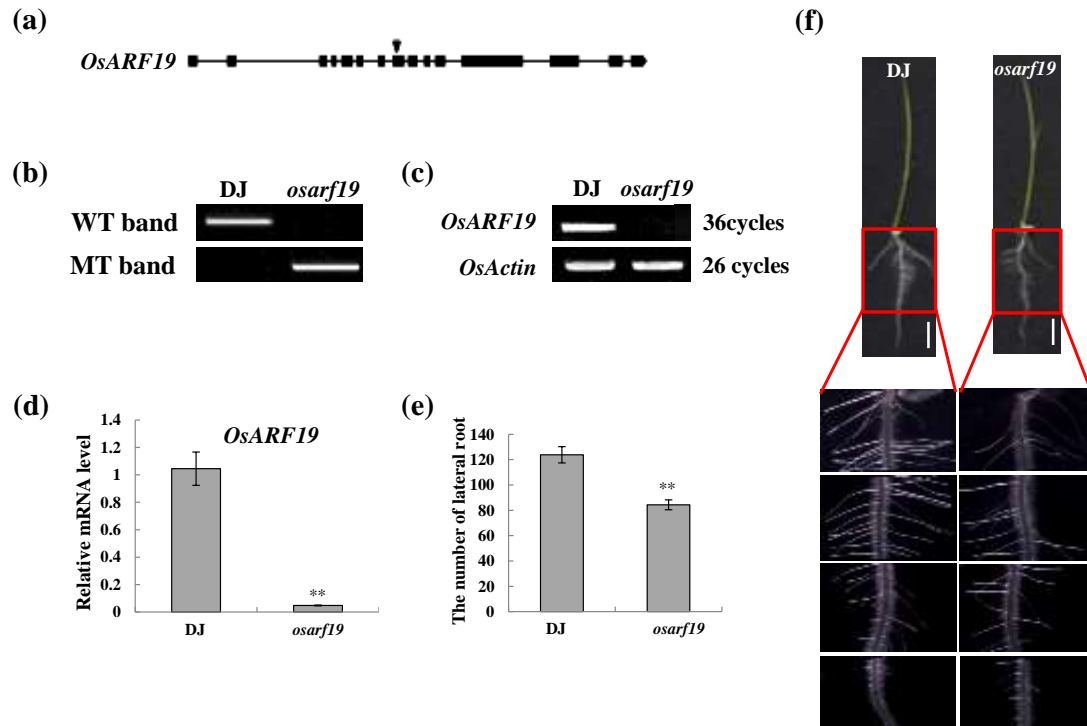**SUPPORTING INFORMATION**

Figure S1. Identification of *osraf19* mutant. (a) T-DNA insertion site in the *OsARF19* gene. Black triangle indicates the T-DNA insertion site. (b) Identification of T-DNA insertion using PCR. (c) *OsARF19* expression in DJ and *osarf19* mutant analyzed by RT-PCR. (d) *OsARF19* expression in DJ and *osarf19* analyzed by qRT-PCR. (e) Lateral root number in DJ and *osarf19*. Ten biological repeats were performed for the measurement of leaf angles. **indicate significant differences at P < 0.01. (f) Phenotypes of WT and *osarf19*. Roots were observed with a Leica MZ95 stereomicroscope (Leica Instrument, Nusslosh, Germany). Bar = 2 cm.
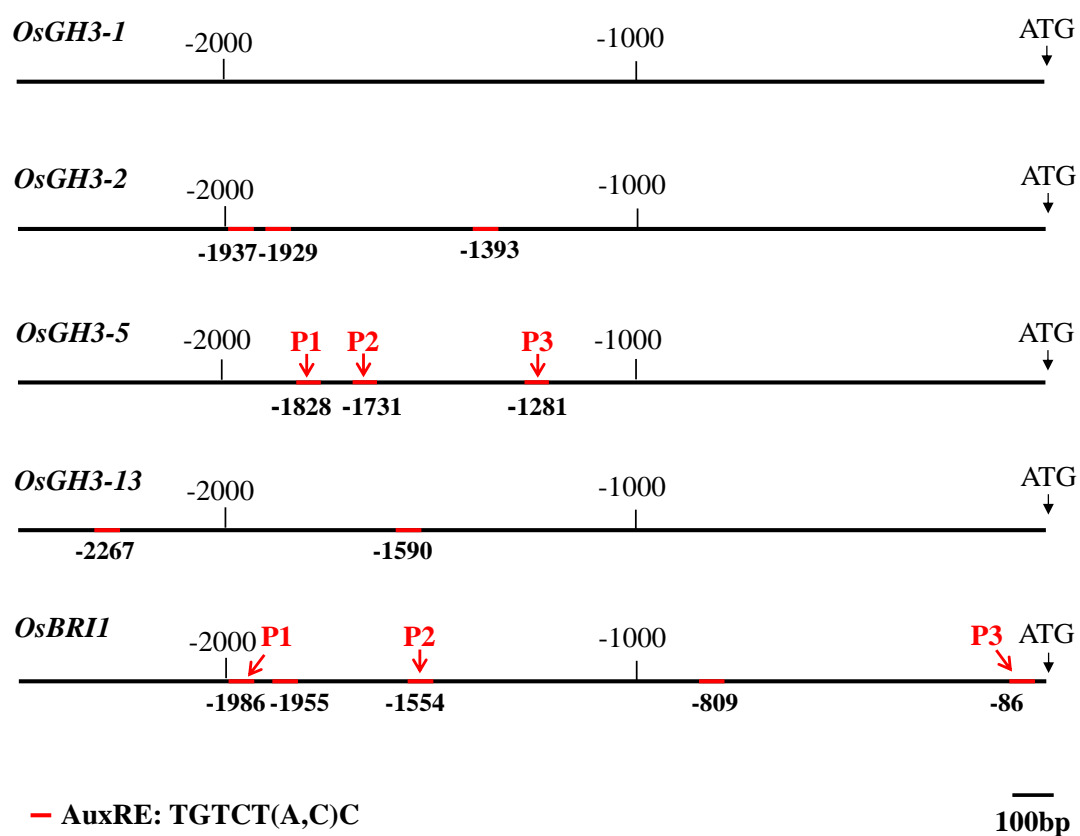
Figure S2. Analysis of AuxRE elements in promoters of *OsGH3* genes and *OsBRI1*. P1, P2 and P3 in *OsGH3-5* and *OsBRI1* promoter indicate the related AuxRE elements in yeast one-hybridization assays, respectively.
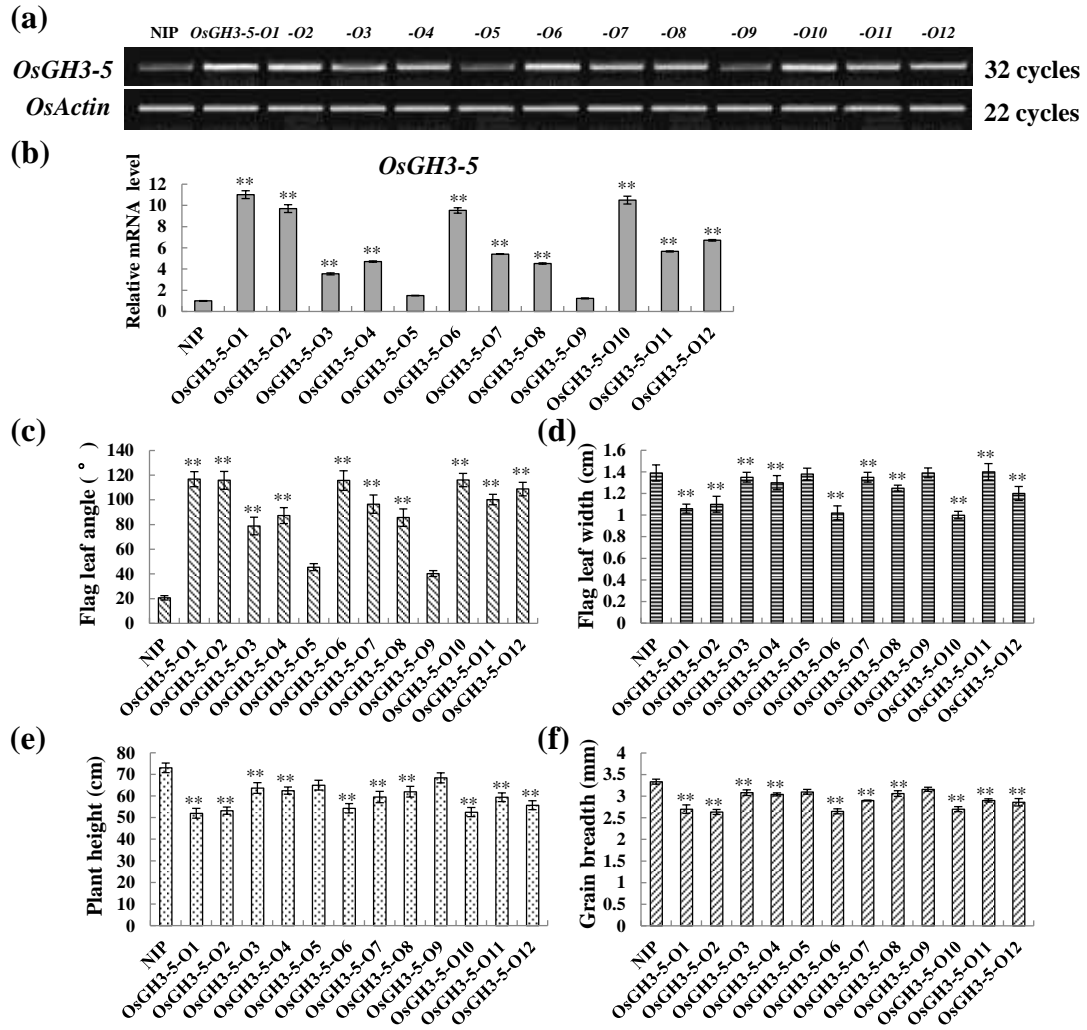
