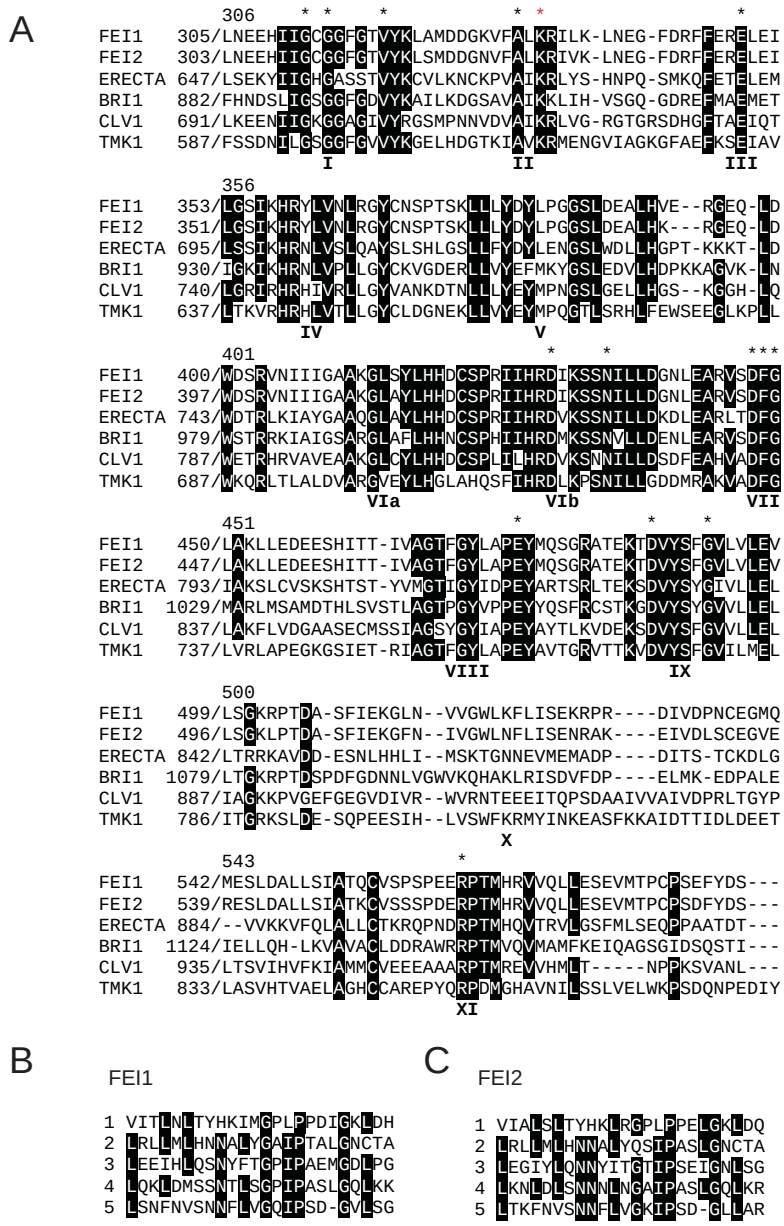
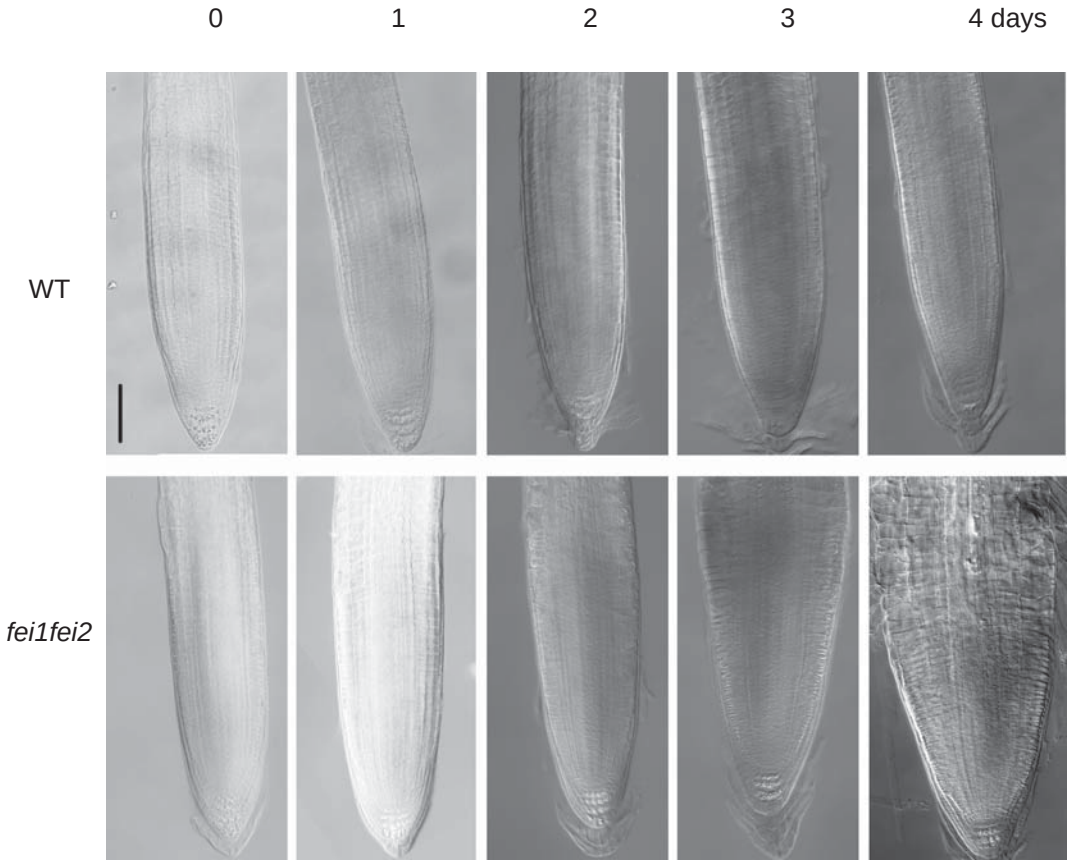
Supplemental Data. Xu et al. (2008). Two leucine-rich repeat receptor kinases mediate signalling linking cell wall biosynthesis and ACC synthase in *Arabidopsis.*



