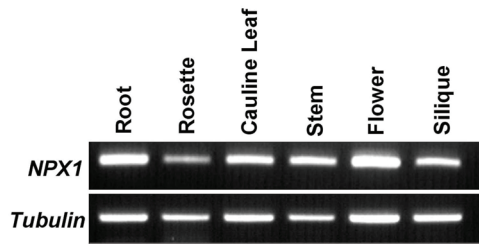
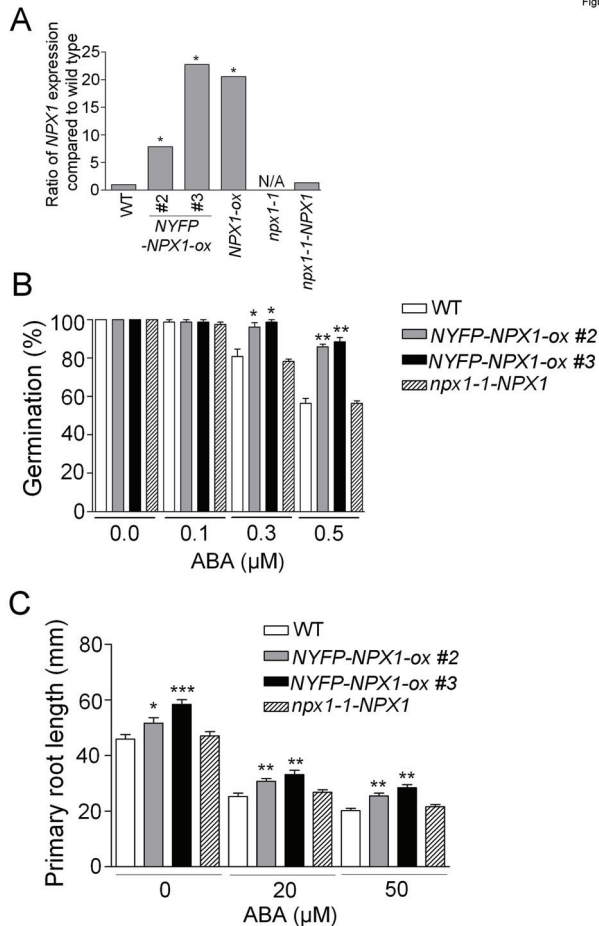


Figure S1



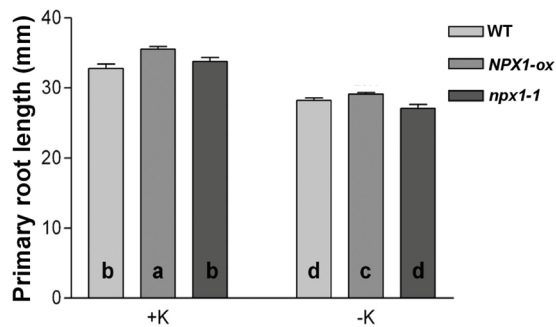
Supplemental Figure S1. RT-PCR analysis of *NPX1* expression in *Arabidopsis* plants. Tissues analyzed were roots, rosette leaf, cauline leaf, stem, flower and developing siliques of 3-week-old *Arabidopsis* plants grown at 22°C with a 16 h daylength. RT-PCR analysis of *NPX1* expression was performed with *NPX1* β -tubulin gene (At5g62690) specific primers. Amplification was performed as follows: 30 s at 94°C, 30 s at 55°C, and 45 s at 72°C for 30 cycles, followed by a 10 min extension at 72°C.

Figure S2



Supplemental Figure S2. Analysis of additional NPX overexpression and knockout lines. A, Quantitative Real-time PCR analysis of *NPX1* expression in wild-type, two NYFP-*NPX1-ox*, *NPX1-ox*, *npx1-1* and *npx1-1-NPX1*. B, The effect of ABA on germination rates of wild-type, two NYFP-*NPX1-ox* and *npx1-1-NPX1* 5 d after germination. Data represent the mean \pm standard deviation of 52 seeds per genotype. C, Comparison of root elongation of wild-type, two NYFP-*NPX1-ox* and *npx1-1-NPX1* seedlings; 6-d-old seedlings were transferred to plates supplemented with ABA, and root elongation was measured after 6 d. Each data point represents the mean \pm standard deviation ($n = 40$). Asterisks indicate a significant difference between wild-type and NYFP-*NPX1-ox* or *npx1-1-NPX1* plants (*: $P < 0.05$; **: $P < 0.01$; ***: $P < 0.001$). These data provide additional genetic evidence for the involvement of NPX1 in ABA sensitivity.

