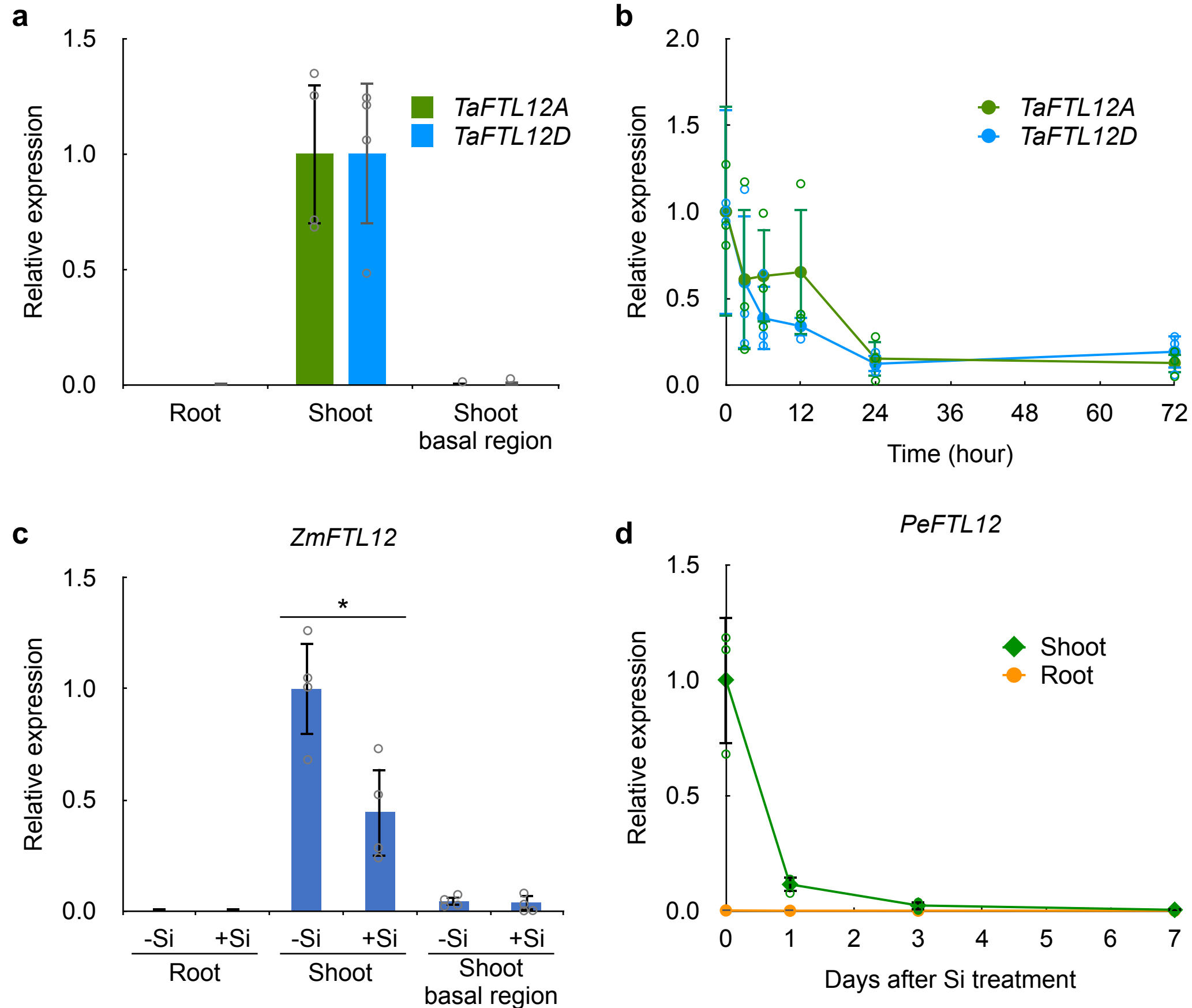


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OsFTL8 1 ----- 1
OsRCN3 1 ----- 1
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OsRCN4 1 ----- 1
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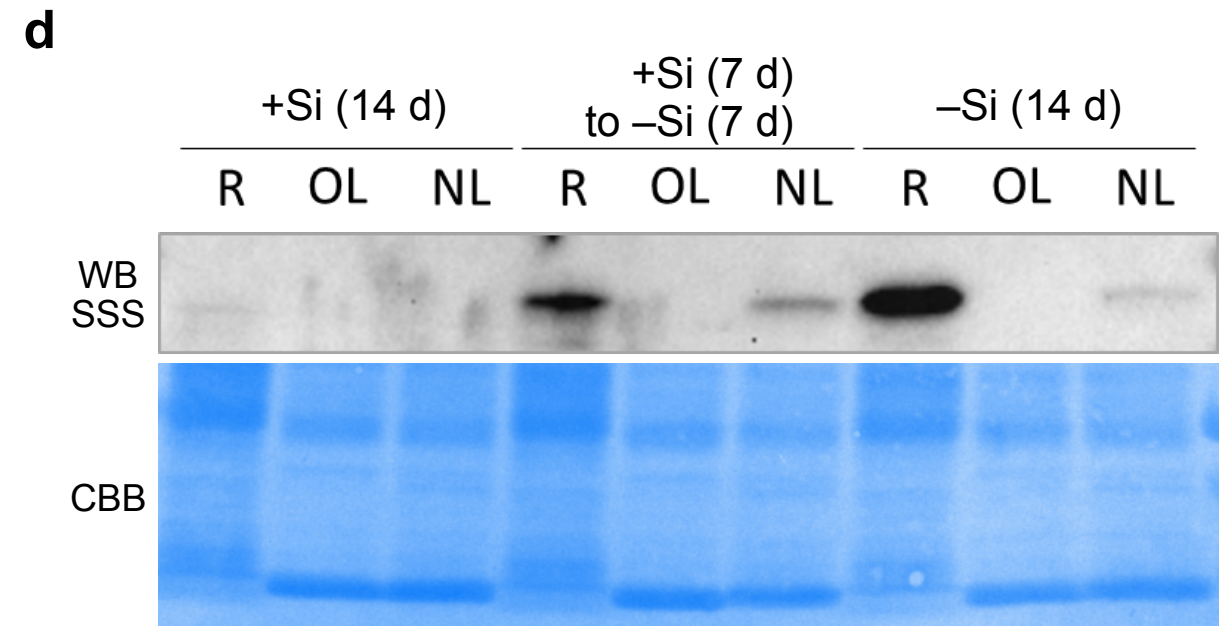
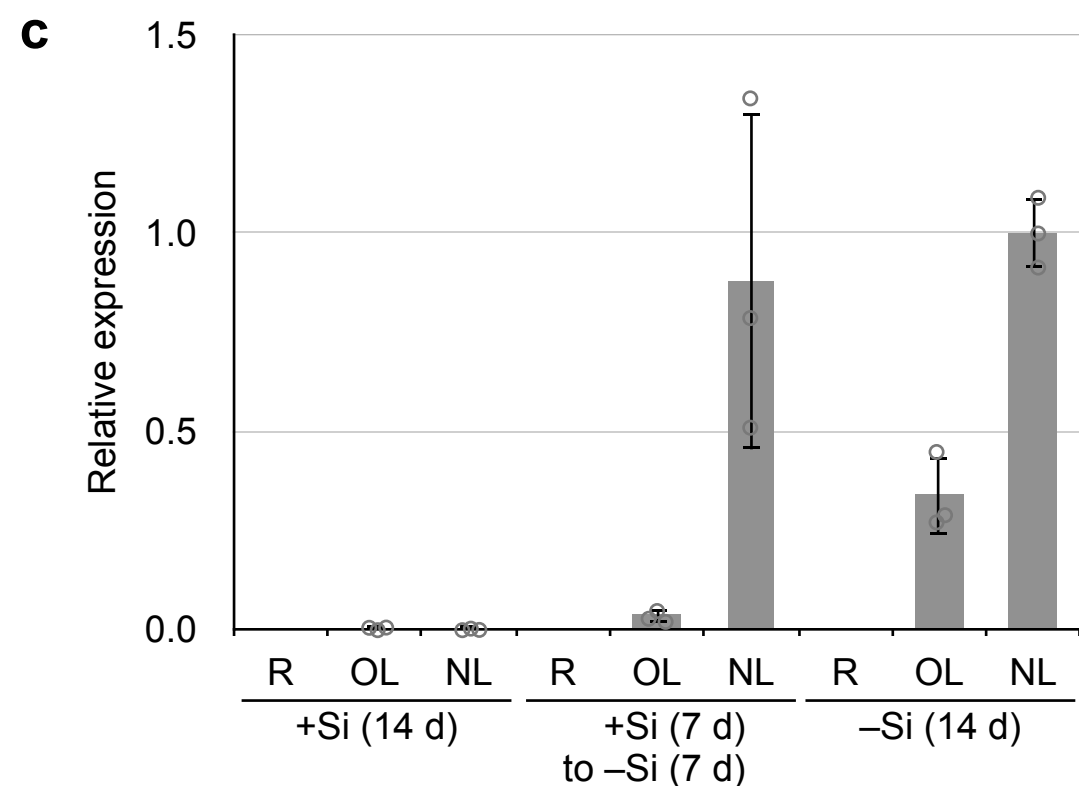
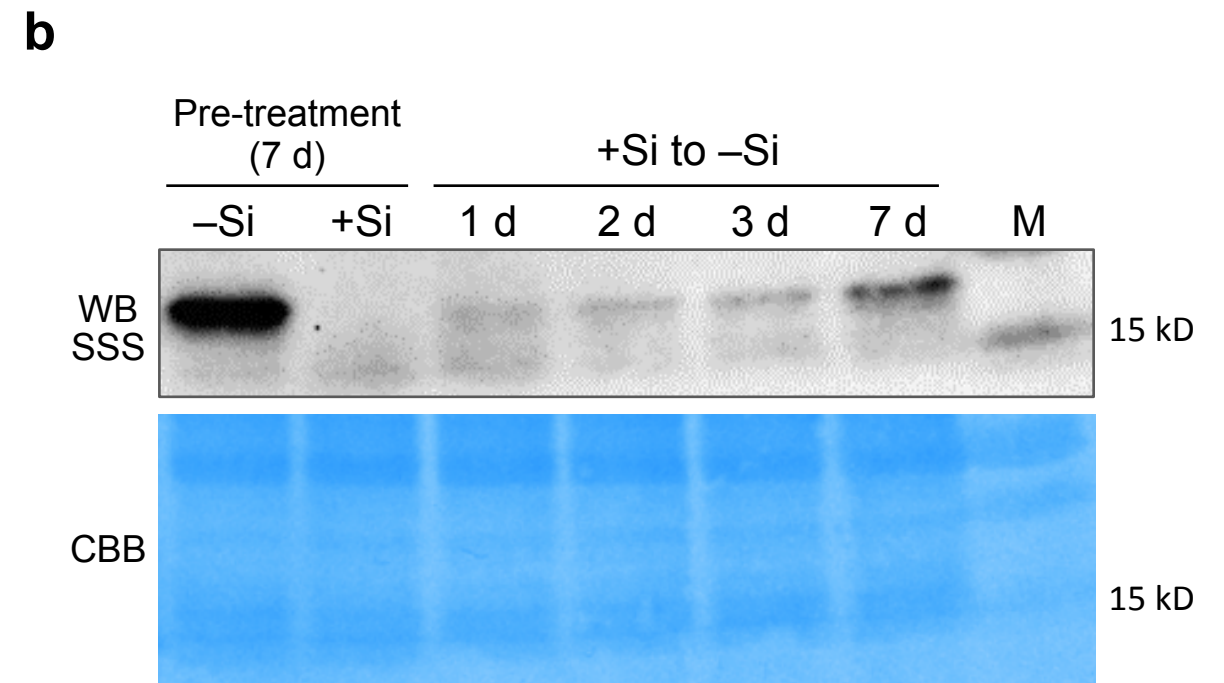
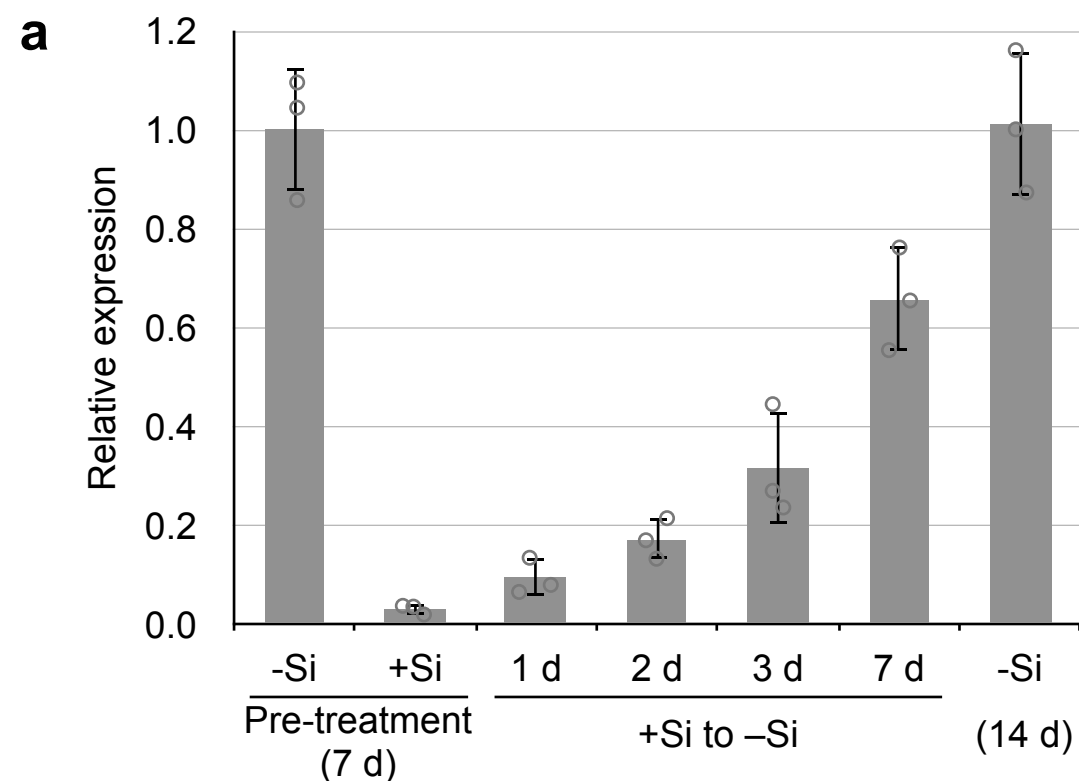
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Supplemental Figure 2.
Amino acid sequence alignment of FT/Hd3a homologs in rice (Os-) and Arabidopsis (At-) together with Moso bamboo (Pe-) and maize (Zm-) FTL12.



