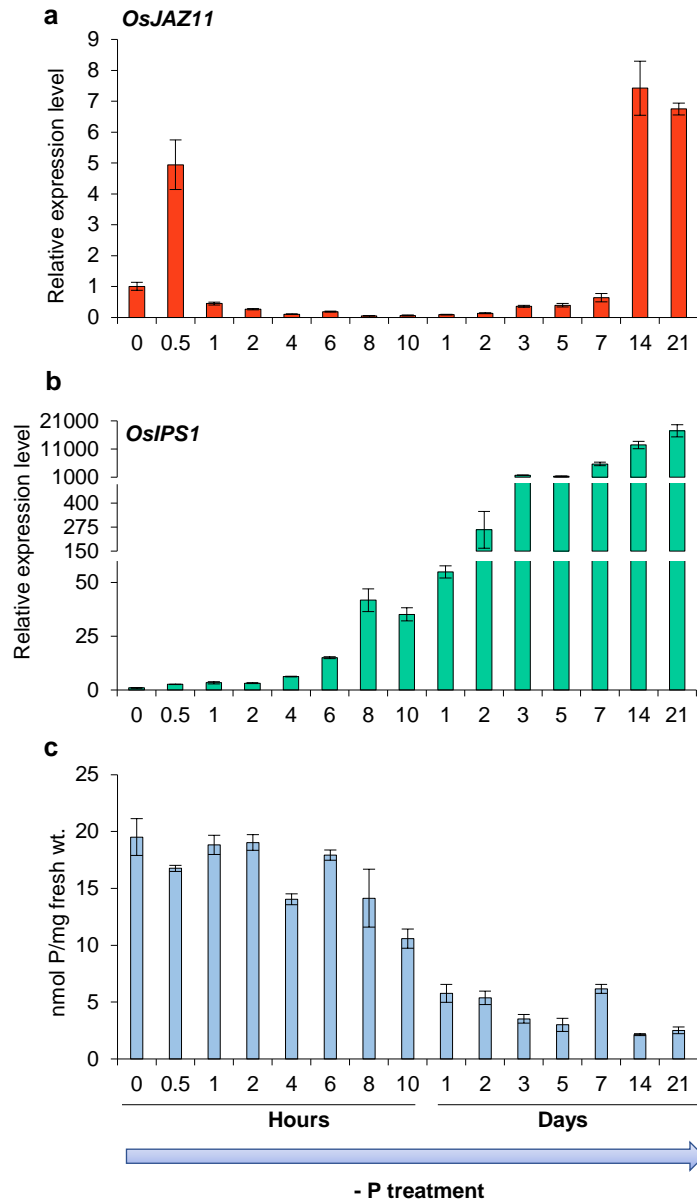


Supplementary Fig. S1 *OsJAZ11* is a JA responsive gene. **a** Schematic representation of gene model of *OsJAZ11* (1551 bp) and open reading frame (ORF) (209 a.a.). Positions of intron/exons in gene structure (above panel) and motifs in ORF (below panel) have been indicated. **b** Expression profile of *OsJAZ11* retrieved from microarray database RiceXPro (Rice Expression Profile Database) version 3.0. Error bars represent standard deviation ($n=3$). **c** Histochemical localization of GUS signals in coleoptiles of *pOsJAZ11:GUS* rice transgenics subjected to different doses of MeJA treatments (0, 1, 10, 50 and 100 μ M) for 1 h.

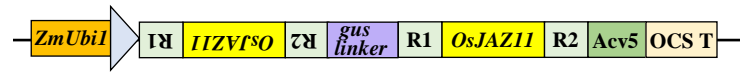


Supplementary Fig. S2 *OsJAZ11* is induced by local and systemic Pi fluctuations. **a-b** Relative expression profiles of *OsJAZ11* and *OsIPS1* in roots of PB1 seedlings. Seven-day-old rice seedlings grown under +P conditions were transferred to -P conditions. *OsIPS1* was used as a marker gene to depict onset of Pi deficiency response at molecular levels. Gene expression levels were measured at indicated time points by RT-qPCR and fold changes were determined with respect to 0 time point. **c** Soluble Pi content in rice seedlings at time points corresponding to time points in panel **a** and **b**. Each bar represents mean of three independent replicates with standard error ($n=3$).

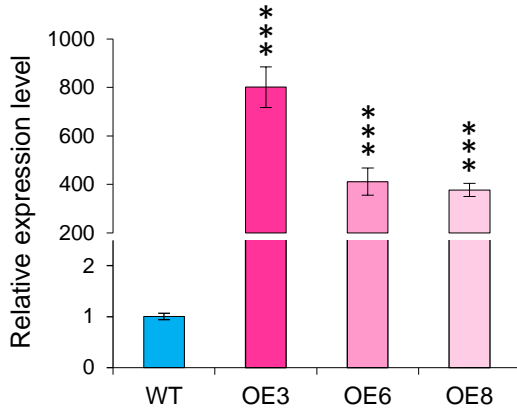
a *OsJAZ11* OE construct



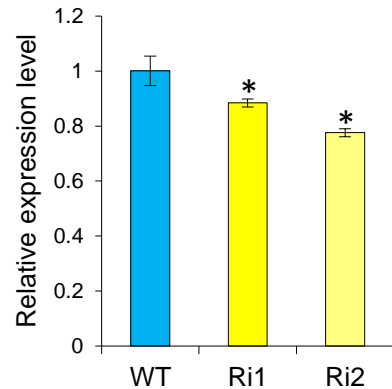
b *OsJAZ11* Ri construct



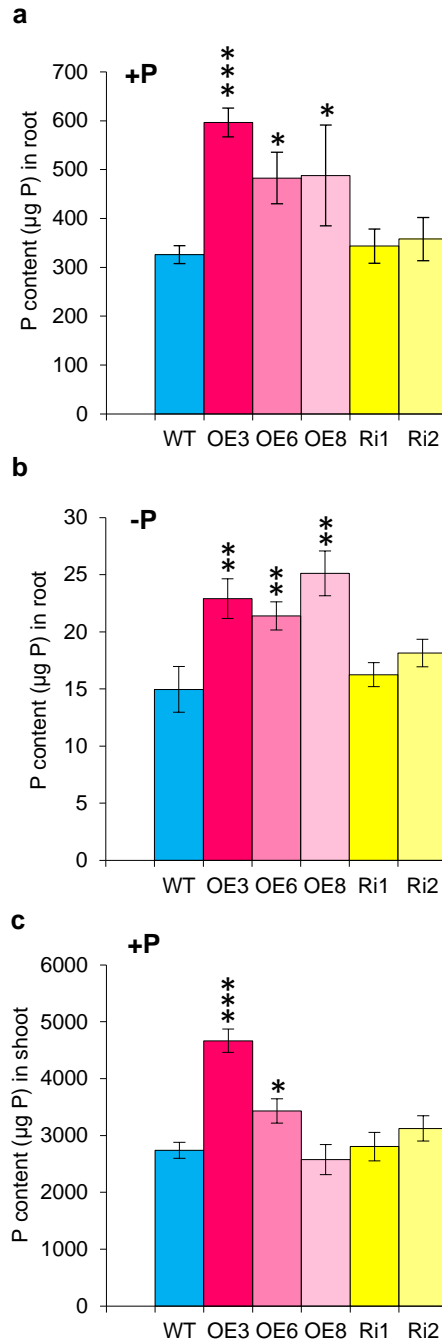
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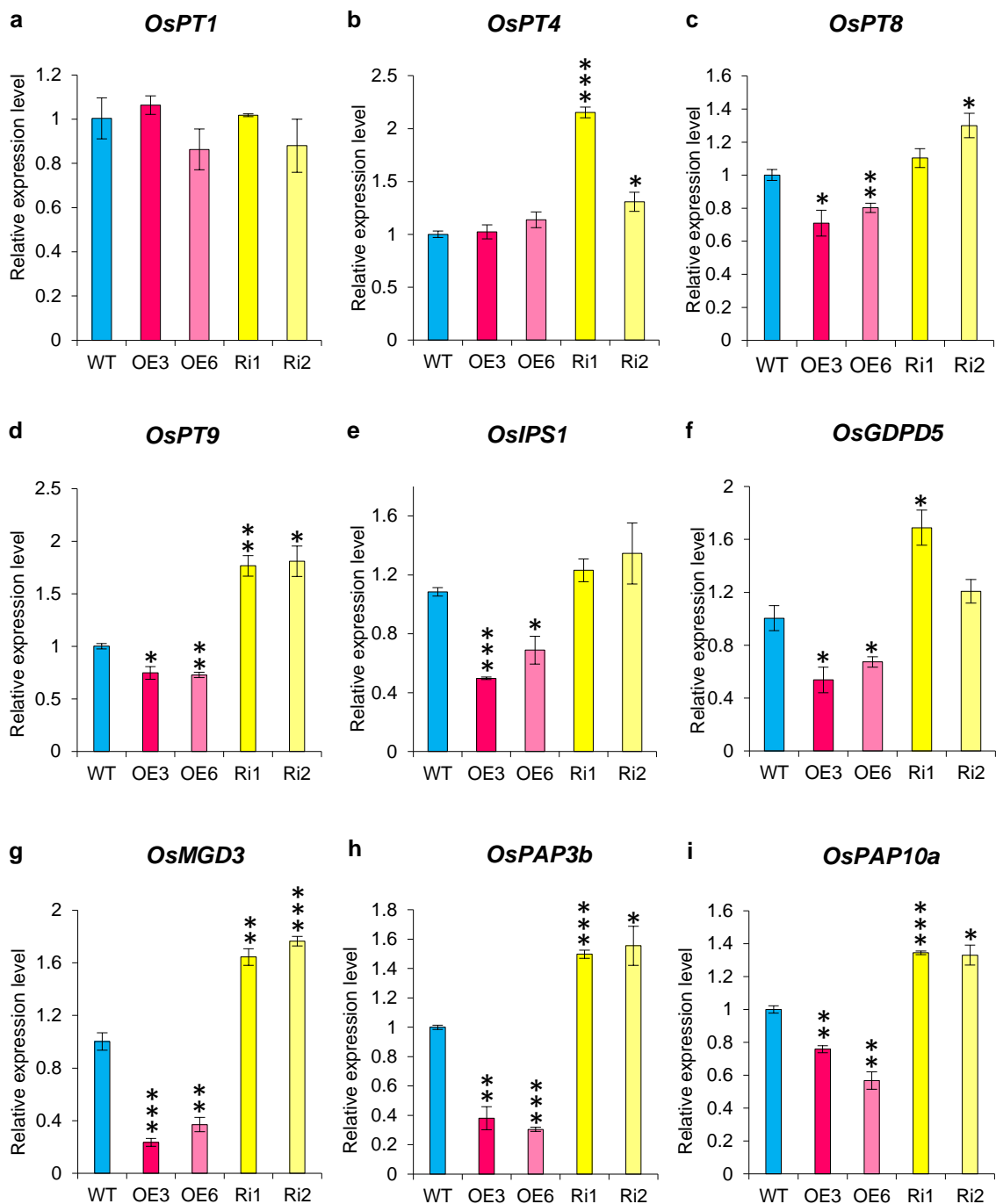
d



