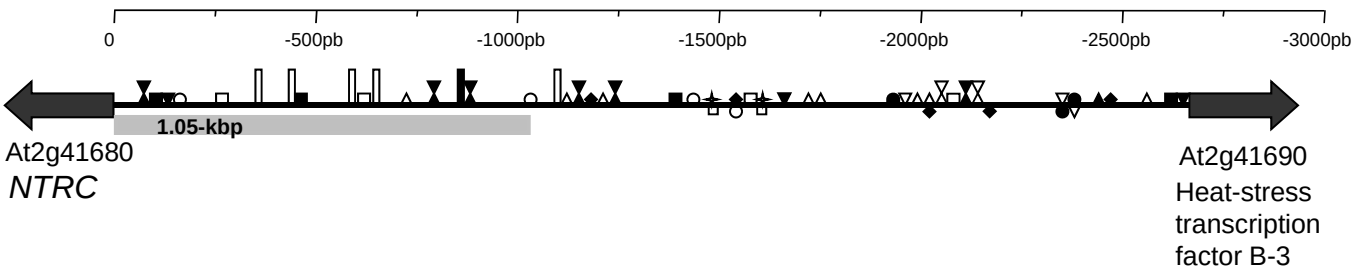
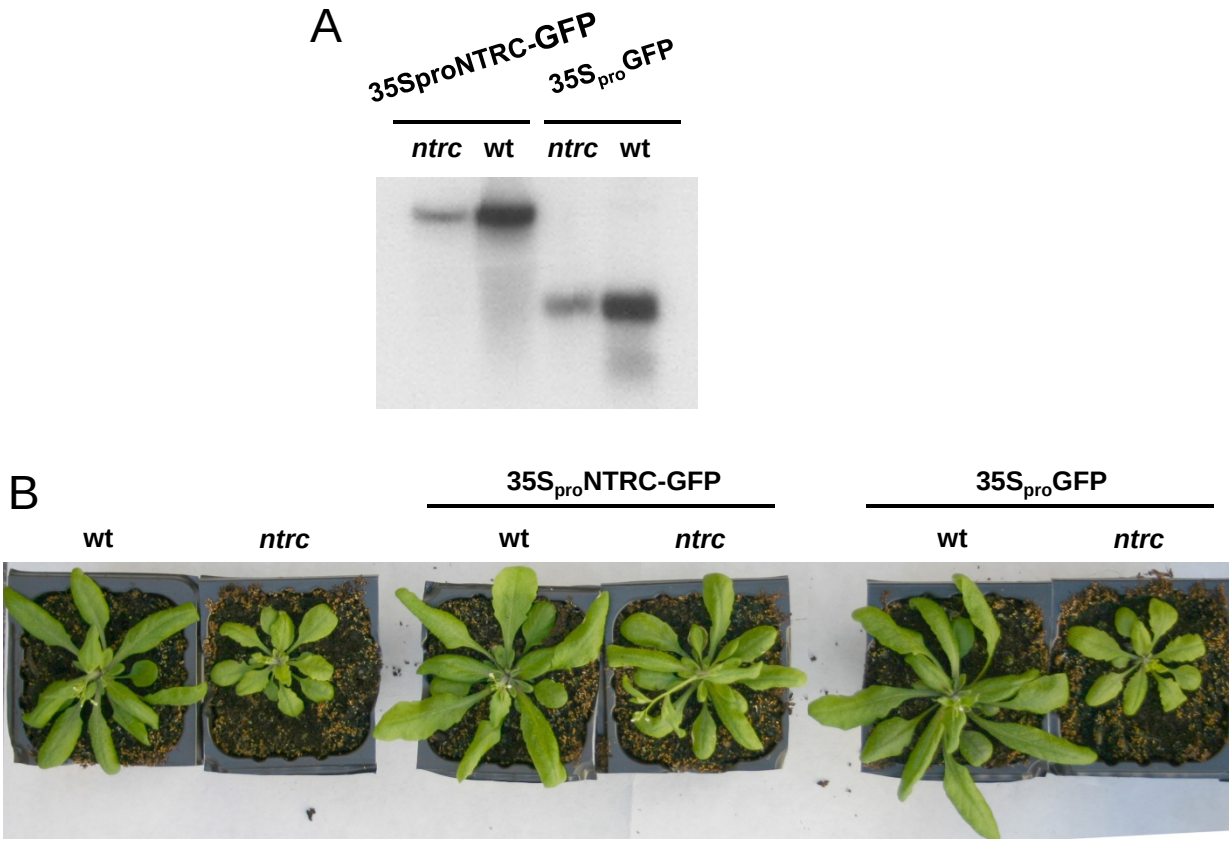
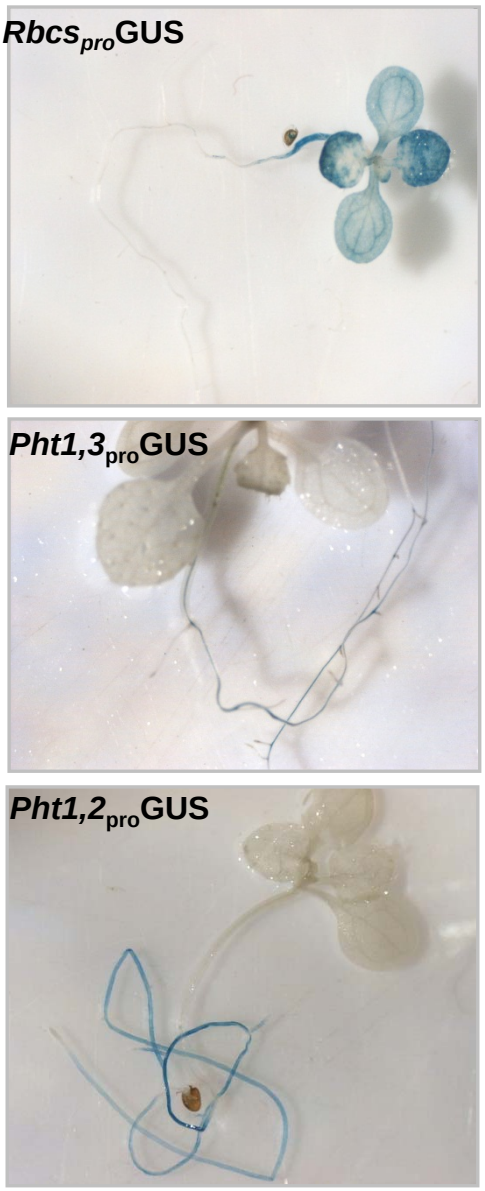


