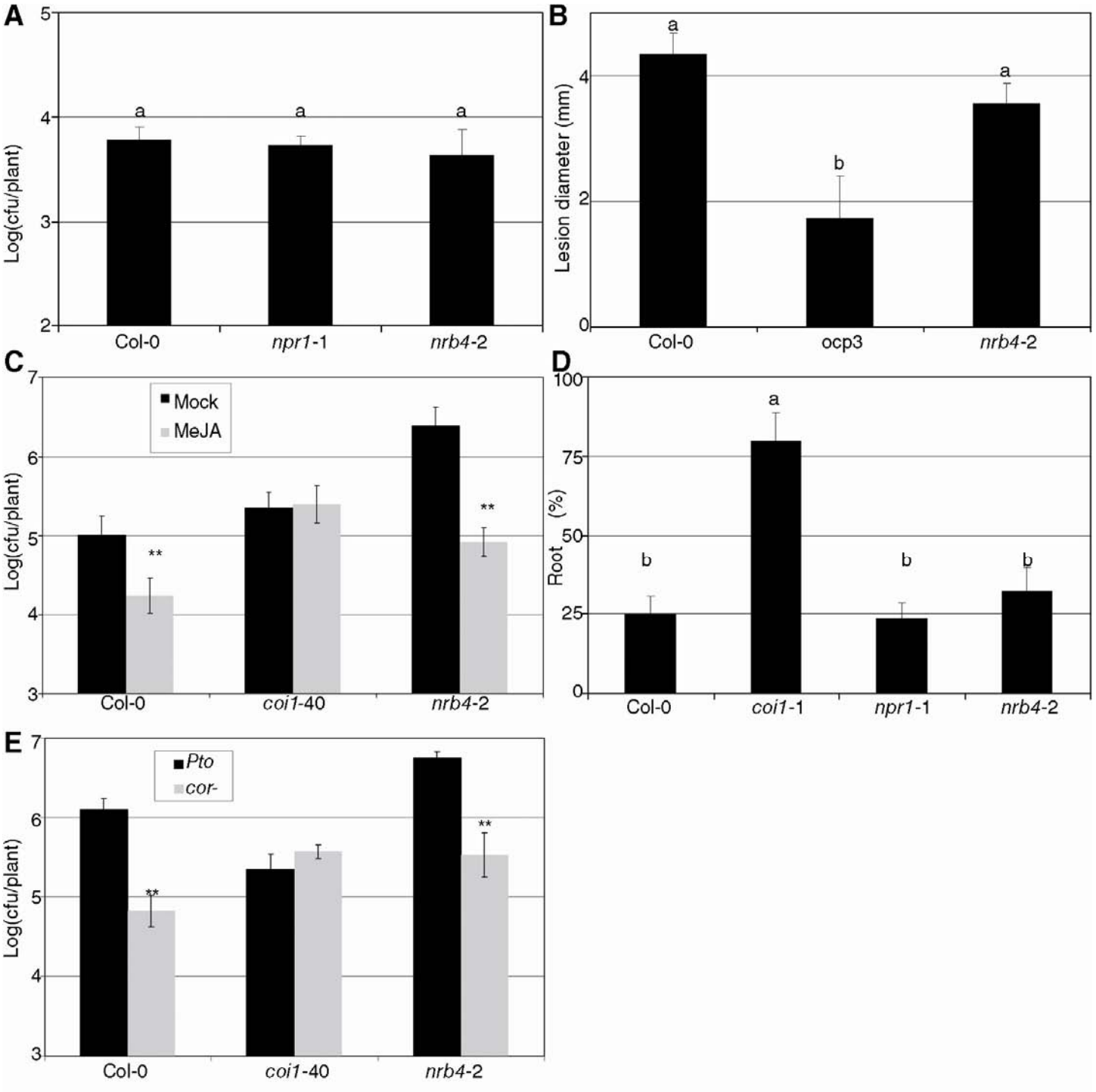
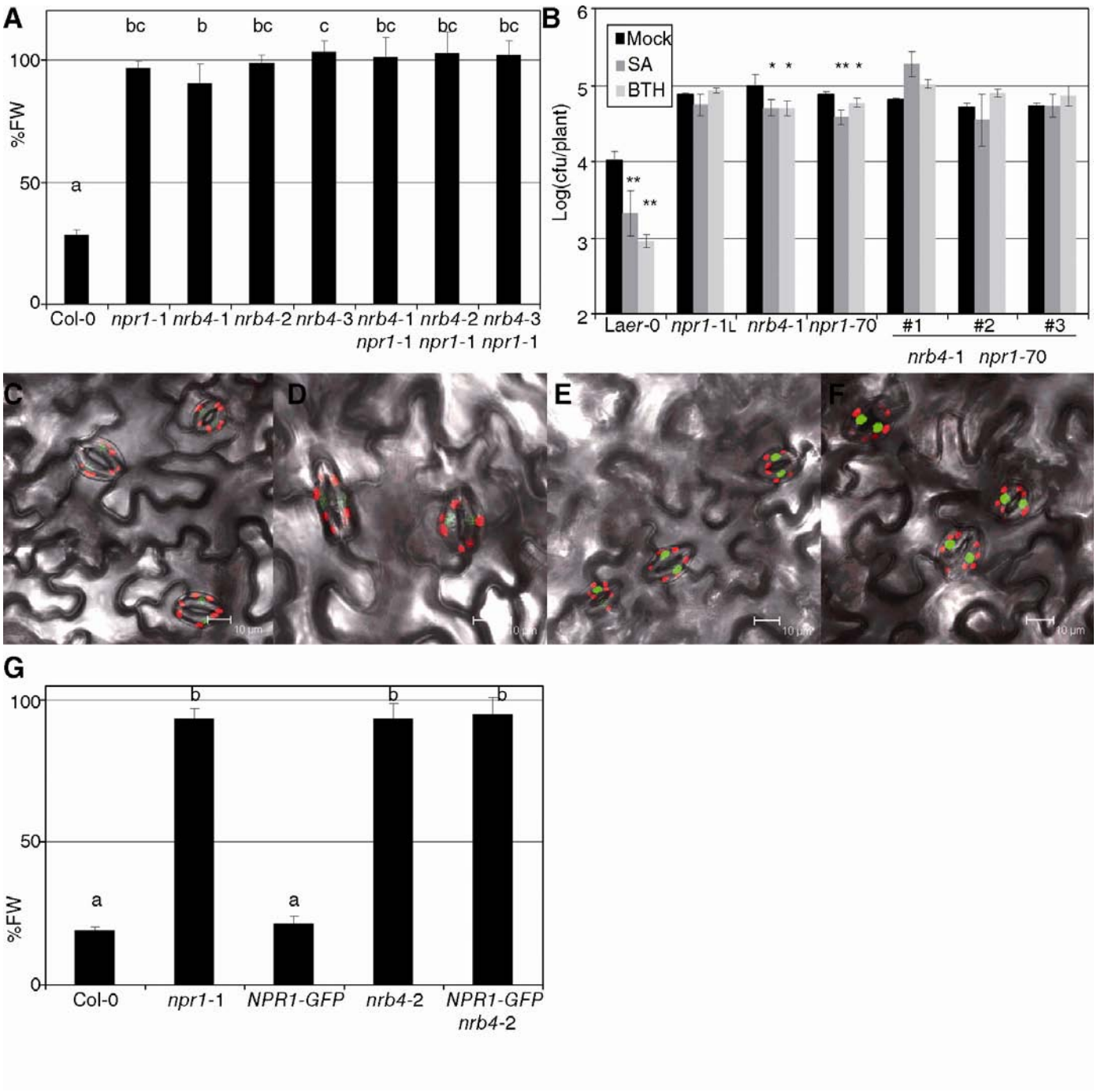
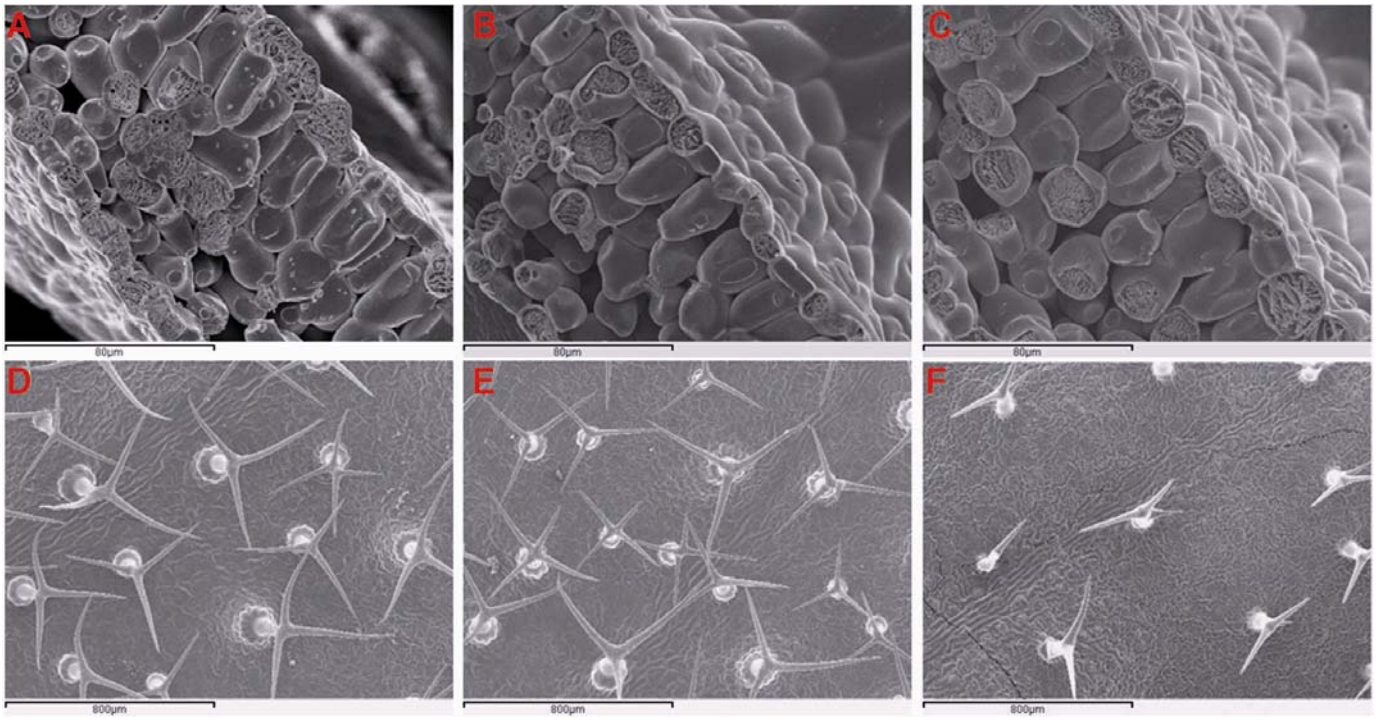

