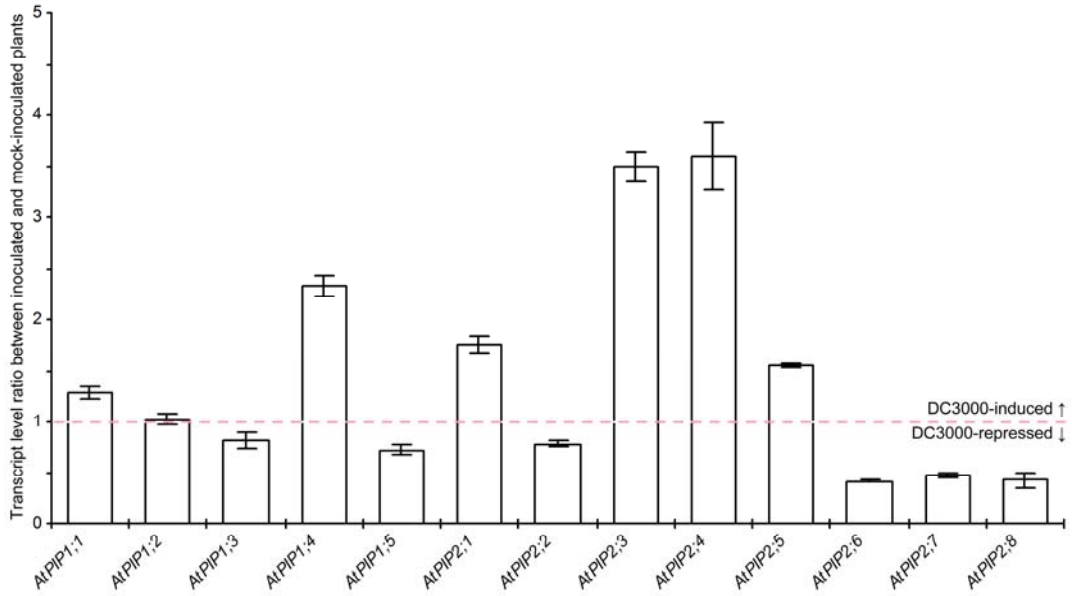


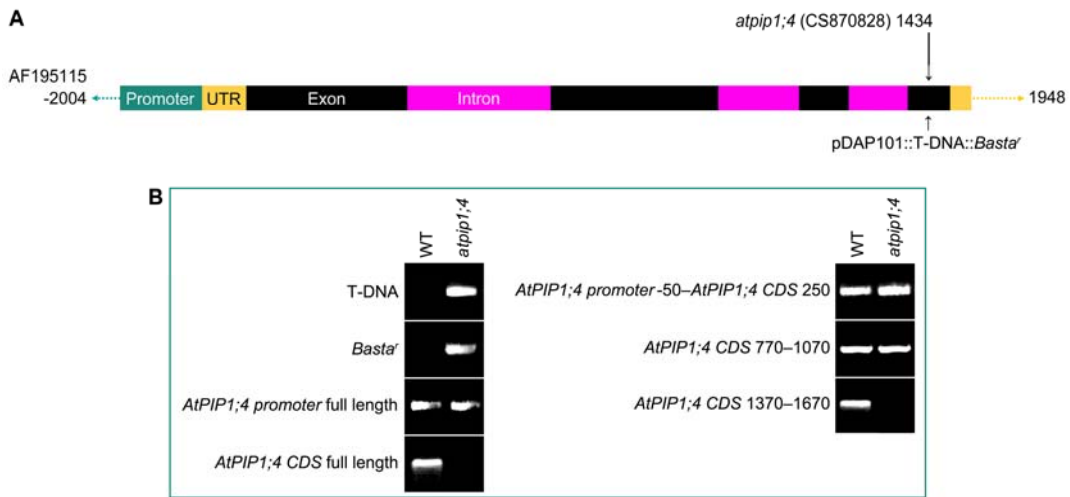
1 **Supplemental Data**

2
3



4
5
6
7
8
9

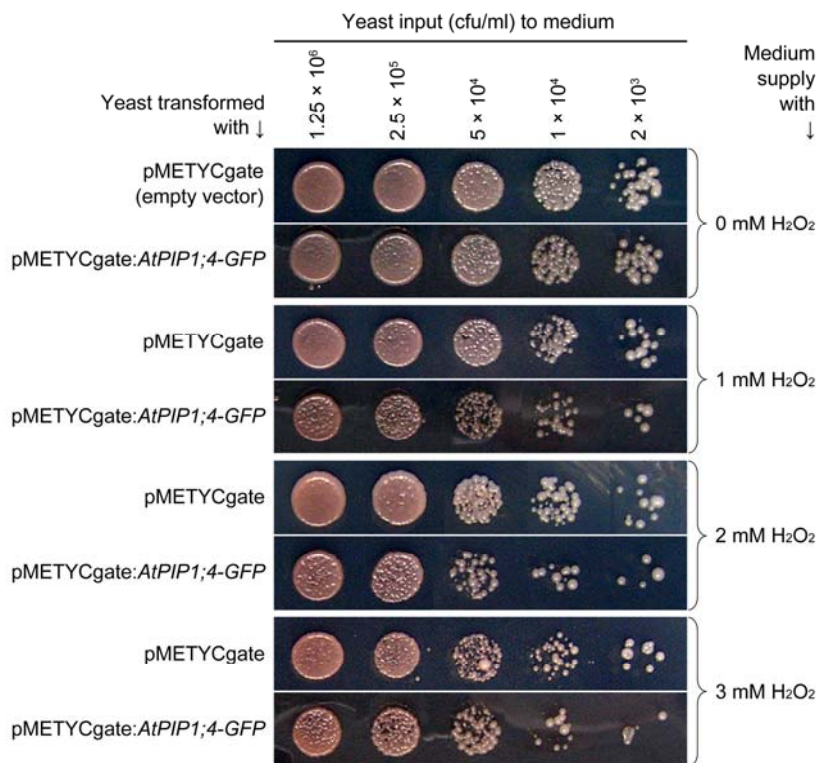
Supplemental Figure S1. Differential expression of *AtPIP* Genes in DC3000-inoculated plants. Gene expression in leaves was analyzed by real-time RT-PCR and expression level of each gene was shown as the ratio (mean \pm SEM; $n = 3$) of transcript quantities between inoculated and mock-inoculated plants.



10

11 **Supplemental Figure S2.** An insertional mutation of *AtPIP1;4*. A, A map showing the
