

Use of natural variation reveals core genes in the transcriptome of iron deficient *Arabidopsis thaliana* roots.

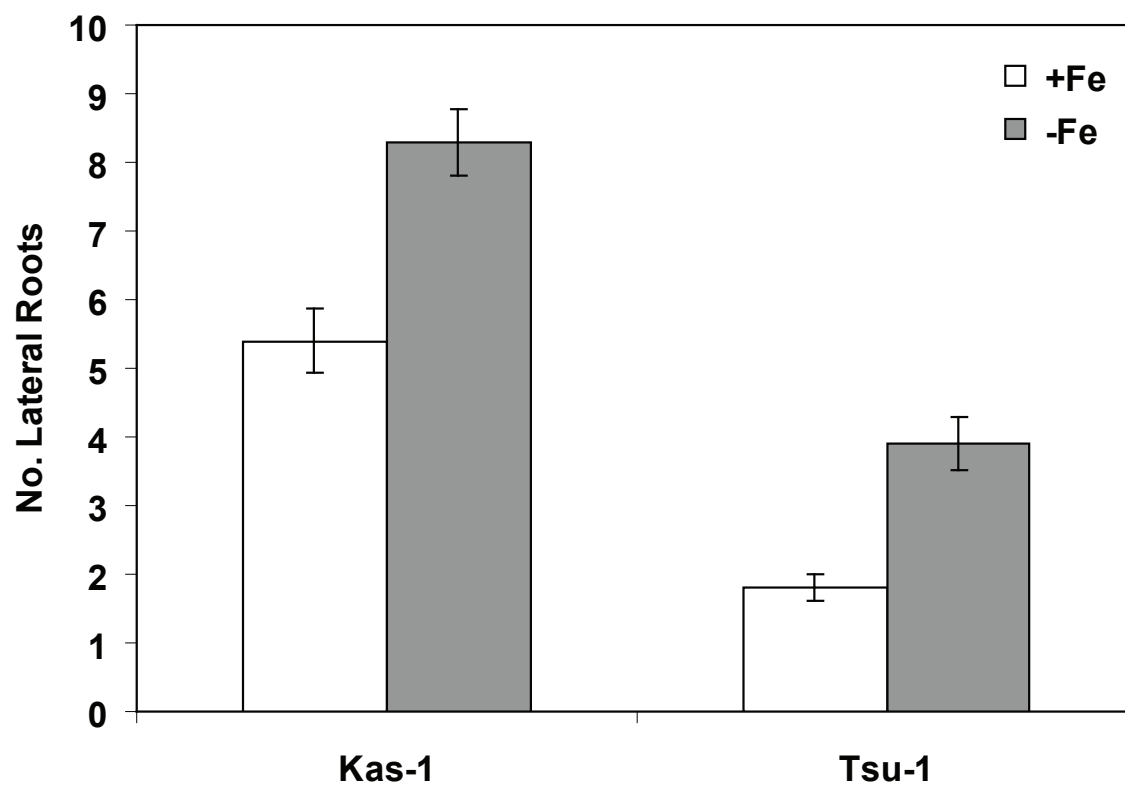
Ricardo J. Stein and Brian M. Waters