A
Log(cfu/plant)
5
4
3
2
a
a
a
Col-0
npr1-1
nrb4-2
B
Lesion diameter (mm)
4
2
0
a
b
a
Col-0
ocp3
nrb4-2
C
Log(cfu/plant)
7
6
5
4
3
Mock
MeJA
**
**
Col-0
coi1-40
nrb4-2
D
Root (%)
100
75
50
25
0
b
a
b
b
Col-0
coi1-1
npr1-1
nrb4-2
E
Log(cfu/plant)
7
6
5
4
3
Pto
cor-
**
**
Col-0
coi1-40
nrb4-2

**Supplemental Figure 1. Additional phenotypes of *nrb4* in defense. A** Responses to *Pto (hrpC-),* a strain that lacks virulence in Arabidopsis (Deng et al., 1998). 18-day-old plants were inoculated at an $OD_{600}$ of 0.1. Three days after inoculation, the growth of *Pto* was evaluated as Logarithm of colony forming units (cfu) per plant. **B** Inoculations with *Plectosphaerella cucumerina*. *P. cucumerina* was provided by Brigitte Mauch-Mani (University of Neuchatel, Switzerland), and used as described (Ton and Mauch-Mani, 2004). **C** Response to Methyl Jasmonate (MeJA) induced resistance. MeJA was applied by spray at 100 µM in 0.1% DMSO and 0.02% Silwet L-77 one day before *Pto* inoculation. **D** Responses to JA-Ile in the length of roots. Plants were grown in Johnson's media (Johnson et al., 1957) with 1 mM $KH_2PO_4$, with or without 50 µM MeJA (Duchefa). The length of the roots was measured with ImageJ software (MIH, Bethesda, MD, USA). **E** Responses to coronatine. *Pto(cfa* $^{-}$*)* a strain that lacks coronatine (Mittal and Davis, 1995) was inoculated, along *Pto*, as indicated in A. The experiments were repeated three times with similar results, and the data represent the average, with the error bars plotting the standard deviation of 15 plants in three groups of five. The letters above the bars indicate different homogeneous groups with statistically significant differences (Fisher's LSD Test, $P < 0.05$). Asterisks indicate statistically significant differences from the mock treatment ($P < 0.05$ one asterisk, $P < 0.01$ two) using the Student's t test (one tail).

