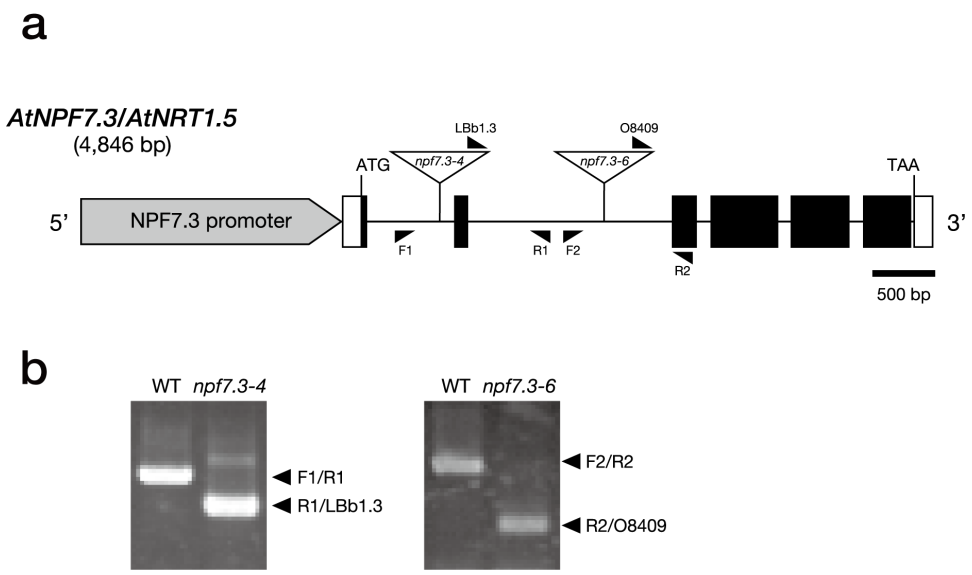
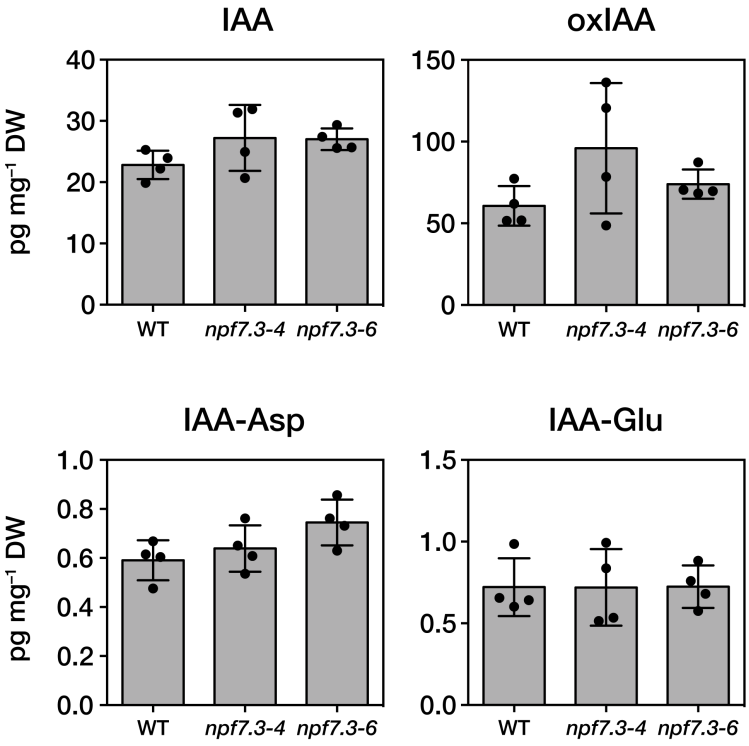
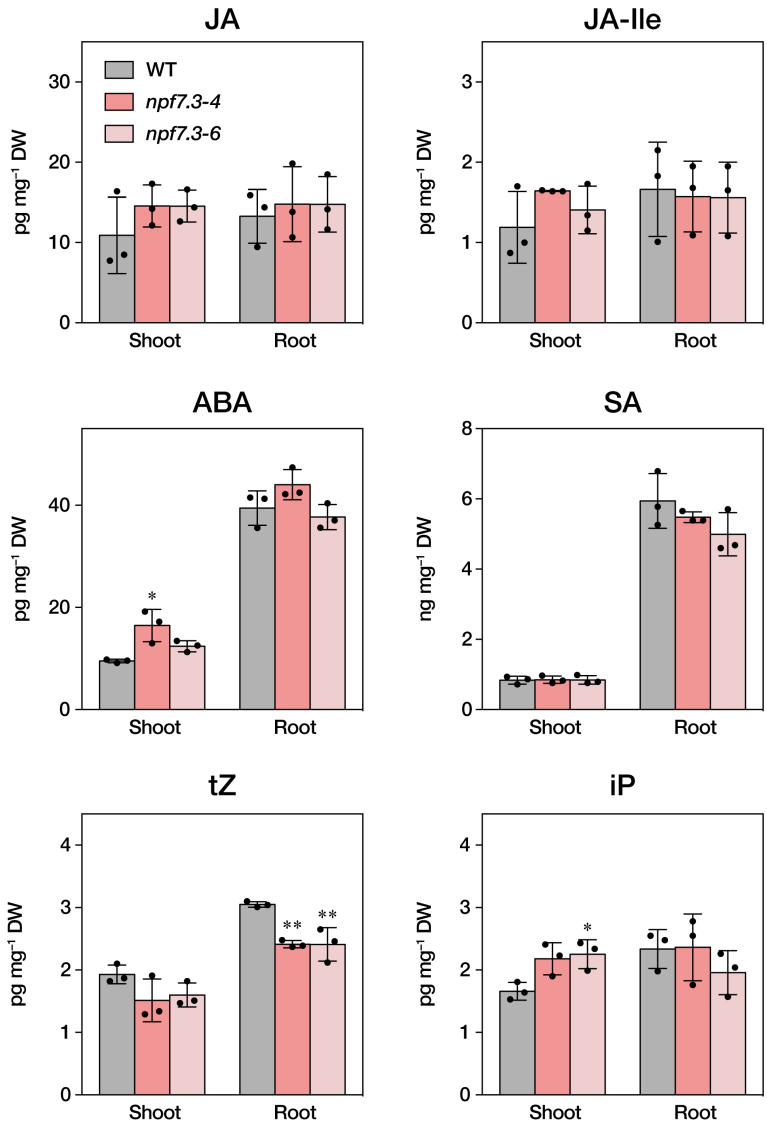