Figure S3. Identification of *OsGH3-5*-overexpression lines. (a) *OsGH3-5* expression in NIP, *OsGH3-5*-overexpression lines analyzed by RT-PCR. (b) *OsGH3-5* expression in NIP, *OsGH3-5*-overexpression lines analyzed by qRT-PCR. Three independent biological replicates were used in the qRT-PCR analysis according to Wang *et al.* (2010). (c) Statistical data of Flag angle. (d) Statistical data of flag leaf width. (e) Statistical data of plant height. (f) Statistical data of grain breadth. Ten biological repeats were employed in each test. Error bars indicate SD (n = 10). ** indicate significant differences at P < 0.01.
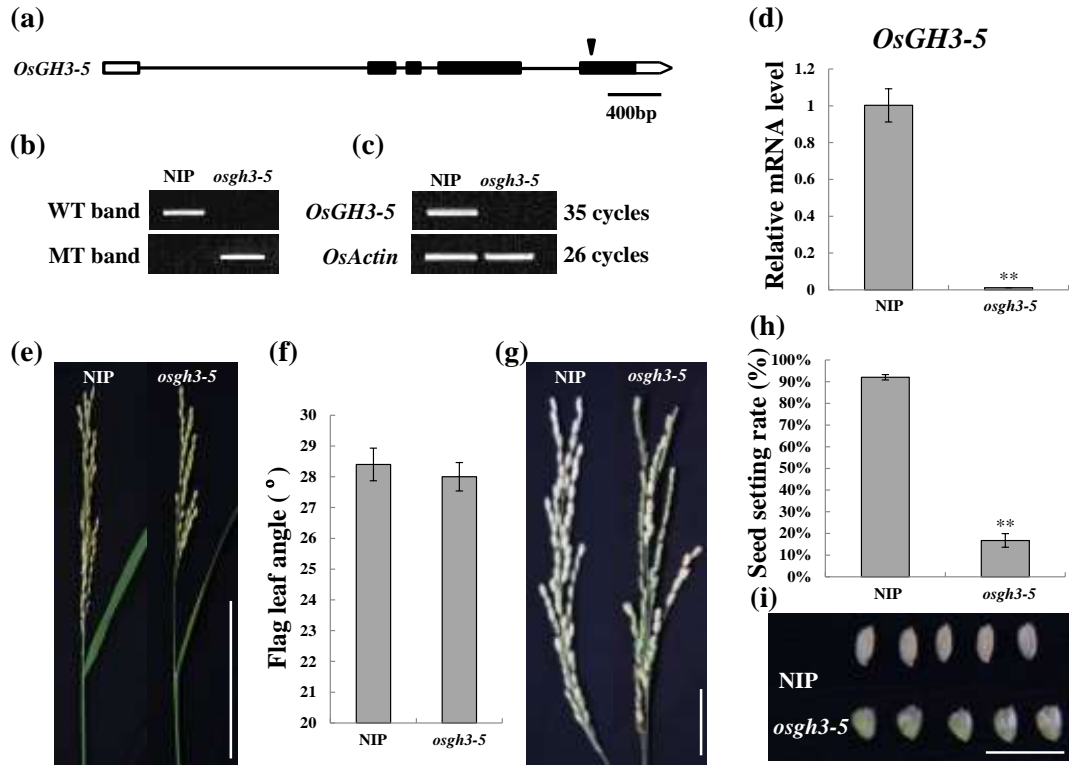
Figure S4. Identification of the *osgh3-5* mutant. (a) TOS17 insertion site in the *OsGH3-5* gene. Black triangle marks the TOS17 insertion site. (b) Identification of the TOS17 insertion using PCR. (c) *OsGH3-5* expression in NIP and *osgh3-5* mutant analyzed by RT-PCR. (d) *OsGH3-5* expression in NIP and *osgh3-5* analyzed by qRT-PCR. Three independent biological replicates were used in the qRT-PCR analysis according to Wang *et al*. (2010). Error bars indicate SD (n = 3). ** indicate significant differences at P < 0.01. All bars = 400μm. (e) Flag Leaf angles at the mature period of NIP and *osgh3-5*. Bar = 10 cm. (f) Statistical data of flag leaf angle of NIP and *osgh3-5*. Ten biological repeats were performed each test. (g) Phenotype of panicle of NIP and *osgh3-5*. Bar = 2 cm. (h) Seed setting rate of NIP and *osgh3-5*. Ten biological repeats were performed for each test. Error bars indicate SD (n = 10). ** indicate significant differences at P < 0.01. Bars = 200μm. (i) Phenotypes of seeds. Bar = 1 cm.
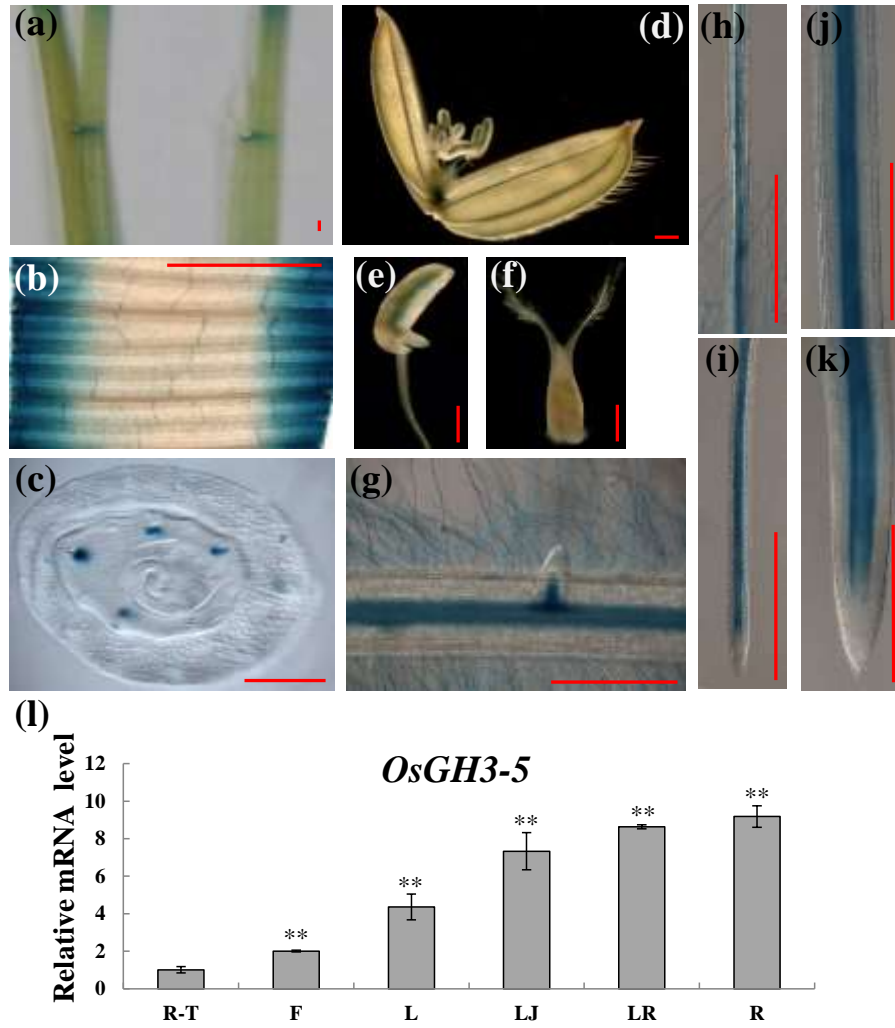
Figure S5. Expression pattern of *OsGH3-5* in rice NIP. (a) Lamina joints of flag leaves for three month-old. (b) Leaf. (c) The cross section of root-stem transition region. (d) Flower and glume. (e) Anther. (f) Stigma. (g) Root hair and lateral root in adventitious root. (h) and (i) Lateral root. Maturation zone (h). Root tip (i). (j) and (k) Primary root. Elongation zone (j). Root tip (k). (l) qRT-PCR analysis of *OsGH3-5* in each tissue of rice NIP. R-T: The cross section of root-stem transition region, F: flower, L: leaf, LJ: lamina joint, LR: lateral root, R: root. Three independent biological replicates were used in the qRT-PCR analysis according to Wang et al

