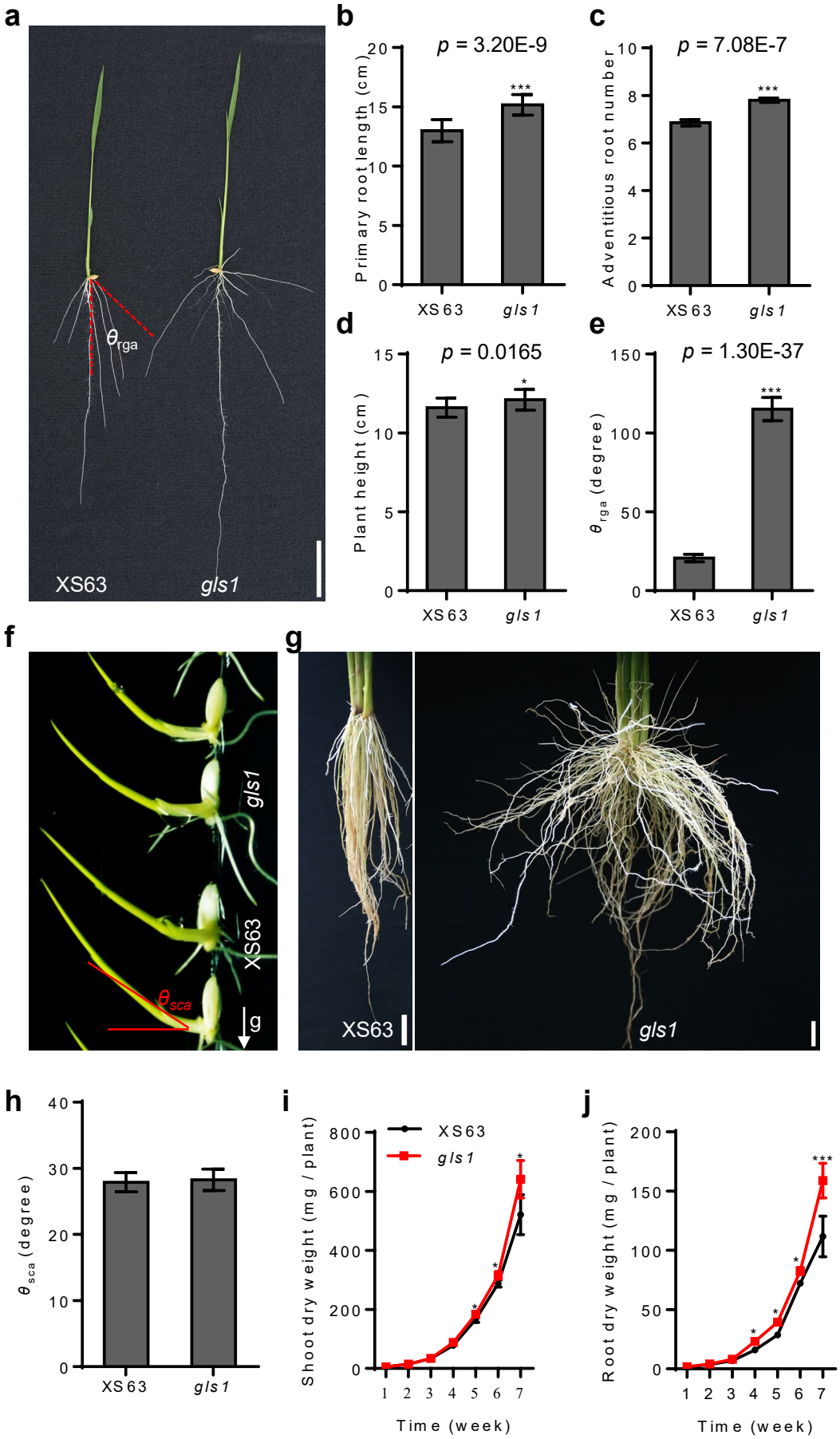
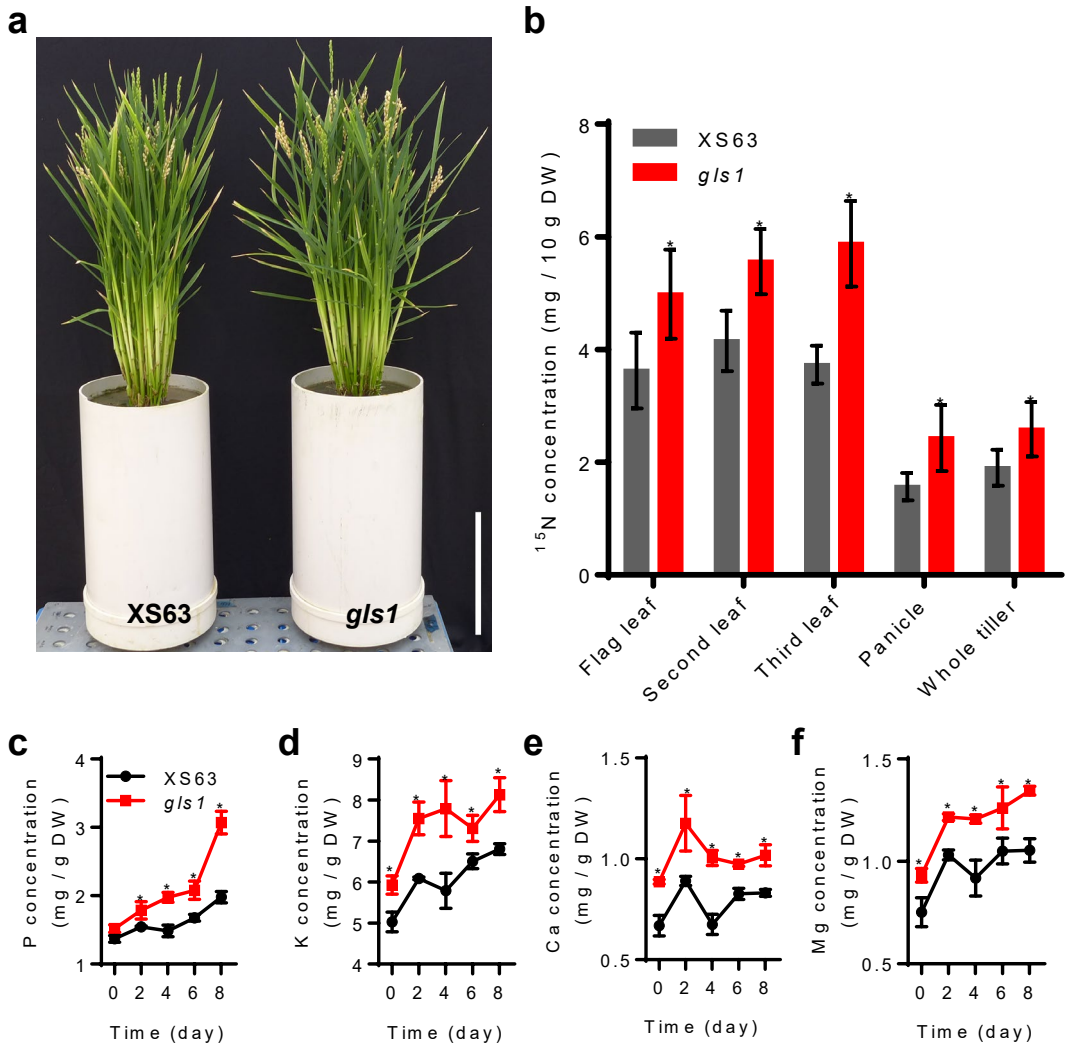
Supplementary figures and tables

Supplementary Fig. 1



Supplementary Fig. 1 Mutation of *OsGLS1* affects root growth and development.
a, Representative photograph of 7-day-old wild-type XS63 and *gls1* seedlings grown in solution culture. Scale bar, 3 cm. **b**–**e**, Primary root length (**b**), adventitious root number (**c**), plant height (**d**) and root growth angle (**e**) of the XS63 and *gls1* seedlings in **a**. **f**, Shoot gravitropic response of 3-day-old XS63 and *gls1* seedlings grown on an agar plate after reorientation by 90º for 6 h. The white arrow indicates the direction of gravity. **g**, Root phenotype of 4-week-old XS63 and *gls1* plants. Scale bars, 3 cm. **h**, Shoot curvature angle (θ_{sca}) of XS63 and *gls1* plants in **f**. **i**, **j**, Shoot dry weight (**i**) and root dry weight (**j**) of XS63 and *gls1* plants grown for different times in solution culture. Data represent means ± standard deviation (SD, $n = 20$ in **b**–**e**, 6 in **h**, 10 in **i** and **j**), *$p < 0.05$ and ***$p < 0.001$, Student's *t*-test.

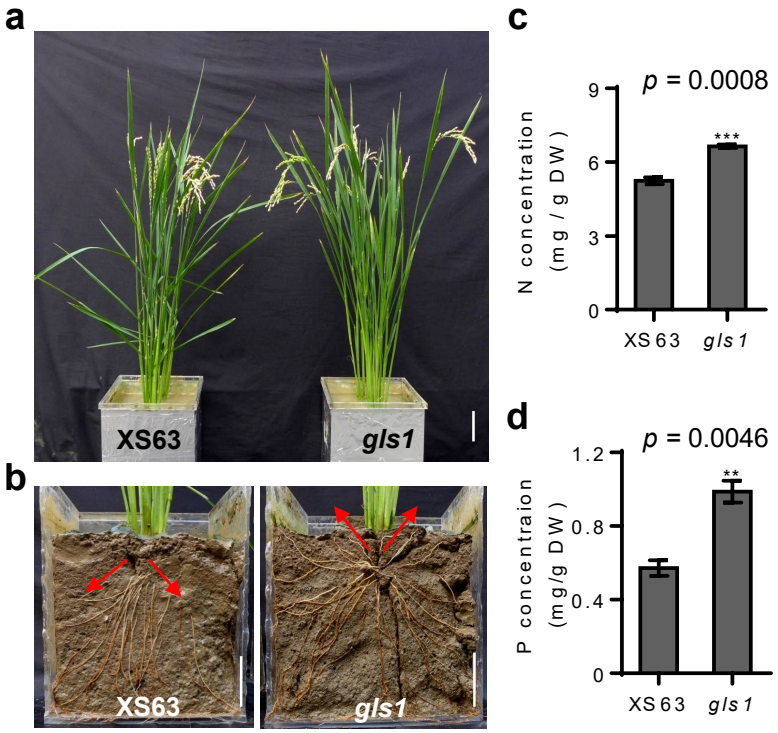
Supplementary Fig. 2



Supplementary Fig. 2 *gls1* shows higher nutrient uptake compared to XS63 in soil culture.

a, Representative photograph of XS63 and *gls1* plants at the maturation stage grown in a soil pot supplied with ^{15}N-labeled urea and other mixed fertilizers. Scale bar, 10 cm. **b**, ^{15}N concentration in different tissues of XS63 and *gls1* at 8 days after onset of fertilization with ^{15}N-labeled urea and other mixed fertilizers. **c**–**f**, Concentration of phosphorus (P; **c**), potassium (K; **d**), calcium (Ca; **e**) and magnesium (Mg; **f**) in rice panicles at different time points after fertilization. Data represent means ± SD (n = 6 in **b**; n = 3 in **c**–**f**). * $p < 0.05$, Student's t test.

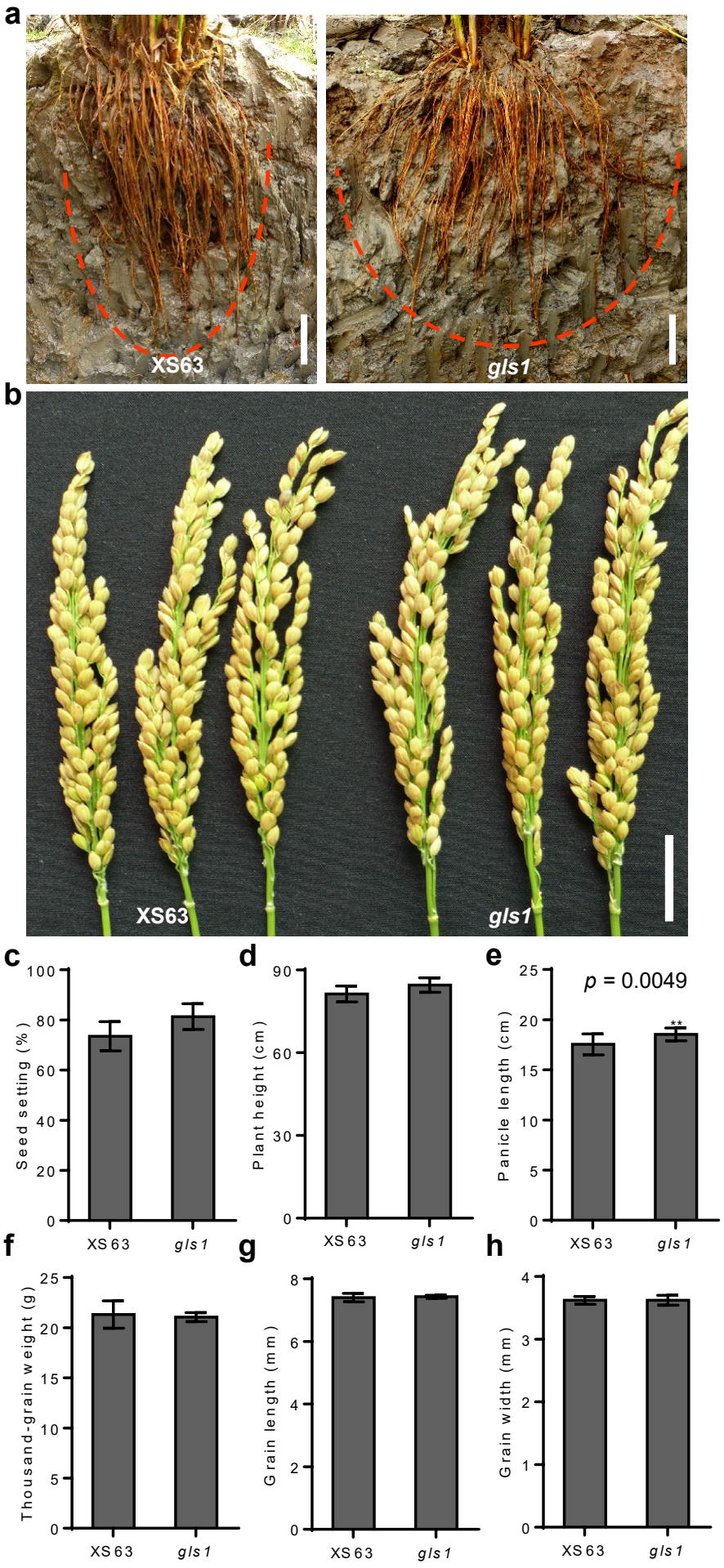
Supplementary Fig. 3



Supplementary Fig. 3 Root phenotype of XS63 and *gls1* in soil pot culture.

