

Figure S1. Effect of different nutrient deficiencies on amino acid profiling. (a-b) Free amino acids in roots of 7-week-old *Arabidopsis* wild type plants that were grown on full nutrient supply, (Ctrl) and depletion of sulfur (-S), iron (-Fe) and potassium (-K) as specified in the material and methods. Bars represent mean \pm SE ($n = 5$). The mean values were converted into x-fold of the concentration in control condition, which was assigned to 1. Control concentrations in pmol mg⁻¹ FW: Ala=569.1, Pro=31.6, Val=42.4, Ile=28.7, Leu=41.9, Phe=16.7, Tyr=11.5, Trp=5.6, Ser=150.3, Thr=148.8, Asp=211.7, Glu=1193.5, His=37.2, Arg=27.8, Asn=109, Gln=1568.1, Lys=22.6. (c) Quantification of total free proteinogenic aminoacids. Different letters indicate statistically significant difference between the nutrient regimes; $P < 0.05$, ANOVA followed by Student-Newman-Keuls test.

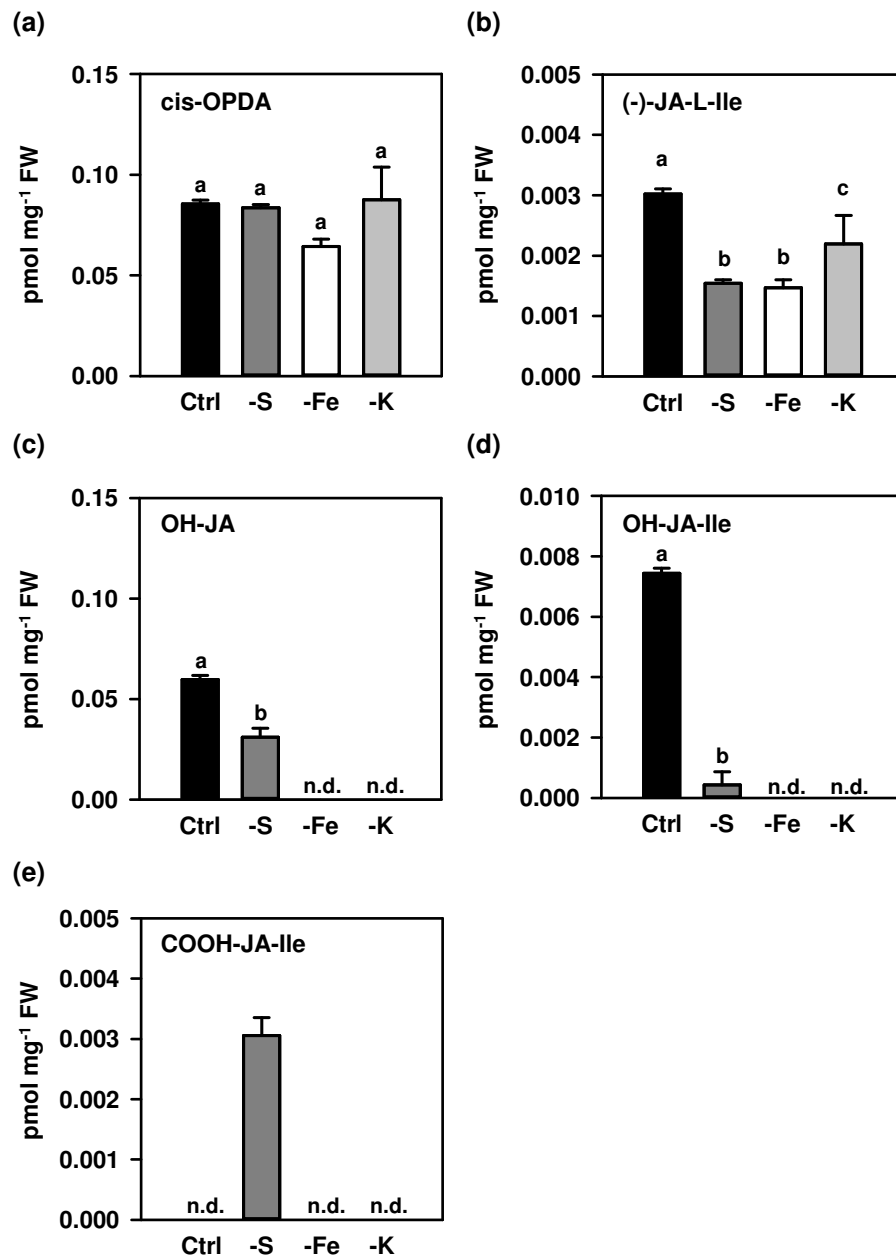


Figure S2. Effect of different nutrient deficiencies on jasmonic acid precursor and its derivatives. (a-e) Steady state levels of cis-OPDA (a), (-)-JA-L-Ile (b), OH-JA (c), OH-JA-Ile (d), COOH-JA-Ile (e) in roots of seven week-old Arabidopsis wild type plants that were grown on full nutrient supply (Ctrl, black bar), or medium depleted of sulfur (-S, dark grey), iron (-Fe, white) or potassium (-K, light grey) as specified in the material and methods. Bars represent mean ± SE (n = 5). Lettering indicates statistical difference by ANOVA (P < 0.05) as determined by Student-Newman-Keuls test.