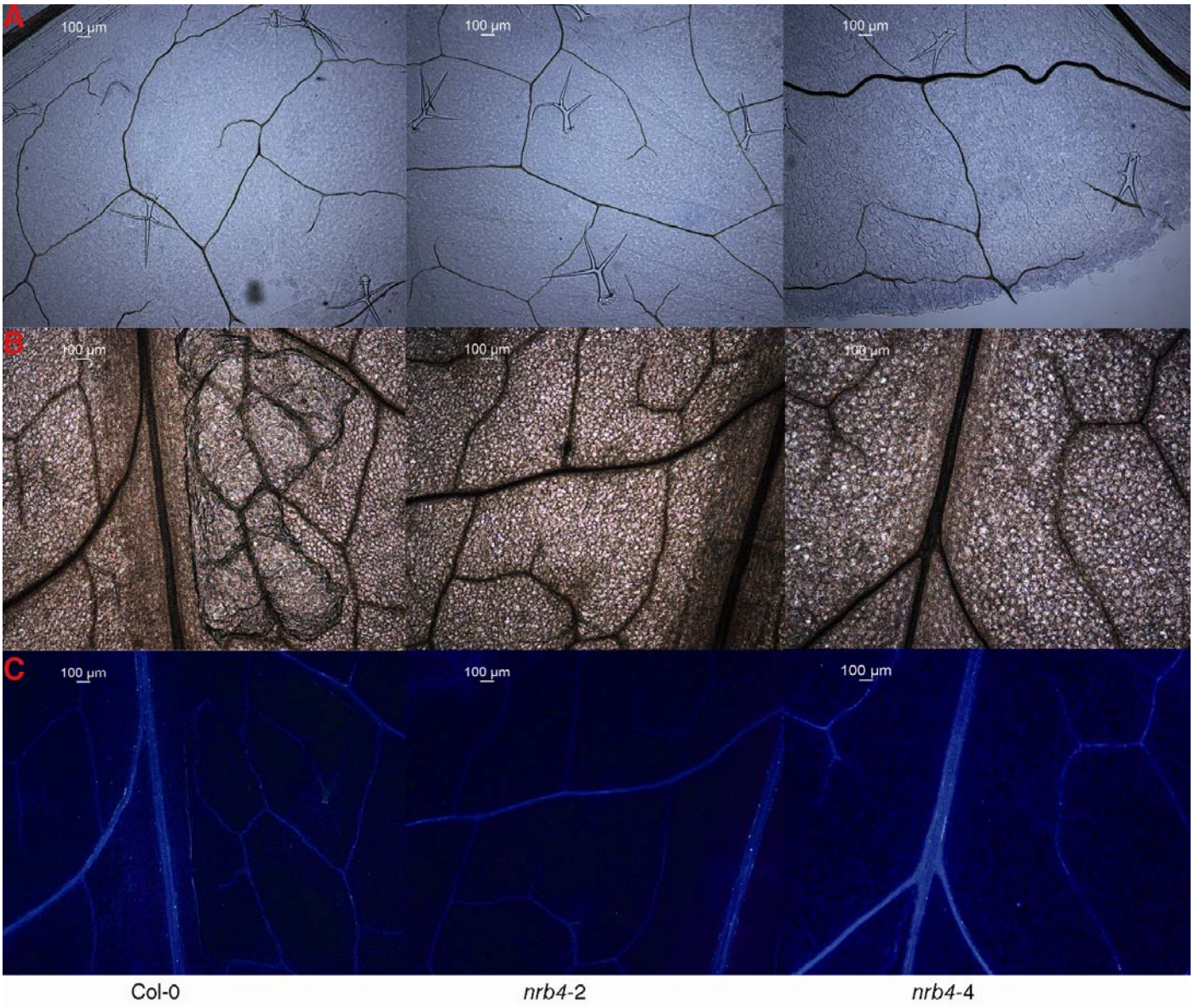

A
%FW
100
50
0
a
bc
b
bc
c
bc
bc
bc
Col-0
npr1-1
nrb4-1
nrb4-2
nrb4-3
nrb4-1 npr1-1
nrb4-2 npr1-1
nrb4-3 npr1-1
B
Log(cfu/plant)
6
5
4
3
2
Mock
SA
BTH
**
**
* *
** *
Laer-0
npr1-1L
nrb4-1
npr1-70
#1
#2
#3
nrb4-1 npr1-70
C
D
E
F
10 µm
G
%FW
100
50
0
a
b
a
b
b
Col-0
npr1-1
NPR1-GFP
nrb4-2
NPR1-GFP nrb4-2

**Supplemental Figure 2. Epistasis of *NRB4* with *NPR1*. A** Three double mutants *nrb4 npr1*-1 and their controls were treated with either mock or 350 µM BTH four times over three weeks, their weights recorded, and the ratio between the BTH and mock treated plants calculated (15 plants in three groups of five). The ratio is expressed as percentage of fresh weight (%FW). **B** Three double mutants *nrb4-1 npr1*-70 were tested for its response to SA and BTH upon *Pto* inoculation. **C** Confocal image of Arabidopsis *35S:NPR1-GFP* in an *npr1*-1 background in mock conditions. **D** Same transgenic in an *nrb4*-2 *npr1*-1 background in mock conditions. **E**. The same line as in C, one day after 350 µM BTH treatment. **F** The same line as in D, one day after 350 µM BTH treatment. **G** The lines described above were tested for its response to BTH. The overexpression of *NPR1*, even if it is detected in the nucleus (F), did not complement the mutation *nrb4*-2. The experiments were repeated three times with similar results, and the data represent the average, with the error bars plotting the standard deviation of 15 plants in three groups of five. The letters above the bars indicate different homogeneous groups with statistically significant differences (Fisher's LSD Test, $P < 0.05$). Asterisks indicate statistically significant differences from the mock treatment ($P < 0.05$ one asterisk, $P < 0.01$ two) using the Student's t test (one tail).

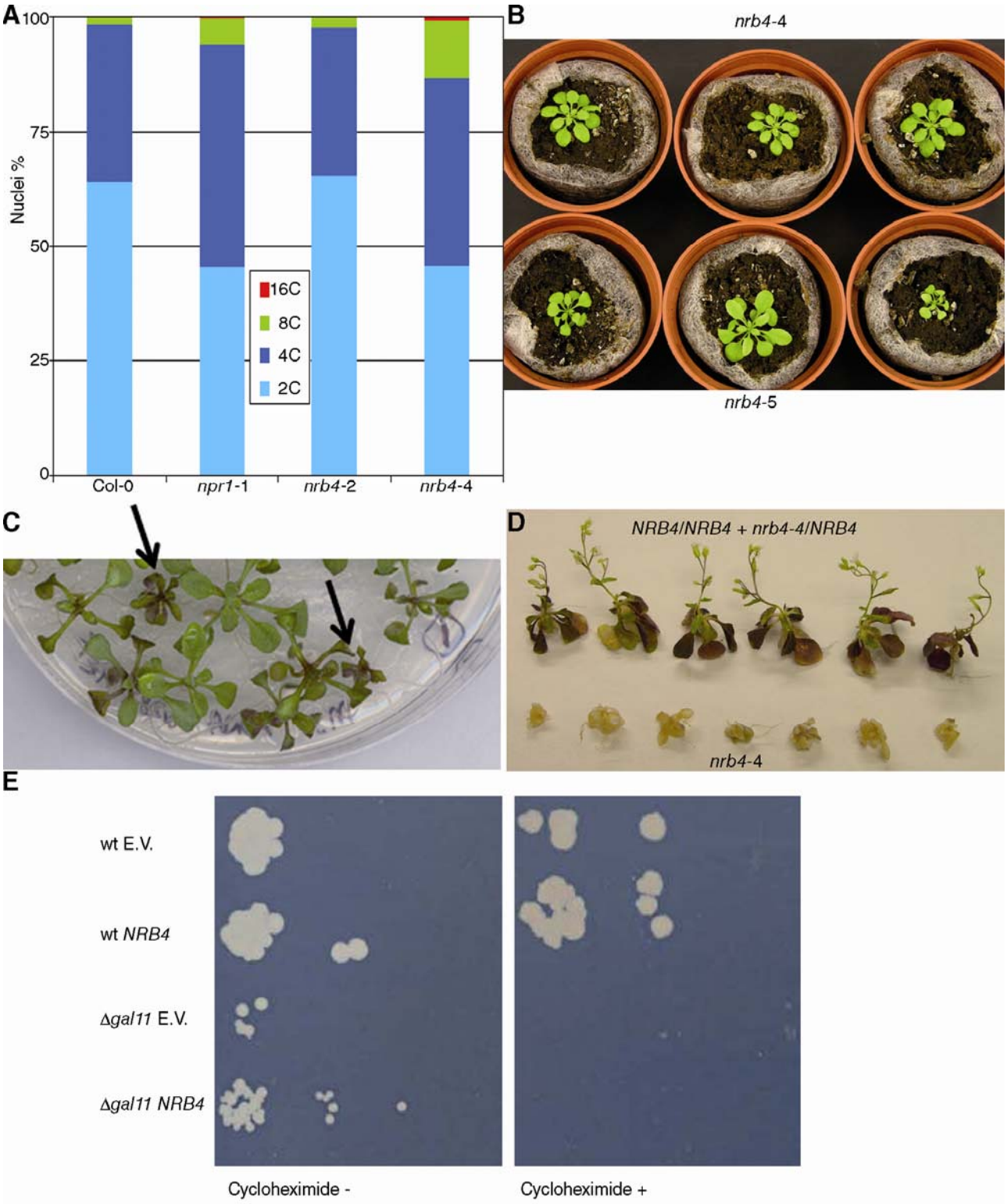

**Supplemental Figure 3. Additional pictures of *nrb4*-4. A** Wild type plant, growing seven weeks in short day and six weeks in long day with no treatment or inoculation. **B** *nrb4*-4 plant of the same age, growing in the same conditions. **C** *nrb4*-4 plant growing seven weeks in short day and eleven weeks in long day, as in A. **D** Detail of the plant in C, note the absence of flowers. **E** *nrb4*-4 plant with flowers. **F** Detail of the plant in E. As a reference, the pots have a diameter of 6 cm.



