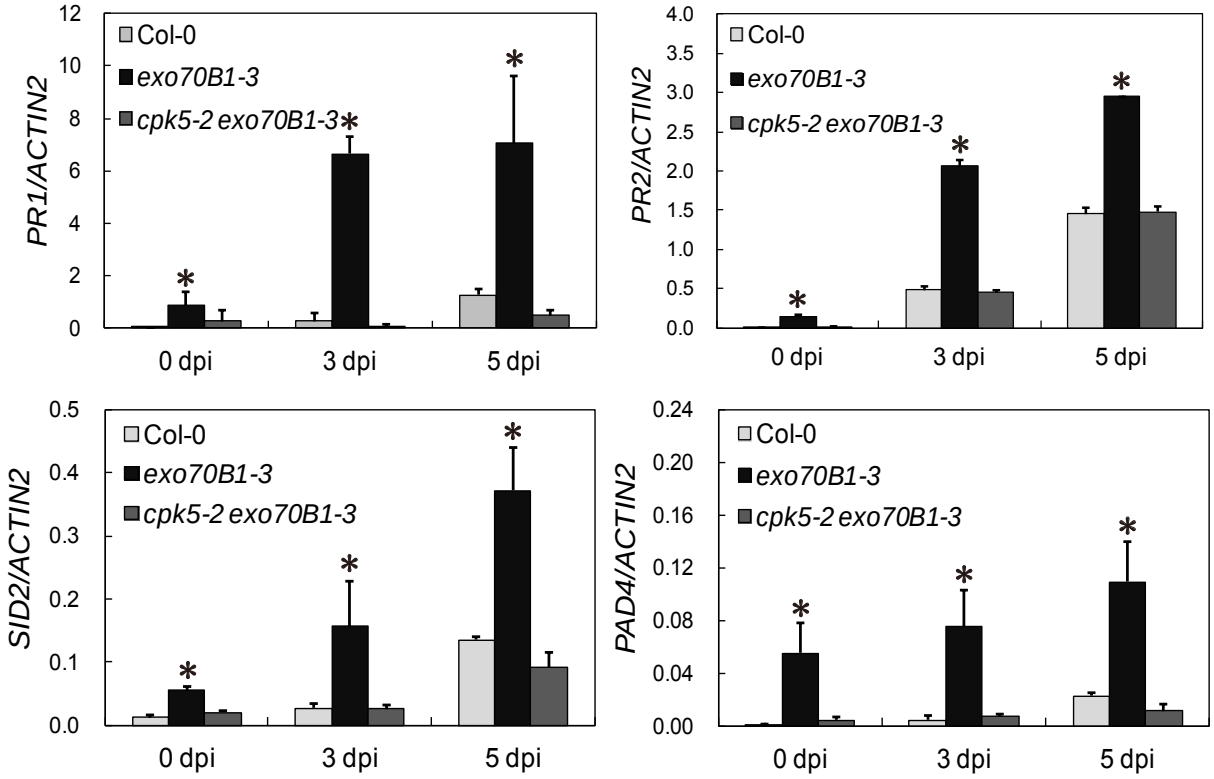
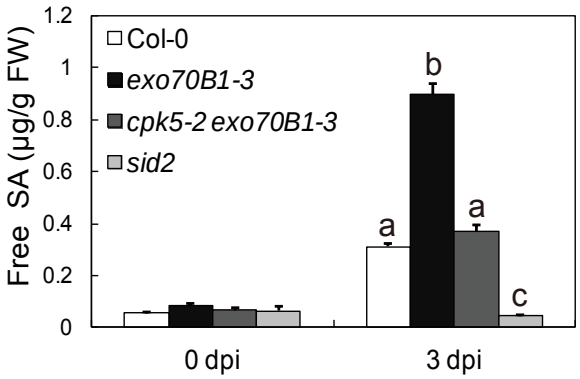



**Supplemental Figure 1. *cpk5-2* suppresses the expression of defense-related genes in *exo70B1-3*.** (Supports Figure 1)

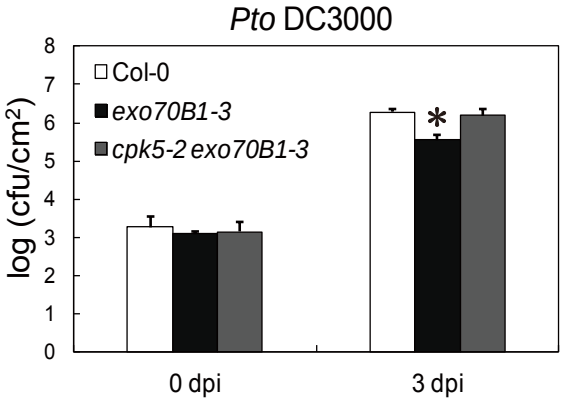
Transcript accumulation of *PR1*, *PR2*, *SID2*, and *PAD4* was examined by reverse transcription quantitative PCR (RT-qPCR). RNA was isolated from leaves of four-week-old plants at different time points after infection with *G. cichoracearum*. *ACT2* was used as an internal control. Results represent mean and standard deviation from three independent biological samples. The asterisks indicate statistically significant differences ($P < 0.05$; one-way ANOVA). The experiments were repeated three times with similar results.