12 pDAP101 vector that contains the selective marker gene *Basta'* (bottom label) and
13 location of a T-DNA insertion in *atpip1;4* mutant. Seed stock number is in parenthesis.
14 Colored bars indicate the gene DNA components, including untranslated region (UTR).
15 B, Identification of T-DNA-indexed *AtPIP1;4* mutation. The genomic DNA was
16 analyzed by PCR using primers specific to gene sequences indicated on left.

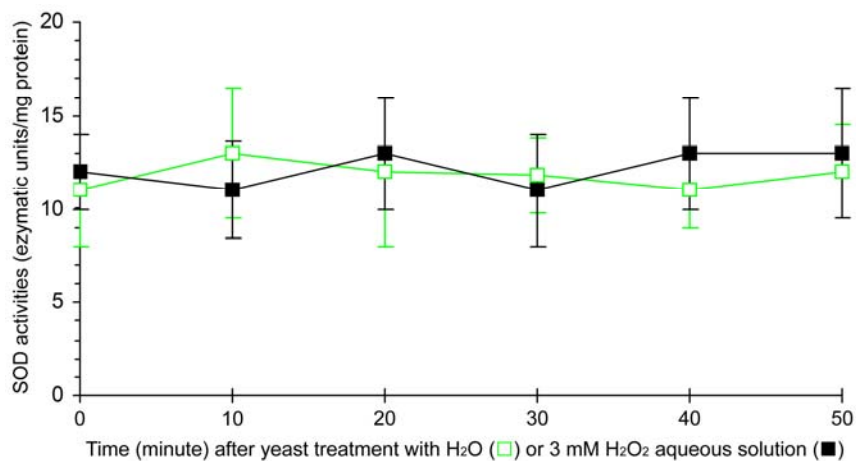
17



18

19 **Supplemental Figure S3.** Yeast colonies grown with H₂O₂ supply at the indicated
 20 concentrations. Colonies were photographed on 3 days after incubation on medium.