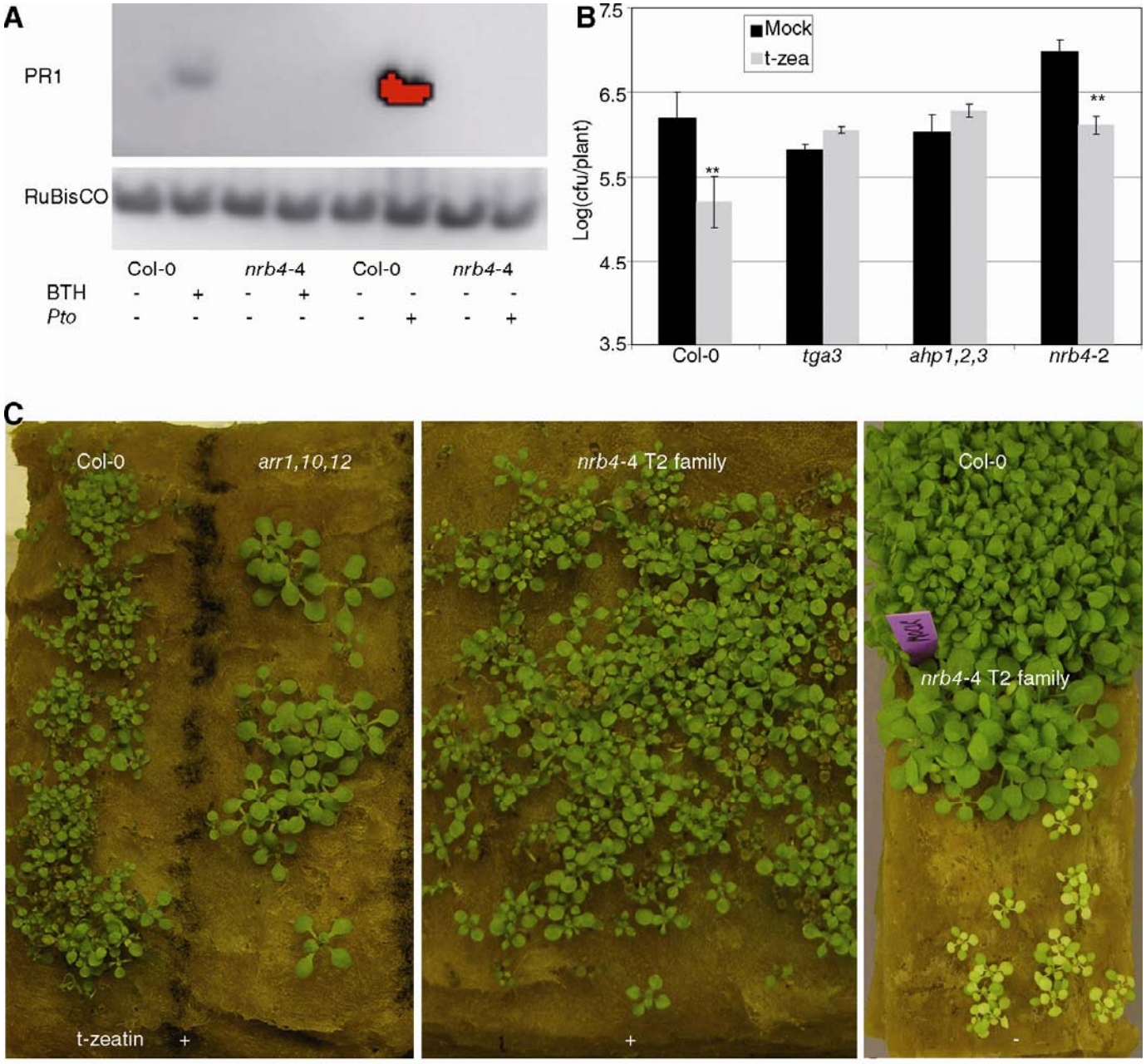

**Supplemental Figure 4. Additional pictures of Cryo-SEM**. **A** Section of Col-0. **B** Section of *nrb4*-2. **C** Section of *nrb4*-4. **D** Surface of a leaf from Col-0. **E** Idem from *nrb4*-2. **F** Idem from *nrb4*-4. The length of the bar in A, B, and C is 80 µm, and in D, E, and F is 800 µm. The leaves were five weeks old for Col-0 and *nrb4*-2 and seven weeks for *nrb4*-4.



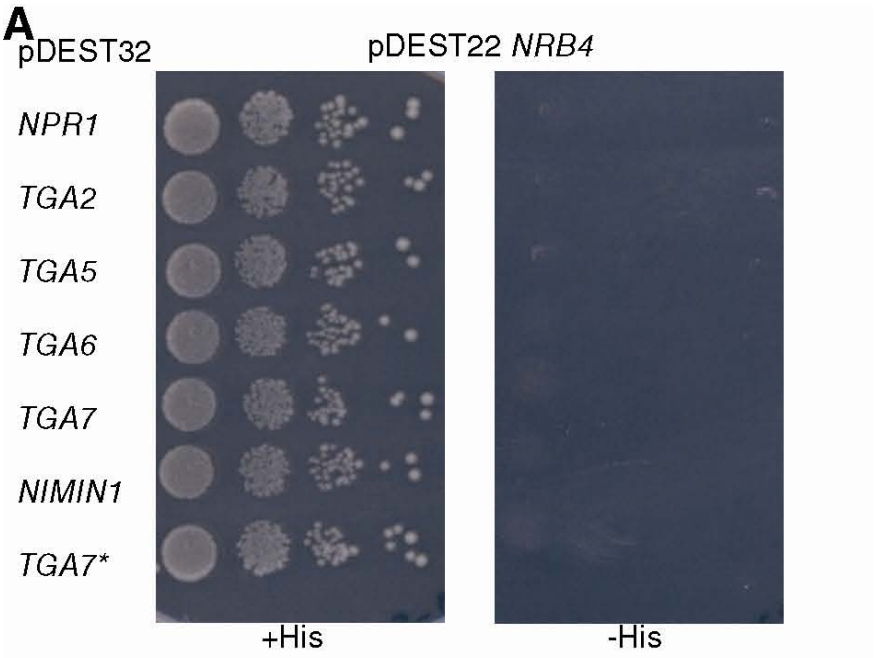

**Supplemental Figure 5. Stainings of *nrb4*.** **A** Trypan blue stains, unveiling cell death and membrane damage in Col-0, *nrb4*-2, and *nrb4*-4. **B** Aniline blue stains under visible light. **C** The same Aniline blue stains under ultraviolet light, which detects callose depositions. Trypan Blue and Aniline Blue staining were performed as described (Tornero et al., 2002; Conrath et al., 1989, respectively). No differences among genotypes were observed with these stains.