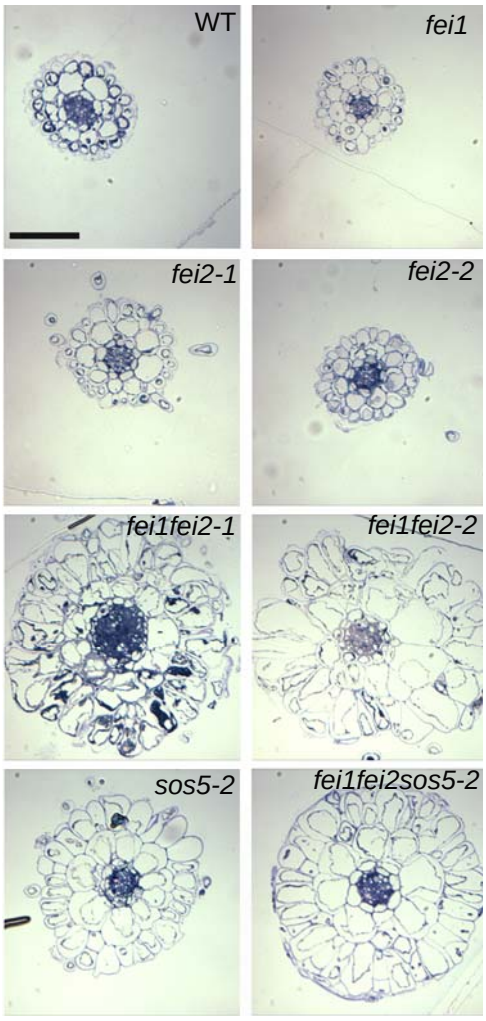
Supplemental Figure 1. Sequence alignments of FEI1 and FEI2.

(A) Alignment of the cytoplasmic kinase domain of FEI1 and FEI2 with the kinase domains of ER, BRI1, CLV1 and TMK1, the four receptor-like kinases in plants. The 12 conserved protein kinase domains are indicated I to XI (Hanks and Quinn, 1991). Residues that are conserved among at least five of the compared sequences are boxed. The 15 invariant amino acids present in the all protein kinases are indicated by asterisks. The conserved lysine in domain II that is involved in ATP binding and which was mutated to create a kinase-dead version of FEI1 is indicated by red asterisk; **(B)-(C)** The alignment of LRR repeats in the FEI1 **(B)** and FEI2 **(C)** proteins. Residues that appear at each position at > 50% frequency are shown by black boxes. Numbers to the left of LRR domain indicate the specific LRR number.