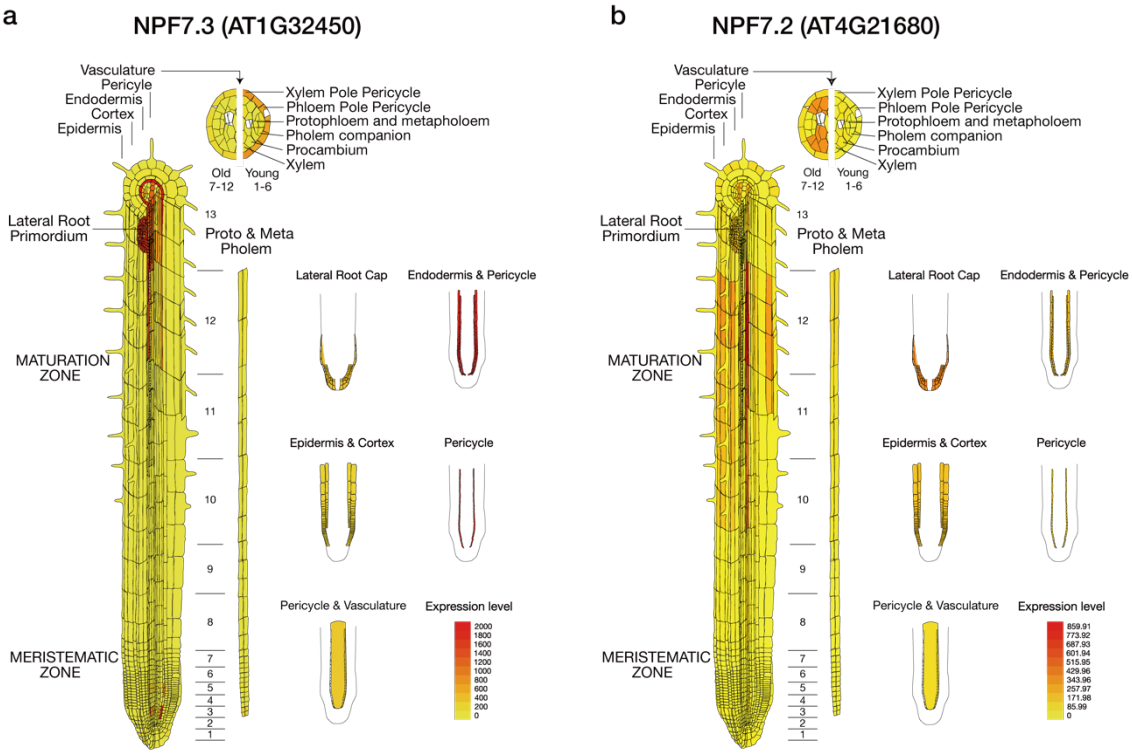
Supplementary Fig. 1. T-DNA insertion mutants of *NPF7.3/NRT1.5* used in this study. a. Structure of the *NPF7.3/NRT1.5* gene and positions of T-DNA insertions in two *npf7.3* alleles. Arrowheads indicate the positions of primers used for PCR-based genotyping of *npf7.3-4* (SALK_063393) and *npf7.3-6* (GK-877E12). **b**. Confirmation of homozygous T-DNA insertions by PCR.



