Supplemental Table 2. Phenotypic characterization of mutant growth and fitness

Experiment and measured parameter	Wild type	*atnth1 atnth2 arp*	*atnth1 atnth2*	*atnth2 arp*	*atnth1*	*atnth2*	*arp*
1 Very high light*							
Seeds/half silique	21.18	21.47					
SD, n = 24	3.06	2.68					
Siliques/plant	192.6	197.6					
SD	32.9	48.3					
Seeds/plant	8118	8484					
SD	1323	2075					
2 Variable light†							
Seeds/half silique	26.67	25.58					
SD, n = 45	2.61	2.53					
Siliques/plant	312.6	308.4					
SD, n = 9	46.9	49.8					
Total seeds/plant	16722	15878					
SD	3113	3381					
3 Variable light‡							
seeds/ half silique	24.97	24.91					
SD, n=31-34	4.18	4.14					
4 Methyl viologen§							
0.125 μM, fresh weight, mg	18.9	19.5	18.7	18.5	19.2	18.3	17.3
SD, n = 7	0. 9	1.3	1.6	0.9	1.6	0.6	1.2
0.25 μM, fresh weight, mg	17.4	16.0	16.7	16.2	17.0	17.6	16.4
SD, n = 6	1.8	1.5	0.7	1.0	1.2	0.7	0.8

5 H_2O_2¶							
10 mM, fresh weight, mg	18.0	19.3	19.7	18.9	20.2	20.6	19.5
SD, n=6-12	1.7	1.2	1.9	1.4	1.4	2.3	0.4

*Plants were grown in short days at low light (~100 μmol photons m^{-2} s^{-1}) for 2 months and then transferred to short days, very high light (VHL, 1,800 μmol photons m^{-2} s^{-1}) for 1 month, at which point the seeds from half of siliques number 12 and 20 on the main inflorescence stem and one randomly selected silique off an axial stem were counted. Plants were returned to VHL and allowed to develop to maturity, at which point total siliques/plant were counted.

†Plants were grown under variable light conditions (subject to fluctuating sunlight in an unshaded greenhouse). At the point when the silique was fully developed but not brittle, seeds from one half of siliques number 10, 12, and 14 from the primary inflorescence stem and 7 and 10 from one axial stem were counted. At maturity, all siliques on each plant were counted.

‡Experiment 3 was similar to Experiment 2, but only siliques 10 and 12 were counted (on more plants), and total siliques were not counted.

§Seedlings were grown in liquid culture in 96-well plates for 12 days. Methyl viologen was then added to a final concentration of 0.125 or 0.25 μM, and plants were grown for 3 more weeks before the fresh weight of each whole plant was determined.

¶Experiment 5 was the same as Experiment 4, but using H_2O_2 at a final concentration of 10 mM.

SD, standard deviation.