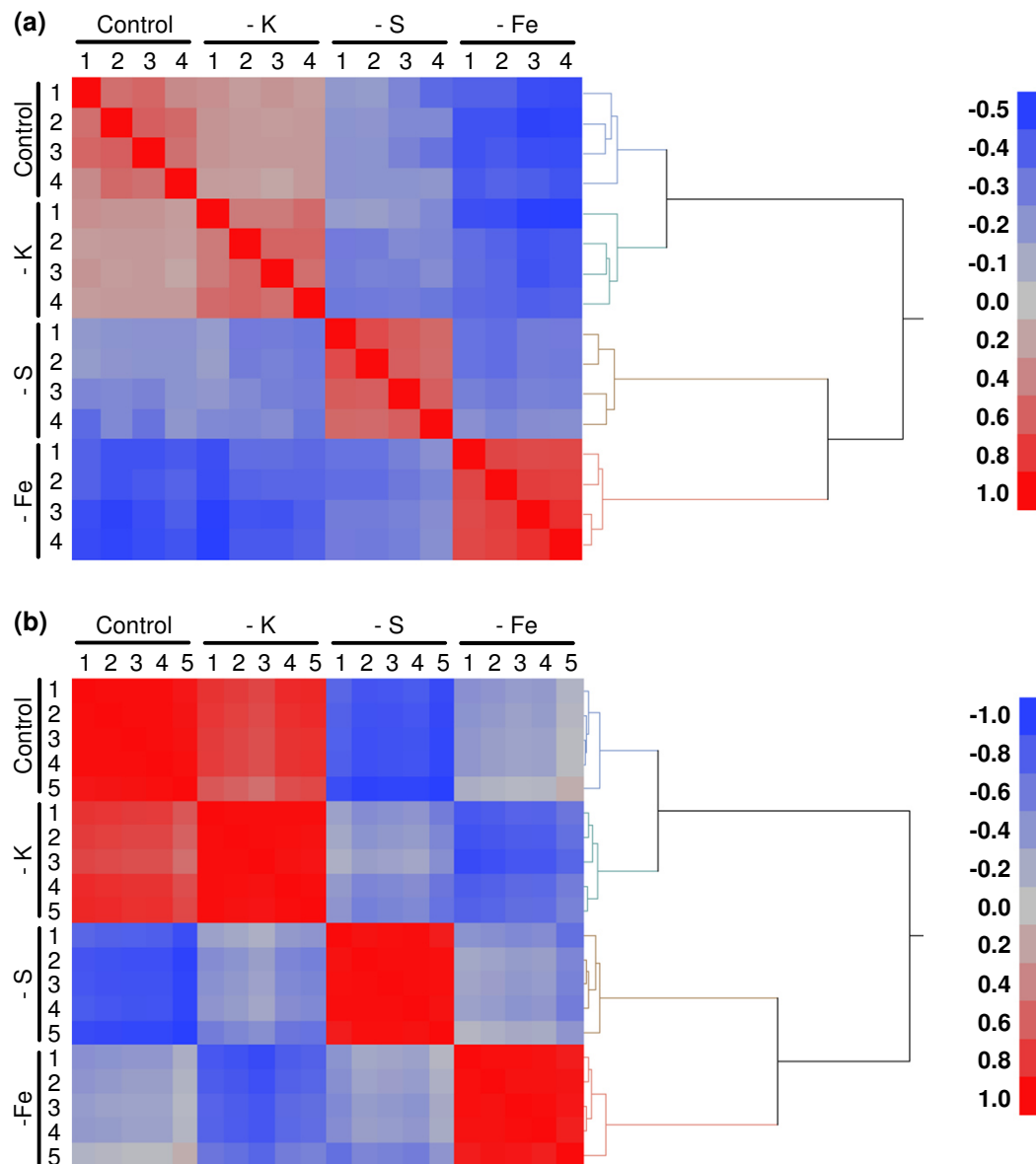


Figure S3. The S and Fe deficiency induced metabolome and transcriptome share higher correlation than the control and the K deficiency induced metabolome and transcriptome. Heat map and dendrogram of nutrient stressed roots compared to control roots. Hierarchical clustering analysis has been performed by using the Pearson correlation coefficient computed for every possible sample comparison of the transcriptome (a) and metabolite (b) data matrix. 2-week old *Arabidopsis* plants were grown for additional 5-weeks under full nutrient supply (Control) or exposed to different nutrient deficiencies (-K, -S, -Fe). The transcriptome and metabolite data were recorded from roots as indicated in Material and Methods. The color legend depicts the degree of correlation, from high (red) to low (blue), between the different samples. Each sample represents a pool of three plants ($n = 4$ for transcriptome and $n = 5$ for metabolite profiling).

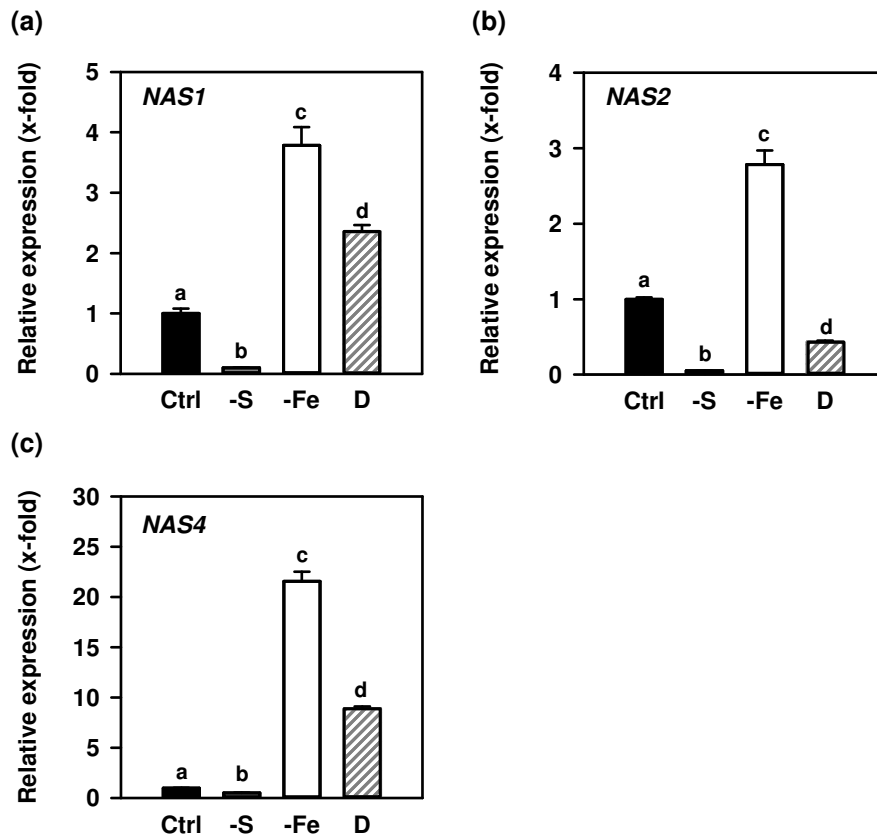


Figure S4. Effect of single and double nutrient deficiencies on the expression of *NAS* isoforms. (a-f) Transcript level of nicotianamine synthase isoforms *NAS1* (a), *NAS2* (b) and *NAS4* (c) in roots of seven-week-old *Arabidopsis* wild type plants hydroponically grown on full medium (Ctrl, black), or medium depleted for sulfur (-S, dark grey), iron (-Fe, white) or both nutrients (D, dashed grey, white) as specified in material and methods. Data are means \pm SE of four individual replicates. Lettering indicates statistical differences by ANOVA ($P < 0.05$) as determined by Student-Newman-Keuls test.

Table S1. Profile of individual glucosinolates in roots of nutrient deficient Arabidopsis plants.

Glucosinolates (nmol mg ⁻¹ FW)	Ctrl	SE	-S	SE	-Fe	SE	-K	SE
3MSOP	0.005	0.000	n.d		0.004	0.002	0.006	0.004
4MSOB	0.054	0.001	n.d		0.021	0.002	0.071	0.029
5MSOP	0.008	0.000	n.d		0.006	0.001	0.009	0.001
4OHI3M	0.065	0.002	0.003	0.000	0.044	0.001	0.099	0.003
7MSOH	0.009	0.001	n.d		0.015	0.002	0.014	0.001
4MTB	0.034	0.001	n.d		0.005	0.001	0.012	0.001
8MSOO	0.164	0.014	n.d		0.079	0.011	0.190	0.016
I3M	0.106	0.002	0.005	0.000	0.088	0.009	0.142	0.004
4MOI3M	0.096	0.001	0.032	0.001	0.213	0.004	0.138	0.001
1MOI3M	0.430	0.011	0.033	0.002	0.504	0.030	0.596	0.048
7MTH	0.053	0.002	n.d		0.045	0.003	0.073	0.001
8MTO	0.668	0.019	n.d		0.138	0.007	0.712	0.017

Total glucosinolates were extracted from 7-week-old Arabidopsis roots grown in full nutrient media (Ctrl) or under sulfur (-S), iron (-Fe) or potassium (-K) limitation and determined as described in the material and methods. Mean of 5 replicates and SE are listed. 3MSOP: 3-methylsulfinylpropyl Gls, 4MSOB: 4-methylsulfinylbutyl Gls, 5MSOP: 5-methylsulfinylpentyl Gls, 4OHI3M: 4-hydroxy-indol-3-yl-methyl Gls, 7MSOH: 7-methylsulfinylheptyl Gls, 4MTB: 4-methylthiobutyl Gls, 8MSOO: 8-methylsulfinyloctyl Gls, I3M: indol-3-yl-methyl Gls, 4MOI3M: 4-methoxy-indol-3-yl-methyl Gls, 1MOI3M: 1-methoxy-indol-3-yl-methyl Gls, 7MTH: 7-methylthioheptyl Gls, 8MTO: 8-methylthiooctyl Gls, n.d.: not detected.

Table S3. List of the 20 most (a) down- and (b) up-regulated genes under Fe limitation in roots of Arabidopsis plants.

