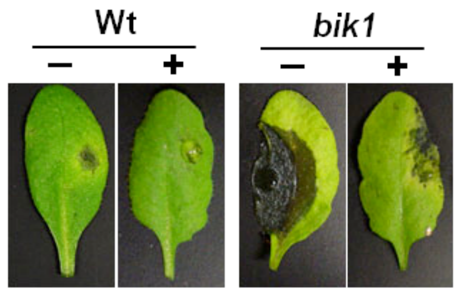
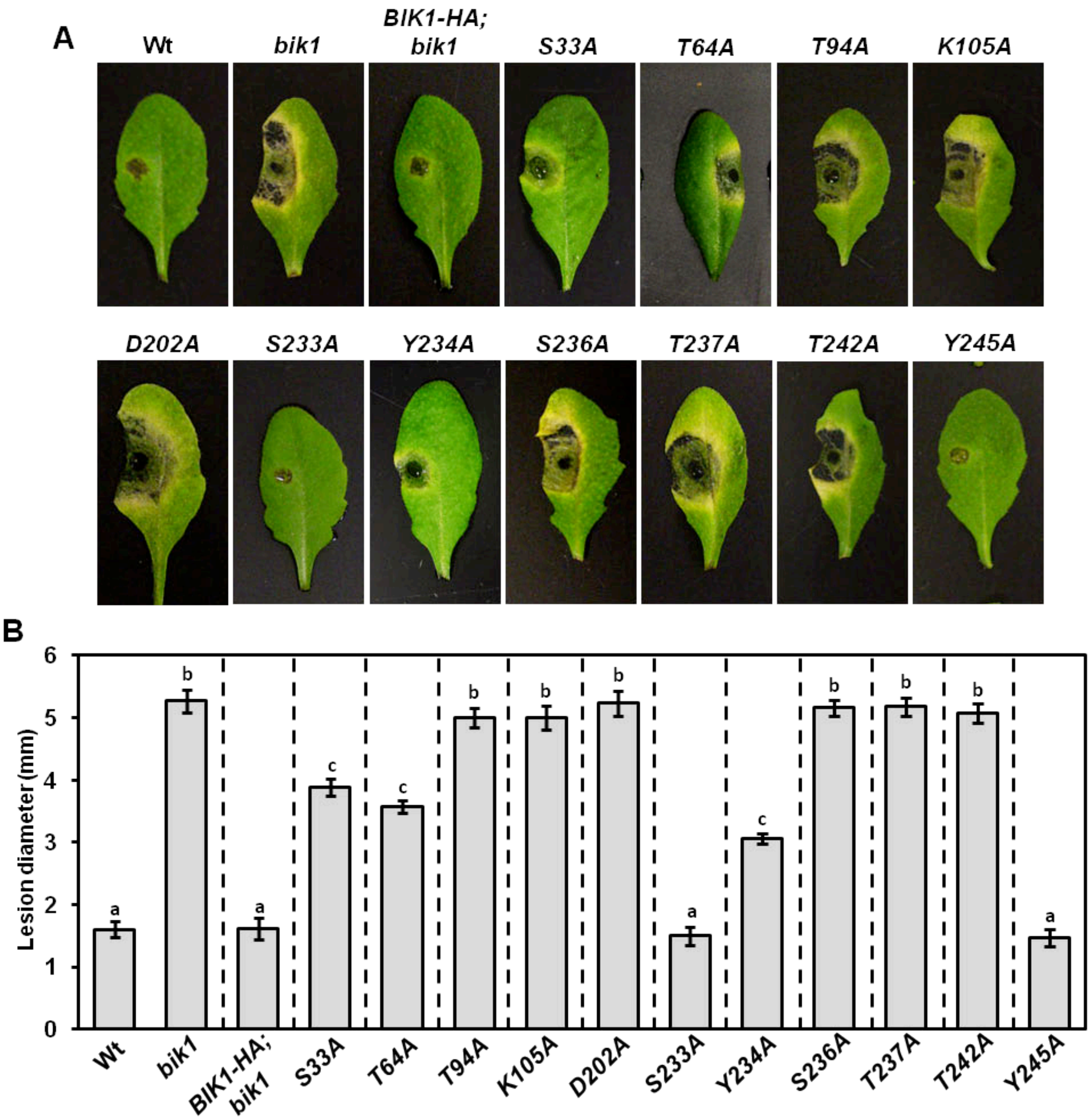
## Supplemental Figures and Tables




**Supplemental Figure 1. Wound-induced immunity to *B. cinerea* requires BIK1**
Disease symptoms of non-wounded (-) and forceps-wounded (+) Arabidopsis leaves 3 days post-drop-inoculation with *B. cinerea* (2.5 x $10^5$ spores/mL). Wt, wild-type.




