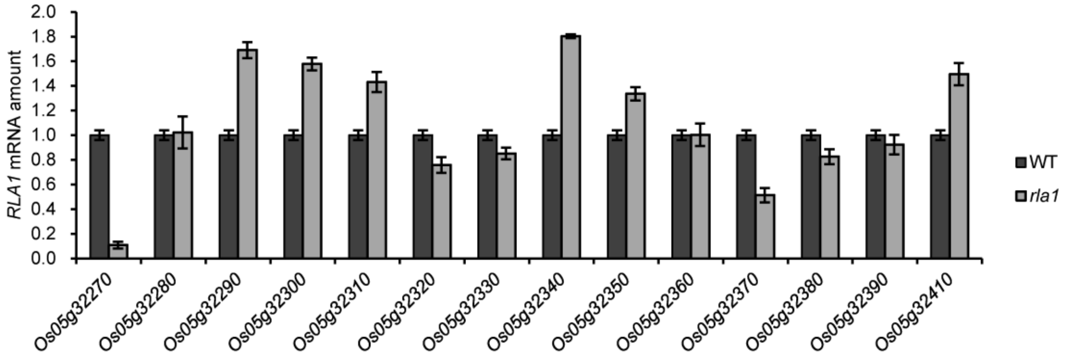
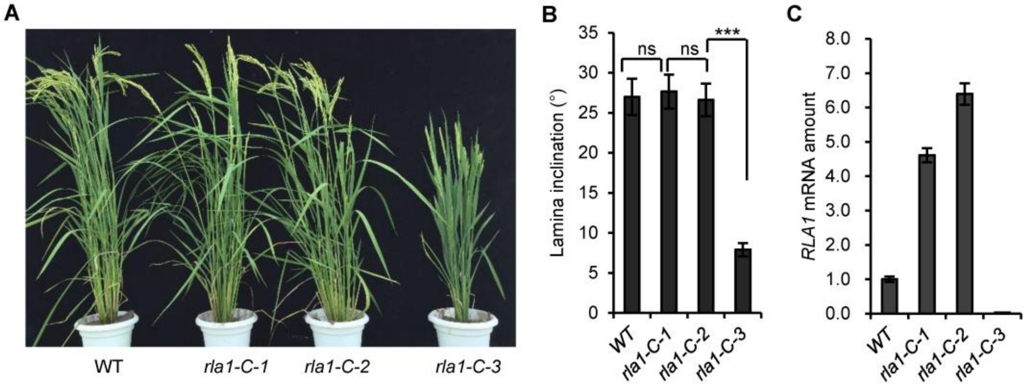
## Supplemental Figures



**Supplemental Figure 1.** Transcript Levels of Genes Located in the Region between the two Markers RM18590 and RM3969 on Chromosome 5.

(Supports Figure 2.)