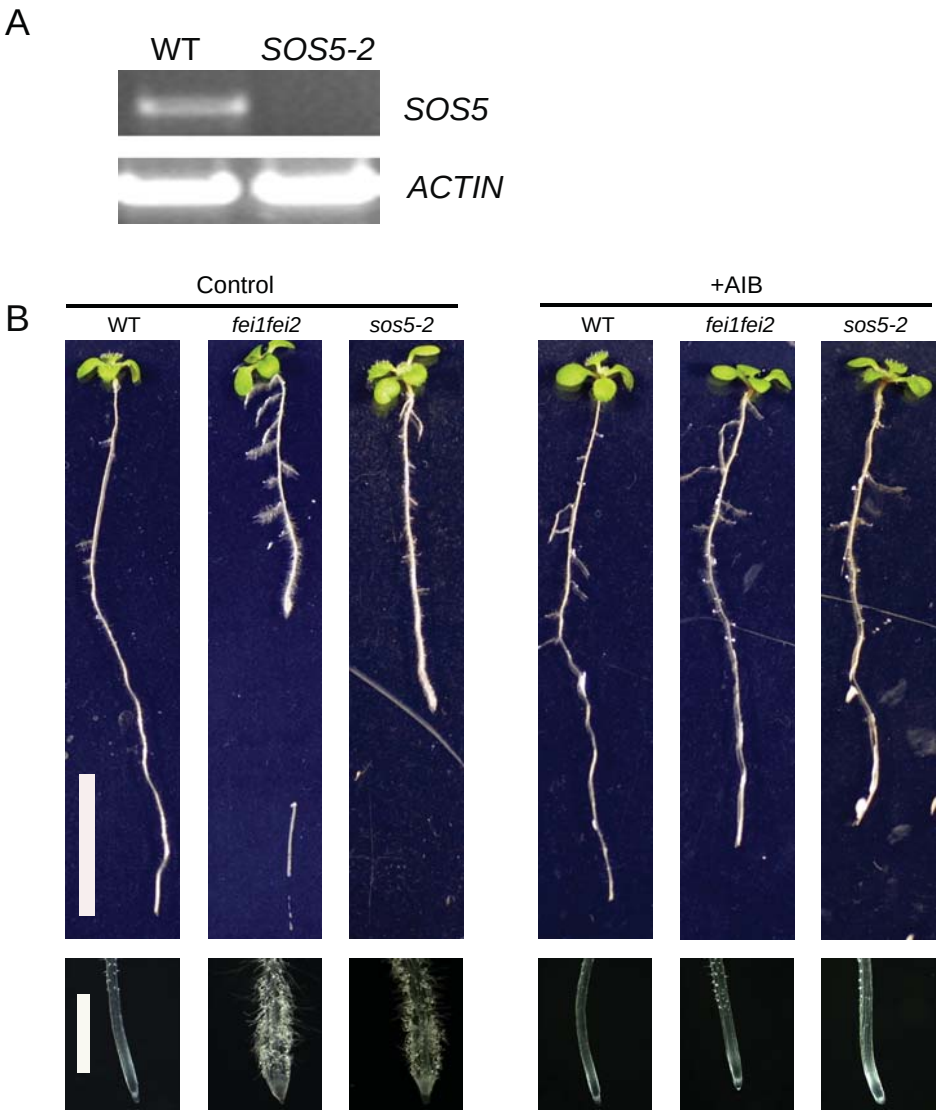
Supplemental Figure 2. Time-course of root swelling following transfer from 0% to 4.5% sucrose media.

Wild-type and *fei1 fei2* root tips were imaged 0, 1, 2, 3, and 4 days after transfer. Bar=100 µm.



Supplemental Figure 3. Transverse sections through the elongation zone of the root from various single, double, and triple mutants.