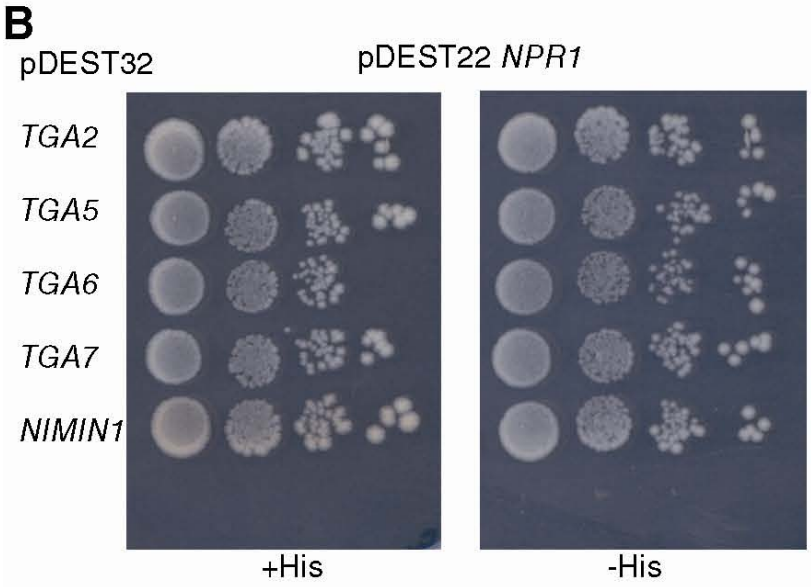

A
100
75
50
25
0
Nuclei %
16C
8C
4C
2C
Col-0
npr1-1
nrb4-2
nrb4-4
B
nrb4-4
nrb4-5
C
D
NRB4/NRB4 + nrb4-4/NRB4
nrb4-4
E
wt E.V.
wt NRB4
Δgal11 E.V.
Δgal11 NRB4
Cycloheximide -
Cycloheximide +

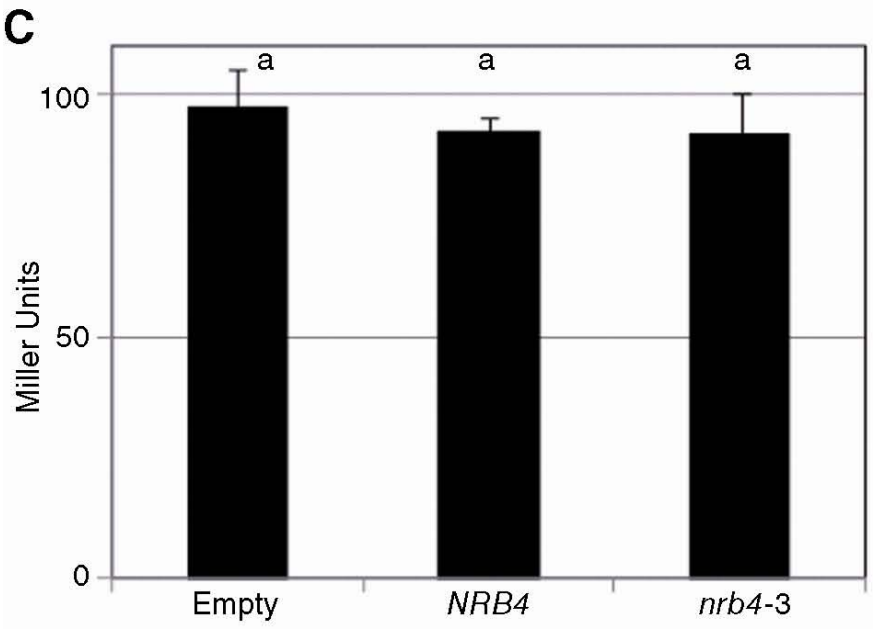
**Supplemental Figure 6. Characterization of *nrb4* null alleles. A** DNA content. Nuclei from the indicated genotypes were extracted, stained with DAPI, and the relative amount of DNA measured with a CyFlow Ploidy Analyzer (Partec GmbH, Münster Germany) following the manufacturer's instructions. At least 5000 nuclei were counted in each measurement, and the same result was obtained in three independent experiments. **B** Phenotypes of *nrb4*-5 in comparison to *nrb4*-4. **C** Phenotypes of a T2 segregating family of *nb4*-4/*NRB4* in MS plates. The arrows point to *nrb4*-4 homozygous plants (confirmed by PCR) Picture taken at two weeks of growing. **D** Plants selected in C were transferred to MS plates with 500 µM SA, and the picture was taken two weeks after the transfer. **E** Lack of complementation in yeast. Empty vector (E.V.) pAG423 (Alberti et al., 2007) and *NRB4* cloned in pAG423 were introduced in wild type (wt) and *Δgal11*. The different strains were grown in liquid and then plated in SD His- plates with or without cycloheximide (0.2µg/ml). The wt and *Δgal1l* strains were obtained from EUROSCARF (Ref. Y00000 and Y01742, respectively).


A
PR1
RuBisCO
Col-0
nrb4-4
Col-0
nrb4-4
BTH - + - + - - - -
Pto - - - - - + - +
B
Mock
t-zea
Log(cfu/plant)
7.5
6.5
5.5
4.5
3.5
**
**
Col-0
tga3
ahp1,2,3
nrb4-2
C
Col-0
arr1,10,12
t-zeatin +
nrb4-4 T2 family
+
Col-0
nrb4-4 T2 family
-

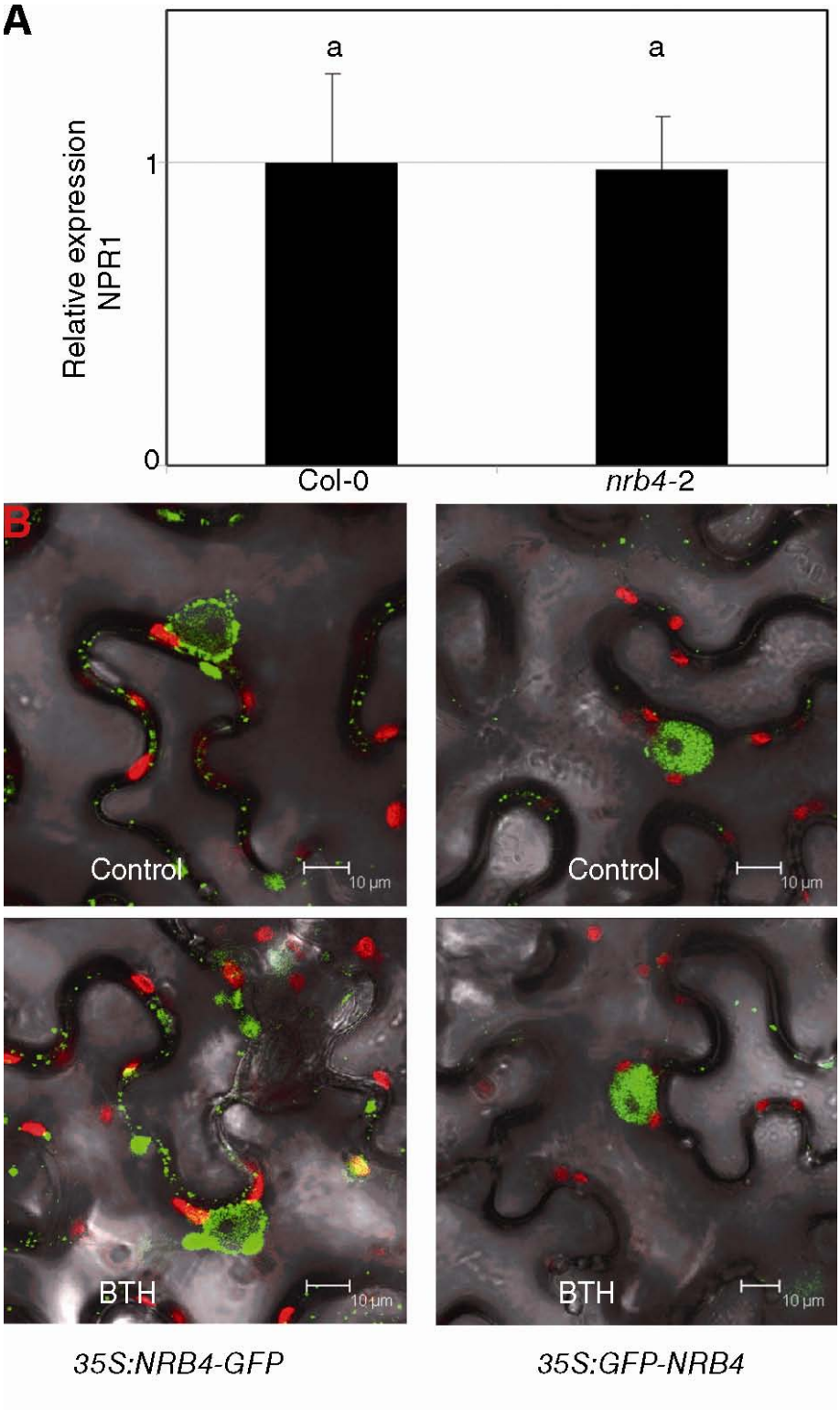
**Supplemental Figure 7. Phenotypes from the transcriptomic analysis. A** PR1 immunoblot of Col-0 and *nrb4*-4 three days after mock or a *Pto* inoculation and one day after mock or 350 µM BTH. The same blot was probed with anti-RuBisCO for loading and transfer control. The red color indicates saturation of the signal. **B** Resistance induced by cytokinins. Trans-zeatin (t-zea) 1 µM or a mock solution was applied one day previous to the inoculation with *Pto*. *tga3* (Choi et al., 2010) and *ahp1 ahp2 ahp3* (Hutchison et al., 2006, abbreviated as *ahp1,2,3*) were included as controls. **C** *nrb4*-4 did not have a specific phenotype with cytokinins. The controls Col-0 and *arr1 arr10 arr12* growing in 5 µM trans-zeatin (left) are the same as in Figure 6B. A T2 family, segregating for *nrb4*-4 (middle) did not produce plants with a different perception to cytokinins. Col-0 and the same T2 family of *nrb4*-4 plants growing in control conditions (right). In the case of *nrb4*-4, the space shown at the bottom of the picture was cleared of wild type plants, to check if the *nrb4*-4 homozygous plants can grow in this media. The experiments were repeated three times with similar results, and the data represent the average, with the error bars plotting the standard deviation of 15 plants in three groups of five. Asterisks indicate statistically significant differences from the mock treatment ($P < 0.05$ one asterisk, $P < 0.01$ two) using the Student's t test (one tail).