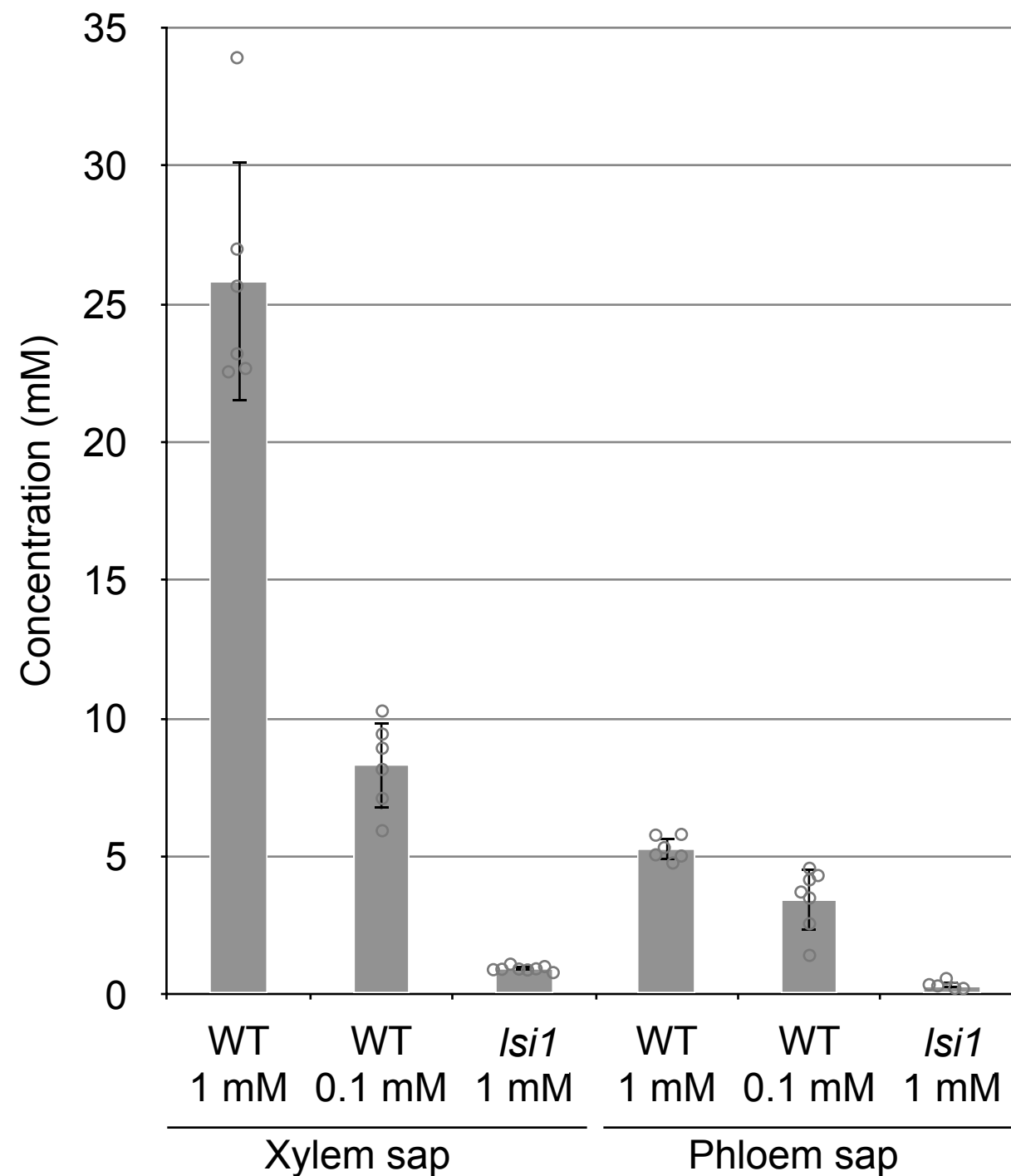
Supplemental Figure 3. Expression of SSS/*OsFTL12* orthologs in wheat, maize and moso bamboo.

(a, b) Wheat seedlings at 4-leaf stage were treated without Si (a) or with 0.5 mM Si (b) and gene expressions of *TaFTL12A*, *TaFTL12B* (not specifically amplified by PCR) and *TaFTL12D* in the root, shoot and shoot basal region (a) or the shoot (b) were measured by real-time RT-PCR at each time point. (c) Maize seedlings at 4-leaf stage were treated with or without 0.5 mM Si for 9 days and gene expressions of *ZmFTL12* (c) in the root, shoot and shoot basal region were measured by real-time RT-PCR. (d) Moso bamboo seedlings at 4-leaf stage were treated with 0.5 mM Si and gene expressions of *PeFTL12* (d) in the shoot and root were measured by real-time RT-PCR at each time point. Data represent mean $\pm$ SD of 4 (a, c) or 3 (b, d) biological replicates. Source data are provided as a Source Data file.



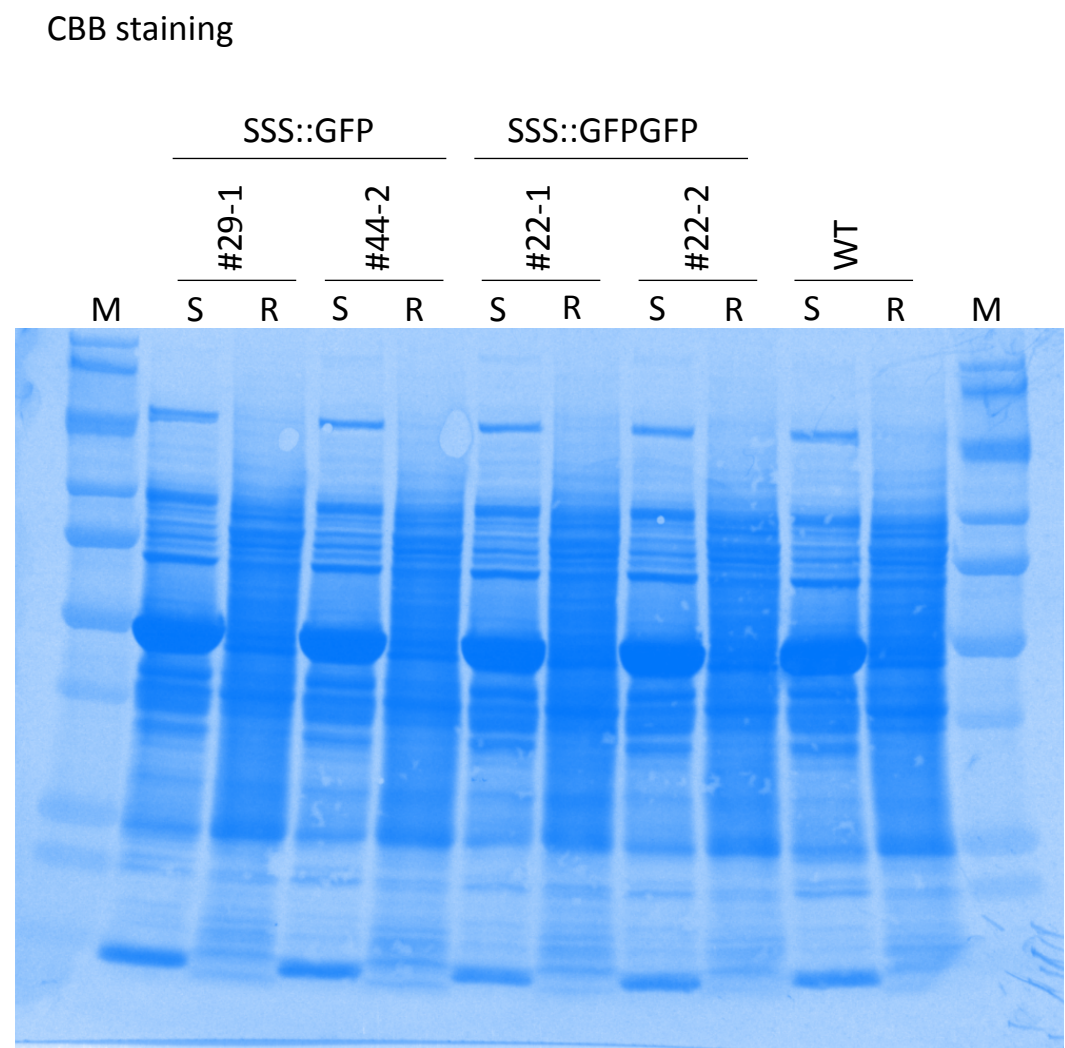
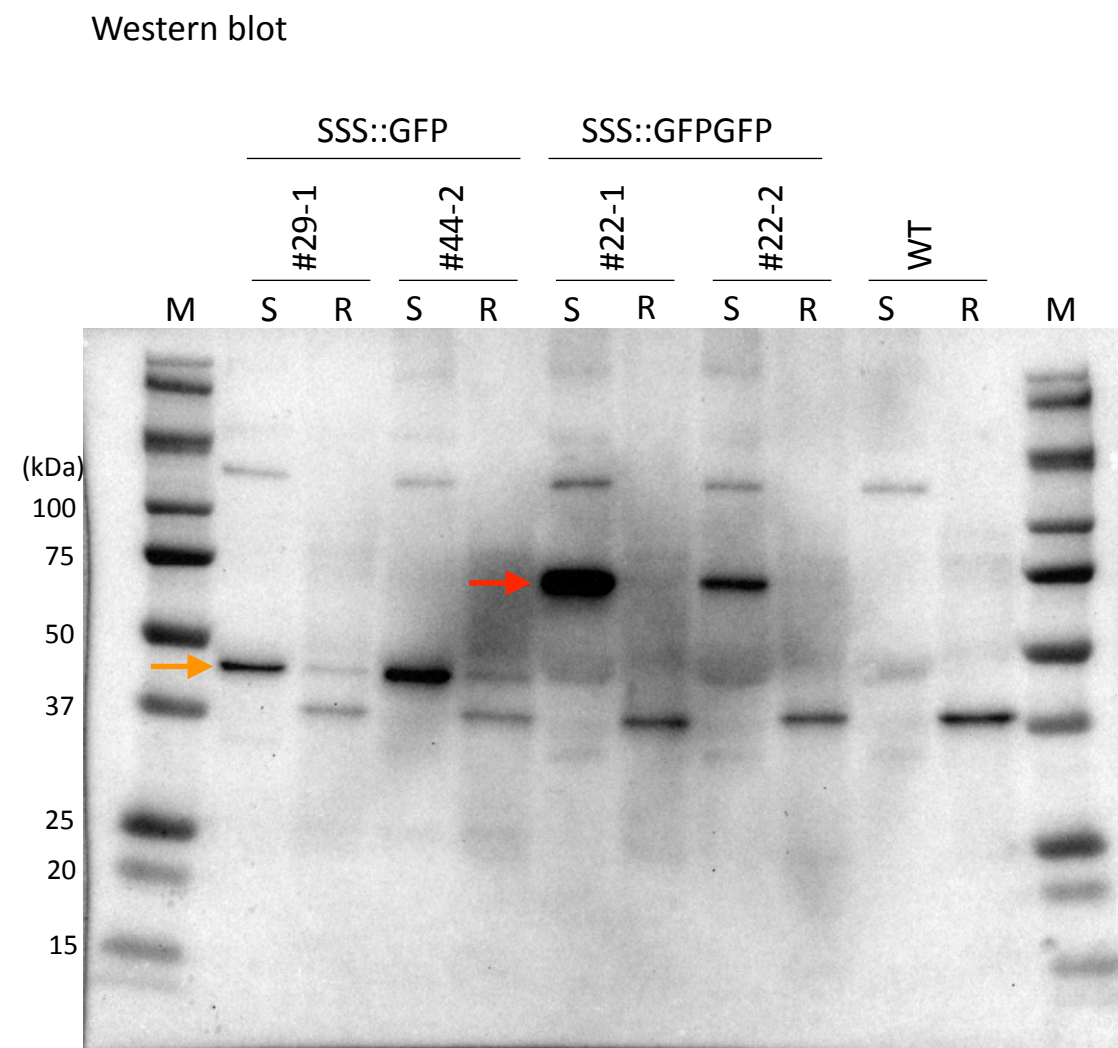
Supplemental Figure 4. Recovery of SSS expression by Si starvation.

Three-week-old WT seedlings pre-treated with or without 1 mM Si for 7 days were subjected to Si starvation treatment for another 7 days. SSS gene expression and SSS protein abundance were measured by real-time RT-PCR and western blot, respectively. Time-course gene expression in shoot (**a**) and protein abundance in root (**b**) response to Si starvation treatment. Gene expression (**c**) and protein abundance (**d**) in root (R), old leaf (OL) and new leaf (NL) after treatment. Gene expression data represent mean $\pm$ SD of 3 biological replicates. For western blot, 10 μ g total protein was loaded in each lane. CBB staining was shown as loading control. Source data are provided as a Source Data file.

