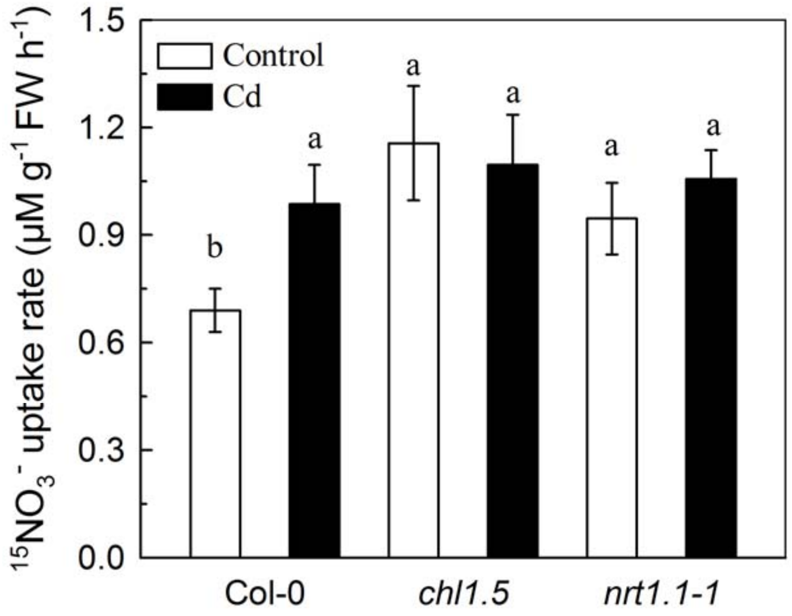
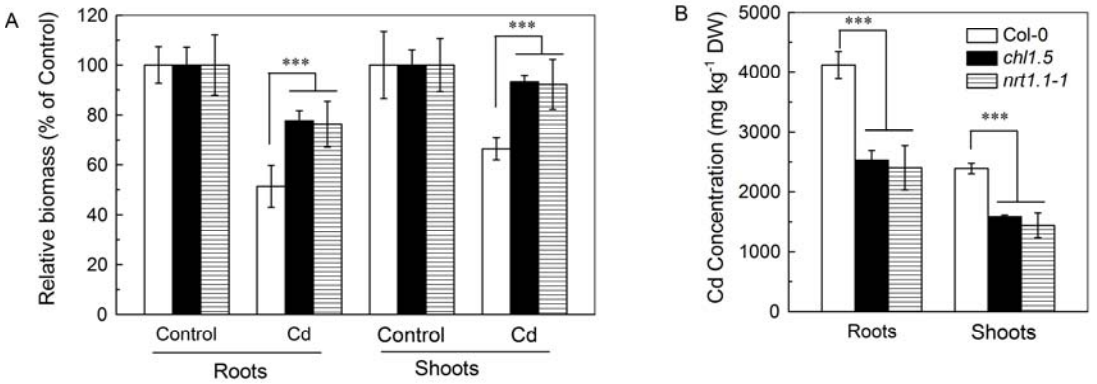
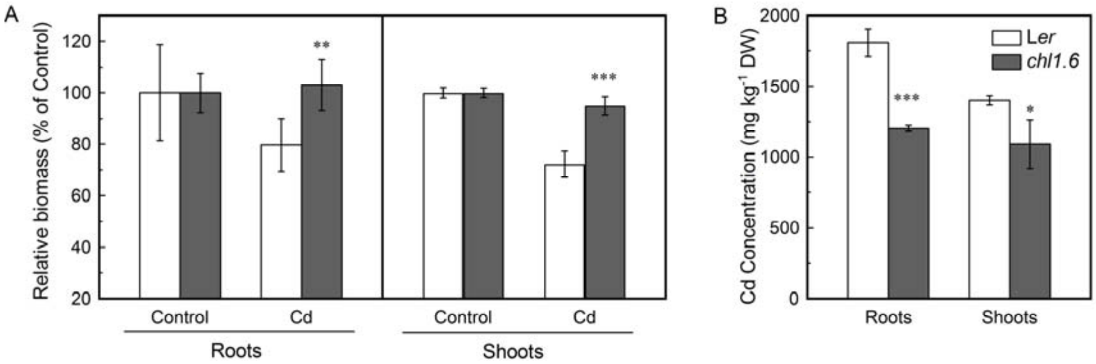


