Supporting Information

Supplementary Table 1. List of primers used in this study

Supplementary Fig. 1. Expression of *AtPrx1*, *AtPrx22*, *AtPrx39* and *AtPrx69* in *bri1-9* and *BRI1-GFP* plants compared with that of the wild type. ANOVA statistical analyses were performed and significant differences are indicated by P values (*: P≤0.004, **: P≤0.002). The unpaired t-test was performed (***: P value = 0.5).

Supplementary Fig. 2. Gross morphologies and H_2O_2 concentrations of T-DNA insertional *AtPrx* mutants. (A) Phenotypes of T-DNA insertional *AtPrx* mutants compared with those of wild type. Pictures were taken of 4-week-old plants grown under long-day conditions. (B) Hydrogen peroxide concentrations were determined from 10-day-old seedlings.

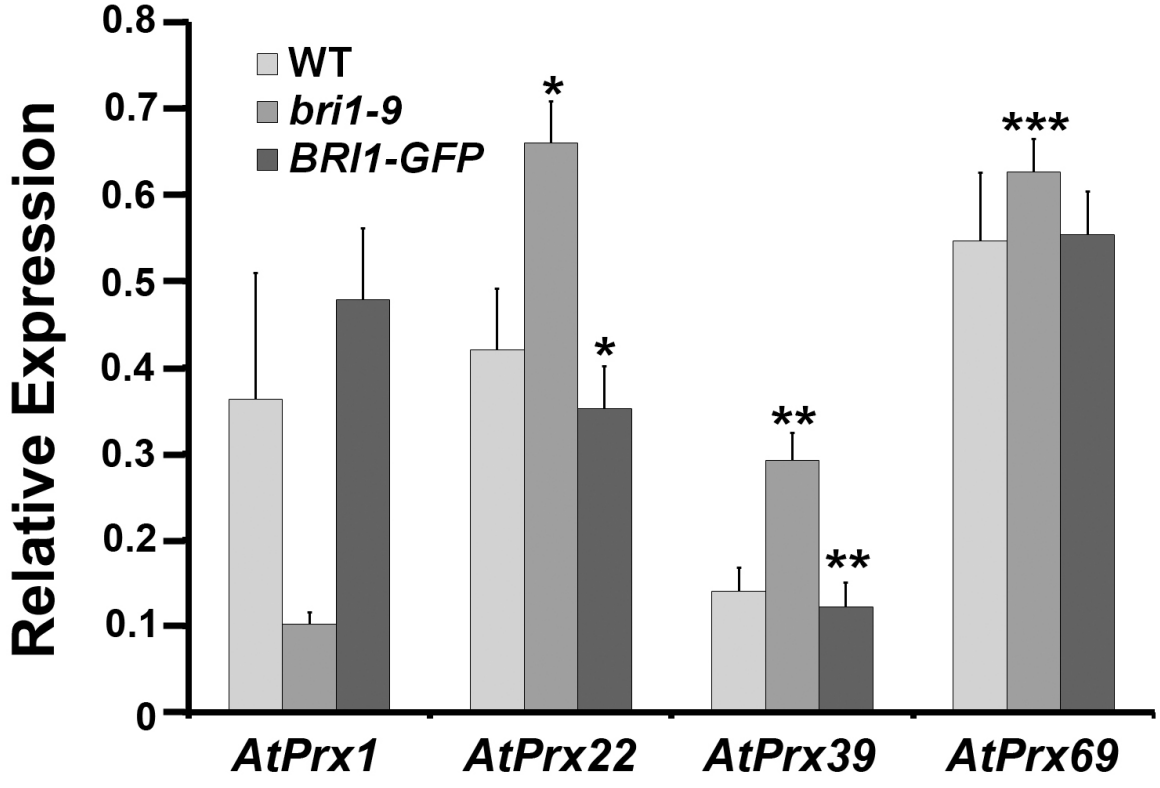
Supplementary Fig. 3. DAB-staining pattern of the *BRI1-GFP* plants transformed with *AtPrx1*, *AtPrx22*, and *AtPrx69* under normal conditions.