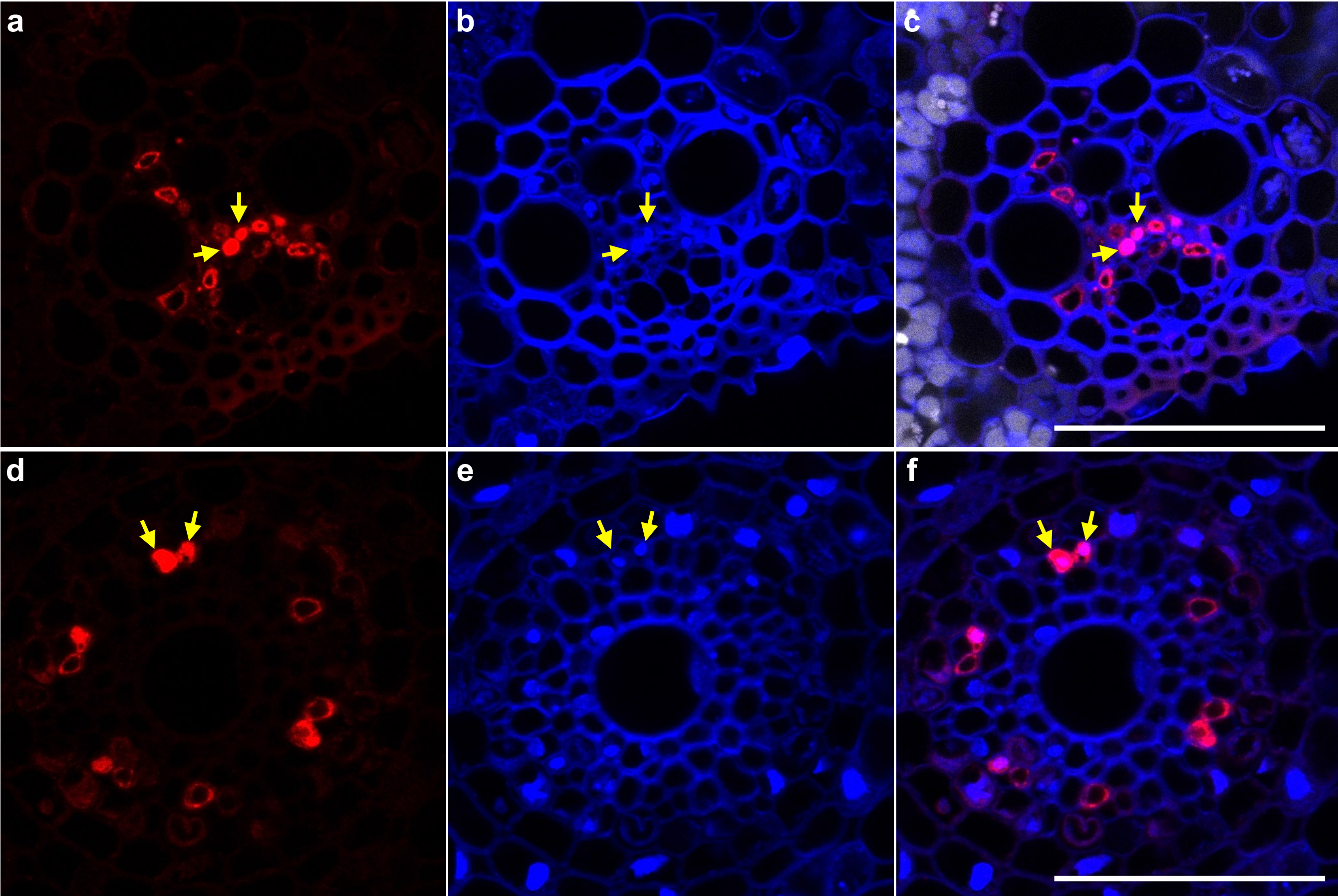


Supplemental Figure 5. Si concentration in xylem and phloem sap

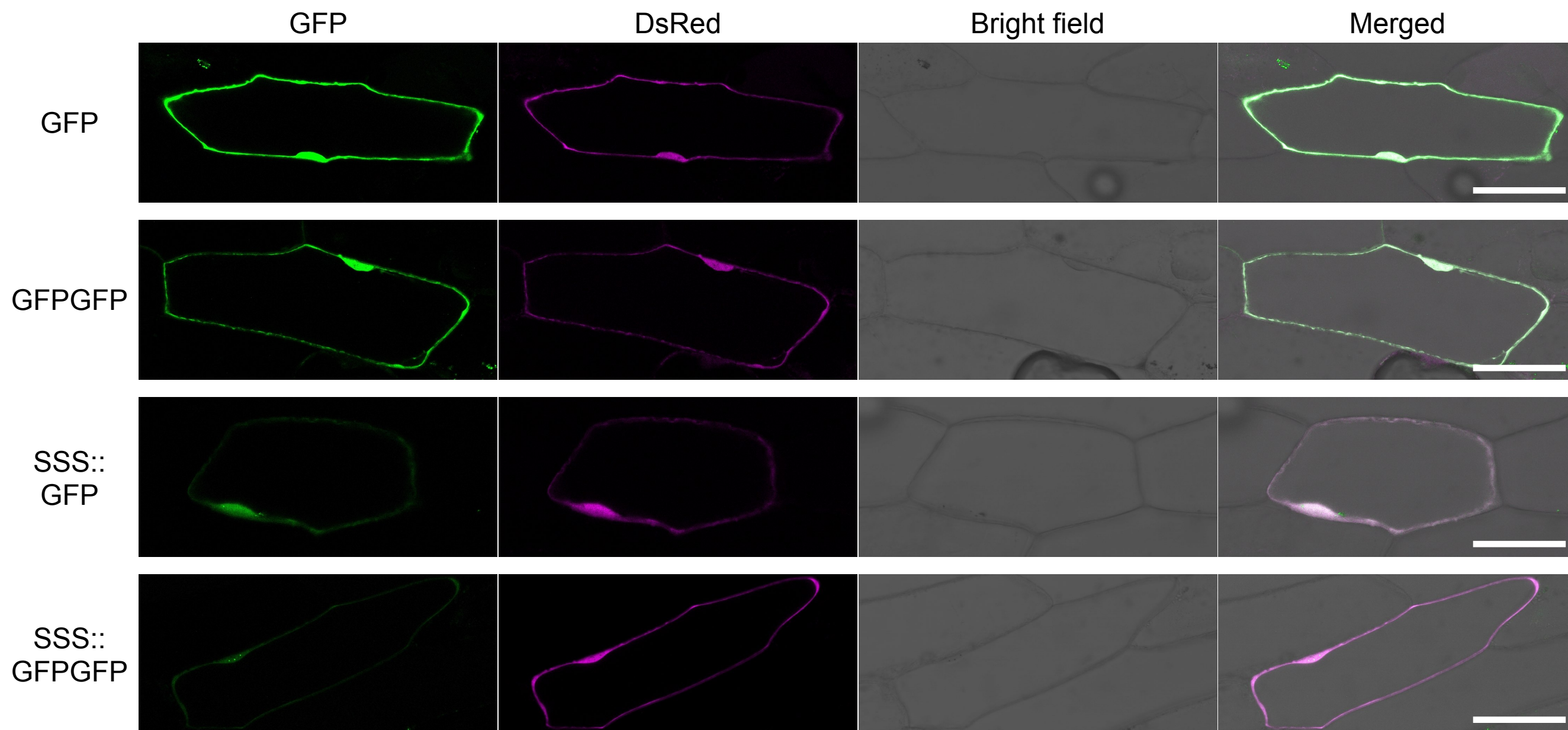
Four-week-old seedlings of WT and *Isi1* mutant grown hydroponically without Si were treated with 1 or 0.1 mM Si and immediately applied for DIY-insect laser method. Phloem saps were acquired during 5 to 32 hours after Si treatment, then the shoots were excised by laser blade and xylem saps were acquired. Xylem and phloem sap samples were diluted by 5% HNO₃ and the Si concentration were measured by ICP-MS. Data represent mean $\pm$ SD of 5~8 biological replicates. Source data are provided as a Source Data file.



Supplemental Figure 6. Western blot of SSS::GFP and SSS::GFPGFP. Three-week-old pSSS-SSS::*GFP/GFPGFP* transgenic lines together with WT grown hydroponically without Si were subjected western blot. Shoot (S) and root (R) 14 µg total protein was loaded in each lane. Orange and red arrows indicate SSS::GFP and SSS::GFPGFP protein, respectively. CBB staining was shown as loading control. M: protein size marker.

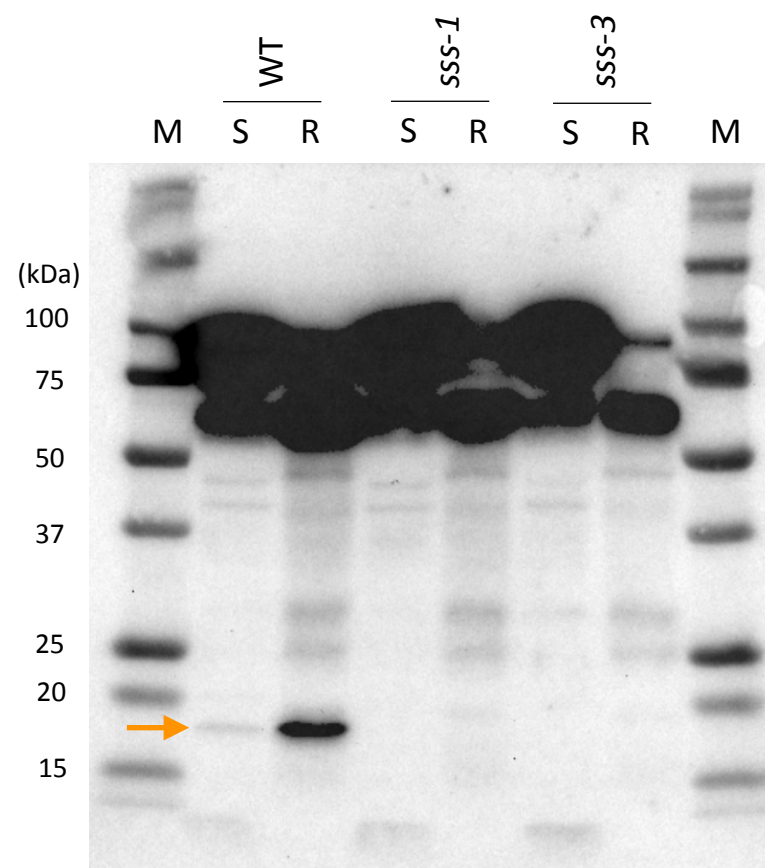


Supplemental Figure 7. Subcellular localization of SSS::GFP fusion protein in leaf and root. Leaf blade (a-c) and root (d-f) of pSSS-SSS::GFP transgenic rice grown hydroponically without Si were used for immunostaining by GFP antibody. Red (a, d) and blue (b, e) colors indicate signals from secondary antibody, and nuclei stained by DAPI together with cell wall autofluorescence, respectively. (c, f) are merged images. Yellow arrows indicate cell examples, which showed both antibody and DAPI signals on a same focal plane. Bar = 50 μ m.

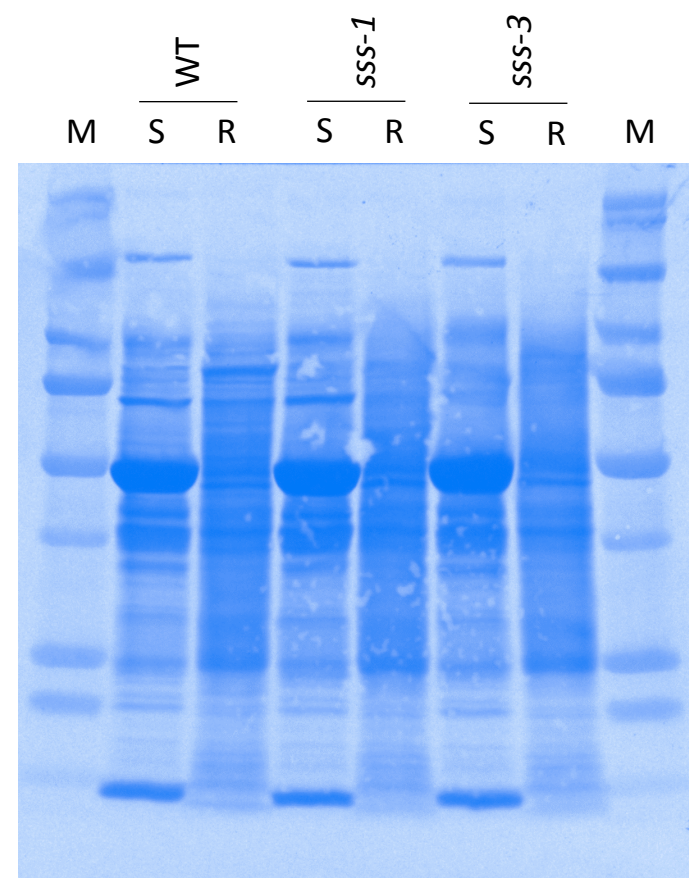


Supplemental Figure 8. Subcellular localization of SSS::GFP and SSS::GFPGFP fusion protein in onion epidermal cell. *GFP*, *GFPGFP*, *SSS::GFP*, and *SSS::GFPGFP* were transiently introduced into onion epidermal cells together with DsRed as a marker of nucleus and cytosol localization by particle bombardment. Bar = 100 μ m.