(2010). Error bars indicate SD (n = 3). ** indicate significant differences at P < 0.01.
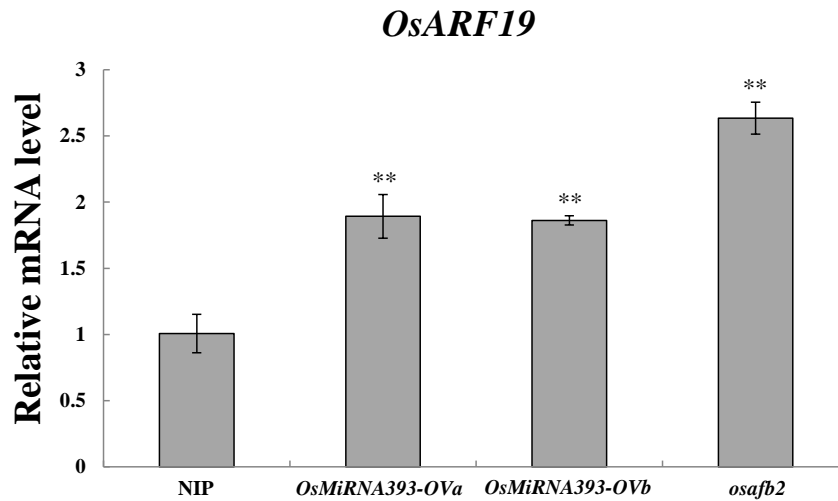
All bars = 400μm.