(a)

TAIR ID	Gene Symbol	Gene Name	Fold change -Fe	P-value -Fe	Fold change -K	P-value -K	Fold change -S	P-value -S
AT1G52820			0.02	0.000	0.94	0.916	0.14	0.000
AT4G11190			0.06	0.000	0.49	0.062	0.18	0.000
AT4G08300	UMAMIT17	Usually multiple acids move in and out Transporters 17	0.06	0.000	0.75	0.199	0.40	0.000
AT4G12510			0.06	0.000	0.85	0.726	0.29	0.002
AT4G37800	XTH7	xyloglucan endotransglucosylase/hydrolase 7	0.07	0.000	1.95	0.104	0.21	0.001
AT1G60050	UMAMIT35	Usually multiple acids move in and out Transporters 35	0.07	0.000	0.85	0.576	0.15	0.000
AT4G35160			0.08	0.000	0.45	0.001	1.02	0.954
AT4G12520			0.08	0.000	0.75	0.328	0.60	0.075
AT1G01190	CYP78A8	cytochrome P450, family 78, subfamily A, polypeptide 8	0.09	0.000	0.88	0.629	0.84	0.489
AT1G34510			0.09	0.000	0.30	0.000	0.54	0.016
AT5G23980	FRO4	ferric reduction oxidase 4	0.09	0.000	0.57	0.106	0.42	0.015
AT5G06900	CYP93D1	cytochrome P450, family 93, subfamily D, polypeptide 1	0.09	0.000	0.56	0.036	0.15	0.000
AT3G22120	CWLP	cell wall-plasma membrane linker protein	0.10	0.002	0.66	0.596	0.07	0.001
AT1G77520			0.10	0.000	0.53	0.015	0.91	0.749
AT4G08380			0.10	0.000	1.05	0.894	2.12	0.014
AT4G28250	EXPB3	expansin B3	0.10	0.000	0.83	0.360	0.18	0.000
AT2G03090	EXPA15	expansin A15	0.11	0.000	0.50	0.001	0.35	0.000
AT3G23290	LSH4	LIGHT SENSITIVE HYPOCOTYLS 4	0.11	0.000	1.49	0.360	0.28	0.003
AT5G13140			0.11	0.000	1.01	0.988	0.10	0.000
AT3G44990	XTH31	XYLOGLUCAN ENDOTRANGLUCOSYLASE/HYDROLASE 31	0.11	0.000	0.65	0.059	0.63	0.042

(b)

TAIR ID	Gene Symbol	Gene Name	Fold change -Fe	P-value -Fe	Fold change -K	P-value -K	Fold change -S	P-value -S
AT1G12030			67.51	0.000	1.12	0.635	116.41	0.000
AT1G13609	IRP4	Iron-responsive protein 4	62.10	0.000	1.02	0.908	1.04	0.834
AT5G67370	CGLD27	CONSERVED IN THE GREEN LINEAGE AND DIATOMS 27	49.64	0.000	0.99	0.968	0.86	0.437
AT2G30766			45.44	0.000	0.46	0.001	0.53	0.004
AT2G41240	BHLH100	basic helix-loop-helix protein 100	42.77	0.000	0.35	0.000	0.15	0.000
AT5G25840			37.14	0.000	0.98	0.955	0.94	0.870
AT2G14247	IRP3	Iron-responsive protein 3	36.99	0.000	0.25	0.000	0.26	0.000
AT2G41730			35.34	0.000	0.78	0.663	7.73	0.000
AT3G56970	bHLH38	basic helix-loop-helix 38	33.25	0.000	0.46	0.002	0.26	0.000
AT1G47395	IRP2	Iron-responsive protein 2	32.50	0.000	0.57	0.104	4.08	0.000
AT5G04150	BHLH101		24.38	0.000	0.51	0.001	0.41	0.000
AT1G47400	IRP1	Iron-responsive protein 1	24.15	0.000	0.59	0.003	3.02	0.000
AT2G30670			20.49	0.000	1.17	0.537	10.49	0.000
AT1G52120			19.43	0.000	1.27	0.215	0.97	0.916
AT3G56980	bHLH39	basic helix-loop-helix 39	18.56	0.000	0.56	0.006	0.96	0.881
AT2G21640			18.42	0.000	0.99	0.974	1.15	0.605
AT2G23170	GH3.3		18.16	0.000	0.90	0.594	0.70	0.038
AT2G04050			17.36	0.000	0.96	0.912	1.14	0.710
AT1G56430	NAS4	nicotianamine synthase 4	16.69	0.000	1.19	0.599	0.56	0.048
AT3G01490			16.00	0.000	0.82	0.228	0.76	0.083

Table S4. List of the 20 most (a) down- and (b) up-regulated genes under S limitation in roots of Arabidopsis plants.

(a)

TAIR ID	Gene Symbol	Gene Name	Fold change -Fe	P-value -Fe	Fold change -K	P-value -K	Fold change -S	P-value -S
AT2G34390	NIP2;1	NOD26-like intrinsic protein 2;1	0.94	0.936	0.04	0.000	0.04	0.000
AT5G10040			1.27	0.844	0.08	0.008	0.06	0.005
AT1G77120	ADH1	alcohol dehydrogenase 1	0.90	0.842	0.08	0.000	0.07	0.000
AT1G01580	FRO2	ferric reduction oxidase 2	3.45	0.000	0.87	0.485	0.07	0.000
AT3G22120	CWLP	cell wall-plasma membrane linker protein	0.10	0.002	0.66	0.596	0.07	0.001
AT3G12900			5.47	0.000	0.69	0.129	0.08	0.000
AT2G25680	MOT1	molybdate transporter 1	0.25	0.000	1.17	0.475	0.09	0.000
AT1G43800	FTM1	FLORAL TRANSITION AT THE MERISTEM1	0.23	0.000	0.11	0.000	0.09	0.000
AT4G19690	IRT1	iron-regulated transporter 1	4.99	0.000	0.99	0.953	0.10	0.000
AT5G13140			0.11	0.000	1.01	0.988	0.10	0.000
AT4G33070			0.39	0.059	0.07	0.000	0.11	0.000
AT5G37260	RVE2	REVEILLE 2	0.78	0.151	0.41	0.000	0.12	0.000
AT2G38600			1.62	0.036	1.83	0.010	0.12	0.000
AT3G22142			0.13	0.002	2.01	0.248	0.12	0.001
AT2G33790	AGP30	arabinogalactan protein 30	0.32	0.000	1.39	0.198	0.13	0.000
AT5G38820			6.89	0.000	0.57	0.065	0.13	0.000
AT3G43190	SUS4	sucrose synthase 4	0.57	0.029	0.19	0.000	0.13	0.000
AT2G41810			0.46	0.000	0.42	0.000	0.14	0.000
AT1G52820			0.02	0.000	0.94	0.916	0.14	0.000
AT4G33560			0.27	0.001	0.17	0.000	0.14	0.000

(b)