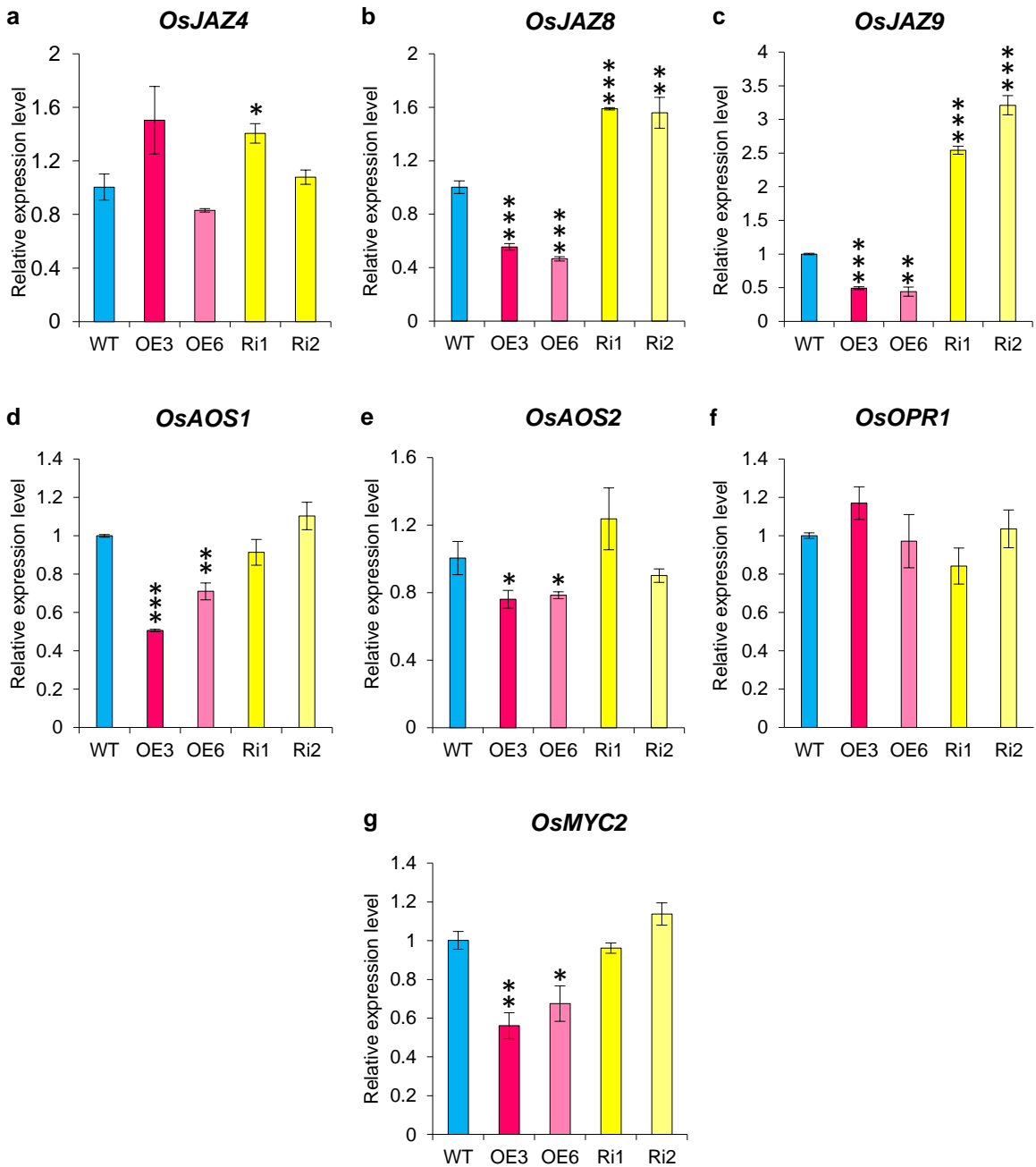
Supplementary Fig. S3 Raising of *OsJAZ11* transgenics. **a** Schematic representation of *OsJAZ11* overexpression construct in Gateway-compatible destination vector, pANIC6B. *OsJAZ11* was overexpressed under maize *Ubiquitin* promoter (*ZmUbi1*). **b** Schematic representation of *OsJAZ11* silencing construct in Gateway-compatible destination vector, pANIC8B. *ZmUbi1* (maize ubiquitin 1 promoter and intron), R1 and R2 (*attR1* and *attR2* recombination sites), AcV5 (epitope tag), *OCS T* (octopine synthase terminator sequence). **c-d** Relative expression levels of *OsJAZ11* in roots of thirty-day-old *OsJAZ11* overexpression (OE) and RNAi (Ri) transgenics compared to WT. Each bar represents mean of three biological replicates with standard error. Significant differences between WT and transgenics were evaluated by Student's *t*-test. Asterisks; * and *** indicate *P* values, ≤ 0.05 and 0.001, respectively ($n=3$).



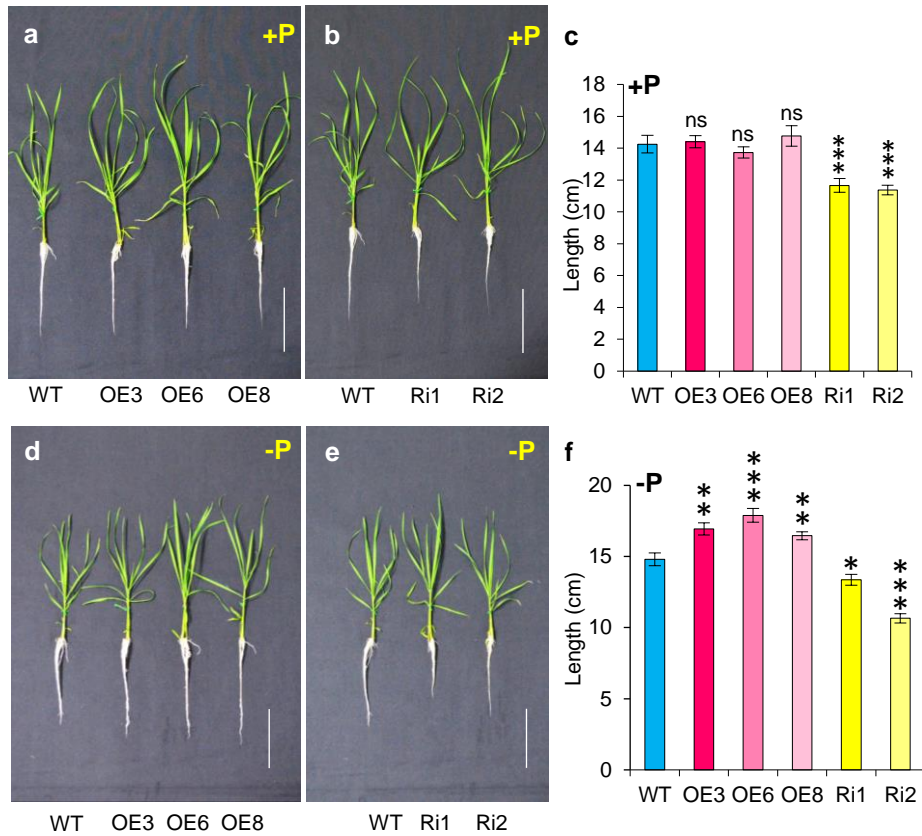
Supplementary Fig. S4 *OsJAZ11* OE lines showed higher phosphorous uptake. **a-b** P content of roots of thirty-day-old plants of WT and *OsJAZ11* transgenics under +P and -P conditions. **c** P content of shoots of thirty-day-old plants of WT and *OsJAZ11* transgenics under +P conditions. Each bar displays means of ten biological replicates with standard error. Significant differences between WT and transgenics were determined by Student's *t*-test. Asterisks; *, ** and *** indicate *P* values, ≤ 0.05 , 0.01 and 0.001, respectively ($n=10$).



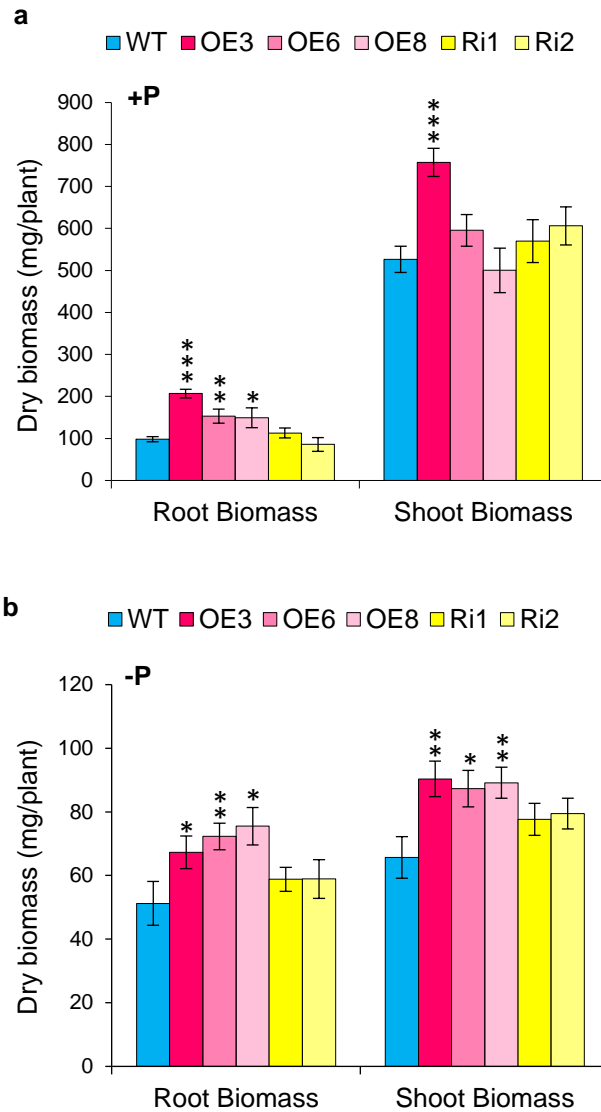
Supplementary Fig. S5 *OsJAZ11* OE lines displayed suppressed phosphate starvation response (PSR). **a-i** Relative expression levels of low Pi marker genes *OsPT1*, *OsPT4*, *OsPT8*, *OsPT9*, *OsIPS1*, *OsGDPD5*, *OsMGD3*, *OsPAP3b* and *OsPAP10a*. Expression levels were measured by RT-qPCR in roots of thirty-day-old WT and *OsJAZ11* transgenics under Pi deficiency. Each bar displays means of three biological replicates with standard error. Significant differences between WT and transgenics were determined by Student's *t*-test. Asterisks; *, ** and *** indicate *P* values, ≤ 0.05 , 0.01 and 0.001, respectively ($n=3$).



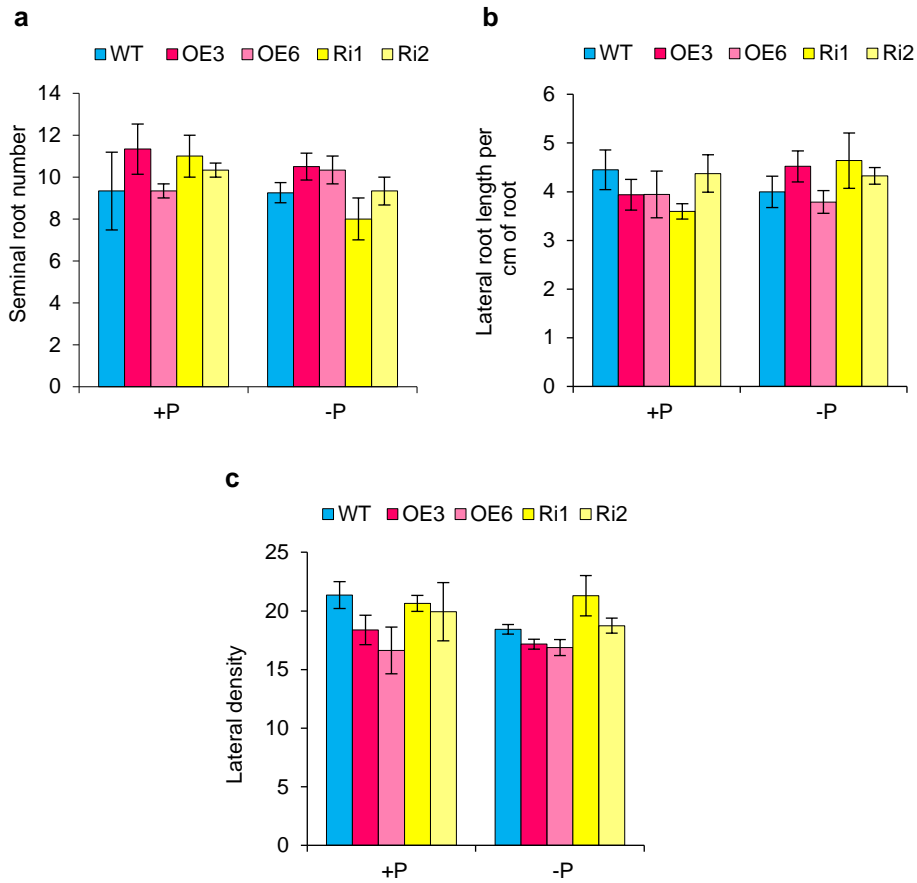
Supplementary Fig. S6 Overexpression of *OsJAZ11* suppressed expression of JA biosynthesis and signalling genes. **a-g** Relative expression levels of *OsJAZ4*, *OsJAZ8*, *OsJAZ9*, *OsAOS1*, *OsAOS2*, *OsOPR1* and *OsMYC2*. Expression levels were measured by RT-qPCR in roots of thirty-day-old WT and *OsJAZ11* transgenics under Pi deficiency. Each bar displays means of three biological replicates with standard error. Significant differences between WT and transgenics were determined by Student's *t*-test. Asterisks; *, ** and *** indicate *P* values, ≤ 0.05 , 0.01 and 0.001 , respectively ($n=3$).



