TaBRI 1-B1 TaBRI 1-A1
consensus

## NDS LRLAI AAALLFLAALAAA- - - DDAQL L DDF RAALPSRDALDGWAARDGACRFPGAV NDSLRLAI AAALLFLAALAAAAAA-DDAQLLDDFRAALPNRDALDGWAARDGACRFPGAV

    LEHLI LDYNGLTGSI PPELAKCKQLNWI SLASNRLSGPI PPWLGKLSNLAI LKLSNNSF
    
## CRGGRLTSLSLAAVALNADFRAVAATLLQLSAVERLSLRGANVSGALAAAAGARCGSKLG CRGGRLTSLSLAAVALNADFRAVAATLLQLSAVERLSLRGANVSGALAAAAGARCGSKLQ CRGGLTSLSLAAVALNADFRAVANTLLQLSAVERLSLRGANVS GALAAAAGARCGSKLQ

 E L DL S GNAALRGS VADVAALAASCGGLKTLNLS GDAVGAAKSAGGGGGGQGF AAL DAL DLE L DL S GNAALRGSVTDVAALAGS CAGLKTLNLS GDAVGTAKTAGAGGGGQGF AAL DAL DL
E L DL S GNAALRGSVADVAALAGSCAGLRTLNLS GGAVGAAKAAGGGGGGQGF AALDTL DL S S NKI TGDADLRWNV GAGL GSVRWL DL AWNKI S GGL S DF TNCS GL QYL DL S GNLI AGDVA
S SNKI AGDADLRWNV GAGL GSVRWL DL AWNKI S GGLS DF TNCS GL QYL DL S GNLI AGDVA
S S NKI AGDADLRWNVGAGL GSVRWL DL AWNKI SGGLSDF TNCS GLQYLDLS GNLI AGDVA

AGAL S GCRSLRALNL S S NHL AGAFPPNI AGLTSLTALNL S NNNF S GDVPADAF T GL QQLQ AGAL S GCRSLRAL NL S S NHL AGAF PPNI AGLTSLTAL NLS NNNF S GEVPADAF TGL QQL AGALSGCRSLRALNLS SNHLAGAFPPNI AGLTSLTAL NL S NNNF S GDVPADAF T GL QQL Q
 SLSLSF NHF SGSI PDS VAALPDLEVLDLS S NNF S GTI PSTLCQDPNSRLRVLYL QNNYLS SLSLSF NHF SGSI PDSVAALPDLEVLDLS SNNF S GTI PSTLCQDPNSRLRVLYL QNNYLS
 GSI PEAVSNCTDLVSLDLSLNYI NGSI PESLGEL GRLQDLI NUQNLLEGEI PASLSSI PG GSI PEAVSNCTDLVSLDLSLNYI NGSI PESLGELGRLQDLI NWQNLLEGEI PASLSSI PG


## GQI PAEL GDCKSLVWL DL NS NQL NGSI PPQL AE QS GKNTVGLII GRPYVYLRNDELS S QC

 GQI PAELGDCKSLVWLDLNSNQLNGSI PPQLAEQSGKNTVGLII GRPYVYLRNDELSS QCRGKGSLLEFSSI RSEDL GRNPSKKLCNFTRNYNGSTEYTFNKNGSNI FLDLSFNQLDSEI RGKGSLLEFSSI RSEDLGRNPSKKLCNF TRNYNGSTEYTF NKNGSNI FLDLSF NQLDSEI RGKGSLLEFSSI RSEDLGRNPSKKLCNF TRNYNGSTEYTF NKNGSNI FLDLSFNQLDSE
TaBRI 1-
TaBRI 1-D1
TaBRI 1-A1
consensus
TaBRI 1-B1 657 NLSSNQLNGTI PELGSLATFPKSQYENNS GLCGFPLPACEPHTGQGSSNGGQSNRRKASL



Figure S1. Multiple alignment of deduced amino acid sequence of TaBRI1 of A (TaBRI1-A1), B (TaBRI1-B1) and D (TaBRI1-D1) genomes. Black regions show identical amino acid residues among the three proteins, and the gray regions show identical amino acid residues among two of the three proteins. The points show the absent amino acid residues. The positions of amino acids are given on the right.


