Supplemental Information

a. **Supplemental Figures**: Figures S1-S17
b. **Supplemental Tables:** Tables S1-S3
c. **Supplemental Text:** Materials and Methods

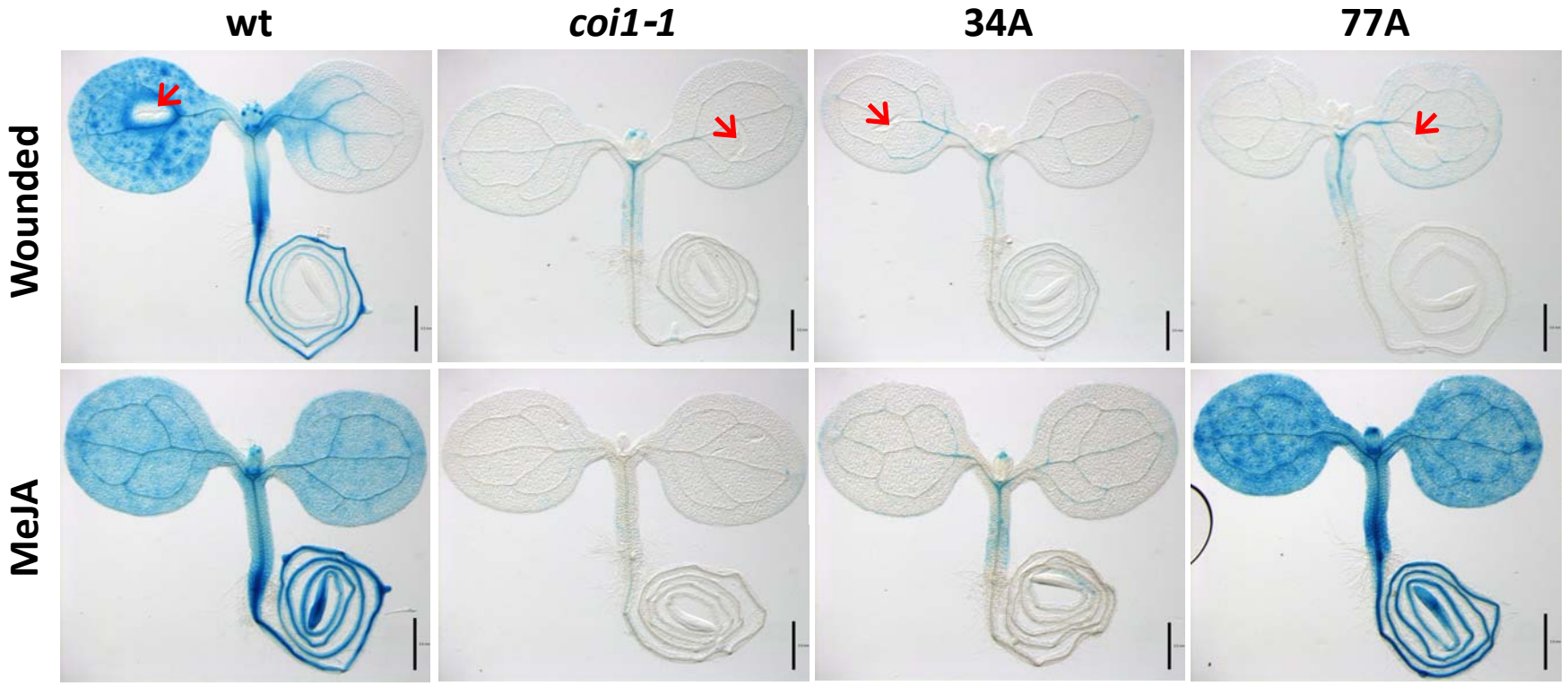

Figure S1. *JAZ10-GusPlus* expression in wt, *coi1-1*, 34A and 77A mutant seedlings 2 h after wounding (red arrows) or treatment with 10 µM methyl jasmonate (MeJA). Three other mutants (44B, 82B and 87A) were identical to *coi1-1* and 34A after treatments. Scale bars = 0.5 mm.

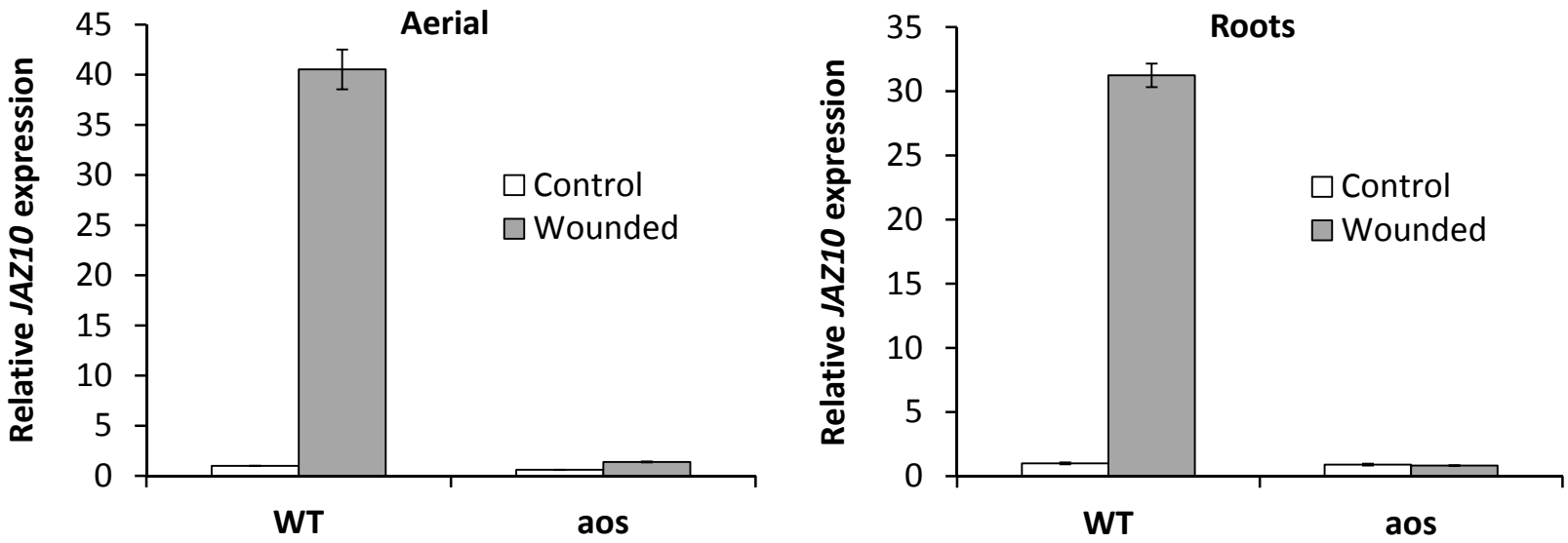

Figure S2. qRT-PCR of *JAZ10* expression 1 h after wounding in wt and *aos*. Quantification was performed separately for aerial organs and roots. *JAZ10* transcript levels were normalized to those of *UBC21* and displayed relative to the expression in the wt unwounded controls. Bars represent the means of two biological replicates (± SD), each containing a pool of organs from ~60 seedlings.