**Supplemental Figure 2. Response of the *BIK1* substitution mutants to *A. brassicicola* infection**
**(A)** Disease symptoms and **(B)** lesion diameters of *bik1* and *BIK1* substitution mutants 4 days post-inoculation with *A. brassicicola* (5 x $10^5$ spores/mL). Data in (B) represent mean ± SE from a minimum of 30 disease lesions. Experiments were repeated at least three times with similar results. Statistical analysis was performed as described in the legend of Figure 2. All substitutions are in the *bik1* background. Wt, wild-type.

BIK1 (AT2G39660) promoter region

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-1287    atttaaacctgtgctcataatttactttacaaattattacttttccataaattgtggaaa
-1227    agttatctgtaacatccgattcaactggagtctagactactatagacattgatacgtttt
-1167    gagtttttagatacttggaagatatatgcatttatgaatacagattacagacacatacta
-1107    gtactactgtatgtctgtatatggatacaaaaaaaatcatgtatgaatactaaaatttta
-1047    ttagaaatctatttttcaattgttgcaacaatcaagttgtcaaatttatttttgtaaccg
-987     ttaaacaaacaaatatcgatttaggtttctaatctgaattgacatctcaaacaaaaaagg
-927     ctgaatactttctgaaaatagtgtatggaatgaaggtggcttttagagccattataaccg
-867     gaagaaaattcaggtgacttttagaaccattataaccggaagaaaaggtgaattttaatt