a, Representative photograph of XS63 and *gls1* plants at the maturation stage grown in a soil pot in the greenhouse. **b**, Root distribution of XS63 and *gls1* in **a**. The red arrows show the growth direction of roots with the largest growth angle. **c**, **d**, Total N concentration (**c**) and total P concentration in the shoots (**d**) of XS63 and *gls1* plants at the maturation stage. Scale bars, 5 cm. Data represent means ± SD ($n = 3$ in **c** and **d**), $^{**}p < 0.01$, $^{***}p < 0.001$, Student's *t*-test.

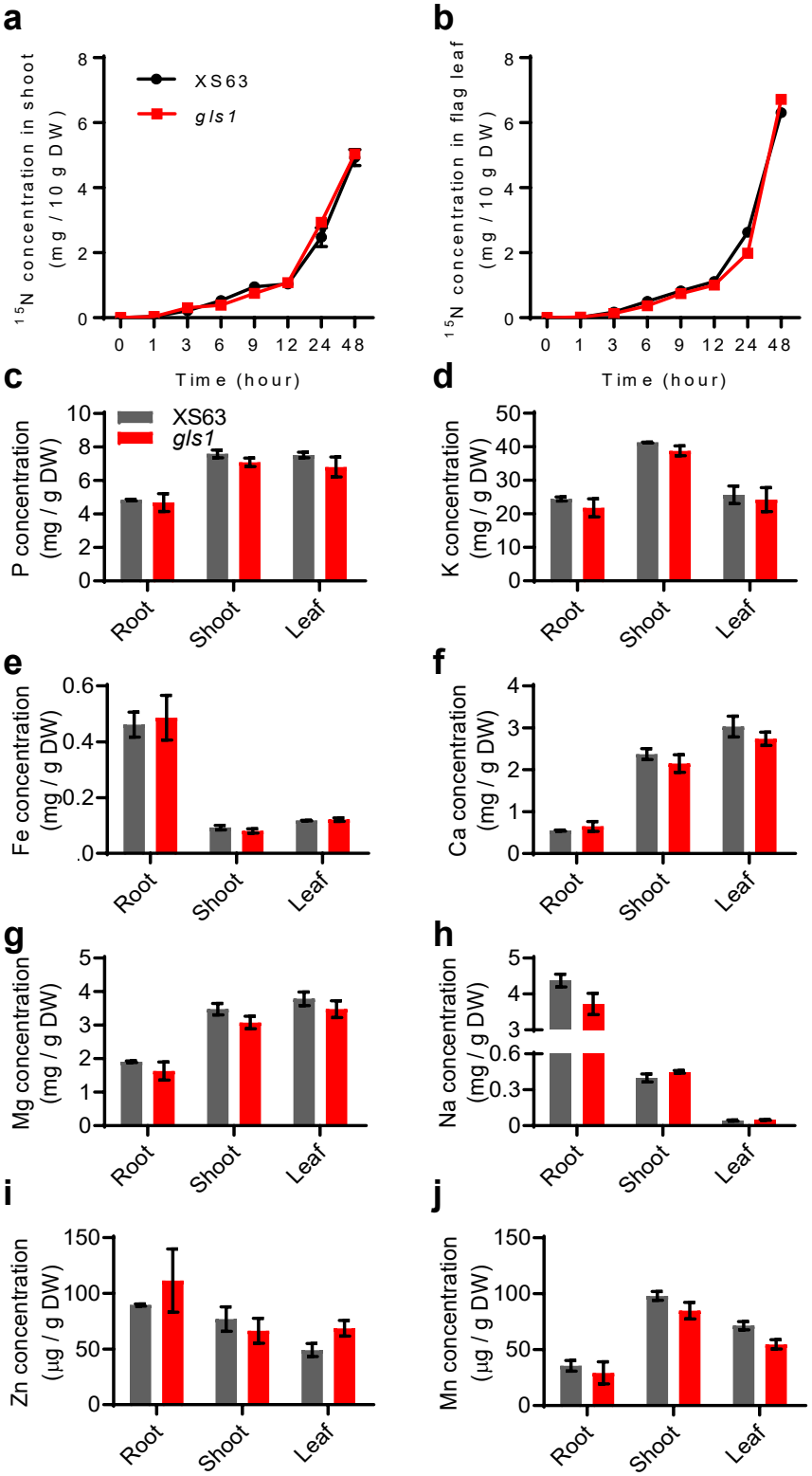
Supplementary Fig. 4



Supplementary Fig. 4 Root and panicle phenotypes of XS63 and *gls1* plants at the maturation stage grown in the paddy field.

a, Root distribution of XS63 (left) and *gls1* (right) plants. Scale bar, 5 cm. **b**, Panicle phenotypes of XS63 and *gls1*. Scale bar, 3 cm. **c**–**h**, Seed setting (**c**), plant height (**d**), panicle length (**e**), thousand-grain weight (**f**), grain length (**g**) and grain width (**h**) of XS63 and *gls1*. Data represent means ± SD (n = 10 in **c**, **d**, **f**, **g** and **h** and ≥ 13 in **e**). ** $p < 0.01$, Student's t-test.

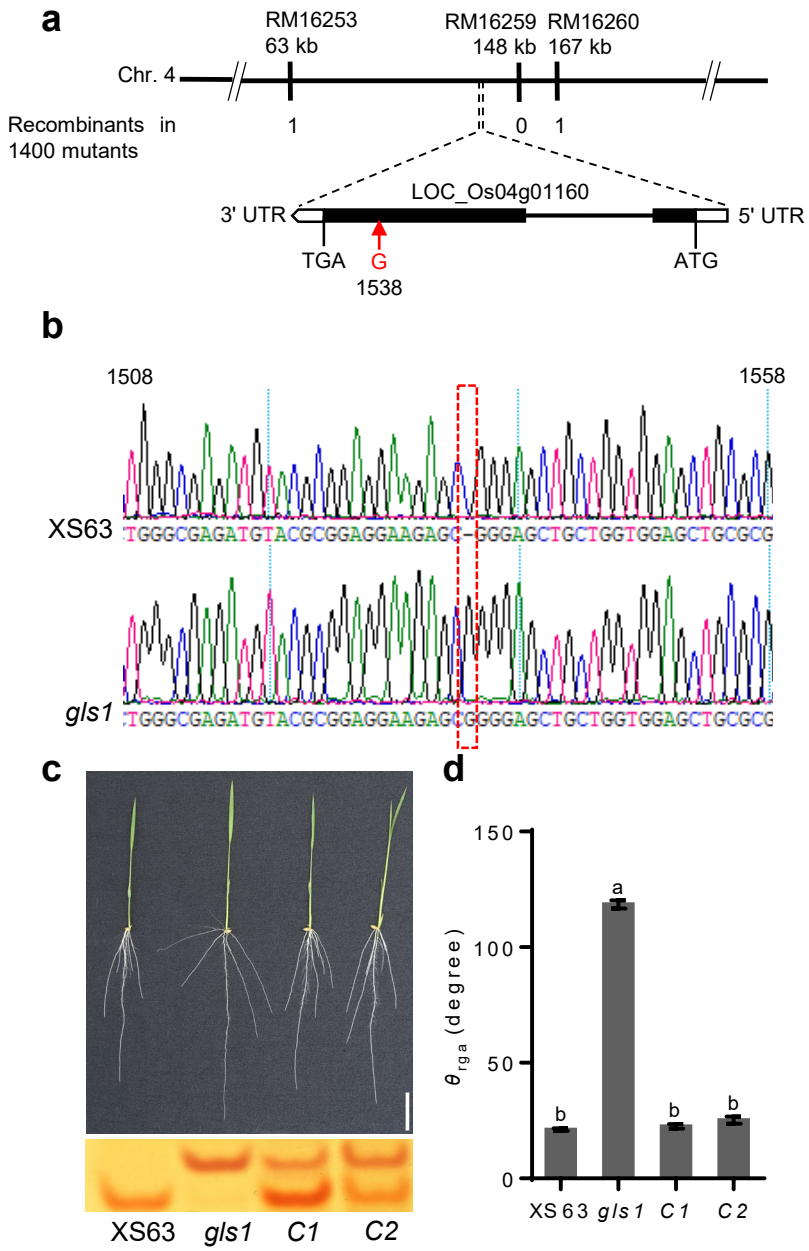
Supplementary Fig. 5



Supplementary Fig. 5 Mutation of *OsGLS1* in rice does not affect nutrient uptake or transport in solution culture.

a, **b**, ^{15}N concentration in the shoot (**a**) and flag leaf (**b**) of XS63 and *gls1* plants grown in solution culture containing ^{15}N-labeled urea. **c**–**j**, Total concentration of P (**c**), K (**d**), iron (Fe; **e**), Ca (**f**), Mg (**g**), sodium (Na; **h**), zinc (Zn; **i**) and manganese (Mn; **j**) in roots, shoots and leaves of XS63 and *gls1* seedlings at 48 h after beginning of fertilization. Data represent means ± SD (n = 3).

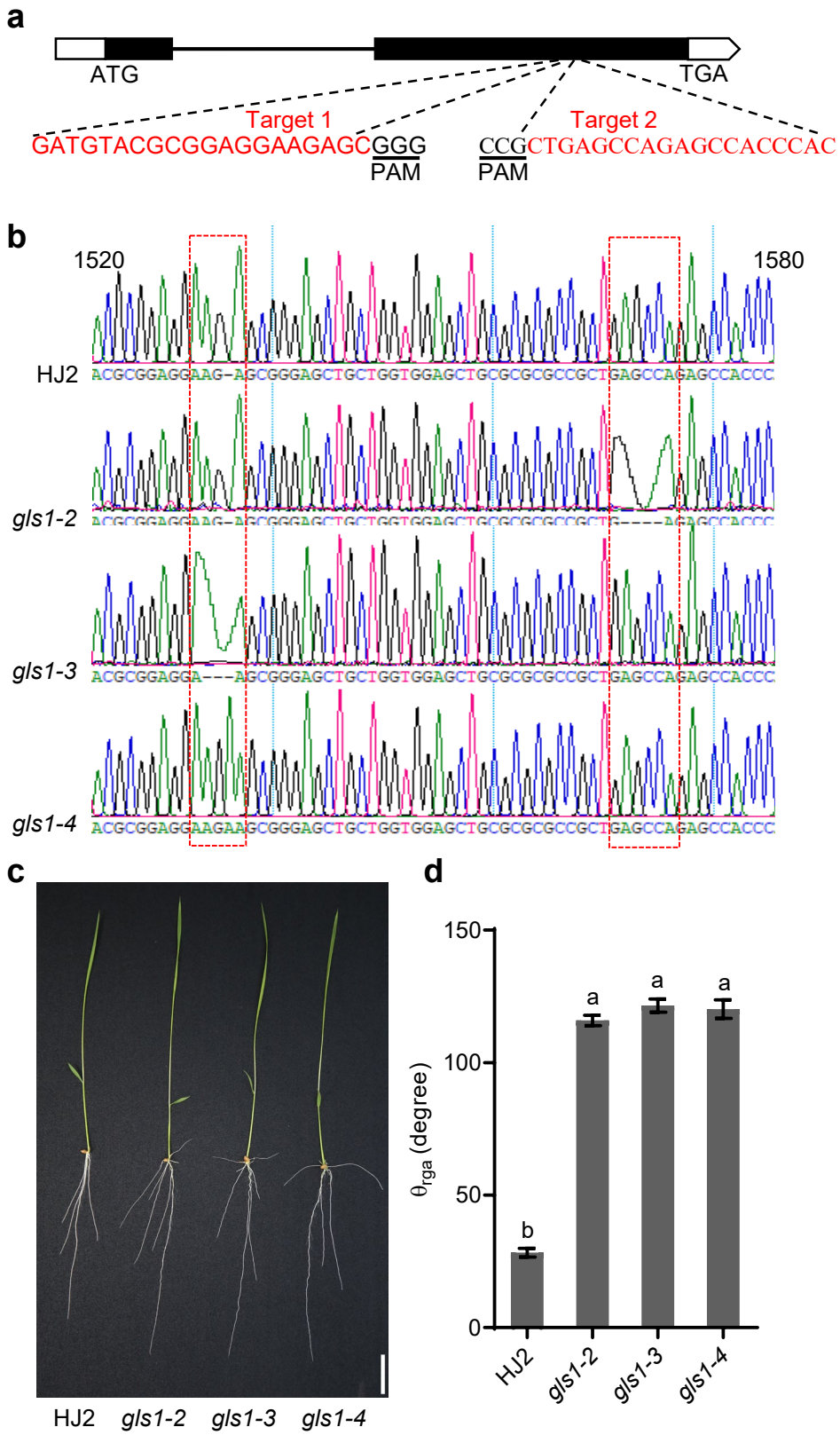
Supplementary Fig. 6



Supplementary Fig. 6 Map-based cloning of *OsGLS1* and complementation analysis.