Western blot

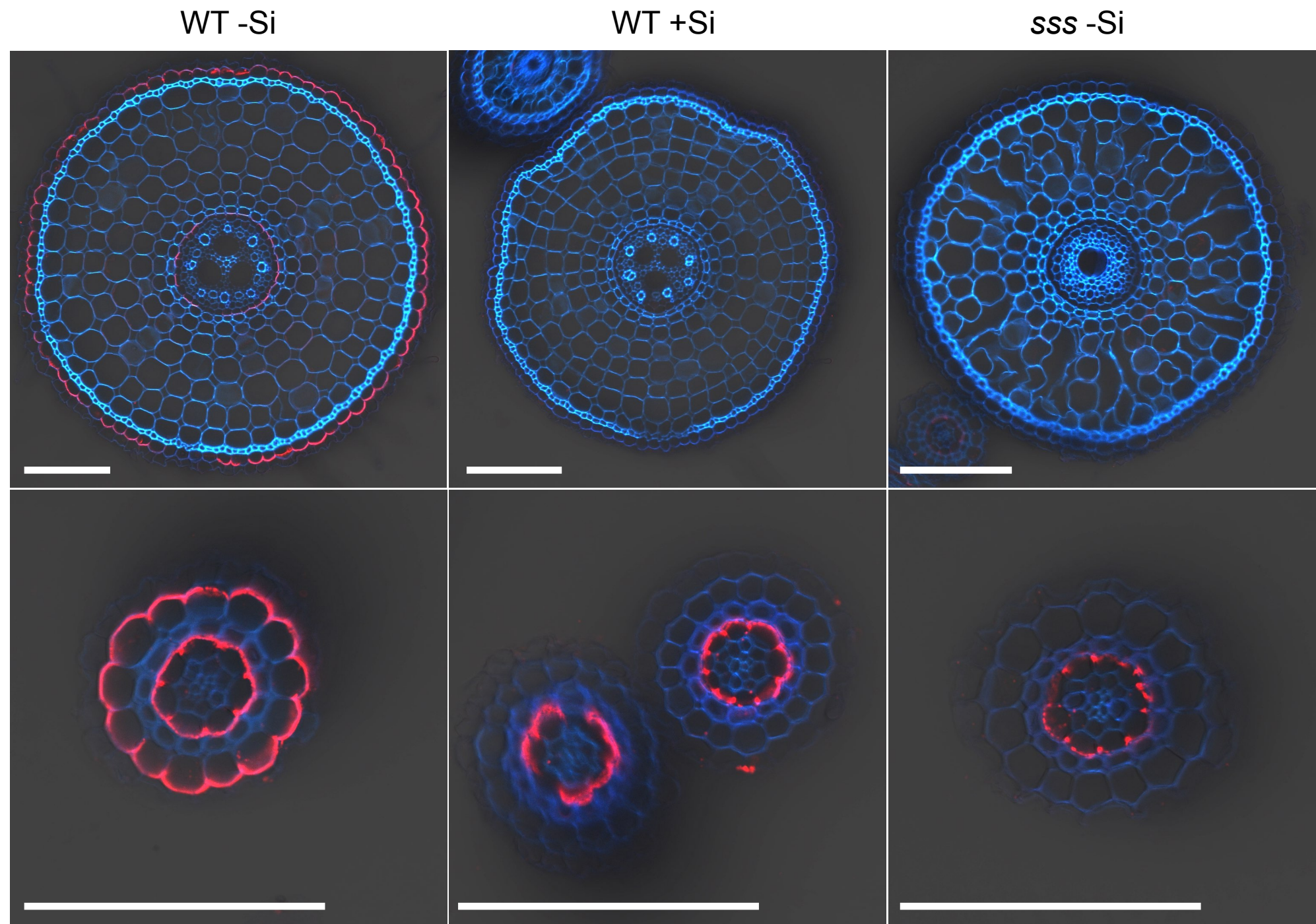


CBB staining

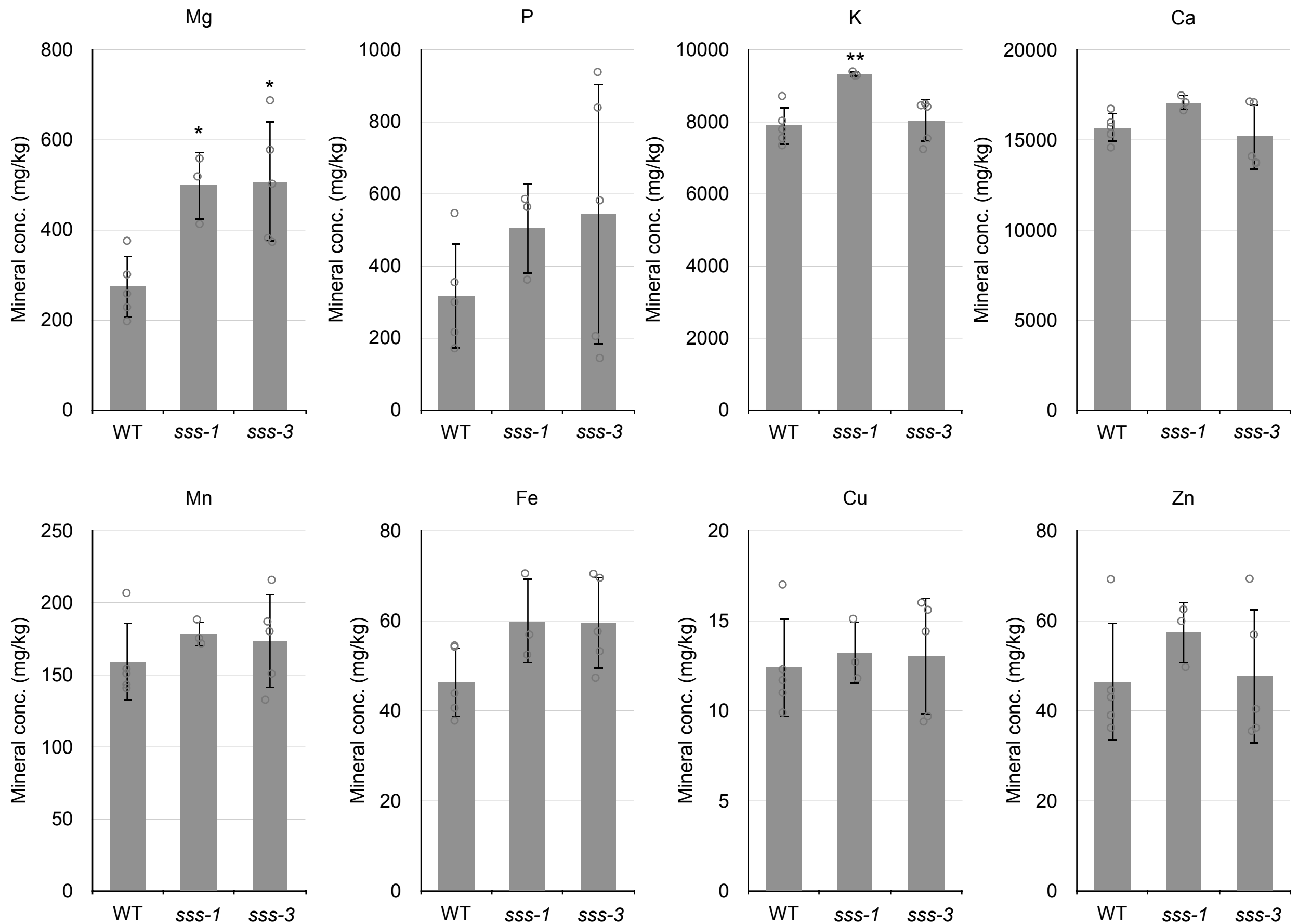


Supplemental Figure 9. Western blot of SSS in mutant root and shoot

Three-week-old WT and two *sss* mutants grown hydroponically without Si were subjected western blot. Shoot (S) and root (R) 14 μ g total protein was loaded in each lane. Orange arrow indicates SSS protein. CBB staining was shown as loading control. M: protein size marker.

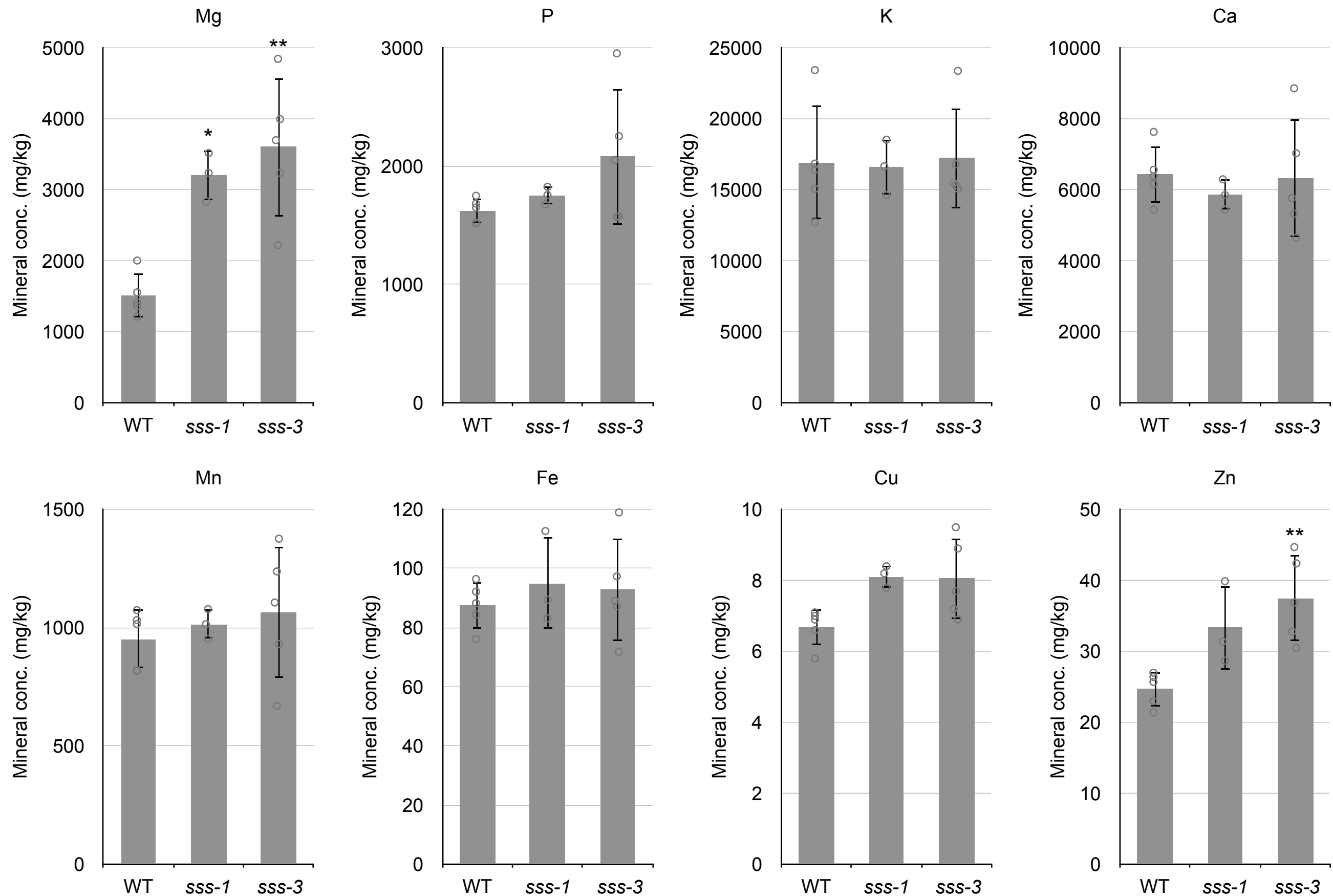


Supplemental Figure 10. Immunostaining of Lsi1 in *sss* mutant. Main root (upper panel) and lateral root (lower panel) of WT and *sss-1* mutant grown hydroponically with or without 1 mM Si for 1 week were used for immunostaining of Lsi1. Red and blue colors indicate signals from secondary antibody and cell wall autofluorescence, respectively. Bar = 100 μ m.



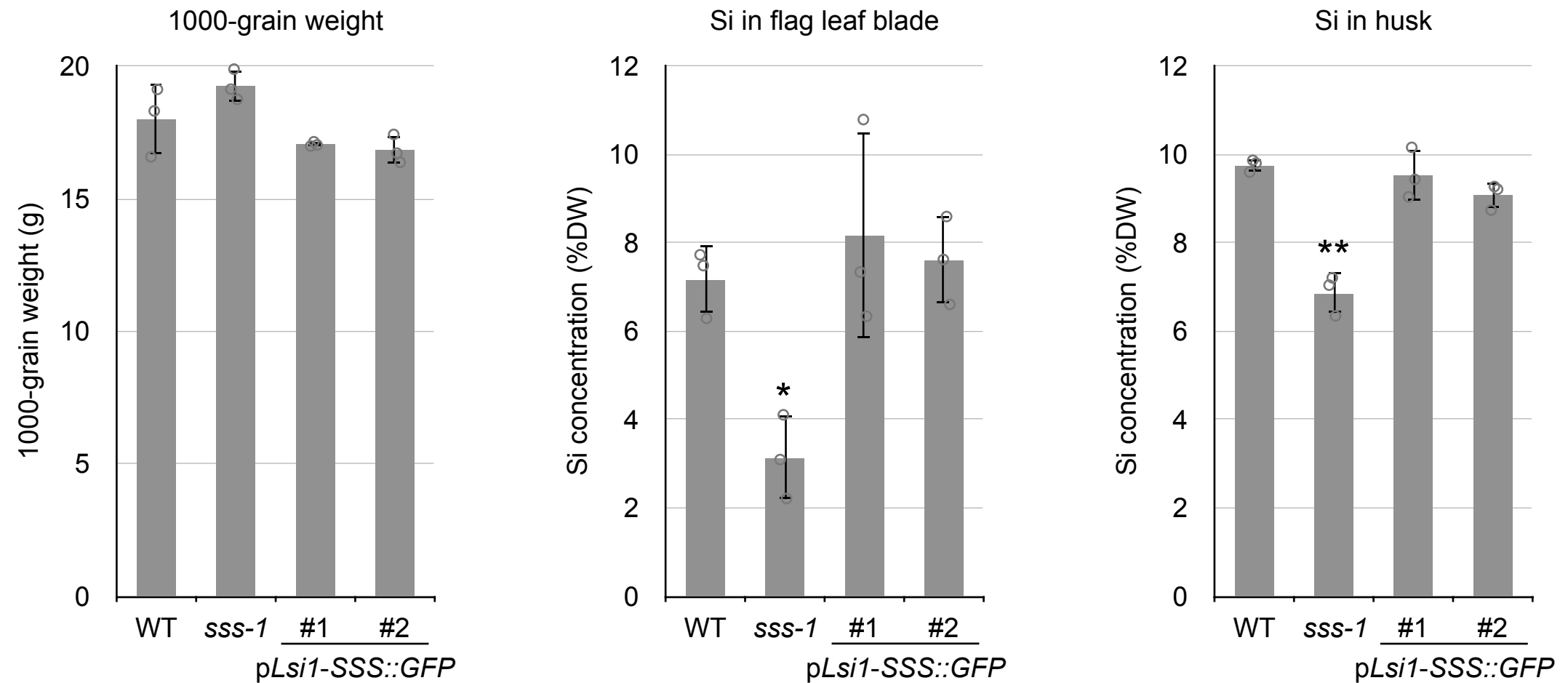
Supplemental Figure 11. Mineral concentration in husk.