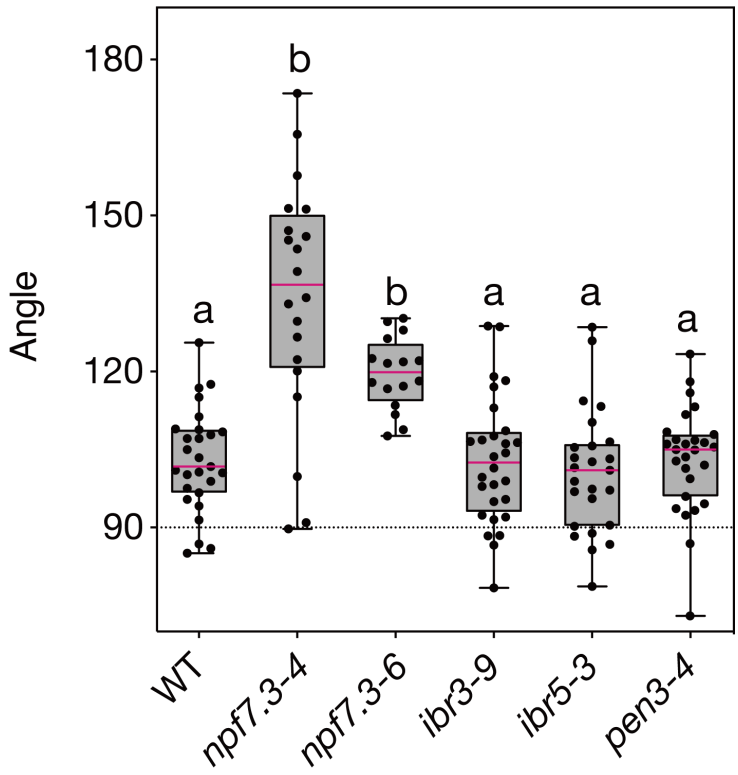
Supplementary Fig. 2. Endogenous levels of IAA derivatives in *npf7.3*. IAA, 2-oxoindole-3-acetic acid (oxIAA), IAA-aspartate (IAA-Asp) and IAA-glutamate (IAA-Glu) were quantified from the roots of 14-day-old wild type (WT) and *npf7.3* (*npf7.3-4* and *npf7.3-6*) seedlings. Bars indicate the standard deviations of the means. Dots represent individual measurements. Asterisks indicate significant differences compared with wild-type (*$P < 0.05$ by Tukey's multiple comparison test).