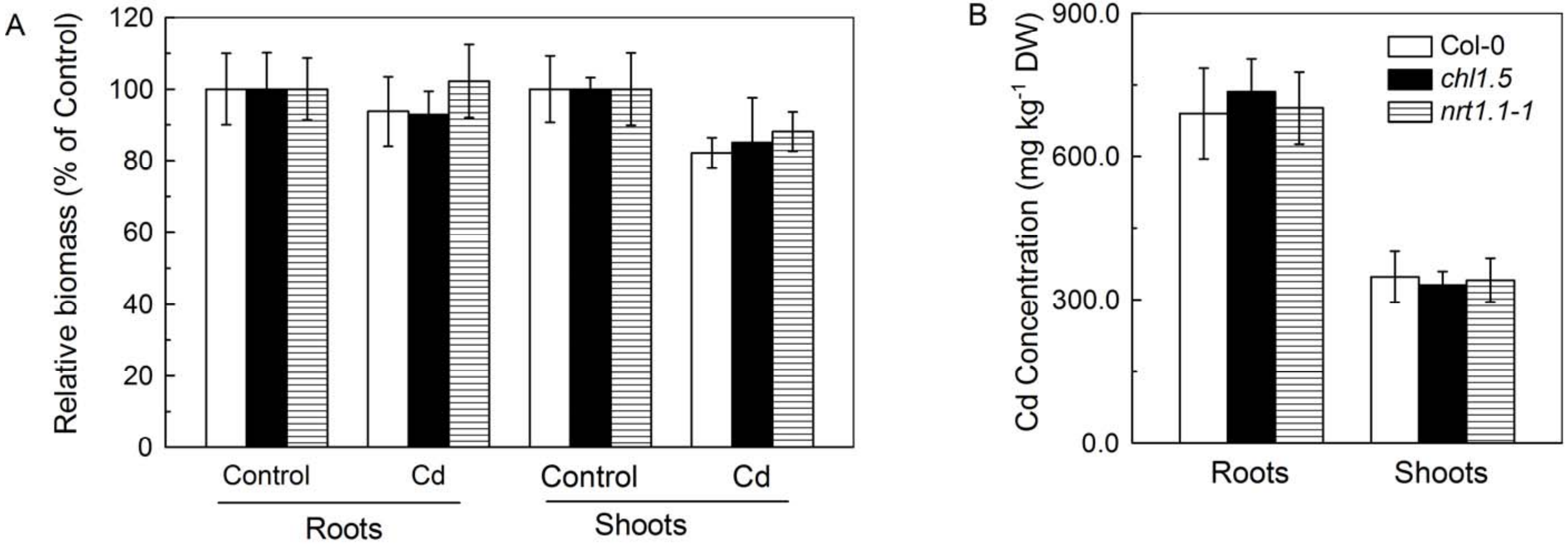
Supplemental Fig. S1. Effect of 10 μM Cd on high-affinity NO_3^- uptake by Col-0, *chl1.5*, or *nrt1.1-1* plants. The treatments were the same as those in Fig. 1. High-affinity NO_3^- uptake was measured using 200 μM $^{15}NO_3^-$ for 5 min. Bars represent the SD (*n* = 6 biological replicates). Different lowercase letters above bars indicate significant differences at $P < 0.05$ (least significant difference test).