-807     tttagctgtgtggaagacacggcaagtccaagtagtaccttcgtacgtcaatattgtcca
-747     accggccgtgtcgaaaatcttcttgagaaaaattggattttcatctataaaaaaaaaaag
-687     tccaagtaataccaaacaaagacagcgacgtgtaaaacaatacaagactcataatcacaa
-627     acctaccacccaagtcaaacctatattccatttagtgaattcttgattatgacttcttga
-567     aatcatttgtattcatatgtataattatttaagtcatttttctgtaagtaaaatttttat
-507     atatctagaataacgagttccctacgacaagatacagttgaacgtaaatgtgacatctca
-447     attttcattggtgtctagtactctagtgattaggttttcgacatttattgtactgattaa
-387     gtaaaaattcatggtacaaacatcgaatatatatttttctgcttacacacaccaattaac
-327     gtggatagaccaattgaaatatttgttacgacaaagcaaaacaaaacaaacgtcatgtt
-267     tcgctgtttgtttgtcgtcccgttaatggtaatctttcagacacatacagtacccaaaca
-207     agtaatttgactaaaattttctctctgtctaaatttcagaagaaaaaaaaactttaggat
-147     atattgccaaaagatcttaaaaatgggtcatatcattttgatcatatagaatccaacgac
-87      ctttatcttttcgccgaactatactttttttgtgtccatttgtttgactttctttcacaca
-27      cacatccacaaagaaaaaaggaccatt
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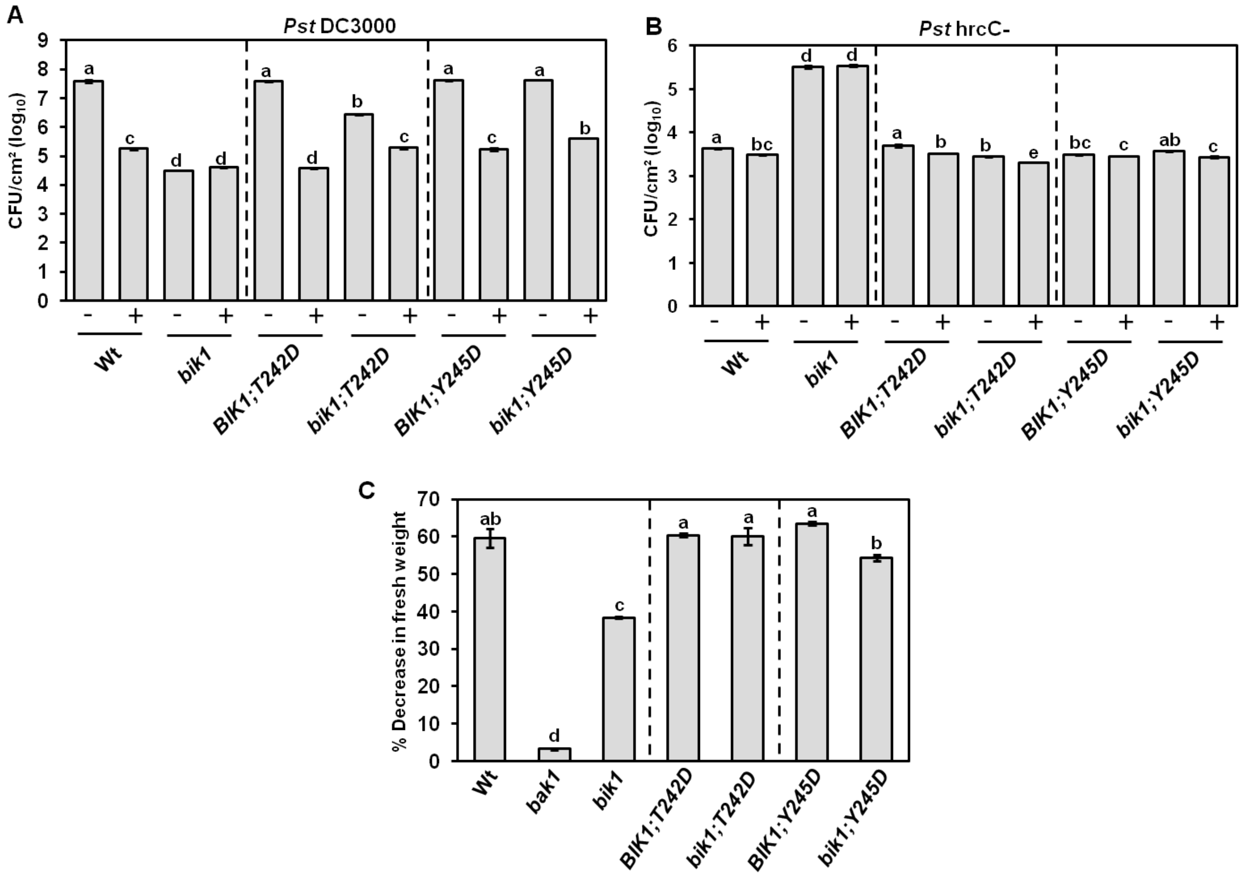
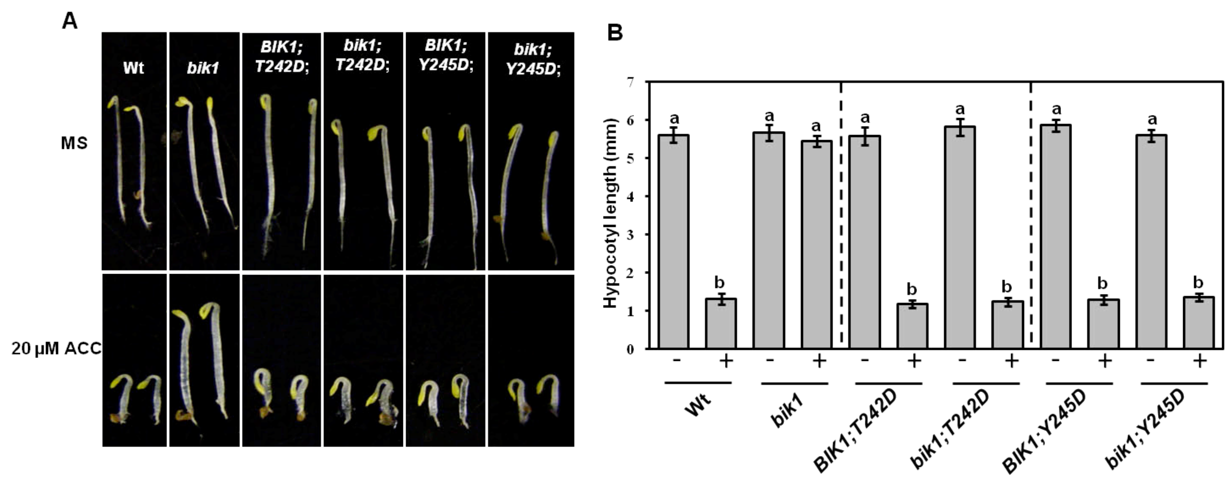
**Supplemental Figure 3. The BIK1 promoter sequence and location of putative EIN3-binding sequences in the *BIK1* promoter.**