No. Supplementary Tables: 1

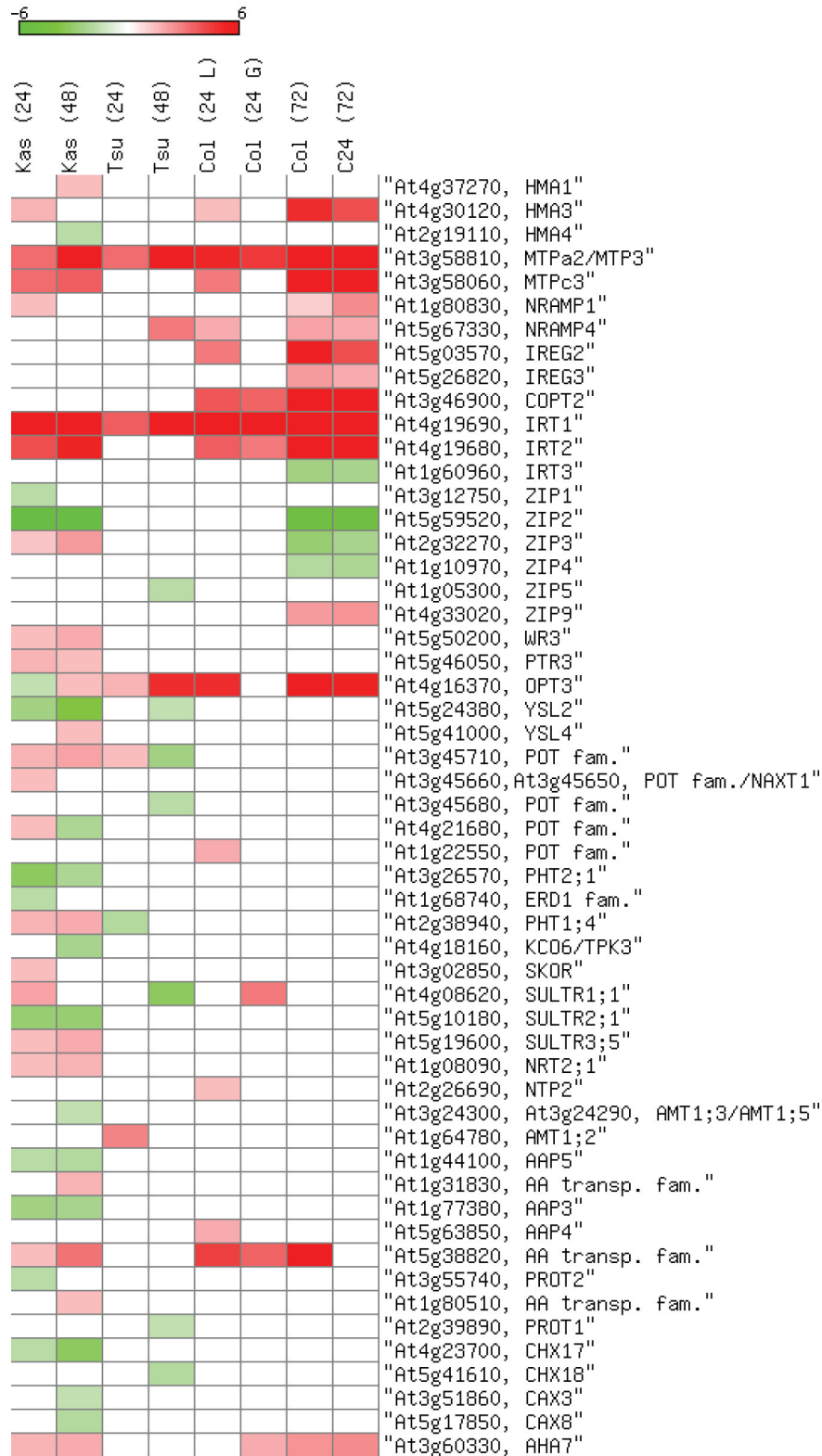
No. Supplementary Figures: 8

Table S1. Overrepresented GO and MIPS categories in Kas-1 and Tsu-1 Fe deficiency