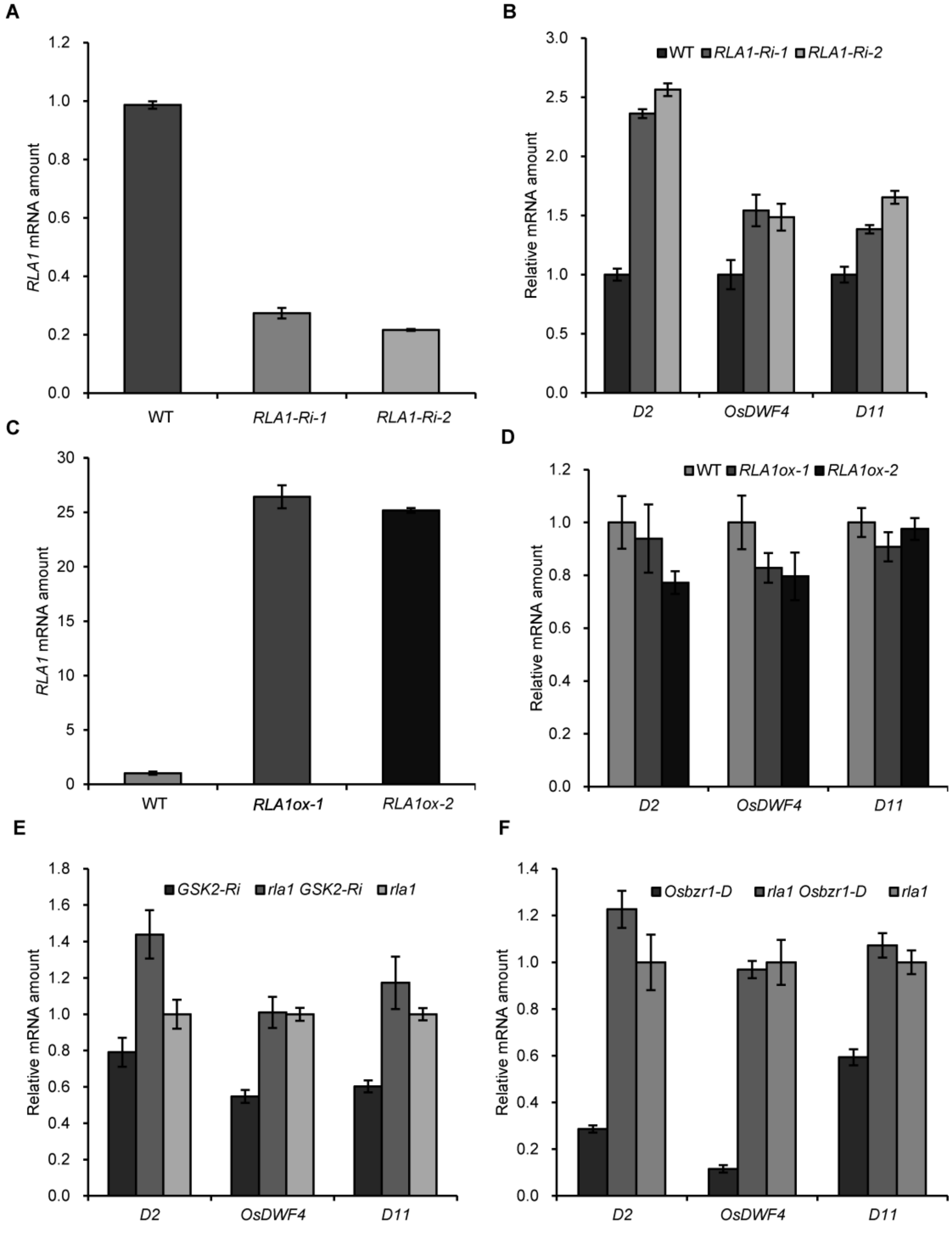
The relative transcript level of each gene in wild type was defined as “1”. Data are means ± SE (n=3).



**Supplemental Figure 2.** Phenotypes and *RLA1* transcript Levels of the *rla1-C* Plants.

(Supports Figure 2.)

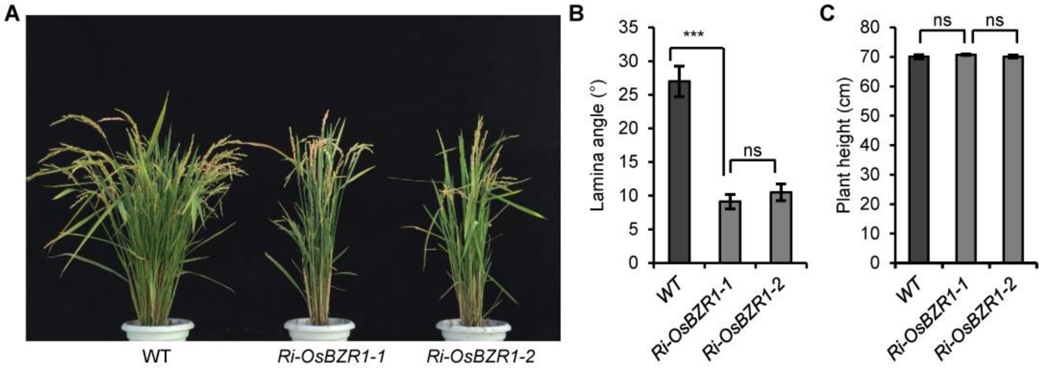
(A) Phenotypes of the wild type and three independent lines of *rla1-C*. (B) The statistical data of the lamina angle of the second lamina joint from plants in A. Data are means ± standard error (SE) (n=20). The comparisons were determined by Student’s *t*-test. *** $P < 0.001$ and “ns” means no significance. (C) The *RLA1* transcript levels in plants from A. The relative transcript level of *RLA1* in the wild type was defined as “1”. Data are means ± SE (n=3).



**Supplemental Figure 3.** Relative Gene Expression in Plants.

(Supports Figure 3.)