a, Chromosome mapping of *gls1* and gene structure of *OsGLS1* (LOC_Os04g01160). Numbers below the molecular markers indicate the number of recombinants among 1400 F_2 plants with the *gls1* mutant phenotype. Black boxes represent exons, white boxes represent untranslated regions (UTRs), lines represent introns and red arrow shows the insertion site of nucleotide G in the *gls1* mutant. **b**, Sequencing results of *OsGLS1* in XS63 and *gls1*. The red dashed box indicates the mutation site. Numbers at the top refer to the nucleotide positions in the coding sequence of *OsGLS1*. **c**, Representative photograph of 7-day-old seedlings from XS63, *gls1* and two complementation lines harboring *GLS1pro:GLS1-GFP* (*C1* and *C2*). Seedlings were grown in solution culture. dCAPS markers (lower panel) were used to genotype *GLS1* in XS63, *gls1*, *C1* and *C2*. Scale bar, 3 cm. **d**, Root growth angle (θ_{rga}) of the corresponding seedlings in **c**. Data represent means ± SD (n = 10). Different letters indicate significant differences ($p < 0.01$; one-way ANOVA with Tukey's honestly significant difference test).

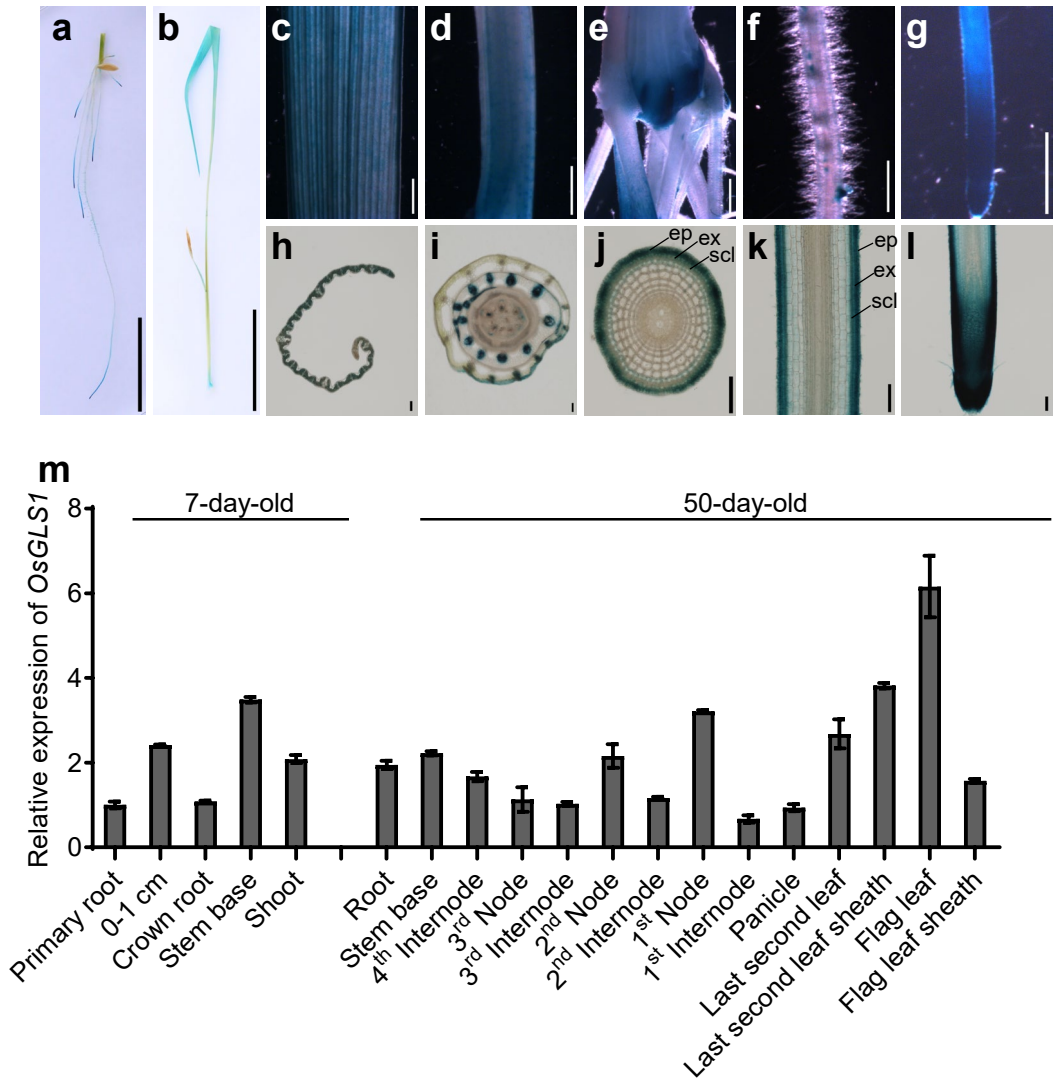
Supplementary Fig. 7



Supplementary Fig. 7 Generation of *gls1* mutants in the HJ2 background using CRISPR/Cas9 gene editing.

a, Diagram of the *OsGLS1* locus and the sgRNA target sites. The sgRNA target sequences are highlighted in red, and the protospacer-adjacent motif (PAM) sequences are in black. **b**, Sequencing results of *OsGLS1* in HJ2 and *gls1* mutant lines (*gls1-2*, *gls1-3* and *gls1-4*). Deletions or insertions in the mutants are indicated in the red boxes. Numbers at the top refer to the nucleotide positions in the coding sequence of *OsGLS1*. **c**, Representative photograph of 7-day-old seedlings from HJ2 and three mutant lines grown in solution culture. Scale bar, 3 cm. **d**, θ_{rga} of the corresponding seedlings. Data represent means ± SD (n = 10). Different letters indicate significant difference ($p < 0.01$; one-way ANOVA with Tukey's honestly significant difference test).

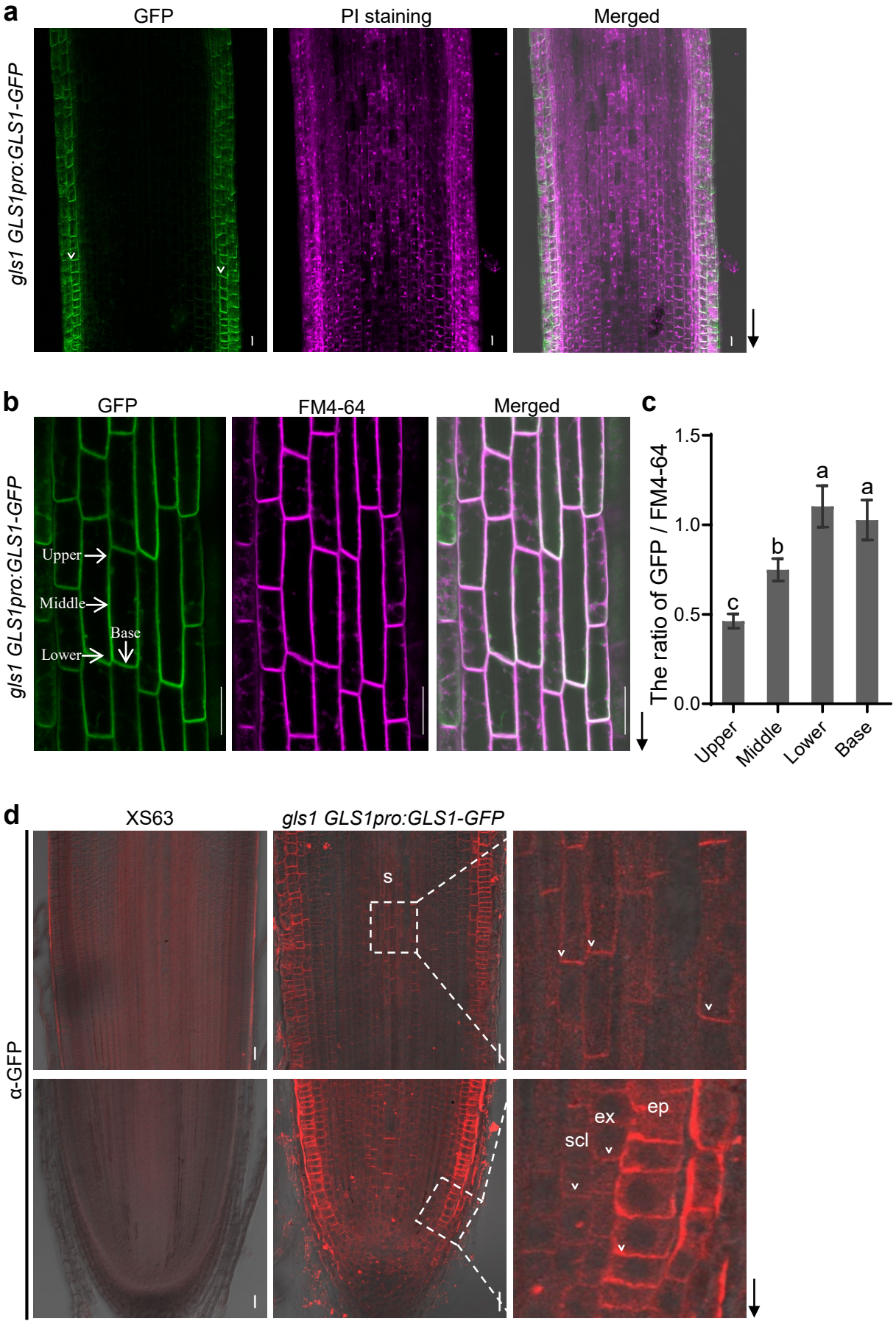
Supplementary Fig. 8



Supplementary Fig. 8 Tissue-specific expression of *OsGLS1*.

a–**l**, GUS staining of 7-day-old *GLS1pro:GUS* seedlings grown in solution culture. Whole root (**a**), shoot (**b**), leaf blade (**c**), stem (**d**), stem base (**e**), primary root with lateral roots (**f**), root tip (**g**), cross section of leaf (**h**), cross section of stem (**i**), root elongation zone (**j**), longitudinal section of primary root elongation zone (**k**) and root tip (**l**). ep, epidermis; ex, exodermis; scl, sclerenchyma. Scale bars, 3 cm in **a** and **b**, 1 mm in **c**–**g**, 100 μm in **h**–**l**. **m**, Relative *OsGLS1* transcript levels in different tissues of 7-day-old seedlings or 50-day-old plants of HJ2 as revealed by RT-qPCR. The 0–1 cm root tip means the length of the root segments relative to the root tip of the primary root. The first to fourth internodes, nodes and leaves from the top of shoots were sampled to analyze *OsGLS1* expression. Data represent means ± SD (n = 3).