Symbol	*Cis*-element	Function
▌	Athb1	Leaf development
▽	Sorlip 1	Light response
○	Tbox	Light response
□	LTRE	Stress response
▲	Ibox	Light response
◗	BoxII	Interaction with TATA complex
⧗	GATA box	Light response
■	Bellringer	Floral development
◆	W-box	Plant defense response
●	CArG	Floral development
▼	ARF1	Auxin response elements
⧖	LFY	Flower development
✦	DRE	Enviromental stress
△	Rav	Floral development
▯	MYB	Enviromental stress
⛉	DPBF1	ABA-responsiveness

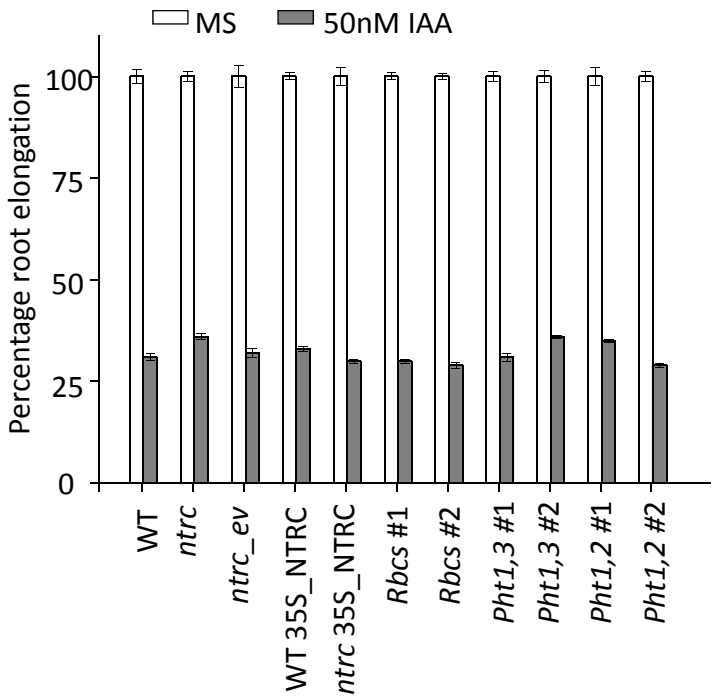
Suppl. Fig. 1. Scheme showing the position of the *NTRC* gene (Atg41680) and the flanking At2g41690 gene in Arabidopsis and distribution of possible *cis*-acting elements. The 1.05-kbp fragment containing the putative *NTRC* gene promoter transcriptionally fused to the GUS reporter gene is indicated. The 3-kbp of 5' regulatory region of NTRC was analyzed for the presence of putative *cis*-acting regulatory elements using Arabidopsis Gene Regulatory Information Server (AGRIS) database (http://arabidopsis.med.ohio-state.edu/AtcisDB) (Davuluri et al., 2003). Based on the AtcisDB Genomic View (http://arabidopsis.med.ohio-state.edu/cgi-bin/gb2/gbrowse/atcisdb/?q=Chr2:17385620..17388800) all the motifs listed in the AGRIS database were mapped.