(A) *RLA1* transcript levels in the *RLA1-Ri* plants in Figure 3A. The relative transcript level of *RLA1* in the wild type was defined as “1”. Data are means ± SE (n=3). (B) The relative transcript level of the BR marker genes in plants from Figure 3A. The relative transcript level of the BR marker genes in the wild type was defined as “1”. Data are means ± SE (n=3). (C) *RLA1* transcript levels in the *RLA1ox* plants in Figure 3C. The relative transcript level of *RLA1* in wild type was defined as “1”. Data are means ± SE (n=3). (D) The relative transcript level of the BR marker genes in plants from Figure 3C. The relative transcript level of the BR marker genes in the wild type was defined as “1”. Data are means ± SE (n=3). (E and F) The relative transcript level of the BR marker genes in plants from Figure 3E and 3G. The relative expression level of BR marker genes in *rla1* was defined as “1”. Data are means ± SE (n=3).



**Supplemental Figure 4.** Phenotypes of *Ri-OsBZR1* Plants*.*

(Supports Figure 5.)

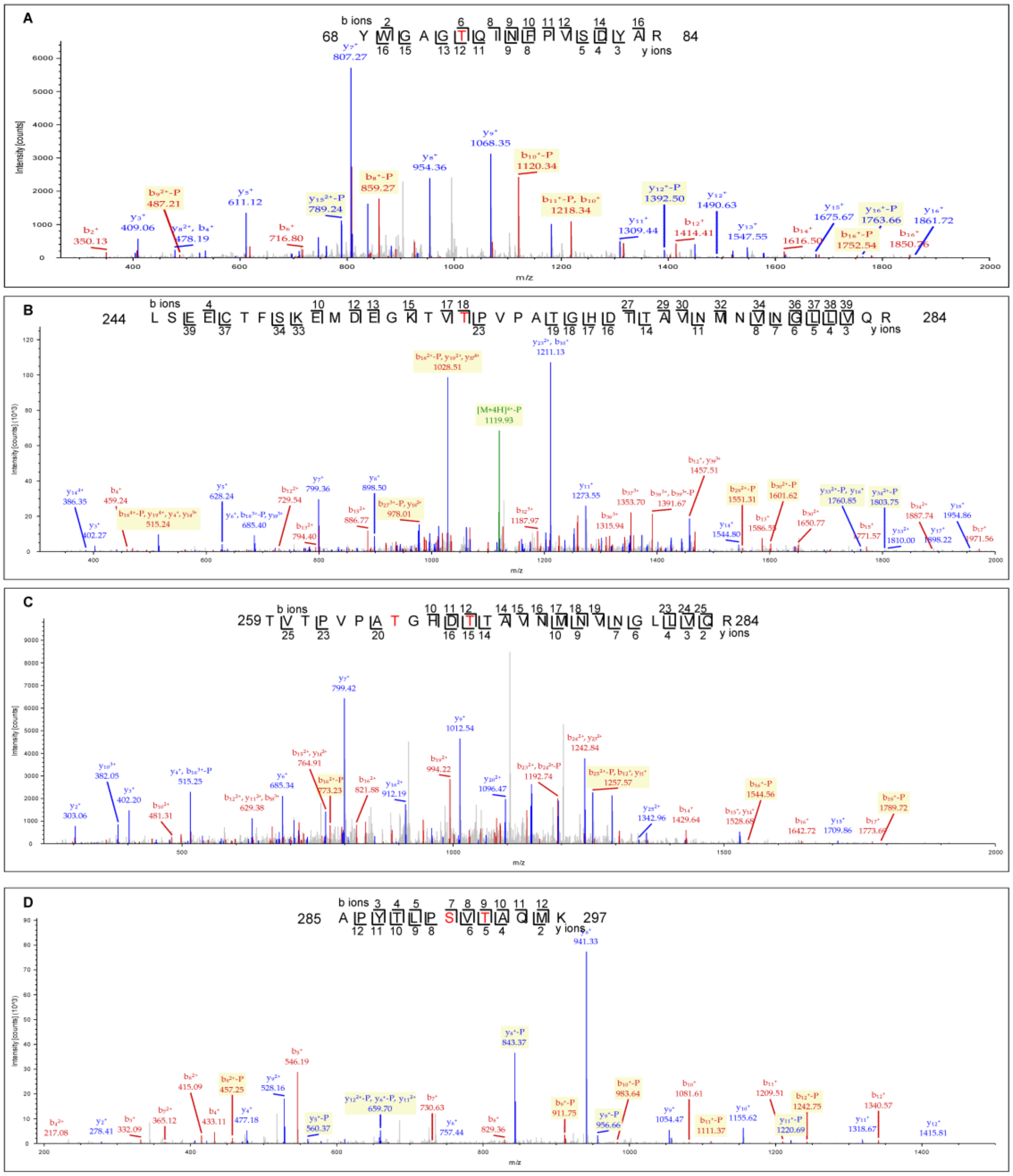
(A) The morphological phenotypes of WT, *Ri-OsBZR1-1* and *Ri-OsBZR1-2*. (B) The statistical data of the lamina angle of the second lamina joint from plants in A. Data are means ± SE (n=20). The comparisons were determined by Student's *t*-test. *** $P < 0.001$ and "ns" means no significance. (C) The statistical data of the plant height from plants in A. Data are means ± SE (n=20). The comparisons were determined by Student's *t*-test. The "ns" means no significance.