The primary ethylene response elements (AYGWAYCT) as described (Kosugi and Ohashi 2000) are highlighted in yellow. Two predicted EIN3 binding regions (Bik1 promoter region A from -1221 to -774 and region B from -494 to -166) are highlighted in red and primers designed for ChIP-PCR are highlighted in blue.

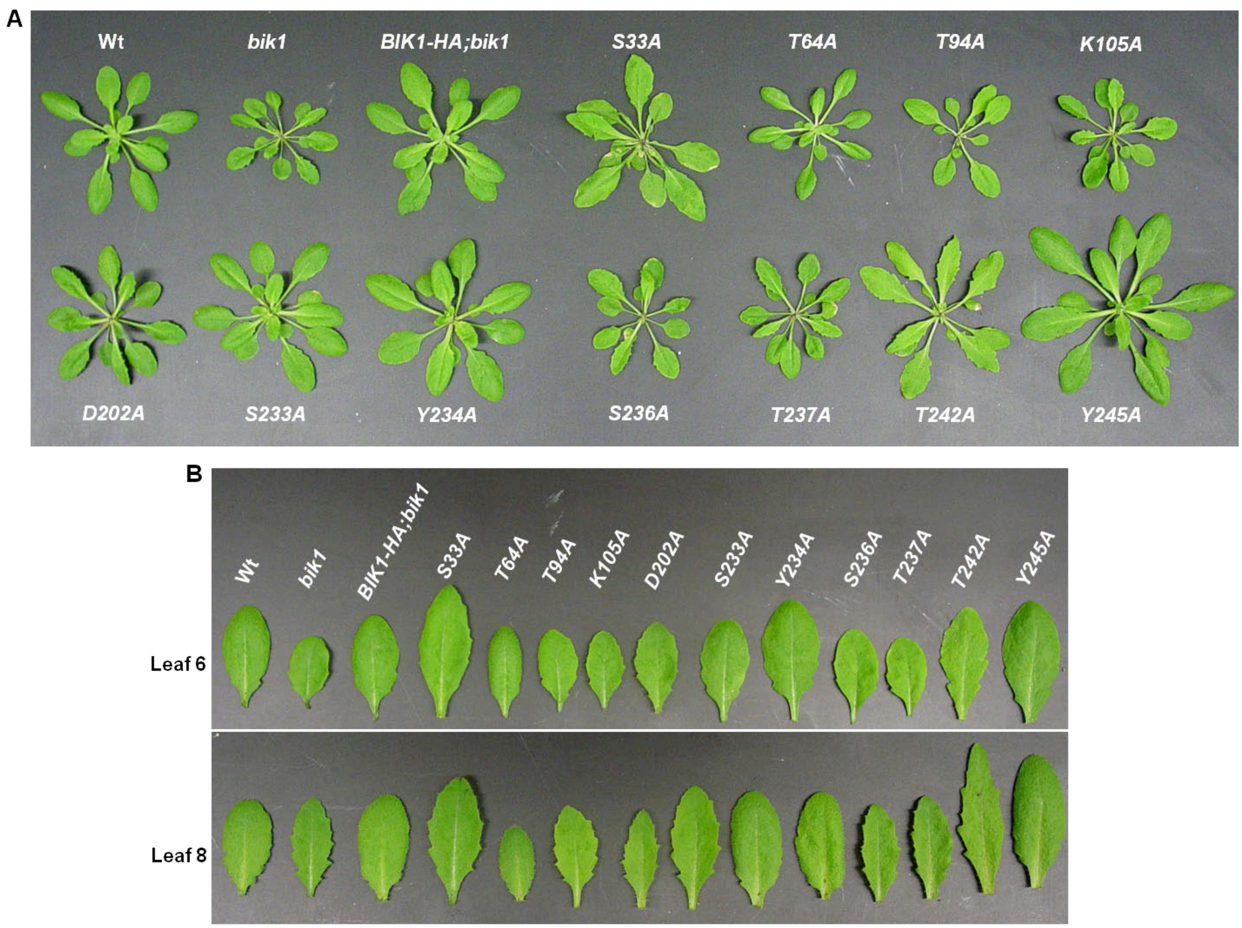



**Supplemental Figure 4. Bacterial and flagellin responses of the BIK1 phospho-mimic mutants** Bacterial growth (colony forming units [CFU]/cm$^2$ leaf area) in water (-) and flg22 (+) pre-treated *bik1* and *BIK1* substitution mutants 3 days post-inoculation with **(A)** *Pst*DC3000 or **(B)** the non-pathogenic *Pst hrp* mutant *hrcC*-. **(C)** Percent decrease in fresh weight of *bik1* and *BIK1* substitution seedlings after growth in 10 nM flg22. Data represent mean values ± SE from three experiments and a minimum of 120 seedlings for bacterial growth and fresh weights, respectively. Experiments were repeated at least three times with similar results. Statistical analysis was performed as described in the legend of Figure 2. Wt, wild-type; CFU, colony-forming units.

