0$ min), increased to 90% solvent B at $t=6$ min, and then held at 90% solvent B for 2 min until $t=8$ min. The gradient was then returned to 20% solvent B at $t=8.1$ min, and stabilized at 20% solvent B for 1.9 min until $t=10$ min before the next injection. The atmospheric pressure ionization (API) source was operated in positive ESI mode. The TSQ quantum mass spectrometer was calibrated with a solution of polytyrosine-1, 3, 6 according to the manufacturer's instructions. The ESI source parameters were optimized for IAA at an LC flow of 200 $\mu\text{L}/\text{min}$ based on preliminary results indicating that IAA was the analyte for which the method had the lowest sensitivity. The optimized source parameters were as follows: sheath gas pressure, 20 (arbitrary units); auxiliary gas flow, 30 (arbitrary units); spray voltage, 4,000 V; capillary temperature, 350 $^{\circ}\text{C}$; and skimmer offset, 10 V. For quantification, the mass spectrometer was set to the data acquisition mode of multiple-reaction monitoring (MRM); the specified acquisition parameters are shown in Supplemental Table 1. Detection of the compounds was performed in the MRM mode with a single time segment containing seven events. The acquisition parameters common to all analytes were: scan width (m/z), 0.10; scan time, 0.05 s; peak width (FWHM), 0.4 for Q1 and 0.7 for Q3; and collision gas pressure, 1.5 mTorr. Data acquisition and analysis were accomplished with Xcalibur software v.1.4 (Thermo, San Jose, CA, USA).