**Supplemental Figure 2. *cpk5-2* suppresses powdery mildew-induced salicylic acid accumulation in *exo70B1-3*.**

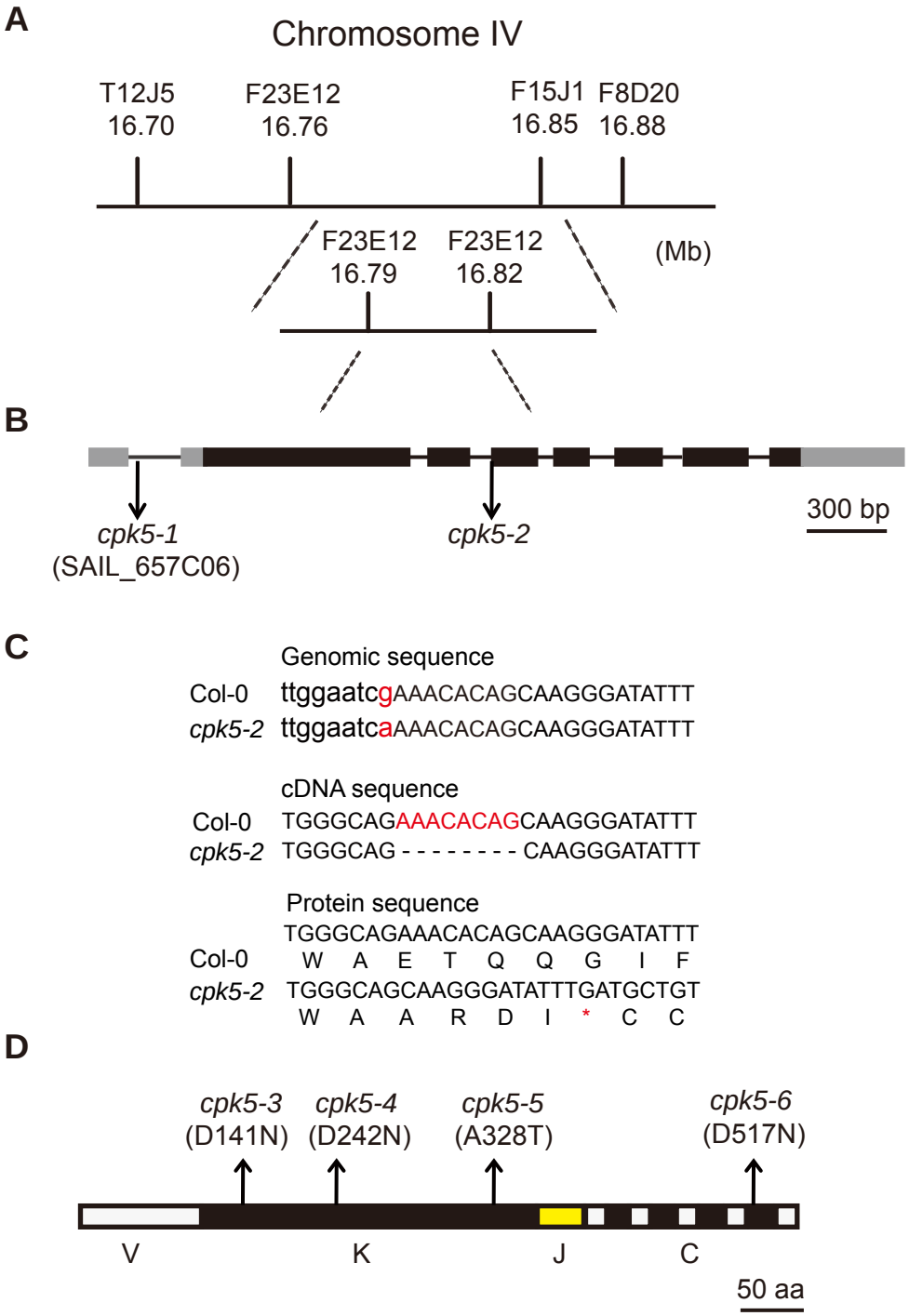
(Supports Figure 1)

Four-week-old plants were infected with *G. cichoracearum*. Salicylic acid was extracted from leaves at 0 dpi and 3 dpi. FW , fresh weight. Bars represent mean and standard deviation from three biological samples. Lower-case letters indicate statistically significant differences ($P < 0.05$, one-way ANOVA).




**Supplemental Figure 3. *cpk5-2* suppresses *exo70B1-3*-mediated resistance to *Pto* DC3000.**
(Supports Figure 1)

Four-week-old plants were inoculated with *Pto* DC3000 at OD600 = 0.0005. The number of bacteria was counted at 3 hours and 3 days post inoculation. Bars represent mean and standard deviation of three biological samples. The asterisk indicates statistically significant difference ($P < 0.05$, one-way ANOVA). The experiment was performed three times with similar results.