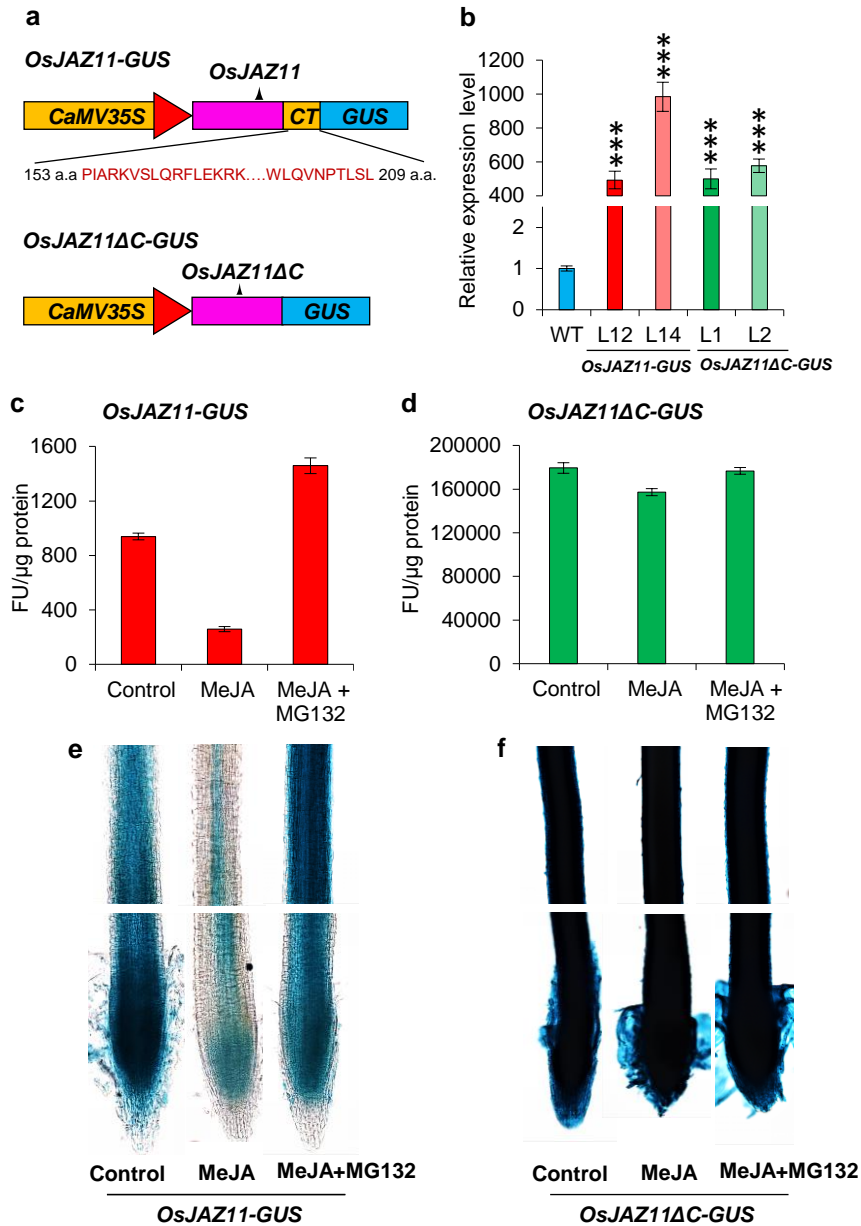
Supplementary Fig. S7 Root length of fifteen-day-old WT and *OsJAZ11* transgenics. Root phenotype of fifteen-day-old *OsJAZ11* overexpression (OE) lines (**a, d**) and silencing (Ri) lines (**b, e**) compared to WT under +P (**a, b**) and -P (**d, e**) conditions. For imaging three representative plants of each line were stacked together. Scale bar = 10 cm. **c** Quantitation of root lengths of WT, OE and Ri lines under +P conditions. **f** Quantitation of root lengths of WT, OE and Ri lines under -P conditions. Each bar represents mean of ten biological replicates with standard error. Significant differences between WT and transgenics were determined by Student's *t*-test. Asterisks; *, ** and *** indicate *P* values, ≤ 0.05 , 0.01 and 0.001, respectively ($n=10$). Ns denotes no significant differences between WT and transgenics.



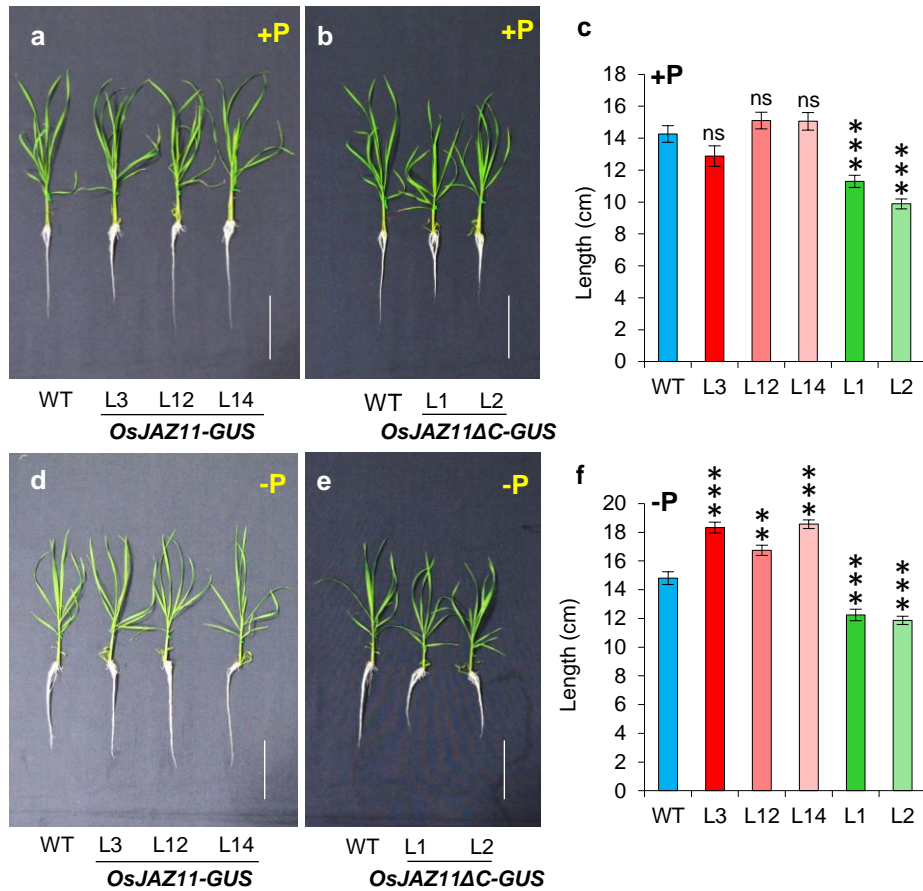
Supplementary Fig. S8 *OsJAZ11* overexpression lines accumulated higher biomass under Pi deficiency. **a-b** Root and shoot dry biomass of thirty-day-old WT and *OsJAZ11* OE and Ri transgenics under +P and -P conditions. Each bar depicts mean of ten biological replicates with standard error. Significant differences between WT and transgenics were determined by Student's *t*-test. Asterisks; *, ** and *** indicate *P* values, ≤ 0.05 , ≤ 0.01 and ≤ 0.001 , respectively ($n=10$).



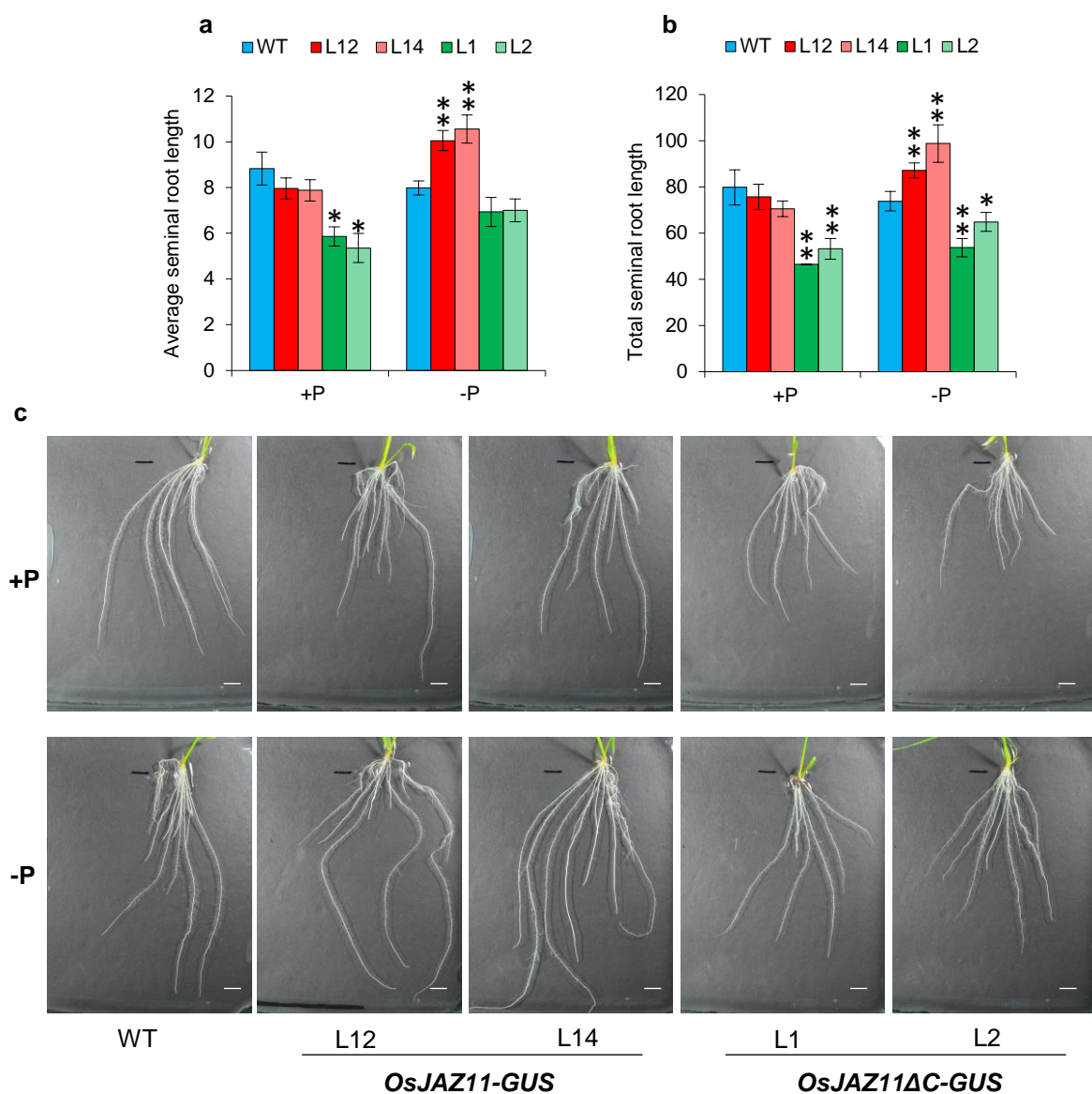
Supplementary Fig. S9 Effect of *OsJAZ11* on different root traits. Seminal root number (a), lateral root length per cm of root (b) and lateral root density (number of laterals per cm of main root) (c). Root traits were measured in roots of fifteen-day-old WT and *OsJAZ11* transgenics under +P and -P conditions. Each bar represents mean of four replicates with standard error ($n=4$).