WT and two independent *sss* knockout mutants were cultivated in soil pots and the mineral concentrations in the brown rice were compared at the harvest. Data represent mean $\pm$ SD of 5 (WT, *sss-3*) or 3 (*sss-1*) biological replicates. Significant differences compared with WT are marked with * $p < 0.05$ or ** $p < 0.01$ by two-sided Tukey's test. Source data are provided as a Source Data file.



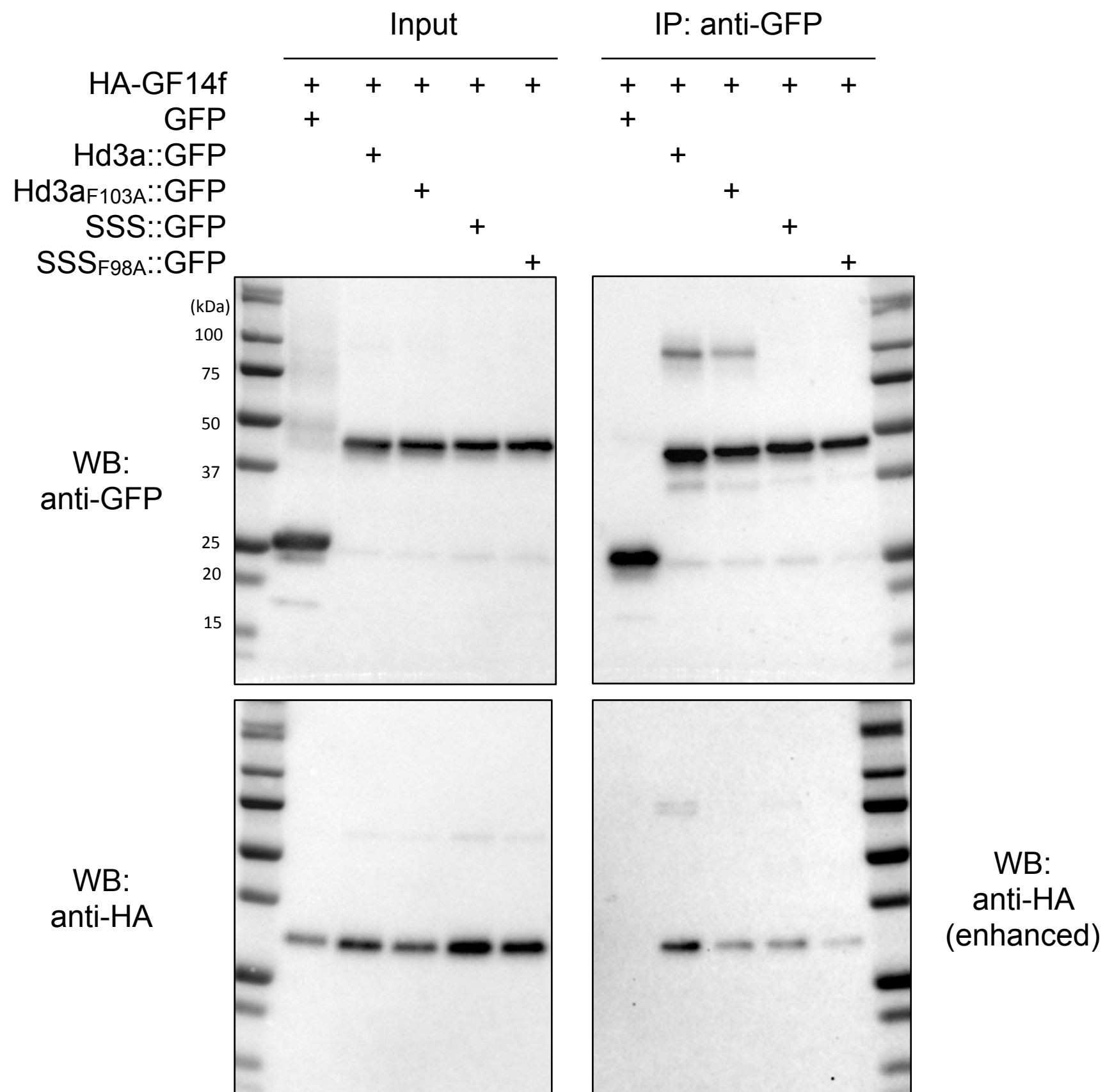
Supplemental Figure 12. Mineral concentration in flag leaf blade.

WT and two independent *sss* knockout mutants were cultivated in soil pots and the mineral concentrations in the flag leaf blade were compared at the harvest. Data represent mean $\pm$ SD of 5 (WT, *sss-3*) or 3 (*sss-1*) biological replicates. Significant differences compared with WT are marked with * $p < 0.05$ or ** $p < 0.01$ by two-sided Tukey's test. Source data are provided as a Source Data file.



Supplemental Figure 13. Phenotype of *pLsi1-SSS::GFP* transgenic rice at the harvest.

WT, *sss-1* and 2 independent *pLsi1-SSS::GFP* transgenic rice lines were cultivated in soil pots until ripening, and the 1000-grain weight and Si concentrations in the flag leaf blade and husk were investigated. Data represent mean $\pm$ SD of 3 biological replicates. Significant differences compared with WT are marked with * $p < 0.05$ or ** $p < 0.01$ by two-sided Tukey's test. Source data are provided as a Source Data file.



Supplemental Figure 14. Interaction between SSS and GF14f

Each protein transiently expressed in rice leaf protoplasts and subjected to immune-precipitation using antibody against GFP. Western blot was conducted with GFP and HA-tag antibodies.

Supplementary Table 1. Proteome analysis of phloem sap. Proteins detected at least two-times in three phloem sap samples (~Si #1, #2 and +Si for 3 days) or Aki et al., 2008 (18) were listed.

	Peptide matches						Name	Aki et al., 2008	Annotation
	-SI #1	Score	-SI #2	Score	+SI	Score			
Os07g0683900	30	855	31	747	20	484	OsEULD1a	+	D-type euonymus-related lectin (EUL), Response to drought stress and ABA treatment, Response to biotic treatment
Os12g0632000	13	584	17	615	10	474	OsGPP162	+	Gly-rich protein, Partner protein of RF5, Fertility restoration
Os01g0963600	15	557	9	317	14	519	OsASR6	+	ASR (abscisic acid, stress and ripening) transcription factor, Suppression of resistance to bacterial diseases caused by Xanthomonas oryzae pv. oryzae (Xoo) and X. oryzae pv. oryzicola (Xoc)
Os01g0910900	11	336	17	409	9	275	-	+	Conserved hypothetical protein.
Os02g0121300	12	409	15	508	10	316	LRT2/OSCYP2	+	Cyclophilin, Peptidyl-prolyl cis-trans isomerase, Auxin signal transduction, Lateral root initiation, Stress tolerance
Os06g0650100 etc.	13	309	15	352	6	216	Ubiquitin	+	Ubiquitin-NEDD8-like protein
Os07g0186000	9	222	15	370	9	272	RPP13-1/OsTR001	+	Phloem sap 13 kDa protein 1, H-type thioredoxin, Regulation of the apoplastic reactive oxygen species, Stress response
Os03g0670700	8	287	9	361	7	351	OsGPP3	-	Similar to Glycine-rich RNA-binding, abscisic acid-inducible protein.
Os05g0116100	8	224	9	218	5	181	OsDHAR	+	Dehydroascorbate reductase, Ascorbate homeostasis, Recycling of ascorbate, Inhibitor of stress-induced protein aggregation
Os07g0684000	6	168	13	289	3	64	OsEULS2	-	S-type euonymus-related lectin (EUL), "Response to salt and drought stress, ABA treatment", Response to biotic treatment
Os04g0508300	4	113	7	257	6	186	OsGRX14	+	Glutaredoxin.
Os01g0910500	5	156	5	121	5	186	-	+	Conserved hypothetical protein.
Os02g0760300	5	233	5	219	5	202	OsFKBP12	+	Rice immunophilin homolog, FK506-binding protein, Negative regulation of biotic and abiotic stress response
Os03g0135100	9	244	3	90	3	71	OsGSTF15	+	Glutathione S-transferase
Os05g0574500	6	138	5	184	3	85	OsRAN2	+	Ras-like nuclear GTPase, Regulation of cell division during cold stress, Cold tolerance, Abiotic stress response
Os03g0134900	7	195	3	106	3	98	OsGSTF14	+	Glutathione S-transferase
Os03g0285700	5	171	6	196	2	126	OsAPX1	+	Cytosolic ascorbate peroxidase, Salt tolerance, Rice blast resistance
Os03g0388900	5	176	3	89	5	166	OsMCI	+	Metacaspase 1, Response to abiotic and biotic stresses
Os08g0129200	3	147	8	194	2	141	OsCSP2	+	Cold shock protein 2
Os08g0191700	4	152	4	160	3	125	OsGLY11	+	Glyoxalase I, Abiotic stress response, requiring Ni(2+) as a cofactor
Os02g0121100	3	99	3	118	3	108	OsCSP1	+	cold shock domain protein 1, Zinc finger, CCHC-type domain containing protein.
Os02g0793700	3	104	4	175	2	65	OsSRP/OsCYB5-9	+	Similar to Membrane steroid-binding protein 1.
Os07g0597000	4	108	5	141	-	-	OsIFSA-1	+	Eukaryotic translation initiation factor 5 A-1, Developmental and environmental responses
Os01g0642200	3	122	2	79	3	100	-	+	Conserved hypothetical protein.
Os08g0374000	1	37	7	231	-	-	OsBetv1	+	Bet v I allergen family protein.
Os03g0327600	2	71	5	112	-	-	OsEULD1b	+	D-type euonymus-related lectin (EUL), "Response to salt and drought stress, hormone treatment", Response to biotic treatment
Os05g0113400	4	111	2	52	1	26	OsADF7	+	Similar to Actin-depolymerizing factor 2 (ADF 2).
Os12g0507200	-	-	5	92	2	42	OsIFSA-2	+	Eukaryotic translation initiation factor 5A
Os02g0628800, Os11g0145400	2	90	2	41	2	94	OsUBL5.1/5.2	-	Ubiquitin-like domain, Similar to GRF zinc finger family protein.
Os03g0718100 etc.	3	85	-	-	3	72	ACT1	+	Actin 1.
Os03g0780400	2	117	3	50	1	29	OsADF2	+	Actin depolymerizing factor, Actin-binding protein, Abiotic stress response
Os05g0188100	1	57	3	101	1	46	-	+	Conserved hypothetical protein.
Os01g0971000	-	-	2	76	2	74	-	+	Conserved hypothetical protein.
Os02g0169300	3	61	1	25	-	-	OsPGK2	+	Phosphoglycerate kinase 2
Os02g0203700	1	26	2	50	1	38	OsSRZ1/LS1	+	stress repressive zinc finger protein 1, Leaf Senescence 1
Os04g0556300	2	86	-	-	2	73	OsGPK1	-	Glutathione peroxidase, Rponse to salt, cold and drought stress
Os06g0152100	1	-	3	82	-	-	OsPRF2	-	Profilin-2, actin binding
Os07g0671000	2	67	2	87	-	-	OsFFL5/ACL1	-	Homologue of Arabidopsis FLOWERING PROMOTING FACTOR1 (FPF1), ACE1 homologue, Control of internode elongation during the reproductive phase
Os08g0366100	1	65	1	55	2	53	EDF	+	Similar to Endothelial differentiation-related factor 1 (EDF-1) (Multiprotein bridging factor 1) (MBF1).
Os01g0104400	2	80	1	92	-	-	OsEULS3	+	S-type euonymus-related lectin (EUL), Response to ABA treatment
Os04g0282400	2	71	1	28	-	-	OsFFL4	+	Modulation of root and flower development, Control of auxin accumulation, Modulation of ROS homeostasis
Os05g0508500	1	71	1	52	1	73	OsTRON2	-	Thioredoxin protein, Bacterial F-box effector (XopI)-interacting protein, Regulation of rice immunity
Os06g0538900	2	26	1	54	-	-	DUF538	+	Protein of unknown function DUF538 domain containing protein.
Os06g0552900	1	44	2	76	-	-	SSS/OsFTL12	+	FT-like gene 12, Flowering Locus T-like 12
Os09g0297100	3	87	-	-	-	-	OsLEV1C	-	ubiquitin-conjugating enzyme variant protein 1C
Os09g0411700	-	-	2	78	1	52	-	-	Peptidyl-prolyl cis-trans isomerase, PpiC-type domain containing protein.
Os09g0458900	1	39	1	37	1	38	EF-hand	-	EF hand domain containing protein.
Os10g0205200	2	75	1	40	-	-	-	+	Similar to Ufm1-conjugating enzyme 1 (Ubiquitin-fold modifier conjugating enzyme 1).
Os12g0515800	1	64	1	38	1	54	OsDX1	-	Green tissue-specific expression gene
Os12g0605400	-	-	3	55	-	-	OsLEV1B	-	Ubiquitin-conjugating enzyme variant protein, Phosphate homeostasis
Os01g0127700	-	-	1	32	1	30	RLCK19	-	Conserved hypothetical protein, Receptor-like Cytoplasmic Kinase 19
Os01g0210600	1	56	1	61	-	-	DUF538	+	Protein of unknown function DUF538 family protein.
Os01g0866600	1	29	-	-	1	18	-	+	Similar to boIA-like protein. 2 iron, 2 sulfur cluster binding
Os02g0300700, Os06g0342200	1	52	-	-	1	22	OsEIF1A-1/2	-	Translation initiation factor 1A
Os02g0583000	1	32	-	-	1	29	-	-	Hypothetical protein.
Os02g0622400	1	32	-	-	1	65	-	+	Glycolipid transfer protein, GLTP domain containing protein.
Os02g0664100	-	-	1	23	1	31	-	-	UDP-glucose:glycoprotein glucosyltransferase
Os03g0820600	2	71	-	-	-	-	OsADF4	+	Similar to Actin-depolymerizing factor 3 (ADF 3) (ZmABP3) (ZmADF3).
Os05g0142400	-	-	2	88	-	-	-	+	Conserved hypothetical protein.
Os06g0498800	-	-	1	43	1	48	OsMFT1	+	Homolog of Arabidopsis MOTHER OF FT AND TFL1, Regulation of heading and panicle architecture
Os08g0162800	-	-	2	83	-	-	OsACBP1	+	Acyl-CoA-binding protein 1, Stress response
Os08g0205400	1	32	1	34	-	-	OsATX1	+	Cu chaperone, Root-to-shoot Cu translocation, Distribution of Cu from old leaves to developing tissues and seeds
Os10g0495600	1	37	-	-	1	38	-	-	Similar to DNA-directed RNA polymerase.
Os10g0543800	2	74	-	-	-	-	OsRPP31/OGSTP6	-	31 kDa rice phloem protein, phloem specific glutathione S-transferase, PHI GLUTATHIONE S-TRANSFERASE 6
Os11g0660500	1	47	1	52	-	-	OsTCTP	+	Translationally controlled tumor protein, Mercury tolerance
Os12g0502000	-	-	2	41	-	-	-	-	Similar to nitrilase-associated protein.
Os01g0170600	1	45	-	-	-	-	OsUSP1	+	universal stress protein 1
Os01g0974200	-	-	1	36	-	-	OsMT2c	+	Metallothionein
Os05g0111300	-	-	1	41	-	-	OsMT2b	+	Metallothionein, Distribution of Zn to grain
Os01g0813400 etc.	-	-	1	60	-	-	OsANFA1a	+	Similar to ADP-ribosylation factor 1.
Os03g0417800	-	-	1	29	-	-	-	+	Nitrilase-associated protein-like
Os09g0529100	1	53	-	-	-	-	-	+	6-phosphogluconolactonase domain containing protein.
Os10g0159700	1	45	-	-	-	-	OsCIA	+	Cold-induced anther protein