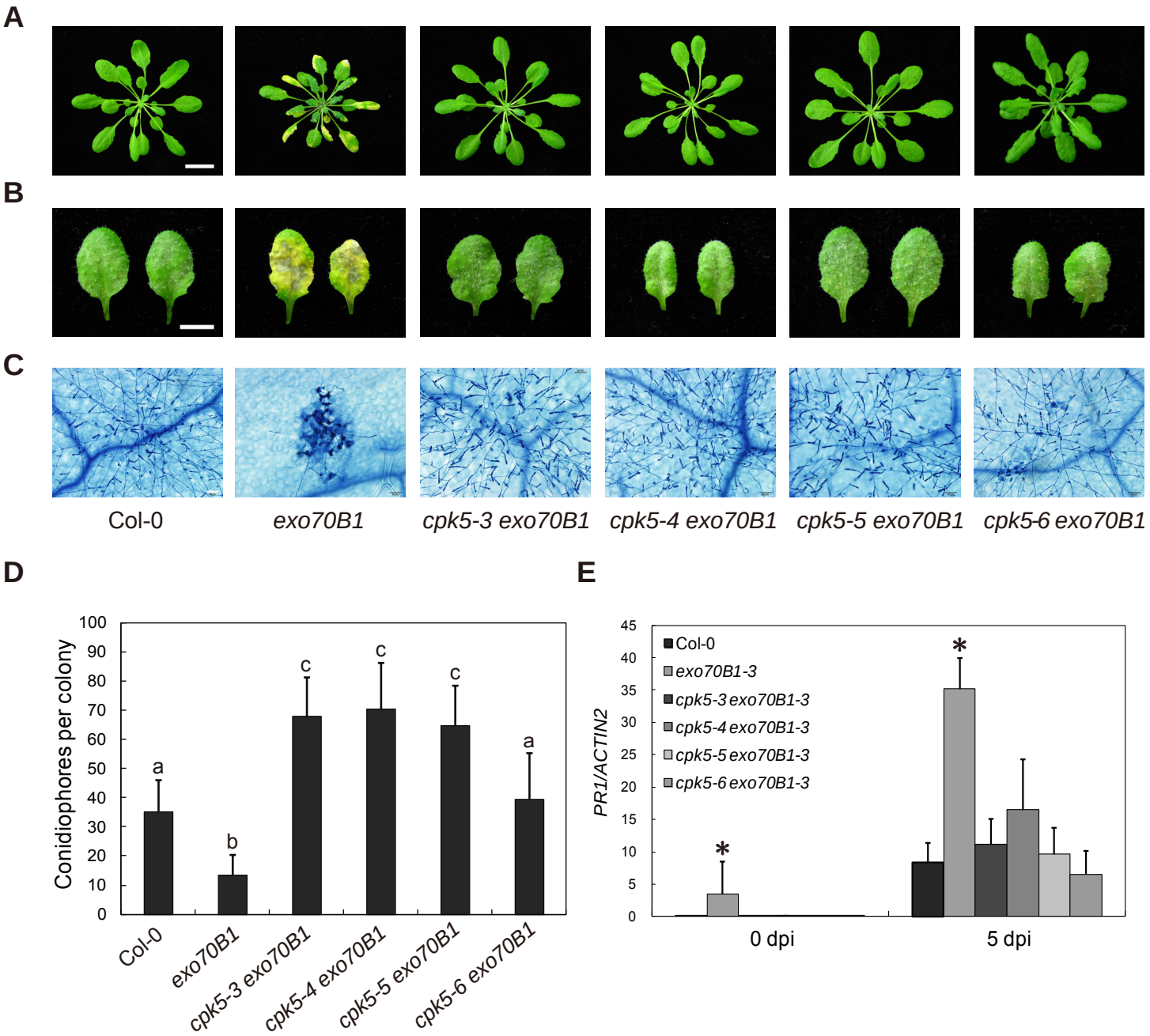

**Supplemental Figure 4. Map-based cloning of *CPK5*.** (Supports Figure 1)

**(A)** The *cpk5-2* mutation was identified by standard map-based cloning. Markers and bacterial artificial chromosome (BAC) clones are indicated.

**(B)** Structure of *CPK5*. The *cpk5-2* mutation is a nucleotide change (G1522A), leading to premature termination. The *cpk5-1* mutant is a previously identified T-DNA insertion mutation; the insertion site is indicated. Lines represent introns, and black and gray boxes represent exons and untranslated regions, respectively.

**(C)** The *cpk5-2* mutation results in a premature stop codon. The *CPK5* genomic DNA, cDNA and protein sequences are shown. In the genomic DNA sequence, the lower-case and upper-case letters represent introns and exons, respectively. The *cpk5-2* mutation (G1522A) in the intron is shown in red. The 8-bp nucleotide deletion in the *CPK5* cDNA sequence resulting from *cpk5-2* mutation is shown in red. The premature stop codon in the *cpk5-2* protein sequence is indicated by red asterisk.

**(D)** Structure of CPK5. V , N-terminal variable domain; K, kinase domain; J, autoinhibitory junction domain; C, CaM-like domain. The arrows indicate four additional *cpk5* mutations identified in an *exo70B1-3* suppressor screen.




**Supplemental Figure 5. The *cpk5* alleles suppress cell death and resistance to *G. cichoracearum* as well as *PR1* accumulation in *exo70B1-3*.** (Supports Figure 1)

**(A)** Six-week-old plants were photographed under short-day conditions. The wild type and *cpk5 exo70B1-3* mutants did not show cell death, but pronounced cell death was observed in the *exo70B1-3* mutant. Bar = 2.4 cm.