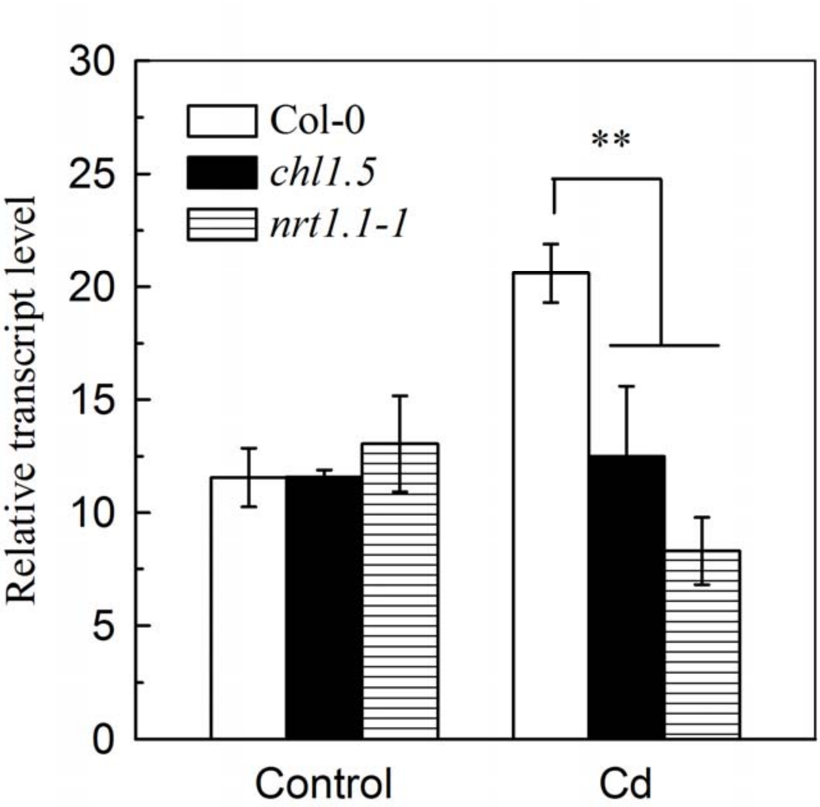
Supplemental Fig. S2. Effect of 20 μM Cd on growth of, and Cd levels in, Col-0, *chl1.5*, and *nrt1.1-1* plants. The plants were pre-cultured as described in Fig. 1 for 5 weeks, then were transferred to complete nutrient solution containing either 0 (Control) or 20 μM $CdCl_2$ (Cd) for 7 days, after which the analyses were performed. A, Relative biomass. B, Cd concentration. Bars represent the SD (*n* = 5–8 biological replicates). Asterisks indicate significant differences compared to the Col-0 plant (***$P < 0.001$; two-tailed Student's *t* test).



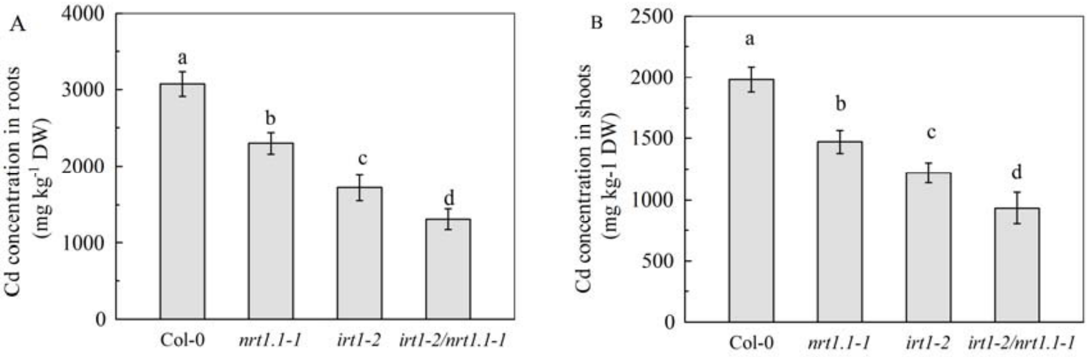
Supplemental Fig. S3. Effect of 10 μM Cd on growth of, and Cd levels in, L*er* and *chl1.6* plants. Treatments were the same as those in Fig. 1. A, Relative biomass calculated as the mean dry weight relative to the control treatment for the same plant line. B, Cd concentrations in Cd-treated plants. Bars represent the SD (*n* = 5–8 biological replicates). Asterisks indicate significant differences compared to L*er* plants (**P* < 0.05, ***P* < 0.01, ****P* < 0.001; two-tailed Student’s *t* test).