Supplementary Table 2 Genes significantly down- or up-regulated (more than two times) in sss -Si compared to WT -Si (FPKM >10 in either WT -Si or sss -Si), FPKM represent mean of 3 biological replicates. Two-sided statistics for differential expression (Q-value of false discovery rate > 0.05) was performed.																						
gene ID	WT -Si	sss -Si	WT +Si	sss +Si	log2(fold change)	p_value	q_value	significant	log2(fold change)	p_value	q_value	significant	log2(fold change)	p_value	q_value	significant	log2(fold change)	p_value	q_value	significant	memo	Note
	mean FPKM in Root				WT-Si vs sss-Si				WT-Si vs WT+Si				sss-Si vs sss+Si				WT+Si vs sss+Si					
Os03g0307300	22.0	1.6	3.0	1.0	(3.793)	0.000	0.001	yes	(2.871)	0.000	0.001	yes	(0.710)	0.014	0.092	no	(1.632)	0.000	0.001	yes	NAS1	Nicotianamine synthase 1 (EC 2.5.1.43) (S-adenosyl-L-methionine:S- adenosyl-L-methionine:S-adenosyl-methionine 3-amino-3- carboxypropyltransferase 1) (OsNAS1). (Os03t0307300-01)
Os04g0127100	12.0	0.9	2.3	0.6	(3.750)	0.000	0.001	yes	(2.380)	0.000	0.001	yes	(0.576)	0.143	0.411	no	(1.945)	0.000	0.001	yes		Peptidase S8, subtilisin-related domain containing protein. (Os04t0127100-01)
Os03g0227700	13.4	1.0	1.8	0.9	(3.725)	0.000	0.001	yes	(2.865)	0.000	0.001	yes	(0.167)	0.381	0.685	no	(1.026)	0.000	0.001	yes		Cytochrome P450 90B2, Brassinosteroid C-22 hydroxylase, Brassinosteroids biosynthesis (Os03t0227700-01)
Os04g0127200	49.6	4.2	17.1	3.7	(3.560)	0.000	0.001	yes	(1.539)	0.000	0.001	yes	(0.169)	0.300	0.609	no	(2.189)	0.000	0.001	yes		Hypothetical conserved gene. (Os04t0127200-01);Similar to Subtilase. (Os04t0127200-02)
Os08g0302000	22.7	2.3	2.0	0.7	(3.337)	0.000	0.001	yes	(3.523)	0.000	0.001	yes	(1.760)	0.000	0.001	yes	(1.574)	0.000	0.001	yes		Similar to Peroxidase 40 precursor (EC 1.11.1.7) (Atperox P40). (Os08t0302000-01)
Os11g0229500	12.4	1.8	15.1	1.7	(2.816)	0.000	0.001	yes	0.286	0.047	0.207	no	(0.031)	0.875	0.959	no	(3.133)	0.000	0.001	yes		Similar to NBS-LRR protein (Fragment). (Os11t0229500-01)
Os06g0129100	12.4	1.8	7.8	2.1	(2.805)	0.000	0.001	yes	(0.672)	0.000	0.001	yes	0.216	0.269	0.577	no	(1.917)	0.000	0.001	yes		Short-chain dehydrogenase/reductase SDR family protein. (Os06t0129100-01)
Os04g0415800	49.8	7.8	6.1	4.0	(2.674)	0.000	0.001	yes	(3.033)	0.000	0.001	yes	(0.977)	0.001	0.013	yes	(0.618)	0.035	0.172	no		Similar to OSIGBa0092M08.2 protein. (Os04t0415800-00)
Os03g0307200	22.4	3.7	3.8	3.6	(2.585)	0.000	0.001	yes	(2.566)	0.000	0.001	yes	(0.073)	0.736	0.904	no	(0.093)	0.669	0.872	no	NAS2	Nicotianamine synthase 2, Nicotianamine biosynthesis (Os03t0307200-01)
Os09g0445600	26.4	5.3	5.6	4.8	(2.328)	0.000	0.001	yes	(2.245)	0.000	0.001	yes	(0.129)	0.571	0.819	no	(0.212)	0.355	0.662	no		Similar to oxidoreductase/ transition metal ion binding protein. (Os09t0445600-01)
Os11g0484700	23.7	4.8	7.9	4.2	(2.320)	0.000	0.001	yes	(1.584)	0.000	0.001	yes	(0.191)	0.587	0.828	no	(0.926)	0.006	0.052	no		Bifunctional inhibitor/plant lipid transfer protein/seed storage domain containing protein. (Os11t0484700-00)
Os10g0175500	17.1	3.4	14.8	3.7	(2.314)	0.000	0.001	yes	(0.213)	0.233	0.535	no	0.115	0.635	0.854	no	(1.986)	0.000	0.001	yes		Hypothetical gene. (Os10t0175500-01)
Os05g0205400	49.7	10.1	12.5	8.9	(2.293)	0.000	0.001	yes	(1.993)	0.000	0.001	yes	(0.188)	0.567	0.816	no	(0.488)	0.123	0.378	no		Conserved hypothetical protein. (Os05t0205400-00)
Os03g0107300	3284.2	681.8	1032.7	362.3	(2.268)	0.000	0.001	yes	(1.669)	0.000	0.001	yes	(0.912)	0.000	0.001	yes	(1.511)	0.000	0.001	yes	Lsi2	Anion transporter, Silicon efflux transporter, Arsenic species (As) uptake (Os03t0107300-01)
Os05g0588900	18.5	4.0	7.2	5.5	(2.204)	0.000	0.001	yes	(1.359)	0.000	0.001	yes	0.460	0.047	0.209	no	(0.385)	0.144	0.411	no		Similar to mitochondrial chaperone BCS1. (Os05t0588900-01)
Os12g0555100	39.9	8.7	20.6	5.3	(2.188)	0.000	0.001	yes	(0.954)	0.000	0.001	yes	(0.718)	0.000	0.003	yes	(1.953)	0.000	0.001	yes		Similar to Probenazole-inducible protein PBZ1. (Os12t0555100-01)
Os12g0555200	48.6	11.2	31.2	11.8	(2.113)	0.000	0.001	yes	(0.636)	0.000	0.001	yes	0.075	0.640	0.857	no	(1.401)	0.000	0.001	yes		Similar to Probenazole-inducible protein PBZ1. (Os12t0555200-01)
Os01g0198500	52.7	12.5	13.0	14.3	(2.078)	0.000	0.001	yes	(2.019)	0.000	0.001	yes	0.201	0.240	0.544	no	0.142	0.404	0.704	no		Conserved hypothetical protein. (Os01t0198500-01)
Os10g0334500	18.2	4.3	10.8	2.8	(2.075)	0.000	0.001	yes	(0.758)	0.000	0.001	yes	(0.635)	0.011	0.077	no	(1.952)	0.000	0.001	yes		Similar to Dirigent-like protein, expressed. (Os10t0334500-00)
Os09g0431300	56.8	13.5	16.7	10.8	(2.074)	0.000	0.001	yes	(1.771)	0.000	0.001	yes	(0.328)	0.050	0.218	no	(0.631)	0.000	0.001	yes		Similar to MYB transcription factor MYB71 (Fragment). (Os09t0431300-00)
Os02g0745100	898.0	219.0	226.0	166.6	(2.036)	0.000	0.001	yes	(1.991)	0.000	0.001	yes	(0.395)	0.014	0.093	no	(0.440)	0.005	0.046	yes	Lsi1	Aquaporin NIP III subfamily protein, Aquaporin, Silicon influx transporter, Arsenic species (As) uptake, Arsenite efflux, Selenite (Se) uptake, Water transport (Os02t0745100-01)
Os09g0379600	20.3	5.0	10.7	5.9	(2.019)	0.000	0.001	yes	(0.920)	0.000	0.001	yes	0.227	0.248	0.553	no	(0.872)	0.000	0.001	yes		Similar to Homeobox-leucine zipper protein HOX25. (Os09t0379600-00)
Os04g0419550	54.3	14.6	29.0	17.8	(1.899)	0.000	0.001	yes	(0.906)	0.000	0.001	yes	0.285	0.098	0.331	no	(0.708)	0.000	0.001	yes		Zinc finger, RING-type domain containing protein. (Os04t0419550-01)
Os10g0527601	22.2	6.2	7.9	6.6	(1.838)	0.000	0.001	yes	(1.501)	0.000	0.001	yes	0.091	0.671	0.873	no	(0.247)	0.244	0.548	no		Glutathione S-transferase, C-terminal-like domain containing protein. (Os10t0527601-00)
Os06g0271600	75.2	21.7	23.5	13.5	(1.796)	0.000	0.001	yes	(1.680)	0.000	0.001	yes	(0.685)	0.001	0.011	yes	(0.801)	0.000	0.002	yes		Zinc finger, RING/FYVE/PHD-type domain containing protein. (Os06t0271600-00)
Os01g0838600	10.2	3.0	4.3	2.6	(1.777)	0.000	0.001	yes	(1.259)	0.000	0.001	yes	(0.174)	0.474	0.756	no	(0.693)	0.004	0.036	yes		Zinc finger, C2H2-like domain containing protein. (Os01t0838600-00)
Os01g0102900	23.4	7.0	11.8	7.5	(1.746)	0.000	0.001	yes	(0.985)	0.000	0.001	yes	0.108	0.593	0.832	no	(0.653)	0.001	0.011	yes		Light-regulated protein, Regulation of light-dependent attachment of LEAF-TYPE FERREDOXIN-NADP+ OXIDOREDUCTASE (LFNR) to the thylakoid membrane (Os01t0102900-01)
Os12g0410050	12.9	3.9	11.0	3.8	(1.743)	0.000	0.001	yes	(0.230)	0.194	0.486	no	(0.010)	0.965	0.989	no	(1.524)	0.000	0.001	yes		Hypothetical conserved gene. (Os12t0410050-01)
Os05g0463100	11.8	3.6	5.0	2.9	(1.710)	0.000	0.001	yes	(1.236)	0.000	0.001	yes	(0.305)	0.306	0.615	no	(0.779)	0.008	0.061	no		Hypothetical gene. (Os05t0463100-01)
Os06g0199700	35.1	10.8	8.7	6.6	(1.705)	0.000	0.001	yes	(2.012)	0.000	0.001	yes	(0.702)	0.007	0.057	no	(0.394)	0.122	0.375	no		Hypothetical conserved gene. (Os06t0199700-00)
Os12g0576100	1625.4	532.6	1144.8	214.6	(1.610)	0.000	0.001	yes	(0.506)	0.002	0.021	yes	(1.312)	0.000	0.001	yes	(2.416)	0.000	0.001	yes		Conserved hypothetical protein. (Os12t0576100-00)
Os08g0417000	18.5	6.3	6.7	5.6	(1.550)	0.000	0.001	yes	(1.454)	0.000	0.001	yes	(0.168)	0.347	0.654	no	(0.264)	0.140	0.406	no		2OG-Fe(II) oxygenase domain containing protein. (Os08t0417000-01)
Os02g0643800	19.9	6.9	16.2	8.1	(1.521)	0.000	0.001	yes	(0.295)	0.092	0.317	no	0.228	0.244	0.548	no	(0.998)	0.000	0.001	yes		Auxin responsive SAUR protein family protein. (Os02t0643800-01)
Os04g0538400	348.1	122.7	67.1	51.1	(1.504)	0.000	0.001	yes	(2.375)	0.000	0.001	yes	(1.263)	0.000	0.001	yes	(0.392)	0.008	0.061	no		Similar to Nodulin 21 (N-21). (Os04t0538400-01)
Os07g0595750	19.9	7.1	13.9	16.0	(1.490)	0.004	0.036	yes	(0.513)	0.167	0.447	no	1.181	0.016	0.099	no	0.204	0.596	0.833	no		Similar to predicted protein. (Os07t0595750-00)
Os10g0349300	11.7	4.2	5.7	2.6	(1.483)	0.000	0.001	yes	(1.033)	0.000	0.001	yes	(0.697)	0.012	0.083	no	(1.146)	0.000	0.003	yes		Similar to Root-specific protein (RCc2 protein). (Os10t0349300-01)
Os06g0169001	837.0	315.4	217.2	192.8	(1.408)	0.000	0.001	yes	(1.947)	0.000	0.001	yes	(0.710)	0.000	0.001	yes	(0.171)	0.262	0.569	no		GOS9 protein. (Os06t0169001-01)
Os01g0174100	73.0	27.5	34.6	24.7	(1.406)	0.000	0.001	yes	(1.078)	0.000	0.001	yes	(0.155)	0.356	0.663	no	(0.483)	0.004	0.039	yes		Conserved hypothetical protein. (Os01t0174100-01)
Os10g0547500	345.9	130.5	131.7	109.1	(1.406)	0.000	0.001	yes	(1.393)	0.000	0.001	yes	(0.258)	0.080	0.291	no	(0.271)	0.066	0.259	no	Lsi3	Si efflux transporter (SIET/Lsi2-like) homolog, Efflux transport of Si, Silicon intervascular transfer (Os10t0547500-01)
Os07g0418700	73.5	27.9	26.7	13.7	(1.397)	0.000	0.001	yes	(1.462)	0.000	0.001	yes	(1.022)	0.000	0.001	yes	(0.957)	0.000	0.001	yes		Proline-rich glycoprotein, ABA-dependent inhibition of root growth (Os07t0418700-01)
Os01g0899387	125.7	47.9	63.0	65.4	(1.393)	0.000	0.001	yes	(0.996)	0.000	0.001	yes	0.450	0.064	0.253	no	0.053	0.814	0.936	no		Conserved hypothetical protein. (Os01t0899387-00)
Os01g0757200	70.0	26.8	15.7	19.8	(1.384)	0.000	0.001	yes	(2.154)	0.000	0.001	yes	(0.436)	0.003	0.032	yes	0.333	0.024	0.132	no		GA 2-oxidase3, GA metabolism (Os01t0757200-01)
Os07g0257200	13.1	5.1	4.9	3.9	(1.369)	0.000	0.001	yes	(1.422)	0.000	0.001	yes	(0.375)	0.014	0.092	no	(0.322)	0.034	0.168	no	Nramp5	Manganese and Cadmium transporter, Mn and Cd uptake (Os07t0257200-01)
Os06g0199000	22.3	8.7	17.6	10.9	(1.353)	0.000	0.001	yes	(0.341)	0.037	0.177	no	0.315	0.076	0.283	no	(0.697)	0.000	0.002	yes		Similar to Glycine-rich cell wall structural protein 2 precursor. (Os06t0199000-01)
Os02g0224100	184.5	73.1	68.1	69.8	(1.335)	0.000	0.001	yes	(1.437)	0.000	0.001	yes	(0.066)	0.652	0.863	no	0.035	0.810	0.935	no		Protein phosphatase 2C domain containing protein. (Os02t0224100-01);Similar to catalytic/ protein phosphatase type 2C. (Os02t0224100-02)
Os02g0223700	42.3	17.0	21.8	18.3	(1.315)	0.000	0.001	yes	(0.955)	0.000	0.001	yes	0.106	0.513	0.783	no	(0.254)	0.114	0.361	no		Protein of unknown function DUF3511 domain containing protein. (Os02t0223700-01)
Os12g0634600	18.0	7.2	12.8	6.6	(1.314)	0.000	0.001	yes	(0.491)	0.011	0.075	no	(0.134)	0.559	0.812	no	(0.958)	0.000	0.001	yes		Conserved hypothetical protein. (Os12t0634600-01)
Os07g0529600	21.5	8.7	13.0	12.2	(1.309)	0.000	0.001	yes	(0.726)	0.000	0.001	yes	0.491	0.005	0.041	yes	(0.092)	0.582	0.825	no		Thiamine synthase, Thiamine accumulation, Bacterial blight resistance, Blast resistance (Os07t0529600-01);Similar to Pathogen-induced defense-responsive protein 8. (Os07t0529600-01)
Os01g0320700	19.6	7.9	12.6	10.6	(1.306)	0.000	0															