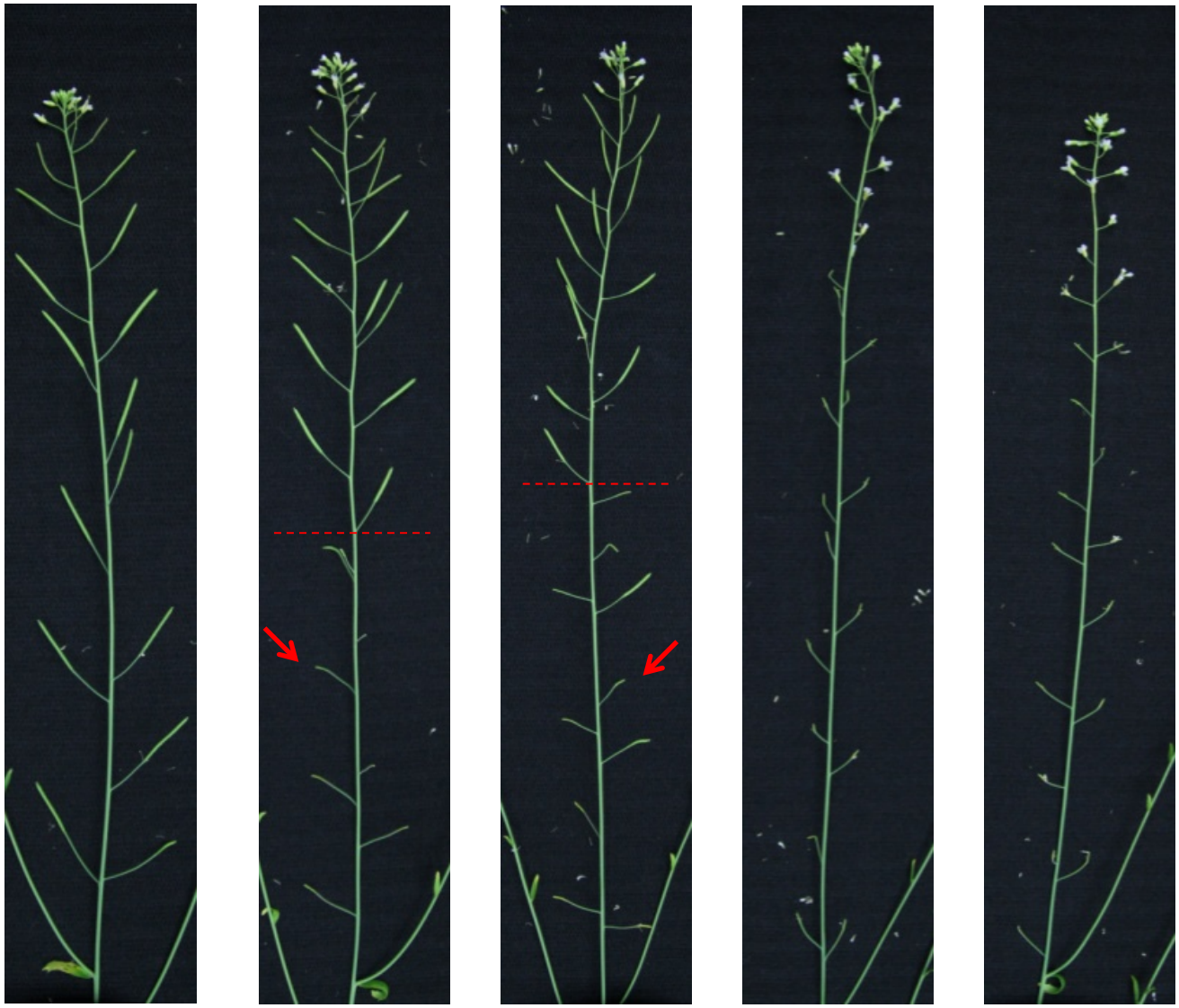

Figure S3. Inflorescences of wt and several mutant lines. The wt is fertile while *coi1-1* and *aos* are completely male sterile. In lines 34A (*coi1-34*) and 77A (*opr3-2*) only the first few flowers are male sterile (e.g. red arrows) and the rest (after red dotted line) are fertile.

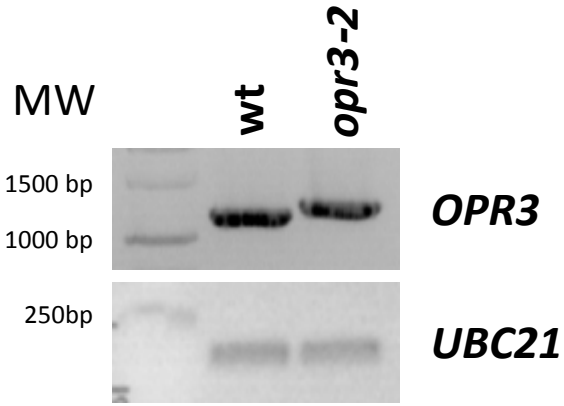

Figure S4. RT-PCR of *OPR3* transcripts in the wt and the *opr3-2* mutant. Note the larger size of the PCR product in the mutant sample. Sequencing of this amplicon revealed the presence of the last intron which remains unspliced due to a G to A transition in the donor splice site at position 1825 of the *OPR3* gene.

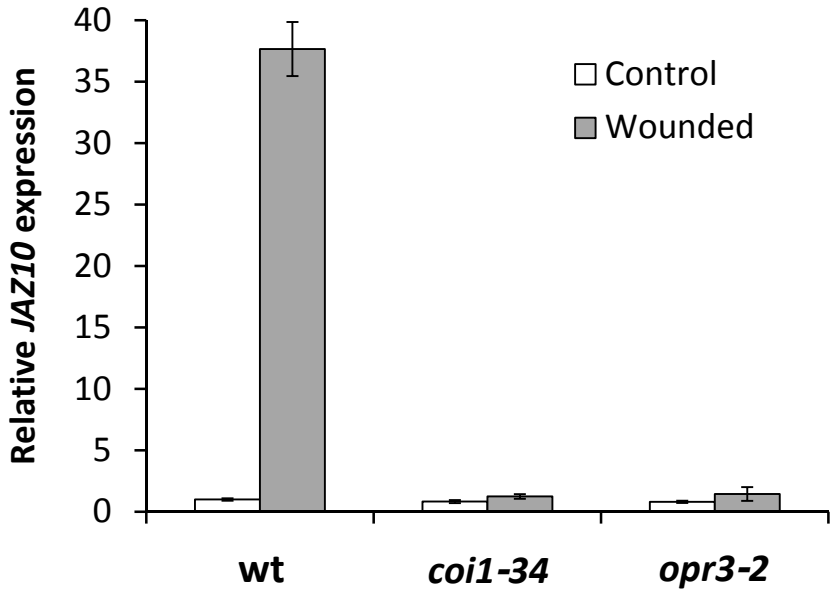

Figure S5. qRT-PCR of *JAZ10* expression 1 h after wounding in whole seedlings of wt, *coi1-34* and *opr3-2* seedlings. *JAZ10* transcript levels were normalized to those of *UBC21* and displayed relative to the expression in the wt control. Bars represent the means of three biological replicates (± SD), each containing a pool of organs from ~40 seedlings.

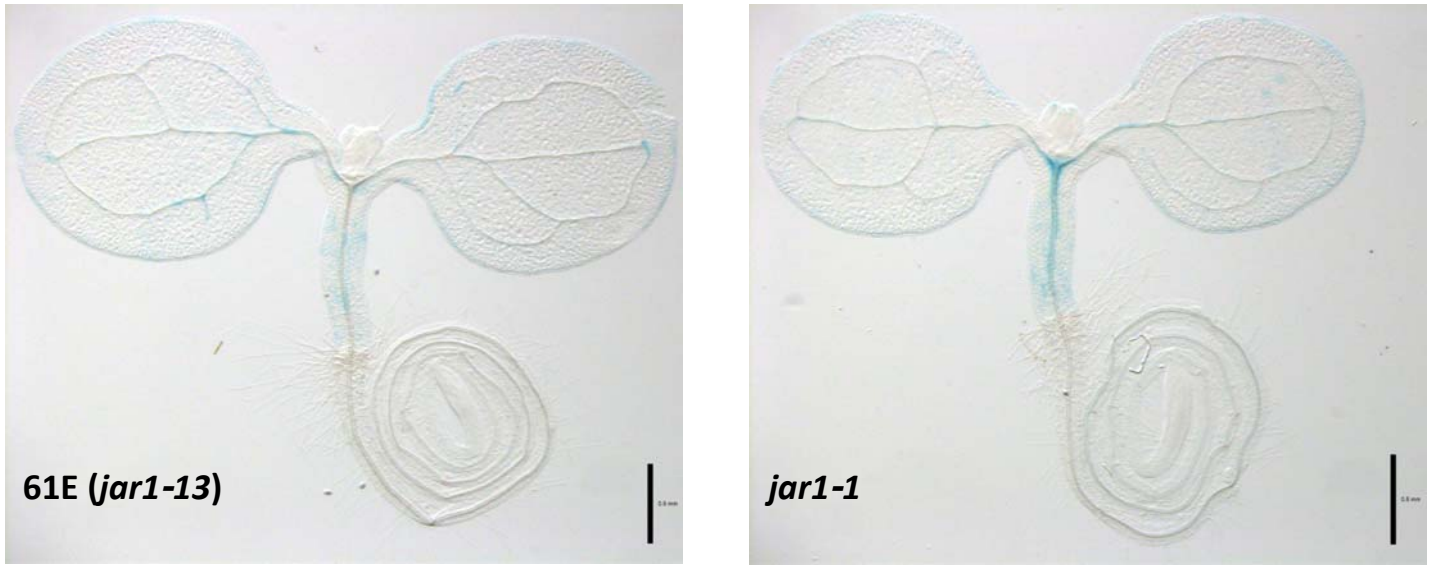

Figure S6. *JGP* expression in unwounded control 61E (*jar1-13*) and *jar1-1* seedlings. Scale bars = 0.5 mm.