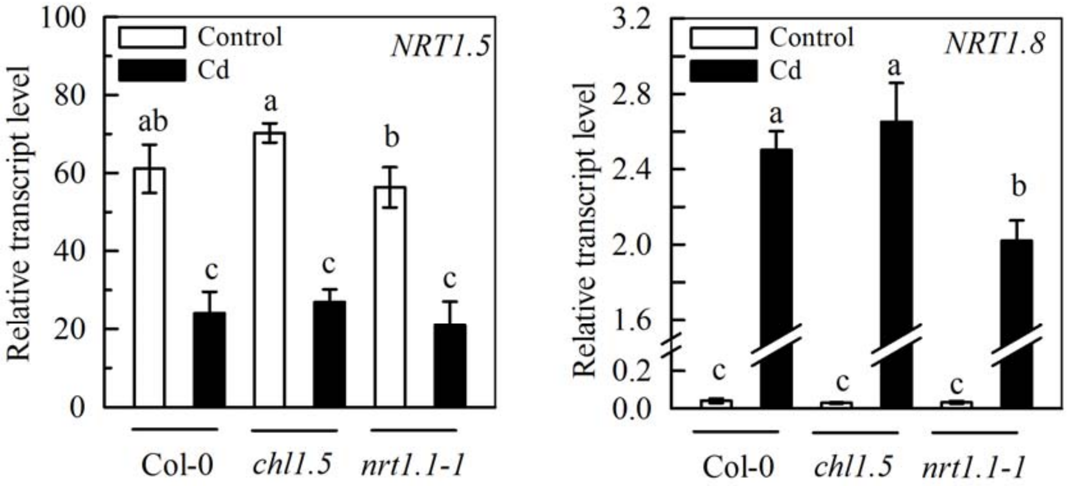
Supplemental Fig. S4. Effect of NO_3^- removal on growth of, and Cd uptake by, Col-0, *chl1.5*, and *nrt1.1-1* plants. The plants were pre-cultured as described in Fig. 1 for 5 weeks, then were grown in NO_3^-–free nutrient solution containing either 0 (Control) or 10 μM $CdCl_2$ (Cd) for 7 days. A, Relative biomass calculated as the mean dry weight relative to the control treatment for the same plant line. B, Cd concentrations. Bars represent the SD (*n* = 5-8 biological replicates).



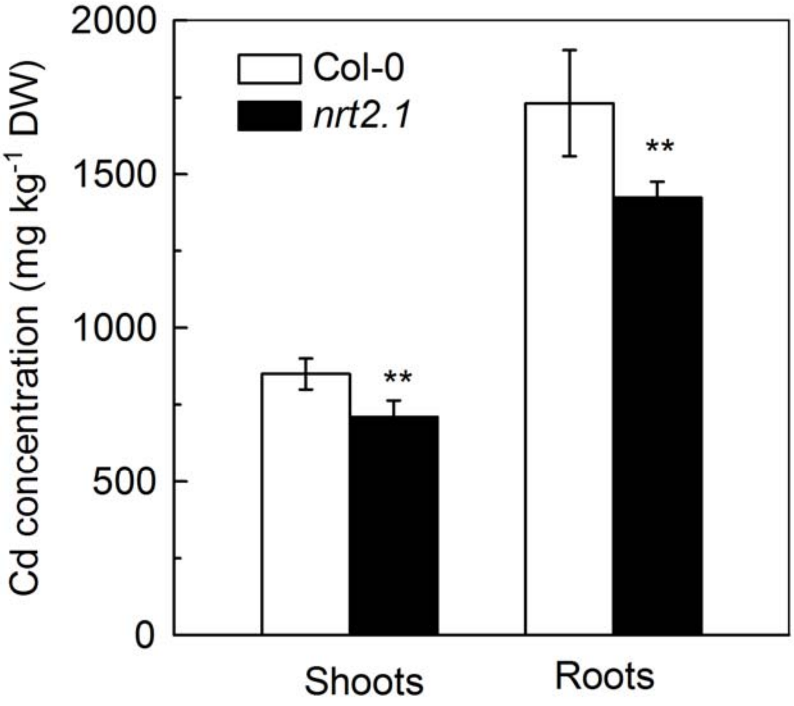
Supplemental Fig. S5. Effect of 10 μM Cd on *IRT1* expression in Col-0, *chl1.5*, and *nrt1.1-1* plants in growth medium containing 10 mM NO_3^-. The plants were pre-cultured as described in Fig. 1 for 5 weeks, then were grown in either Cd-free (Control) or 10 μM Cd-containing (Cd) nutrient solution containing 10 mM KNO_3 for 7 days. Transcript levels were normalized to *UBQ10* mRNA levles (100%). Bars represent the SD (*n* = 5 biological replicates). Asterisks indicate significant differences compared to Col-0 plants (***P* < 0.01; two-tailed Student's *t* test).



Supplemental Fig. S6. Cd levels in Col-0, *nrt1.1-1*, *irt1-2*, and *irt1-2/nrt1.1-1* plants after 7 days of exposure to Cd in 10 mM NO_3^- medium. The plants were pre-cultured as described in Fig. 1 for 5 weeks, then were grown in nutrient solution containing 10 μM Cd and 10 mM KNO_3 for 7 days. A, Cd concentrations in roots. B, Cd concentrations in shoots. Bars represent the SD (n = 5 biological replicates). Different lowercase letters above bars indicate significant differences at $P < 0.05$ (least significant difference test).