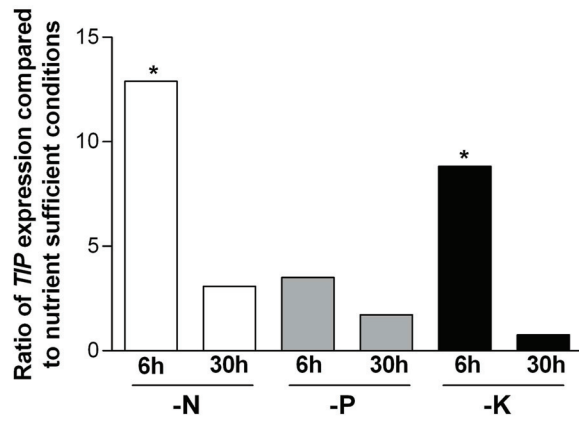
Figure S3



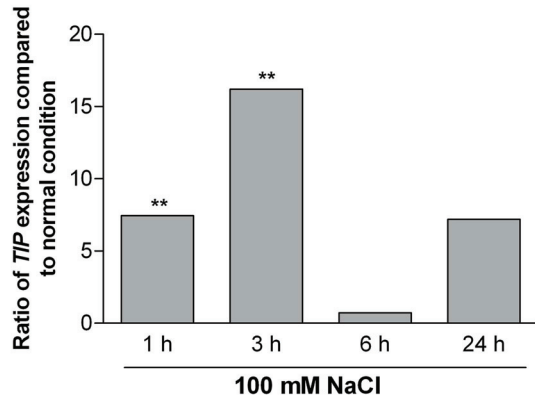
Supplemental Figure S3. Overexpression of *NPX1* enhances primary root growth.

+K indicates full nutrients and -K indicates full nutrients with limiting 10 μM K^+ . Bars represent standard errors. Different letters indicates a significant difference between means at $P < 0.05$ (TUKEY HSD) ($n \geq 70$ plants).

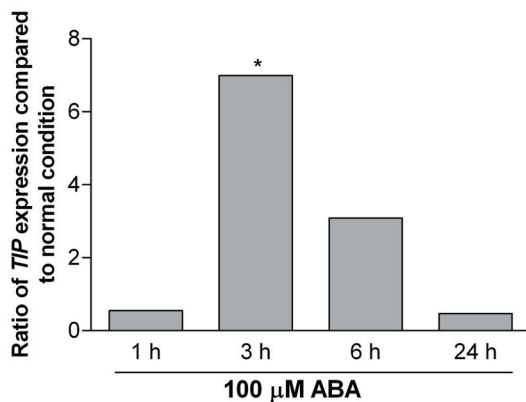
A



B

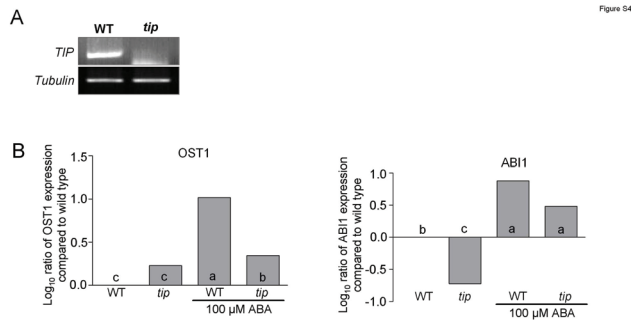


C



Supplemental Figure S4. The expression of *TIP* was up-regulated by nutrient deprivation and abiotic stresses. A-C, Quantitative real-time PCR analysis of *TIP* under nutrient deprived, NaCl and ABA treatment expressed in relation to control conditions. A, *Arabidopsis* Col-0 roots: grown under full nutrient conditions; K⁺ deficiency (-K); N

deficiency (-N) and P deficiency (-P). B and C, Expression of *TIP* after treatment with 100 mM NaCl (B), or 100 μ M ABA for 1, 3, 6 and 24 h (C). Data are the mean of three biological replicates. Asterisks indicate a significant change (*: $P < 0.05$; **: $P < 0.01$; Student's t-test).



Supplemental Figure S5. Disruption of *TIP* alters the expression of ABA-signaling genes. A, RT-PCR analysis of *TIP* expression in wild-type and *tip* plants after 100 μ M ABA treatment. B, Quantitative real-time PCR analysis of *OST1* and *ABI1* expression in wild-type and *tip* before and after 100 μ M ABA treatment. Different letters indicate a significant difference between means at $P < 0.05$ (Student's t-test).