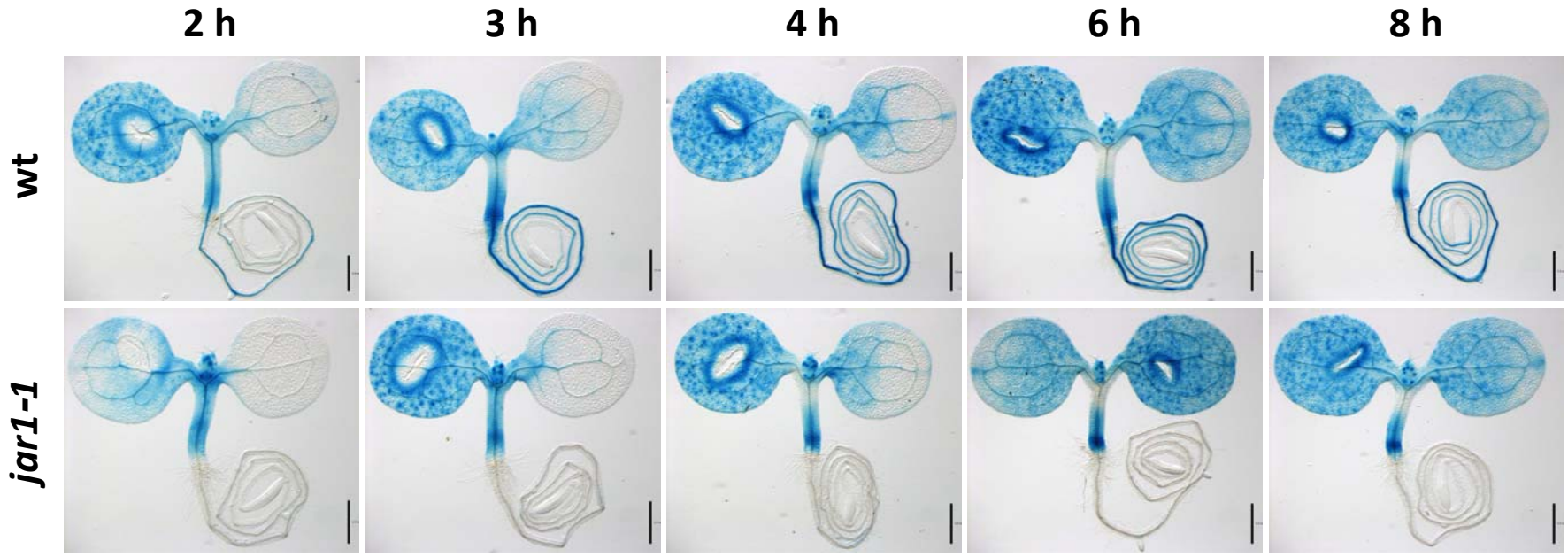

Figure S7. Progression of *JGP* expression at several time points after cotyledon wounding in wt and *jar1-1*. Note the lack of expression in *jar1-1* roots at all time points and the sharp separation between responsive and unresponsive tissues at the hypocotyl-root interface. Scale bars= 0.5 mm.

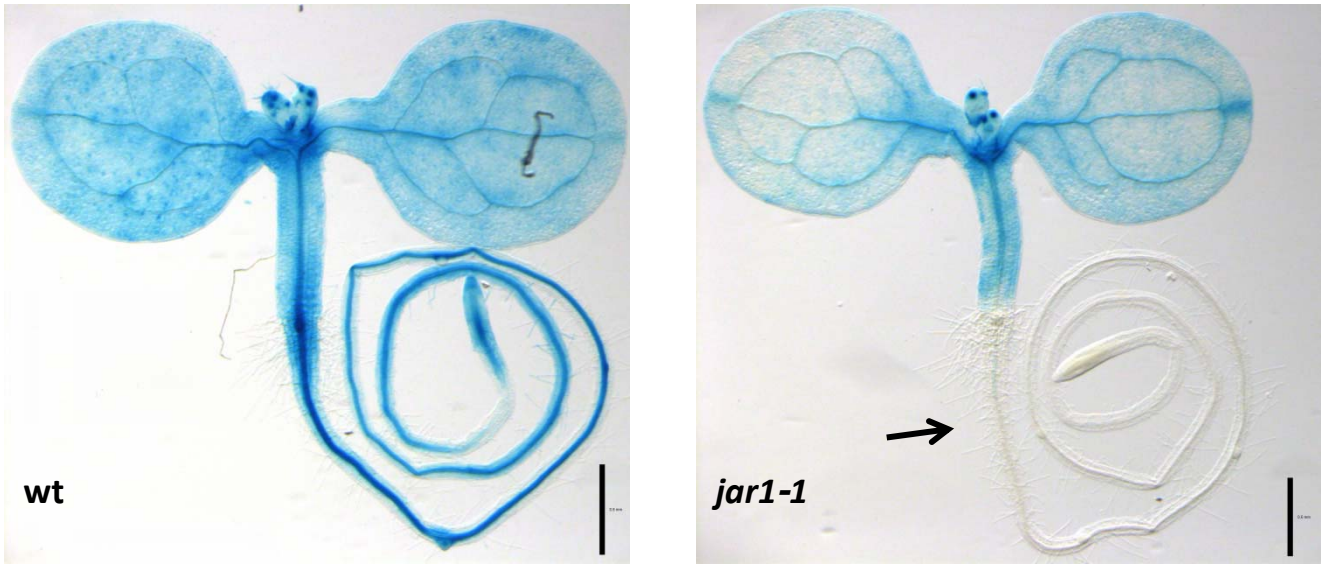

Figure S8. *JGP* expression in wt and *jar1-1* mutant seedlings after a 2 h treatment with 10 µM MeJA. Note the lack of expression in *jar1-1* roots (black arrow) and the slightly weaker response in its cotyledons. Scale bars = 0.5 mm.

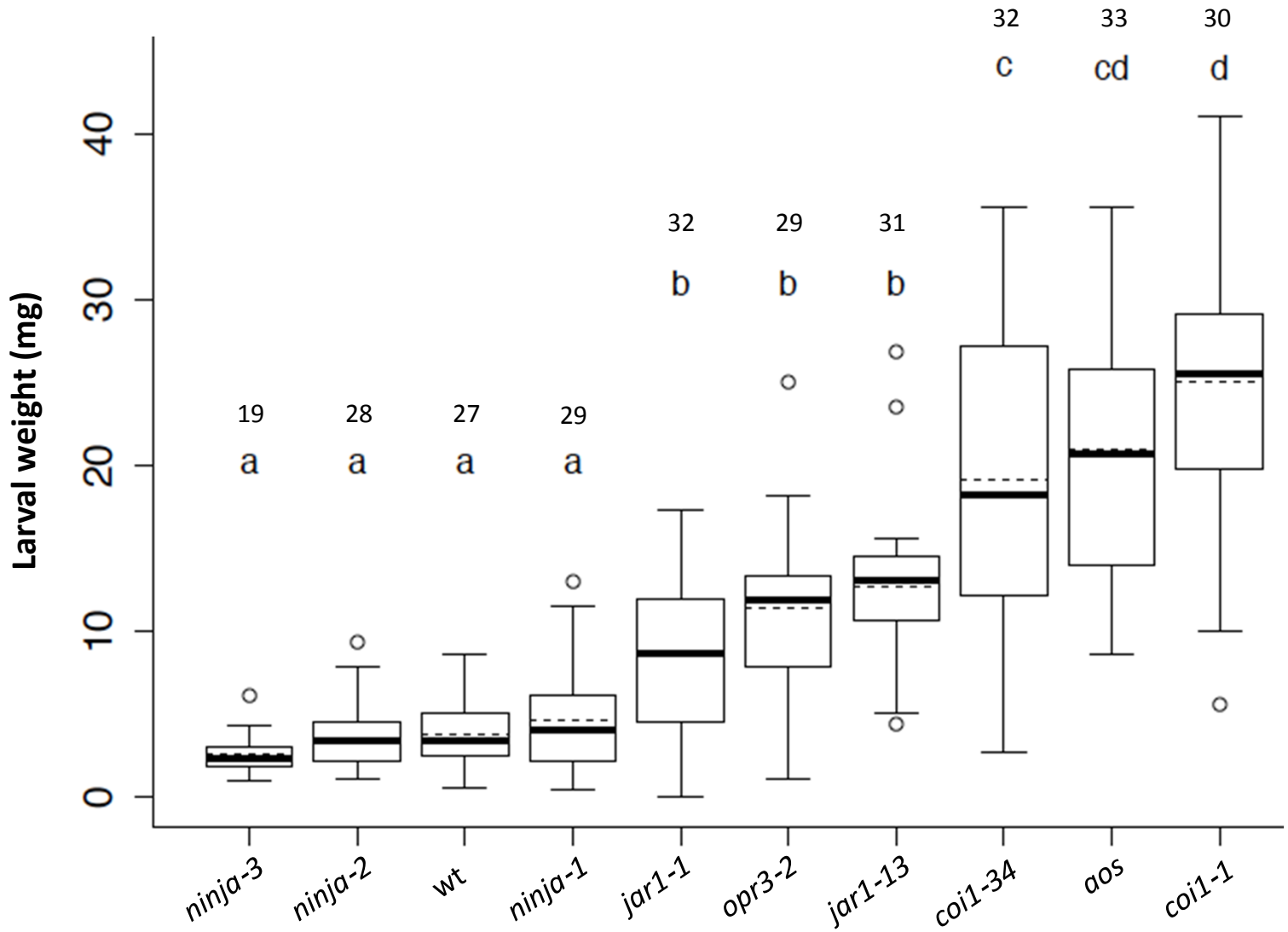

Figure S9. Differential response of JA signaling mutants to herbivore attack. Box plot summary of *S. littoralis* larval weights after feeding for 10 d on different genotypes of adult *Arabidopsis* plants. Medians and means are represented inside the boxes by solid and dotted lines respectively. Circles depict outlier data points beyond ±1.5X the interquartile range defined by the whiskers and numbers indicate *n*. Letters indicate statistically significant differences between pairs as determined by Tukey's HSD test ($P < 0.003$, except in two cases where $P = 0.04$ and 0.02).