Supplementary Table 1. Primer Sequences

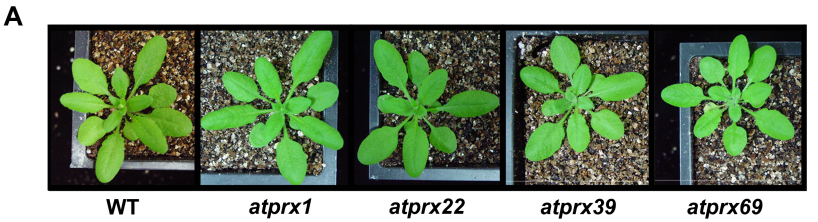
Primer Name	Sequence (5' to 3')	Use
AtPrx1 RT F	GGGGGTCACACCATTGGAATCTC	Confirmation of null *AtPrx1* expression in the *atprx1* mutant
AtPrx1 RT R	GGAGGGAGAATGGCCTGAGTCTG	
AtPrx22 RT F	GACATGTCCGTGTTCTTTCGAGCATTCA	Confirmation of null *AtPrx22* expression in the *atprx22* mutant
AtPrx22 RT R	TATTAGTCGAAATTGTTCTCACGTGCG	
AtPrx39 RT F	CACCGGCGTTGGAGACCAAGATCC	Confirmation of null *AtPrx39* expression in the *atprx39* mutant
AtPrx39 RT R	CTCCGATCCTCCGGCGAAGCGTTTG	
AtPrx69 RT F	CTGCTGGCTGCGGTCTAGTAAGGGG	Confirmation of null *AtPrx69* expression in the *atprx69* mutant
AtPrx69 RT R	GGCTCGGGTCTCGGGATCCTTCC	
Tubulin F	ACCATGAGCAGCTTTCTGTGCCTG	Amplification of Arabidopsis *tubulin* for nomalization
Tubulin R	CGCCGACTTCCTCATAGTCCTTC	
AtrbohD F	GGAAGGATGGACTGGCATTGTG	Monitoring the *AtrbohD* expression in response to cold
AtrbohD R	GTACGCTCAGGTAATCGTCTCCG	
AtrbohF F	GAACGATCGGCGACGGTGGTCATTTG	Monitoring the *AtrbohF* expression in response to cold
AtrbohF R	CGAAATCGGAGCGATAGATGTAACCATT	
AtPrx1 F	GGGGTACCATGGCGATCAAGAACATTCTCGC	Amplification of full length *AtPrx1* for overexpression construct
AtPrx1 R	ACGCGTCGACTTAGTTAGGGAAGGCGCATCTC	
AtPrx22 F	GGGGTACCATGGGGTTTTCTCCTTCATTTTC	Amplification of full length *AtPrx22* for overexpression construct
AtPrx22 R	ACGCGTCGACTCAGATAGAACTCACAACACCAT	
AtPrx69 F	TCCCCCCGGGATGGGTCGTGGTTACAATTTGC	Amplification of full length *AtPrx69* for overexpression construct
AtPrx69 R	GCGTCGACTTAGTTGATGGCGGAACAAACC	

RNA was purified from the seedlings grown for 10 days in normal conditions and then exposed to cold for 24 hours. The RNA samples were treated with RNase-free RQ1 DNase (Promega) and used for first-strand cDNA synthesis with the Superscript^{III}-MMLV reverse transcriptase (Invitrogen) using oligo d(T_{15}) as the primer. Second-strand synthesis was performed using the same aliquot of first-strand cDNA as the template. PCR conditions were as follows: pre-denaturation at 94°C for 4 min., denaturation at 94°C for 30 sec., primer-annealing at 52°C for 30 sec., elongation at 72°C for 30 sec. for 25 cycles or 28 cycles depending on the experiment, and post-elongation at 72°C for 7 min. The expression of each gene was normalized to β-*Tubulin*.

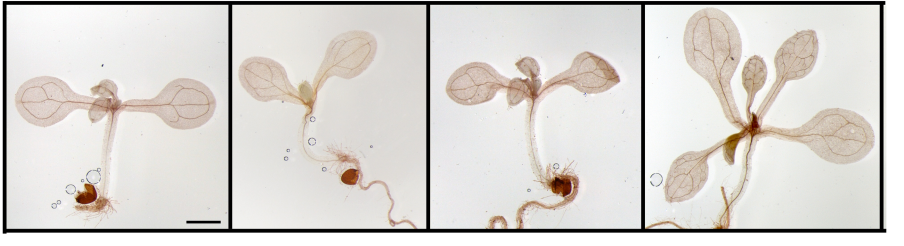
Supplementary Fig.1 Kim *et al*.



Supplementary Fig. 2 Kim *et al*.



Supplementary Fig. 3 Kim *et al.*



BRI1-GFP ***AtPrx1OE/ BRi1-GFP*** ***AtPrx22OE/ BRI1-GFP*** ***AtPrx69OE/ BRI1-GFP***