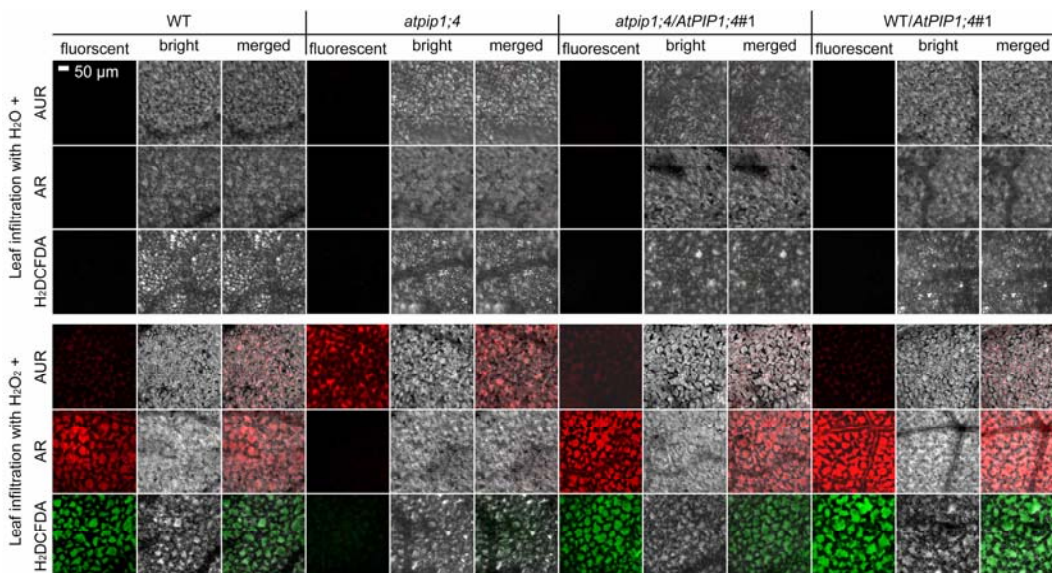
21



22

23 **Supplemental Figure S4.** Yeast SOD activity measurements. Data shown are means ±
 24 SEMs ($n = 3$).