A
pDEST32
pDEST22 NRB4
NPR1
TGA2
TGA5
TGA6
TGA7
NIMIN1
TGA7*
+His
-His

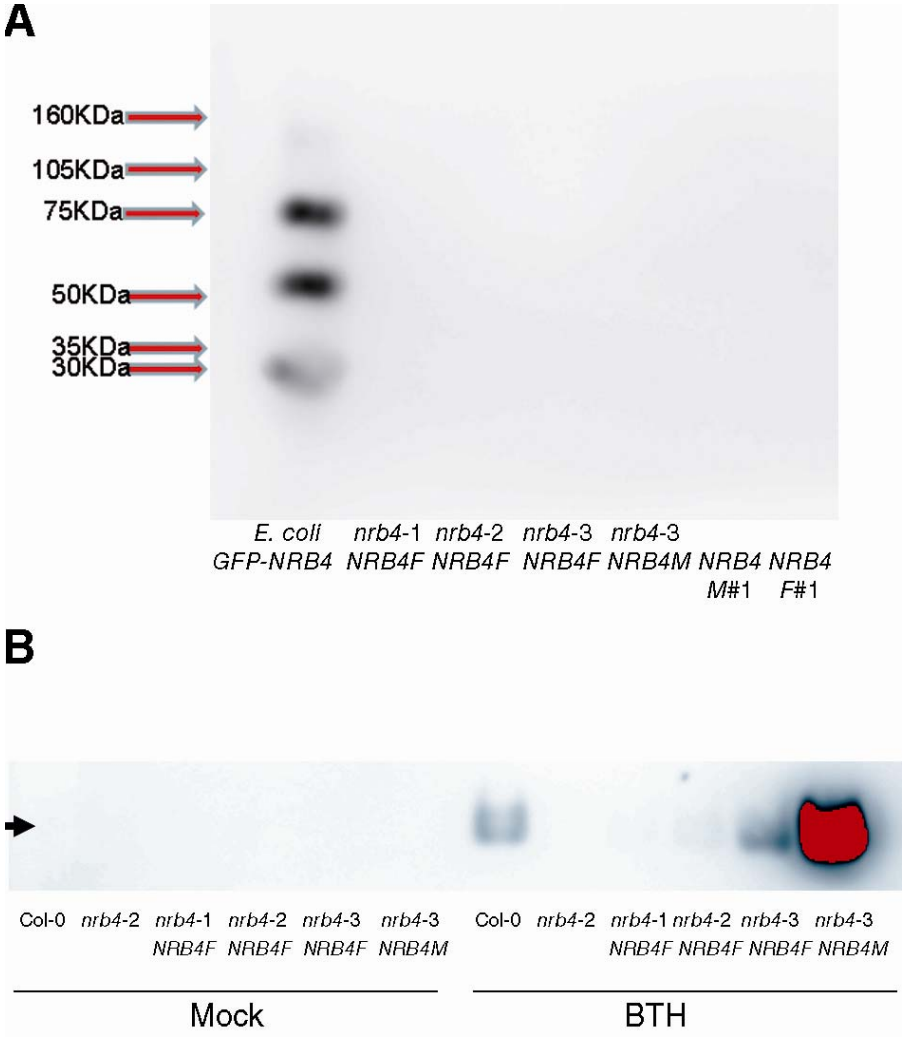

B
pDEST32
pDEST22 NPR1
TGA2
TGA5
TGA6
TGA7
NIMIN1
+His
-His


C
a
a
a
100
50
0
Miller Units
Empty
NRB4
nrb4-3

**Supplemental Figure 8. Yeast n-hybrid interactions. A** Interactions between NRB4 and proteins that have a role in SA perception. The yeasts that had NRB4 and any of these proteins were able to grow in His+ plates, but not in His- plates. Therefore, there was not detectable interaction. TGA7* stands for an additional control with an empty pDEST22, since TGA7 was able to autoactivate the system with no 3AT (the His- plates contained 5 mM 3AT). **B** As a control, interactions between NPR1 and the rest of proteins that have a role in SA perception. **C** NRB4 did not alter the interaction between NPR1 and TGA2. *NRB4* was cloned in a third vector, and introduced in the first yeast of B. There was no statistical difference between introducing *NRB4*, respect *nrb4*-3, or to the empty vector. All the plates were Lys-, Trp-, Leu-, and 100 µM SA. Similar experiments with no SA produced the same results. Similarly, bimolecular fluorescence complementation between *NRB4* and *NPR1* or *TGA2* did not produce a positive result in *Nicotiana benthamiana.* The pictures were taken 3-5 days after growing at 28°C. *NRB4* was cloned in three different versions for detection of interactions in the yeast two hybrid system: a short version, from 1 to 112 aa, included the KIX domain; an intermediate version, from 1 to 670 aa, spanned half of the coding sequence; and a full version. The full version when fused to the GAL4 BD was autoactivated, even with mutated versions of *NRB4* that recreated the EMS mutations herein described. The three versions of the wild type protein fused with the GAL4 AD were tested for interaction in yeast with genes described in SA response. The experiment shown in this figure corresponds to the full version of NRB4. The experiments were repeated three times with similar results, and the data represent the average, with the error bars plotting the standard deviation of three colonies. The letters above the bars indicate different homogeneous groups with statistically significant differences (Fisher's LSD Test, $P < 0.05$).


A
a
a
Relative expression NPR1
1
0
Col-0
nrb4-2
B
Control
10 µm
Control
10 µm
BTH
10 µm
BTH
10 µm
35S:NRB4-GFP
35S:GFP-NRB4

**Supplemental Figure 9. Expression of *NPR1* and *NBR4*. A** *NPR1* was detectable in *nrb4*-2 at normal levels. The levels of expression of *NPR1*, measured by RT-qPCR, are normalized to three reference genes and to the level of Col-0. The RNA was extracted from three-week-old plants, from three independent samples of 100 mg each. **B** The nuclear localization did not change with the application of 350 µM BTH. *35S:NRB4-GFP* (left) and *35S:GFP-NRB4* (right) were infiltrated in *N. benthamiana*. Then, a mock or a 350 µM BTH was applied one day before these pictures were taken. The controls correspond to the Figure 7C and D, respectively. The experiments were repeated three times with similar results, and the data represent the average, with the error bars plotting the standard deviation of three independent RT-qPCRs. The letters above the bars indicate different homogeneous groups with statistically significant differences (Fisher's LSD Test, $P < 0.05$).