Suppl. Fig. 2. Characterization of transgenic plants expressing the NTRC-GFP fusion protein or GFP under the control of the CaMV 35S promoter in wild type and *ntrc* mutant backgrounds.
(A) Total RNA isolated from leaves of Arabidopsis wild type, *ntrc* mutant and transgenic lines, were analysed by RNA gel blot probed with ^{32}P-labelled GFP cDNA, which shows expression of the transgenes in both wild type and *ntrc* backgrounds. **(B)** Complementation of the *ntrc* phenotype by the expression of the NTRC-GFP fusion protein. Plants were grown in standard long-day conditions (16/8) for 28 days.



Suppl. Fig. 3. Histochemical localization of GUS expression under the control of organ-specific promoters.
GUS staining of Arabidopsis seedlings expressing the GUS reported gene under the control of leaf-specific (*Rbcs*) or root-specific (*Pht1,2* and *Pht1,3*) promoters.



Suppl. Fig. 4. Effect of IAA treatment on root growth inhibition. Seedlings of the different Arabidopsis lines under analysis, as indicated, were grow for 5 days on MS medium under long day conditions. Then seedlings were transferred to media containing 50 nM IAA for an additional period of 3 days. Root length was expressed as a percentage of root elongation of seedling not treated with IAA. Mean values ± standard errors are indicated.

Suppl. Table 1. Expression of genes encoding NTRC, 2-Cys PRX A and 2-Cys PRX B in different Arabidopsis organs based on data obtained from Genevestigator.

Gene	Leaves	Roots	Stems	Flowers
NTRC (At2g41680)	High 9396 ± 122	Low 1362 ± 30	High 6024 ± 396	High 3235 ± 125
2-Cys PRX A (At3g11630)	High 57385 ± 627	High 12252 ± 258	High 51023 ± 1859	High 25984 ± 934
2-Cys PRX B (At5g06290)	High 21025 ± 227	Medium 2266 ± 78	High 15077 ± 566	High 7950 ± 403

Suppl. Table 2. Expression of genes encoding the alternative pathway for redox regulation in root amyloplasts based on data obtained from Genevestigator.

Gene	Leaves	Roots
FNR1 (At5g66190)	High 46488 ± 513	Low 1446 ± 169
FNR2 (At1g20020)	High 43957 ± 530	Low 548 ± 76
RFNR1 (At4g05390)	Medium 3099 ± 78	High 7029 ± 186
RFNR2 (At1g30510)	Medium 1979 ± 36	High 23583 ± 569
Fd1 (At1g10960)	High 46436 ± 622	Medium 7383 ± 346
Fd2 (At1g60950)	High 108053 ± 1097	High 8433 ± 339
FTRA (At5g23440)	High 5418 ± 55	Low 1054 ± 15
FTRB (At2g04700)	High 25140 ± 225	Medium 3590 ± 56
Trxf1 (At3g02730)	High 31856 ± 395	Low 1081 ± 82
Trxf2 (At5g16400)	High 9637 ± 136	Low 580 ± 36

Suppl. Table 3. Gene-specific oligonucleotides used for qPCR analysis.