Os05g0355400	206.2	86.9	92.1	84.1	(1.246)	0.000	0.001	yes	(1.163)	0.000	0.001	yes	(0.048)	0.741	0.907	no	(0.131)	0.376	0.680	no		UspA domain containing protein. (Os05t0355400-01)
Os09g0425500	41.1	17.4	15.7	15.3	(1.245)	0.000	0.001	yes	(1.389)	0.000	0.001	yes	(0.184)	0.370	0.676	no	(0.040)	0.847	0.949	no		Hypothetical gene. (Os09t0425500-01)
Os11g0127951	37.1	15.8	18.2	10.7	(1.234)	0.000	0.005	yes	(1.030)	0.002	0.019	yes	(0.565)	0.131	0.391	no	(0.769)	0.039	0.186	no		Hypothetical protein. (Os11t0127951-00)
Os05g0241300	20.8	8.8	10.3	6.8	(1.232)	0.000	0.001	yes	(1.004)	0.000	0.001	yes	(0.385)	0.057	0.237	no	(0.613)	0.002	0.025	yes		Conserved hypothetical protein. (Os05t0241300-01)
Os06g0594400	43.8	18.9	29.3	20.4	(1.216)	0.000	0.001	yes	(0.580)	0.000	0.002	yes	0.111	0.500	0.774	no	(0.526)	0.001	0.014	yes		KMD family of F-box protein, Negative regulation of cytokinin signalling (Os06t0594400-02)
Os06g0283100	31.8	13.7	17.1	16.7	(1.215)	0.000	0.001	yes	(0.890)	0.000	0.001	yes	0.291	0.069	0.267	no	(0.034)	0.830	0.943	no		Similar to UDP-glycosyltransferase. (Os06t0283100-00)
Os06g0329300	52.7	23.0	23.4	16.3	(1.194)	0.000	0.001	yes	(1.173)	0.000	0.001	yes	(0.502)	0.004	0.039	yes	(0.523)	0.003	0.029	yes		Conserved hypothetical protein. (Os06t0329300-01)
Os01g0177400	19.5	8.6	9.9	10.5	(1.192)	0.000	0.001	yes	(0.978)	0.000	0.001	yes	0.292	0.105	0.343	no	0.077	0.664	0.870	no		GA 3 beta-hydroxylase2, GA metabolism (Os01t0177400-01)
Os03g0159900	276.7	121.8	130.2	87.9	(1.184)	0.000	0.001	yes	(1.088)	0.000	0.001	yes	(0.471)	0.002	0.025	yes	(0.566)	0.000	0.005	yes		Hypothetical conserved gene. (Os03t0159900-01);Hypothetical conserved gene. (Os03t0159900-02)
Os01g0304400	10.2	4.5	5.2	3.3	(1.179)	0.000	0.001	yes	(0.971)	0.000	0.001	yes	(0.458)	0.063	0.251	no	(0.665)	0.006	0.053	no		Conserved hypothetical protein. (Os01t0304400-00)
Os10g0456100	125.3	55.7	60.3	46.4	(1.170)	0.000	0.001	yes	(1.055)	0.000	0.001	yes	(0.264)	0.091	0.316	no	(0.379)	0.014	0.091	no		Similar to Brn1-like protein. (Os10t0456100-00)
Os01g0915000	74.9	33.6	38.0	24.2	(1.156)	0.000	0.001	yes	(0.980)	0.000	0.001	yes	(0.475)	0.003	0.026	yes	(0.651)	0.000	0.003	yes		Protein of unknown function DUF506, plant family protein. (Os01t0915000-01)
Os02g0108400	18.9	8.5	14.8	10.4	(1.152)	0.000	0.001	yes	(0.351)	0.036	0.174	no	0.295	0.095	0.323	no	(0.506)	0.003	0.031	yes		Protein of unknown function DUF1677, Oryza sativa family protein. (Os02t0108400-00)
Os05g0148800	54.2	24.6	35.9	27.2	(1.139)	0.000	0.001	yes	(0.595)	0.000	0.001	yes	0.142	0.376	0.681	no	(0.402)	0.010	0.072	no		Hypothetical conserved gene. (Os05t0148800-00)
Os02g0753700	17.2	7.9	10.6	9.1	(1.133)	0.000	0.001	yes	(0.697)	0.000	0.001	yes	0.214	0.289	0.598	no	(0.222)	0.256	0.562	no		VQ domain containing protein. (Os02t0753700-01)
Os11g0666100	24.3	11.1	11.8	8.8	(1.128)	0.000	0.001	yes	(1.047)	0.000	0.001	yes	(0.335)	0.107	0.348	no	(0.416)	0.043	0.196	no		Similar to Receptor kinase-like protein. (Os11t0666100-01)
Os01g0881300	20.3	9.4	12.7	10.1	(1.115)	0.000	0.001	yes	(0.678)	0.000	0.001	yes	0.109	0.484	0.764	no	(0.328)	0.032	0.163	no		Non-protein coding transcript. (Os01t0881300-01);MtN3 and saliva related transmembrane protein family protein. (Os01t0881300-02)
Os08g0101500	99.5	45.9	46.8	46.7	(1.115)	0.000	0.001	yes	(1.087)	0.000	0.001	yes	0.025	0.868	0.957	no	(0.003)	0.983	0.994	no	MOT1;1	Molybdate transporter, Uptake and translocation of molybdate (Os08t0101500-01)
Os02g0197600	14.0	6.5	14.7	8.6	(1.109)	0.000	0.001	yes	0.065	0.679	0.877	no	0.398	0.019	0.115	no	(0.777)	0.000	0.001	yes		Chlorophyll a/b-binding protein type III (Fragment). (Os02t0197600-01);Similar to Chlorophyll a/b-binding protein type III (Fragment)
Os11g0246200	1092.1	506.7	522.3	418.6	(1.108)	0.000	0.001	yes	(1.064)	0.000	0.001	yes	(0.275)	0.088	0.309	no	(0.319)	0.044	0.201	no		Kelch-type beta propeller domain containing protein. (Os11t0246200-00)
Os03g0266300	138.7	65.3	158.7	78.9	(1.087)	0.000	0.001	yes	0.194	0.172	0.454	no	0.273	0.064	0.253	no	(1.008)	0.000	0.001	yes		17.9 kDa class I small heat shock protein, Heat tolerance (Os03t0266300-01);Class I low-molecular-weight heat shock protein 17.9. (Os03t0266300-03)
Os05g0385400	14.5	6.8	8.6	3.4	(1.087)	0.000	0.001	yes	(0.752)	0.000	0.003	yes	(1.013)	0.000	0.001	yes	(1.348)	0.000	0.001	yes		Conserved hypothetical protein. (Os05t0385400-01)
Os07g0416900	10.8	5.1	5.9	5.1	(1.083)	0.000	0.001	yes	(0.876)	0.000	0.001	yes	0.004	0.979	0.993	no	(0.203)	0.293	0.602	no		Similar to Omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 2 (EC 1.14.19.-). (Os07t0416900-01)
Os06g0535200	51.4	24.3	23.6	20.0	(1.082)	0.000	0.001	yes	(1.121)	0.000	0.001	yes	(0.279)	0.087	0.307	no	(0.240)	0.141	0.407	no		Zinc finger, RING/FYVE/PHD-type domain containing protein. (Os06t0535200-01)
Os09g0545320	39.2	18.6	25.4	17.4	(1.079)	0.000	0.001	yes	(0.629)	0.001	0.010	yes	(0.095)	0.651	0.862	no	(0.545)	0.009	0.066	no		Conserved hypothetical protein. (Os09t0545320-01)
Os01g0237750	29.7	14.1	14.4	12.1	(1.075)	0.000	0.001	yes	(1.047)	0.000	0.001	yes	(0.224)	0.306	0.615	no	(0.253)	0.249	0.554	no		Hypothetical conserved gene. (Os01t0237750-00)
Os02g0102300	33.0	15.8	13.5	14.5	(1.059)	0.000	0.001	yes	(1.285)	0.000	0.001	yes	(0.130)	0.556	0.810	no	0.096	0.657	0.866	no	HAC1;1	Arsenate reductase, Sulfurtransferase/rhodanese-like protein, Regulation of arsenic accumulation (Os02t0102300-01)
Os09g0447300	62.1	30.0	39.8	25.5	(1.051)	0.000	0.001	yes	(0.640)	0.000	0.001	yes	(0.231)	0.114	0.361	no	(0.642)	0.000	0.001	yes		Cytochrome P450 family protein. (Os09t0447300-01)
Os04g0457000	11.7	5.6	13.8	6.1	(1.048)	0.000	0.001	yes	0.240	0.168	0.448	no	0.116	0.547	0.804	no	(1.173)	0.000	0.001	yes		Similar to Chlorophyll a/b-binding protein CP24, photosystem II (Fragment). (Os04t0457000-01)
Os12g0581900	521.6	253.6	278.3	246.4	(1.040)	0.000	0.001	yes	(0.906)	0.000	0.001	yes	(0.041)	0.777	0.922	no	(0.175)	0.221	0.522	no		Zinc finger, C2H2-like domain containing protein. (Os12t0581900-01)
Os03g0700400	12.7	6.2	6.8	6.4	(1.038)	0.000	0.001	yes	(0.914)	0.000	0.001	yes	0.055	0.717	0.896	no	(0.069)	0.646	0.860	no		Lipoxxygenase-3, Generation of stale flavor (Os03t0700400-01)
Os01g0501800	39.1	19.1	42.1	24.8	(1.037)	0.000	0.001	yes	0.105	0.482	0.762	no	0.377	0.015	0.099	no	(0.765)	0.000	0.001	yes		Similar to Photosystem II oxygen-evolving complex protein 1 (Fragment). (Os01t0501800-01)
Os11g0246250	14.9	7.3	8.6	7.0	(1.031)	0.000	0.001	yes	(0.799)	0.000	0.001	yes	(0.053)	0.773	0.920	no	(0.284)	0.123	0.378	no		Non-protein coding transcript. (Os11t0246250-01)
Os04g0389100	14.1	6.9	9.0	7.7	(1.029)	0.000	0.001	yes	(0.646)	0.000	0.001	yes	0.148	0.386	0.689	no	(0.236)	0.160	0.438	no		OSIGBa0096P03.6 protein. (Os04t0389100-00)
Os10g0166300	19.5	9.6	13.4	10.0	(1.027)	0.000	0.001	yes	(0.547)	0.002	0.022	yes	0.059	0.761	0.915	no	(0.421)	0.024	0.135	no		Hypothetical gene. (Os10t0166300-01)
Os02g0799700	47.1	23.1	26.6	19.2	(1.027)	0.000	0.001	yes	(0.825)	0.000	0.001	yes	(0.267)	0.108	0.350	no	(0.468)	0.004	0.040	yes		Similar to serine-rich protein. (Os02t0799700-01)
Os09g0484200	2238.4	1103.5	1243.2	1217.4	(1.020)	0.000	0.001	yes	(0.848)	0.000	0.001	yes	0.142	0.424	0.720	no	(0.030)	0.865	0.956	no		Hypothetical protein. (Os09t0484200-01);Hypothetical gene. (Os09t0484200-02)
Os01g0795700	171.4	84.9	118.9	96.3	(1.014)	0.000	0.001	yes	(0.528)	0.000	0.006	yes	0.181	0.241	0.545	no	(0.304)	0.044	0.199	no		Non-protein coding transcript. (Os01t0795700-01)
Os02g0185300	23.9	11.8	21.9	15.2	(1.012)	0.000	0.001	yes	(0.128)	0.385	0.689	no	0.357	0.022	0.125	no	(0.527)	0.001	0.011	yes		Cytochrome P450 family protein. (Os02t0185300-01)
Os09g0545300	35.5	17.7	23.4	16.1	(1.005)	0.000	0.001	yes	(0.598)	0.000	0.004	yes	(0.138)	0.456	0.743	no	(0.545)	0.004	0.033	yes		SAUR family protein, Negative regulator of auxin synthesis and transport (Os09t0545300-01)
Os08g0190100	1008.2	502.9	538.0	559.5	(1.003)	0.000	0.001	yes	(0.906)	0.000	0.001	yes	0.154	0.323	0.632	no	0.057	0.717	0.896	no		Germin-like protein 8-11, Disease resistance (Os08t0190100-01)
Os07g0539900	72.8	151.5	50.9	85.4	1.058	0.000	0.001	yes	(0.515)	0.000	0.003	yes	(0.827)	0.000	0.001	yes	0.746	0.000	0.001	yes		Similar to Beta-1,3-glucanase-like protein. (Os07t0539900-01)
Os06g0513943	79.5	166.5	123.6	94.2	1.066	0.000	0.001	yes	0.637	0.000	0.001	yes	(0.822)	0.000	0.001	yes	(0.393)	0.010	0.070	no		Conserved hypothetical protein. (Os06t0513943-01)
Os11g0676200	6.9	14.5	7.6	12.5	1.067	0.000	0.001	yes	0.136	0.427	0.722	no	(0.214)	0.181	0.468	no	0.717	0.000	0.001	yes		Similar to NBS-LRR-like protein NBA2 (Fragment). (Os11t0676200-00)
Os09g0564400	5.5	11.5	7.8	14.9	1.070	0.000	0.001	yes	0.507	0.007	0.054	no	0.367	0.028	0.148	no	0.930	0.000	0.001	yes		Hypothetical conserved gene. (Os09t0564400-00)
Os06g0701700	15.0	31.5	13.7	20.9	1.073	0.000	0.001	yes	(0.134)	0.384	0.687	no	(0.592)	0.000	0.002	yes	0.614	0.000	0.001	yes	HKT	Ion transporter , Na+/K+ symport (Os06t0701700-01);Similar to Cation transporter HKT1. (Os06t0701700-02)
Os04g0173800	5.0	10.7	9.0	8.9	1.114	0.000	0.001	yes	0.852	0.000	0.002	yes	(0.272)	0.128	0.386	no	(0.010)	0.959	0.986	no		Lectin precursor (Agglutinin). (Os04t0173800-01)
Os10g0113100	10.4	23.2	8.9	7.3	1.154	0.000	0.001	yes	(0.224)	0.192	0.483	no	(1.672)	0.000	0.001	yes	(0.295)	0.105	0.344	no		Aldo/keto reductase family protein. (Os10t0113100-01);Similar to cDNA clone:J033143K18, full insert sequence. (Os10t0113100-02)
Os02g0586000	15.7	35.9	32.0	43.8	1.189	0.000	0.001	yes	1.026	0.000	0.001	yes	0.289	0.063	0.251	no	0.452	0.003	0.031	yes		Quinonprotein alcohol dehydrogenase-like domain containing protein. (Os02t0586000-01)
Os07g0689600	30.5	69.7	26.6	65.6	1.192	0.000	0.001	yes	(0.197)	0.193	0.485	no	(0.089)	0.537	0.798	no	1.301	0.000	0.001	yes	NAS3	Nicotianamine synthase 3, Mitigation of excess Fe stress, Fe detoxification, Transport of iron (Os07t0689600-01)
Os10g0127900	5.3	12.4	19.4	16.7	1.232	0.000	0.001	yes	1.876	0.000	0.001	yes	0.431	0.003	0.032	yes	(0.214)	0.146	0.415	no		Similar to F-box domain containing protein, expressed. (Os10t0127900-01);Similar to F-box domain containing protein, expressed. (Os10t0127900-02);F-box domain containing protein,
Os05g0412800																						