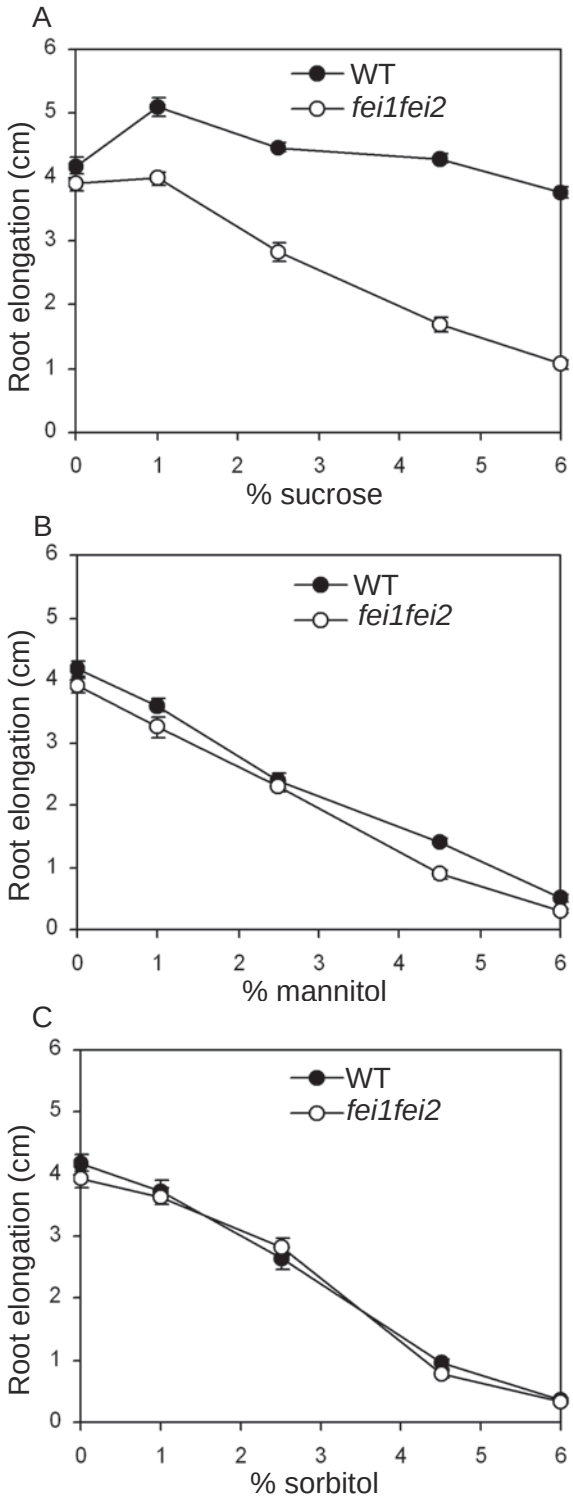
Bar =100 μm.



Supplemental Figure 4. Analysis of the *sos5-2* mutant.

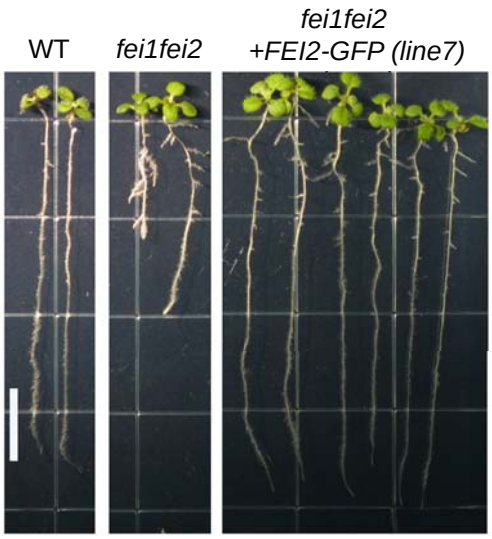
(A) RT-PCR analysis shows no full length transcript was detected in *sos5-2* mutant. The actin fragment was amplified as control. *SOS5* and *ACTIN* were amplified for 30 cycles.

(B) Phenotype of seedlings of WT, *fei1fei2* and *sos5-2* four days after being transferred to media containing 50 mM NaCl in the absence or presence of 2 mM AIB. Top bar = 1 cm; Bottom bar = 1 mm.