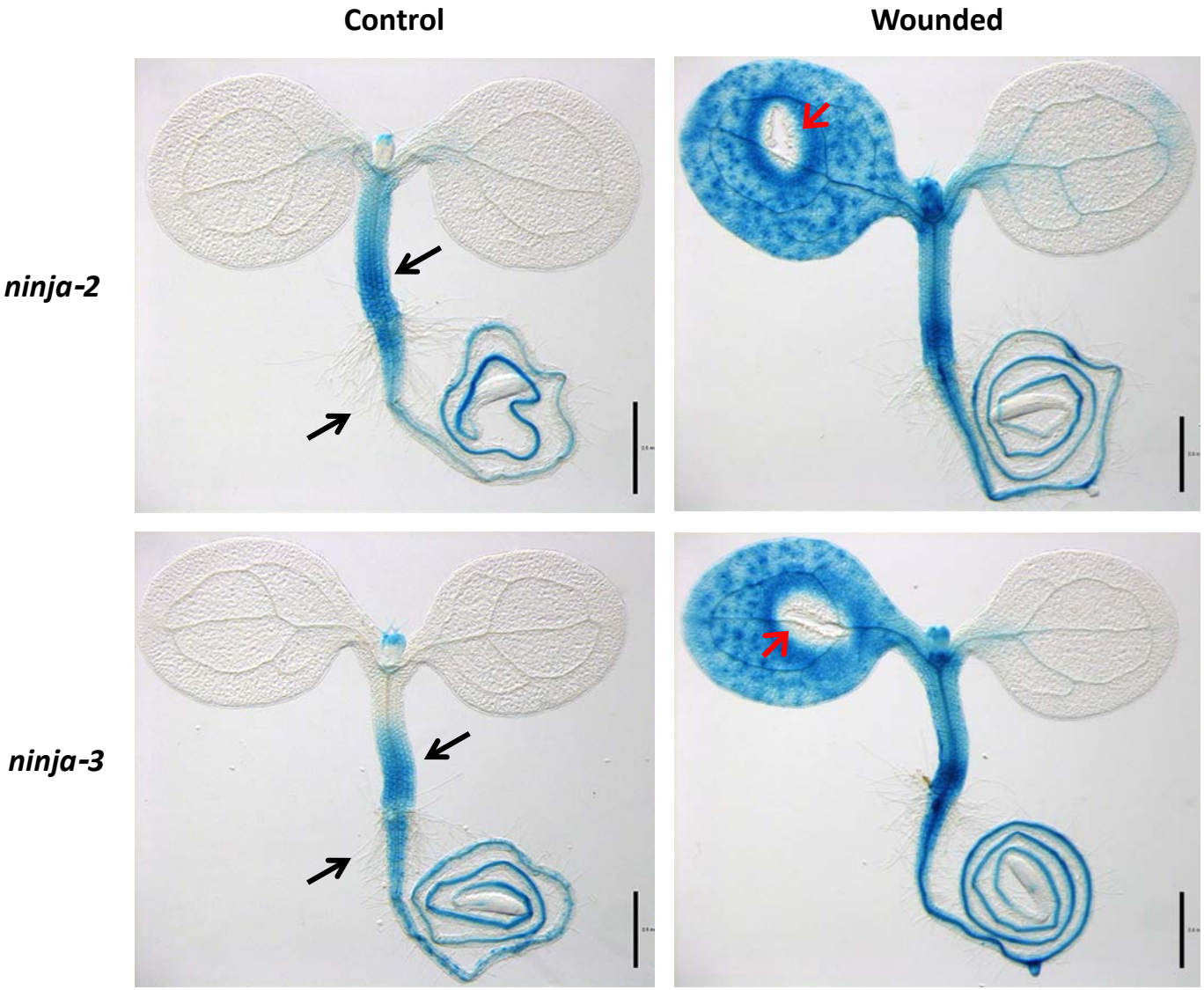

Figure S10. *JGP* expression in control and wounded seedlings of two *ninja* mutant alleles. Arrows indicate constitutive reporter activity in hypocotyl and roots (black) and cotyledon wounding sites (red). Scale bars = 0.5 mm.

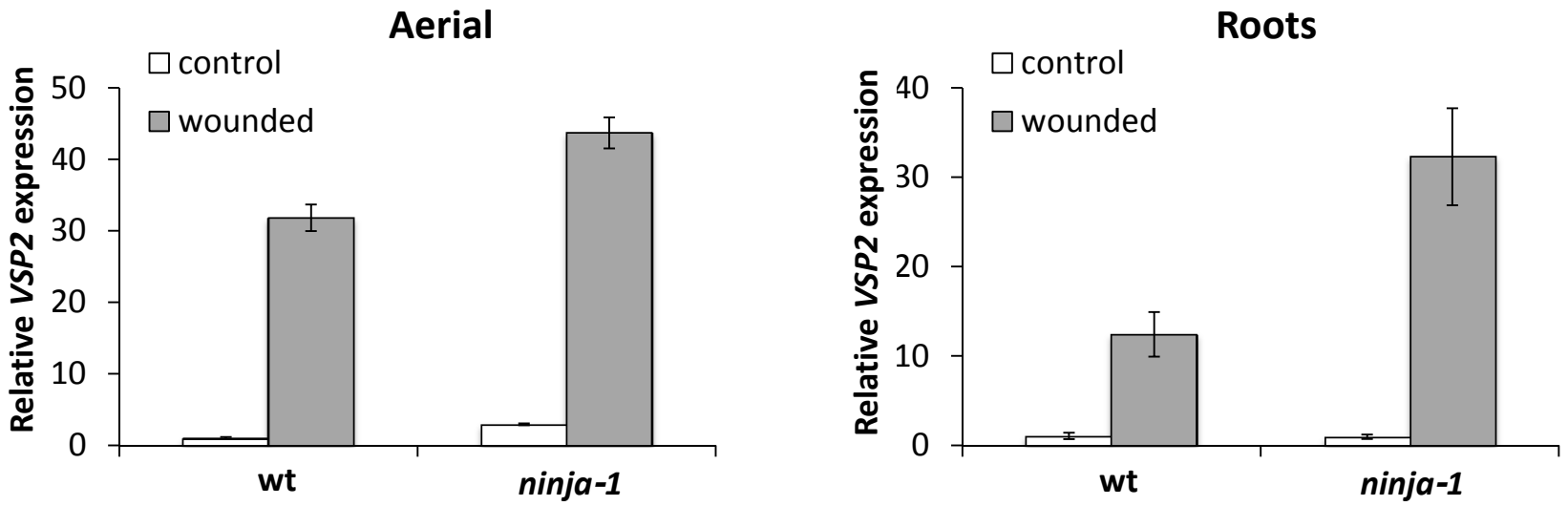

Figure S11. qRT-PCR of *VSP2* expression 1 h after wounding in wt (*JGP*) and *ninja-1* seedlings. For each sample, *VSP2* transcript levels were normalized to those of *UBC21* and displayed relative to the expression in the wt unwounded controls. Bars represent the means of three biological replicates (± SD), each containing a pool of organs from ~60 seedlings.

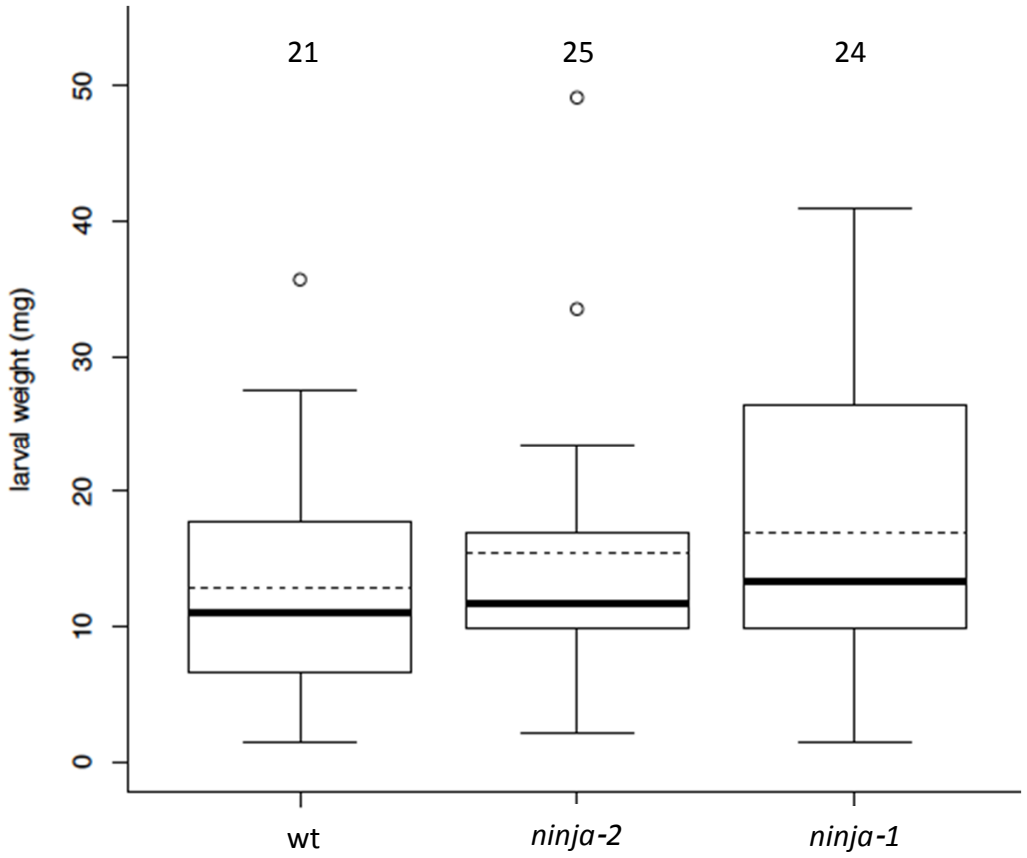

Figure S12. Box plot summary of *S. littoralis* larval weights after feeding for 14 d on adult plants of wt, *ninja-1* and *ninja-2* mutants. Medians and means are represented inside the boxes by solid and dotted lines respectively. Circles depict outlier data points beyond ±1.5X the interquartile range defined by the whiskers and numbers indicate *n*. No statistically significant differences were found by ANOVA ($P = 0.374$).