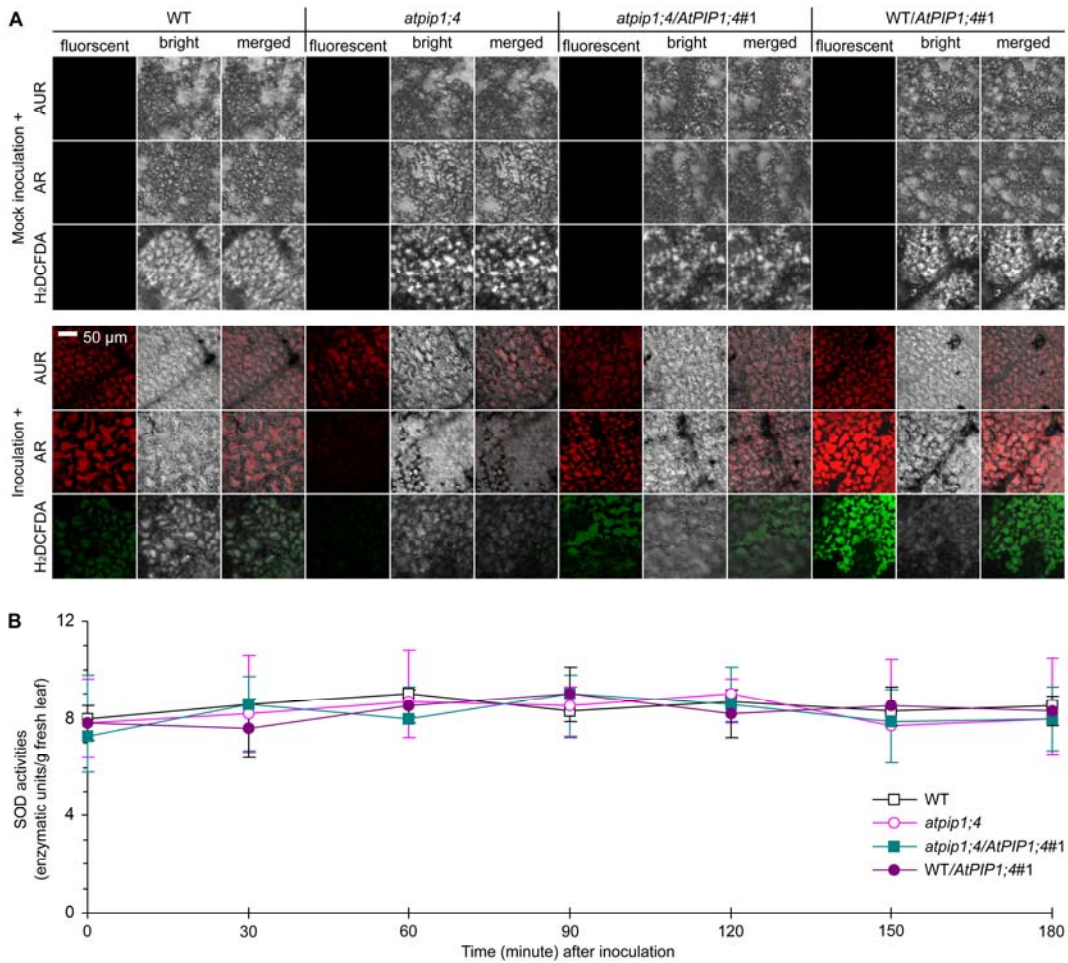
25



26

27 **Supplemental Figure S5.** Imaging of apoplastic H₂O and cytoplasmic H₂O₂ or ROS in
28 leaves of plants treated with H₂O₂ or H₂O. Leaves were observed by confocal
29 microscopy on 45 minutes after infiltration treatment with agents shown on left. AUR
30 and AR visualized apoplastic and cytoplasmic H₂O₂, respectively, and H₂DCFDA
31 detected cytoplasmic ROS.

32

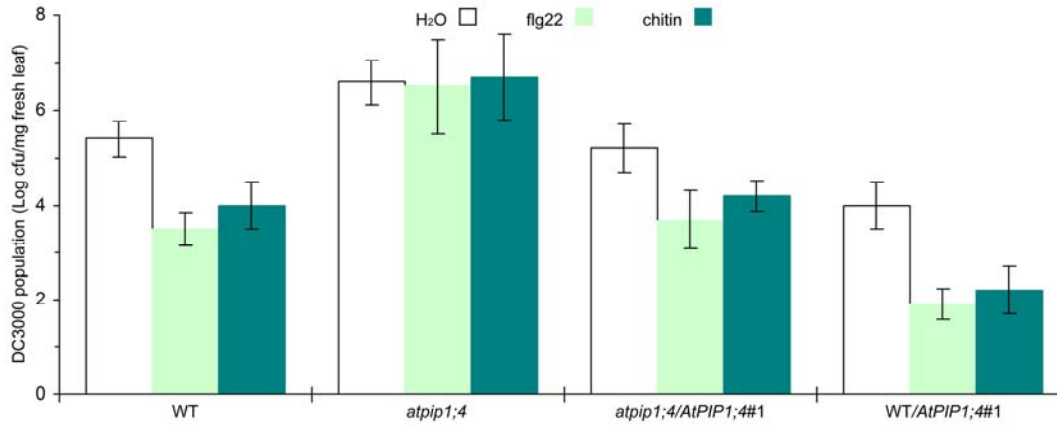


33

34 **Supplemental Figure S6.** H₂O₂ or ROS visualization and SOD activities in leaves of
 35 inoculated and mock-inoculated plants. A, Leaf imaging by confocal microscopy at one
 36 hour after inoculation or mock inoculation. AUR and AR visualized apoplastic and
 37 cytoplasmic H₂O₂, respectively, and H₂DCFDA detected cytoplasmic ROS.