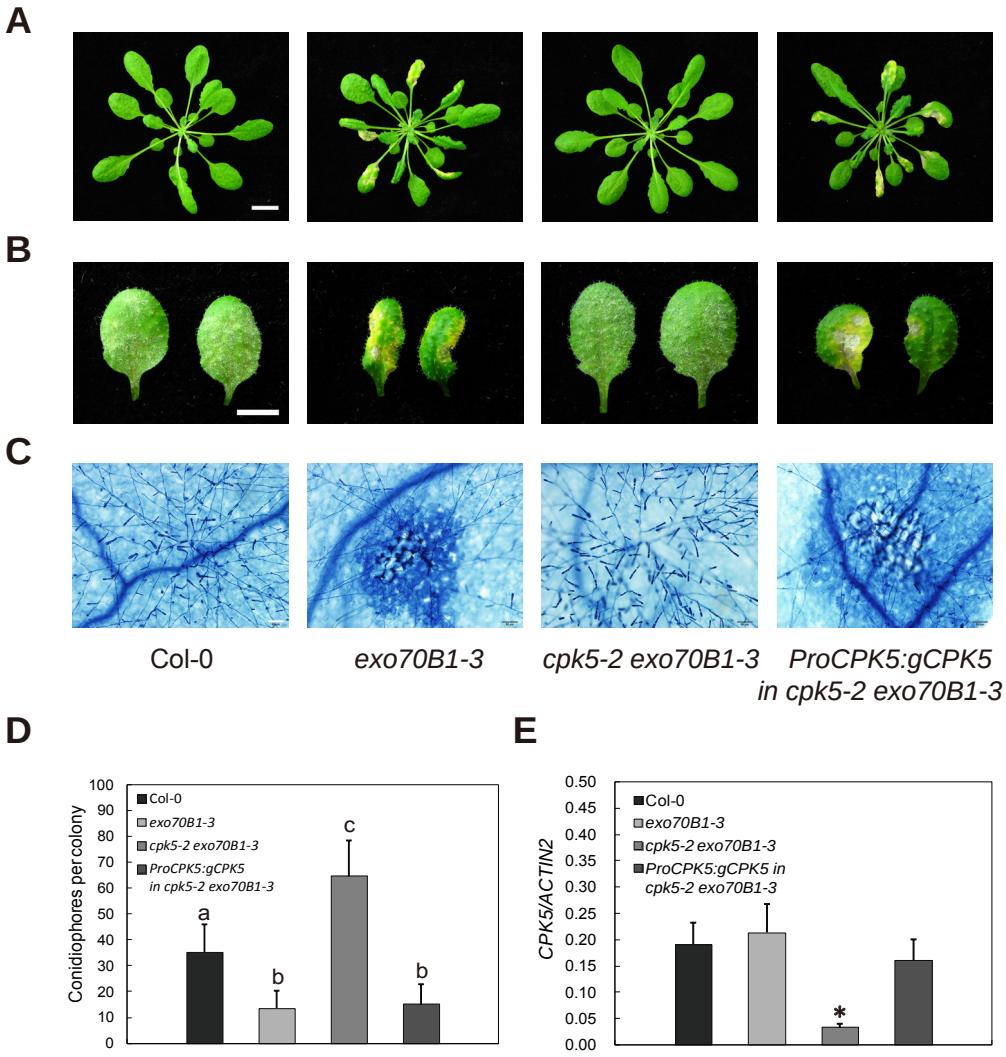
**(B)** Four-week-old plants were infected with *G. cichoracearum*. The leaves were detached and photographed at 8 dpi. The wild type and *cpk5 exo70B1-3* mutants were susceptible, but *exo70B1-3* was resistant to *G. cichoracearum*. Bar = 0.5 cm.

**(C)** The leaves were stained with trypan blue after infection with *G. cichoracearum* at 8 dpi. Bar = 50 µm.

**(D)** Quantification of fungal growth in plants at 5 dpi by counting the number of conidiophores per colony. Bars represent means and standard deviation ( $n \geq 24$). Lower-case letters indicate statistically significant differences ($P < 0.05$, one-way ANOVA). The experiments were repeated two times with similar results.