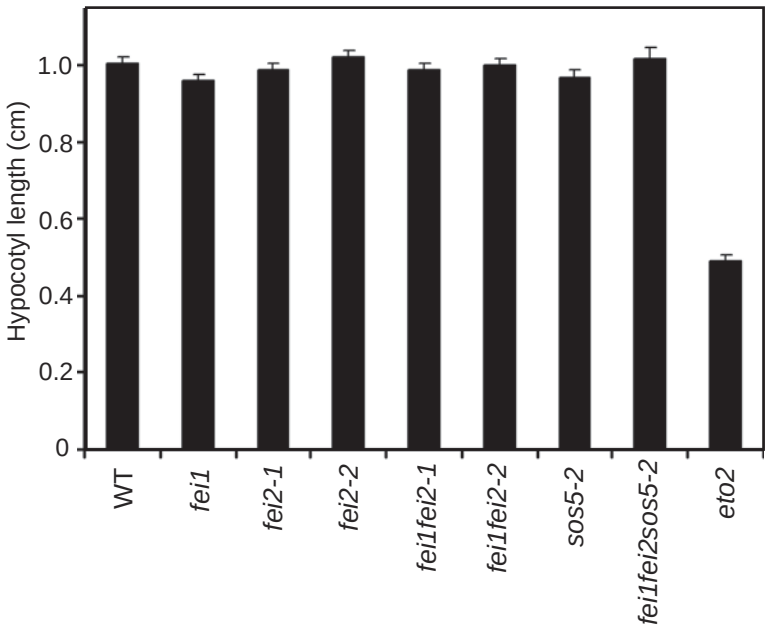
Supplemental Figure 5. The *fei1fei2* mutant phenotype in response to sucrose is not the result of increased osmoticum.

Root elongation (days 4 – 8) of WT and *fei1fei2* after being transferred to media containing the indicated amount of **(A)** sucrose; **(B)** mannitol; **(C)** sorbitol. Plants were grown on MS media plates containing 0% sucrose for 4 days before the transfer. Closed circles, wild type; Open circles, *fei1fei2*. Values shown are average ± se (n= 15).



Supplemental Figure 6. The FEI2-GFP fusion is functional.

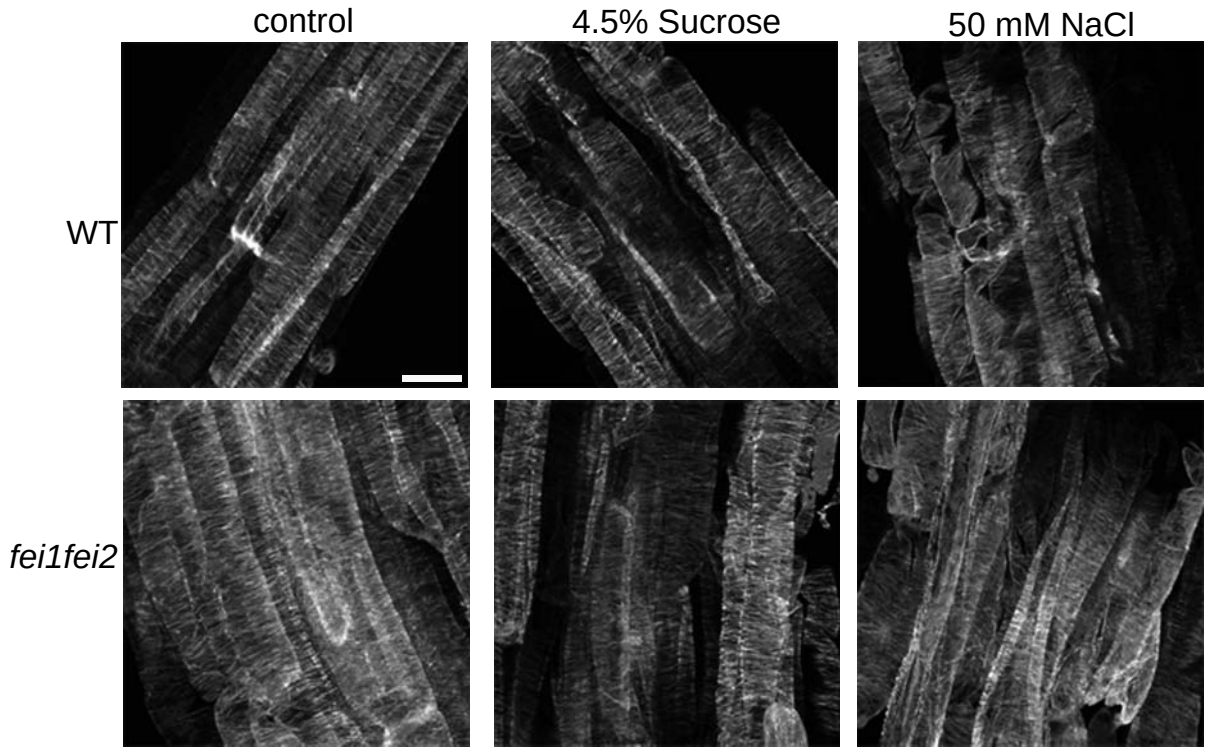
A 35S: *FEI2*-GFP genomic construct was introduced into the *fei1fei2* mutant. Six seedlings from one of the transformed lines are shown. The WT, *fei1fei2* and transgenic seedlings were grown on MS media containing 4.5% sucrose for nine days.