38 B, SOD activity quantification (means ± SEMs; *n* = 3).

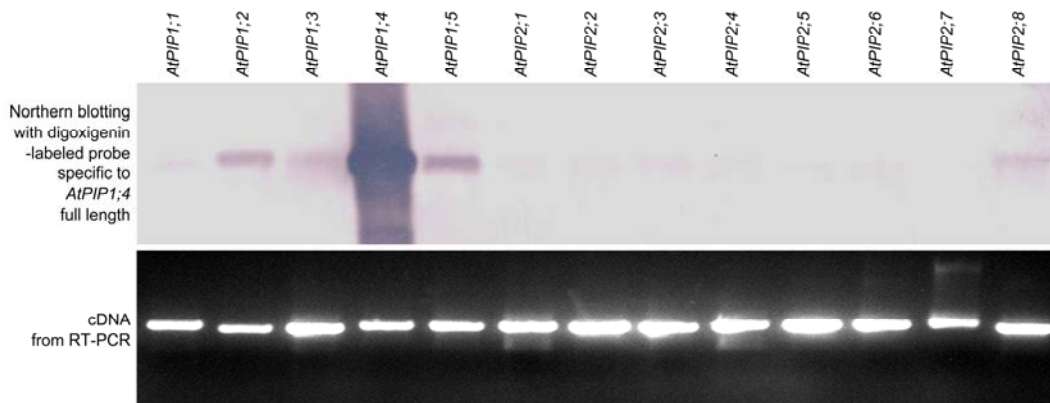
39



40

41 **Supplemental Figure S7.** The effects of PAMPs on DC3000 population growth in
 42 plant leaves. Data shown are means \pm SEMs ($n = 3$) of bacterial population in
 43 inoculated leaves 3 dpi (5 days after treatment with the indicated agents).

44



45

46 **Supplemental Figure S8.** Northern blotting analysis with *AtPIP1;4* probe hybridized to
 47 RT-PCR products of *AtPIPs*. RT-PCR was performed with specific primers and total
 48 RNA isolated from leaves of the WT plant. RNA was used at 1 μ g in a 25 μ l reaction
 49 solution to produce cDNA; uniformly 5 μ g cDNA was used in electrophoresis for every
 50 *AtPIP* gene.

51

52 **Supplemental Table S1.** Relative levels of *MPK6* expression in leaves

Treatment group	Plant genotype			
	WT	<i>atpip1;4</i>	<i>atpip1;4/AtPIP1;4#1</i>	WT/ <i>AtPIP1;4#1</i>
H ₂ O (control)	1 ± 0.017	0.86 ± 0.096	1.17 ± 0.414	1.14 ± 0.092
Flg22	0.85 ± 0.159	0.66 ± 0.07	0.99 ± 0.248	1.03 ± 0.037
Chitin	0.83 ± 0.162	0.78 ± 0.19	1.05 ± 0.414	1.03 ± 0.108