Supplemental Table 3. Oligonucleotide primers used

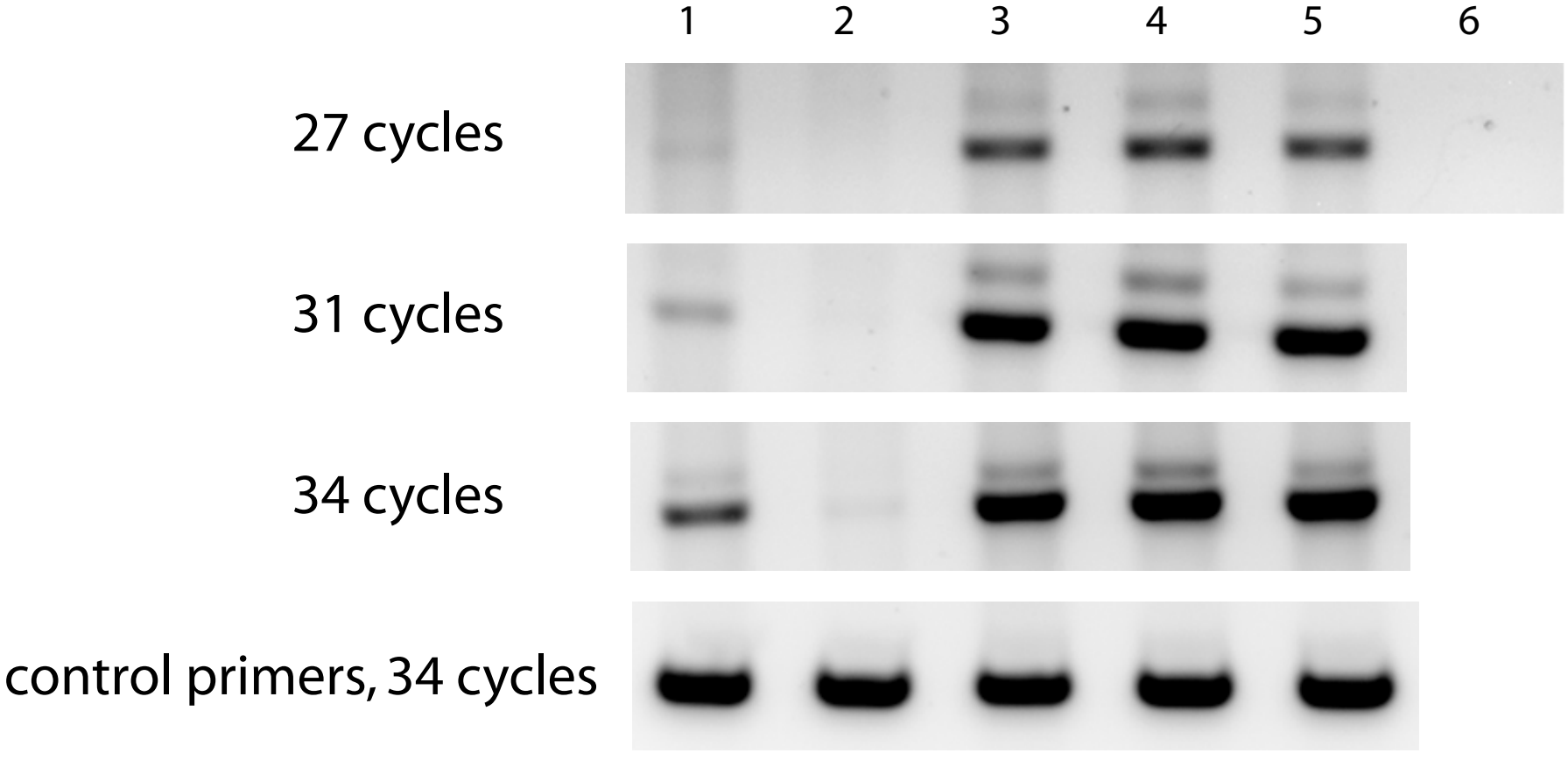
Number	Descriptive name	Sequence, 5' -> 3'
BG1	At2g41460cDNAL	GGTTCTTTGCCTCTCCTTCC
BG2	At2g41460cDNAR	AAAAGCTGGGAATGGTGAAA
BG3	05900adaptL	GATCGTCGACCCAGGCCAGAAGGAGATATAA
BG4	05900adaptR	GTACCCATGGCCACCTGTTTCGTTCCAGGTTTA
BG5	At2g31450gfpR	TCGACCATGGTTCGGTTAGATTTCTTCA
BG6	At2g41460GFPL	TCCTGTCGACTCTCGAGTTTGTGCCCTTT
BG7	At2g41460GFPR	GCTACCATGGAACCGACACCAGGA
BG8	05900.2cDNAL	AAACACAAAAATTGATTGGCTCT
BG9	05900.2cDNAR	GCTCTTGCATTCCCCATAAA
BG10	05900.2+12	GCTAACGTAGGACATATGAATCCAGAGCCAAAGCAA
BG11	05900-19	AAGTGCACTGAACCATATGAATCGCCGTAT
BG12	Salk LBa1	TGGTTCACGTAGTGGGCCATCG
BG13	013055L(05900L)	GCTTCCTTGAAAGGTCGATG
BG14	013055R(05900R)	AGGCCATTTTGATGAAGTCG
BG15	054181L	CGGTTGACAAAGCTGATGAA
BG16	054181R	CCTGGAAGAGACAGCAGGTC
BG17	SAIL LB1	GCCTTTTCAGAAATGGATAAATAGCCTTGCTTCC
BG18	866_H10L	AAGGAAATTGAGGCGATGACT
BG19	866_H10R	AGTAGGCTCTTCCCTGTTGCT
BG20	05900expressionL	CCACCTGAAAACTGGGAAAA
BG21	05900expressionR	GGACCAACTCCTGGAAGTGA
BG22	31450expression2L	TCCCACGGAAAGAAGATTTG
BG23	31450expressionR	TTGAATGCAGCAGGACAAAG
BG24	41460expressionL	CGTTGAGGAAACTTGGGGTA
BG25	41460expressionR	TCTGGTAGAGGGGGAGGTCT
BG26	30480expressionL	GCTTGGGAAATCAGAGCAAG
BG27	30480expressionR	GAACTGGAGCCAACTCGTTC

Supplemental Figure Legends

Supplemental Fig. 7. RT-PCR of *AtNTH1* expression in mutants and wild type. Agarose-gel analysis of PCR reactions (27-34 cycles) using first-strand cDNA template generated from total RNA and gene-specific primers. Lane 1, *atnth1 atnth2 arp* triple mutant; lane 2, *atnth1*; lane 3, *atnth2*; lane 4, *arp*; lane 5, wild type (Col-0); lane 6, no RNA control. Bottom row, detection of control mRNA (At1g40380) to confirm the presence of RNA. *AtNTH1* transcript is present at a very reduced level in the mutant and at a slightly greater, but not wild-type, level in the triple mutant. *AtNTH1* transcript is present at wild-type levels in the *atnth2* and *arp* mutant backgrounds.

Supplemental Fig. 8. Photos of wild type and T-DNA insertional mutants grown under standard short-day conditions. The triple mutant is *atnth1 atnth2 arp*.

Supplemental Fig. 9. Absence of AP sites in OsO_4-treated plasmid DNA substrate. Supercoiled plasmid substrate prepared as for glycosylase-lyase/endonuclease activity assay was incubated 15 min at 37°C with the indicated enzymes: T4 endonuclease V (PDG) (lanes 1-2), *E. coli* Nth as a positive control (lanes 3-4 and 9-10), no enzyme (lanes 5-6 and 11-12), and human Ape1 (lanes 7-8). The substrate and product were then separated on a 1% agarose gel. +, lanes with OsO_4-treated plasmid; -, untreated control plasmid; OC, relaxed open circular plasmid product; SC, supercoiled plasmid substrate.


1
2
3
4
5
6
27 cycles
31 cycles
34 cycles
control primers, 34 cycles

Col-0

atnth1

atnth2

arp

atnth1 atnth2

arp atnth2

atnth1 arp

triple mutant

Gutman supplemental fig. 9