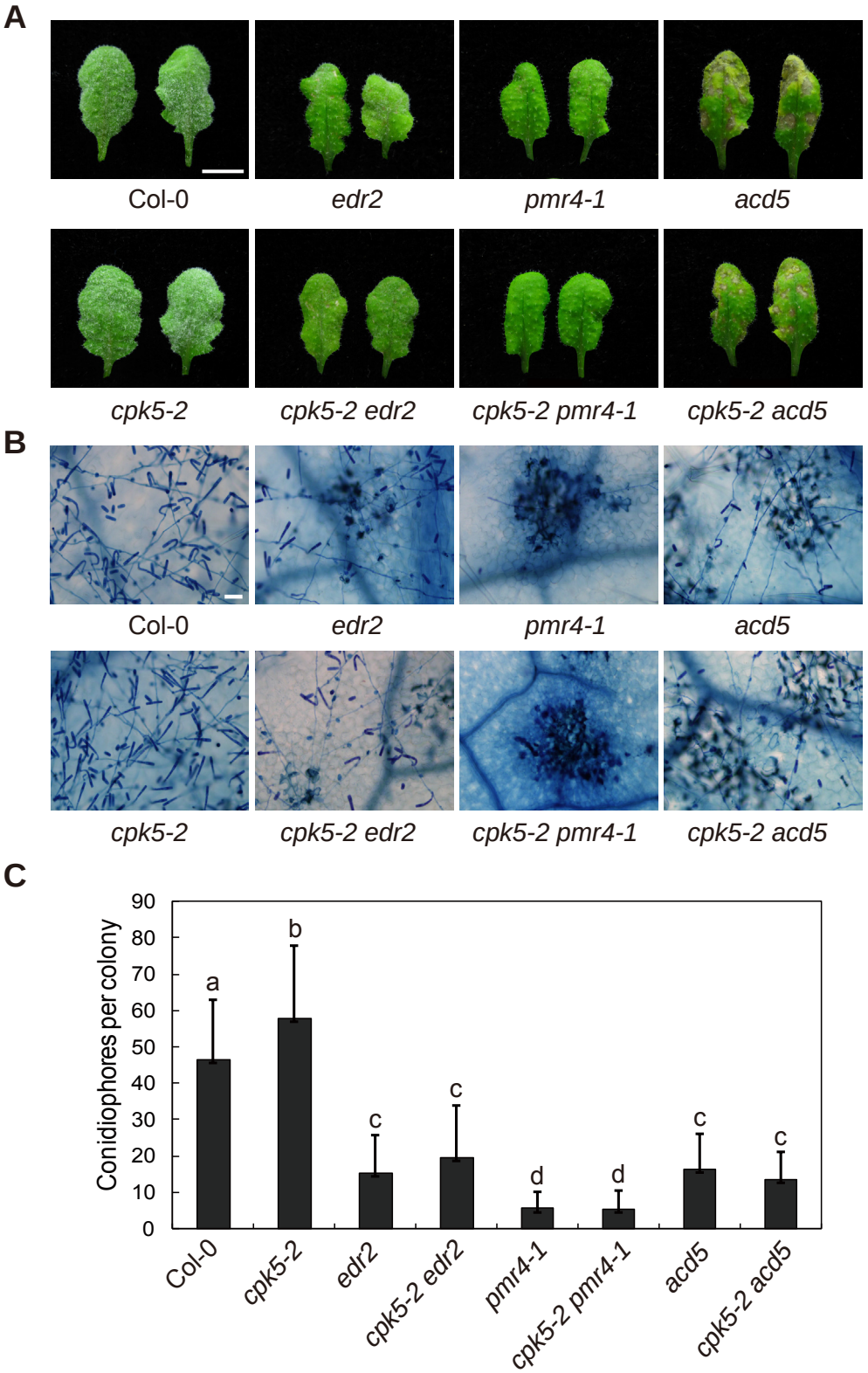
**(E)** *PR1* transcript level was examined by RT-qPCR. RNA was isolated from four-week-old plants at indicated time points after infection with *G. cichoracearum*. *ACT2* was used as an internal control. Bars represent standard deviation from three independent biological samples. Three technical replicates for each biological sample were performed. The asterisks indicate statistically significant differences ($P < 0.05$; one-way ANOVA). The experiments were repeated two times with similar results.

"*exo70B1*" indicates plants carrying the *exo70B1-3* allele.




**Supplemental Figure 6. Complementation of the *cpk5-2* mutation.**
(Supports Figure 1)

**(A)** Six-week-old plants were photographed under short-day conditions. The *CPK5* genomic sequence under its native promoter was transformed into *cpk5-2 exo70B1-3* plants. The *CPK5* genomic clone complemented the *cpk5-2* mutation. Bar = 2.4 cm.
**(B)** Four-week-old plants were infected with *G. cichoracearum* and the leaves were photographed at 8 dpi. Bar = 0.5 cm.
**(C)** Infected leaves were stained with trypan blue at 8 dpi to visualize fungal structures and dead cells. Bar = 50 µm.
**(D)** Fungal growth was assessed by counting the number of conidiophores per colony at 5 dpi. Bars represent means and standard deviation ( $n \geq 24$). Lower-case letters indicate statistically significant differences ($P < 0.05$, one-way ANOVA). The experiments were repeated two times with similar results.
**(E)** *CPK5* transcript level was examined by RT-qPCR. RNA was isolated from five-week-old plants. Bars represent standard deviation from three independent biological samples. Three technical replicates for each biological sample were performed. The asterisks indicate statistically significant differences ($P < 0.05$; one-way ANOVA). The experiments were repeated two times with similar results.

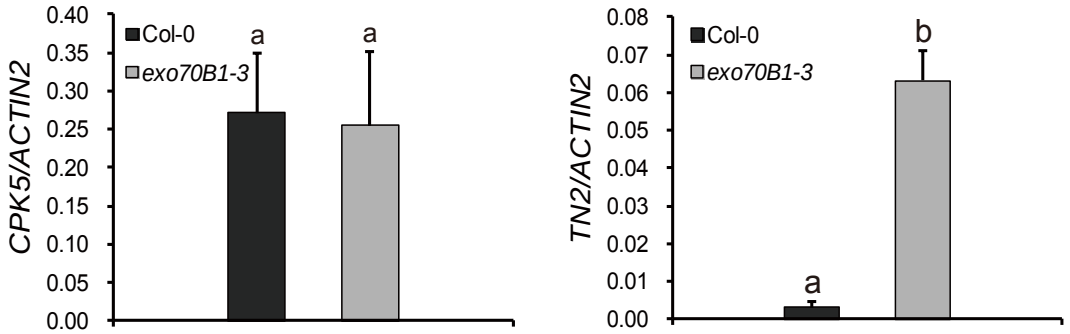



**Supplemental Figure 7. *cpk5-2* does not suppress *edr2*-, *pmr4*-, or *acd5*-mediated resistance to *G. cichoracearum*.** (Supports Figure 3)