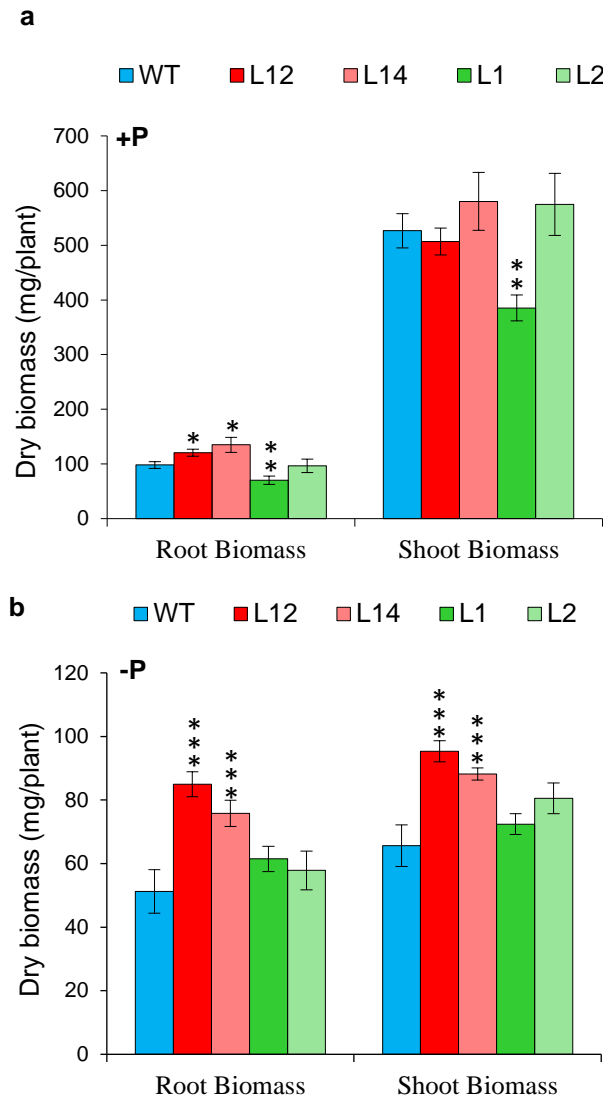
Supplementary Fig. S10 *OsJAZ11* shows *in vivo* repressor activity. **a** Raising of *OsJAZ11* translational reporters. Schematic representation of *OsJAZ11-GUS* (with Jas motif) and *OsJAZ11ΔC-GUS* (without Jas motif) fusion constructs in pCAMBIA1301. In *OsJAZ11ΔC-GUS*, 57 a.a. (153- 209 a.a.) from C-terminal (CT) end of *OsJAZ11* ORF was deleted. This deleted region also contains Jas motif. **b** Relative expression levels of *OsJAZ11* in WT, *OsJAZ11-GUS* (L12, L14) and *OsJAZ11ΔC-GUS* (L1, L2) transgenics. Expression levels were measured by RT-qPCR in roots of thirty-day-old plants. Each bar represents mean of three biological replicates with standard error. Significant differences between WT and transgenics were determined by Student's *t*-test. Asterisks; *** indicate *P* value, ≤ 0.001 ($n=3$). **c-d** Fluorometric quantitation of GUS signals in roots of fifteen-day-old *OsJAZ11-GUS* (L14) and *OsJAZ11ΔC-GUS* (L1) transgenics subjected to MeJA and/or MG132 treatments. Plants were treated with 100 μ M MeJA with or without the proteasome inhibitor 100 μ M MG132 for 1 h. DMSO treated seedlings were used as control. Each bar represents mean of four biological replicates with standard error ($n=4$). **e-f** Representative images showing GUS signals in root tips of fifteen-day-old *OsJAZ11-GUS* (L14) and *OsJAZ11ΔC-GUS* (L1) transgenics treated MeJA and/or MG132 treatments.



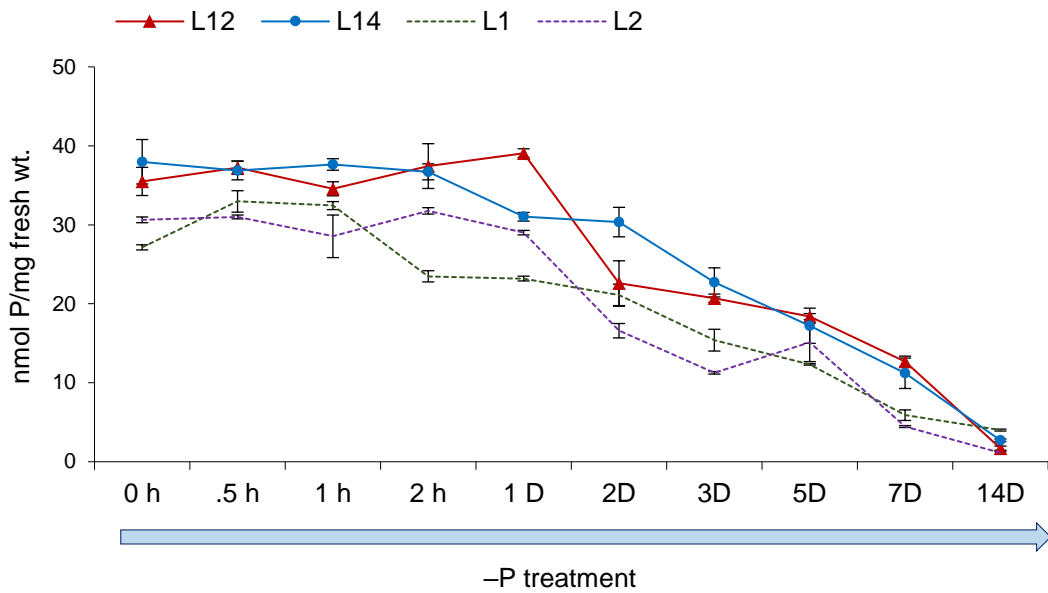
Supplementary Fig. S11 Root length of fifteen-day-old WT and *OsJAZ11* translational reporters. Root phenotype of fifteen-day-old *OsJAZ11-GUS* (**a**, **d**) and *OsJAZ11ΔC-GUS* lines (**b**, **e**) compared to WT under +P (**a**, **b**) and -P (**d**, **e**) conditions. For imaging three representative plants of each line were stacked together. Scale bar = 10 cm. **c** Quantitation of root lengths of WT and translational reporters under +P conditions. **f** Quantitation of root lengths of WT and translational reporters under -P conditions. Each bar represents mean of ten biological replicates with standard error. Significant differences between WT and transgenics were determined by Student's *t*-test. Asterisks; ** and *** indicate *P* values, ≤ 0.01 and 0.001 , respectively. Ns denotes no significant differences between WT and transgenics ($n=10$).



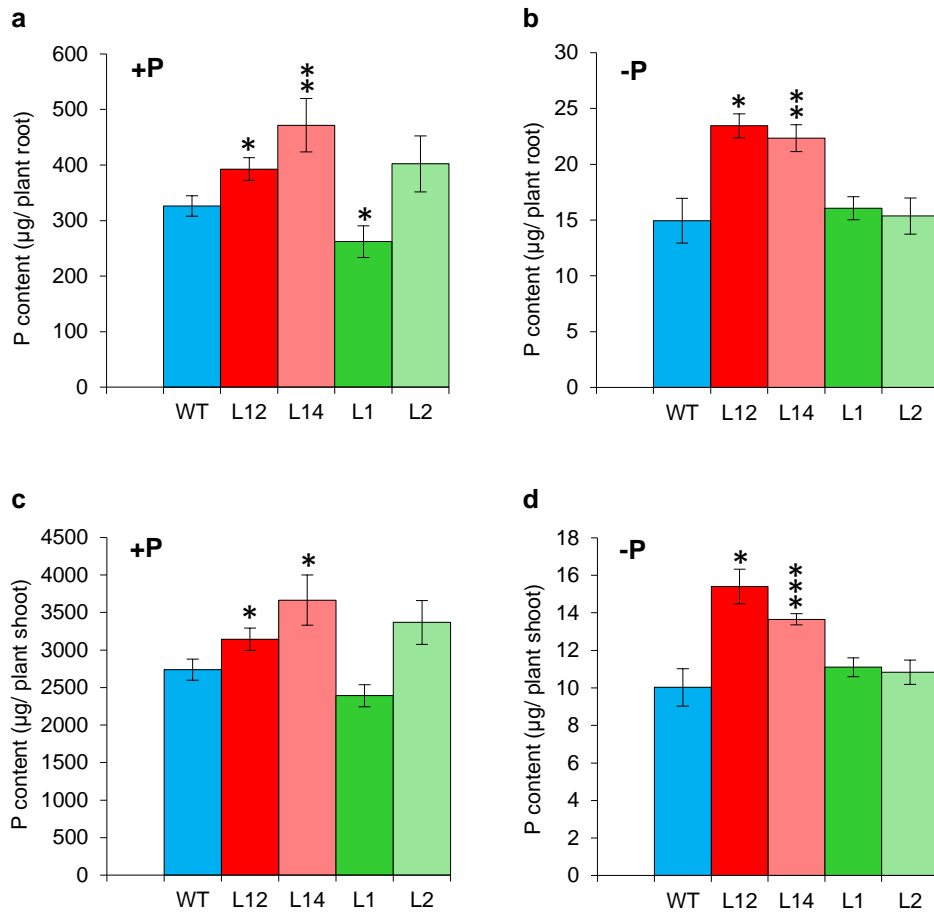
Supplementary Fig. S12 *OsJAZ11-GUS* lines developed longer seminal roots. Average seminal root length (a) and total seminal root length (b) of fifteen-day-old WT, *OsJAZ11-GUS* (L12, L14) and *OsJAZ11ΔC-GUS* (L1, L2) lines under +P and -P conditions. Each bar represents mean from four replicates with standard error. Significant differences between WT and transgenics were determined by Student's *t*-test. Asterisks; * and ** indicate *P* values, ≤ 0.05 and 0.01 , respectively ($n=4$). c Representative images of fifteen-day-old WT and *OsJAZ11* translational reporters under +P and -P conditions. White line at bottom of each image denotes scale of 1 cm.



Supplementary Fig. S13 *OsJAZ11-GUS* lines accumulated more biomass under Pi deficiency. Root and shoot dry biomass of thirty-day-old WT, *OsJAZ11-GUS* (L12, L14) and *OsJAZ11ΔC-GUS* (L1, L2) lines under +P (a) and -P (b) conditions. Each bar represents mean of ten biological replicates with standard error. Significant differences between WT and transgenics were determined by Student's *t*-test. Asterisks; *, ** and *** indicate *P* values, ≤ 0.05 , 0.01 and 0.001, respectively ($n=10$).



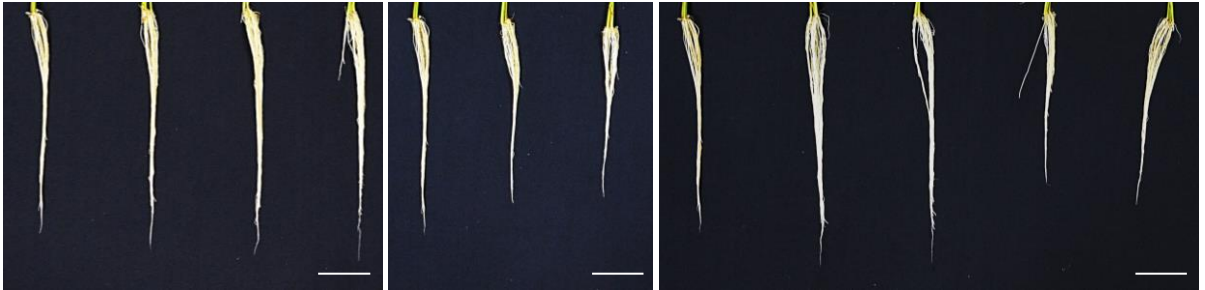
Supplementary Fig. S14 *OsJAZ11*-GUS transgenics accumulated higher Pi than *OsJAZ11ΔC*-GUS transgenics. Seven-day-old rice seedlings of *OsJAZ11*-GUS (L12, L14) and *OsJAZ11ΔC*-GUS (L1, L2) lines grown under +P conditions were transferred to -P conditions. Soluble Pi was measured at indicated time-points. Means were calculated from three biological replicates. Error bars indicate standard error ($n=3$).