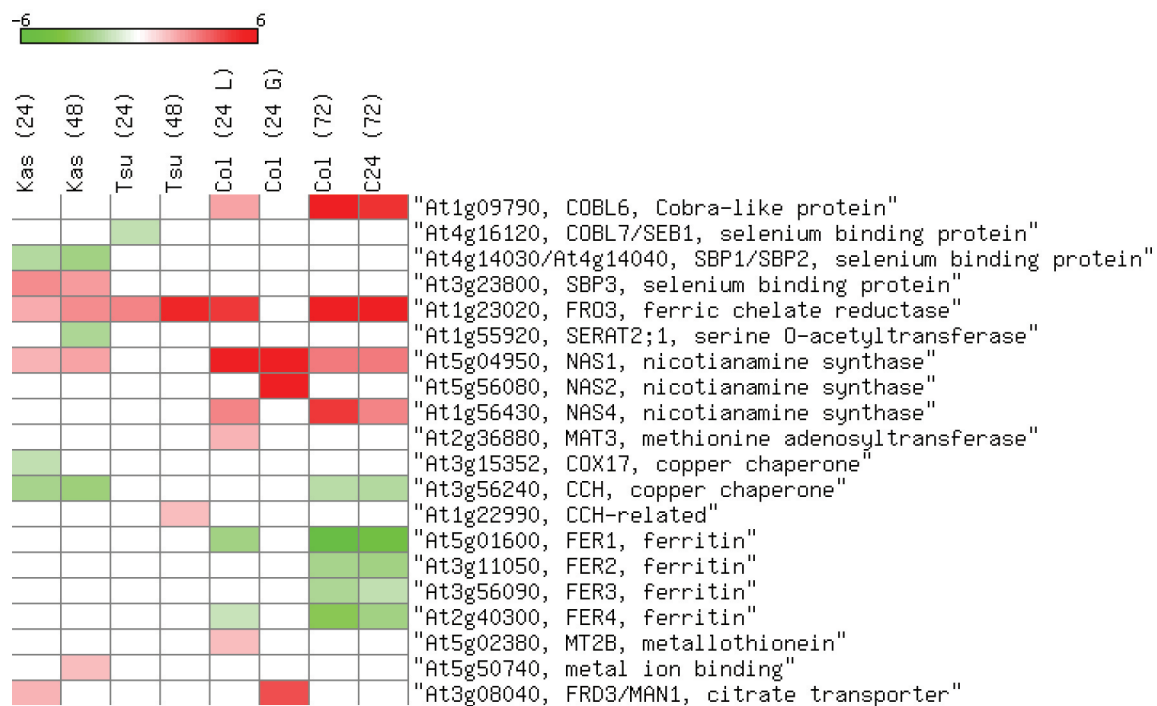
	<u>Observed</u> Frequency	<u>Expected</u> Frequency	p-value
<i>Kas-1 downregulated genes</i>			
<u>GO Term</u>			
response to stimulus	17.30%	10.80%	4.01E-06
response to chemical stimulus	11.00%	5.00%	1.04E-09
response to stress	10.30%	6.30%	2.12E-03
response to endogenous stimulus	6.50%	3.10%	1.20E-04
response to abiotic stimulus	6.20%	3.60%	0.038
response to hormone stimulus	5.40%	2.70%	5.35E-03
amino acid and derivative metabolic process	4.50%	2.00%	1.97E-03
secondary metabolic process	4.20%	1.60%	4.13E-05
response to external stimulus	3.20%	1.00%	3.23E-05
response to abscisic acid stimulus	2.90%	1.00%	1.15E-03
aromatic compound metabolic process	2.70%	1.10%	0.036
response to oxidative stress	2.50%	0.90%	0.014
response to osmotic stress	2.40%	0.90%	0.048
response to jasmonic acid stimulus	1.90%	0.60%	0.022
response to wounding	1.60%	0.50%	0.028
nitrogen compound catabolic process	1.20%	0.20%	5.44E-05
amino acid catabolic process	1.10%	0.10%	3.40E-04
amine catabolic process	1.10%	0.10%	3.40E-04
cellular response to stimulus	1.10%	0.20%	0.014
response to extracellular stimulus	1.10%	0.20%	0.042
<u>MIPS Term</u>			
metabolism	27.30%	20.70%	8.30E-04
interaction with the environment	10.70%	6.10%	8.37E-05
cellular sensing and response to external stimulus	10.30%	5.50%	5.89E-06
cell rescue, defense and virulence	9.60%	5.70%	1.75E-03
chemoperception and response	7.40%	3.20%	1.04E-06
stress response	6.60%	3.40%	9.90E-04
systemic interaction with the environment	5.60%	2.80%	1.70E-03
plant / fungal specific systemic sensing and response	5.20%	2.50%	1.54E-03
plant hormonal regulation	4.70%	2.20%	3.43E-03
secondary metabolism	4.50%	1.80%	1.10E-04
amino acid metabolism	4.10%	1.50%	3.53E-05
metabolism of the pyruvate family (alanine, isoleucine, leucine, valine) and D-alanine	1.50%	0.20%	2.61E-06
response to wounding	1.40%	0.30%	0.016
metabolism of leucine	1.00%	0.10%	2.20E-04
cell aging	1.00%	0.20%	0.035
metabolism of lignins	1.00%	0.20%	0.049
unannotated	0.70%	0.00%	0
metabolism of glycosinolates and derivatives	0.60%	0.10%	0.025
<i>Kas-1 upregulated</i>			
<u>GO Term</u>			
cell wall organization and biogenesis	3.30%	1.00%	1.60E-04
external encapsulating structure organization and biogenesis	3.30%	1.00%	1.90E-04
plant-type cell wall organization and biogenesis	2.30%	0.50%	3.57E-05
<u>MIPS Term</u>			
cell wall	4.40%	1.70%	6.50E-04
cell wall	4.00%	1.10%	7.03E-07
chitin metabolism	0.70%	0.10%	0.013
chitin catabolism	0.70%	0.10%	0.013
unannotated	0.60%	0.00%	0
<i>Tsu-1 downregulated</i>			
<u>G.O. Term</u>			
(none)			
<u>MIPS Term</u>			
unannotated	0.90%	0.00%	0
<i>Tsu-1 upregulated</i>			
<u>G.O. Term</u>			
suberin biosynthetic process	0.60%	0.00%	0.033
<u>MIPS Term</u>			
mitochondrion	18.70%	11.60%	0.023