Os06g0200800	5.0	33.4	7.1	33.4	2.732	0.000	0.001	yes	0.507	0.209	0.506	no	0.001	0.998	0.999	no	2.225	0.000	0.001	yes		Conserved hypothetical protein. (Os06t0200800-01)
Os11g0454300	1.8	12.8	1.4	2.3	2.823	0.000	0.001	yes	(0.342)	0.286	0.595	no	(2.487)	0.000	0.001	yes	0.678	0.035	0.172	no		Group 2 late embryogenesis abundant (LEA) protein, Salt tolerance (Os11t0454300-01)
Os08g0203350	2.9	21.1	1.3	20.1	2.880	0.000	0.001	yes	(1.115)	0.006	0.048	yes	(0.067)	0.724	0.899	no	3.928	0.000	0.001	yes		Conserved hypothetical protein. (Os08t0203350-01)
Os10g0386300	1.4	11.3	1.5	2.3	3.022	0.000	0.001	yes	0.149	0.607	0.839	no	(2.332)	0.000	0.001	yes	0.541	0.054	0.227	no		Hypothetical protein. (Os10t0386300-01)
Os07g0122000	1.2	11.6	1.1	9.8	3.216	0.000	0.001	yes	(0.191)	0.431	0.726	no	(0.238)	0.152	0.425	no	3.169	0.000	0.001	yes		Protein of unknown function DUF1719, Oryza sativa family protein. (Os07t0122000-01)
Os03g0266900	3.6	41.0	3.3	75.8	3.492	0.000	0.001	yes	(0.159)	0.538	0.799	no	0.887	0.000	0.001	yes	4.538	0.000	0.001	yes		17.4 kDa class I small heat shock protein, Heat tolerance (Os03t0266900-02)
Os03g0426350	5.8	67.1	7.7	69.8	3.527	0.000	0.001	yes	0.407	0.056	0.234	no	0.057	0.698	0.887	no	3.178	0.000	0.001	yes		Conserved hypothetical protein. (Os03t0426350-00)
Os10g0472501	1.7	19.5	1.9	21.4	3.534	0.000	0.001	yes	0.202	0.655	0.865	no	0.132	0.530	0.794	no	3.465	0.000	0.001	yes		Hypothetical conserved gene. (Os10t0472501-00)
Os01g0537250	4.7	65.6	9.2	76.2	3.815	0.000	0.001	yes	0.974	0.000	0.001	yes	0.216	0.139	0.404	no	3.057	0.000	0.001	yes		Protein of unknown function DUF3778 domain containing protein. (Os01t0537250-01)
Os05g0103800	1.1	18.1	1.6	15.3	4.082	0.000	0.001	yes	0.542	0.043	0.198	no	(0.235)	0.126	0.382	no	3.305	0.000	0.001	yes		Conserved hypothetical protein. (Os05t0103800-00)
Os12g0113600	0.4	12.7	0.3	13.1	5.008	0.000	0.001	yes	(0.348)	1.000	1.000	no	0.047	0.801	0.931	no	5.403	0.000	0.001	yes		Hypothetical protein. (Os12t0113600-01)
Os03g0299700	1.2	315.3	1.5	333.7	8.077	0.000	0.001	yes	0.405	0.140	0.406	no	0.082	0.585	0.827	no	7.754	0.000	0.001	yes		Conserved hypothetical protein. (Os03t0299700-01)
Os01g0356951	0.1	35.3	0.1	31.7	8.391	0.003	0.027	yes	(0.526)	1.000	1.000	no	(0.153)	0.360	0.667	no	8.764	0.250	0.555	no		Putative long noncoding RNA, Regulation of panicle architecture (Os01t0356951-01)
Os07g0511400	0.7	1300.4	0.4	1160.9	10.933	0.000	0.001	yes	(0.728)	0.174	0.458	no	(0.164)	0.306	0.615	no	11.497	0.000	0.001	yes		Hypothetical protein. (Os07t0511400-01)
Os03g0115800	0.2	648.1	0.1	711.1	11.681	0.000	0.001	yes	(1.426)	1.000	1.000	no	0.134	0.422	0.719	no	13.240	0.000	0.002	yes		Conserved hypothetical protein. (Os03t0115800-01);Conserved hypothetical protein. (Os03t0115800-02)

Supplementary Table 3. Primer sequences used in this study.

Primer name	Forward (5'-3')	Reverse (5'-3')	Purpose
SSS CRISPR-A	gttgAGGTTTCATCGAGACTGCCG	aaacCGGCAGTCTCGATGAAACCT	CRISPR/Cas9 target sequence
SSS CRISPR-B	gttgAACTCCTTGCCATTAAACAC	aaacGTGTTTAATGGCAAGGAGTT	CRISPR/Cas9 target sequence
SSS ORF	GCAAGGCCTGTTAGCATTTcTAGAGCTAG	ttcatgactccGGTTGGCCTCCTCCCACCTG	SSS ORF without stop codon cloning
GFP ORF	aaTGTACATGGTGAGCAAGGGCGAGGAG	tGCGGCCGCTTTACTTaTACAGCTCG	GFP ORF without stop codon cloning
SSS promoter	aaaaGCTTTCGCGTGGGACAGACG	CTAGCTCTAgAAATGCTAACAGGCCTTGC	SSS promoter cloning
SSS downstream	agcggccgCTGATCTGATCAATATCGATCGATC	tgaaTTCTTCTTACCAATGCCTACCTC	SSS downstream cloning
SSS qPCR	CACATCATGGCAAATGACTCATTG	ATTAGGAGCATCAGGATCCACC	qPCR of rice SSS
Lsi1 qPCR	TGTACTACGGCGAGAAGGCC	CGTCATGAACACCAGCAGGA	qPCR of rice Lsi1
Lsi2 qPCR	CGTACCAACGGTGCTTCTTATG	GATGGGTCGATGAGATGAGATC	qPCR of rice Lsi2
Ubiquitin qPCR	AGAAGGAGTCCACCCTCCACC	GCATCCAGCACAGTAAACACG	Internal standard of qPCR in rice
HistoneH3 qPCR	AGTTTGGTCGCTCTCGATTTCG	TCAACAAGTTGACCACGTCACG	Internal standard of qPCR in rice
TaFTL12A qPCR	GGCACGCCAGAGCTTCAACTC	CATTGCCGTCGGCTGGGCTG	qPCR of wheat TaFTL12A
TaFTL12B qPCR	GGCACGCCAGAGCTTCAACTC	GTGAGCTCAGGCGGCGACGA	qPCR of wheat TaFTL12B
TaFTL12D qPCR	GGCACGCCAGAGCTTCAACTC	CATTGCCGTCGGCTGGGCCG	qPCR of wheat TaFTL12D
Actin qPCR	CACTGGAATGGTCAAGGCTG	CTCCATGTCATCCCAGTTG	Internal standard of qPCR in wheat
ZmFTL12 qPCR	GGCCACATAATCGGGGATGTC	CGACGCCCGAAACTCCATCC	qPCR of maize ZmFTL12
Tubulin qPCR	ATGGCATCCAGGCTGATGGT	TATGGCTCAACTACCGAAGT	Internal standard of qPCR in maize
PeFTL12 qPCR	TCCTGGTGTTGTATCAACAACTG	TCAGGTGAACCTTCTCCCACC	qPCR of moso bamboo PeFTL12
PeHistoneH3 qPCR	GACGTCATCAACTCGTTGATCC	CTTACAACATCTGTTTGCTTAGCC	Internal standard of qPCR in moso bambo
Hd3a ORF	agtcgacATGGCCGGAAGTGGCAGG	acatgTAGGGGTAGACCCTCCTGCC	Hd3a ORF cloning
Hd3a_F103A	GCAGCGTCAGCTGGGCAAGAGGTG	CTCTTGCCCAGCTGACGCTGCAGT	Introduce Hd3a_F103A mutation
Hd3a infusion	TACAATTACAGTCGAATGGCCGGAAGTGGCAGG	TGCAGCCGGGCGGCCTTACTTGACAGCTCGTCC	Hd3a sub-cloning
GF14f ORF	CGACGTACCAGATTACGCTATGTCGCCTGCTG	gcggccgcTTAGTGGCCCTCTCCTTCAGG	GF14f ORF cloning
HA tag-GF14f	gtcgacATGTACCCATACGACGTACCAG	gcggccgcTTAGTGGCCCTCTCCTTCAGG	HA tag attachment to GF14f
SSS_F98A	ATCGACGGACGATAGCgcTGGG	ATCTCCCGCCCAgcGCTATCG	Introduce SSS_F98A mutation