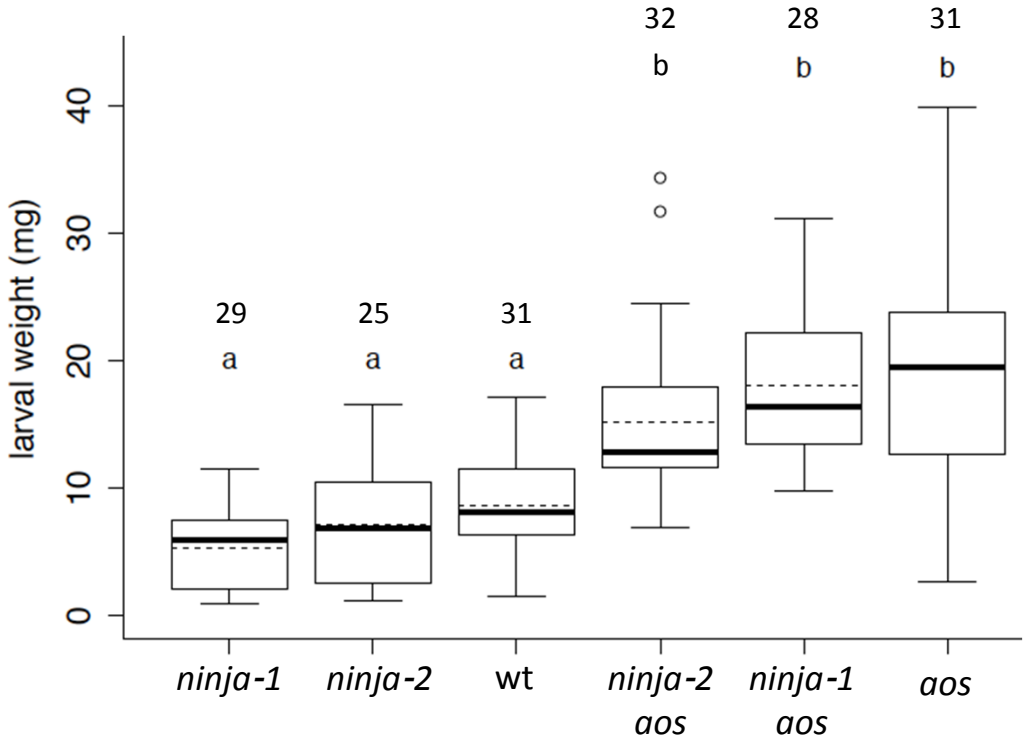

Figure S13. Box plot summary of *S. littoralis* larval weights after feeding for 10 d on adult plants of indicated genotypes. Medians and means are represented inside the boxes by solid and dotted lines respectively. Circles depict outlier data points beyond ±1.5X the interquartile range defined by the whiskers and numbers represent *n*. Letters indicate statistically significant differences between pairs as determined by Tukey's HSD test ($P < 0.04$).

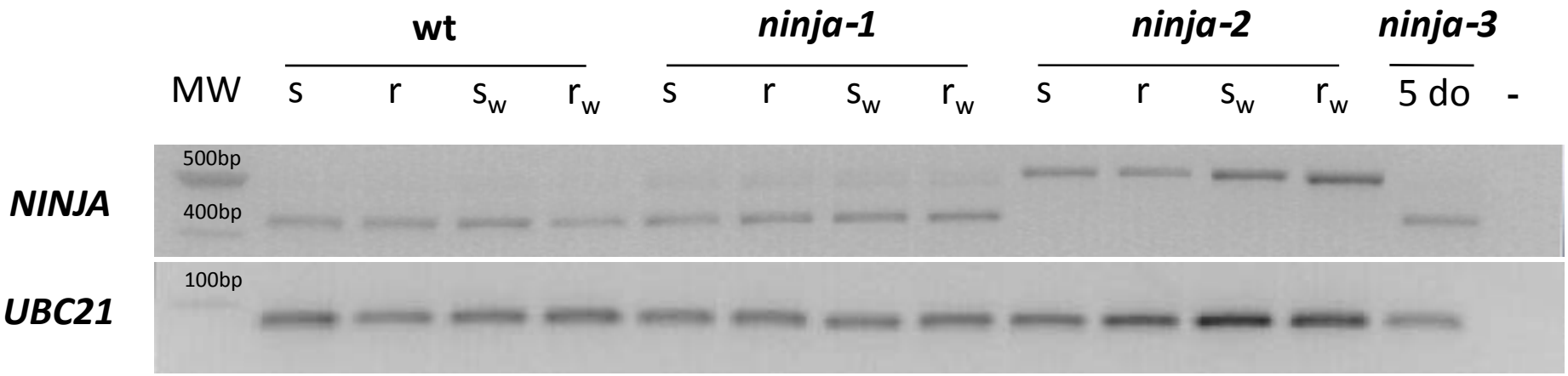

Figure S14. RT-PCR of a *NINJA* transcript fragment in wt and *ninja* mutants. Note the larger size of the PCR product in *ninja-2* due to the presence of the unspliced last intron, which was confirmed by sequencing. MW = molecular weight marker, s = shoots, r = roots, sw or rw = refer respectively to aerial or root tissue collected 1 h after wounding one cotyledon, 5 do = 10 unwounded 5-do whole seedlings, - = negative control (no DNA)

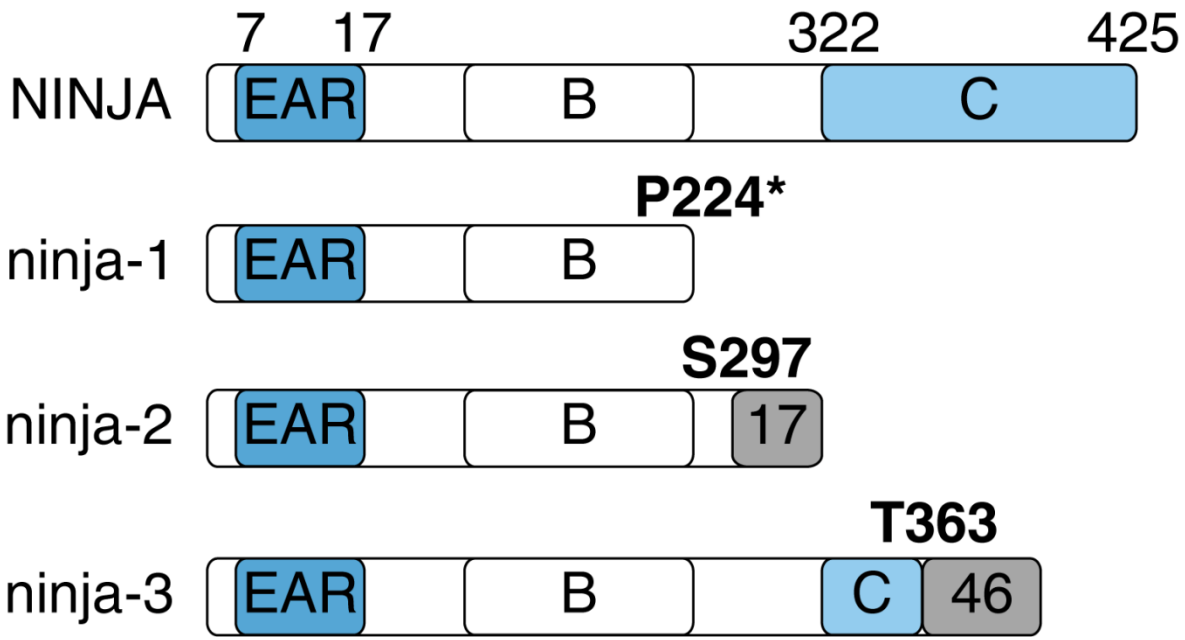

Figure S15. Protein functional domains of wt NINJA compared to predicted domains in 3 *ninja* mutant alleles. Amino acid positions in bold are the sites where the normal NINJA protein sequence is truncated in the mutants. Grey boxes indicate the number of altered amino acids before a premature STOP codon is found in *ninja-2* and *ninja-3*.