TAIR ID	Gene Symbol	Gene Name	Fold change -Fe	P-value -Fe	Fold change -K	P-value -K	Fold change -S	P-value -S
AT5G48850	ATSDI1	SULPHUR DEFICIENCY-INDUCED 1	1.01	0.987	2.51	0.034	209.49	0.000
AT1G12030			67.51	0.000	1.12	0.635	116.41	0.000
AT3G55790			0.94	0.732	1.42	0.028	105.84	0.000
AT2G44460	BGLU28	beta glucosidase 28	1.42	0.229	1.09	0.820	84.53	0.000
AT3G49580	LSU1	RESPONSE TO LOW SULFUR 1	1.13	0.398	0.96	0.813	77.78	0.000
AT5G26220			0.78	0.484	1.61	0.139	77.16	0.000
AT1G23730	BCA3	beta carbonic anhydrase 3	1.31	0.248	0.92	0.778	76.20	0.000
AT3G05400			1.67	0.004	1.40	0.044	59.94	0.000
AT3G49570	LSU3	RESPONSE TO LOW SULFUR 3	0.79	0.210	1.29	0.175	55.23	0.000
AT1G58320			4.39	0.000	1.56	0.022	43.05	0.000
AT5G24660	LSU2	RESPONSE TO LOW SULFUR 2	0.65	0.334	2.81	0.016	40.88	0.000
AT4G31330			4.12	0.000	0.73	0.032	34.64	0.000
AT2G32487			1.23	0.193	1.09	0.636	28.72	0.000
AT1G03020			0.67	0.063	0.83	0.399	22.23	0.000
AT2G29220			2.26	0.000	1.80	0.001	20.84	0.000
AT1G69795	MIR395E	microRNA395E	0.95	0.755	1.00	0.996	20.30	0.000
AT3G08860	PYD4	PYRIMIDINE 4	7.97	0.000	1.00	0.998	16.00	0.000
AT1G26985	MIR395C	microRNA395C	0.97	0.945	1.18	0.673	15.97	0.000
AT4G35640	SERAT3;2	serine acetyltransferase 3;2	1.01	0.945	1.16	0.349	15.95	0.000
AT3G60140	DIN2	DARK INDUCIBLE 2	8.66	0.002	0.29	0.045	15.12	0.000

Table S5. List of the 20 most (a) down- and (b) up-regulated genes under K limitation in roots of Arabidopsis plants.

(a)

TAIR ID	Gene Symbol	Gene Name	Fold change -Fe	P-value -Fe	Fold change -K	P-value -K	Fold change -S	P-value -S
AT2G34390	NIP2;1	NOD26-like intrinsic protein 2;1	0.94	0.936	0.04	0.000	0.04	0.000
AT4G33070			0.39	0.059	0.07	0.000	0.11	0.000
AT1G77120	ADH1	alcohol dehydrogenase 1	0.90	0.842	0.08	0.000	0.07	0.000
AT5G10040			1.27	0.844	0.08	0.008	0.06	0.005
AT1G43800	FTM1	FLORAL TRANSITION AT THE MERISTEM1	0.23	0.000	0.11	0.000	0.09	0.000
AT5G39890			0.64	0.110	0.12	0.000	0.18	0.000
AT1G67865			0.12	0.000	0.16	0.000	0.40	0.001
AT4G33560			0.27	0.001	0.17	0.000	0.14	0.000
AT4G26050	PIRL8	plant intracellular ras group-related LRR 8	2.41	0.000	0.18	0.000	0.74	0.021
AT2G39510	UMAMIT14	Usually multiple acids move in and out Transporters 14	0.24	0.003	0.19	0.001	0.55	0.194
AT3G43190	SUS4	sucrose synthase 4	0.57	0.029	0.19	0.000	0.13	0.000
AT5G15120			0.75	0.209	0.20	0.000	0.41	0.000
AT1G12805			0.45	0.015	0.22	0.000	0.14	0.000
AT1G08090	NRT2:1	nitrate transporter 2:1	0.56	0.090	0.22	0.000	0.14	0.000
AT1G33055			1.27	0.502	0.23	0.000	0.38	0.004
AT3G10040			0.61	0.136	0.23	0.000	0.33	0.002
AT2G16060	HB1	hemoglobin 1	1.06	0.836	0.24	0.000	0.23	0.000
AT2G14247			36.99	0.000	0.25	0.000	0.26	0.000
AT2G14210	AGL44	AGAMOUS-like 44	1.38	0.059	0.26	0.000	0.68	0.028
AT4G10270			0.80	0.473	0.26	0.000	0.27	0.000

(b)

TAIR ID	Gene Symbol	Gene Name	Fold change -Fe	P-value -Fe	Fold change -K	P-value -K	Fold change -S	P-value -S
AT4G13420	HAK5	high affinity K+ transporter 5	2.69	0.000	11.86	0.000	0.72	0.176
AT5G25980	TGG2	glucoside glucohydrolase 2	0.99	0.978	5.59	0.000	0.82	0.674
AT5G26000	TGG1	thioglucoside glucohydrolase 1	0.85	0.507	4.98	0.000	0.67	0.076
AT1G67090	RBCS1A	ribulose biphosphate carboxylase small chain 1A	0.85	0.788	4.95	0.002	0.57	0.252
AT4G17090	CT-BMY	chloroplast beta-amylase	0.97	0.942	4.27	0.000	0.85	0.621
AT5G52700			2.13	0.002	4.20	0.000	0.91	0.736
AT1G78230			1.06	0.898	4.12	0.000	0.47	0.018
AT3G28510			2.13	0.000	3.95	0.000	1.47	0.028
AT1G22770	GI	GIGANTEA	2.73	0.000	3.69	0.000	9.88	0.000
AT2G02120	PDF2.1		1.64	0.049	3.58	0.000	0.31	0.000
AT4G21840	MSRB8	methionine sulfoxide reductase B8	2.87	0.023	3.51	0.008	1.84	0.190
AT5G13220	JAZ10	jasmonate-zim-domain protein 10	2.40	0.156	3.47	0.042	0.72	0.650
AT1G52130			4.36	0.000	3.46	0.000	0.94	0.835
AT5G44110	ABCI21	ATP-binding cassette A21	0.70	0.424	3.32	0.006	1.34	0.529
AT1G56600	GolS2	galactinol synthase 2	1.70	0.002	3.24	0.000	0.95	0.792
AT4G23700	CHX17	cation/H+ exchanger 17	4.94	0.000	3.21	0.005	1.00	0.995
AT3G60700			0.48	0.001	3.12	0.000	0.62	0.014
AT5G22570	WRKY38	WRKY DNA-binding protein 38	1.07	0.888	3.09	0.004	1.18	0.702
AT3G53600			1.80	0.048	3.02	0.001	3.46	0.000
AT3G23120	RLP38	receptor like protein 38	3.21	0.000	2.99	0.000	1.65	0.050

Table S6. List of the 20 most (a) down- and (b) up-regulated genes under Fe and S limitation in roots of Arabidopsis plants.

(a)

TAIR ID	Gene Symbol	Gene Name	Fold change -Fe	P-value -Fe	Fold change -K	P-value -K	Fold change -S	P-value -S
AT1G52820			0.02	0.000	0.94	0.916	0.14	0.000
AT4G11190			0.06	0.000	0.49	0.062	0.18	0.000
AT4G08300	UMAMIT17	Usually multiple acids move in and out Transporters 17	0.06	0.000	0.75	0.199	0.40	0.000
AT4G12510			0.06	0.000	0.85	0.726	0.29	0.002
AT4G37800	XTH7	xyloglucan endotransglucosylase/hydrolase 7	0.07	0.000	1.95	0.104	0.21	0.001
AT1G60050	UMAMIT35	Usually multiple acids move in and out Transporters 35	0.07	0.000	0.85	0.576	0.15	0.000
AT5G23980	FRO4	ferric reduction oxidase 4	0.09	0.000	0.57	0.106	0.42	0.015
AT3G22120	CWLP	cell wall-plasma membrane linker protein	0.10	0.002	0.66	0.596	0.07	0.001
AT4G28250	EXPB3	expansin B3	0.10	0.000	0.83	0.360	0.18	0.000
AT3G23290	LSH4	LIGHT SENSITIVE HYPOCOTYLS 4	0.11	0.000	1.49	0.360	0.28	0.003
AT5G13140			0.11	0.000	1.01	0.988	0.10	0.000
AT3G44990	XTH31	XYLOGLUCAN ENDOTRANSGLUCOSYLASE/HYDROLASE 31	0.11	0.000	0.65	0.059	0.63	0.042
AT1G09750			0.11	0.000	1.27	0.517	0.17	0.000
AT4G38770	PRP4	proline-rich protein 4	0.12	0.000	1.03	0.916	0.28	0.000
AT4G01430	UMAMIT29	Usually multiple acids move in and out Transporters 29	0.12	0.000	0.99	0.986	0.22	0.000
AT2G32990	GH9B8	glycosyl hydrolase 9B8	0.12	0.000	0.70	0.007	0.40	0.000
AT5G38020			0.13	0.000	0.82	0.502	0.43	0.003
AT3G22142			0.13	0.002	2.01	0.248	0.12	0.001
AT1G62280	SLAH1	SLAC1 homologue 1	0.14	0.000	0.95	0.888	0.25	0.000
AT2G33850			0.14	0.000	1.32	0.455	0.47	0.031