**Supplemental Figure 10. Characterization of *NRB4* complementation. A** In the stable transgenic lines, GFP was not detectable by immunoblot. A immunoblot with antibody raised against GFP (Roche, Madrid, Spain) was performed in different extracts. The first line of the immunoblot is a *GFP-NRB4* fusion expressed in *E. coli*, which shows partial processing. The rest of lines correspond to plant extracts from the same lines described in Figure 8. The arrows point the position of the weight markers. **B** The complemented *nrb4* alleles express PR1 upon BTH application. The lines described in Figure 8 were treated with BTH and PR1 detected as in Figure 2B. There is a low expression of PR-1 in the lines that contain *35S:NRB4-GFP* (*NRB4F*) in *nrb4*-1 and *nrb4*-2, a expression similar to Col-0 in the *35S:NRB4* in *nrb4*-3, and a very strong expression in the lines that overexpress the first 670 AA of NRB4 plus GFP (*NRB4M*) in *nrb4*-3. The red color indicates saturation of signal.

**Supplemental Table 1. Evaluation of segregations.**

| **Population** | **Observed** | | | **Expected** | | | | |
|---|---|---|---|---|---|---|---|---|
| | | | | **(3/4)** | **(1/4)** | | | |
| | **wt** | **mut** | **Total** | **wt** | **mut** | **$\chi^2$** | **d.f.** | **p** |
| F2 Col-0 x *nrb4*-1 | 297 | 108 | 405 | 303.75 | 101.25 | 0.600 | 1 | 0.44 |
| F2 Col-0 x *nrb4*-2 | 248 | 87 | 335 | 251.25 | 83.75 | 0.168 | 1 | 0.68 |
| F2 Col-0 x *nrb4*-3 | 345 | 104 | 449 | 336.75 | 112.25 | 0.808 | 1 | 0.37 |
| | | | | **(1/2)** | **(1/2)** | | | |
| F1 *nrb4*-4 het x *nrb4*-1 | 25 | 23 | 48 | 24 | 24 | 0.083 | 1 | 0.77 |
| F1 *nrb4*-4 het x *nrb4*-2 | 26 | 30 | 56 | 28 | 28 | 0.286 | 1 | 0.59 |
| F1 *nrb4*-4 het x *nrb4*-3 | 28 | 30 | 58 | 29 | 29 | 0.069 | 1 | 0.79 |
| | | | | **(3/4)** | **(1/4)** | | | |
| F1 *nrb4*-5 het x *nrb4*-4 het | 40 | 11 | 51 | 38.25 | 12.75 | 0.320 | 1 | 0.57 |

Segregations observed in the indicated populations. The phenotypic classes were evaluated with the $\chi^2$ statistics. The p value gives the probability that any deviation from expected results is due to chance only. Since in all the cases the p value is bigger than the standard value of 0.05, the segregations fit the proposed model.

**Supplemental Table 2. Evaluation of phenotypes in T-DNA insertion lines.**

| AGI | NASC | T-DNA | Status | Position | Phenotype (% wt) |
|---|---|---|---|---|---|
| | Col-0 | | | | 100 |
| | *npr1*-1 | | Homoz | | 0 |
| AT1G07950 | N656591 | SALK_065283C | Homoz | Exon | 100 |
| AT1G11760 | N665553 | SALK_023845C | Homoz | 5' | 100 |
| AT1G11760 | N678300 | SALK_028490C | Homoz | 5' | 100 |
| AT1G15780 | N835429 | SAIL_792_F02 | Heteroz | Intron, *nrb4*-4 | 75 |
| AT1G15780 | | GABI_955_E02 | Heteroz | Intron, *nrb4*-5 | 75 |
| AT1G16430 | N870082 | SAIL_9_E04 | Heteroz | Exon | 100 |
| AT1G23230 | N659417 | SALK_060062C | Homoz | Exon | 100 |
| AT1G23230 | N671536 | SALK_074015C | Homoz | Exon | 100 |
| AT1G25540 | N679089 | SALK_129555C | Homoz | Exon | 100 |
| AT1G25540 | N677751 | SALK_059316C | Homoz | Exon | 100 |
| AT1G26665 | | No info | | | |
| AT1G29940 | N876306 | SAIL_726_H01 | Heteroz | Exon | 100 |
| AT1G31360 | N661000 | SALK_087178C | Homoz | Exon | 100 |
| AT1G44910 | N521070 | SALK_021070 | Heteroz | Exon | 100 |
| AT1G54250 | N679260 | SALK_151800C | Homoz | Exon | 100 |
| AT1G55080 | N529118 | SALK_029118 | Heteroz | Exon | 100 |
| AT1G55325 | N861503 | SAIL_1169_H11 | Homoz | Exon | 100 |
| AT1G60850 | N655705 | SALK_088247 | Homoz | Exon | 100 |
| AT2G03070 | N682656 | SALK_092406C | Homoz | Exon | 100 |
| AT2G22370 | N677657 | SALK_027178C | Homoz | Intron | 100 |
| AT2G28230 | | No info | | | |
| AT2G29540 | N507414 | SALK_007414 | Heteroz | Exon | 100 |
| AT2G38250 | N667374 | SALK_133090C | Homoz | 5' | 100 |
| AT2G48110 | N671698 | SALK_092499C | Homoz | 5' | 100 |
| AT2G48110 | N667838 | SALK_015532C | Homoz | Exon | 100 |
| AT3G01435 | | No info | | | |
| AT3G04740 | N521711 | SALK_021711 | Heteroz | Exon | 100 |
| AT3G09180 | N512449 | SALK_012449 | Heteroz | Exon | 100 |
| AT3G10690 | N506294 | SALK_006294 | Heteroz | 3' | 100 |
| AT3G21350 | N662531 | SALK_055723C | Homoz | 5' | 100 |
| AT3G21350 | N656864 | SALK_110696C | Homoz | 5' | 100 |
| AT3G23590 | N667150 | SALK_119561C | Homoz | Exon | 100 |
| AT3G23590 | N661810 | SALK_022477C | Homoz | Exon | 100 |
| AT3G25940 | N562311 | SALK_062311 | Heteroz | 3' | 100 |
| AT3G52860 | N685672 | SALK_037570C | Homoz | 5' | 100 |
| AT3G57660 | N673273 | SALK_116823C | Homoz | 3' | 100 |
| AT3G57660 | N673356 | SALK_122465C | Homoz | 3' | 100 |
| AT3G59600 | | No info | | | |