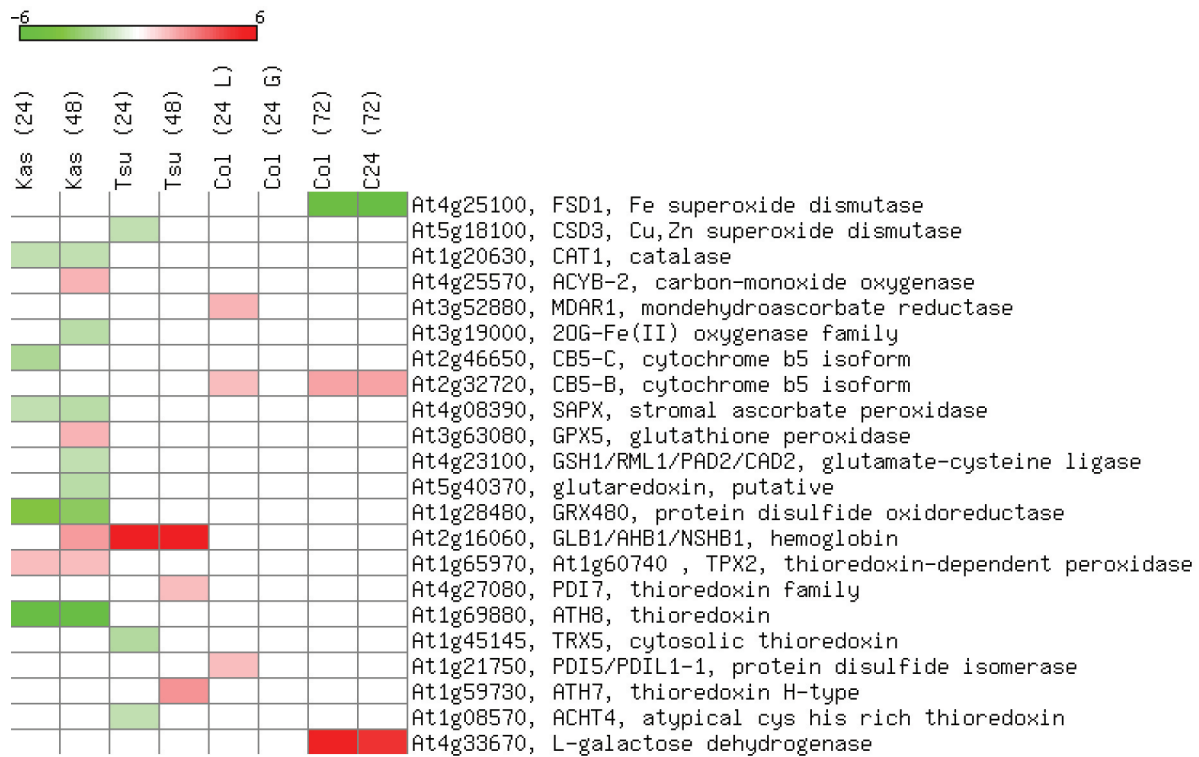
Supplementary Figure S1. Number of lateral roots of Kas-1 and Tsu-1 seedlings. Imbibed seeds were planted onto agar media (0.8 %) supplemented with 1% sucrose and mineral nutrients as described for hydroponic growth. Plates were placed under fluorescent lighting of a 16h photoperiod and held upright to keep root growth on surface of media. Number of lateral roots were counted 8 d after planting. Values are means \pm s.e.