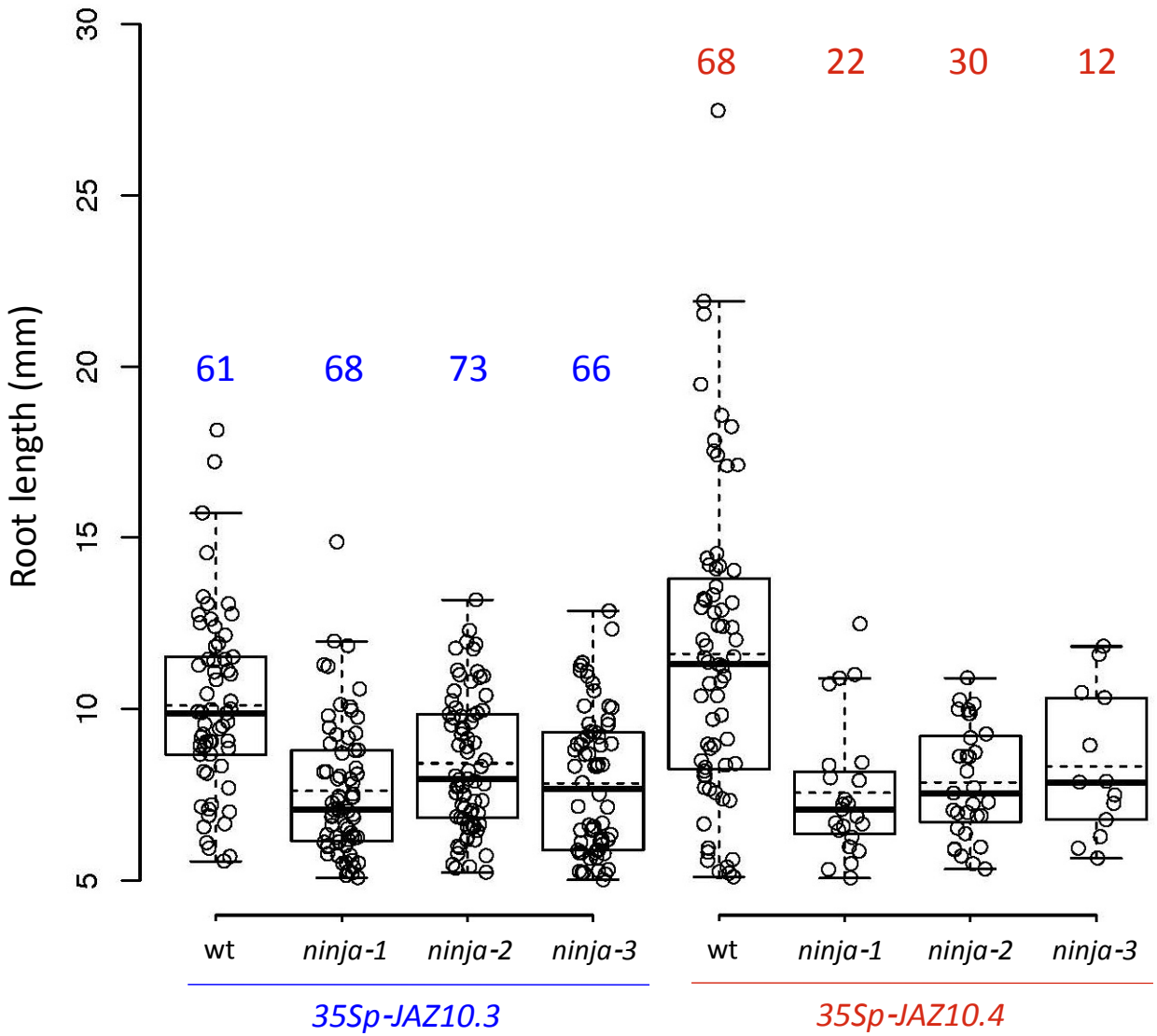

Figure S16. Box plots summarizing the root length distribution of T_1 *JGP* (wt) and *ninja* lines carrying *35Sp-JAZ10.3* (blue) or *35Sp-JAZ10.4* (red) constructs. Transformed T_1 seeds expressing red fluorescence protein were selected by microscopy and grown for 9 d in media supplemented with 25 µM MeJA. The number of independent T_1 analyzed per genotype is shown above the boxes and circles represent individual measurements. Medians and means are represented inside the boxes by solid and dotted lines respectively. Note in wt the shift in root length distribution and the higher fraction of T_1 individuals displaying long roots.

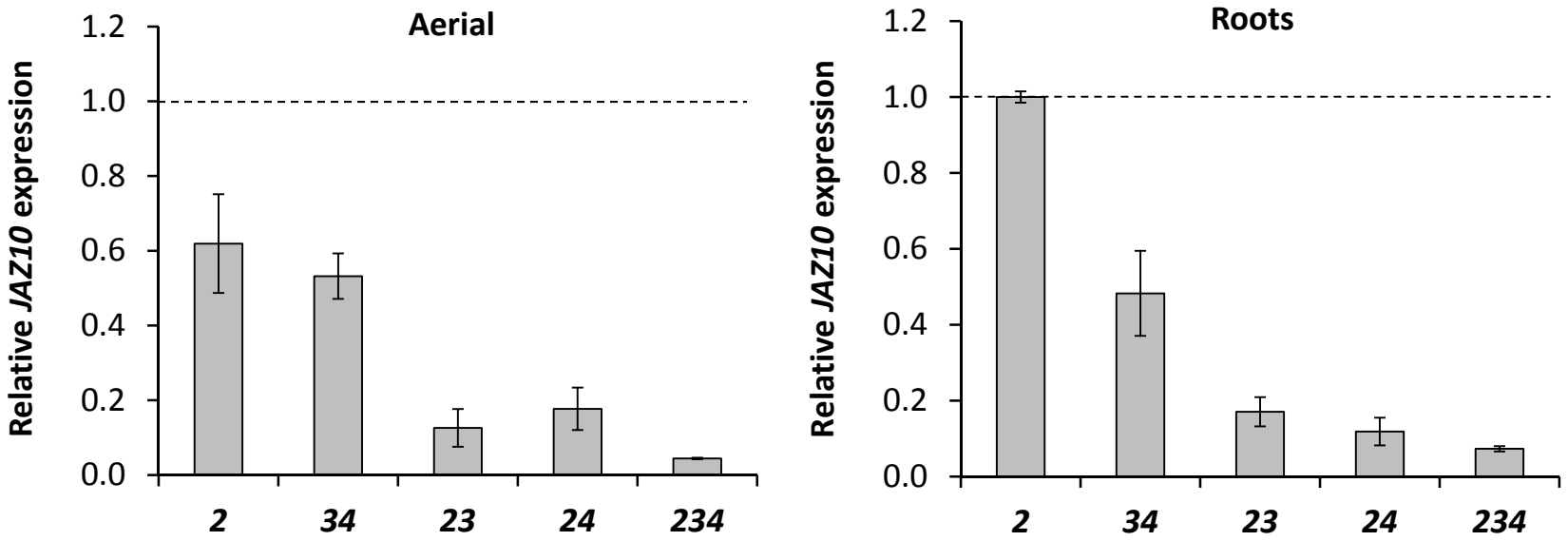

Figure S17. qRT-PCR of *JAZ10* expression 1 h after wounding in a *myc2* single mutant (2: *jin1-2*) and several combinations of *myc2, myc3* and *myc4* mutants (34: *myc3 myc4*; 23: *myc2 myc3*; 24: *myc2 myc4*; 234: *myc2 myc3 myc4*). *JAZ10* transcript levels were normalized to those of *UBC21* and displayed relative to the expression of wt wounded samples (dotted line). Bars represent the means of three biological replicates (± SD), each containing a pool of organs from ~60 seedlings. The full qRT-PCR data is in Supplemental Dataset 2.

Supplemental TABLES

Table S1. Mutant alleles identified in this study

Allele	Mutant line	Mutation	Location in gene (nt)
coi1-32	44B	G→A transition in last base of intron 2; probably destroys acceptor splice site; putative transcript including this intron contains early stop codon	1832
coi1-33	87A	G→A transition; causes G399D substitution in helix 194	2056
coi1-34	34A	G→A transition; causes A442T substitution in strand 219	2184
coi1-8$_L$	82B	G→A transition; causes E543K substitution in strand 223	2487
opr3-2	77A	G→A transition in first base of last intron; destroys donor splice site; transcript containing 81-bp intron encodes a protein with 27 extra amino acids (GLYVSSLSTRKSYKGLGNFI TFLSLCI) between A116 and V117	1825
jar1-13	61E	C→T transition; causes T448I substitution	1719
ninja-1	346C	C→T transition; causes P224STOP substitution	673
ninja-2	347D	G→A transition in first base of last intron; destroys donor splice site; transcript including this intron codes for 17 altered amino acids after position S297 and prior to a premature STOP codon	893
ninja-3	55B-b	2-bp deletion; causes frameshift that codes for 46 altered amino acids after position T363 and prior to a premature STOP codon	1164-1165

Table S2. Cortex cell length in the differentiation zone of the primary root

Genotype	Cell length (µm) *
wt	181 ± 38
aos	185 ± 41
ninja-1	148 ± 34
ninja-2	150 ± 30
ninja-3	147 ± 32
ninja-1 aos	150 ± 31

* Values represent average cell length ± standard deviation (*n* = 270)

Table S3. Relative *JAZ10* expression in 5 do seedlings of wt (*JGP*) and Col-0

Genotype	Aerial control	Aerial wounded	Roots control	Roots wounded
wt (*JGP*)	1 ± 0.02	36.38 ± 0.18	1 ± 0.06	45.4 ± 9
Colombia	1.07 ± 0.16	41.51 ± 1.42	0.95 ± 0	61.32 ± 22
t-test p-value	0.66	0.17	0.25	0.45

JAZ10 transcript levels were normalized to those of *UBC21* and displayed relative to the expression in the wt (*JGP*) unwounded controls. Values represent the means of two biological replicates (± SD), each containing a pool of organs from ~60 seedlings. No significant difference was detected between the two genotypes.