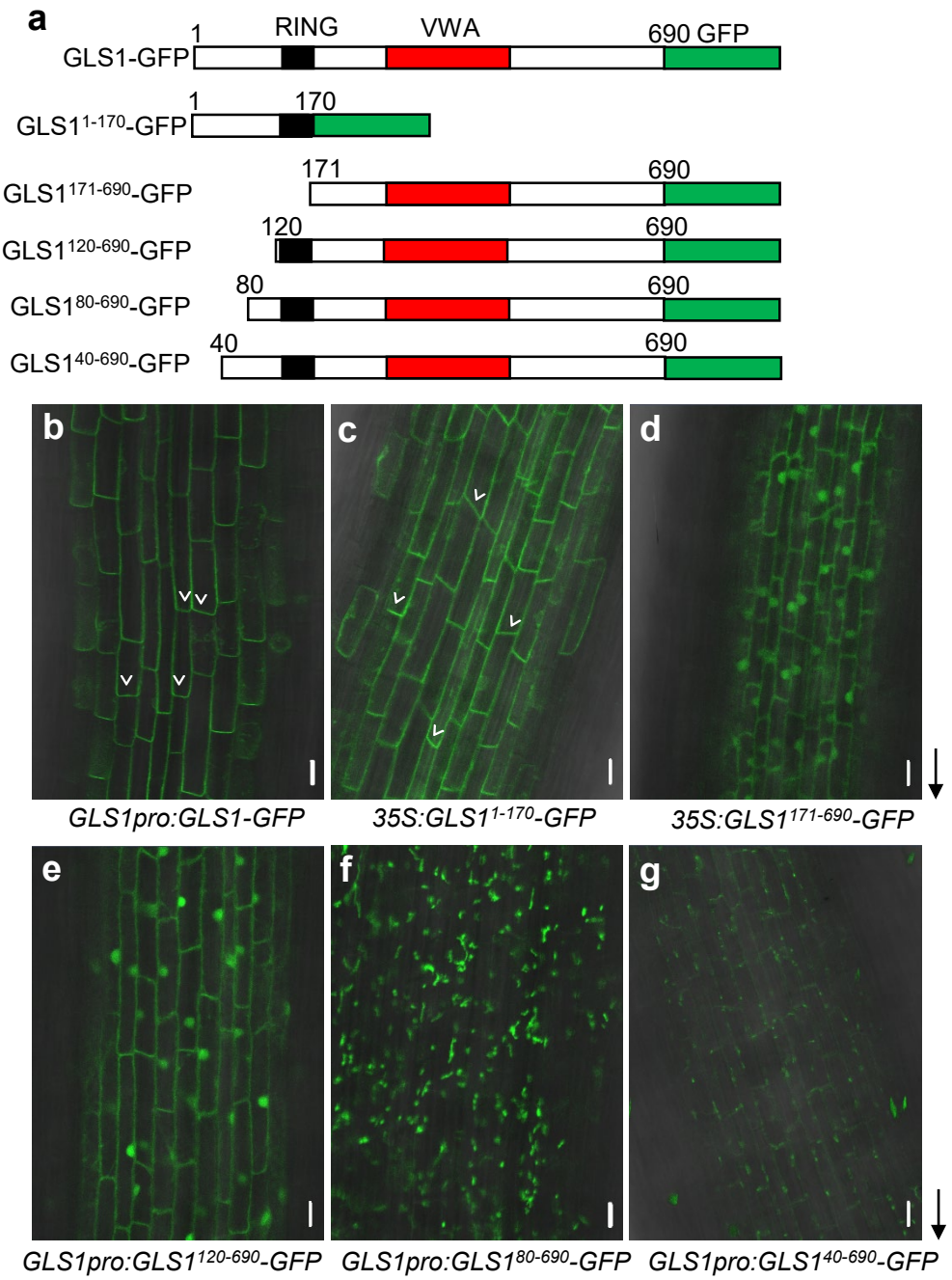
Supplementary Fig. 9



Supplementary Fig. 9. Subcellular localization of OsGLS1 in root cells.

a, GLS1-GFP (green fluorescence) and PI staining (magenta fluorescence) in a longitudinal section of the root meristematic zone of 7-day-old *gls1 GLS1pro:GLS1-GFP* transgenic seedlings. **b**, Localization of GLS1-GFP (green fluorescence) and FM4-64 (magenta fluorescence) in epidermal cells of the primary root tip of the *gls1 GLS1pro:GLS1-GFP* transgenic lines. **c**, The ratio of the GFP fluorescence intensity to FM4-64 at different PM sites as indicated in **b**. Data represent means ± SD (n = 15). Different letters indicate significant difference ($p < 0.01$; one-way ANOVA with Tukey's honestly significant difference test). **d**, Immunostaining of GLS1-GFP in a longitudinal section of the root meristematic zone (upper panel) and root tip (lower panel) of the primary root of 7-day-old XS63 and *gls1 GLS1pro:GLS1-GFP* transgenic seedlings detected using an anti-GFP antibody (α-GFP; red fluorescence). The boxed areas are magnified in the images to the right. s, stele; ep, epidermis; ex, exodermis; scl, sclerenchyma. White arrowheads in **a** and **d** indicate the polarity of fluorescent signals. Black arrow indicates the direction of the root tip. Scale bars, 20 μm.

Supplementary Fig. 10



Supplementary Fig. 10 Subcellular localization of different truncated OsGLS1.

a, Diagram showing various truncated OsGLS1 variants fused to GFP used in the subcellular localization analysis. Numbers at the top refer to the positions of the first or last amino acid of OsGLS1 truncations. **b**–**g**, Subcellular localization of full-length or truncated GLS1-GFP variants in the roots of seedlings from *GLS1pro:GLS1-GFP* (**b**), *35S:GLS1*$^{1\text{-}170}$*-GFP* (**c**), *35S:GLS1*$^{171\text{-}690}$*-GFP* (**d**), *GLS1pro:GLS1*$^{120\text{-}690}$*-GFP* (**e**), *GLS1pro:GLS1*$^{80\text{-}690}$*-GFP* (**f**) and *GLS1pro:GLS1*$^{40\text{-}690}$*-GFP* (**g**) transgenic lines. The white arrowheads in **b** and **c** indicate the polarity of protein localization. The black arrows indicate the direction of root tips. Scale bars, 20 μm.

Supplementary Fig. 11

a

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001 MGTGWRRALC TSVRRDPEQQ EVKRRGEAPS PRCGGGSRLG GFFSAISSSH SSSNPATTTP TLRCRTKPKP QSSSSDHQQQ
081 LPSSAPAPKK RMPLLQALSV PSSPRSPSRF ALLKASILPN KSRCGVCSHG VKTGAAAVFT AECSHSFHFP CIAAHAHALA
161 AATALSCPVC AAPWRQAPFI NKRTTTTDDH KRKSYDDDEP LLAPKAAAGA FNPIPEDDED DATEFRGFFP ARPRSGLAVT
241 LAPDAALVSA GRRHGKYVVA VRVKAPALRS SPSTRAPIDL VTVLDVSQGM MGDKLHMLKR GMRLVIASLG PADRLAIVAF
321 SGAAKRLLPL RRMTRQGQRS ARQIVDRLVV CAAAQGQEQP QAVCVGDALR KATKVLEDRR DRNPVATVML LSDTQQQQQQ
401 QQDAIRRPPA APPATRFTHV EIPIGPGEEP ARSALVAEED DDQFSEHAFA KCLGGLVSVV MQEVQLELAF PTGEITAVYS
481 CGHGQQAVAL GGGGGGAAVS VSLGEMYAEE ERELLVELRA PLSQSHPHSL SVRCSYREPA SQETVRGAEQ QLVVPALHGG
561 SSSRRLHDLF VATRAVAESR RLAELNDYAT AIHLLSSARA VVVQSAEQGL VGSLDTELSD MRWRRGQSAG RRRGGESEET
641 PVGTPRARGG EPLTPTSAWR AAEQLAKVAI MRKSMNRVSD LHGFENARF
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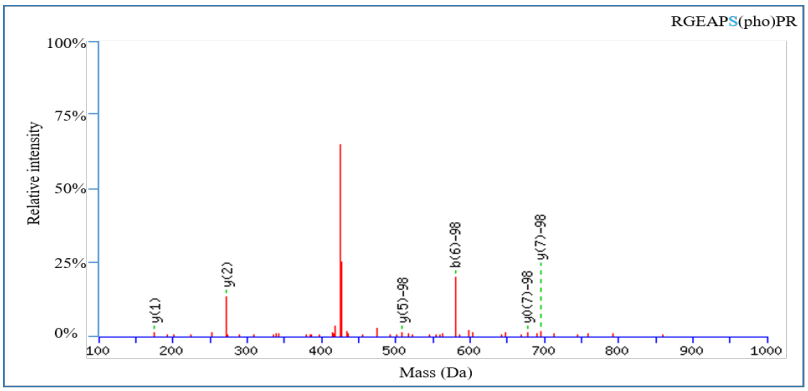
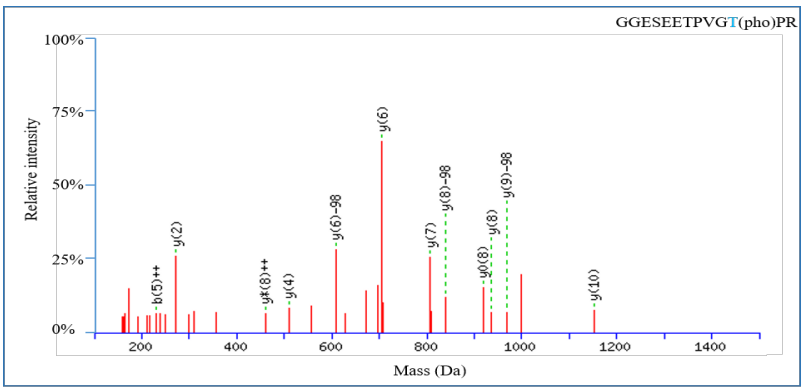
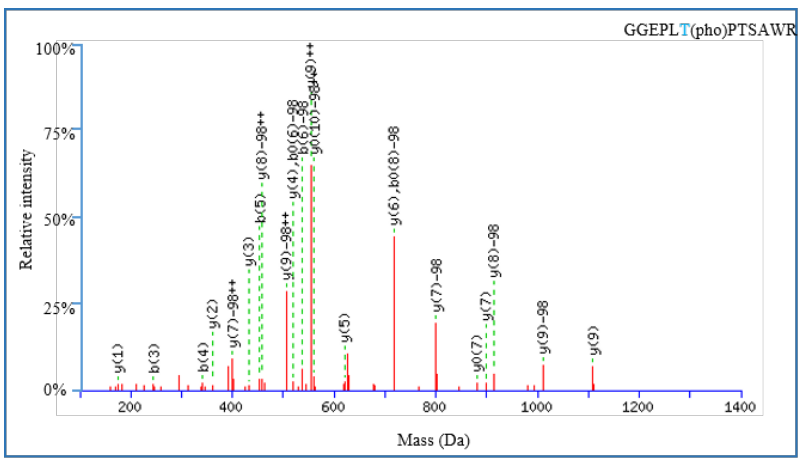
b



c



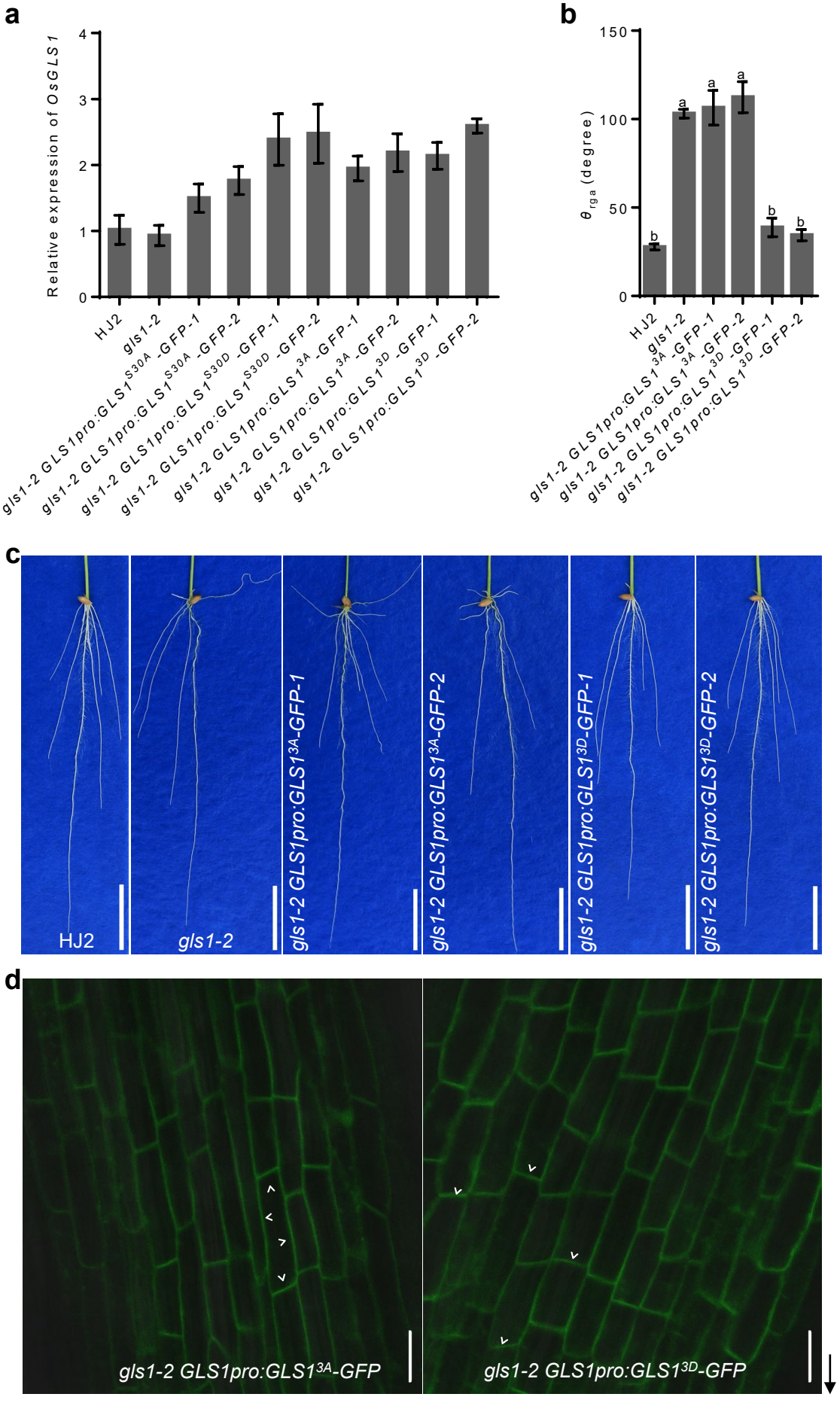
d



Supplementary Fig. 11 *In planta* phosphorylation of OsGLS1 as revealed by LC–MS/MS.

a, Amino acid sequence coverage for OsGLS1 based on analysis by liquid chromatography–tandem mass spectrometry (LC-MS/MS). Total proteins were extracted from roots of *gls1-2 GLS1pro:GLS1-GFP* transgenic seedlings and immunoprecipitated with anti-GFP antibody–conjugated beads. Peptides that were detected by LC-MS/MS are shown in red, those not detected are shown in black and detected phosphorylated amino acids are shown in blue. **b**–**d**, LC-MS/MS spectra for the phosphorylated amino acids Ser-30 (**b**), Thr-644 (**c**) and Thr-654 (**d**) in OsGLS1.