| | | | | | |
|---|---|---|---|---|---|
| AT4G00450 | N678935 | SALK_108241C | Homoz | Exon | 100 |
| AT4G04780 | | No info | | | |
| AT4G04920 | N548091 | SALK_048091 | Heteroz | Intron | 100 |
| AT4G09070 | N553156 | SALK_053156 | Heteroz | 3' | 100 |
| AT4G25210 | N599954 | SALK_099954 | Heteroz | Exon | 100 |
| AT4G25210 | N607213 | SALK_107213 | Heteroz | 5' | 100 |
| AT4G25630 | N682661 | SALK_093373C | Homoz | Exon | 100 |
| AT5G02850 | N622082 | SALK_122082 | Heteroz | Exon | 100 |
| AT5G02850 | N683125 | SALK_007367C | Homoz | 5' | 100 |
| AT5G03220 | N678464 | SALK_049958C | Homoz | 5' | 100 |
| AT5G03500 | N676132 | SALK_088220C | Homoz | Intron | 100 |
| AT5G12230 | N657910 | SALK_037435C | Homoz | 5' | 100 |
| AT5G12230 | N658182 | SALK_034955C | Homoz | Intron | 100 |
| AT5G19480 | | No info | | | |
| AT5G19910 | N682219 | SALK_035522C | Homoz | Exon | 100 |
| AT5G20170 | N663678 | SALK_111977C | Homoz | Exon | 100 |
| AT5G28540 | N675173 | SALK_054493C | Homoz | 3' | 100 |
| AT5G28540 | N675862 | SALK_079156C | Homoz | 5' | 100 |
| AT5G41010 | N549327 | SALK_049327 | Heteroz | Intron | 100 |
| AT5G41910 | N663226 | SALK_087920C | Homoz | 5' | 100 |
| AT5G41910 | N678994 | SALK_115673C | Homoz | 5' | 100 |
| AT5G42020 | N659850 | SALK_047956C | Homoz | Exon | 100 |
| AT5G42060 | N669407 | SALK_014079C | Homoz | 5' | 100 |
| AT5G63480 | N654793 | SALK_095631C | Homoz | Intron | 100 |
| AT5G64680 | N685462 | SALK_023879 | Homoz | 5' | 100 |
| AT5G67240 | N542641 | SALK_042641 | Heteroz | Exon | 100 |

Phenotypes observed in the indicated populations, either homozygous or heterozygous T-DNA insertions in Arabidopsis genes with homology with Mediator genes. The phenotypic classes were evaluated visually, as described by Canet et al., 2010.

**Supplemental Table 3. Lack of homologs in Arabidopsis for several nuclear receptors.**

| Name | Organism | AA | Max. E value | Identities | Positives |
|---|---|---|---|---|---|
| Pdr1p | Yeast | 1068 | 7.7 | 37/143 | 58/143 |
| PDR3p | Yeast | 976 | 2.3 | 27/99 | 47/99 |
| Oaf1p | Yeast | 1047 | 0.38 | 24/90 | 46/90 |
| PPARα | H. sapiens | 468 | 2.3 | 13/42 | 24/42 |
| NHR-49 | C. elegans | 501 | 0.41 | 18/62 | 29/62 |

The mentioned proteins were used to search in the Arabidopsis genome with BLASTP (TAIR10, www.arabidopsis.org), with the default settings. The column “AA” indicates the number of aa of the original protein. The “Max. E value” indicates the maximal E value obtained with BLASTP, while the “Identities” and “Positives” columns indicate the ratio of aa either identical or similar in the best stretch of homology.

**Supplemental Table 4. Primers used**

| Name | Sequence | Objective |
|---|---|---|
| 5249817-NlaIII-F | TGAGCAGCAAGAAAGATGATG | nrb4 mapping |
| 5249817-NlaIII-R | CTTAGCAGAGGTACGAGGATCA | nrb4 mapping |
| 5346165-DdeI-F | CACCAAACACCACACTTCTCA | nrb4 mapping |
| 5346165-DdeI-R | CATATCTTCAAAATCTTTGAGTTGG | nrb4 mapping |
| 5377218-NlaIII-F | CTGGATTTTGGTCGAGTTAGC | nrb4 mapping |
| 5377218-NlaIII-R | GTGGCAATAGAGGCACAAGT | nrb4 mapping |
| 5393430-CauI-F | GAAGAGTGGTTGCAAGCGTA | nrb4 mapping |
| 5393430-CauI-R | TTTTTGCGAGTCCACGTTC | nrb4 mapping |
| 5406030-NlaIII-F | AGTTGGTCGGAGCTTTTCCT | nrb4 mapping |
| 5406030-NlaIII-R | GATTCTCCACACCACCCACT | nrb4 mapping |
| 5425793-SecI-F | AGAACGAGCTCGAACACGAA | nrb4 mapping |
| 5425793-SecI-R | CTGAAACATTGAATCCCATTTG | nrb4 mapping |
| 5440252-MseI-F | TGCTTTCAATAATCGTTGTGTT | nrb4 mapping |
| 5440252-MseI-R | CACACCAAAACAAGCTTCTGC | nrb4 mapping |
| 5455705-HinfI-F | GAATCTTGATGCTTGCTTGG | nrb4 mapping |
| 5455705-HinfI-R | CCATGTCCGGGAAACTTATC | nrb4 mapping |
| 5494532-RsaI-F | GTTGATCGGAAAGGAAAAGTAAAA | nrb4 mapping |
| 5494532-RsaI-F | AAAAACGGATAACCAAACATGG | nrb4 mapping |
| F10B6.1-F | ATTATATTGTTCAACATCAACTGCACAT | nrb4 mapping |
| F10B6.1-R | TTTATCTCTTAAACAAGTTCGTAAACCAAC | nrb4 mapping |
| T16N11.1-F | AATAGATTAGAAATGAACAGGAGAATTGACT | nrb4 mapping |
| T16N11.1-R | TGGCATTTTAATAACATCCTCACC | nrb4 mapping |
| 15780.1 | TAACAAAAAATCCCAATCACGTGTG | NRB4 sequencing |
| 15780.2 | AACAATTGGAGGCCTTCTCTTCC | NRB4 sequencing |
| 15780.3 | AAATATTGCACGCCAACAAGCA | NRB4 sequencing |
| 15780.4 | AAGGCGTTCAATAGGCAGCTCA | NRB4 sequencing |
| 15780.5 | TATGCACAGGCCGAGGAAGC | NRB4 sequencing |
| 15780.6 | GCATCTGCGGATTTGTTTGG | NRB4 sequencing |
| 15780.7 | CAAGCCTCTGGTATCCATCAGC | NRB4 sequencing |
| 15780.8 | TCTGTTGGATGCCTGAGCTATTTG | NRB4 sequencing |
| 15780.9 | AATCTATGGATGTGCCATTATTAGCG | NRB4 sequencing |
| 15780.10 | TGCGCAGAATGGAAACACTAAA | NRB4 sequencing |
| 15780.11 | TTCCGGTGGGATTGGCTATT | NRB4 sequencing |
| 15780.12 | GAATGAAATCTACCAGAGAGTTGCA | NRB4 sequencing |
| 15780.13 | TGGTTTGGGACAGCAACGG | NRB4 sequencing |
| NRB4FP2-attb1 | GGGGACAAGTTTGTACAAAAAAGCAGGCTTCGAAG GAGATAGAACCATGGATAATAACAATTGGAGGCCT | NRB4 Cloning in pDONR221, C-terminal |
| NRB4RP1-attb2 | GGGGACCACTTTGTACAAGAAAGCTGGGTCTATGG ATGTGCCATTATTAGC | NRB4S Cloning in pDONR221 |
| NRB4RP2-attb2 | GGGGACCACTTTGTACAAGAAAGCTGGGTAAGCCA CCTTATCTTTTAATGC | NRB4M Cloning in pDONR221 |
| NRB4RP3-attb2 | GGGGACCACTTTGTACAAGAAAGCTGGGTGGGAAG CTGCTACATATTTCTC | NRB4F Cloning in pDONR221 |
| NRB4FP4-attb1 | GGGGACAAGTTTGTACAAAAAAGCAGGCTTCATGG ATAATAACAATTGGAGG | NRB4 Cloning in pDONR221, N-terminal |

| | | |
|---|---|---|
| qRT NPR1.1 | GAAGAATCGTTTCCCGAGTTCC | NPR1 RT-qPCR |
| qRT NPR1.2 | CATCACCGGGTGTAAAGATAGCA | NPR1 RT-qPCR |
| qRT NRB4.3 | TTGCCACCTGATTCTCGTCA | NRB4 RT-qPCR |
| qRT NRB4.4 | CTCTGGTCCGGAAAATGGAA | NRB4 RT-qPCR |

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