Table S1. Proteins that interact with NPX1 as determined by yeast two hybrid screening

# of clone	Locus	Description	β -galactosidase activity ^b	Gene expression after ABA treatment ^c	Cellular localization ^d
1	At5g42530	unknown protein	56.6 \pm 11.2	N/A	endomembrane
2	At5g39320	UDP-glucose 6-dehydrogenase, putative	70.0 \pm 9.2	no change	cytosol/nucleus
3	At4g30220	RUXF (Small nuclear ribonucleoprotein F)	61.9 \pm 7.7	no change	nucleus
4	At5g44130	FLA13 (Fasciclin-like arabinogalactan protein 13 precursor)	55.8 \pm 9.6	down	cell wall
7	At5g08520	MYB family transcription factor	68.2 \pm 8.5	no change	nucleus
8	At1g01620	PIP1;3 (Plasma membrane intrinsic protein 1;3)	83.1 \pm 19.4	up	plasma membrane
9	At1g17745 (2)^a	3-Phosphoglycerate dehydrogenase	69.1 \pm 20.0	up	chloroplast/ cytosol/nucleus
19	At3g06390 (2)	integral membrane family protein	149.6 \pm 35.6	up	N/A
24	At2g32487	unknown protein	153.6 \pm 19.1	N/A	endomembrane
26	At1g60989	SCR (S locus cysteine-rich protein) similar	150.6 \pm 7.1	no change	endomembrane
27	At5g27450	Mevalonate kinase	127.2 \pm 12.2	down	cytosol
28	At4g11280	a member of the 1-aminocyclopropane-1-carboxylate (ACC) synthase	94.7 \pm 15.2	up	N/A
29	At4g12420	SKU5	123.2 \pm 10.5	down	cell wall/plasma membrane
32	At4g13940 (2)	SAHH1(S-adenosyl-L-homocysteine hydrolase)	92.6 \pm 21.7	down	membrane/ vacuole
39	At1g60950	Ferredoxin 2	120.3 \pm 25.4	down	chloroplast
40	At5g24590	TIP (TCV-interacting protein)	54.3 \pm 9.7	up	nucleus
41	At4g39260	GRP8 (Glycine rich protein 8)	77.0 \pm 25.0	down	peroxisome

^a Selected repeatedly in the yeast two-hybrid screen

^b The liquid culture assay using o-nitrophenyl- β -D-galactopyranoside as substrate

^c Determined by the AtGenExpress Database (Arabidopsis eFP Browser)

^d Determined by the TAIR Database

N/A-not available

Supplemental Table S1. Proteins that interact with NPX1 as determined by yeast two hybrid screening.

Table S2. Gene information used for real-time PCR analysis

Gene name	Locus	Description
AREB1	At1g45249	ABSCISIC ACID RESPONSIVE ELEMENTS-BINDING FACTOR 2; Leucine zipper transcription factor that binds to the abscisic acid (ABA)-responsive element (ABRE) motif in the promoter region of ABA-inducible genes
MYC2	At1g32640	Encodes a MYC-related transcriptional activator with a typical DNA binding domain of a basic helix-loop-helix leucine zipper motif
MYB2	At2g47190	Encodes a MYB transcription factor that possesses an R2R3 MYB DNA binding domain and is known to regulate the expression of salt- and dehydration-responsive genes
RD29A	At5g52310	RESPONSIVE TO DESSICATION 29A; Cold regulated gene, the 5' region of cor78 has cis-acting regulatory elements that can impart cold-regulated gene expression
ABI1	At4g26080	ABA INSENSITIVE 1; Involved in abscisic acid (ABA) signal transduction
ABI2	At5g57050	ABA INSENSITIVE 2; Encodes a protein phosphatase 2C and is involved in ABA signal transduction
AtrbohD	At5g47910	ARABIDOPSIS THALIANA RESPIRATORY BURST OXIDASE HOMOLOGUE D;NADPH/respiratory burst oxidase protein D
AtrbohF	At1g64060	ARABIDOPSIS THALIANA RESPIRATORY BURST OXIDASE HOMOLOG F; Interacts with AtrbohD gene to fine tune the spatial control of ROI production and hypersensitive response to cell in and around infection site
OST1	At4g33950	OPEN STOMATA 1; Encodes calcium-independent ABA-activated protein kinase
NCED3	At3g14440	NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 3; Encodes 9-cis-epoxycarotenoid dioxygenase, a key enzyme in the biosynthesis of abscisic acid
ABA2	At1g52340	ARABIDOPSIS THALIANA ABA DEFICIENT 2; Encodes a cytosolic short-chain dehydrogenase/reductase involved in the conversion of xanthoxin to ABA-aldehyde during ABA biosynthesis

Supplemental Table S2. Information on Genes used for real-time PCR analysis.