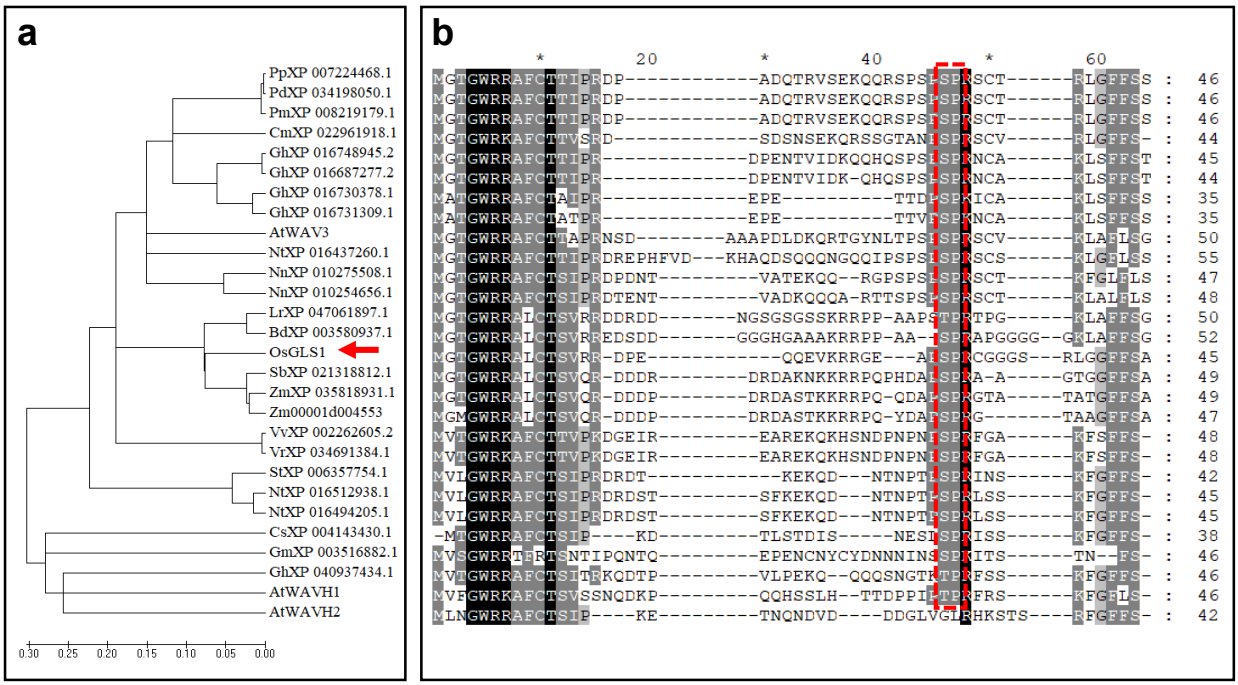
Supplementary Fig. 12



Supplementary Fig. 12 Root phenotype and subcellular localization of OsGLS1 phosphomimic mutation or nonphosphorylatable mutation in related transgenic plants.

a, RT-qPCR analysis of relative *OsGLS1* transcript levels in the wild-type HJ2 and different transgenic lines. **b**, Root growth angle of HJ2 and related transgenic lines. GLS1^{30A}, Ser-30 replaced with Ala; GLS1^{30D}, Ser-30 replaced with Asp; GLS1^{3A}, Ser-30, Thr-644 and Thr-654 replaced with Ala; GLS1^{3D}, Ser-30, Thr-644 and Thr-654 replaced with Asp. **c**, Root phenotypes of 7-day-old seedlings grown on germination paper. Scale bars, 3 cm. **d**, Subcellular localization of GLS1^{3A}-GFP and GLS1^{3D}-GFP in roots of related transgenic seedlings. The white arrowheads indicate the polar localization of proteins. Scale bars, 20 μm. Data represent means ± SD (n = 3 in **a** and 12 in **b**), different letters indicate significant difference (p < 0.01; one-way ANOVA with Tukey's honestly significant difference test).

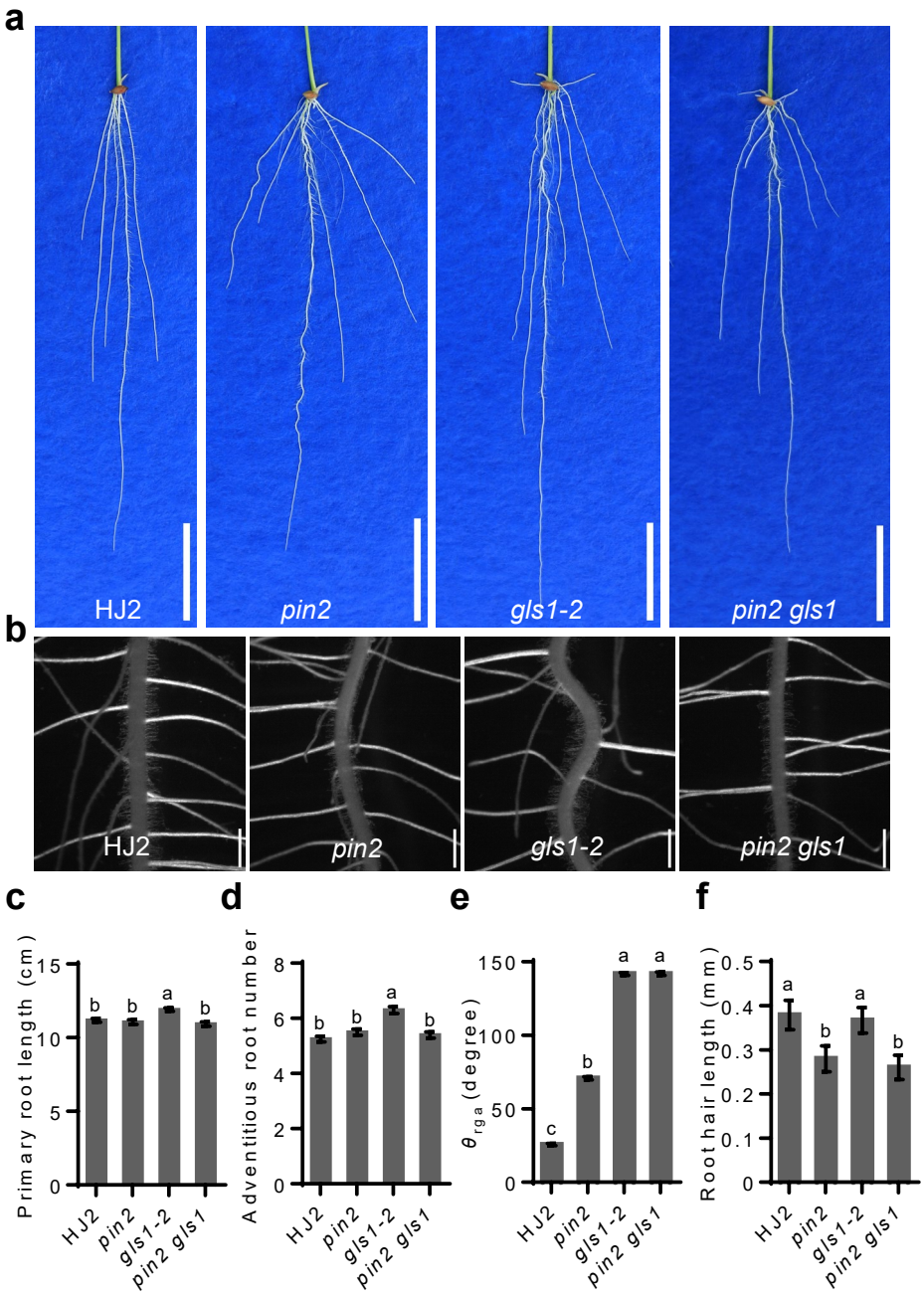
Supplementary Fig. 13



Supplementary Fig. 13 Phylogenetic relationships and N-terminal sequence alignment of OsGLS1 and its homologous proteins from different plant species.

a, Phylogenetic tree of OsGLS1 and its homologs, reconstructed using the neighbor-joining method with 1000 bootstrap replicates in MEGA 7.0 software. The red arrow points to OsGLS1. **b**, Alignment of the N terminus of OsGLS1 and its homologs. The red box shows conserved phosphorylatable amino acids Ser/Thr-Pro in GLS1-related proteins. The tree is drawn to scale in **a**, with branch lengths measured according to the relative number of substitutions per site. *Pp*, *Prunus persica*; *Pd*, *Prunus dulcis*; *Pm*, *Prunus mume*; *Cm*, *Cucurbita moschata*; *Gh*, *Gossypium hirsutum*; *At*, *Arabidopsis thaliana*; *Nt*, *Nicotiana tabacum*; *Nn*, *Nelumbo nucifera*; *Lr*, *Lolium rigidum*; *Bd*, *Brachypodium distachyon*; *Os*, *Oryza sativa*; *Sb*, *Sorghum bicolor*; *Zm*, *Zea mays*; *Vv*, *Vitis vinifera*; *Vr*, *Vitis riparia*; *St*, *Solanum tuberosum*; *Cs*, *Cucumis sativus*; *Gm*, *Glycine max*.

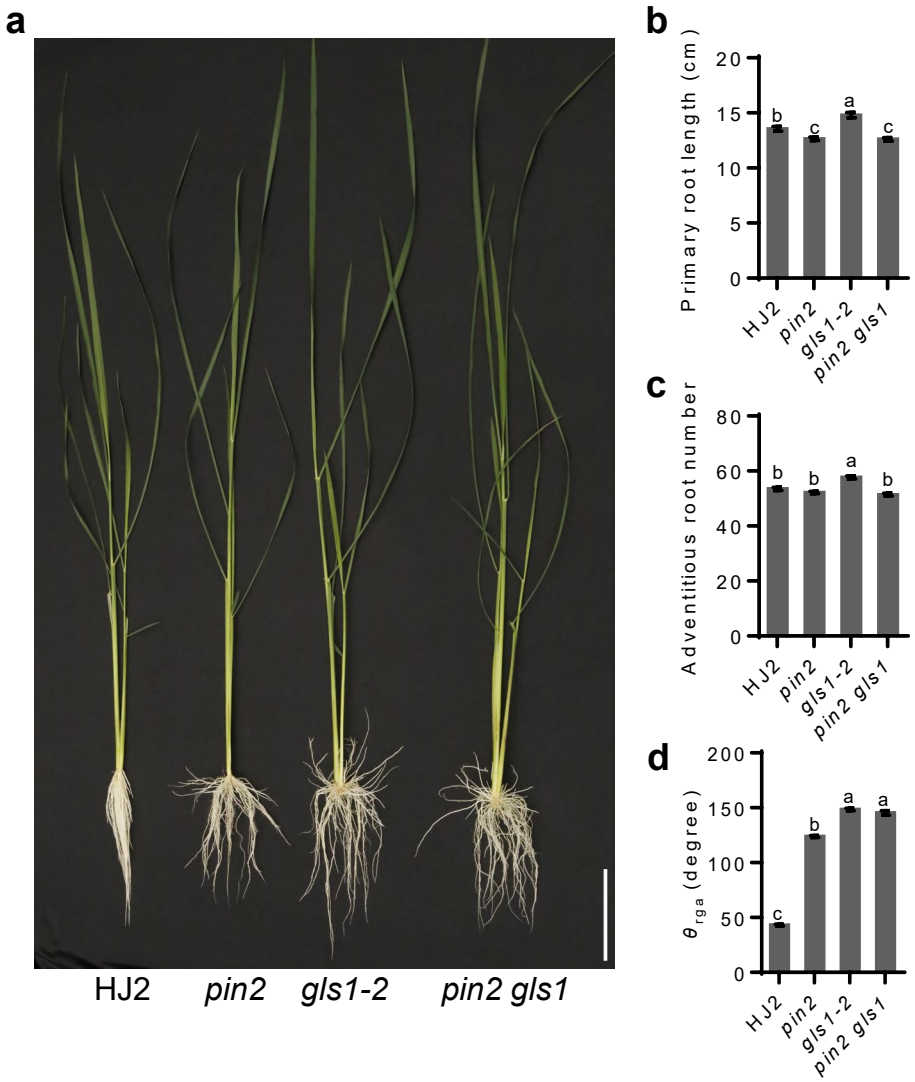
Supplementary Fig. 14



Supplementary Fig. 14 Phenotypes of 7-day-old HJ2, *pin2*, *gls1-2* and *pin2 gls1* seedlings grown on germination paper.

a, Representative photographs of the root from the indicated genotypes. Scale bars, 3 cm. **b**, Stereomicroscope images of root maturation zones. Scale bars, 1 mm. **c**–**e**, Primary root length (**c**), adventitious root number (**d**) and θ_{rga} (**e**) of the corresponding seedlings in **a**. **f**, Root hair length of the corresponding seedlings in **b**. Data represent means ± SD (n = 20 in **c**–**e** and 15 in **f**). Different letters indicate significant difference ($p < 0.01$; one-way ANOVA with Tukey's honestly significant difference test).