Materials and Methods

Plant material and growth conditions. *Arabidopsis thaliana* accession Columbia (Col) was the wt background of the *JGP* reporter and all previously described mutant and knock-down lines: *aos* (1), *coi1-1* (2), *jar1-1* (3), *NINJA* RNAi (4), *jin1-2* and *jin1-7* (5), and *myc23*, *myc24*, *myc34*, *myc234* (6). After seed stratification for 2 d at 4°C, plants were grown at 21°C under 100 µE m^{-2} s^{-1} of light with photoperiod depending on the application (seedlings: 14 h light, 10 h dark; soil-grown plants for herbivory assays: 10 h light, 14 h dark; soil-grown plants for crosses and seed propagation: 24 h light). For seedling growth, seeds were surfaced-sterilized with a 70% ethanol, 0.05% (v/v) Triton X-100 solution for 3 min; washed once in ethanol for 1 min; dried under a sterile hood for at least 30 min after ethanol removal; and resuspended in sterile water for plating. Seedlings were grown on half-strength Murashige and Skoog solid medium (0.5X MS, 2.15 g/L, pH 5.7; Duchefa, Haarlem, The Netherlands) supplemented with 0.5 g/L of MES hydrate (Sigma, Buchs, Switzerland) and 0.7% agar (for horizontally-grown seedlings) or 0.8% agar (for vertically-grown seedlings). For horizontal seedling growth, 100 or 120 seeds were equidistantly plated by pipetting on a 6 cm x 6 cm nylon mesh resting on solid MS medium in a standard 94-mm round petri dish. The nylon mesh (200 µm pore size; product number AH03444, Lanz-Anliker AG, Rohrbach, Switzerland) provided a solid support that allowed all seedlings to grow straight and uniform with a horizontal cotyledon surface that was easily accessible for wounding.

Plant treatments. For wounding, we used 5-day-old (do) horizontally grown seedlings (~4 d after germination). Wounding was routinely performed between 8 and 10 am, except for screening with non-destructive GUS staining when it was performed at 12 pm. Plates were placed under a stereomicroscope and seedlings were wounded once in one of the two cotyledons with a 25G x 5/8" needle (0.5 mm x 16 mm). Plates were brought back to the growth chamber and incubated for different times before tissue collection depending on the type of experiment: 1 h for qPCR analysis of *JAZ10* expression; 2 h for normal β-glucuronidase (GUS) histochemical detection; and 2 to 6 h for non-destructive GUS staining (see below). For short-term MeJA treatments 5 do horizontally or vertically-grown seedlings were carefully transferred to a 10 µM MeJA solution and incubated for 2 h before tissue collection for GUS histochemical detection.

Generation of *JGP* reporter. A 2,121 bp fragment containing the promoter and most of the 5'-UTR of the *JAZ10* gene was amplified by PCR with primers SS44 (GCCGAATTCgcgagcaaaccttacgcaaa) and SS45 (ATACCATGGatcaagacagagagatatggg), which added *EcoRI* and *NcoI* restriction sites respectively (uppercase letters in sequence). These were used to clone the *JAZ10p* amplicon upstream of the *GUSPlus*™ gene in the vector pCAMBIA1305.2 (CAMBIA Labs, Australia). The *GUSPlus* gene, isolated from *Staphylococcus sp*. and codon-optimized for expression in plants, encodes a β-glucuronidase that is more sensitive, stable and fixative-tolerant than *E. coli* GUS (7). Moreover, the particular version of GUSPlus encoded in pCAMBIA1305.2 contains a plant secretion signal peptide that sends the protein to the apoplastic space allowing a non-destructive assay of β-glucuronidase activity.

The *JGP* construct was transformed with *Agrobacterium tumefaciens* (strain GV3101::pMP90) using the floral dip method (8). T_1 lines were selected on MS plates containing hygromycin (30 µg/ml). Reporter activation upon 2 h MeJA treatment was tested in 11 independent T_2 progenies and a single line displaying strong activation and apparently segregating for a single transgene insertion was further propagated. Homozygous T_3 progeny was identified by MeJA- and wound-induced reporter activation. Later on, T-DNA insertion mapping (9) and high-throughput genome sequencing of the chosen *JPG* reporter line showed that it contained 3 copies of the *JGP* transgene inserted at 2 different loci (Chr. 3: 20515350..20515403; Chr. 5: 26767148). Moreover, the double T-DNA insertion most likely caused a reciprocal translocation of the distal ends of chromosomes 3 and 5 (approximately 3.0 and 0.2 Megabases respectively). In such a situation gametes of hemizygous transgenic plants are viable only if genetically-balanced, that is, they carry either no transgene or both transgenic loci. This leads to the false impression of a single insertion segregating in the progeny of those plants. Notwithstanding this genomic defect, the *JGP* reporter line displayed normal wound-induced *JAZ10* expression (Fig. 1; SI Appendix, Fig. S1, Table S3).

Histochemical detection of GUS activity. Regularly, between 30 and 60 seedlings were analysed for each treatment. They were collected in 90% acetone, incubated for at least 20 min and washed with 50 mM sodium phosphate buffer pH 7.0 for 5-10 min. The rinsing solution was replaced with staining mix (50 mM sodium phosphate buffer pH 7.0, 0.1% Triton X-100, 0.5 mM $K_4Fe(CN)_6$, 0.5 mM $K_3Fe(CN)_6$, 0.5 mg/ml X-Gluc). Seedlings were then vacuum-infiltrated for 5 min at room temperature then incubated at 37°C in the dark for 2 h. The reaction was stopped by replacing the staining solution with 70% ethanol, which was exchanged several times to remove the remaining chlorophyll. Final tissue clearing was achieved with a chloral hydrate : glycerol : water solution (8:2:1) and mounted in the same solution on microscope slides for photography in a stereomicroscope (Leica MZ16A fitted with a DFC310FX camera) or an upright microscope (Leica DM5500 fitted with a DFC420 camera).

The non-destructive assay of GUS activity in *Arabidopsis* seedlings ("live staining") was used to assess reporter activity in seedlings that could then be rescued and grown to maturity. Live staining was performed in the afternoon (5-7 pm). The nylon mesh containing horizontally-grown seedlings was carefully lifted with forceps, floated in 1.0-1.5 ml of "live" staining solution (150 mM sodium phosphate buffer pH 7.0, 0.2 mg/ml X-Gluc) in a clean petri dish and incubated overnight in the growth chamber. GUS staining was assessed next day between 8-10 am by observing roots under a stereomicroscope. Seedlings of interest were carefully transferred to a fresh 0.5X MS plate where they recovered for a few days before being transferred to soil.

Genetic screen. Approximately 20,000 T_4 seeds of the *JGP* reporter were subjected to mutagenesis with ethyl methanesulfonate (EMS) essentially as described (10), except that the seed treatment with 0.2% EMS was done for 8 h and the seeds rinsed 11 times afterwards. About 10,000 M_1 plants were grown and their progeny collected in a total of 600 pools each containing M_2 seeds of 16-17 plants. Two different genetic screens were performed on horizontally-grown M_2 seedlings that were evaluated for *JGP* activity by live staining. In one we screened for loss of GUS staining in the root after cotyledon wounding and in the other we screened for constitutive GUS activity in the root of unwounded seedlings. More than 32,000 M_2

seedlings were analyzed in each screen, covering 90 M_1 pools in the wound response screen and another 120 M_1 pools in the constitutive *JGP* expression screen. Putative mutants were rescued from live-staining and about 50% survived and grew to maturity.

Identification of mutant genes by Next Generation Sequencing (NGS). The *opr3-2*, *ninja-1*, *ninja-2* and *ninja-3* alleles were identified by whole genome sequencing with a HiSeq 2000 system (Illumina, San Diego, CA, USA). Three independent samples were multiplexed in a single sequencing lane, which yielded an average of 60 to 80 reads per nucleotide per sample. Sequencing was done in a pool of ≥100 mutant individuals selected by live GUS staining from a segregating BC_nF_2 (n = 1 - 5) population. The mutant SNPs in such a pool segregate at different frequencies: f = 1 for the SNP mutation causing the phenotype; ~0.5 < f < 1 for SNPs linked to the mutant locus; and f ≈ 0.5 for the SNPs in unlinked genomic regions. Genomic DNA was extracted with the CTAB method (10). EMS-generated SNPs were identified essentially as described (11). In brief, sequence reads were mapped to the TAIR10 release of the *Arabidopsis thaliana* genome (including the sequence of the *JGP* transgene) with the Burrows-Wheeler Aligner software (BWA) version 0.5.9-r16 (12) using default parameters. The alignment in SAM (Sequence Alignment/Map) format was converted to BAM format with SAMtools version 0.1.18-dev (13). SNPs were called with the Unified Genotyper tool of the Genome Analysis Toolkit (GATK) version v1.4-24-g6ec686b (14, 15). SNPs in Variant Call Format (VCF) were filtered with BEDTools utilities version v2.14.2 (16) for SNPs also present in the *JGP* wt line [whose whole genome sequence was also obtained with the HiSeq 2000 system]. SNPs falling in annotated transposons were filtered out based on the TAIR10 Gene File Format (GFF3) annotation file "TAIR10_GFF3_genes_transposons.gff". The predicted effect of the remaining SNPs in coding regions was assessed with SNPEff version 2.0.4 RC1 (17). SNP frequencies (the number of reads supporting a given SNP over the total number of reads covering the SNP location) were extracted using the Unix command awk and plotted with R 2.15.1 (18).