MPPCAAGKRSSIYRGVTRHRWTGRYEAHLWDK
STWNQNQNKKGKQVYLGAYDDEEAAARAYDLA
ALKYWGAGTQINFPVSDYARDLEEMQMISKEDY
LVSLRRKSSAFSRGLPKYRGLPRQLHNSRWDAS
LGHLLGNDYMSLGKDITLDGKFAGTFGLERKIDL
TNYIRWWLPKKTRQSDTSKMEEVTDEIRAIESSM
QRTEPYKFPSLGLHSNSKPSSVVLSACDILSQSD
AFKSFSEKSTKLSEECTFSKEMDEGKTVTPVPAT
GHDTTAVNMNVNGLLVQRAPYTLPSVTAQMKNT
WNPADPSADPLFWTNFILPASQPVTMATIATTTF
AKNEVSSSDPFHGQE

**Supplemental Figure 5.** There are 10 Potential Phosphorylation Motifs of GSK2 in RLA1.

(Supports Figure 7.)

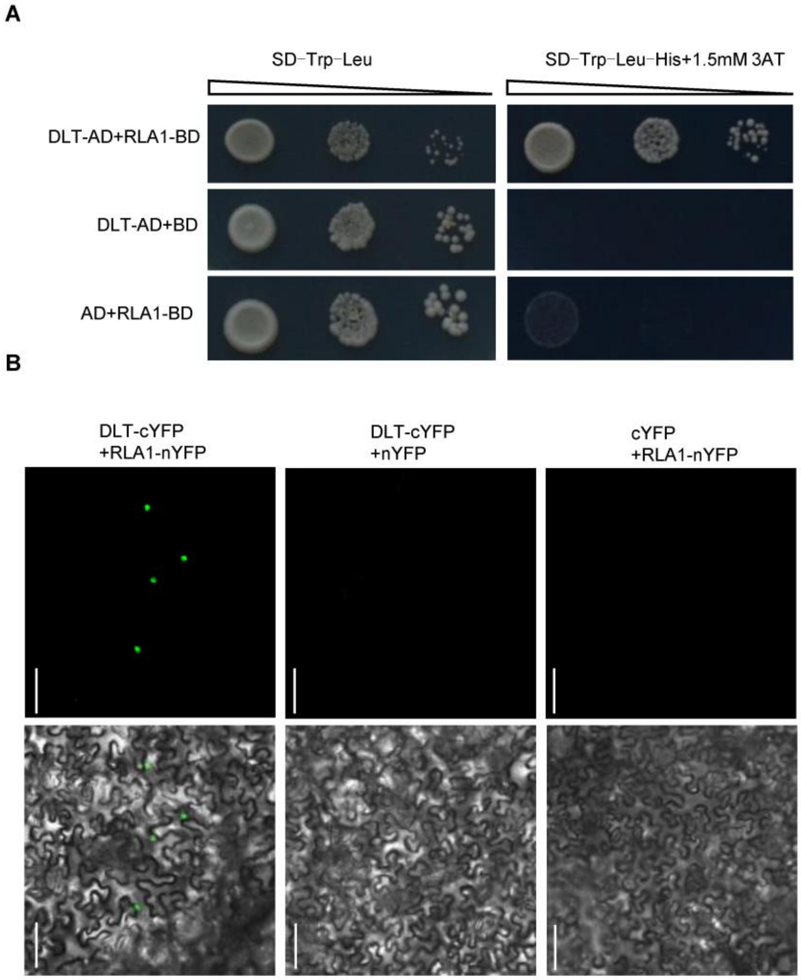
The potential phosphorylation sites are indicated by red font.