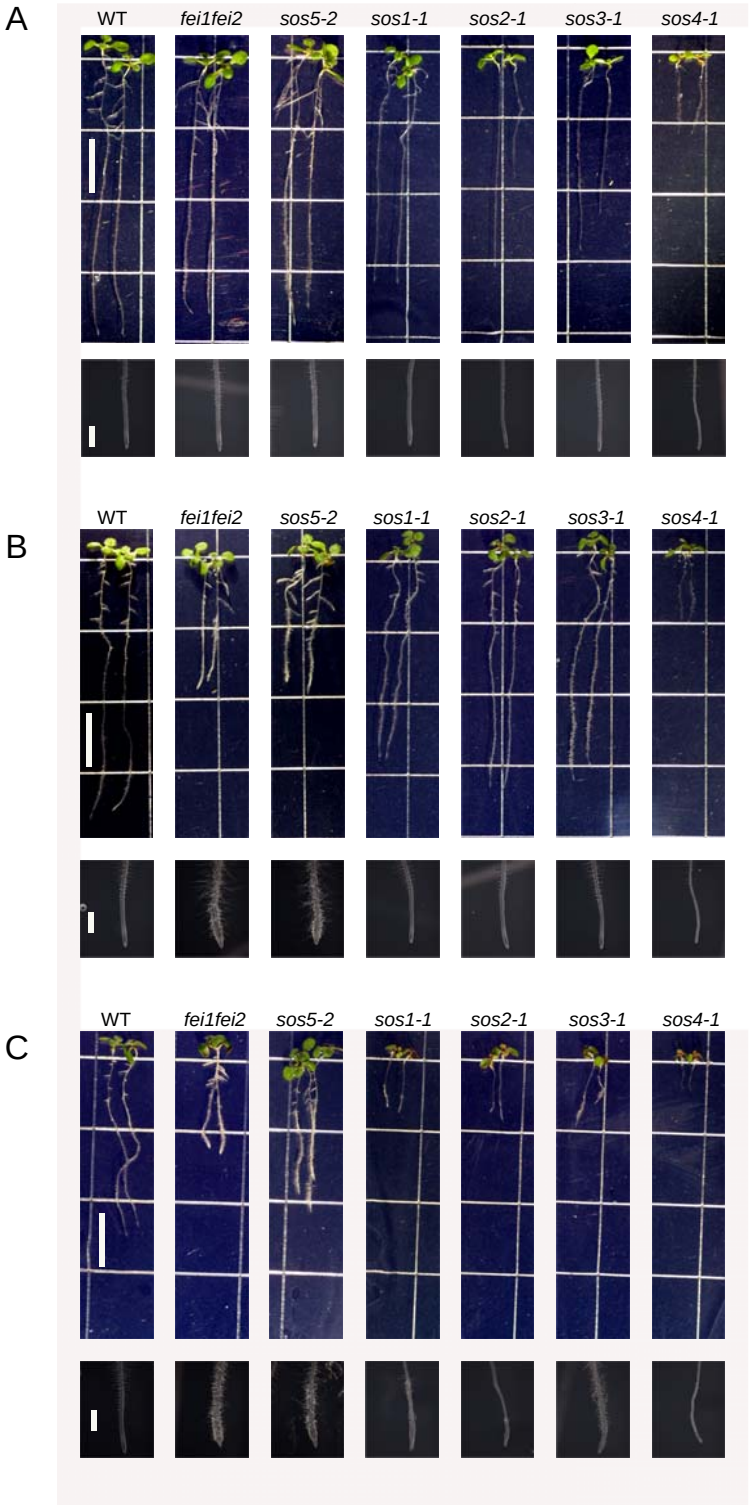
Supplemental Figure 7. Hypocotyl length is not affected in the *fei* mutants.