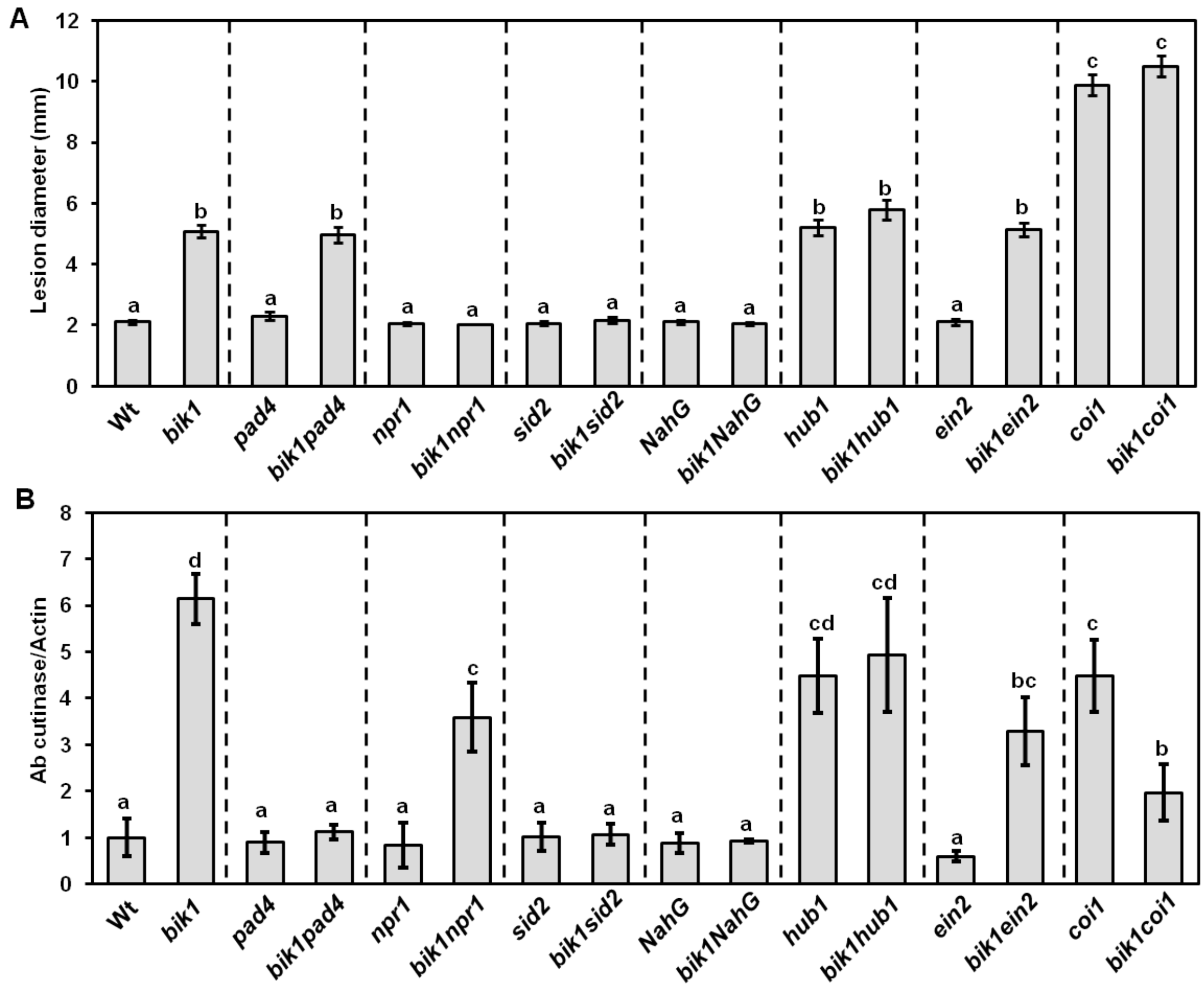



**Supplemental Figure 5. The triple response of BIK1 T242 and Y245 phospho-mimic mutations at 20 µM ACC**

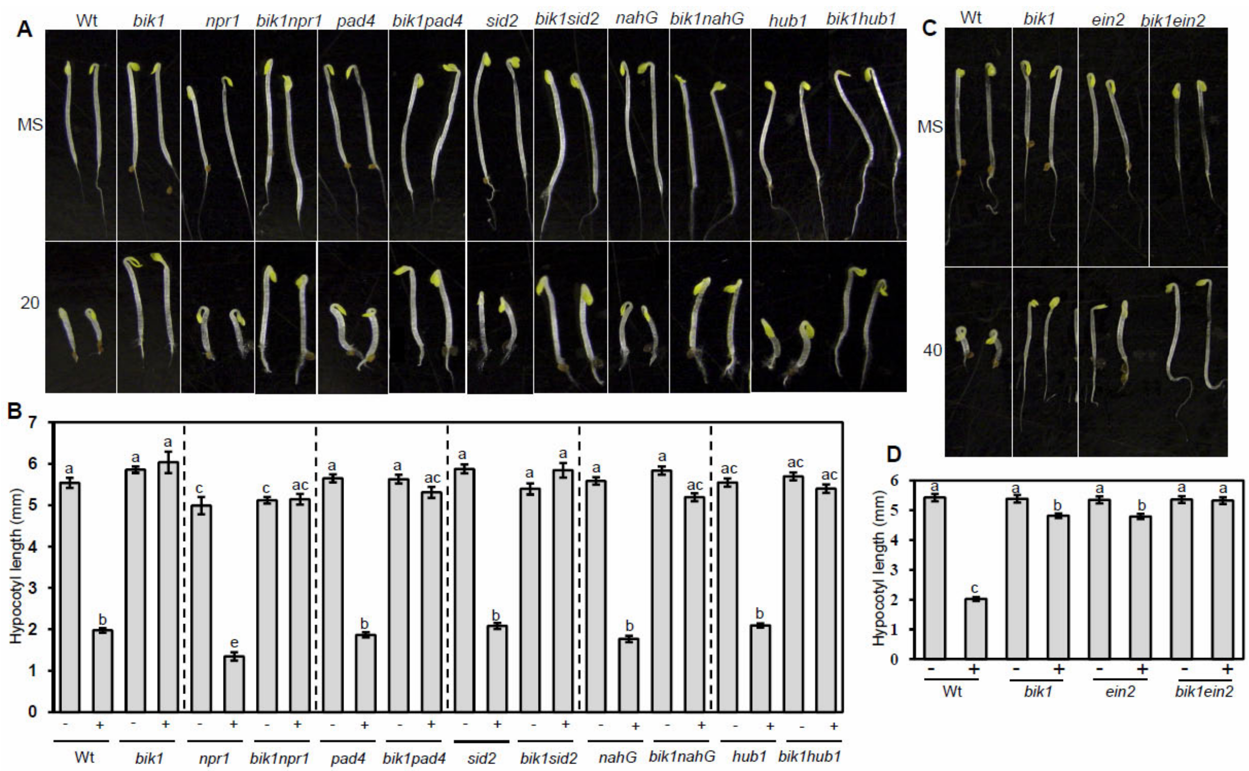
**(A)** Triple response and **(B)** average hypocotyl length of the BIK1$^{T242D}$ and BIK1$^{Y245D}$ substitution mutants on 20 µM ACC. Data in (B) represents mean ± SE from a minimum of 60 seedlings. Experiments were repeated at least three times with similar results. Statistical analysis was performed as described in the legend of Figure 2. Wt, wild-type.