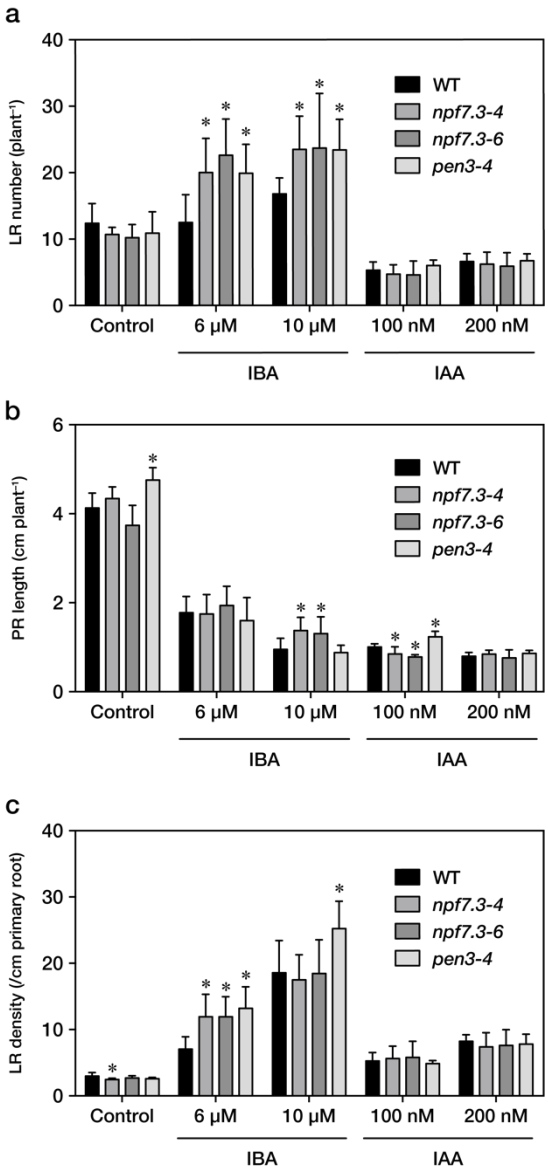
Supplementary Fig. 3. Endogenous plant hormone levels in *npf7.3*. Endogenous levels of jasmonic acid (JA), JA-Ile, ABA, salicylic acid (SA), *trans*-zeatin (tZ) and isopentenyl adenine (iP) were measured in shoot and root tissues excised from 14-day-old wild-type and *npf7.3* (*npf7.3-4* and *npf7.3-6*). Bars indicate standard deviations of the means. N.D, not detected. Asterisks indicate significant differences as compared with wild type within each treatment group (*$P < 0.05$; **$P < 0.01$ by Tukey's multiple comparison test).



Supplementary Fig. 4. Expression pattern of *NPF7.3* Spatial expression patterns of *NPF7.3* (**a**) and *NPF7.2* (**b**) obtained from the Arabidopsis eFP Browser (http://bar.utoronto.ca/efp/cgi-bin/efpWeb.cgi)[1-3] are shown.



Supplementary Fig. 5. Root gravitropism of IBA-related mutants. Gravitropic responses of mutants defective in IBA-to-IAA conversion (*ibr3-9*), responses to auxin (*ibr5-3*) and IBA export (*pen3-4*) were analyzed. Vertical plates containing seven-day-old seedlings were rotated 90º, and root angles were measured one day after plate rotation. Dots represent individual measurements, and whiskers represent the entire spread of the data. Different letters indicate statistically significant differences by Dunn's multiple comparison test ($P < 0.05$).