Supplemental Fig. S7. Effect of 10 μM Cd on expression of *NRT1.5* and *NRT1.8* in Col-0, *chl1.5*, and *nrt1.1-1* plants. Treatments were the same as those in Fig. 1. Gene expression was analyzed by real-time qPCR and transcript levels normalized to *UBQ10* mRNA levels (100%). Bars represent the SD (n = 5 biological replicates). Different lowercase letters above bars indicate significant differences at $P < 0.05$ (least significant difference test).



Supplemental Fig. S8. Cd levels in Col-0 plants and *nrt2.1* mutants grown for 7 days in 200 µM NO_3^- medium. The plants were pre-cultured as described in Fig. 1 for 5 weeks, then grown in nutrient solution containing 10 µM Cd and 0.2 mM KNO_3 for 7 days. Bars represent the SD (*n* = 5 biological replicates). Asterisks indicate significant differences compared to Col-0 plants (***P* < 0.01; two-tailed Student's *t* test).

Supplemental Table S1. Effect of Cd treatment on the expression in roots of genes related to uptake of metal cations. Gene expression was measured by Illumina mRNA-Seq analysis. A statistical cutoff of *$p<0.1$* after Bonferroni correction (see gray scale) was used to determine which genes were differentially expressed. A positive ratio indicates that gene expression was induced and a negative ratio that gene expression was repressed.

Gene_id	**Annotation**	**Control**				**Cd**			
		FPKM		**Ratio [log2 (chl1.5/Col-0)]**	***P value***	***FPKM***		**Ratio [log2 (chl1.5/Col-0)]**	***P value***
		Col-0	***chl1.5***			**Col-0**	***chl1.5***		
AT1G05300	Zinc transporter 5 precursor	12.40	24.48	0.98	4.66E-02	23.97	26.46	0.14	7.50E-01
AT1G10970	Zinc transporter 4 precursor	6.13	4.96	-0.31	6.25E-01	17.99	15.17	-0.25	5.97E-01
AT1G55910	Zinc transporter 11 precursor	6.90	8.35	0.28	6.57E-01	17.39	21.33	0.29	5.41E-01
AT1G60960	Iron regulated transporter 3	25.64	36.20	0.50	2.42E-01	57.78	69.28	0.26	5.34E-01
AT2G29410	Metal tolerance protein B1	1.47	1.04	-0.50	7.93E-01	1.14	1.72	0.59	7.41E-01
AT2G30080	ZIP metal ion transporter family	16.58	12.17	-0.45	4.19E-01	16.53	16.61	0.01	9.90E-01
AT2G32270	Zinc transporter 3 precursor	76.78	94.18	0.29	4.87E-01	112.75	129.72	0.20	6.44E-01
AT2G46800	Zinc transporter of Arabidopsis thaliana	71.33	71.28	0.00	9.98E-01	60.62	51.61	-0.23	6.53E-01
AT3G12750	Zinc transporter 1 precursor	11.50	6.66	-0.79	5.65E-01	35.59	29.98	-0.25	7.79E-01
AT3G58810	Metal tolerance protein A2	25.41	18.92	-0.43	3.35E-01	42.87	53.55	0.32	4.63E-01
AT5G59520	ZRT/IRT-like protein 2	18.51	11.83	-0.65	2.02E-01	69.82	66.76	-0.06	8.77E-01
AT4G19690	Iron-regulated transporter 1	146.59	79.77	-0.88	6.77E-02	229.67	180.38	-0.35	5.09E-01
AT4G19680	Iron regulated transporter 2	0.87	1.22	0.49	7.23E-01	4.65	4.96	0.09	9.08E-01
AT1G15960	NRAMP metal ion transporter 6	18.94	16.99	-0.16	8.58E-01	32.09	33.38	0.06	9.49E-01
AT1G47240	NRAMP metal ion transporter 2	14.15	16.55	0.23	6.64E-01	14.98	14.23	-0.07	8.86E-01
AT1G80830	NRAMP metal ion transporter 1	316.07	255.78	-0.31	5.77E-01	283.74	227.85	-0.32	5.53E-01
AT2G23150	NRAMP metal ion transporter 3	14.77	22.90	0.63	1.55E-01	14.55	13.07	-0.15	7.41E-01
AT5G03280	NRAMP metal ion transporter family protein	30.26	28.57	-0.08	8.49E-01	20.78	20.75	0.00	9.97E-01
AT5G67330	NRAMP metal ion transporter 4	21.34	20.07	-0.09	8.35E-01	45.53	43.33	-0.07	8.64E-01
AT1G16010	Magnesium transporter 2	28.49	28.66	0.01	9.86E-01	28.94	30.93	0.10	8.56E-01
AT1G29820	Magnesium transporter CorA-like family protein	18.14	18.65	0.04	9.27E-01	16.13	15.57	-0.05	9.09E-01
AT1G29830	Magnesium transporter CorA-like family protein	3.48	2.53	-0.46	4.88E-01	3.94	2.90	-0.44	5.88E-01
AT1G61790	Magnesium transporter family protein	135.13	129.51	-0.06	8.86E-01	151.67	148.29	-0.03	9.40E-01
AT1G80900	Magnesium transporter 1	5.99	10.15	0.76	2.45E-01	8.01	8.81	0.14	8.37E-01
AT2G03620	Magnesium transporter 3	11.45	13.34	0.22	6.56E-01	12.81	14.96	0.22	6.41E-01
AT2G04305	Magnesium transporter CorA-like family protein	23.42	24.36	0.06	8.93E-01	20.90	23.15	0.15	7.30E-01
AT2G19340	Magnesium transporter family protein	19.93	15.03	-0.41	5.10E-01	17.64	18.53	0.07	9.09E-01
AT2G42950	Magnesium transporter CorA-like family protein	5.03	7.03	0.48	4.07E-01	7.22	7.41	0.04	9.46E-01
AT3G19640	Magnesium transporter 4	38.95	35.11	-0.15	7.20E-01	40.13	39.21	-0.03	9.36E-01
AT3G58970	Magnesium transporter 6	21.81	22.17	0.02	9.55E-01	20.65	21.22	0.04	9.28E-01