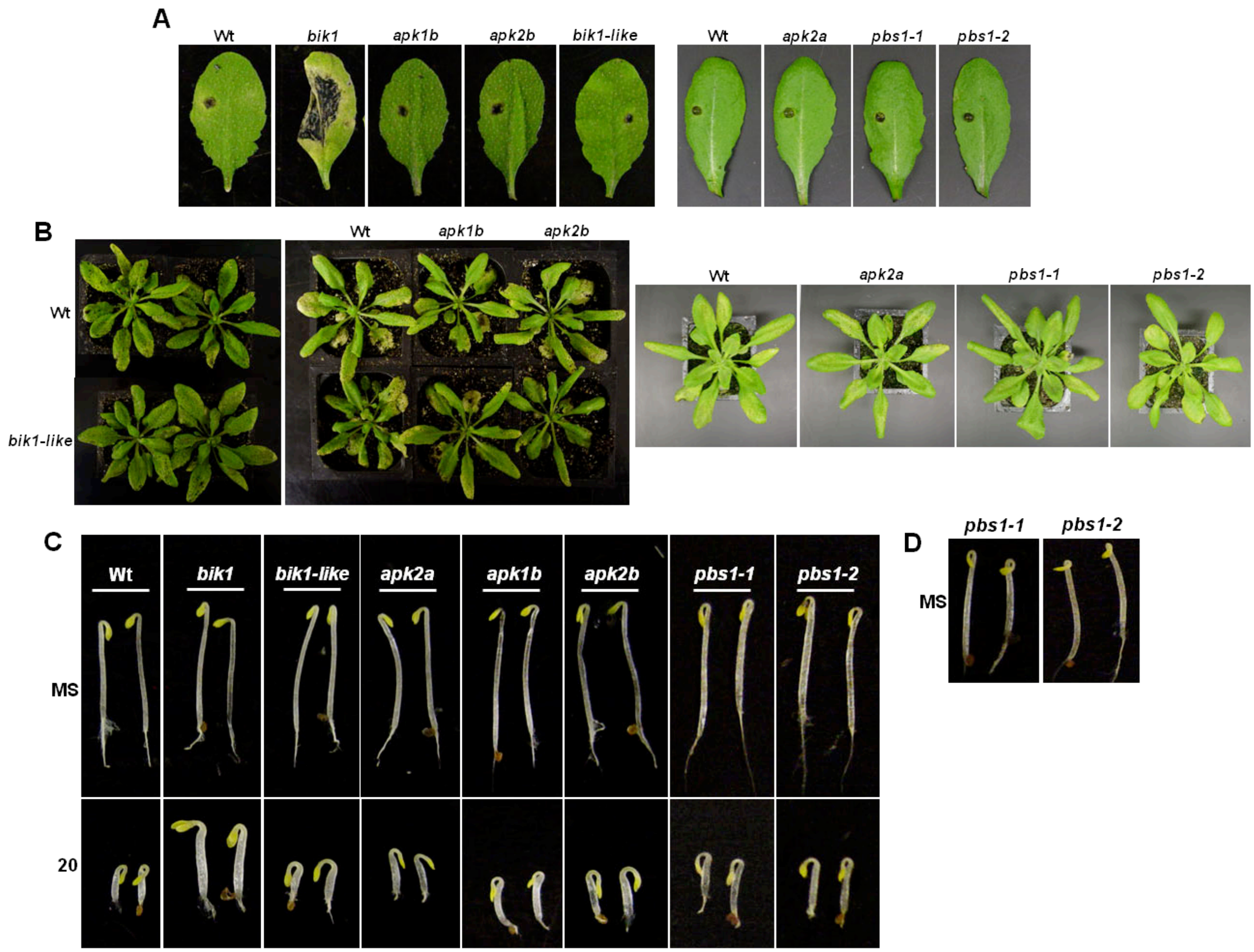

**Supplemental Figure 6. Growth morphology of the *BIK1* substitution mutants**
**(A)** Comparison of rosettes from 4-week old wild-type (Wt) and *bik1* plants with those of the substitution mutants. **(B)** Close-up images of rosette leaves 6 (upper panel) and 8 (lower panel).




**Supplemental Figure 7. Disease responses of the *bik1* double mutants to *A. brassicicola***
**(A)** Lesion diameter and **(B)** fungal growth in single and double mutants 4 days post-inoculation with *A. brassicicola* (5 x $10^5$ spores/mL). Fungal accumulation based on qPCR amplification of *A. brassicicola CutinaseA* relative to Arabidopsis *Actin2*. Data in (A) represents the mean ± SE from a minimum of 30 disease lesions. Experiments were repeated at least three times with similar results. Statistical analysis was performed as described in the legend of Figure 2. Wt, wild-type.




**Supplemental Figure 8. The BIK1-regulated ET growth response is independent of SA**
**(A, C)** Triple response and **(B, D)** average hypocotyl lengths of single and double mutants on 20 or 40 μM ACC (+) and un-supplemented MS media (MS; -). Data in (B) and (D) represent mean ± SE from a minimum of 60 seedlings. Experiments were repeated at least three times with similar results. Statistical analysis was performed as described in the legend of Figure 2. Wt, wild-type.




**Supplemental Figure 9. BIK1 function in necrotrophic defense and ET-responses is unique among related protein kinases**

Disease response phenotypes of T-DNA insertion alleles of *APK1B*, *APK2B*, *BIK1-LIKE*, and *PBS1* in response to **(A)** *A. brassicicola* and **(B)** *B. cinerea* 4 and 3 days post-inoculation, respectively. **(C)** Triple response of *bik1* and the related kinase mutant alleles on 20 µM ACC. **(D)** Constitutive triple response phenotype of *pbs1-1* and *pbs1-2* seedlings when grown in the dark on un-supplemented MS media (MS).

**Supplemental Table 1. Primers used in the *BIK1* study.** Sequences read 5' to 3'.

(For pGEX-4T)
BIK1 full length-F: CTAGGATCCATGGGTTCTTGCTTCAGTTCTCGAGT
BIK1 full length-R: AAGGAATTCCTACACAAGGTGCCTGCCAAAAGGTT

(For pCAMBIA 99-1-3xHA)
BIK1 full length-F: AGACGGTGGATGGGTTCTTGCTTCAGTTCT
BIK1 full length-R: GCGCCCGGGCACAAGGTGCCTGCCAAAAGG