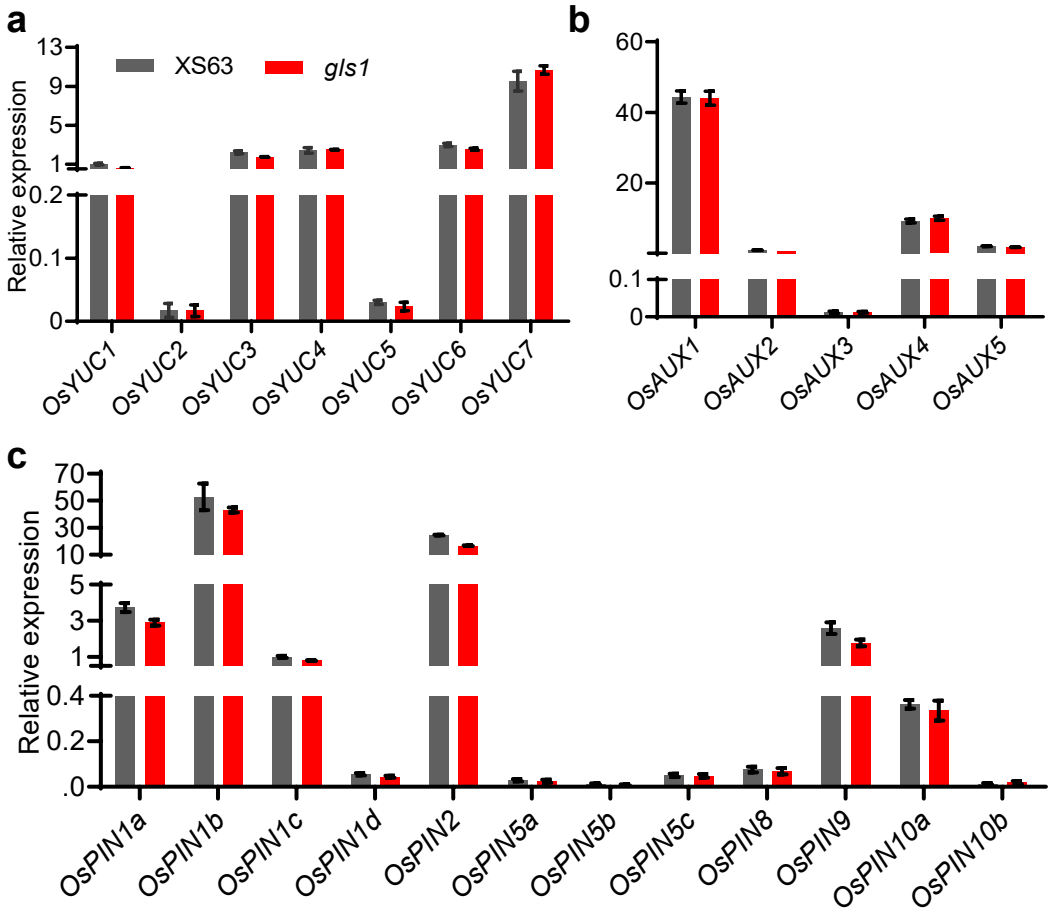
Supplementary Fig. 15



Supplementary Fig. 15 Phenotypes of 4-week-old HJ2, *pin2*, *gls1-2* and *pin2 gls1* plants grown in solution culture.

a, Representative photograph of 4-week-old plants in solution culture. Scale bar, 10 cm. **b**–**d**, Primary root length (**b**), adventitious root number (**c**) and θ_{rga} (**d**) of the corresponding plants in **a**. Data represent means ± SD (n = 10 in **b** and **c** and 17 in **d**). Different letters indicate significant difference ($p < 0.01$; one-way ANOVA with Tukey's honestly significant difference test).

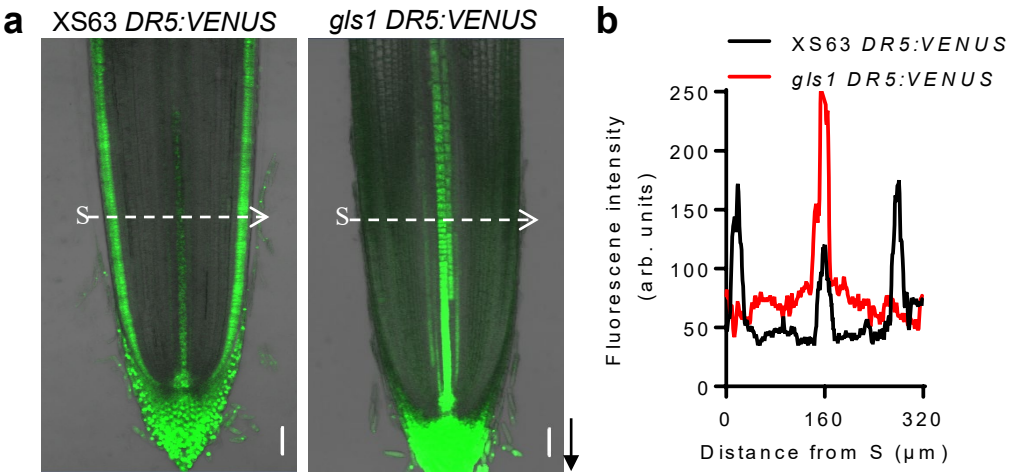
Supplementary Fig. 16



Supplementary Fig. 16 RT-qPCR analysis of the transcript levels of genes related to auxin biosynthesis and transport in XS63 and *gls1*.

Relative transcript levels of *OsYUC* (**a**), *OsAUX* (**b**) and *OsPIN* genes (**c**) in the root of 7-day-old XS63 and *gls1* seedlings as revealed by RT-qPCR. Data represent means ± SD (n = 3).

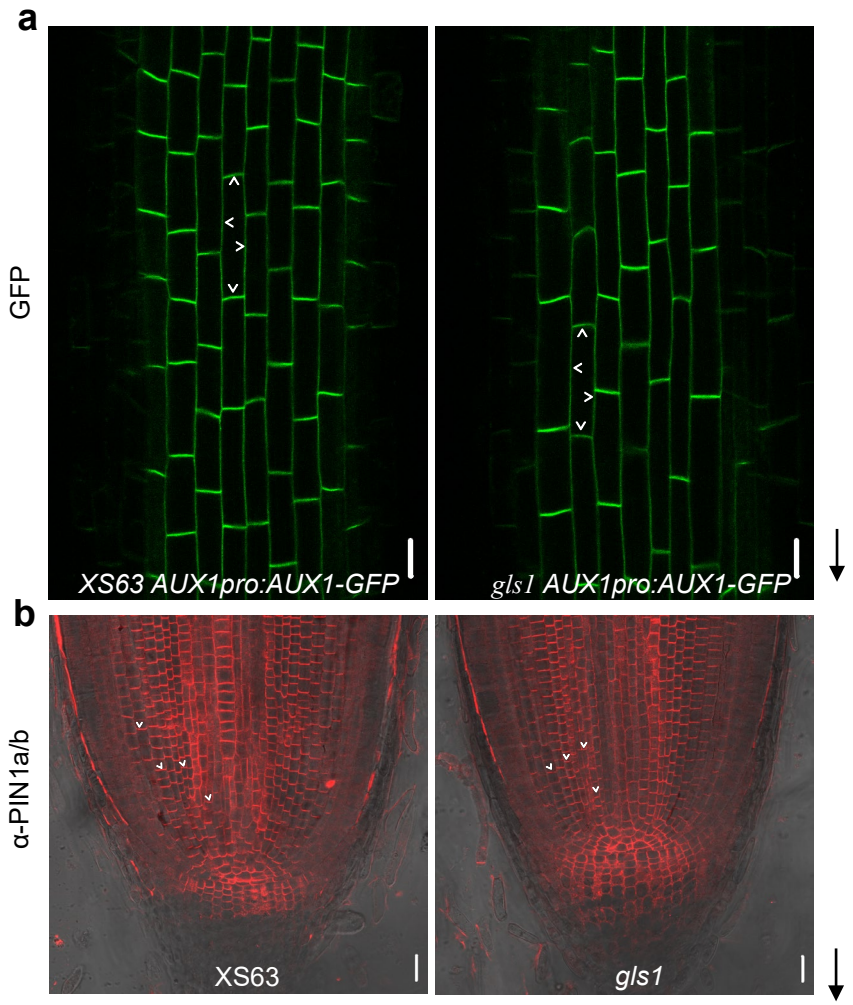
Supplementary Fig. 17



Supplementary Fig. 17 Auxin distribution pattern is altered in *gls1*.

a, Expression pattern of *DR5:VENUS* in the root tips of 7-day-old XS63 (left) and *gls1* (right) seedlings. **b**, Relative fluorescence intensity of VENUS along the white dashed arrow in **a**.

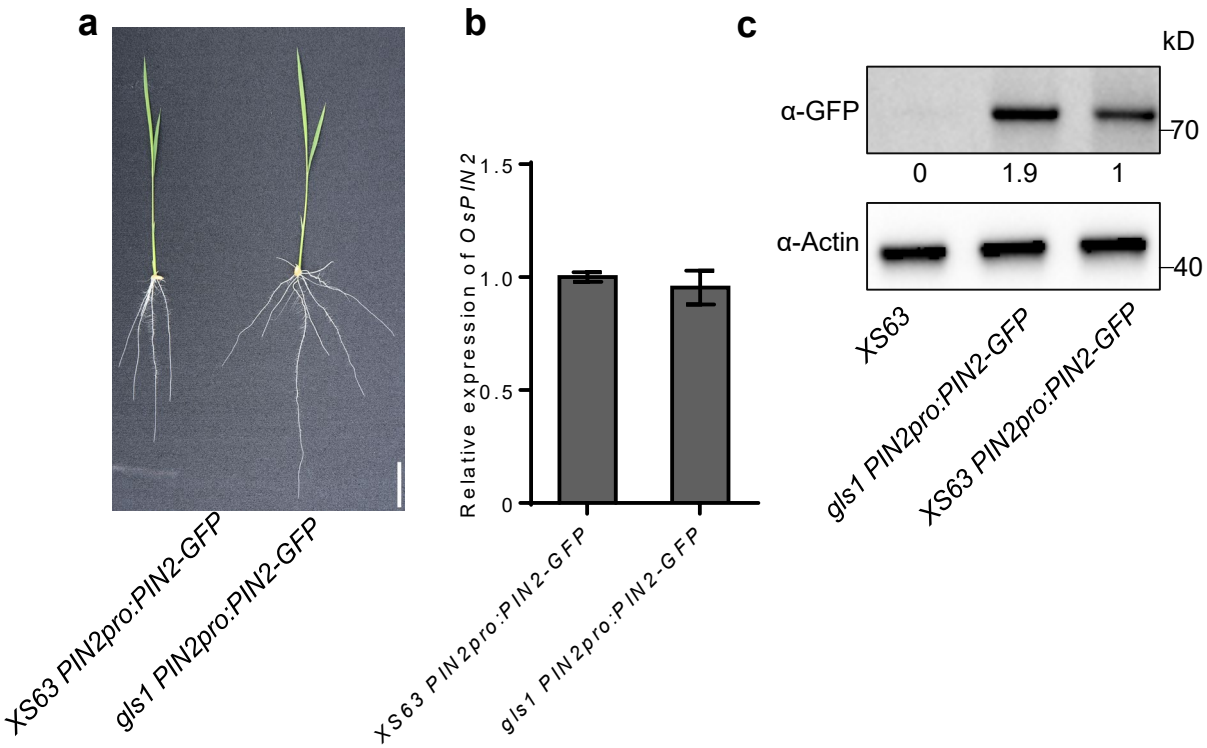
Supplementary Fig. 18



Supplementary Fig. 18 The subcellular localization of OsAUX1 and OsPIN1a/b does not change in the root tips of *gls1*.

a, GFP fluorescence (green) in the primary root tip of the *AUX1pro:AUX1-GFP* transgenic lines in the XS63 and *gls1* backgrounds. **b**, Immunostaining of OsPIN1a/b along longitudinal sections of the primary root tips of XS63 (left) and *gls1* (right) using an antibody against OsPIN1a/b (α-PIN1a/b; red fluorescence). The black arrows show the direction of the root tip, and the white arrowheads indicate the polarity of the proteins. Scale bars, 20 μm.

