SUPPLEMENTARY MATERIAL FOR MANUSCRIPT

Functional analysis of the pathways for 2-Cys peroxiredoxin reduction in *Arabidopsis thaliana* chloroplasts

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Legends for Supplementary Figures

Fig. S1. A, Schematic representation of the structure of *2cpA* and *2cpB* genes from Arabidopsis showing the location of the T-DNA insertions, as previously reported (Kirchsteiger et al., 2009), used for construction of the double mutant. The position of the oligonucleotides used for PCR analysis is marked with arrows. B, PCR analysis of the presence of the T-DNA insertions in genomic DNA isolated from the wild type and homozygous double mutant (Hom) for both insertions. DNA size markers, in kbp, were loaded on the left. T denotes the primer specific for the T-DNA insertion, while a, a', b and b' represent the gene specific primers as shown in A.

Fig. S2. A, Schematic representation of the structure of the Trx *x* gene from Arabidopsis showing the position of the T-DNA insertion in line SALK_125897 and the oligonucleotides used for PCR analysis. B, PCR analysis of genomic DNA isolated from wild type and a homozygous line for the T-DNA insertion in the *trxx* gene. DNA size markers, in kbp, are shown on the left. T denotes the primer specific for the DNA insertion, c and d represent the gene specific primers as shown in A.

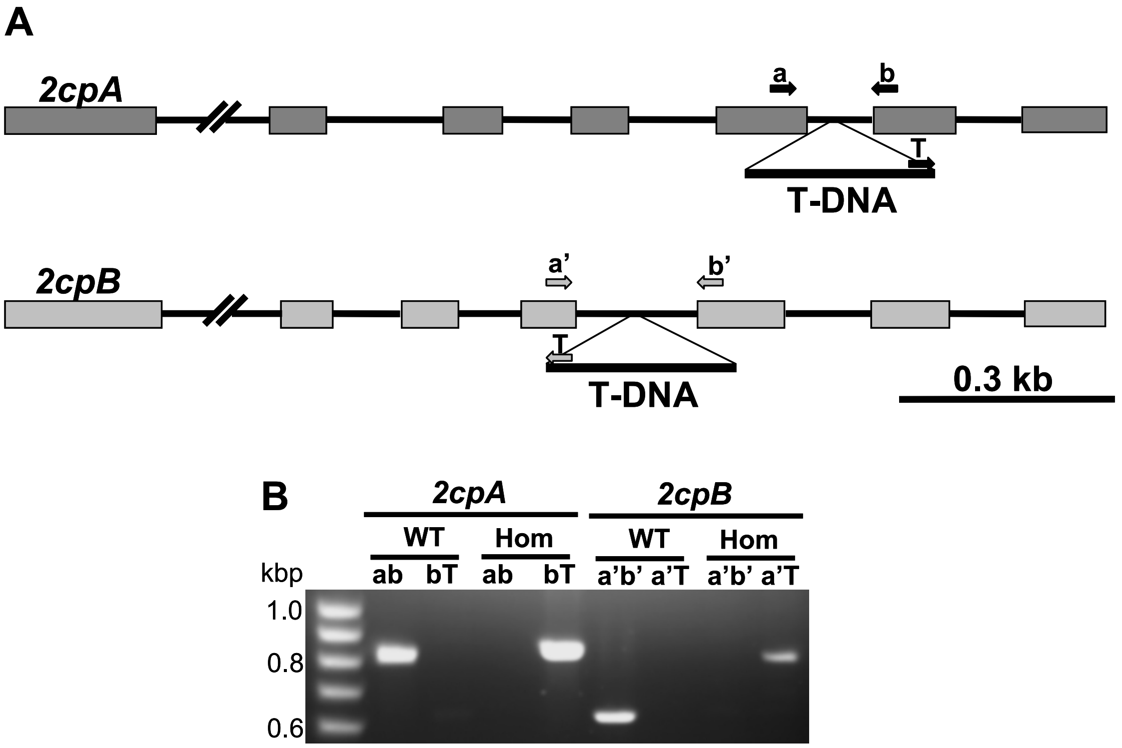
A
2cpA
a
b
T
T-DNA
2cpB
a'
b'
T
T-DNA
0.3 kb
B
2cpA
2cpB
WT
Hom
WT
Hom
kbp
ab
bT
ab
bT
a'b'
a'T
a'b'
a'T
1.0
0.8
0.6