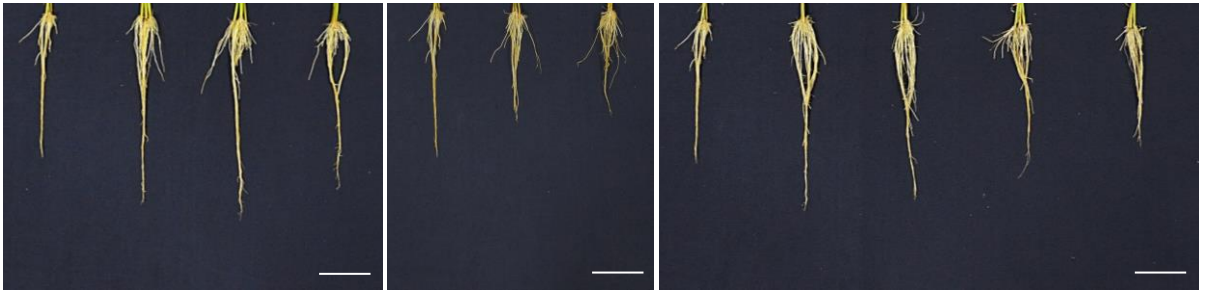
Supplementary Fig. S15 *OsJAZ11-GUS* lines showed higher phosphorous uptake under Pi deficiency. **a-b** P content of roots of thirty-day-old plants of WT, *OsJAZ11-GUS* (L12, L14) and *OsJAZ11ΔC-GUS* (L1, L2) lines under +P and -P conditions. **c-d** P content of shoots of thirty-day-old plants of WT, *OsJAZ11-GUS* (L12, L14) and *OsJAZ11ΔC-GUS* (L1, L2) lines under +P and -P conditions. Each bar displays means of ten biological replicates with standard error. Significant differences between WT and transgenics were determined by Student's *t*-test. Asterisks; *, ** and *** indicate *P* values, ≤ 0.05 , 0.01 and 0.001, respectively ($n=10$).

a

Control

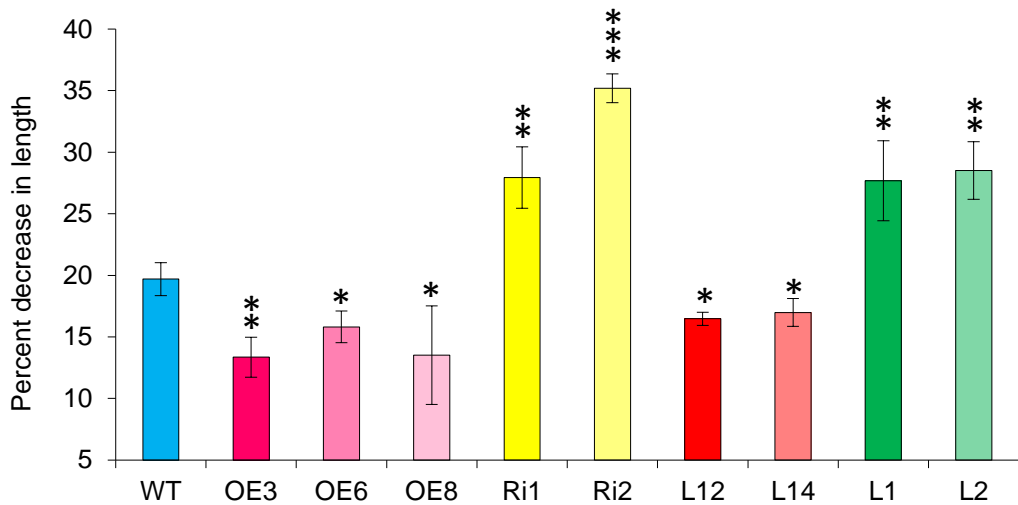


+ MeJA

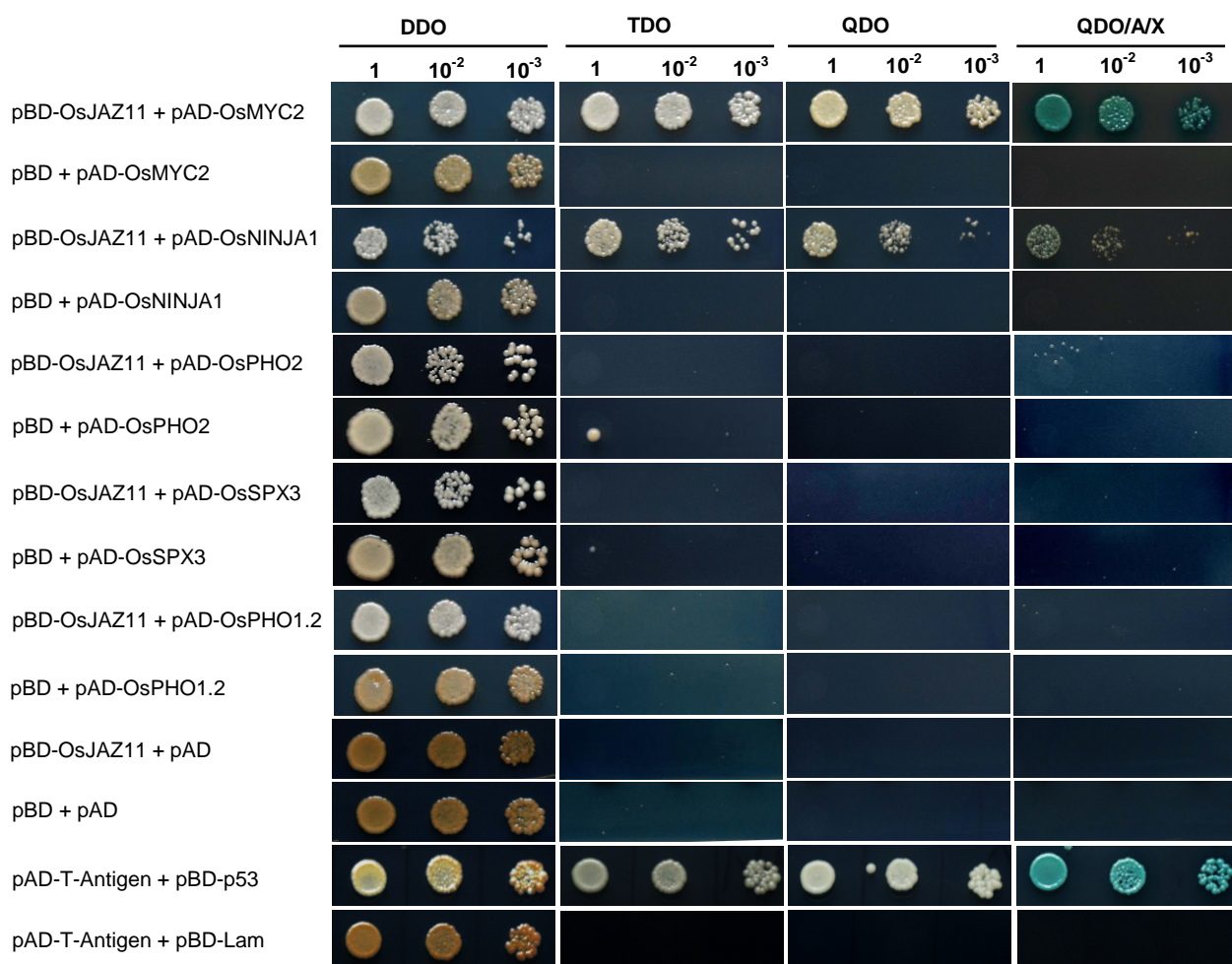


WT OE3 OE6 OE8 WT Ri1 Ri2 WT L12 L14 L1 L2
pZmUbi1:OsJAZ11 *OsJAZ11 RNAi* *OsJAZ11-GUS OsJAZ11ΔC-GUS*

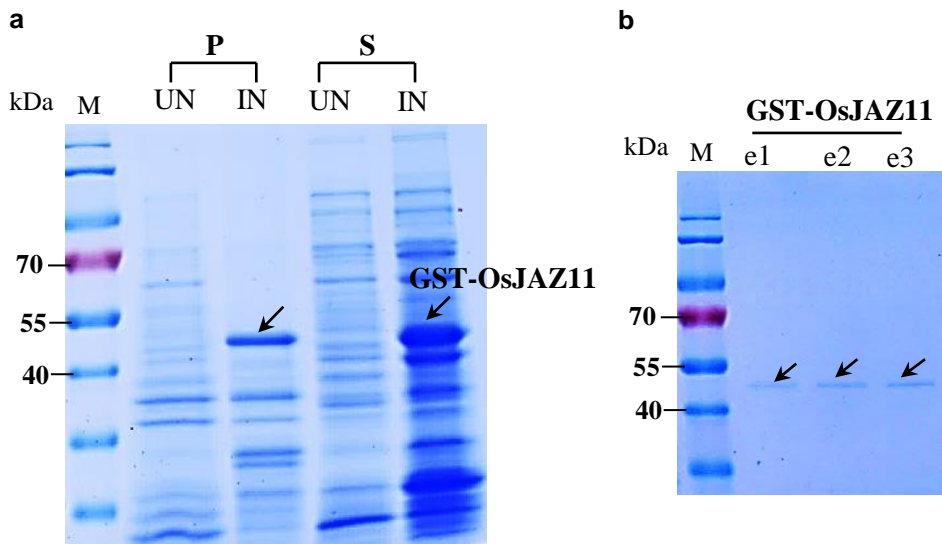
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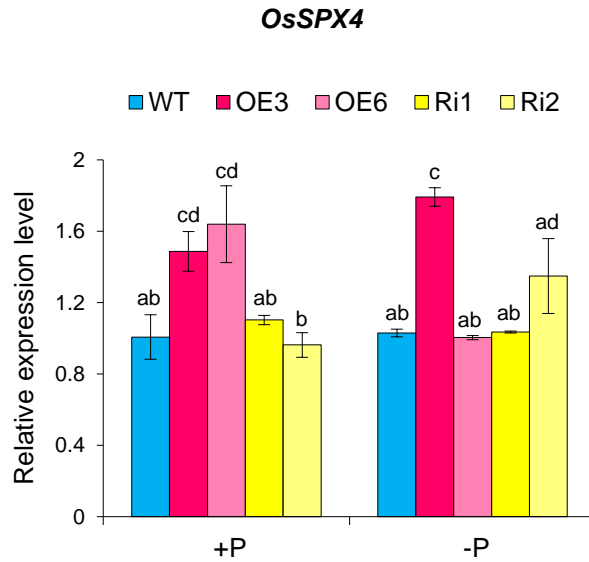
Supplementary Fig. S16 JA sensitivity assay of *OsJAZ11* transgenics. **a** Root images of WT and *OsJAZ11* transgenics subjected to DMSO (control) and MeJA (10 μ M) treatment. Seven-day-old rice seedlings were treated with 10 μ M MeJA or DMSO (control) for 14 days. For imaging three representative plants of each line were stacked together. Scale bar = 5 cm. **b** Percent reduction in root lengths of WT and *OsJAZ11* transgenics after MeJA treatment. Reduction in root length under MeJA treatment was compared to control conditions ($n=10$). Significant differences between WT and transgenics were determined by Student's *t*-test. Asterisks; *, ** and *** indicate *P* values, ≤ 0.05 , 0.01 and 0.001, respectively ($n=10$).



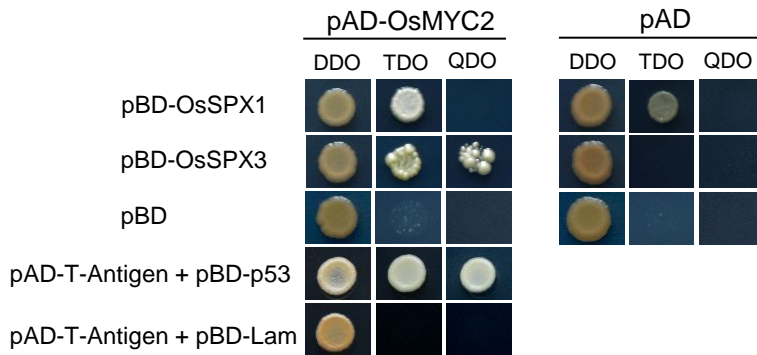
Supplementary Fig. S17 Interactions assays of OsJAZ11 with JA and Pi signaling proteins. Yeast two-hybrid interaction assays between bait plasmid, pBD-OsJAZ11 and prey plasmids, pAD-OsMYC2, pAD-OsNINJA1, pAD-OsPHO2, pAD-OsSPX3, pAD-OsPHO1.2. Serial dilutions of Y2H Gold strain co-transformed with AD (prey) and BD (bait) clones were spotted on DDO (SD-Leu/-Trp), TDO (SD- Leu/-Trp/-His), QDO (SD- Leu/-Trp/-His/-Ade) and QDO/A/X (QDO + Aureobasidin A + X- α -Gal). pBD and pAD indicates empty BD (pGBKT7) and AD (pGADT7) vectors, respectively. Interaction between pAD-T-Antigen and pBD-p53 was used as positive control whereas interaction between pAD-T-Antigen and pBD-Lam was used as a negative control.