(b)

TAIR ID	Gene Symbol	Gene Name	Fold change -Fe	P-value -Fe	Fold change -K	P-value -K	Fold change -S	P-value -S
AT1G12030			67.51	0.000	1.12	0.635	116.41	0.000
AT3G05400			1.67	0.004	1.40	0.044	59.94	0.000
AT4G31330			4.12	0.000	0.73	0.032	34.64	0.000
AT3G08860	PYD4	PYRIMIDINE 4	7.97	0.000	1.00	0.998	16.00	0.000
AT3G60140	DIN2	DARK INDUCIBLE 2	8.66	0.002	0.29	0.045	15.12	0.000
AT1G15125			4.19	0.002	1.92	0.124	12.60	0.000
AT5G24860	FPF1	FLOWERING PROMOTING FACTOR 1	1.60	0.005	0.61	0.004	11.26	0.000
AT2G30670			20.49	0.000	1.17	0.537	10.49	0.000
AT2G29150			3.69	0.004	1.01	0.989	10.37	0.000
AT2G41730			35.34	0.000	0.78	0.663	7.73	0.000
AT3G53820			2.19	0.001	1.09	0.721	7.18	0.000
AT4G21680	NRT1.8	NITRATE TRANSPORTER 1.8	10.85	0.000	0.55	0.048	6.88	0.000
AT2G26560	PLA2A	phospholipase A 2A	7.32	0.000	1.10	0.808	6.56	0.000
AT5G39110			3.00	0.000	0.83	0.419	5.56	0.000
AT4G16260			4.57	0.000	1.37	0.247	5.52	0.000
AT5G02780	GSTL1	glutathione transferase lambda 1	7.10	0.000	0.85	0.305	5.01	0.000
AT2G17640	ATSERAT3;1		2.00	0.000	0.88	0.138	4.93	0.000
AT1G05340			2.21	0.000	1.30	0.129	4.91	0.000
AT1G67160			4.13	0.000	1.14	0.518	4.71	0.000
AT4G14580	CIPK4	CBL-interacting protein kinase 4	1.93	0.000	1.44	0.009	4.69	0.000

Table S7. List of the 20 most (a) down- and (b) up-regulated genes under Fe, S and K limitation in roots of *Arabidopsis* plants.

(a)

TAIR ID	Gene Symbol	Gene Name	Fold change -Fe	P-value -Fe	Fold change -K	P-value -K	Fold change -S	P-value -S
AT1G34510			0.09	0.000	0.30	0.000	0.54	0.016
AT5G06900	CYP93D1	cytochrome P450, family 93, subfamily D, polypeptide 1	0.09	0.000	0.56	0.036	0.15	0.000
AT2G03090	EXPA15	expansin A15	0.11	0.000	0.50	0.001	0.35	0.000
AT2G27402			0.12	0.000	0.58	0.008	0.15	0.000
AT1G67865			0.12	0.000	0.16	0.000	0.40	0.001
AT4G28850	XTH26	xyloglucan endotransglucosylase/hydrolase 26	0.12	0.000	0.49	0.004	0.60	0.032
AT4G12545			0.14	0.000	0.37	0.000	0.61	0.025
AT4G02850			0.14	0.000	0.47	0.003	0.46	0.002
AT4G25250			0.15	0.000	0.56	0.004	0.52	0.002
AT5G59520	ZIP2	ZRT/IRT-like protein 2	0.19	0.000	0.60	0.000	0.56	0.000
AT2G38750	ANNAT4	annexin 4	0.20	0.000	0.49	0.001	0.39	0.000
AT4G22230			0.20	0.000	0.40	0.000	0.42	0.000
AT3G20460			0.21	0.000	0.65	0.016	0.48	0.000
AT3G02620			0.21	0.000	0.27	0.000	0.46	0.014
AT4G11210			0.23	0.000	0.56	0.010	0.44	0.001
AT1G26790			0.23	0.000	0.41	0.000	0.18	0.000
AT3G57920	SPL15	squamosa promoter binding protein-like 15	0.23	0.000	0.59	0.001	0.30	0.000
AT1G43800	FTM1	FLORAL TRANSITION AT THE MERISTEM1	0.23	0.000	0.11	0.000	0.09	0.000
AT4G37160	sks15	SKU5 similar 15	0.23	0.000	0.54	0.000	0.25	0.000
AT5G51520			0.27	0.000	0.62	0.045	0.27	0.000

(b)

TAIR ID	Gene Symbol	Gene Name	Fold change -Fe	P-value -Fe	Fold change -K	P-value -K	Fold change -S	P-value -S
AT1G58320			4.39	0.000	1.56	0.022	43.05	0.000
AT2G29220			2.26	0.000	1.80	0.001	20.84	0.000
AT1G09080	BIP3	binding protein 3	5.15	0.000	2.52	0.003	13.28	0.000
AT1G22770	GI	GIGANTEA	2.73	0.000	3.69	0.000	9.88	0.000
AT1G53625			3.50	0.000	2.38	0.001	9.51	0.000
AT1G63590			7.59	0.000	1.68	0.030	9.38	0.000
AT2G43570	CHI	chitinase, putative	2.15	0.000	1.76	0.000	6.29	0.000
AT3G22370	AOX1A	alternative oxidase 1A	10.48	0.000	1.69	0.016	5.89	0.000
AT1G53610			2.22	0.000	1.77	0.006	5.63	0.000
AT4G11170			2.91	0.000	1.95	0.001	5.02	0.000
AT5G52720			4.93	0.000	2.34	0.000	4.43	0.000
AT5G10410			1.54	0.019	1.84	0.002	4.33	0.000
AT1G12200	FMO	flavin monooxygenase	3.88	0.000	1.69	0.001	4.08	0.000
AT4G28460			3.00	0.000	1.94	0.002	4.00	0.000
AT5G18470			2.95	0.000	2.14	0.004	3.77	0.000
AT3G53600			1.80	0.048	3.02	0.001	3.46	0.000
AT5G39120			1.72	0.026	1.78	0.019	3.30	0.000
AT5G25260			1.67	0.000	1.91	0.000	3.25	0.000
AT3G63380			2.72	0.000	2.27	0.000	3.22	0.000
AT1G74590	GSTU10	glutathione S-transferase TAU 10	4.69	0.000	1.82	0.001	2.79	0.000

Table S8. List of the 20 genes (a) most up-regulated under -S and down-regulated under -Fe and (b) most down-regulated under -S and up-regulated under -Fe in roots of Arabidopsis plants.