Supplementary Fig. 6. Effects of IBA and IAA on lateral root formation and primary root elongation in *npf7.3*. a-c. lateral root (LR) numbers (**a**), primary root (PR) lengths (**b**) and LR densities (**c**) of wild type (WT), *npf7.3* (*npf7.3-4* and *npf7.3-6*) and *pen3-4* treated with IBA or IAA. Two days after germination on half-strength MS media, seedlings were transferred to media containing IBA or IAA at the indicated concentrations. After further incubation for five days, LR numbers and PR lengths were measured. LR densities were calculated as the LR numbers divided by the PR lengths. Asterisks indicate significant differences.

Supplementary Table 1. Primers used in this study.

Target*	Use for	Forward primer		Reverse primer	
		Name	Sequence (5'-3')	Name	Sequence (5'-3')
***npf7.3* mutant isolation**					
NPF7.3/NRT1.5	PCR genotyping	NPF7.3g- F1	CACGTTCACGTAAAATTCGAAG	NPF7.3g- R1	AGCATGATCAAAAGGACATGC
NPF7.3/NRT1.5		NPF7.3g- F2	AAAACGCGAGTTAGGAAGAGC	NPF7.3g- R2	TAGAAAAACCCCAACCACATG
T-DNA		LBb1.3	ATTTTGCCGATTTCGGAAC		
T-DNA		O8409	ATATTGACCATCATACTCATTGC		
Complementation test					
NPF7.3 promoter	Construction of pENTR-NPF7.3pro	NPF7.3pro-topo-F	CACCCATCCCGTATGAGTATCAACCCAAAC	NPF7.3pro-R	TTTGCGATGATATATGATTATATGTATGTGAG
NPF7.3 promoter	Construction of pDONR-NPF7.3pro:NPF	NPF7.3pro-attL1-IF-F	GCCGCCCCCTTCACCCATCCCGTATGAGTATCAAC	AtNPF7.3pro-NPF7.3CDS-IF-R	CTCTAGGCAAGACATTTTGCGATGATATATGATTA
pDONR207-NPF7.3 CDS	7.3	NPF7.3CDS-IF-F	ATGTCTTGCCTAGAGATTTA	pDONR-attL1-R	GGTGAAGGGGGCGGCCGCGGAGCCTGCTTTTTTGTA
NPF7.3 promoter	Construction of pENTR-NPF7.3pro:NPF	NPF7.3pro-attL1-IF-F	GCCGCCCCCTTCACCCATCCCGTATGAGTATCAAC	AtNPF7.3pro-NPF7.2CDS-IF-R	AACTTTTTGATCCATTTTGCGATGATATATGATTA
pENTR-NPF7.2 CDS	7.2	NPF7.2CDS-IF-F	ATGGATCAAAAAGTTAGACA	pENTR-attL1-R	GGTGAAGGGGGCGGCCGC
NPF7.3 promoter	Construction of pENTR-NPF7.3pro:NPF	NPF7.3pro-attL1-IF-F	GCCGCCCCCTTCACCCATCCCGTATGAGTATCAAC	AtNPF7.3pro-NPF4.6CDS-IF-R	TTCTTCCACTTCCATTTTGCGATGATATATGATTA
pENTR-NPF4.6 CDS	4.6	NPF4.6CDS-IF-Fp	ATGGAA GTGGAAGAAG AGGT	pENTR-attL1-R	GGTGAAGGGGGCGGCCGC
NPF7.3 promoter-reporter analysis					
NPF7.3 promoter	Construction of pENTR-NPF7.3pro:GUS	NPF7.3pro-IF-F	GCCCCCTTCACCATGCATCCCGTATGAGTATCAAC	NPF7.3pro-GUS-IF-R	TACAGGACGTAACATTTTGCGATGATATATGATTATAT
GUS		GUS-F	ATGTTACGTCCTGTAGAAAC	GUS-IF-R	AGCTGGGTCGGCGCGCTCATTGTTTGCCTCCCTGC
pENTR		pENTR-F	AAGGGTGGGCGCGCCGACC	pENTR-R	GGTGAAGGGGGCGGCCGCG
NLS	Construction of	GFP-NLS-IF-F	CTGTACAAGTCCGGACTCAGATCTCGAG	GFP-NLS-IF-R	CTGGGTCTAGATATCTCGATTATCTAGATCCG
GFP	pENTR4-GFP-NLS	GFP-IF-F	AAAAGCAGGCTCCACCATGATGGTGAGCAAGGGCGAG	GFP-IF-R	TGAGTCCGGACTTGTACAGCTCGTCCATGC
GFP-NLS	Construction of pENTR4-NPF7.3pro:GFP-NLS	NRT7.3pro-GFP-NLS-IF-F	ATAATCATATATCATCGCAAAATGGTGAGCAAGGGCGAG	NRT7.3pro-GFP-NLS-IF-R	AGAAAGCTGGGTCGGCGCGTTATCTAGATCCGGTGAATCCTACC
pENTR-NPF7.3pro	Construction of pENTR4-NPF7.3pro:GFP-NLS	pENTR-NPF7.3pro-F	CGCGCCGACCCAGCTTTCTTGTACA	pENTR-NPF7.3pro-R	TTTGCGATGATATATGATTATATGTATGTGAG