OsARF19

Figure S6. *OsARF19* expression in *OsMiRNA393*-overexpression lines and *osafb2* *(OsTIR1-RNAi)* mutant. Three independent biological replicates were used in the qRT-PCR analysis according to Wang et al (2010). Error bars indicate SD (n = 3). ** indicate significant differences at P < 0.01.
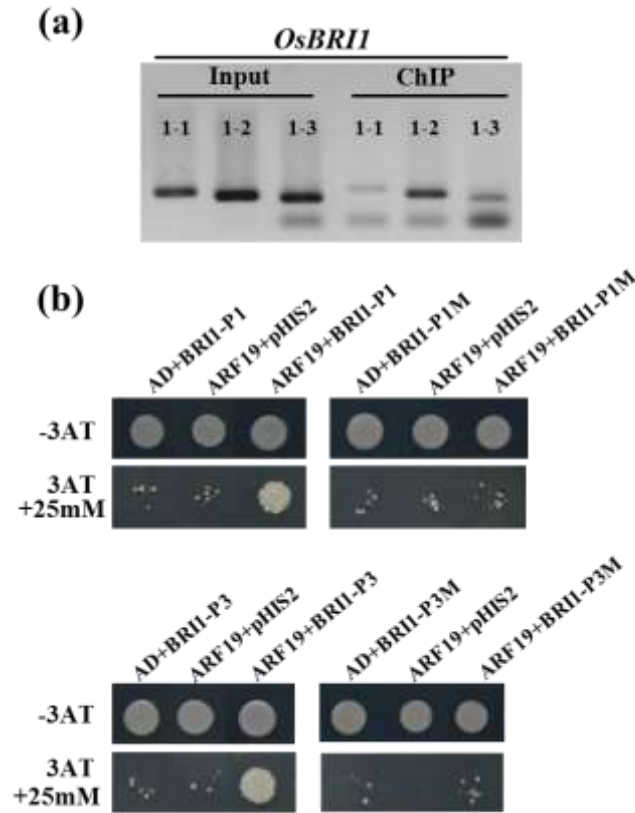
Figure S7. ChIP assay and yeast one hybrid of OsARF19 and *OsBRI1*.

(a) ChIP-PCR analysis. OsARF19 ChIP assays were performed as described under Fig. 4a. DNA products were amplified using three specific primers (listed in Supporting Information Table S4) with the AuxRE elements in *OsBRI1* promoters.

(b) YOH assay between OsARF19 and *OsBRI1*. The bait vector containing the *OsBRI1*-promoter fragments P1 or P3 and the mutated P1M or P3M fused HIS2 reporter gene, and the prey vector containing OsARF19 fused a GAL4 activation domain were co-transformed into yeast cells (Y187). Growth condition of yeast cells were tested as indicated under Fig. 4b.