Gene	Primers
NTRC (At2g41680)	5’-TCACCAACATGTGGCCC-3’ 5’-TTCTTCATCTTCACACCCGA-3’
2-Cys PRX A (At3g11630)	5’-ACTCTCATCTCTTCTCCC-3’ 5’-AGGAGAAGAAAGGGTTCGAA-3’
2-Cys PRX B (At5g06290)	5’-CACCACCCTACTCTCTT-3’ 5’-GGAAGAGGGTATGATTCTGG-3’
Fd1 (At1g10960)	5’-CATCACACCTGAGGGAGAACAAGA -3’ 5’- GAAGTCGGATAAGCCACACAG-3’
Fd2 (At1g60950)	5’-CGTGGTGGACGTGTCACAG-3’ 5’-CAACAGATCCAGACACAACTTTACC-3’
FNR1 (At5g66190)	5’-CTACCGAGGCACCACCAG-3’ 5’-CGATTGTCCTTCTCTGTACGG-3’
FNR2 (At1g20020)	5’-GAACAGATACTCCTACTCCTGCAAAG-3’ 5’-CGATTGTCCTTCTCTGTACGG-3’
RFNR1 (At4g05390)	5’-GGACAATGGAGCTCATATTTACTTC-3’ 5’-CTTTCTTGGTTGAGTTACACTGTG-3’
RFNR2 (At1g30510)	5’-GGACAATGGAGCTCATATTTACTTC-3’ 5’-CAAAACCAACAAATTTCAGATATTATC-3’
FTRA (At5g23440)	5’-GCCACTACTGCTACCGCCAC-3’ 5’-CGCTTCCGCTTCGATTTCTTC-3’
FTRB (At2g04700)	5’-CTCGATGAATCTTCAAGCTGTTTC-3’ 5’-CAAAGCGGTGCACCATATGAATC-3’
Trxf1 (At3g02730)	5’-GGTGTGGTCCATGTAAAGTGATTGC-3’ 5’-GACTGGTTCATCCGGAAGCAG-3’
Trxf2 (At5g16400)	5’-GGTGATAAGATTGTTGTCCTCGAC-3’ 5’-CTTCAATGGCTGCAAGTAAGTCTTC-3’

Suppl. Table 4. Oligonucleotides used for constructs to generate transgenic lines.

Transgenic line	Oligonucleotides
NTRCpro:GUS	F-NOSter-NotI (5'AATTGCTACCGCGGCCGCGAATTT-3') R-NOSter-SacI (5'CAGTGAGCTCCCGATCTAGTAACATAGAT-3') FpNtrc-HindIII (5'GTAAGCTTCACGCGTCTGTAAAT-3') RpNtrc-XbaI (5'-GGTCTAGAATTTTTTTTGATTGCCTTACC-3') F-GUS-XbaI (5'-AACACGGGGGACTCTAGAGGATCC-3') R-GUS-NotI (5'-ACGCGGCCGCAGTTGTTGATTCATTGTTT-3')
NTRC-GFP	Ntrc-F-KpnI (5'-CAGGTACCATGGCTGCGTCTCC-3') Ntrc-R-SmaI (5'-GACCCGGGa**TCA**TTTATTGGCCTCAATG-3')
Pht1,2pro:NTRC	*P ht1,2*-Fw (5´- TAGGATCCGATCACTATACAACTCTGC-3´) *Pht1,2*-Rev (5´- GAGGTACCTCTCTTGTCTTTCC-3´)
Pht1,3pro:NTRC	*Pht1,3*-Fw (5´- TAGGATCCTAATGAGTATAAGAG-3´) *Pht1,3*-Rev (5´- CTGGTACCTCTCCTATTTTGCAC-3´)
Rbcs1Apro:NTRC	*Rbcs*-Fw (5´- TGGGATCCTGAGTCTCAAAGTGGC-3´) *Rbcs*-Rev (5´- TGGTACCTCTTCTTTACTCTTTG-3´)
GATEWAY tails	AttB1 tail (5´-GGGGACAAGTTTGTACAAAAAAGCAGGCT-3') AttB2 tail (5´- GGGGACCACTTTGTACAAGAAAGCTGGGT-3')
NTRC cDNA	(5´- CAGGTACCATGGCTGCGTCTC-3´) (5´- GAGAGCTCTCATTTATTGGCCTCA-3´)