BIK1mS33A-F: CGGAAATCGGCGTCGACTGTA
BIK1mS33A-R: TACAGTCGACGCCGATTTCCG

BIK1mT35A-F: TCGTCTTCGGCGGATGCGGCG
BIK1mT35A-R: CGCCGCATCCGCCGAAGACGA

BIK1mT64A-F: AAACTCGCCGCGAGAAACTTC
BIK1mT64A-R: GAAGTTTCTCGCGGCGAGTTT

BIK1mS71A-F: AGACCAGATGCGGTGATCGGA
BIK1mS71A-R: TCCGATCACCGCATCTGGTCT

BIK1mT94A-F: CTCACTCCGGCGAAACCTGGA
BIK1mT94A-R: TCCAGGTTTCGCCGGAGTGAG

BIK1mK105A-F: ATCGCCGTTGCGAAGCTTAAC
BIK1mK105A- R: GTTAAGCTTCGCAACGGCGAT

BIK1mS206A -F: ATTAAAGCCGCGAACATCTTA
BIK1mS206A -R: TAAGATGTTCGCGGCTTTAAT

BIK1mS233A-F: GGTGATTTGGCGTATGTTAGT
BIK1mS233A-R: ACTAACATACGCCAAATCTCC

BIK1mY234A-F: GATTTGAGTGCGGTTAGTACA
BIK1mY234A-R: TGTACTAACCGCACTCAAATC

BIK1mS236A-F: AGTTATGTTGCGACAAGGGTC
BIK1mS236A-R: GACCCTTGTCGCAACATAACT

BIK1mT237A-F: TATGTTAGTGCGAGGGTCATG
BIK1mT237A-R: CATGACCCTCGCACTAACATA

BIK1mY243A-F: ATGGGTACTGCGGGGTACGCC

BIK1mY243A-R: GGCGTACCCCGCAGTACCCAT

BIK1mY245A-F: ACTTATGGGGCGGCCGCGCCT
BIK1mY245A-R: AGGCGCGGCCGCCCCATAAGT

BIK1mS253A-F: TACATGTCAGCGGGTCACTTG
BIK1mS253A-R: CAAGTGACCCGCTGACATGTA

BIK1mS274A-F: GAGATTTTAGCGGGTAAGCGA
BIK1mS274A-R: TCGCTTACCCGCTAAAATCTC

BIK1mS333A-F: CAGTGTCTCGCGTTTGAACCC
BIK1mS333A-R: GGGTTCAAACGCGAGACACTG

BIK1mY245D-F: ACTTATGGGGACGCCGCGCCT
BIK1mY245D-R: AGGCGCGGCGTCCCCATAAGT

BIK1mT242D-F: GTCATGGGTGACTATGGGTAC
BIK1mT242D-R: GTACCCATAGTCACCCATGAC

*qA. brassicicola CutinaseA*-F: CACTGCGCCCAATGATGAAC
*qA. brassicicola CutinaseA*-R: GTAGCCGAACAACACGACACC

*qPR1*-F: GTGGGTTAGCGAGAAGGCTA
*qPR1*-R: ACTTTGGCACATCCGAGTCT

*qERF4*-F: ATGGGGATCGGTAACGTAGG
*qERF4*-R: CGATCTAAACGCCGATGTC

*qORA59*-F: TCGCGGCCGAGATAAGAGACTC
*qORA59*-R: TCCGGAGAGATTCTTCAACGACATCC

*qERF104*-F: CACGGCAGTGTCGTAAGTCCCA
*qERF104*-R: GAGTGAGACGAAGACCGTGGG

*qMKK9*-F: CAGTTGATGCGAGAGATGGA
*qMKK9*-R: GCGAGTTTTTGCTCCGTTAC

*qMPK6*-F: CGTCCCGGGATGGACGGTG
*qMPK6*-R: ATAGCGGCCGCCTATTCGTGATAT

*qPDF1.2*-F: TTCTCTTTGCTGCTTTCGACGCA
*qPDF1.2*-R: TTGCATGATCCATGTTTGGCTCCTT

*qA. thaliana Actin2*-F: GTCGTACAACCGGTATTGTGCTG
*qA. thaliana Actin2*-R: CTCTCTCTGTAAGGATCTTCATGAGGT

*qFRK1*-F: ATCTTCGCTTGGAGCTTCTC

*qFRK1*-R: TGCAGCGCAAGGACTAGA

*qBIK1*-F: ACTTATGGGTACGCCGCGCCTGAGT
*qBIK1*-R: GGCACGGACCACTTGGTCCA

*qPDF1.2*-F: TTCTCTTTGCTGCTTTCGACGCA
*qPDF1.2*-R: TTGCATGATCCATGTTTGGCTCCTT

*qA. thaliana Actin2*-F: GTCGTACAACCGGTATTGTGCTG
*qA. thaliana Actin2*-R: CTCTCTCTGTAAGGATCTTCATGAGGT

*qFRK1*-F: ATCTTCGCTTGGAGCTTCTC
*qFRK1*-R: TGCAGCGCAAGGACTAGA

*qBIK1*-F: ACTTATGGGTACGCCGCGCCTGAGT
*qBIK1*-R: GGCACGGACCACTTGGTCCA

**ChIP primers**
Actin F: 5′-CGTTTCGCTTTCCTTAGTGTTAGCT-3′
Actin R: 5′-AGCGAACGGATCTAGAGACTCACCTTG-3′

BIK1 promoter region A-F: 5′- CTGTAACATCCGATTCAACTGGAG-3′
BIK1 promoter region A-R: 5′- TACTTGGACTTGCCGTGTCTTCCA-3′

BIK promoter region B-F: 5′- CGAGTTCCCTACGACAAGATAC-3′
BIK promoter region B-R:5′- CTTCTGAAATTTAGACAGAGAGAA-3′

**References:**
**Kosugi S, Ohashi Y** (2000) Cloning and DNA-binding properties of a tobacco Ethylene-Insensitive3 (EIN3) homolog. Nucleic acids research **28:** 960-967