AT4G29870	Magnesium transporter family protein	84.56	82.14	-0.04	9.21E-01	78.70	80.59	0.03	9.36E-01
AT5G09690	Magnesium transporter 7	17.64	16.68	-0.08	8.86E-01	16.38	17.14	0.07	9.07E-01
AT5G09710	Magnesium transporter CorA-like family protein	1.89	1.45	-0.38	7.02E-01	3.07	2.39	-0.36	6.82E-01
AT5G09720	Magnesium transporter CorA-like family protein	5.16	3.30	-0.64	3.89E-01	11.27	9.35	-0.27	6.44E-01
AT5G22830	Magnesium transporter 10	8.28	7.31	-0.18	8.00E-01	4.44	4.67	0.07	9.34E-01
AT5G64560	Magnesium transporter 9	6.11	7.60	0.31	5.91E-01	8.91	11.37	0.35	5.02E-01
AT2G17780	PLAC8 family protein	0.11	0.37	1.68	2.83E-01	1.35	0.54	-1.31	2.02E-01
AT4G35920	PLAC8 family protein	50.28	47.48	-0.08	8.64E-01	30.43	33.50	0.14	7.69E-01
AT2G22950	Cation transporter/ E1-E2 ATPase family protein	0.94	1.29	0.46	5.65E-01	0.60	0.49	-0.31	7.48E-01
AT4G37640	Calcium ATPase 2	31.28	37.40	0.26	5.47E-01	36.51	35.80	-0.03	9.48E-01
AT5G01490	Cation exchanger 4	19.72	25.88	0.39	3.76E-01	20.51	24.58	0.26	5.55E-01
AT5G17860	Calcium exchanger 7	0.19	1.86	3.29	3.91E-03	0.05	0.15	1.53	4.00E-01
AT1G08960	Cation exchanger 11	4.85	4.49	-0.11	8.53E-01	6.44	6.31	-0.03	9.58E-01
AT1G54115	Cation calcium exchanger 4	19.86	18.25	-0.12	7.76E-01	21.21	21.33	0.01	9.84E-01
AT1G55730	Cation exchanger 5	25.81	29.48	0.19	6.56E-01	27.93	28.86	0.05	9.10E-01
AT2G38170	Cation exchanger 1	15.35	26.89	0.81	7.61E-02	25.93	27.00	0.06	8.96E-01
AT3G13320	Cation exchanger 2	30.03	35.87	0.26	5.39E-01	36.57	32.68	-0.16	6.98E-01
AT3G14070	Cation exchanger 9	4.60	7.26	0.66	2.55E-01	5.12	6.70	0.39	4.99E-01
AT3G51860	Cation exchanger 3	4.59	2.78	-0.73	2.81E-01	21.95	17.47	-0.33	4.50E-01
AT5G01490	Cation exchanger 4	19.72	25.88	0.39	3.76E-01	20.51	24.58	0.26	5.55E-01
AT5G17860	Calcium exchanger 7	12.28	15.99	0.38	4.22E-01	0.05	0.15	1.53	4.00E-01
AT1G04690	Potassium channel beta subunit 1	78.41	67.55	-0.22	6.10E-01	97.78	81.38	-0.26	5.36E-01
AT1G31120	K$^+$ uptake permease 10	18.21	22.00	0.27	5.15E-01	13.39	13.09	-0.03	9.39E-01
AT1G60160	Potassium transporter family protein	4.52	2.81	-0.69	2.50E-01	1.54	0.79	-0.97	2.41E-01
AT1G70300	K$^+$ uptake permease 6	34.91	46.40	0.41	3.37E-01	38.63	47.47	0.30	4.89E-01
AT2G26650	K$^+$ transporter 1	84.77	56.62	-0.58	2.43E-01	63.94	53.64	-0.25	5.90E-01
AT2G30070	Potassium transporter 1	6.17	4.96	-0.31	5.64E-01	4.28	4.72	0.14	8.07E-01
AT2G35060	K$^+$ uptake permease 11	9.55	9.92	0.05	9.05E-01	8.83	8.32	-0.09	8.56E-01
AT2G40540	Potassium transporter 2	13.99	11.52	-0.28	5.66E-01	27.87	20.31	-0.46	3.04E-01
AT3G02050	K$^+$ uptake transporter 3	5.40	4.55	-0.25	6.43E-01	4.64	4.06	-0.19	7.30E-01
AT3G02850	STELAR K$^+$ outward rectifier	56.70	24.75	-1.20	9.62E-03	8.80	11.76	0.42	4.70E-01
AT3G09030	BTB/POZ domain-containing protein	14.02	11.74	-0.26	5.93E-01	14.33	13.09	-0.13	7.83E-01
AT4G00630	K$^+$ efflux antiporter 2	20.11	20.86	0.05	9.14E-01	16.71	13.15	-0.35	5.07E-01
AT4G01840	Ca^{2+}-activated outward rectifying K+ channel 5	7.00	16.02	1.20	2.34E-02	13.44	16.84	0.33	4.91E-01
AT4G04850	K$^+$ efflux antiporter 3	1.75	1.56	-0.17	8.16E-01	1.44	1.14	-0.34	6.59E-01
AT4G10310	High-affinity K+ transporter 1	40.27	14.83	-1.44	1.05E-04	35.40	33.56	-0.08	8.54E-01
AT4G13420	High affinity K+ transporter 5	9.88	40.92	2.05	3.38E-06	51.09	97.20	0.93	4.10E-02
AT4G18160	Ca^{2+}-activated outward rectifying K+ channel 6	8.89	7.57	-0.23	6.82E-01	5.57	5.68	0.03	9.62E-01
AT4G19960	K$^+$ uptake permease 9	6.98	6.58	-0.08	8.65E-01	7.41	5.69	-0.38	4.48E-01
AT4G23640	Potassium transporter family protein	25.98	26.67	0.04	9.29E-01	24.45	26.96	0.14	7.36E-01
AT4G23700	Cation/H$^+$ exchanger 17	4.28	6.47	0.59	2.64E-01	5.96	7.29	0.29	5.60E-01
AT4G32650	Potassium channel in Arabidopsis thaliana 3	52.27	51.41	-0.02	9.58E-01	55.60	49.27	-0.17	6.90E-01
AT4G33530	K$^+$ uptake permease 5	18.18	21.76	0.26	5.35E-01	14.66	12.34	-0.25	5.60E-01
AT5G09400	K$^+$ uptake permease 7	18.73	19.36	0.05	9.09E-01	19.36	19.75	0.03	9.46E-01
AT5G14880	Potassium transporter family protein	66.20	51.53	-0.36	4.05E-01	35.14	43.57	0.31	4.61E-01