**(A)** Four-week-old plants were infected with *G. cichoracearum*. Representative leaves were removed and photographed at 8 dpi. The *edr2*, *pmr4-1*, and *acd5* mutants were more resistant to *G. cichoracearum* than wild type, and the resistance of the *cpk5-2 edr2*, *cpk5-2 pmr4-1*, and *cpk5-2 acd5* double mutants was similar to that of the respective single mutants. Bar = 0.5 cm.

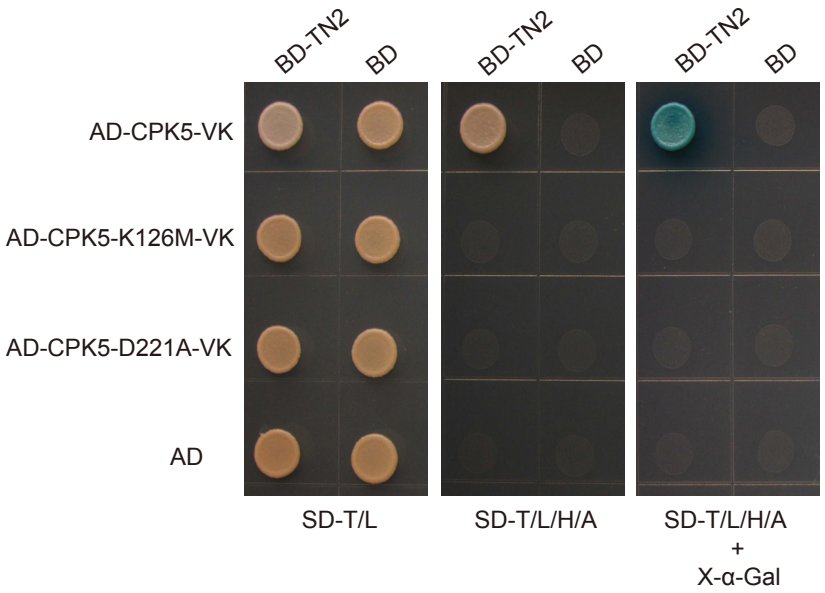
**(B)** Leaves were stained with trypan blue after infection with *G. cichoracearum* at 8 dpi. Bar = 50 μm.

**(C)** Fungal growth in plants was quantified at 5 dpi by counting the number of conidiophores per colony. Bars represent means and standard deviation ($n \geq 27$). Lower-case letters indicate statistically significant differences ($P < 0.05$, one-way ANOVA). The experiment was performed three times with similar results.