**Supplemental Figure 6.** Identification of RLA1 Phosphorylation Sites by GSK2 Kinase Using LC-MS/MS.

(Supports Figure 8.)

Potential phosphorylation sites of RLA1: (A) T73, (B) T261, (C) T266 and T270, and (D) S291 and T293.



**Supplemental Figure 7.** RLA1 Interacts with DLT.

(A) Interaction between RLA1 and DLT in yeast two-hybrid assays. (B) Interaction between RLA1 and DLT in BiFC assays. Bars = 100 μm.

**Supplemental Table 1.** Primers used in this study.

| Purpose | Primer name | Primer sequence (5' to 3') |
|---|---|---|
| *RLA1* genomic sequence | RLA1-C-F | CGGAATTCGGTCGTCGCACCAGTTGAACTAAGC |
| | RLA1-C-R | GCGTCGACATGCCTACTAGTTCCTGCTAAAGGACAACC |
| RT-qPCR | RT-OsACTIN1-F | AAGACTGTAATACCTATTG |
| | RT-OsACTIN1-R | ATAGAATAATCGCAACTC |
| | RT-RLA1-F | CTCTTCCGTGGTCCTATC |
| | RT-RLA1-R | GGTAACTGTCTTTCCTTCATC |
| | RT-D2-F | TCGCTGACGGAGCTGATG |
| | RT-D2-R | ACTTGAGGTGGGAGGACTTG |
| | RT-OsDWF4-F | CTCCACCTTCTCCGCTCAG |
| | RT-OsDWF4-R | GCCGCTCCGTCTCTTCC |
| | RT-D11-F | TGGCGACATTGAGAAGATTGC |
| | RT-D11-R | CAGAAGGCGATGACATTGACC |
| | RT-ILI1-F | ATGTCGAGCAGCCGGAGGTCG |
| | RT-ILI1-R | AAGCTCGGCGATCTGGTCCTC |
| ChIP-qPCR | 1-F | TGGCCCAAAGGTAAATGGTCA |
| | 1-R | TAGGGCACTCTAGTTTCGTGA |
| | 2-F | TATCATGAGCCGTAGGACGGA |
| | 2-R | GTCCCAAAACACAGTACATGGC |
| | 3-F | ATCGCCATGGCATGAACACT |
| | 3-R | AGTAGCTCTTGTTGGTACTGC |
| | 4-F | CTCCCACACAGCTTGAGACA |
| | 4-R | AGGTGCATATGGGGGTAGACT |
| | 5-F | CCCCACAAACACCTTTGCAT |
| | 5-R | GTACGGGGAGAGCAAGTCAC |
| | 6-F | CTTGCCCCATACCATCCCTC |
| | 6-R | TGCAATTTCACTGGCATTACCT |
| | 7-F | AGCATGAACGGCATCGATCT |
| | 7-R | TACTTGCATTTTGGCCGCTG |
| | 8-F | CGCAACACATGCTCAAGACT |
| | 8-R | TTGTAATTGTGCGACAGCGAG |
| | 9-F | CTCGCTGTCGCACAATTACA |
| | 9-R | GATGCCTGAGATTGGCAGTTG |
| | 10-F | AACTGCCAATCTCAGGCATCA |
| | 10-R | ACCACTTGCAGTGCAGCTATC |

| | | |
|---|---|---|
| | P-OsDWF-F | CTCCTCTTCCAGCACAAGCA |
| | P-OsDWF-R | TGAGTGACCTCTCCCTCCTC |
| | P-D2-F | TCAGTGTCTCAGCTGCCATC |
| | P-D2-R | CTTGGCCTGATGACCACACA |
| | P-OsDWF4-F | CAAAGCAGCCAGCAGAAAGG |
| | P-OsDWF4-R | TTCCCTCTTGCTCGCCAAAT |
| | P-D11-F | AGGCTCCATCCATGCTTCTT |
| | P-D11-R | CCTATAGCCTCACACCAGGC |
| | P-IBH1-F | GCACAGTATATGCATGCAGCC |
| | P-IBH1-R | AGGGAGTGATGGAAAGGGGT |