AT5G37500	Gated outwardly-rectifying K^+ channel	3.84	5.99	0.64	2.34E-01	4.60	5.23	0.19	7.29E-01
AT5G46370	Ca^{2+}-activated outward rectifying K^+ channel 2	4.48	9.29	1.05	8.91E-02	2.11	3.28	0.63	4.21E-01
AT5G55630	Outward rectifying potassium channel protein	21.19	18.48	-0.20	6.80E-01	27.24	32.56	0.26	5.47E-01
AT4G33530	K^+ uptake permease 5	18.18	21.76	0.26	5.35E-01	14.66	12.34	-0.25	5.60E-01
AT5G09400	K^+ uptake permease 7	18.73	19.36	0.05	9.09E-01	19.36	19.75	0.03	9.46E-01
AT5G14880	Potassium transporter family protein	66.20	51.53	-0.36	4.05E-01	35.14	43.57	0.31	4.61E-01
AT2G37925	Copper transporter 4	9.18	4.11	-1.16	2.17E-01	1.01	3.72	1.89	1.45E-01
AT3G46900	Copper transporter 2	12.66	2.16	-2.55	4.77E-03	153.14	137.69	-0.15	7.13E-01
AT5G20650	Copper transporter 5	231.41	210.72	-0.14	7.61E-01	241.01	276.87	0.20	6.57E-01
AT5G59030	Copper transporter 1	4.29	4.07	-0.07	9.31E-01	5.41	3.69	-0.55	5.06E-01