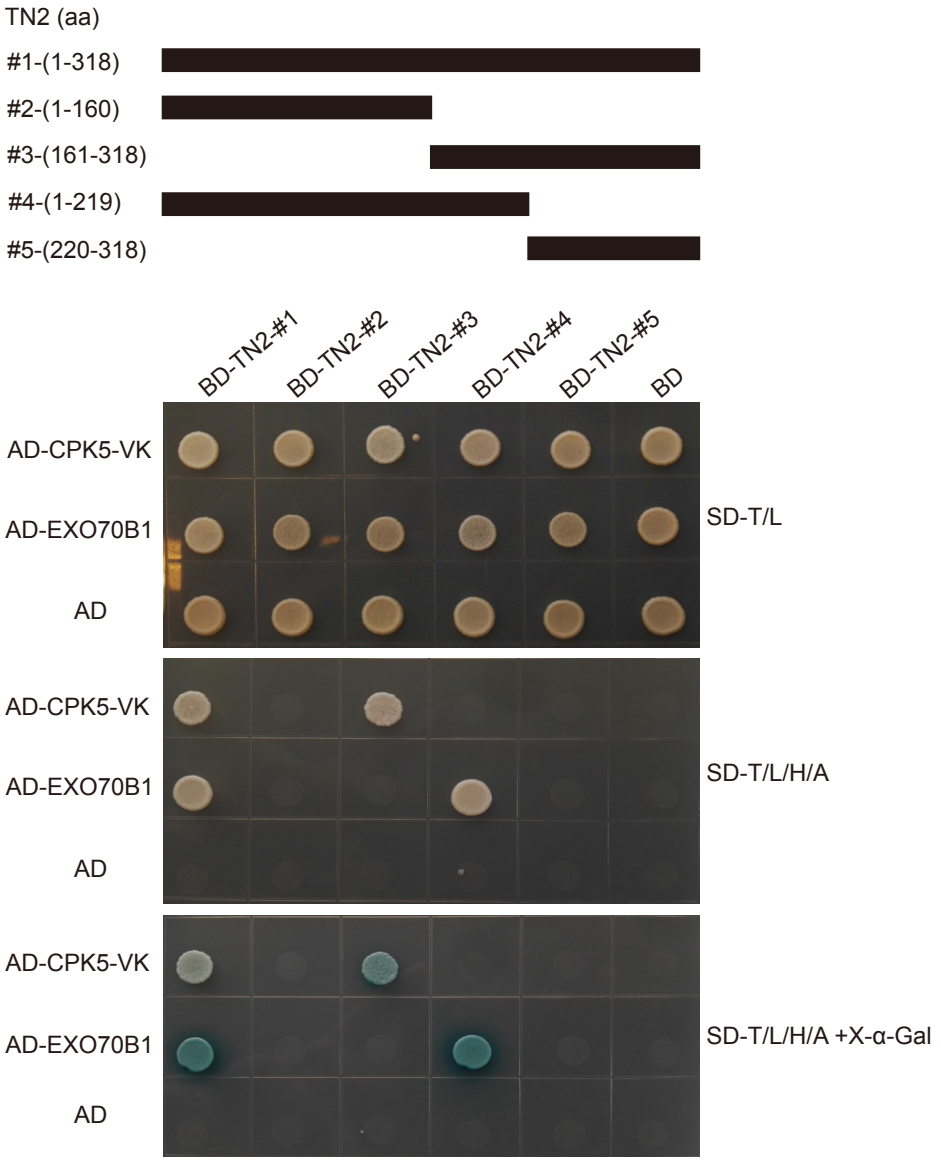

**Supplemental Figure 8. *CPK5* transcript level was not significantly changed in *exo70B1-3*.**
(Supports Figure 5)

*CPK5* and *TN2* transcript levels were examined by RT-qPCR. The RNA was extracted from five-week-old plants. Bars represent standard deviation from three independent biological samples. Three technical replicates for each biological sample were performed. The lower-case letters indicate statistically significant differences ($P < 0.05$; Student's *t*-test). This experiment was performed three times with similar results.



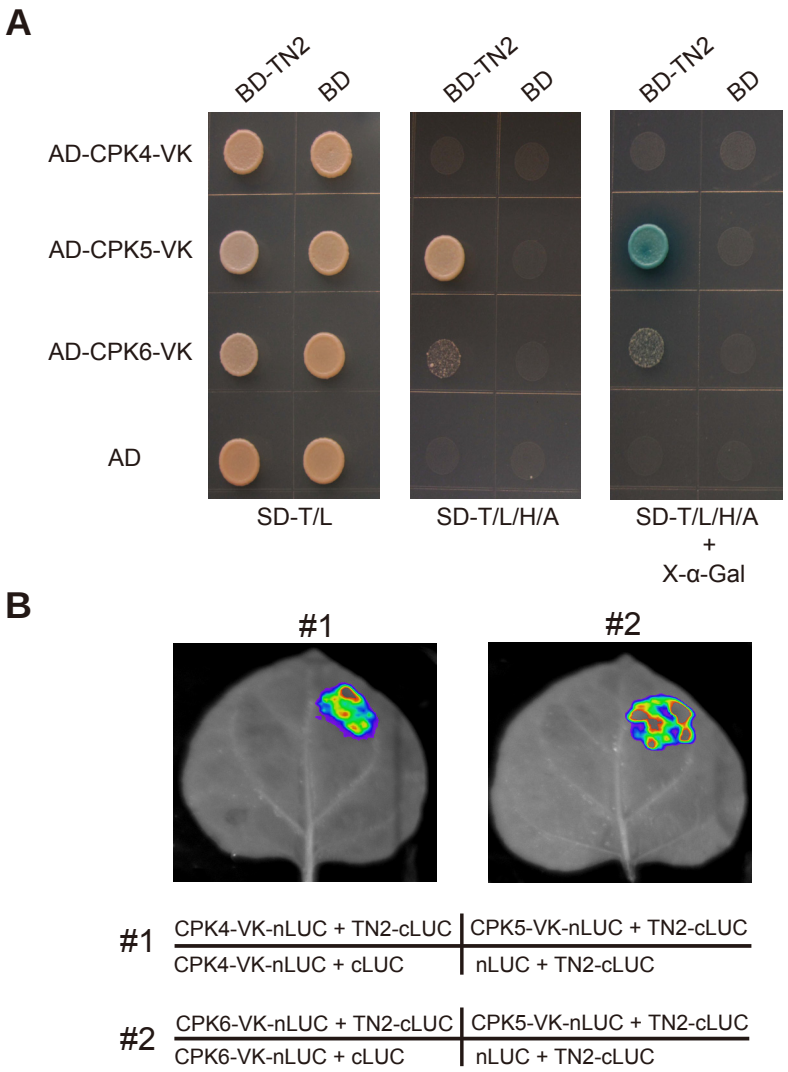

**Supplemental Figure 9. The K126 and D221 residues of CPK5 are critical for the interaction between CPK5-VK and TN2.**
(Supports Figure 5)

Yeast two-hybrid assay. The coding sequences of CPK5-VK-K126M and CPK5-VK-D221A were fused to the AD. The coding sequences of TN2 were fused to BD. Different pairs of constructs were cotransformed into AH109. Yeast cells with the indicated plasmids were dropped onto SD-Leu-Trp or SD-Ade-His-Leu-Trp with or without X-α-Gal, respectively. Photographs were taken after 5 days of incubation.