53 Note: data are *MPK6* transcript quantity ratios to *ACTIN2*.

54

55 **Table S2.** Information on genes tested and primers used in this study

Gene (locus code)	Primers / product size (bp) / subjects
<i>Actin2</i> (AT3G18780)	5'-GGCTCCTCTTAACCCAAAGG-3', 5'-CCCTCGTAGATTGGCACAGT-3' / 183 / real-time RT-PCR (qRT-PCR)
<i>AtPIP1;1</i> (AT3G61430)	5'-CTTGCTGCTCTTTACCATGTGG-3', 5'-AGCAACTAAGGACAAGGCCAG-3' / 121 / qRT-PCR
	5'-ATGGAAGGCAAGGAAGAAG-3', 5'-GCTTCTGGACTTGAAGGG-3' / 858 / RT-PCR for Northern blotting
<i>AtPIP1;2</i> (AT2G45960)	5'-ACTACCTGTGTGTAACGTGTGT-3', 5'-TGCCTGCTTGAGATAAACCCA-3' / 159 / qRT-PCR
	5'-ATGGAAGGTAAAGAAGAAGA-3', 5'-TCCGATAATTGAAACCTTAC-3' / 822 / RT-PCR for Northern blotting
<i>AtPIP1;3</i> (AT1G01620)	5'-TTTGCTGTGGATGATCTGGT-3' 5'-CGAGAAACCAAGCCGAAACA-3' / 188 / qRT-PCR
	5'-ATGGAAGGGAAGAAGAGG-3' 5'-GGATCTGGACTTGAATGGAA-3' / 858 / RT-PCR for Northern blotting
<i>AtPIP1;4</i> (AT4G00430)	5'-(1056)TGGCAAAGGGTCTCTGAAGTC(1076)-3', 5'-(1234)CCCCACATTCACGAAGTCA(1215)-3' / 179 / qRT-PCR
	5'-ATGGAAGGCAAAGAAGAAGATG-3', 5'-CTAACTCTTGCTCTTGAAAGGA-3' / 864 / RT-PCR for Northern blotting
	5'-GGATGGAAGGCAAAGAAGAA-3', 5'-CGACTCTTGCTC TTGAAAGGA-3' / 864 / hybridization probe
	5'-GGGGTACCATGGAAGGCAAAGAAGAA-3' (<i>Kpn</i> I), 5'-CGGGATCCACTCTTGCTC TTGAAAGGA-3' (<i>Bam</i> H I) / 864 / CDS cloning by RT-PCR and overexpression construction
<i>AtPIP1;5</i> (AT4G23400)	5'-AAGTTGGTGGTGATAGAGTGAG-3', 5'-TGGTTCCTTATAGTCCTTGCTCTCC-3' / 136 / qRT-PCR
	5'-ATGGAAGGCAAAGAAGAA-3',