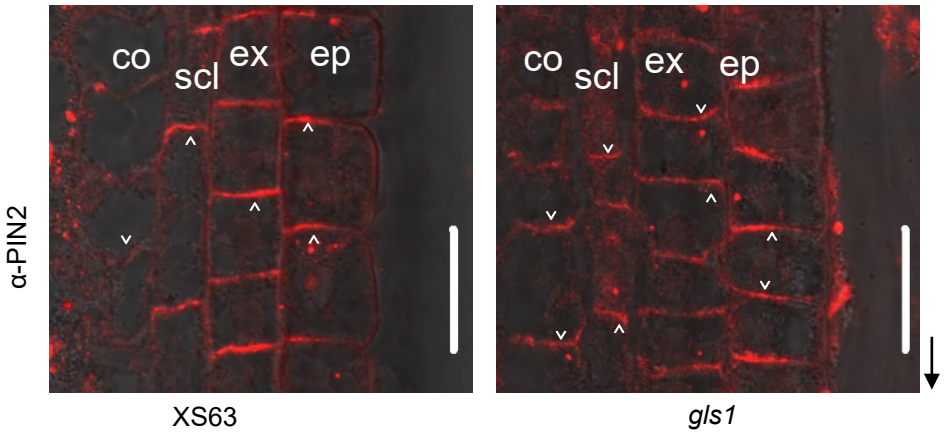
Supplementary Fig. 19



Supplementary Fig. 19 Abundance of PIN2-GFP in the roots of XS63 and *gls1*.

a, Representative photograph of 7-day-old seedlings from *PIN2pro:PIN2-GFP* transgenic lines in the XS63 and *gls1* backgrounds grown in solution culture. Scale bar, 3 cm. **b**, Relative *OsPIN2* transcript levels in the roots of related seedlings. Data represent means ± SD (n = 3). **c**, PIN2-GFP protein levels in roots of *PIN2pro:PIN2-GFP* transgenic lines in the XS63 and *gls1* backgrounds. Numbers under each band indicate the relative band intensity based on quantification with Image Lab software. OsACTIN1 was used as a loading control.

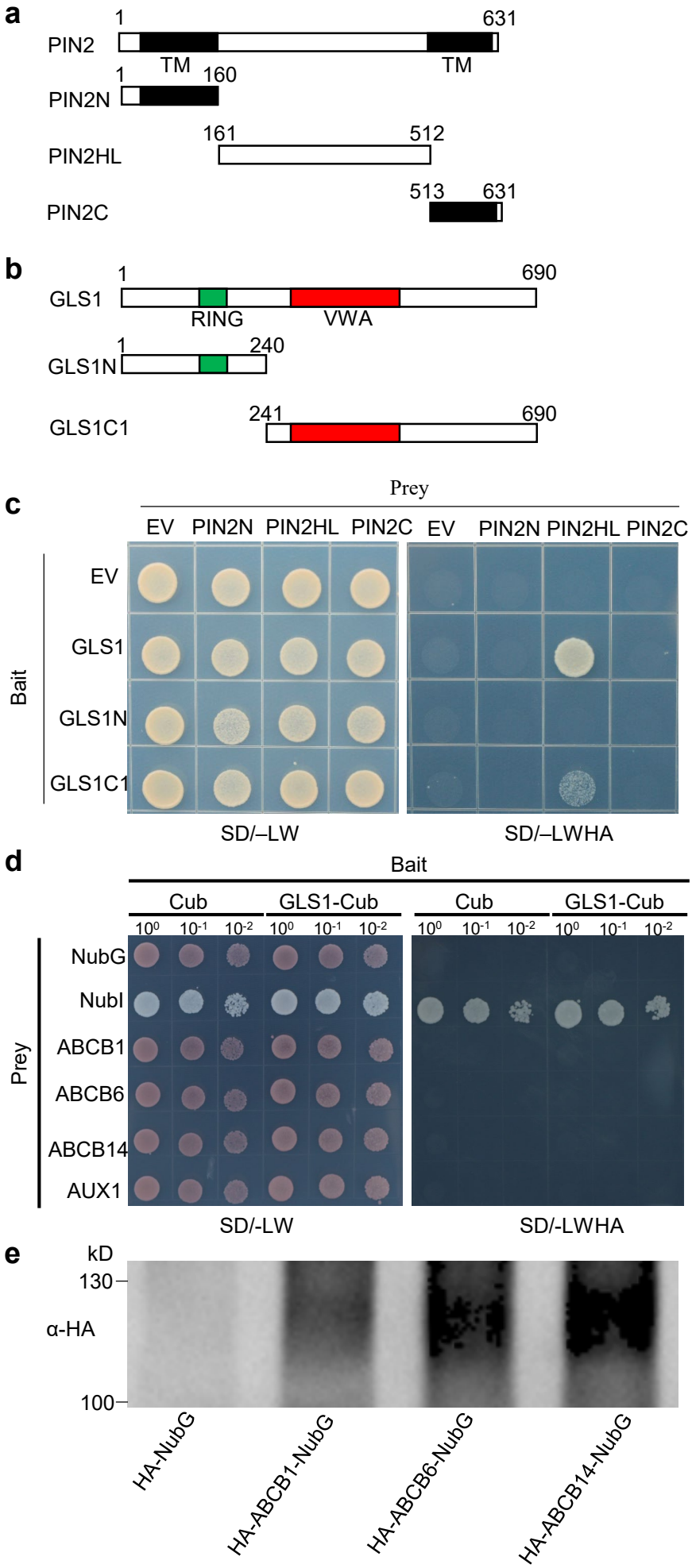
Supplementary Fig. 20



Supplementary Fig. 20 Immunolocalization of OsPIN2 in the root elongation zone of XS63 and *gls1*.

The root elongation zones of 5-day-old seedlings from XS63 (left) and *gls1* (right) were subjected to immunostaining using an antibody against OsPIN2. ep, epidermis; ex, exodermis; scl, sclerenchyma; co, cortex. The black arrow indicates the direction of the root tip. The white arrowheads indicate the polarity of the protein at the plasma membrane. Scale bars, 20 μm.

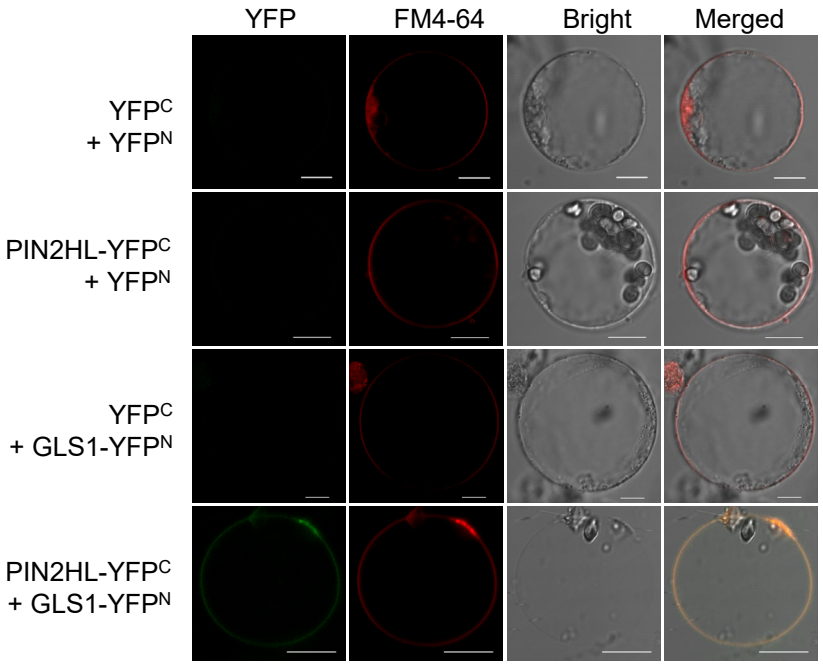
Supplementary Fig. 21



Supplementary Fig. 21. Interaction between OsGLS1 and OsPIN2 truncated variants in yeast two-hybrid assay.

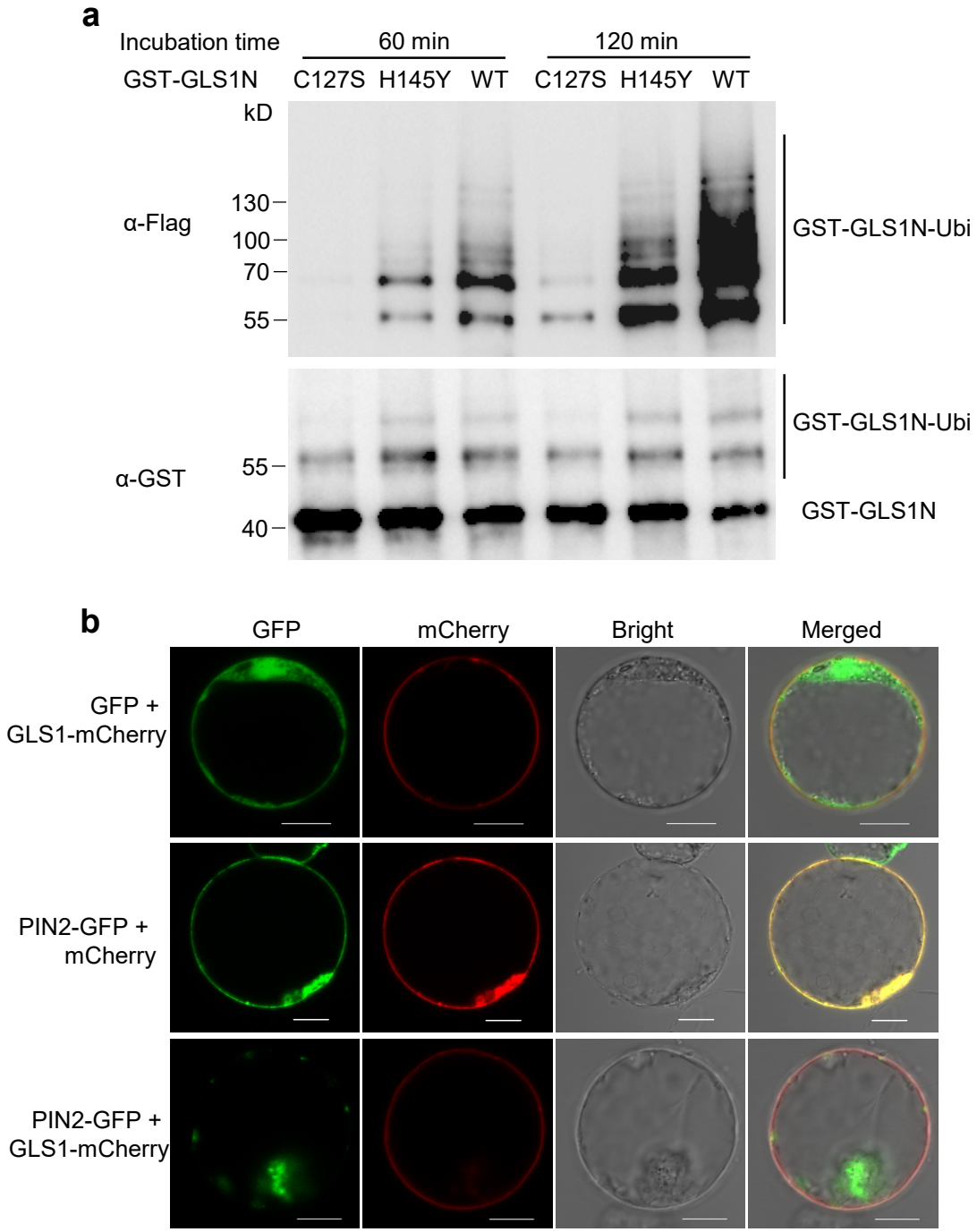
a, **b**, Diagrams of the full-length and truncated OsPIN2 (**a**) and OsGLS1 (**b**) variants used in the yeast two-hybrid assay. Numbers at the top refer to the positions of the first or last amino acid in each truncation. **c**, Yeast two-hybrid results of the interaction between truncated OsPIN2 and OsGLS1. EV, empty vector. **d**, Split-ubiquitin yeast two-hybrid analysis of the interaction between OsGLS1 and OsABCB1, OsABCB6, OsABCB14 or OsAUX1. Cub, C-terminal ubiquitin. NubI and NubG, the wild type and mutated N-terminal fragment of ubiquitin. Yeast cells were grown on synthetic defined (SD) medium lacking leucine and tryptophan (SD/–LW) or lacking leucine, tryptophan, histidine, and adenine (SD/–LWHA). **e**, Western bolting analysis of the expression of OsABCBs in related yeast cells in **d**. α-HA, HA tag antibody.

Supplementary Fig. 22



Supplementary Fig. 22. BiFC analysis of the interaction between OsGLS1 and OsPIN2HL in rice protoplasts. OsGLS1 and OsPIN2HL were fused with the N-terminal (YFP^N) and C-terminal (YFP^C) portion of YFP, respectively. Combinations of YFP^N or YFP^C with the corresponding OsGLS1 and OsPIN2HL fusion constructs were used as negative controls. The fluorescence was observed using confocal microscope. Scale bars, 10 μm.

Supplementary Fig. 23



Supplementary Fig. 23. *In vitro* ubiquitination assay and co-localization of OsGLS1 and OsPIN2.

a, Recombinant GST-GLS1N, GST-GLS1N^{C127S} and GST-GLS1N^{H145Y} proteins were purified and assayed for ubiquitination in the presence of E1, E2 and ubiquitin-Flag for 60 min or 120 min. The results were analyzed by immunoblotting using anti-Flag or anti-GST antibodies. C127S, Cys-127 was replaced with Ser; H145Y, His-145 was replaced with Tyr. **b**, Co-localization of GLS1-mCherry and PIN2-GFP fusion proteins in protoplast. *35S:GLS1-mCherry* or *35S:mCherry* with *35S:GFP* or *PIN2pro:PIN2-GFP* were expressed in rice protoplasts. Scale bars, 20 μm.