Supplementary Figure S2. Heat map of the MapMan "Transport" functional bin, with genes encoding metal/mineral, oligopeptide, or amino acid transporters. Genes downregulated ≥ 1.5 -fold are shaded in green, genes upregulated ≥ 1.5 -fold are in red.



Supplementary Figure S3. Heat map of the MapMan "Metal handling" functional bin. Genes downregulated ≥ 1.5 -fold are shaded in green, genes upregulated ≥ 1.5 -fold are in red.



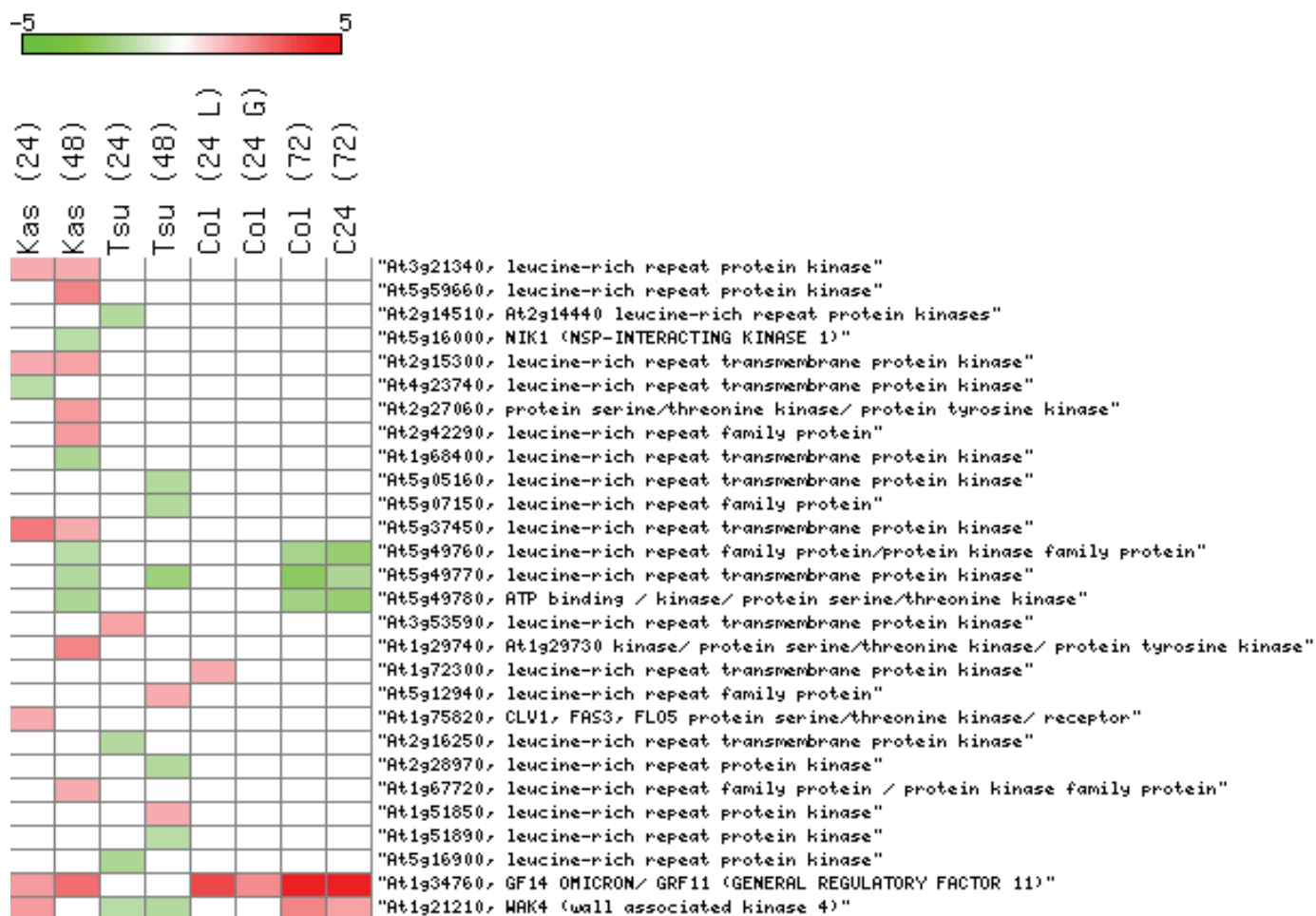
Supplementary Figure S4. Heat map of the "Redox" functional bin. Genes downregulated ≥ 1.5 -fold are shaded in green, genes upregulated ≥ 1.5 -fold are in red.