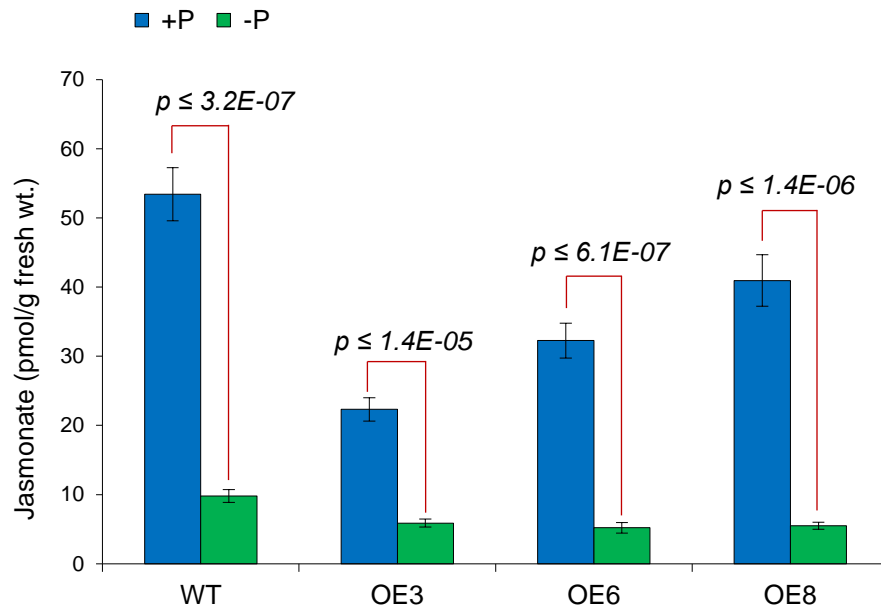
Supplementary Fig. S18 Induction and purification of OsJAZ11-GST. **a** Overexpression of OsJAZ11-GST in *E. coli* BL21(DE3) induced by IPTG. Induced (IN) and uninduced (UN) total protein fractions were resolved on 12% SDS-PAGE gel. Gel was stained with Coomassie blue. P and S implies proteins in pellet (insoluble) and supernatant (soluble) fractions. 20 μ g of total protein was loaded in each lane. **b** Coomassie-stained SDS-PAGE gel showing 49.9 kDa purified recombinant OsJAZ11-GST protein.



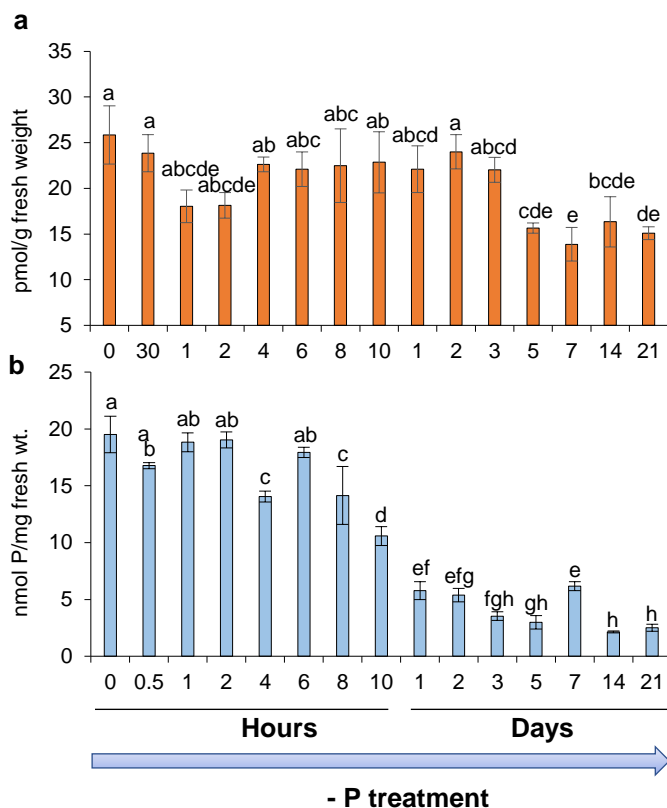
Supplementary Fig. S19 Expression of *OsSPX4* in WT and *OsJAZ11* transgenics. Relative expression levels of *OsSPX4* in roots of thirty-day-old WT and *OsJAZ11* transgenics under +P and -P conditions. Each bar is the mean of three independent replicates with standard error. Different letters on top of each bar denotes significant differences determined by one-way ANOVA followed by Duncan's multiple comparison test ($\alpha < 0.05$) ($n=3$).



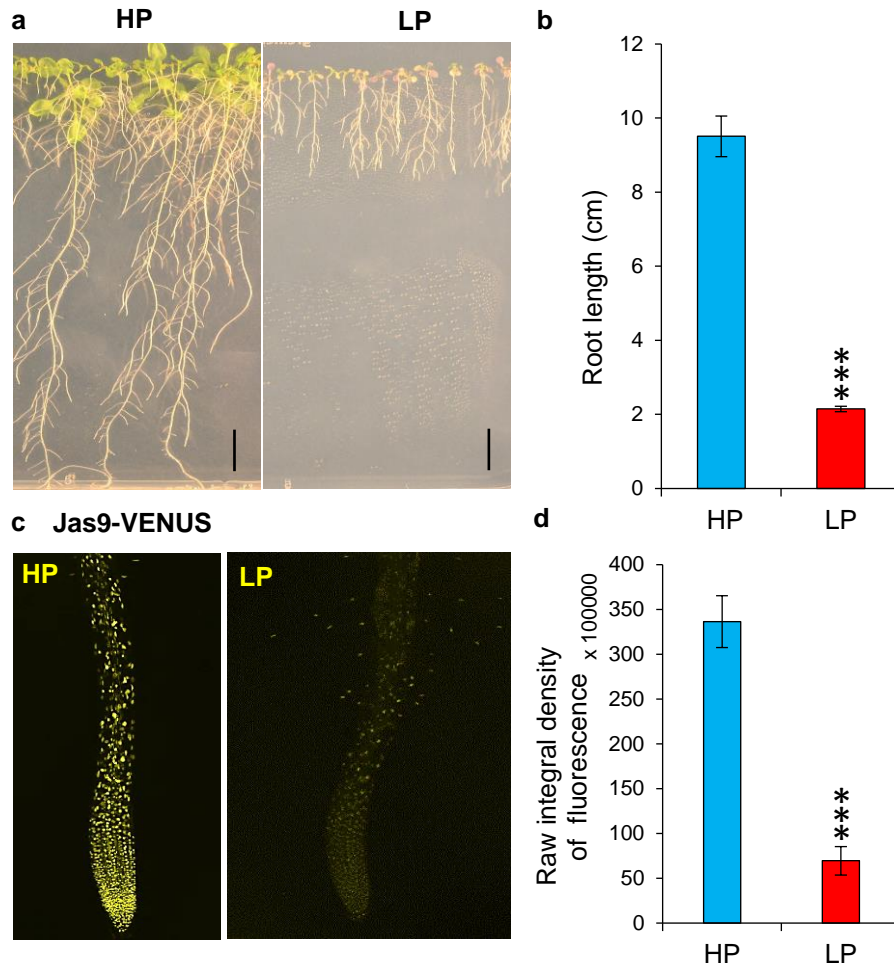
Supplementary Fig. S20 Interactions assays of OsMYC2 with SPX proteins. Yeast two-hybrid interaction assays between pAD-OsMYC2 and pBD-OsSPX (OsSPX1 and OsSPX3). Cells of yeast strain, Y2H Gold co-transformed with AD (prey) and BD (bait) clones were spotted on DDO (SD-Leu/-Trp), TDO (SD-Leu/-Trp/-His) and QDO (SD- Leu/-Trp/-His/-Ade). pBD and pAD indicates empty BD (pGBKT7) and AD (pGADT7) vectors, respectively. Interaction between pAD-T-Antigen and pBD-p53 was used as positive control whereas interaction between pAD-T-Antigen and pBD-Lam was used as a negative control.



Supplementary Fig. S21 Pi deficiency reduces JA levels in rice. JA content in roots of thirty-day-old WT and *OsJAZ11* OE transgenics grown under +P and -P conditions. Each bar represents mean of six independent replicates with standard error. Significant differences between WT and transgenics were evaluated by Student's *t*-test ($n=6$).



Supplementary Fig. S22 JA levels in rice under progressive Pi deficiency. JA levels (a) and soluble Pi content (b) in roots of PB1 seedlings. Seven-day-old rice seedlings grown under +P conditions were transferred to -P conditions. Soluble Pi and JA levels were measured at indicated time-points. For JA and Pi measurements means were calculated from six ($n=6$) and four ($n=4$) biological replicates, respectively. Error bars indicate standard error. Different letters on top of each bar denotes significant differences determined by one-way ANOVA followed by Duncan's multiple comparison test ($\alpha < 0.05$).



Supplementary Fig. S23 Pi deficiency leads to root length inhibition and increased JA levels in *Arabidopsis*. **a** Plant phenotype of ten-day-old *Arabidopsis* seedlings (Col-0) grown under Pi sufficient (HP) and deficient (LP) conditions. Scale bar = 1 cm. **b** Quantitation of primary root length of *Arabidopsis* seedling grown under Pi sufficient (HP) and deficient (LP) conditions. Each bar represents mean of ten replicates with standard error. **c** Representative SP5 confocal images showing Jas9-VENUS fluorescence in primary root tips of *Arabidopsis* under HP and LP conditions. **d** Quantitation of VENUS fluorescence under HP and LP conditions. Significant differences between HP and LP conditions were determined by Student's *t*-test. Asterisks; *** indicate *P* value ≤ 0.001 ($n=10$).