(a)

TAIR ID	Gene Symbol	Gene Name	Fold change -Fe	P-value -Fe	Fold change -K	P-value -K	Fold change -S	P-value -S
AT1G63560			0.19	0.000	1.50	0.287	12.83	0.000
AT3G61400			0.57	0.032	1.17	0.599	9.82	0.000
AT4G36570	RL3	RAD-like 3	0.31	0.000	0.31	0.000	9.06	0.000
AT1G62180	APR2	5'adenylylphosphosulfate reductase 2	0.46	0.001	1.00	0.999	8.57	0.000
AT4G10540			0.38	0.003	1.28	0.478	6.07	0.000
AT2G36020	HVA22J	HVA22-like protein J	0.49	0.001	1.04	0.890	5.46	0.000
AT4G25220	G3Pp2	glycerol-3-phosphate permease 2	0.27	0.000	0.75	0.264	4.49	0.000
AT1G10480	ZFP5	zinc finger protein 5	0.51	0.001	1.05	0.828	4.42	0.000
AT1G09180	SARA1A	secretion-associated RAS super family 1	0.49	0.002	1.06	0.829	4.40	0.000
AT3G53590			0.62	0.017	1.04	0.881	3.75	0.000
AT1G62975			0.37	0.002	1.38	0.296	3.59	0.000
AT2G21010			0.46	0.000	0.75	0.096	3.37	0.000
AT4G04610	APR1	APS reductase 1	0.55	0.012	1.04	0.895	3.37	0.000
AT1G24575			0.41	0.000	0.62	0.012	3.35	0.000
AT3G29110			0.31	0.000	0.67	0.006	3.26	0.000
AT5G37990			0.24	0.000	0.89	0.722	3.22	0.000
AT1G19050	ARR7	response regulator 7	0.26	0.000	0.69	0.033	3.15	0.000
AT4G19800			0.40	0.001	0.55	0.017	3.14	0.000
AT4G21250			0.13	0.000	0.85	0.508	3.07	0.000
AT3G44320	NIT3	nitrilase 3	0.53	0.002	0.84	0.399	2.99	0.000

(b)

TAIR ID	Gene Symbol	Gene Name	Fold change -Fe	P-value -Fe	Fold change -K	P-value -K	Fold change -S	P-value -S
AT1G01580	FRO2	ferric reduction oxidase 2	3.45	0.000	0.87	0.485	0.07	0.000
AT3G12900			5.47	0.000	0.69	0.129	0.08	0.000
AT4G19690	IRT1	iron-regulated transporter 1	4.99	0.000	0.99	0.953	0.10	0.000
AT2G38600			1.62	0.036	1.83	0.010	0.12	0.000
AT5G38820			6.89	0.000	0.57	0.065	0.13	0.000
AT3G46900	COPT2	copper transporter 2	3.64	0.000	1.17	0.234	0.19	0.000
AT4G35770	SEN1	SENESCENCE 1	11.19	0.000	0.90	0.850	0.19	0.000
AT3G57157			2.05	0.023	1.22	0.570	0.21	0.000
AT3G17180	scpl33	serine carboxypeptidase-like 33	1.62	0.016	1.23	0.319	0.27	0.000
AT3G07720			2.86	0.000	1.05	0.828	0.28	0.000
AT4G13300	TPS13	terpenoid synthase 13	6.64	0.000	1.72	0.008	0.31	0.000
AT2G02120	PDF2.1		1.64	0.049	3.58	0.000	0.31	0.000
AT5G49360	BXL1	beta-xylosidase 1	2.46	0.000	1.30	0.078	0.32	0.000
AT5G22920			1.63	0.049	0.62	0.055	0.33	0.000
AT3G45130	LAS1	lanosterol synthase 1	2.74	0.000	0.79	0.201	0.36	0.000
AT5G46730			1.86	0.037	1.02	0.966	0.37	0.002
AT3G57520	SIP2	seed imbibition 2	1.74	0.000	1.11	0.303	0.39	0.000
AT4G26290			5.94	0.000	0.73	0.285	0.39	0.002
AT1G30720			2.55	0.000	1.21	0.449	0.40	0.000
AT3G06850	BCE2		4.61	0.000	1.28	0.031	0.40	0.000

Table S9. Analysis in public available databases (Genevestigator® V3) of the expression in roots of the 14 genes belonging to S assimilation that were specifically down-regulated by -Fe. Fold changes relative to the respective controls are shown, <-1.2 fold-change and <0.05 P-value are light grey, <-1.5 fold-change and <0.05 P-value are dark grey.

Reference	Deficiency	SULTR3;5		ATPS1		APK2		APK3		SOT6		SOT8		SOT9/SOT10		SIR		OAS-TL A		OAS-TL B		OAS-TL C		GCL			
		fold change	P-value	fold change	P-value	fold change	P-value	fold change	P-value	fold change	P-value	fold change	P-value	fold change	P-value	fold change	P-value	fold change	P-value	fold change	P-value	fold change	P-value	fold change	P-value		
[1]	Fe (3h and 6h)	0.53	0.083	-0.19	0.410	0.19	0.608	0.27	0.193	-0.09	0.745	-0.62	0.023	0.32	0.022	-0.04	0.459	-0.24	0.209	0.18	0.262	0.03	0.774	-0.03	0.926	0.22	0.343
[1]	Fe (12h and 24h)	0.10	0.731	-0.26	0.468	0.25	0.262	0.04	0.802	-0.03	0.907	-1.48	0.039	0.31	0.125	-0.86	0.042	-0.23	0.045	0.00	0.993	0.07	0.624	-0.40	0.194	0.19	0.285
[1]	Fe (48h and 72h)	0.18	0.093	0.72	0.000	0.43	0.044	0.02	0.898	-2.55	0.001	-4.26	0.000	-0.58	0.063	-1.56	0.001	-1.21	0.005	-0.72	0.009	-0.50	0.001	-1.35	0.002	0.17	0.124
[2]	Fe (1h)	-0.02	0.932	-0.17	0.130	-0.18	0.243	-0.04	0.860	-0.02	0.946	-0.04	0.932	0.37	0.197	-0.05	0.748	-0.17	0.411	-0.05	0.449	0.11	0.004	-0.06	0.671	-0.05	0.495
[2]	Fe (6h)	-0.33	0.404	0.06	0.776	-0.14	0.508	0.00	0.995	0.53	0.193	0.29	0.454	0.30	0.011	-0.18	0.042	0.09	0.689	-0.05	0.710	0.01	0.972	-0.27	0.127	0.03	0.803
[2]	Fe (24h)	0.05	0.737	-0.06	0.774	-0.13	0.795	-0.05	0.518	-0.05	0.925	0.06	0.605	0.03	0.874	-0.20	0.482	-0.01	0.983	-0.11	0.544	-0.14	0.373	-0.26	0.070	0.05	0.647
[3]	Fe (5 days)	0.46	0.105	0.29	0.131	0.21	0.174	-0.06	0.521	-0.11	0.714	-0.48	0.111	-0.38	0.043	-0.36	0.090	0.02	0.655	-0.09	0.119	0.23	0.199	-0.12	0.324	-0.14	0.585
[4]	Fe (7 days)	0.19	0.889	0.22	0.362	0.36	0.194	-0.06	0.805	-0.27	0.744	-0.27	0.803	-0.01	0.988	-0.22	0.200	0.24	0.145	-0.06	0.649	0.09	0.728	0.07	0.635	-0.08	0.382
[5]	Fe (10 days)	-1.94	0.001	0.05	0.541	0.11	0.660	-0.17	0.073	-0.50	0.089	-0.90	0.011	-0.60	0.036	-0.36	0.001	-0.20	0.005	-0.15	0.340	-0.06	0.396	-0.45	0.013	-0.02	0.736
[6]	S (24h)	-0.13	0.028	0.20	0.109	-0.85	0.005	0.00	0.978	-0.19	0.271	-0.46	0.001	-0.07	0.592	-0.17	0.007	-0.10	0.183	-0.01	0.843	-0.17	0.004	-0.31	0.011	-0.19	0.014
[7]	S (3h)	0.05	0.924	1.44	0.004	1.01	0.009	0.29	0.397	0.38	0.029	0.69	0.190	-0.43	0.270	0.55	0.002	-0.09	0.750	0.21	0.285	0.07	0.644	0.33	0.312	-0.02	0.444
[7]	S (12h)	-0.06	0.875	0.68	0.009	-0.16	0.554	-0.05	0.645	0.50	0.016	0.07	0.753	-0.15	0.669	0.16	0.098	-0.09	0.416	0.25	0.236	-0.11	0.525	-0.15	0.593	-0.07	0.101
[7]	S (24h)	-0.06	0.810	0.57	0.020	-0.69	0.035	-0.08	0.529	0.39	0.012	-0.83	0.049	-0.29	0.414	0.25	0.034	0.02	0.848	0.32	0.151	-0.23	0.195	-0.05	0.858	-0.03	0.563
[7]	S (48h)	-0.01	0.906	0.05	0.532	-0.73	0.097	-0.14	0.217	0.43	0.008	-0.56	0.104	-0.29	0.415	0.32	0.027	-0.05	0.623	0.38	0.113	-0.16	0.338	-0.19	0.507	-0.04	0.340
[7]	S (72h)	-0.87	0.050	-0.39	0.215	-1.45	0.021	-0.08	0.449	0.37	0.019	-0.48	0.135	-0.20	0.589	0.23	0.004	-0.08	0.470	0.40	0.107	-0.11	0.459	-0.17	0.544	-0.20	0.079