*Gene symbol provided by TAIR (http://www.arabidopsis.org/) except for T-DNA.

Supplementary Table 2. Conditions of LC.

Solvent A	Solvent B	Gradient (composition of solvent B)	Column
Water containing 0.01% (v/v) acetic acid	MeCN containing 0.05% (v/v) acetic acid	Constant at 20% for 1 min	ZORBAX Eclipse XDB-C18 column, 2.1 x 50 mm i.d., 18 μm (Agilent)
		Linear gradient from 20 to 35% over 4 min	
		Linear gradient from 35 to 98% over 0.1 min	
		Constant at 98% for 0.9 min	
		Linear gradient from 98 to 20% over 0.1 min	
		Constant at 20% for 0.9 min	

Supplementary Table 3. Parameters of tandem mass spectrometer.

Compound	Material	Retention time on LC (min)	Polarity of ESI	IonSpray voltage (kV)	Desolvation temperature (°C)	Declustering potential (V)	Collision energy (V)	Precursor ion (*m*/*z*)	Scan range (*m*/*z*)	Qualifier ion (*m*/*z*)
[$^{13}C_8$, $^{15}N_1$]IBA	Arabidopsis	4.0	+	5.5	600	90	20	213.15	50-1000	195
IBA		4.0	+	5.5	600	90	20	204.15	50-1000	186
[methylene-$^2H_2$]IAA		2.5	+	5.5	600	90	15	178.20	50-1000	132
IAA		2.5	+	5.5	600	90	15	176.20	50-1000	130
[methylene-$^2H_2$]IBA	Yeast	4.0	–	–3.5	600	–90	–22	204.15	50-1000	160
IBA		4.0	–	–3.5	600	–90	–22	202.15	50-1000	158
[methylene-$^2H_2$]IAA		2.5	–	–3.5	600	–90	–15	176.20	50-250	132
IAA		2.5	–	–3.5	600	–90	–15	174.20	50-250	130

Supplementary References

1 Brady, S. M. *et al.* A high-resolution root spatiotemporal map reveals dominant expression patterns. *Science* **318**, 801-806, doi:10.1126/science.1146265 (2007).

2 Gifford, M. L., Dean, A., Gutierrez, R. A., Coruzzi, G. M. & Birnbaum, K. D. Cell-specific nitrogen responses mediate developmental plasticity. *Proc Natl Acad Sci U S A* **105**, 803-808, doi:10.1073/pnas.0709559105 (2008).

3 Winter, D. *et al.* An "Electronic Fluorescent Pictograph" browser for exploring and analyzing large-scale biological data sets. *PLoS One* **2**, e718, doi:10.1371/journal.pone.0000718 (2007).