Supplementary Table 1. Primers used for plasmid construction

Primer	Sequence (5'-3')	Note
U3GLS1F	GGCAATGTACGCGGAGGAAGAGC	*CRISPR/Cas9-GLS1*
U3GLS1R	AAACGCTCTTCCTCCGCGTACAT	
U6aGLS1F	GCCGGTGGGTGGCTCTGGCTCAG	
U6aGLS1R	AAACCTGAGCCAGAGCCACCCAC	
JCGLS1F	GTCAGCGTGGTGATGCAGGA	Detection primer
JCGLS1R	CGCTGACACGGTTCATGGAC	
dGLS1F	GGCGCGGCGGTGAGTGTC	dCAPS primer
dGLS1R	CGCAGCTCCACCAGCAG	
proGLS1F	CTTGCATGCCTGCAGGTCGACAAATTTGACCTCTACCTTTT	*GLS1p::GUS*
proGLS1R	CCTCAGATCTACCATGGTACCCACACACACACTCTCTCTCT	
IFGLS1F	GCCAAGCTTGCATGCCTGCAGTTTGACCTCTACCTTTTCTA	*GLS1p::GLS1-GFP*
GLS1F	GAGAGTGTGTGTGTGATGGGGACGGGGTGG	
GLS1R	CCACCCCGTCCCCATCACACACACACTCTC	
IFGLS1R	GCCCTTGCTCACCATGGTACCGAATCTGGCGTTCTCGAAAC	
GLS40F	GAGAGAGTGTGTGTGTGATGGGCTTCTTCTCCGCCATCTC	*GLS1p::Δ40GLS1-GFP*
GLS40R	GAGATGGCGGAGAAGAAGCCCATCACACACACACTCTCTC	
GLS80F	GAGAGAGTGTGTGTGTGATGCTTCCGTCGTCCGCGCCGGC	*GLS1p::Δ80GLS1-GFP*
GLS80R	GCCGGCGCGGACGACGGAAGCATCACACACACACTCTCTC	
GLS120F	GAGAGAGTGTGTGTGTGATGAAGAGCCGGTGCGGCGTGTG	*GLS1p::Δ120GLS1-GFP*
GLS120R	CACACGCCGCACCGGCTCTTCATCACACACACACTCTCTC	
GLS1NF	AACTGGTACCATGGGGACGGGGTGGCGG	*35S::GLS1$^{1-170}$-GFP*
GLS1NF	GCGCTCTAGAGCAGACGGGGCAGGAGAG	
GLS1CF	AACTGGTACCATGGCCGCGCCATGGCGC	*35S::GLS1$^{171-690}$-GFP*
GLS1CF	GCGCTCTAGAGAATCTGGCGTTCTCGAAAC	
GLS30DF	GAGGCCCCAGACCCCCGGTG	*GLS1p::GLS1^{30A}-GFP* *GLS1p::GLS1^{30D}-GFP* *GLS1p::GLS1^{3A}-GFP* *GLS1p::GLS1^{3D}-GFP*
GLS30DR	CACCGGGGGTCTGGGGCCTC	
GLS30AF	GAGGCCCCAGCCCCCCGGTG	
GLS30AR	CACCGGGGGGCTGGGGCCTC	
GLS644654DF	GGGGACCCGCGGGCGCGGGGGGGAGAGCCGCTGGACCCG	
GLS644654DR	CGGGTCCAGCGGCTCTCCCCCCCGCGCCCGCGGGTCCCC	
GLS644654AF	GGGGCGCCGCGGGCGCGGGGGGGAGAGCCGCTGGCGCCG	
GLS644654AR	CGGCGCCAGCGGCTCTCCCCCCCGCGCCCGCGGCGCCCC	
AUX1F	AAAATCTAGAGGACCGAGTTTGAGCAATCTCTC	*AUX1p::AUX1-GFP*
AUX1R	AAAATCTAGAAGTGGTGCGGCAATGGCAC	
PIN2F0	CCATGATTACGAATTCCGTTGCTTCCCTGGACATAG	*PIN2p::PIN2-GFP*
PIN2R0	TCTAGAGGATCCCCGGGTACCTCTTGCCATGCACTGTGGAA	
PIN2F1	ACTCCCAAAGGTACCATGGTGAGCAAGGGC	
PIN2R1	GCCCTTGCTCACCATGGTACCTTTGGGAGT	
PIN2F2	GACGAGCTGTACAAGGGATCCTCTAGAGGG	
PIN2R2	CCCTCTAGAGGATCCCTTGTACAGCTCGTC	
PIN2HLF1	AACTGGTACCATGGAGTACCGCGGCGCC	*35S::PIN2HL-GFP*

PIN2HLR1	GCGCTCTAGACTTTATTATTGAAGGCATTTG	
PIN2HLF2	CACGGGGGACTCTAGAATGGAGTACCGCGGCGCC	*35S::PIN2HL-FLAG*
PIN2HLR2	CGGGGGATCCTCTAGACTTTATTATTGAAGGCATTTG	
PIN2HLF3	TGGCTTAATTAACATGGAGTACCGCGGCGCC	YFP^{C}-PIN2HL
PIN2HLR3	TAATGGCGCGCCCTACTTTATTATTGAAGGCATTTG	
GLS1F1	TGGCTTAATTAACATGGGGACGGGGTGGCGG	YFP^{N}-GLS1
GLS1R1	TAATGGCGCGCCTCAGAATCTGGCGTTCTC	
GSTGLS1CF	CTGGTTCCGCGTGGATCCGGCTTCTTCTCCGCCATCTC	GST-GLS1C
GSTGLS1CR	ACGATGCGGCCGCTCGAGGAATCTGGCGTTCTCGAAAC	
GSTGLS1NF	ATTAGGATCCATGGGGACGGGGTGGCGGAG	GST-GLS1N
GSTGLS1NR	AGGGCTCGAGGGTGACGGCCAGCCCGCTCCT	
GLSC127SF	TGCGGCGTGTCCTCCCACG	GST-GLS1^{C127S}N
GLSC127SR	CGTGGGAGGACACGCCGCA	
GLSH145YF	GGCGGAGTGCTCCTAC TCCTTCC	GST-GLS1^{H145Y}N
GLSH145YR	GGAAGGAGTAGGAGCACTCCGCC	
HISPIN2HLF	AAAACATATGGAGTACCGCGGCGCCAAGGC	HIS-PIN2HL
HISPIN2HLR	AAAACTCGAGCTTTATTATTGAAGGCATTTG	
GLS1pDHB1F	ATTAACAAGGCCATTACGGCCATGGGGACGGGGTGGCGG	GLS1-Cub
GLS1pDHB1R	AACTGATTGGCCGAGGCGGCCGAATCTGGCGTTCTCGAAAC	
PIN2pPR3F	ATTAACAAGGCCATTACGGCCATGATCACCGGACGCGACAT	PIN2-pPR3
PIN2pPR3R	AACTGATTGGCCGAGGCGGCCCCTATCCCAAGAAGCACATA	
AUX1pPR3F	TATGACGTCAGTGGCCATTACGGCCTTATGGTGCCGCGCGAGCA	AUX1-pPR3
AUX1pPR3R	GAATTCTCGAGAGGCCGAGGCGGCCCCGTGGTGCGGCAATGGC	
ABCB1pPR3F	ATTAACAAGGCCATTACGGCCTTATGCCGGAGTCTTGGAGAGAC	ABCB1-pPR3
ABCB1pPR3R	AACTGATTGGCCGAGGCGGCCCCTGAAGAAGCTGCTGAATGAA	
ABCB14pPR3F	ATTAACAAGGCCATTACGGCCTTATGGCGGATGAGTCAGGGAG	ABCB14-pPR3
ABCB14pPR3R	AACTGATTGGCCGAGGCGGCCCCGCCGTGGTGTAGCTGCAGCT	
ABCB16pPR3F	ATTAACAAGGCCATTACGGCCTTATGGACGCGGCGGCGAACGG	ABCB16-pPR3
ABCB16pPR3R	AACTGATTGGCCGAGGCGGCCCCTGATGAGCCTGAACGGAGTT	
BDGLS1F	TCAGAGGAGGACCTGCATATGATGGGGACGGGGTGGCGG	GLS1-BD
BDGLS1R	TCGACGGATCCCCGGGAATTCTCAGAATCTGGCGTTCTC	
BDGLS1NF	TCAGAGGAGGACCTGCATATGATGGGGACGGGGTGGCGG	GLS1N-BD
BDGLS1NR	TCGACGGATCCCCGGGAATTCGGTGACGGCCAGCCCGCTC	
BDGLS1CF	TCAGAGGAGGACCTGCATATGCTCGCCCCGGACGCCGCCC	GLS1C-BD
BDGLS1CR	TCGACGGATCCCCGGGAATTCTCAGAATCTGGCGTTCTC	
ADPIN2NF	ACCAGATTACGCTCATATGATGATCACCGGACGCGACA	PIN2N-AD
ADPIN2NR	GCCCACCCGGGTGGAATTCCTAGAAGAGGAAGAGCATGAG	
ADPIN2HLF	ACCAGATTACGCTCATATGGAGTACCGCGGCGCCAAG	PIN2HL-AD
ADPIN2HLR	GCCCACCCGGGTGGAATTCCTACTTTATTATTGAAGGCATT	
ADPIN2CF	GTACCAGATTACGCTCATATGGGCTCAATATCAATATTGTC	PIN2C-AD
ADPIN2CR	GCCCACCCGGGTGGAATTCCTATATCCCAAGAAGCACAT	

Supplementary Table 2. Primers used for qPCR.

Primer	Forward primer sequence (5′-3′)	Reverse primer sequence (5′-3′)
OsGLS1-qRT-F/R	GCCACCCACACTCGCTGTCCG	GCCGTCGCGTAGTCGTTCAGC
OsAUX1-qRT-F/R	GCCTGCGCGAGTAACATCTA	CAGCACCAGCTTGGTTGGAC
OsAUX2-qRT-F/R	GATCTACCTGATGGCGACGCTGT	CTTGAAGAGGCTGCGGCAGTCG
OsAUX3-qRT-F/R	TTGGAATTTTGCAGGTGGCG	ACCACTGGATGACGTGGTTC
OsAUX4-qRT-F/R	GAATGTGGGACTGGCCTTCA	GATGTACGTCCATGTCCGCT
OsAUX5-qRT-F/R	GTGTTCTACGGGCTGATGGG	CACTGGATGACATGGTTGCG
OsYUCCA1-qRT-F/R	TCATCGGACGCCCTCAACGTCGC	GGCAGAGCAAGATTATCAGTC
OsYUCCA3-qRT-F/R	GTGAGAACGGGCTCTACTCGGTC	GCTTATGCATGACCGATGAACACG
OsYUCCA4-qRT-F/R	GCAGAATGGCCTGTACGCTGTTG	CAGACCAGCACATGACGTGTCTA
OsYUCCA6-qRT-F/R	CCATTCCCAGATGGTTGGAAGG	CATGTTGCGCCTCAAGATATTTG
OsYUCCA7-qRT-F/R	CACTGCTGTGTCCTACAATATCA	GGAGGTGCATCTCCGTCATCTTC
OsPIN1a-qRT-F/R	GTTCAGGTTTTTAGTACAGGGC	CTAATCAAAGCCGAAGCATTGT
OsPIN1b-qRT-F/R	CTGAGCTGAGCTGTGAAATAGT	GTCATCACGTGGTAGAAGTCC
OsPIN1c-qRT-F/R	GATAGGTCAGCTTAGTGATGCT	GATGCCTGTTGTCACTAATGTG
OsPIN1d-qRT-F/R	TGATCAGGAACCCAAACACTTA	GCATCTGAAAGGATCGAAATCG
OsPIN2-qRT-F/R	GCAGGGCTAGGAATGGCTATG	CAGCTGGACCAGTCAAGAACC
OsPIN5a-qRT-F/R	TGGCGGATCTTCACGAGG	CCGACGACAAGCGAGTTG
OsPIN5b-qRT-F/R	GTCCTGCACCTCGCCATCAT	GCGTAATATGCAATCAGAATCGG
OsPIN5c-qRT-F/R	CGAAATTCATTCGCCAAGTT	CATCACGAGCAGTTTCATCG
OsPIN8-qRT-F/R	CATTTCCACAACCGATCCTT	CTTTGGAAATGGCTGCAAAT
OsPIN9-qRT-F/R	GATACAAGATAGCGTCGTTCTC	ATGATGTCTGCGTGGACCT
OsPIN10a-qRT-F/R	CCTCATCCTCATAATGGTGTGG	GAACAATCCCAGGCTAAACATG
OsPIN10b-qRT-F/R	GCACATATCTCTTTCCGTGTTC	CTCTGTTGAGAGTCGAGACTAC
OsUBQ5-qRT-F/R	ACCACTTCGACCGCCACTACT	ACGCCTAAGCCTGCTGGTT
OseEF-1a-qRT-F/R	TTTCACTCTTGGTGTGAAGCAGAT	GACTTCCTTCACGATTTCATCGTAA
OsGAPDH2-qRT-F/R	AAGCCAGCATCCTATGATCAGATT	CGTAACCCAGAATACCCTTGAGTTT
OsACTIN1-qRT-F/R	GAGACATTCAGCGTTCCAGC	CGTAGATTGGGACTGTGTGAC