References: [1] Dinnyen J.R., Long T.A., Wang J.Y., Jung J.W., Mace D., Pointer S., Barron C., Brady S.M., Schiefelbein J. & Benfey P.N. (2008) Cell identity mediates the response of Arabidopsis roots to abiotic stress. *Science*, **320**, 942-945. [2] Buckhout T., Yang T. & Schmidt W. (2009) Early iron-deficiency-induced transcriptional changes in Arabidopsis roots as revealed by microarray analyses. *BMC Genomics*, **10**, 147. [3] Long T.A., Tsukagoshi H., Busch W., Lahner B., Salt D.E. & Benfey P.N. (2010) The bHLH transcription factor POPEYE regulates response to iron deficiency in Arabidopsis roots. *Plant Cell*, **22**, 2219-2236. [4] Schuler M., Keller A., Backes C., Philipp K., Lenhof H.P. & Bauer P. (2011) Transcriptome analysis by GeneTrail revealed regulation of functional categories in response to alterations of iron homeostasis in *Arabidopsis thaliana*. *BMC Plant Biol*, **11**, 87. [5] Sivitz A.B., Hermand V., Curie C. & Vert G. (2012) Arabidopsis bHLH100 and bHLH101 control iron homeostasis via a FIT-independent pathway. *PLoS One*, **7**, e44843. [6] Goda H., Sasaki E., Akiyama K., Maruyama-Nakashita A., Nakabayashi K., Li W., Ogawa M., Yamauchi Y., Preston J., Aoki K., Kiba T., Takatsuto S., Fujiooka S., Asami T., Nakano T., Kato H., Mizuno T., Sakakibara H., Yamaguchi S., Nambara E., Kamiya Y., Takahashi H., Hirai M.Y., Sakurai T., Shinzaki K., Saito K., Yoshida S. & Shimada Y. (2008) The AtGenExpress hormone and chemical treatment data set: experimental design, data evaluation, model data analysis and data access. *Plant J*, **55**, 526-542. [7] Iyer-Pascuzzi A.S., Jackson T., Cui H., Petricka J.J., Busch W., Tsukagoshi H. & Benfey P.N. (2011) Cell identity regulators link development and stress responses in the Arabidopsis root. *Dev Cell*, **21**, 770-782.

Table S10. Analysis in public available databases (Genevestigator® V3) of the expression in roots of the 3 genes belonging to Fe assimilation that were specifically regulated by -S. Fold changes relative to the respective controls are shown, <-1.5 fold-change and <0.05 P-value are dark grey.

Reference	Deficiency	NRAMP3		NRAMP6		ZIP5	
		fold change	P-value	fold change	P-value	fold change	P-value
[1]	Fe (3h and 6h)	-0.15	0.606	-0.10	0.664	0.02	0.935
[1]	Fe (12h and 24h)	-0.24	0.012	-0.13	0.628	-1.00	0.128
[1]	Fe (48h and 72h)	1.16	0.004	-0.35	0.071	-2.97	0.000
[2]	Fe (1h)	0.19	0.363	-0.09	0.383	-0.37	0.540
[2]	Fe (6h)	-0.09	0.586	-0.03	0.758	-0.62	0.367
[2]	Fe (24h)	0.08	0.797	0.05	0.624	-1.24	0.299
[3]	Fe (5 days)	-0.12	0.172	-0.16	0.009	-0.56	0.020
[4]	Fe (7 days)	0.30	0.421	-0.19	0.248	-0.21	0.759
[5]	Fe (10 days)	0.65	0.040	0.14	0.241	-1.41	0.008
[6]	S (24h)	0.10	0.162	-0.07	0.444	-0.20	0.382
[7]	S (3h)	-0.46	0.122	-0.07	0.097	0.27	0.368
[7]	S (12h)	0.58	0.152	-0.02	0.754	0.06	0.730
[7]	S (24h)	1.30	0.074	0.15	0.171	-0.64	0.114
[7]	S (48h)	-0.03	0.914	0.01	0.752	0.00	0.973
[7]	S (72h)	0.01	0.916	0.08	0.606	0.02	0.929

References: [1] Dinneny J.R., Long T.A., Wang J.Y., Jung J.W., Mace D., Pointer S., Barron C., Brady S.M., Schiefelbein J. & Benfey P.N. (2008) Cell identity mediates the response of Arabidopsis roots to abiotic stress. *Science*, **320**, 942-945. [2] Buckhout T., Yang T. & Schmidt W. (2009) Early iron-deficiency-induced transcriptional changes in Arabidopsis roots as revealed by microarray analyses. *BMC Genomics*, **10**, 147. [3] Long T.A., Tsukagoshi H., Busch W., Lahner B., Salt D.E. & Benfey P.N. (2010) The bHLH transcription factor POPEYE regulates response to iron deficiency in Arabidopsis roots. *Plant Cell*, **22**, 2219-2236. [4] Schuler M., Keller A., Backes C., Philippar K., Lenhof H.P. & Bauer P. (2011) Transcriptome analysis by GeneTrail revealed regulation of functional categories in response to alterations of iron homeostasis in *Arabidopsis thaliana*. *BMC Plant Biol*, **11**, 87. [5] Sivitz A.B., Hermand V., Curie C. & Vert G. (2012) Arabidopsis bHLH100 and bHLH101 control iron homeostasis via a FIT-independent pathway. *PLoS One*, **7**, e44843. [6] Goda H., Sasaki E., Akiyama K., Maruyama-Nakashita A., Nakabayashi K., Li W., Ogawa M., Yamauchi Y., Preston J., Aoki K., Kiba T., Takatsuto S., Fujioka S., Asami T., Nakano T., Kato H., Mizuno T., Sakakibara H., Yamaguchi S., Nambara E., Kamiya Y., Takahashi H., Hirai M.Y., Sakurai T., Shinozaki K., Saito K., Yoshida S. & Shimada Y. (2008) The AtGenExpress hormone and chemical treatment data set: experimental design, data evaluation, model data analysis and data access. *Plant J*, **55**, 526-542. [7] Iyer-Pascuzzi A.S., Jackson T., Cui H., Petricka J.J., Busch W., Tsukagoshi H. & Benfey P.N. (2011) Cell identity regulators link development and stress responses in the Arabidopsis root. *Dev Cell*, **21**, 770-782.