Figure S1

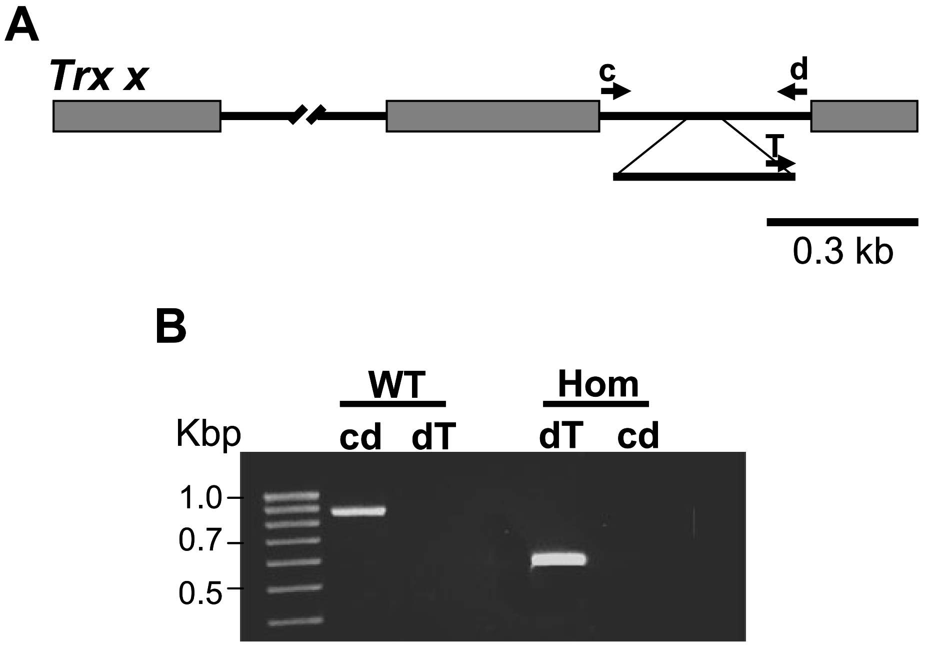

Figure S2

Table S1. Gene-specific oligonucleotides used for qPCR analysis

Gene	Oligonucleotides
Ubiquitin 10	F: 5’-GATCTTTGCCGGAAAACAATTGGAGGATGGT-3’ R: 5’-CGACTTGTCATTAGAAAGAAAGAGATAACAGG-3’
2cpA	F: 5’-ACTCTCATCTCTTCTCCC-3’ R: 5’-AGGAGAAGAAAGGGTTCGAA-3’
2cpB	F: 5’-CACCACCCTACTCTCTT-3’ R: 5’-GGAAGAGGGTATGATTCTGG-3’
Trxx	F: 5’-CTAGTTCGGTGATAAGATGC-3’ R: 5’-ATTGAGTTCAAGAGACCATC-3’
NtrC	F: 5’-TCACCAACATGTGGCCC-3’ R: 5’- TTCTTCATCTTCACACCCGA-3’
FeSOD1	F: 5'- GCTGTCACCGCAAACTAC -3' R: 5'- GTAAGTGCTGTGGATAATGTGC -3'
FeSOD2	F: 5'- AAAGAAACGGAAAGAGACGG -3' R: 5'- GATCCGTGCCTAAGATTTGC -3'
FeSOD3	F: 5'- CAGTTAGGGAAAGATGATAGACTC-3' R: 5'- ATCTGCTCAAGAACACCCT -3'
CuZnSOD2	F: 5’- TTGGGAGACCTGGGAACAC-3’ R: 5'- TAGTTTTCTCCAACCCCTGCG -3'
APX1	F: 5'- GTCCATTCGGAACAATGAGGTTTGAC -3' R: 5'- GTGGGCACCAGATAAAGCGACAAT -3'
APX3	F: 5'- CCCAAAATCACATACGCAGACCTGTA -3' R: 5'- AGTTGTCAAACTTCAGCGGCTCTTG -3'

APX4	F: 5'- CTACTAAATCCGGGGGAGCCAATG -3' R: 5'- CTCTGTTGCATCACTCCTTCCAAAAT -3'
APX5	F: 5'- AGCTAAACCGTCCACACAACAAAGGT -3' R: 5'- GTCCCAAAGTGTGACCTCCAGAGAGA -3'
APX6	F: 5'- TGCAAAACGAAATAAGGAAAGTGGTG -3' R: 5'- CACTCAGGGTTTCTGGAGGTAGCTTG -3'
sAPX	F: 5'- TGCTAATGCTGGTCTTGTGAATGCTT -3' R: 5'- CCACTACGTTCTGGCCTAGATCTTCC -3'
tAPX	F: 5'- CAGAATGGGACTTGATGACAAGGAAA -3' R: 5'- ATGCAGCCACATCTTCAGCATACTTC -3'