Table S1a. Statistical data of phenotypical characterization in WT/NIP, *OsARF19*-overexpression lines, WT/DJ and *osarf19*.

	Plant height (cm)	Tiller number	Flag leaf width (cm)	Flag leaf length (cm)	Panicle length (cm)
NIP	72.50±2.65	7.67±0.58	1.41±0.04	45.70±1.47	17.69±0.65
OsARF19-O1	49.25±2.50 **	9.67±0.58 *	1.05±0.06 **	27.63±0.91 **	13.49±0.85 **
OsARF19-O2	51.30±1.25 **	9.33±0.58 *	1.17±0.06 **	26.42±1.31 **	14.03±0.33 **
OsARF19-O3	50.52±1.56 **	9.50±0.41 *	1.09±0.04 **	2.51±1.64 **	13.51±0.56 **
OsARF19-O4	65.35±1.25 **	8.52±0.39 *	1.25±0.16 **	33.02±1.67 **	15.9±0.24 **
OsARF19-O5	68.09±2.05	7.92±0.23	1.31±0.09	38.43±1.47 **	16.5±0.86 *
OsARF19-O6	58.66±2.18 **	9.13±0.48 *	1.18±0.03 **	30.27±1.45 **	14.51±0.44 **
OsARF19-O7	53.74±1.09 **	9.40±0.31 *	1.10±0.06 **	27.04±1.90 **	13.83±0.64 **
OsARF19-O8	49.96±2.17 **	9.60±0.64 *	1.05±0.04 **	27.52±1.46 **	13.53±0.65 **
OsARF19-O9	69.80±2.07	7.84±0.32	1.35±0.05	40.49±1.37	17.03±0.66
OsARF19-O10	50.35±1.46 **	9.53±0.08 *	1.08±0.08 **	27.52±1.78 **	13.51±0.51 **
OsARF19-O11	64.38±2.41 **	8.18±0.67 *	1.23±0.13 **	35.37±1.61 **	15.43±0.40 **
DJ	80.00±2.55	7.40±0.55	1.56±0.05	48.38±0.97	17.82±0.29
osarf19	79.70±1.10	7.00±1.00	1.48±0.04 *	45.50±1.12 **	17.56±0.29

All values are the averages of 10 seedlings for 3 month-old plants (±SD).

* Significant difference from wild type at 5% by student's *t* test.

** Significant difference from wild type at 1% by student's *t* test.

Table S1b. Statistical data of phenotypical characterization in WT/NIP, *OsARF19*-overexpression lines, WT/DJ and *osarf19*.

	Flag leaf angle (°)	Grain number/panicle	Seed setting rate (%)	Grain breadth (mm)	Grain length (mm)	100-grain weight (g)
NIP	28.83±2.48	70.50±2.74	92.95±1.25	3.33±0.06	7.34±0.04	2.50±0.01
OsARF19-O1	124.80±3.13 **	44.75±4.72 **	33.64±2.75 **	2.70±0.10 **	7.25±0.05	1.95±0.03 **
OsARF19-O2	116.67±4.63 **	43.25±4.03 **	36.98±2.41 **	2.63±0.06 **	7.26±0.05	1.90±0.01 **
OsARF19-O3	119.33±3.89 **	44.75±4.36 **	33.4±2.39 **	2.68±0.16 **	7.25±0.07	1.94±0.04 **
OsARF19-O4	78.53±3.14 **	58.69±4.05 **	45.09±2.23 **	2.95±0.09 **	7.28±0.17	2.19±0.06 **
OsARF19-O5	45.64±2.10 **	65.66±4.18 **	52.13±2.40 **	3.10±0.03	7.29±0.15	2.25±0.07
OsARF19-O6	100.59±4.03 **	49.94±4.32 **	35.40±2.31 **	2.85±0.17 **	7.27±0.06	2.11±0.04 **
OsARF19-O7	118.97±4.21 **	44.54±4.34 **	34.50±2.64 **	2.74±0.04 **	7.26±0.09	1.91±0.05 **
OsARF19-O8	121.02±4.34 **	44.61±4.17 **	33.54±2.32 **	2.70±0.05 **	7.25±0.07	1.94±0.08 **
OsARF19-O9	40.57±2.87 **	68.06±4.22 *	57.34±2.10 **	3.25±0.08	7.31±0.08	2.3±0.03
OsARF19-O10	120.27±4.31 **	44.55±4.19 **	33.40±2.08 **	2.69±0.13 **	7.25±0.03	1.94±0.02 **
OsARF19-O11	89.60±3.26 **	55.38±4.41 **	40.18±2.67 **	2.91±0.23 **	7.28±0.08	2.15±0.09 **
DJ	32.80±1.92	77.40±4.00	95.6±2.00	3.43±0.05	7.44±0.02	2.72±0.04
osarf19	31.2±2.28	76.40±3.05	76.50±3.53 **	3.25±0.06 **	7.26±0.04 **	2.49±0.03 **

Data are measured with 4 month-old seedlings at least 10 plants (±SD).