Table S11. GSEA of down- or up-regulated genes specifically under Fe limitation. Enriched GO biological processes, P-value and false discovery rates (FDR in percent) are reported.

Biological Process	Fold Enrichment	P-value	FDR
<i>DOWN_GO biological process</i>			
Nucleotide-sugar biosynthetic process	8.5	1.8E-03	2.842
Purine salvage	7.6	0.012	18.202
Cell wall polysaccharide biosynthetic process	7.6	0.012	18.202
Lignin/aromatic compound catabolic process	7.2	5.5E-05	0.089
Glucosinolate catabolic process	5.9	8.1E-03	12.447
Regulation of DNA replication	5.5	0.011	16.208
Cellular amino acid derivative catabolic process	5.3	6.4E-05	0.105
Serine family amino acid biosynthetic process	5.1	8.7E-05	0.142
Hexose biosynthetic process	5.1	5.0E-03	7.826
Alcohol biosynthetic process	5.0	1.6E-05	0.026
Plant-type cell wall biogenesis	4.6	9.2E-07	1.5E-03
Glucosinolate metabolic process	4.5	1.7E-05	0.028
Sulfur amino acid biosynthetic process	4.3	1.4E-05	0.022
Transmembrane receptor protein tyrosine kinase signaling pathway	4.2	2.9E-13	4.7E-10
Trichoblast differentiation	4.2	1.9E-04	0.313
Branched chain family amino acid biosynthetic process	4.2	0.012	18.313
Protein polymerization	4.1	2.7E-03	4.337
<i>UP_GO biological process</i>			
L-phenylalanine catabolic process	10	4.4E-03	6.977
Cadmium ion transport	9.8	9.2E-04	1.493
Response to zinc ion	7.0	0.016	23.248
Cellular amino acid catabolic process	4.7	1.3E-05	0.021
Zinc ion transport	4.5	8.9E-03	13.524
Iron ion transport	4.4	4.0E-03	6.376
Organic acid catabolic process	4.0	1.6E-07	2.7E-04

Table S12. GSEA of down- or up-regulated genes specifically under S limitation. Enriched GO biological processes, P-value and false discovery rates (FDR in percent) are reported.

Biological Process	Fold Enrichment	P-value	FDR
<i>DOWN_GO biological process</i>			
Chromosome condensation	25	3.6E-04	0.560
Nicotianamine metabolic process	22	6.7E-03	10.125
DNA methylation on cytosine	19	0.010	14.577
Chromosome segregation	10	5.1E-05	0.081
Brassinosteroid metabolic process	10	6.8E-03	10.167
Mitosis	9.1	4.7E-06	7.4E-03
Iron ion homeostasis	8.8	0.010	14.295
DNA topological change	8.3	0.011	16.611
Cytokinesis	8.2	1.1E-05	0.017
Nuclear division	8.2	1.1E-05	0.017
Pyruvate metabolic process	7.9	0.013	19.080
DNA methylation	7.2	1.3E-03	1.984
Glutamine family amino acid metabolic process	7.2	1.0E-03	1.641
Negative regulation of gene expression, epigenetic	7.1	0.018	24.422
Meiosis	6.8	1.5E-04	0.236
Microtubule-based process	6.4	4.2E-06	6.6E-03
M phase	6.1	1.1E-06	1.8E-03
Organelle fission	5.6	6.9E-05	0.108
Cell cycle process	5.3	1.5E-08	2.4E-05
Cellular amino acid catabolic process	5.1	6.1E-03	9.221
Cell division	4.4	1.4E-07	2.2E-04
<i>UP_GO biological process</i>			
Immune response	22	2.6E-07	2.27E-05
Apoptosis	14	2.2E-04	0.059
Cellular response to extracellular stimulus	14	3.0E-05	0.059
Cellular response to nutrient levels	7.2	3.9E-05	6.717
Posttranscriptional gene silencing by RNA	5.4	4.4E-04	0.124
Cellular response to starvation	4.9	8.2E-05	0.045
Cellular response to sulfate starvation	4.3	1.5E-08	0.164

Table S13. GSEA of down- or up-regulated genes specifically under K limitation. Enriched GO biological processes, P-value and false discovery rates (FDR in percent) are reported.

Biological Process	Fold Enrichment	P-value	FDR
<i>DOWN_GO biological process</i>			
Sepal development	117	2.6E-04	0.332
Regulation of anthocyanin biosynthetic process	70	7.7E-04	0.983
Petal development	44	2.0E-03	2.560
Regulation of secondary metabolic process	24	6.6E-03	8.139
Gene silencing by miRNA	13	3.2E-03	4.015
Auxin mediated signaling pathway	12	1.3E-04	0.168
Response to gibberellin stimulus	7.8	0.014	16.323
Response to carbohydrate stimulus	7.0	1.5E-03	1.888
Shoot development	5.8	1.2E-03	1.487
Response to auxin stimulus	5.5	5.1E-04	0.656
Response to hormone stimulus	4.1	3.7E-06	0.005
<i>UP_GO biological process</i>			
Response to desiccation	21	8.3E-03	11.321
Cold acclimation	19	0.010	13.744
Protein-chromophore linkage	14	0.018	23.266
Photosynthesis	14	1.3E-15	0.000
Response to red light	11	9.0E-04	1.292
Polysaccharide catabolic process	6.9	0.019	24.637
Response to water deprivation	6.6	6.4E-05	0.092
Response to wounding	5.2	5.6E-03	7.748
Heterocycle biosynthetic process	4.9	0.019	24.169
Carbohydrate catabolic process	4.4	5.0E-03	6.917
Response to abscisic acid stimulus	4.1	1.6E-03	2.309

Table S14. List of primers used for qRT-PCR.

Oligonucleotide sequence (5'-3')	Description	Gene locus
GCCATCACAATCGCTCTCCAA	SULTR1;1_for	AT4G08620
TTGCCAATTCCACCCATGC	SULTR1;1_rev	
GGATCCAGAGATGGCTACATGA	SULTR1;2_for	AT1G78000
TCGATGTCCGTAACAGGTGAC	SULTR1;2_rev	
GATGAGGCACCAACTGTTCTTCGTG	TIP41-like_for	AT4G34270
CTGACTGATGGAGCTCGGGTCG	TIP41-like_rev	
GCCACATCTGCGTATCAAGTT	FRO2_for	AT1G01580
TCCCAAACAAGCTACGACCA	FRO2_rev	
GTGTTTAATCGCGCTCTTC	IRT1_for	AT4G19690
GTTAAGCCCATTTGGCGATA	IRT1_rev	
TGTAATCTCAAGGAAGCTAGGTG	NAS4_for	AT1G56430
CAGTTACACGCGAGATCCG	NAS4_rev	
CCTCCCAACACAACGTTCC	NAS2_for	AT5G56080
GGTCTAACCCTCCTTAGCG	NAS2_rev	
GTCCGATGCCTCTCACATCCATC	NAS1_for	AT5G04950
GAAGCGAGTGTGTTTGC GTGTG	NAS1_rev	
CCTTAGATGGGACATGCTTCG	FIT_for	AT2G28160
TCCACAGCTTCAGGTTAGGC	FIT_rev	
GCCTCTGGCCAATCGAAGAA	BHLH039_for	AT3G56980
ACCTGAAATTTGCACCAAGAGC	BHLH039_rev	
CTCCCACCAATCAAACGAAGTT	BHLH100_for	AT2G41240
CTTGCTCTTGACAGCTCTGGT	BHLH100_for	
AACAAGGCCGTTCTGTGAGAG	PYE_for	AT3G47640
GATTCAGTTCAAGAGTATCGGCT	PYE_rev	