Gene expression analysis. At the time of tissue collection, forceps were used to gently lift from the growth mesh 10 consecutive seedlings. While held together at the hypocotyls, roots and aerial organs were separated by carefully pulling at the root-hypocotyl boundary with a second pair of forceps. Separated tissues were immediately frozen in liquid N_2. The operation was repeated until material from between 40 and 60 seedlings was collected for each biological replica. RNA isolation and quantitative RT-PCR of *JAZ10* (At5g13220) and *UBC21* (At5g25760) transcripts were done as described (19). *VSP2* transcripts were quantified using primers vsp2F (CATCATAGAGCTCGGGATTGAACCC) and vsp2R (AGATGCTTCCAGTAGGTCACGC). RT-PCR was performed with GoTaq DNA polymerase (Promega) as indicated by the manufacturer, with the following primer pairs. *OPR3*: ATGACGGCGGCACAAGGGAAC (P177) and TCAGAGGCGGGAAAAAGGA (P178). *NINJA*: TGGTGGTTCTTCTTCCAACC (NINJA.2F) and GCAACAGGTTGTTTGCCTTC (NINJA.2R).

Herbivory assay. Plants were grown for 4 weeks as indicated above with the exception of *coi1-1*, which was first grown from a 1:1 segregating population on vertical 0.5X MS plates containing 25 μM MeJA; after 7 d, MeJA-insensitive *coi1-1* seedlings were transferred to soil. At the start of the bioassay, 11 pots per genotype containing individual plants were transferred into 20 x 30 x

20 cm plexiglas boxes after placing 3 newly hatched *Spodoptera littoralis* larvae on each plant. Boxes were brought back to the growth chamber and larvae were allowed to feed for 10 or 14 d. Surviving larvae were collected and individually weighted. Experiments were repeated at least three times with similar results.

Plant transformation with *35Sp-JAZ10.3* and *35Sp-JAZ10.4*. The *JAZ10.3* and JAZ10.4 transcript variants were amplified by PCR with primer pairs SS25/SS29 and P227/P228, respectively (SS25: ACAAGTTTGTACAAAAAAGCAGGCTcaaagaagatgtcgaaag, SS29: ACCACTTTGTACAAGAAAGCTGGGTttacctctccttgcgc, P227: ACAAGTTTGTACAAAAAAGCAGGCTtgatgtcgaaagctaccatagaactcg, P228: ACCACTTTGTACAAGAAAGCTGGGTctaatctctccttgcgcttc). JAZ10.4 was amplified from a previously generated plasmid containing this particular variant. Primers added Gateway attB recombination sites (uppercase letters) to clone inserts into pDONR™/ZEO (Invitrogen) by Gateway recombination technology. The final overexpression constructs were obtained with a double Gateway reaction of the respective ENTRY clones and pEN-L4-2-R1, containing the CaMV 35S promoter (20), into the destination vector pEDO097pFR7m24GW. This vector was generated by Ester M. N. Dohmann (University of Lausanne) inserting the fluorescence-accumulating seed technology (FAST) cassette (21) into pH7m24GW (Invitrogen). The overexpressor constructs were transformed into wt (*JGP*) and *ninja* mutant plants with *A. tumefaciens* as described above. Transformed seeds (T_1) expressing red fluorescence protein (RFP) were selected by fluorescence microscopy and directly sowed in 0.5X MS medium containing 25 µM MeJA to test root sensitivity.

Root phenotypic measurements. Plates of 7 do seedlings grown vertically in 0.5X MS (alone or supplemented with 25 µM MeJA), were scanned and root lengths measured with the ImageJ software (http://rsb.info.nih.gov/ij/). At least 20 seedlings were analyzed per genotype. For root cellular measurements a minimum of 10 primary roots per genotype were analyzed. In brief, vertically grown 5 do seedlings were mounted in chloral hydrate : glycerol : water (8:2:1) and observed with a Leica DM5500 upright microscope fitted with a Leica DFC420 camera. The number of cells in the meristematic zone was counted in the cortex cell file between the quiescent center and the first elongating cell (22). In the same sample, cortex cell length measurements were initiated in the differentiation zone, at the place were root hairs and xylem vessels were first observed, and acquired for a minimum of 27 cells shootward with the ruler function of the LAS V4.1 Software (Leica).

Statistical analysis. Statistical significance in pair-wise comparisons was evaluated by Student's t test. Box plot drawing and multiple comparisons [analysis of variance (ANOVA) followed by Tukey's HSD test] were performed in R 2.15.1 (18).

References

1. Park JH*, et al.* (2002) A knock-out mutation in allene oxide synthase results in male sterility and defective wound signal transduction in *Arabidopsis* due to a block in jasmonic acid biosynthesis. *Plant J* 31(1):1-12.

2. Feys B, Benedetti CE, Penfold CN, & Turner JG (1994) Arabidopsis mutants selected for resistance to the phytotoxin coronatine are male sterile, insensitive to methyl jasmonate, and resistant to a bacterial pathogen. *Plant Cell* 6(5):751-759.
3. Staswick PE, Su W, & Howell SH (1992) Methyl jasmonate inhibition of root growth and induction of a leaf protein are decreased in an *Arabidopsis thaliana* mutant. *Proc Natl Acad Sci USA* 89(15):6837-6840.
4. Pauwels L*, et al.* (2010) NINJA connects the co-repressor TOPLESS to jasmonate signalling. *Nature* 464(7289):788-791.
5. Lorenzo O, Chico JM, Sanchez-Serrano JJ, & Solano R (2004) *JASMONATE-INSENSITIVE1* encodes a MYC transcription factor essential to discriminate between different jasmonate-regulated defense responses in Arabidopsis. *Plant Cell* 16(7):1938-1950.
6. Fernandez-Calvo P*, et al.* (2011) The Arabidopsis bHLH transcription factors MYC3 and MYC4 are targets of JAZ repressors and act additively with MYC2 in the activation of jasmonate responses. *Plant Cell* 23(2):701-715.
7. Broothaerts W*, et al.* (2005) Gene transfer to plants by diverse species of bacteria. *Nature* 433(7026):629-633.
8. Clough SJ & Bent AF (1988) Floral dip: a simplified method for *Agrobacterium*-mediated transformation of *Arabidopsis thaliana*. *Plant J* 16:735-743.
9. O'Malley RC, Alonso JM, Kim CJ, Leisse TJ, & Ecker JR (2007) An adapter ligation-mediated PCR method for high-throughput mapping of T-DNA inserts in the *Arabidopsis* genome. *Nat Protoc* 2(11):2910-2917.
10. Weigel D & Glazebrook J (2002) *Arabidopsis: A laboratory manual* (Cold Spring Harbor Laboratory Press, New York).
11. Depuydt S*, et al.* (2013) Suppression of *Arabidopsis* protophloem differentiation and root meristem growth by CLE45 requires the receptor-like kinase BAM3. *Proc Natl Acad Sci U S A* 110(17):7074-7079.
12. Li H & Durbin R (2009) Fast and accurate short read alignment with Burrows-Wheeler transform. *Bioinformatics* 25(14):1754-1760.
13. Li H*, et al.* (2009) The Sequence Alignment/Map format and SAMtools. *Bioinformatics* 25(16):2078-2079.
14. McKenna A*, et al.* (2010) The Genome Analysis Toolkit: a MapReduce framework for analyzing next-generation DNA sequencing data. *Genome Res* 20(9):1297-1303.
15. DePristo MA*, et al.* (2011) A framework for variation discovery and genotyping using next-generation DNA sequencing data. *Nat Genet* 43(5):491-498.
16. Quinlan AR & Hall IM (2010) BEDTools: a flexible suite of utilities for comparing genomic features. *Bioinformatics* 26(6):841-842.
17. Cingolani P*, et al.* (2012) A program for annotating and predicting the effects of single nucleotide polymorphisms, SnpEff: SNPs in the genome of *Drosophila melanogaster* strain *w1118; iso-2; iso-3*. *Fly (Austin)* 6(2):80-92.
18. R Core Team (2012). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-07-0, URL: www.r-project.org
19. Gfeller A*, et al.* (2011) Jasmonate controls polypeptide patterning in undamaged tissue in wounded Arabidopsis leaves. *Plant Physiol* 156(4):1797-1807.
20. Karimi M, Bleys A, Vanderhaeghen R, & Hilson P (2007) Building blocks for plant gene assembly. *Plant Physiol* 145(4):1183-1191.
21. Shimada TL, Shimada T, & Hara-Nishimura I (2010) A rapid and non-destructive screenable marker, FAST, for identifying transformed seeds of Arabidopsis thaliana. *Plant J* 61(3):519-528.

22. Casamitjana-Martinez E*, et al.* (2003) Root-specific *CLE19* overexpression and the *sol1/2* suppressors implicate a CLV-like pathway in the control of *Arabidopsis* root meristem maintenance. *Curr Biol* 13(16):1435-1441.