* Significant difference from wild type at 5% by student's *t* test.

** Significant difference from wild type at 1% by student's *t* test.

Table S2. Primer sequences for *OsARF19* gene.

Name	Primer sequences (5'-3')
OVARF19U/L	GGTACCATGATGAAGCAGGCGCAGCA/CAGCTGTCATTCGAATTGTTCATATGAAC
RTARF19U/L	GTCCTACTGAATTTGTTATC/CAGATAGAAACCCTATTTCG
ProARF19U/L	GGATCCATATGCCAAGCCAAGGTTA/GGTACCGACCTCAGACCAGACAG
ARF19-LP	GCCAGGGATTTGCATGATAA
ARF19-RP	CATCCCAACCAACCTGTAAGTT
Ngus-RB	AACGCTGATCAATTCCACAG
OsACTIN U/L	TCAGCAACTGGGATGATATGGAG/GCCGTTGTGGTGAATGAGTAAC

Table S3. Primer sequences for *OsGH3* genes.

Name	Primer sequences (5'-3')
OsGH3-1-qRT-U/L	CGGGAACAAGCAATGGAACA /CAGATCATCACCCTCTAGCTTCAA
OsGH3-2-qRT-U/L	TCATGCCCGTCATGAACTTG /TCGTCTCCGACTTGATGAACAG
OsGH3-5-qRT-U/L	CACGGAAAGCCCAAGTTCATT/TTATGACTTGCTTGCTACCATAA
OsGH3-13-qRT-U/L	TGTGTAATGTCAAACGTTGCTCAT/TGATTCATAAAGAACACTGCTCGTATT
OVGH3-5U/L	CACCATGACGATCTGCAGCTG/AAATCCATAGGCAGTACTGAAATAA
ProGH3-5-GUSU/L	GTCGACCAGAAAGTTTTTCAGAGATAACAG/GGTACCGAGAGAGAGGTTGGTGATGG
GH3-5-LP/RP	GCCAGACTCACCAATAACAT/CACCACCAAGGCTTAGGAAA
TOS17 tail16	AGGTTGCAAGTTAGTTAAGA(3'end of Tos 17)

Table S4. Primer sequences for ChIP-PCR analysis.

Name	Primer sequences (5'-3')
35S:ARF19-sGFP-U/L	GGTACCATGATGAAGCAGGCGCAGCA/GTCGACTTCGAATTGTTCATATGAACCATTG
pGH3-1-1U/L	GTATCGTCCAGAGTTCCACAC/CATTTCCTAACACCCCTTGTG
pGH3-1-2U/L	ATGTATCGTGGTGTTAAGTG/TTCAACCGTATTGTTTTAGT
pGH3-1-3U/L	ACATCTTCTCCATCTCCACG/GAGCTTGGTTTGTGTGAGCG
pGH3-2-1U/L	CAGATTTACTGTAGATCCTCG/ATCTGTCGATCGAGTTGTTCC
pGH3-2-2U/L	ACAGAAAGGGGATAGATAGG/AAAATTAGCACGTCACAAA
pGH3-2-3U/L	GTGGCGCTGCACACTACTG/GTTGTGTAGTTGTTCGTCTCC
pGH3-5-1U/L	TAATCTCCTTTCTTTGCGTCT/AGTTTTAATACCTCGTTGACC
pGH3-5-2U/L	TGTCGGCAATAAAGTTCCAC/GTAGAATCCTGGCTTTACCAC
pGH3-5-3U/L	CCTTTCCTCCATTGTAGGGTG/CGCGAAATTTTGGACGAACCG
pGH3-13-1U/L	TTGTTTTCCTCCTCTTTTCC/CTGTTGTTTTATTGTTTGCTA
pGH3-13-2U/L	CTTTTGGGAGGAGGTAGTAAC/AGATGTGAGATGATTTAGCC
pGH3-13-3U/L	GGCTGAAGAAGTAGAAGAAG/TTGACAGTCCAAAGGTTATT
pBRI1-1U/L	CAGTAAAACCTGAAAGTGCAT/CACCCCTACTTGTCACGGA
pBRI1-2U/L	GGTTCCCTCCACGAGTCCA/AGGTTAAATCCCGATCCGA
pBRI1-3U/L	GCTTAATGGAAGGCTCGCAAG/CAATATGCCCACGACGACGTT

Table S5. Primer sequences for Yeast one-hybrid.