Figure S2. The leaf angle in the wild type (WT), tabri1 mutants, and corresponding. $\mathrm{BC}_{1} \mathrm{~F}_{2}$ homozygous individuals for tabri1 deletion identified with TaBRI1-A1 and TaBRI1-D1 specific primers at 14 DPA. DPA represents days post-anthesis. Data are means $\pm$ SE of fifteen plants.


Figure S3. The root length of WT and tabri1 mutants at seedling stage. (A) Root morphology in WT and tabri1 mutants. Bar $=5 \mathrm{~cm}$; (B) Statistic analysis of root length in WT and tabri1 mutants. All values are means $\pm \mathrm{SE}(\mathrm{n}=15)$. * indicates significant differences between WT and tabri1 mutants at $P<0.05$.


Figure S4. The yield traits in WT and tabri1 mutants. (A) Spike number per plant; (B) Number of grains per spike; (C) Grain yield per plant. All phenotypic data were measured from field-grown plants under normal cultivation conditions. All values are means $\pm \mathrm{SE}$ ( $\mathrm{n}=$ 15).



Figure S5. Photosynthesis parameters in WT and tabri1 mutants during the whole post-anthesis period. (A) Transpiration rate, Tr ; (B) Stomatal conductance, gs; (C) Intercellular $\mathrm{CO}_{2}$ partial pressure, Ci . All values are means $\pm \mathrm{SE}(\mathrm{n}=8)$. ${ }^{*}$ and ${ }^{* *}$ indicate significant differences between WT and tabri1 deletion plants at $P<0.05$ and $P<0.01$, respectively.

Table S1. Primers used in this work.

| Experiment | Name | Sequence |
| :---: | :---: | :---: |
| realtime PCR | TaBRI1(QP)F | GCCACCAGAGTACTACCAGAGCTTC |
| realtime PCR | TaBRI1(QP)R | GCGATTTTCAAATGCTCCAGC |
| realtime PCR | TaBRI1-A1(QP)F | CTGGAGCTGGAGCTGCTGGAG |
| realtime PCR | TaBRI1-A1(QP)R | TaBRI1.1specifeic(R) |
| realtime PCR | TaBRI1-D1(QP)F | GTGATGACGATGTTCAAGGAGATCC |
| realtime PCR | TaBRI1-D1(QP)R | TaBRI1.2specifeic(R) |
| realtime PCR | ACTINF | ACCTTCAGTTGCCCAGCAAT |
| realtime PCR | ACTINR | CAGAGTCGAGCACAATACCAGTTG |
| realtime PCR | TaDWARF4(QP)F | GGTTGCCCTAAAGCCGTTGAA |
| realtime PCR | TaDWARF4(QP)R | CGTTGCCCTTCCATCTCCAAG |
| realtime PCR | TaCPD1(QP)F | GAGATGGCAGAGCAACAACAAAC |
| realtime PCR | TaCPD1(QP)R | CGAGTGGTGGGAAAGAAGACGAG |
| realtime PCR | TaCYC90D1(QP)F | CTCGCCGTCAAGTTCCTCAG |
| realtime PCR | TaCYC90D1(QP)R | CATGCTGCGTGAATGACAAGGAC |
| VIGS | TaBRI1(VIGS)F | AGCTAGCCAGAGCTTGGTTCTC |
| VIGS | TaBRI1(VIGS)R | TGCTAGCGGTACTTGCCTCATC |
| Chromosome location | TaBRI1(RACE)F1 | GCCACCAGAGTACTACCAGAGCTTC |
| Chromosome location | TaBRI1.1specifeic(R) | CCCGGCCCCAAACTGGATGG |
| Chromosome location | TaBRI1.2specifeic(R) | GGTATCAGCATCTGAGAGACTGTG |
| Chromosome location | TaBRI1.3specifeic(R) | CAGCTCCGGGTCAAACACATCC |
| TaBRI1 amplification | TaBRI1(F) | CTTCTCGCATGGTCTCAAGGTAG |
| TaBRI1 amplification | TaBRI1(R3) | GCGATTTTCAAATGCTCCAGC |
| Vector construction | TaBRI1(pri)F | TaBRI1(pri)R |