Table S1. List of primers used in the study

	F (5'-3')	R (5'-3')
<i>OsJAZ11_pANIC6B</i>	CACCGAAGGTTTCGTCCTCGTT	CCATAGGTCCGACAGGCATCAA
<i>OsJAZ11_pANIC8B</i>	CACCAAGAAAGACGATGGC	TATAAGATCAGCATGCATGAAG
<i>OsJAZ11_pMDC163</i>	CACCATCAATGCACCTAGGTGC	GTTGTAGCTCTAGCAAAATCAGCTAG
<i>OsJAZ11_pCAMBIA1301</i>	TGCTTAAGATCTAATGGCCGTA GTAGCGA	TGCTTAAGATCTACCAGGCTG AGAGTGGGGT
<i>OsJAZ11ΔC_pCAMBIA1301</i>	TGCTTAAGATCTAATGGCCGTA GTAGCGA	TGCTTAAGATCTACCATGTCT GGTAGGCAAGGC
<i>OsJAZ11_pGEX4T1</i>	TGCTTAGGATCCATGGCCGGTAG TAGCGAGC	GAGTTCGAATTCTCACAGGCT GAGAGTGGGGT
<i>OsSPX1_pET28a</i>	AATTGGATCCATGAAGTTTGGGA AGAGCCTGAGTAG	GATCGAATTCTCATTTGGCGG CCTGCTC
<i>OsJAZ11_qRT_pCAMBIA</i>	ACGCTGAAAGACACGCAAGA	TGGTCAGCTGCGCCTTCT
<i>OsJAZ11_qRT_pANIC6B/ pANIC8B</i>	AATTCTTTCATGCATGCTGATCT TA	AGGTCCGACAGGCATCAATC
<i>OsSPX1_qRT</i>	TATATGAAGGGCACGGTCGC	ACAGTAGAGCTCCGCTTCG
<i>OsSPX2_qRT</i>	CACCACCGACCTCCTCTACAA	GTTCGTTTCGTCCGCATGAG
<i>OsSPX3_qRT</i>	GACGTACGGGCGGTTCTCG	GGATCGGATCGGATGGACTG
<i>OsSPX4_qRT</i>	GCCAGCCACGTGATGAATG	AGGGCCTCGGAGGATTAAC
<i>OsSPX5_qRT</i>	ATGCCACATATTGCGACGAG	TCGATTTCAATTTGCTGCCAA AAG
<i>OsPT1_qRT</i>	CCTCGACATCGCCTTCTACAG	CACCCGACCTTGCTGAAGAT
<i>OsPT4_qRT</i>	TCGGCGTGCGCAACT	GGCACCAGGAACGTGAAGAA
<i>OsPT8_qRT</i>	GTCCCGGGCTACTGGTTCA	TGAAAAACCCTAGCAGCTGG AT
<i>OsPT9_qRT</i>	CCGGCTACATCGTGCTCTACT	AGGATGAAGGTGGTGGTGTT G
<i>OsIPS1_qRT</i>	AAGGGCAGGGCACACTCCACAT TATC	ATTAGAGCAAGGACCGAAAC ACAAAC
<i>OsGDPD5_qRT</i>	TCCCCAACCGATCTTGTC	GAAAGTGTATGGATGCACCT GAAG
<i>OsMGDG3_qRT</i>	AGTCGGGAATGTGCCTTACG	CTCGGGTCCTTGGAGAACAC
<i>OsPAP3b_qRT</i>	GCTCGATTGCGCTTCTACGA	TTTGCTGAAGCTCCAGTGGT
<i>OsPAP10a_qRT</i>	CGCCATCCTGGACATCAAG	TTGCGGTGCCACGTGTAG
<i>OsJAZ4_qRT</i>	GAGTGCCAATGACAACAAGTCA TC	TGATTCGTCGCGGTTGCT
<i>OsJAZ8_qRT</i>	GAAGGCTCAACAGCTGACCAT	TTGGTGGACGGGAAGTTCTC
<i>OsJAZ9_qRT</i>	CGGTCGAGTTGGAAGATGGTT	GGTCAGGCTCGGCGAAAT
<i>OSAOS1_qRT</i>	CGCCTCGGCATTGCA	AGCGTCGGGAACAGGATCTT
<i>OsAOS2_qRT</i>	TGCCATGATCATCGAGGAT	ACGCGTACAGCGCCTTGTA
<i>OsOPR1_qRT</i>	TCGCTGCTGGCGGGTAT	TAGCCATCAGCCACCACCTT
<i>OsMYC2_qRT</i>	AAATCCATTCCACCCCATACC	CCGTCCAAAGGTTTCATCGAT
<i>OsUBQ5_qRT</i>	ACCACTTCGACCGCCACTACT	ACGCCTAAGCCTGCTGGTT
<i>OsJAZ11_P1BS EMSA</i>	GAGTCACATCGGATATACATAC ACATATTT	AAATATGTGTATGTATATCCG ATGTGACTC
<i>OsJAZ11_mP1BS EMSA</i>	GAGTCACATCTGCGCGAAATAC ACATATTT	AAATATGTGTATTTTCGCGCAG ATGTGACTC
<i>OsSPX2_P1BS EMSA</i>	TATCCCGTACGAATATTCCTC TTCTCC	GGAGGAAGAGGAATATTCGT GACGGGGATA
<i>OsJAZ11_BD</i>	CACCATGGCCGGTAGTAGC	CAGGCTGAGAGTGGGGTTC

<i>OsSPX1_AD/BD</i>	CACCATGAAGTTTGGGAAGAGC CTG	TTTGGCGGCCTGCTCAATCAC
<i>OsSPX3_AD/BD</i>	CACCATGAAGTTTGGGAAGAG	GGCATAAAAAAACTGTAAAC TTGGA
<i>OsMYC2_AD</i>	CACCATGTGGGTTTTGTTATCTC CTCTCCTCACCAC	CCGGGCGGCAGGTGCCAG
<i>OsPHO1;2_AD/BD</i>	CACCATGGTGAAGTTCTCGAGG	ATCAGTTTCAAGTTCACGGA ATGGTAAT
<i>OsPHO2_AD</i>	CACCATGGATCTATATGCAATTG ACTCGGACACT	CGGGCTGCAGGGGATGCC
<i>OsNINJA1_AD</i>	AGAATTCCATATGGACGATGAG AATGGCCT	TGCTTAGAATTCTTAGTTTTG GGCTGAGGCTG

Table S2. List of interacting proteins identified in *OsJAZ11* OE lines using MS using Exactive™ Plus Orbitrap Mass Spectrometer

Accession	Description	Sum PEP Score	Coverage [%]	No. of Peptides	No. of AAs	MW [kDa]	pI	Biological Process	Molecular Function	Gene Symbol	KEGG Pathways
Q8GRS2	Protein TIFY 11c OS= <i>Oryza sativa</i> subsp. japonica OX=39947 GN=TIFY11C PE=1 SV=1	15.393	31	5	209	22	5.74	metabolic process; regulation of biological process; response to stimulus	protein binding	Os03g0180900; LOC4331833	Plant hormone signal transduction
Q0J8A4	Glyceraldehyde-3-phosphate dehydrogenase 1, cytosolic OS= <i>Oryza sativa</i> subsp. japonica OX=39947 GN=GAPC1 PE=1 SV=1	15.044	27	7	337	36.4	7.11	metabolic process	catalytic activity; nucleotide binding	Os08g0126300; LOC4344564	Biosynthesis of secondary metabolites; Metabolic pathways; Biosynthesis of amino acids; Carbon fixation in photosynthetic organisms; Glycolysis / Gluconeogenesis; Carbon metabolism
Q7FAH2	Glyceraldehyde-3-phosphate dehydrogenase 2, cytosolic OS= <i>Oryza sativa</i> subsp. japonica OX=39947 GN=GAPC2 PE=1 SV=1	10.571	17	5	337	36.8	6.81	metabolic process	catalytic activity; nucleotide binding	Os04g0486600; LOC4336216	Biosynthesis of secondary metabolites; Metabolic pathways; Biosynthesis of amino acids; Carbon fixation in photosynthetic organisms; Glycolysis / Gluconeogenesis; Carbon metabolism
Q2R8Z5	Alcohol dehydrogenase 1 OS= <i>Oryza sativa</i> subsp. japonica OX=39947 GN=ADH1 PE=2 SV=2	6.257	6	1	379	41	6.65	metabolic process	catalytic activity; metal ion binding	Os11g0210300; LOC4350053	Biosynthesis of secondary metabolites; Fatty acid degradation; Metabolic pathways; Glycolysis / Gluconeogenesis; Tyrosine metabolism; alpha-Linolenic acid metabolism
P93438	S-adenosylmethionine synthase 2 OS= <i>Oryza sativa</i> subsp. japonica OX=39947 GN=SAM2 PE=2 SV=1	5.578	15	3	394	42.9	6.05	metabolic process	catalytic activity; metal ion binding; nucleotide binding	OSJNBa0011P19.5; Os01g0323600; LOC4326996	Cysteine and methionine metabolism; Biosynthesis of secondary metabolites; Metabolic pathways; Biosynthesis of amino acids
Q2QS14	UDP-glucose 6-dehydrogenase 4 OS= <i>Oryza sativa</i> subsp. japonica OX=39947 GN=UGD4 PE=2 SV=1	4.755	9	3	480	52.8	6.13	metabolic process	catalytic activity; nucleotide binding	Os12g0443500; LOC4352146	Pentose and glucuronate interconversions; Metabolic pathways; Ascorbate and aldarate metabolism; Amino sugar and nucleotide sugar metabolism
Q9XGP7	Tricin synthase 1 OS= <i>Oryza sativa</i> subsp. japonica OX=39947 GN=ROMT-15 PE=1 SV=1	3.858	17	2	252	27.8	5.31	metabolic process	catalytic activity; metal ion binding	Os08g0498100; LOC4345934	
Q2QS13	UDP-glucose 6-dehydrogenase 5 OS= <i>Oryza sativa</i> subsp. japonica OX=39947 GN=UGD5 PE=2 SV=1	3.607	9	3	480	52.9	6.13	metabolic process	catalytic activity; nucleotide binding	Os12g0443600; LOC4352147	Pentose and glucuronate interconversions; Metabolic pathways; Ascorbate and

											aldarate metabolism; Amino sugar and nucleotide sugar metabolism
P31924	Sucrose synthase 1 OS=Oryza sativa subsp. japonica OX=39947 GN=SUS1 PE=1 SV=1	3.247	2	1	816	92.8	6.38	metabolic process; response to stimulus	catalytic activity	Os03g0401300; LOC4333062	Starch and sucrose metabolism; Metabolic pathways
Q9FR35	Peroxiredoxin-2C OS=Oryza sativa subsp. japonica OX=39947 GN=PRXIIC PE=1 SV=1	3.075	14	1	162	17.3	5.88	cellular homeostasis; metabolic process; regulation of biological process	antioxidant activity; catalytic activity	Os01g0675100; LOC4325511	
Q0J7U6	Protein TOPLESS-RELATED PROTEIN 2 OS=Oryza sativa subsp. japonica OX=39947 GN=TPR2 PE=1 SV=1	2.898	3	3	1133	124.7	7.28	metabolic process; regulation of biological process	protein binding	Os08g0162100; LOC4344728	
P51823	ADP-ribosylation factor 2 OS=Oryza sativa subsp. japonica OX=39947 GN=ARF PE=2 SV=2	2.698	25	3	181	20.7	6.95	metabolic process; regulation of biological process; response to stimulus; transport	catalytic activity; nucleotide binding; protein binding; signal transducer activity; transporter activity	Os05g0489600; LOC4339157	Endocytosis
A3C6D7	Actin-2 OS=Oryza sativa subsp. japonica OX=39947 GN=ACT2 PE=2 SV=1	2.319	8	2	377	41.7	5.49		nucleotide binding	Os10g0510000; LOC4349087	
P45960	Tubulin beta-4 chain OS=Oryza sativa subsp. japonica OX=39947 GN=TUBB4 PE=2 SV=1	1.976	5	2	447	50.3	4.86	cell organization and biogenesis; cellular component movement	catalytic activity; nucleotide binding; structural molecule activity	Os01g0805900; LOC4327550	
Q53M52	Tubulin alpha-2 chain OS=Oryza sativa subsp. japonica OX=39947 GN=TUBA PE=2 SV=1	1.432	4	1	451	49.7	4.96	cell organization and biogenesis	catalytic activity; nucleotide binding; structural molecule activity	Os11g0247300; LOC4350197	Phagosome
Q2QLY4	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 2 OS=Oryza sativa subsp. japonica OX=39947 GN=Os12g0624000 PE=2 SV=1	1.141	2	1	766	84.6	6.3	metabolic process	catalytic activity; metal ion binding	Os12g0624000; LOC4352833	Selenocompound metabolism; Cysteine and methionine metabolism; Biosynthesis of secondary metabolites; Metabolic pathways; Biosynthesis of amino acids
Q0J4P2	Heat shock protein 81-1 OS=Oryza sativa subsp. japonica OX=39947 GN=HSP81-1 PE=3 SV=2	1.019	4	1	699	80.1	5.07	metabolic process; response to stimulus	nucleotide binding; protein binding	OJ1118_A06.20; Os08g0500700; LOC4345951	Plant-pathogen interaction; Protein processing in endoplasmic reticulum
P93431	Ribulose biphosphate carboxylase/oxygenase activase, chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=RCA PE=1 SV=2	0.969	4	1	466	51.4	5.62	regulation of biological process	enzyme regulator activity; nucleotide binding	Os11g0707000; LOC4351224	