Seedlings of the indicated genotype were grown for four days in the dark on MS media containing 1% sucrose and the hypocotyl length measured. The *eto2* mutant is included as a control. Data shown is the mean ± se (n= 15).

Supplemental Figure 8. Phloroglucinol staining for lignin in wild type and *fei1 fei2* seedlings grown on MS media for three days in the dark.

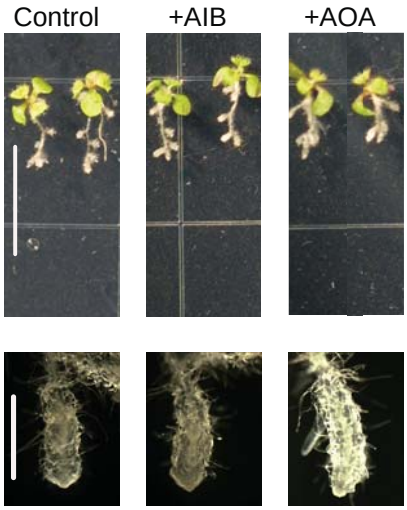


Supplemental Figure 9. Organization of microtubules is not altered in the *fei1fei2* mutant. Seedlings were grown on MS media containing 1% sucrose for four days and then transferred to media containing 1% sucrose (control), 4.5% sucrose, or 1% sucrose + 50 mM NaCl as indicated. Three days after transfer, seedlings were fixed and microtubules in the cells of the elongation zone were localized by immunocytochemistry. At this time, mutant roots had begun to swell but were not so swollen as to impede imaging. Similar treatment of *sos5-2* also showed no apparent disruption of the microtubules (not shown). Scale bar = 10 μm.



Supplemental Figure 10. Growth in the presence of elevated sucrose does not affect other *sos* mutants.

The indicated seedlings were grown on MS media containing 0% sucrose for four days and then transferred for four days to MS media containing: **(A)** 0% sucrose; **(B)** 4.5% sucrose; **(C)** 1% sucrose and 75 mM NaCl.



Supplemental Figure 11. Effect of inhibition of ethylene biosynthesis on *cob* mutant. Seedlings grown on MS media containing 0% sucrose for four days and then transferred to media containing 4.5% sucrose plus nothing (control), AOA (0.375 mM) or AIB (1 mM). Scale bars: Top = 1 cm; Bottom = 1mm.

Table S1. Primers utilized in this study.

	Primers	Sequence
T-DNA characterization		
fei1	FEI1-Sense	5’ GAAGCTGGAAATGTTGAATGAAGA 3’
	FEI1-A5	5’ TTAATCAGAGCTGGAATCATAAAATTC 3’
	T-DNA left border primer-JMLB1	5' GGCAATCAGCTGTTGCCCGTCTCACTGGTG-3'
fei2-1	FEI2-S5	5’ ACAAATCGATATTGTGTGCAATGACAG 3’
	FEI1-A5	5’ TCAATCGGAGCTGGAGTCGTAGAAG 3’
	T-DNA left border primer	5' TTACCCAACTTAATCGCCTTGCAGCACAT3'
fei2-2	FEI2-S5	as above
	FEI2-A5	as above
	T-DNA left border primer-JMLB1	as above
sos5-2	SOS5-S2	5’ CACCATGGCCGCCGCAATTAACGTCACC 3’
	SOS5-A2	5’ GCCGGAAGAAACTATCTCACGC 3’
	T-DNA left border primer-JMLB1	as above
ein2	EIN2-S1	5 'GGTACATTGAGCTATACACAGCAAC 3'
	EIN2-A1	5' CATGAGAGACAAGTCAAGGACACG 3'
	T-DNA left border primer-JMLB1	as above
***fei2-1* screening**		
fei2-1	AICKinS	5’ GCTGCTCATGGTTTCTTTTGATCTCGTTT 3’
	AICKinA	5’ AGATCAATTGAGGCGTGTCACCAATCT 3’
RT-PCR		
fei1	FEI1-S9	5’ AAGCACTTCATGTAGAGAGAGG 3’
(for cDNA only)	FEI1-A2	5’GCGGCCGCATCAGAGCTGGAATCATAAAATTCG 3’
fei1 5’	FEI1-S4	5’ ATATGGAGCAATACCTACAGC 3’
	FEI1-A6	5’ TGATGCGCTAATCAGCAGCTTACCAG 3’
fei2	FEI2-S3	5’ GAAACTGGAATCTCTTAATGAAGAGC 3’
	FEI2-A2	5’GCGGCCGCATCGGAGCTGGAGTCGTAGAAG3’
sos5-2	SOS5-S1	5' CACCATGGCGAACGTAATCTCAATTTCC 3'
	SOS5-A1	5' TACCAAAACATAACAAAATGCTATAC 3'
ACTIN	Actin-S1	5’GTTGGGATGAACCAGAAGGA 3'
	Actin-A1	5’GAACCACCGATCCAGACACT 3'
Promoter: GUS		
FEI1: GUS	FEI1-PROM-F1	5’ GTCGAC TCGTCTTTAGAACAAGAAGCATTCA 3’
	FEI1-PROM-R1	5’ GCGGCCGCGGCACTGTCCAAGCATAATATAACT 3’