Name	Primer sequences (5'-3')
OsGH3-5-P3-pHIS2-U	AATTCGCGGGGGATGCTGCTCCCTGAGCCTGTGTGTGTCTCTTGATTTTTCTTTCTTTGCTCGCAGAGCT
OsGH3-5-P3-pHIS2-L	CTGCGAGCAAAGAAAGAAAAATCAAGAGACACACACAGGCTCAGGGAGCAGCATCCCCCGCG
OsGH3-5-P3M -pHIS2-U	AATTCGCGGGGGATGCTGCTCCCTGAGCCTGTGTGAAAAAATTGATTTTTCTTTCTTTGCTCGCAGAGCT
OsGH3-5-P3M-pHIS2-L	CTGCGAGCAAAGAAAGAAAAATCAATTTTTTCACACAGGCTCAGGGAGCAGCATCCCCCGCG
OsBRI1-P1-pHIS2-U	AATTCGTACCTCTAACATGCGTACACAATTCTTACTGTCTCAGGTCATACCAAGGAAGATCTTATGAGCT
OsBRI1-P1-pHIS2-L	CATAAGATCTTCCTTGGTATGACCTGAGACAGTAAGAATTGTGTACGCATGTTAGAGGTACG
OsBRI1-P1M-pHIS2-U	AATTCGTACCTCTAACATGCGTACACAATTCTTACAAAAAAAGGTCATACCAAGGAAGATCTTATGAGCT
OsBRI1-P1M-pHIS2-L	CATAAGATCTTCCTTGGTATGACCTTTTTTTGTAAGAATTGTGTACGCATGTTAGAGGTACG
OsBRI1-P3-pHIS2-U	AATTCTCCTCCTCATCACTTCCCACTCTCCCCCTTCTGTCTCTCTACTTTCTCTCTCTACCGCCGGAGCT
OsBRI1-P3-pHIS2-L	CCGGCGGTAGAGAGAGAAAGTAGAGAGACAGAAGGGGGAGAGTGGGAAGTGATGAGGAGGAG
OsBRI1-P3M-pHIS2-U	AATTCTCCTCCTCATCACTTCCCACTCTCCCCCTTCAAAAAATCTACTTTCTCTCTCTACCGCCGGAGCT
OsBRI1-P3M-pHIS2-L	CCGGCGGTAGAGAGAGAAAGTAGATTTTTTGAAGGGGGAGAGTGGGAAGTGATGAGGAGGAG
OsARF19-orf-ADU/L	CCATCGATGGATGATGAAGCAGGCGC/CCGCTCGAGTCATTCGAATTGTTCATATGA

Table S6. Primer sequences for co-expression analysis.

Name	Primer sequences (5'-3')
OVARF19U/L	GGTACCATGATGAAGCAGGCGCAGCA/CAGCTGTCATTCGAATTGTTCATATGAAC
ProGH3-5-sGFPU/L	GAATTCCAGAAAGTTTTTCAGAGATAACAG/GGATCCTAATGGTAGAATCCTGGCTTTAC

Table S7. Primer sequences for qRT-PCR analysis.

Name	Primer sequences (5'-3')
OsIAA1-qRT-U/L	CTCGACTTCGAGGACACCGC/GATGGTGAAGTGGGAGAAGAAC
OsARF23-qRT-U/L	GAGCTGGTGGCCAAGGATCT/CTAGGCTTGTAGTAGACAGTGAA
OsTIR1-qRT-U/L	TGCTCGAGGAGCTCAGCTTCA/AGCCTTATGAAGGAGGCTAGCA
OsBZR1-qRT-U/L	CGTCGCCCACCTACAACCTC/TCGCCCAAATCGCAGCAT
OsBRI1-qRT-U/L	TACCAGAGCTTC AGATGCACC A/AGTAGCTCAGGGTCGAAGACAT
OsD2-qRT-U/L	AGCTGCCTGGCACTAGGCTCTACAGATCAC/ATGTTGTCGGAGATGAGCTCGTCGGTGAGC
OsD11-qRT-U/L	TTGGGTCATGGCATGGCAAGAGCAAGGA/TTGTTGCTGGAGCCAGCATTCCTCCTCT
OsDWARF-qRT-U/L	ATGGTGTTGGTGGCGATTGGGGTGGTTG/ATGTTGTTCCGCCCCAGGATGTCCAGCA