O64937	Elongation factor 1-alpha OS=Oryza sativa subsp. japonica OX=39947 GN=REFA1 PE=2 SV=2	0.823	2	1	447	49.3	9.06	metabolic process	catalytic activity; nucleotide binding; RNA binding	Os03g0177900; LOC4331812; Os03g0178000; LOC4331813; Os03g0177400; LOC4331810; Os03g0177500; LOC4331811	RNA transport
P14655	Glutamine synthetase, chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=GLN2 PE=1 SV=1	0.799	4	1	428	46.6	6.34	metabolic process; response to stimulus	catalytic activity; nucleotide binding	Os04g0659100; LOC4337272	Arginine biosynthesis; Nitrogen metabolism; Metabolic pathways; Biosynthesis of amino acids; Alanine, aspartate and glutamate metabolism; Glyoxylate and dicarboxylate metabolism
Q10L71	Villin-2 OS=Oryza sativa subsp. japonica OX=39947 GN=VLN2 PE=2 SV=1	0.699	2	1	966	106.1	5.82	cell organization and biogenesis; regulation of biological process; response to stimulus	protein binding	Os03g0356700; LOC4332869	
P42211	Aspartic proteinase OS=Oryza sativa subsp. japonica OX=39947 GN=RAP PE=2 SV=2	0.631	5	1	496	54.1	6.15	metabolic process	catalytic activity	Os05g0137400; LOC4337744	
P51431	Ubiquitin-40S ribosomal protein S27a-2 OS=Oryza sativa subsp. japonica OX=39947 GN=RPS27AB PE=2 SV=3	0.612	10	1	155	17.7	9.8	metabolic process	metal ion binding; protein binding; structural molecule activity	Os05g0160200; LOC4337883	Ribosome
Q01859	ATP synthase subunit beta, mitochondrial OS=Oryza sativa subsp. japonica OX=39947 GN=ATPB PE=1 SV=2	0.585	7	1	552	58.9	6.37	metabolic process; transport	catalytic activity; nucleotide binding; transporter activity	Os05g0553000; LOC4339546	Oxidative phosphorylation; Metabolic pathways
Q9MAX5	Coatomer subunit zeta-1 OS=Oryza sativa subsp. japonica OX=39947 GN=COPZ1 PE=2 SV=1	0.571	11	1	177	19.4	4.73	transport		Os05g0461000; LOC4339020	
Q5VRW2	Transcription factor NIGTH1 OS=Oryza sativa subsp. japonica OX=39947 GN=NHO1 PE=1 SV=2	0.528	5	1	507	53	6.02	cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus	DNA binding; protein binding	Os01g0176700; LOC4326224	
Q10HL3	Endoribonuclease Dicer homolog 2a OS=Oryza sativa subsp. japonica OX=39947 GN=DCL2A PE=2 SV=1	0.5	1	1	1410	158.4	6.86	metabolic process; regulation of biological process; response to stimulus	catalytic activity; DNA binding; metal ion binding; nucleotide binding; protein binding; RNA binding	Os03g0583900; LOC4333337	
O82451	Probable glutathione S-transferase GSTF2 OS=Oryza sativa subsp.	0.5	9	1	215	24	6.13	metabolic process	catalytic activity; protein binding	Os01g0764000; LOC4326887	Glutathione metabolism

	japonica OX=39947 GN=GSTF2 PE=1 SV=3										
Q9AUV6	UDP-glucose 6-dehydrogenase 3 OS=Oryza sativa subsp. japonica OX=39947 GN=UGD3 PE=2 SV=1	3.607	9	3	480	52.9	6.13	metabolic process	catalytic activity; nucleotide binding	Os03g0757900; LOC4334169	Pentose and glucuronate interconversions; Metabolic pathways; Ascorbate and aldarate metabolism; Amino sugar and nucleotide sugar metabolism
Q10NY2	Protein TPR3 OS=Oryza sativa subsp. japonica OX=39947 GN=TPR3 PE=1 SV=1	2.898	3	3	1133	125.1	7.14	regulation of biological process	protein binding	Os03g0254700; LOC4332285	
Q06396	ADP-ribosylation factor 1 OS=Oryza sativa subsp. japonica OX=39947 GN=Os01g0813400 PE=2 SV=3	2.698	25	3	181	20.7	6.95	regulation of biological process; response to stimulus; transport	catalytic activity; nucleotide binding; protein binding; signal transducer activity; transporter activity	Os01g0813400; LOC4327591	Endocytosis
Q76FS2	Tubulin beta-8 chain OS=Oryza sativa subsp. japonica OX=39947 GN=TUBB8 PE=2 SV=1	1.976	5	2	446	49.6	4.89	cell organization and biogenesis	catalytic activity; nucleotide binding; structural molecule activity	Os03g0661300; LOC4333632	Phagosome
Q43594	Tubulin beta-1 chain OS=Oryza sativa subsp. japonica OX=39947 GN=TUBB1 PE=2 SV=2	1.976	5	2	447	50.3	4.83	cell organization and biogenesis	catalytic activity; nucleotide binding; structural molecule activity	Os01g0282800; LOC4326917	Phagosome
P46265	Tubulin beta-5 chain OS=Oryza sativa subsp. japonica OX=39947 GN=TUBB5 PE=1 SV=1	1.976	5	2	447	50.1	4.83	cell organization and biogenesis; cellular component movement	catalytic activity; nucleotide binding; structural molecule activity	Os02g0167300; LOC4328420	Phagosome
Q76FS3	Tubulin beta-6 chain OS=Oryza sativa subsp. japonica OX=39947 GN=TUBB6 PE=2 SV=1	1.976	5	2	444	49.9	4.91	cell organization and biogenesis	catalytic activity; nucleotide binding; structural molecule activity	Os05g0413200; LOC4338790	Phagosome
P37832	Tubulin beta-7 chain OS=Oryza sativa subsp. japonica OX=39947 GN=TUBB7 PE=2 SV=2	1.976	5	2	444	49.8	4.87	cell organization and biogenesis; cellular component movement	catalytic activity; nucleotide binding; structural molecule activity	Os03g0780600; LOC4334309	Phagosome
Q40665	Tubulin beta-3 chain OS=Oryza sativa subsp. japonica OX=39947 GN=TUBB3 PE=2 SV=2	1.976	5	2	446	50.1	4.83	cell organization and biogenesis	catalytic activity; nucleotide binding; structural molecule activity	Os06g0671900; LOC4341810	Phagosome
Q8H7U1	Tubulin beta-2 chain OS=Oryza sativa subsp. japonica OX=39947 GN=TUBB2 PE=2 SV=1	1.976	5	2	447	50.2	4.83	cell organization and biogenesis	catalytic activity; nucleotide binding; structural molecule activity	Os03g0105600; LOC4331315	Phagosome
P28752	Tubulin alpha-1 chain OS=Oryza sativa subsp. japonica OX=39947 GN=TUBA1 PE=1 SV=1	1.432	4	1	450	49.6	5.06	cell organization and biogenesis	catalytic activity; nucleotide binding;	Os07g0574800; LOC4343694	Phagosome

									structural molecule activity		
Q2QLY5	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 1 OS=Oryza sativa subsp. japonica OX=39947 GN=Os12g0623900 PE=2 SV=1	1.141	2	1	766	84.5	6.3	metabolic process	catalytic activity; metal ion binding	Os12g0623900; LOC4352832	Selenocompound metabolism; Cysteine and methionine metabolism; Biosynthesis of secondary metabolites; Metabolic pathways; Biosynthesis of amino acids
POCH34	Ubiquitin-60S ribosomal protein L40-1 OS=Oryza sativa subsp. japonica OX=39947 GN=Ub-CEP52-1 PE=2 SV=1	0.612	12	1	129	14.8	9.92	metabolic process	protein binding; structural molecule activity	Os03g0234200; LOC4332169; Os09g0568400; LOC4347896	Ribosome
POC031	Ubiquitin-NEDD8-like protein RUB2 OS=Oryza sativa subsp. japonica OX=39947 GN=RUB2 PE=2 SV=2	0.612	10	1	153	17.1	6.06		protein binding	Os06g0650100; LOC4341684	
Q9ARZ9	Ubiquitin-40S ribosomal protein S27a-1 OS=Oryza sativa subsp. japonica OX=39947 GN=RPS27AA PE=2 SV=1	0.612	10	1	155	17.7	9.77	metabolic process	metal ion binding; protein binding; structural molecule activity	Os01g0328400; LOC4326977	Ribosome
POC030	Ubiquitin-NEDD8-like protein RUB1 OS=Oryza sativa subsp. japonica OX=39947 GN=RUB1 PE=2 SV=2	0.612	10	1	153	17.1	6.06		protein binding	Os09g0420800; LOC4347085	
Q58G87	Polyubiquitin 3 OS=Oryza sativa subsp. japonica OX=39947 GN=UBQ3 PE=2 SV=2	0.612	17	1	381	42.7	7.58	response to stimulus	protein binding	OSJNBa0089N06.4; Os04g0628100; LOC4337080	
Q69LX2	Endoribonuclease Dicer homolog 2b OS=Oryza sativa subsp. japonica OX=39947 GN=DCL2B PE=2 SV=2	0.5	1	1	1377	154.7	7.15	metabolic process; regulation of biological process; response to stimulus	catalytic activity; DNA binding; metal ion binding; nucleotide binding; protein binding; RNA binding	Os09g0315100; LOC4346696	
Q6K5G8	Glyceraldehyde-3-phosphate dehydrogenase 3, cytosolic OS=Oryza sativa subsp. japonica OX=39947 GN=GAPC3 PE=2 SV=1	6.657	9	3	337	36.5	7.88	metabolic process	catalytic activity; nucleotide binding	Os02g0601300; LOC4329892	Biosynthesis of secondary metabolites; Metabolic pathways; Biosynthesis of amino acids; Carbon fixation in photosynthetic organisms; Glycolysis / Gluconeogenesis; Carbon metabolism
Q0DKY4	S-adenosylmethionine synthase 1 OS=Oryza sativa subsp. japonica OX=39947 GN=SAM1 PE=2 SV=1	4.233	12	2	396	43.2	6.14	metabolic process	catalytic activity; metal ion binding; nucleotide binding	Os05g0135700; LOC4337733	Cysteine and methionine metabolism; Biosynthesis of secondary metabolites; Metabolic pathways; Biosynthesis of amino acids
Q9LGU6	S-adenosylmethionine synthase 3 OS=Oryza sativa subsp. japonica OX=39947 GN=METK3 PE=2 SV=1	4.233	12	2	396	43.3	5.41	metabolic process	catalytic activity; metal ion binding; nucleotide binding	Os01g0293000; LOC4325163	Cysteine and methionine metabolism; Biosynthesis of secondary metabolites;

											Metabolic pathways; Biosynthesis of amino acids
Q5NBT9	Protein TPR1 OS= <i>Oryza sativa</i> subsp. japonica OX=39947 GN=TPR1 PE=1 SV=1	2.042	2	2	1129	125	7.18	regulation of biological process	protein binding	Os01g0254100; LOC4327709	
Q75GS4	UDP-glucose 6-dehydrogenase 1 OS= <i>Oryza sativa</i> subsp. japonica OX=39947 GN=UGD1 PE=3 SV=1	1.223	3	1	481	52.3	6.04	metabolic process	catalytic activity; nucleotide binding	Os03g0425600; LOC4333156	Pentose and glucuronate interconversions; Metabolic pathways; Ascorbate and aldarate metabolism; Amino sugar and nucleotide sugar metabolism
B7F958	UDP-glucose 6-dehydrogenase 2 OS= <i>Oryza sativa</i> subsp. japonica OX=39947 GN=UGD2 PE=2 SV=1	1.223	3	1	482	53.1	7.18	metabolic process	catalytic activity; nucleotide binding	Os03g0604200; LOC4333410	Pentose and glucuronate interconversions; Metabolic pathways; Ascorbate and aldarate metabolism; Amino sugar and nucleotide sugar metabolism
P0C540	Actin-7 OS= <i>Oryza sativa</i> subsp. japonica OX=39947 GN=ACT7 PE=3 SV=1	0.84	4	1	376	41.6	5.39		nucleotide binding	Os01g0866100; LOC4325068	
Q10DV7	Actin-1 OS= <i>Oryza sativa</i> subsp. japonica OX=39947 GN=ACT1 PE=2 SV=1	0.84	4	1	377	41.8	5.49		nucleotide binding	Os03g0718100; LOC4333919	
Q10AZ4	Actin-3 OS= <i>Oryza sativa</i> subsp. japonica OX=39947 GN=ACT3 PE=2 SV=1	0.84	4	1	377	41.7	5.49		nucleotide binding	Os03g0836000; LOC4334702	