	1.00E-04	1.00E-03	5.00E-02	1.00E-01	1
P value	░	▒	▓	▓	█

Supplemental Table S2. Primers used in this work.

Gene	Primer	Sequence (5'-3')	Method
AT4G05320	*UBQ10* F	ACCCTAACGGGAAAGACGA	Real-time qPCR
	UBQ10 R	GGAGCCTGAGAACAAGATGAA	
AT1G12110	*NRT1.1* F	TTCTCGTGACAATCGTCG	Real-time qPCR
	NRT1.1 R	TGGAATACTCGGCTCATCAT	
AT1G69850	*NRT1.2* F	GGATTCGGTGTTTCTACCAT	Real-time qPCR
	NRT1.2 R	CGCAATGATTTGAGGGAC	
AT1G08090	*NRT2.1* F	AACAAGGGCTAACGTGGATG	Real-time qPCR
	NRT2.1 R	CTGCTTCTCCTGCTCATTCC	
AT1G08100	NRT2.2 F	CAGGTGGAAACAGAGCTGCCATGG	Real-time qPCR
	NRT2.2 R	GACCATAGATACAACGGCAGTGACGAG	
AT5G50200	*NRT3.1* F	GGCCATGAAGTTGCCTATG	Real-time qPCR
	NRT3.1 R	TCTTGGCCTTCCTCTTCTCA	
AT5G60770	*NRT2.4* F	CCGTCTTCT CCA TGTCTTTC	Real-time qPCR
	NRT2.4 R	CTGACCATTGAACATTGTG	
AT1G32450	*NRT1.5* F	TGTCATTGGACTTTCATCGC	Real-time qPCR
	NRT1.5 R	CCCACAACCTCTTGGTCTAATC	
AT4G21680	*NRT1.8* F	GGCTTCAGATTCTTGGATAG	Real-time qPCR
	NRT1.8 R	AACCACAGAGTAGAGGATGG	
AT4G19690	*IRT1* F	AAGCTTTGATCACGGTTGG	Real-time qPCR
	IRT1 R	TTAGGTCCCATGAACTCCG	
AT4G19690	Salk_054554 LP	CAAGTAAAACCAGCGCTTTTG	Genotyping
	Salk_054554 RP	GCTCTTTGCTTCCATCAAATG	
AT1G12110	Salk_097431 LP	ATATTGGAATCCCTTTCTCGG	Genotyping
	Salk_097431 RP	ATATTGGAATCCCTTTCTCGG	
AT1G08090	CS859604 LP	GCAAGCGACTATCATCACTCC	Genotyping
	CS859604 RP	GTTCTCCATGAGCTTCGTGAG	
pBIN-pROK2 T-DNA	Lab1.3	ATTTTGCCGATTTCGGAAC	Genotyping