	5'-TGTCTTGGACTTGAAAGG-3' / 861 / RT-PCR and Northern blotting
<i>AtPIP2;1</i> (AT3G53420)	5'-GCTGCCAACGTCTAAACACA-3', 5'-ACACAACGCATAAGAACCTCT-3' / 232 / qRT-PCR
	5'-ATGGCAAAGGATGTGGAA-3', 5'-GACGTTGGCAGCACTTCTG-3' / 861 / RT-PCR and Northern blotting
<i>AtPIP2;2</i> (AT2G37170)	5'-CAACGTTTGTAGTTTTTGCCAC-3', 5'-CATTGGCATTGGCACATAATCA-3' / 187 / qRT-PCR
	5'-ATGGCCAAAGACGTGGAAG-3', 5'-AACGTTGGCTGCACTTCTG -3' / 855 / RT-PCR and Northern blotting
<i>AtPIP2;3</i> (AT2G37180)	5'-TCCACTCGTATCTTAGCTTCTTCC-3', 5'-ACACCAAACCTACATACGTTGC-3' / 111 / qRT-PCR
	5'-ATGGCTAAAGACGTGGAAG-3', 5'-AACGTTGGCTGCACTTCT-3' / 855 / RT-PCR for Northern blotting
<i>AtPIP2;4</i> (AT5G60660)	5'-AGAAACATATCCTCTTTTCCACTCG-3', 5'-CGTTGCAAAGATGAATTGAAAAACA-3' / 112 / qRT-PCR
	5'-ATGGCAAAGACTTGGATG-3', 5'-AGCAAAGCTCCTAAAGGAG-3' / 873 / RT-PCR for Northern blotting
<i>AtPIP2;5</i> (AT3G54820)	5'-ACCTGAACCTCTATTTCGACGC-3', 5'-CACTGGTCAGGATTCAGGGCT-3' / 159 / qRT-PCR
	5'-ATGACGAAGGAAGTGGTTGG-3', 5'-AACGTGAGGCTGGCTCCT-3' / 858 / RT-PCR for Northern blotting
<i>AtPIP2;6</i> (AT2G39010)	5'-ATTCTTTGGGCCAGGAAGGG-3', 5'-TCCCCACAAAGCCACAAAT-3' / 129 / qRT-PCR
	5'-ATGACGAAGGATGAGTTGACG-3', 5'-AGCATGGAGCTCATGAAGC-3' / 867 / RT-PCR for Northern blotting
<i>AtPIP2;7</i> (AT4G35100)	5'-TGAGAGAGATGGTGGATTGATGT-3', 5'-AGAGAAACCAAAGGCAAACGA-3' / 105 / qRT-PCR
	5'-ATGTCGAAAGAAGTGAGCG-3', 5'-ATTGGTTGCGTTGCTTCG-3' / 840 / RT-PCR for Northern blotting
<i>AtPIP2;8</i> (AT2G16850)	5'-TCATCTTTGTCCGTTGCTTTCT-3', 5'-TGCATGTGGGTTTATATAAACTTG-3' / 106 / qRT-PCR
	5'-ATGTCAAAGAAGTGAGTGAAG-3', 5'-ATTGGTTGGGTTGCTGC-3' / 834 / PCR for Northern blotting
<i>ARPI</i> (AT5G44300)	5'-CCATCTCCGACGAATCTCCA-3', 5'-CCACTTCCGACCAGATCCT-3' / 131 / qRT-PCR
<i>GFP</i> (U56995)	5'-TGCTCTAGAAATGGTGAGCAAGGGCGAGGAGC-3' (<i>Xba</i> 1), 5'-ACGCGTCTGACTTACTTGTACAGCTCGTCCATGCCGAGA-3' (<i>Sal</i> 1) / 738 bp / cloning and recombination

<i>GSL5</i> (AT4G03550)	5'-GATGGGATTTCCACCCTATACT-3', 5'-GTGCCAATGTCTGACCTCTGTA-3' / 166 / qRT-PCR
<i>MPK3</i> (AT3G45640)	5'-CTCACAATGAGGATGCGAAA-3', 5'-ATTCGGGTCGTGCAATTTAG-3' / 197 / qRT-PCR
<i>MPK6</i> (AT2G43790)	5'-CCCGACAGTGCATCCTTTAG-3', 5'-TGCAACGAGTTCAGGTATGG-3' / 114 / qRT-PCR
<i>NbEF1α</i> (AY206004)	5'-ACCCTTCTTGAGGCTCTTGAC-3', 5'-GTCAGACCAGTAGGTCCAAAGG-3' / 179/qRT-PCR
<i>NbRbohB</i> (AB079499)	5'-TTGGAACCAGTGTCGGAACC-3', 5'-CCAATAAAGCCAGCTCGGGA-3' / 150/ qRT-PCR
<i>NbWIPK</i> (AB098729)	5'-ATACGGAGCTGAATGAGATGGT-3', 5'-GTAACGGTGGAGGAATCACATC-3' / 156 / qRT-PCR
<i>NPRI</i> (At1G64280)	5'-CGACACTGCTGAGAAACGAC-3', 5'-CCGACGACGATGAGAGAGTT-3' / 182 / qRT-PCR
<i>PR-1</i> (At2G14610)	5'-TTCTTCCCTCGAAAGCTCAA-3', 5'-AAGGCCACCAGAGTGATG-3' / 174 / qRT-PCR
<i>PR-2</i> (At3G57260)	5'-ATTCGACGAAATCTCGACT-3', 5'-ATAGCTTCCCTGGCCTTCT-3' / 195 / qRT-PCR