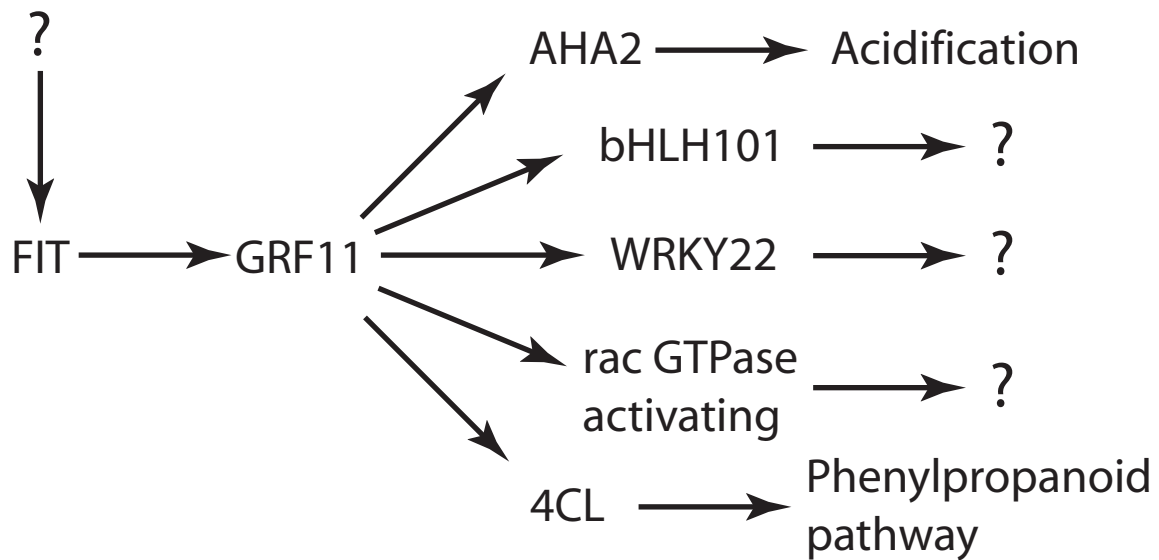
Supplementary Figure S5. Heat map of the "Miscellaneous" functional bin, with genes encoding cytochrome P450 and peroxidases proteins. Genes downregulated ≥ 1.5 -fold are shaded in green, genes upregulated ≥ 1.5 -fold are in red.



Supplementary Figure S6. Heat map of the "Regulation" functional bin, with genes encoding transcription factors of the bHLH, MYB, NAC/NAM, and WRKY families. Genes downregulated ≥ 1.5 -fold are shaded in green, genes upregulated ≥ 1.5 -fold are in red.



Supplementary Figure S7. Heat map of the "Signaling" functional bin, including leucine-rich repeat protein kinase genes, a 14-3-3 gene, and WAK4 wall-associated kinase genes. Genes downregulated ≥ 1.5 -fold are shaded in green, genes upregulated ≥ 1.5 -fold are in red.



Supplementary Figure S8. Model of the involvement of GF14/GRF11, a 14-3-3 protein, in a potential network of root Fe-deficiency regulated responses. Solid arrows represent transcriptional activation, dashed arrows represent protein-protein interactions or biochemical activity. FIT protein responds to an unknown upstream signal (?) to upregulate expression of GRF11. GRF11 protein has been confirmed to activate AHA2 protein activity, and AHA2 transcripts are also increased under Fe deficiency. GRF11 may interact with 14-3-3 consensus motifs in 4CL to alter the phenylpropanoid pathway, a rac GTPase activating protein, and bHLH101 and WRKY22 transcription factors to activate unknown downstream targets.