FEI2 : GUS	FEI1-PROM-F2	5'CCATGG CTGGAAATGTTGGTTACTGAAGAGG 3
	FEI2-PROM-R2	5'GCGGCCGCTGGCACCGTTCAAGCATAATATAG 3
Complementation		
FEI1:FEI1-Myc	FEI1-S7	5' CACCGGTGAAACAACGGACAACAATGGCTTC 3'
	FEI1-A3	5' ATCAGAGCTGGAATCATAAAATTCG 3'
FEI2:FEI2-Myc	FEI2-S7	5' CACCAGCTGAAAATACAAGAATTGTCCC 3'
	FEI2-A4	5' ATCGGAGCTGGAGTCGTAGAAGTC 3'
35S:*FEI2*-GFP	FEI2-S8	5' CACCATGGGCATCTGTCTAATGAAGCGCTGC 3'
	FEI2-A4	as above
Kinase assay		
Kinase domain of FEI1	FEI1-C2	5' CACCATGAAAAAGCTTGGTAGAGTTGAG 3'
	FEI1-A5	as above
Kinase-inactive		
	Wild-type sequence of *FEI1*	5' CTTTGCATTGAAGAGAATTCT 3'
Mutagenesis for FEI1	FEI1-M2F	5' GGCAAAGTCTTTGCATTGAGGAGAATTCTAAAG 3'
	FEI1-M2R	5' CTTTAGAATTCTCCTCAATGCAAAGACTTTGCC 3'
	Wild-type sequence of *FEI2*	5' TTGCGCTGAAAAGAATTGTTAAG 3'
Mutagenesis for FEI2	FEI2-M2F	5'GGCAATGTTTTTGCGCTGAGAAGAATTGTTAAG 3'
	FEI2-M2R	5' CTTAACAATTCTTCTCAGCGCAAAAACATTGCC 3'
Yeast two hybrid		
FEI1 kinase domain	FEI1-C2	as above
	FEI1-A5	as above
FEI2 kinase domain	FEI2-C2	5' CACCATGAAAAAGCTTGGTAGAGTTGAG 3'
	FEI2-A5	as above
ERECTA kinase domain	ERECTA-C2	5' CACCATGCTTGATGGATCACTTGACAAACC 3'
	ERECTA-A5	5' CTACTCACTGTTCTGAGAAATAACTTG 3'
ACS5	ACS5-S1	5'CCATGGCTAAACAGCTTTCGACAAAAGTG 3'
	ACS5-A1	5'GCGGCCGCTCATCGTTCATCAGGTACACG 3'
eto2	Same as ACS5 primers	
ACS9	ACS9-S1	5'CCATGGCTAAACAACTGTCGAGAAAAGTG 3'
	ACS9-A1	5' GCGGCCGCTCATCGTTCATCAGGTACACG G 3'
eto3	Same as ACS9	
ACS2	ACS2 sen	5' CACCATGGGTCTTCCGGGAAA
	ACS2 anti	5' GCCTTAAGATTTTCATGCTCGG