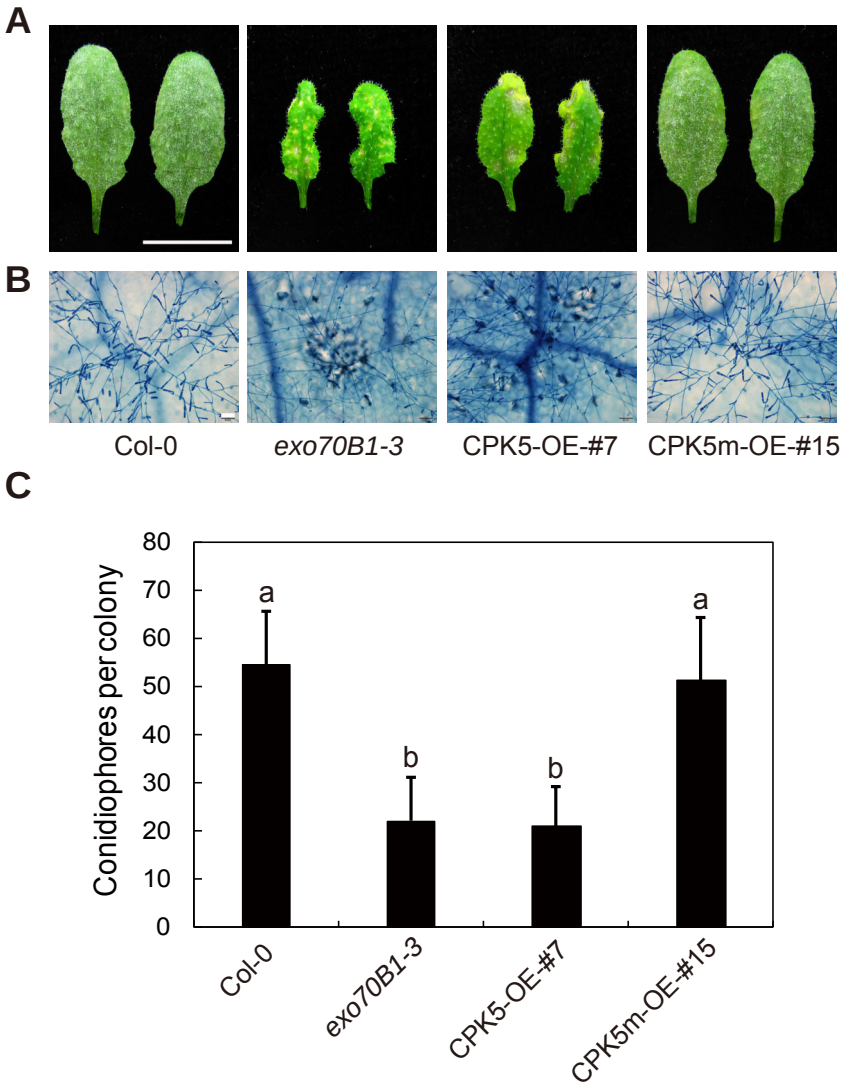

**Supplemental Figure 10. CPK5-VK interacts with the TN2-NBS domain, but not the TIR domain.** (Supports Figure 5)

Yeast two-hybrid assay. Different truncated fragments of TN2 and CPK5-VK were fused to BD and AD, respectively. Different pairs of constructs were cotransformed into AH109. Yeast cells containing the indicated plasmids were spotted onto SD-Leu-Trp or SD-Ade-His-Leu-Trp with or without X-α-Gal, respectively. Photographs were taken after 5 days incubation.



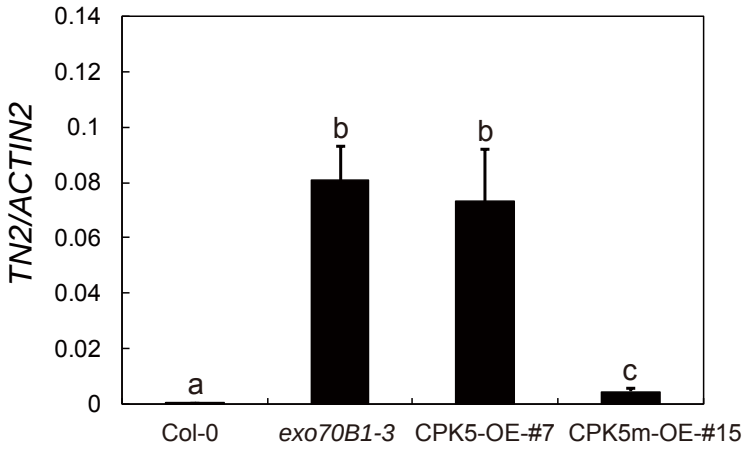

**Supplemental Figure 11. CPK4-VK and CPK6-VK do not interact with TN2.**
(Supports Figure 5)

**(A)** Yeast two-hybrid assay. The coding sequences of CPK4-VK and CPK6-VK were fused to AD. The coding sequence of TN2 was fused to BD. Different pairs of constructs were cotransformed into AH109. A 10 µL suspension (OD600 = 0.5) of each cotransformant was dropped onto Synthetic Dropout (SD) medium lacking Leu and Trp and SD medium lacking Ade, His, Leu, and Trp with or without X-α-Gal, respectively. Photographs were taken after 5 days of incubation.
**(B)** Firefly luciferase complementation imaging (LUC) assay. *N. benthamiana* leaves were co-infiltrated with agrobacterium strains containing different pairs of constructs. LUC images were captured using a cooled CCD imaging apparatus.



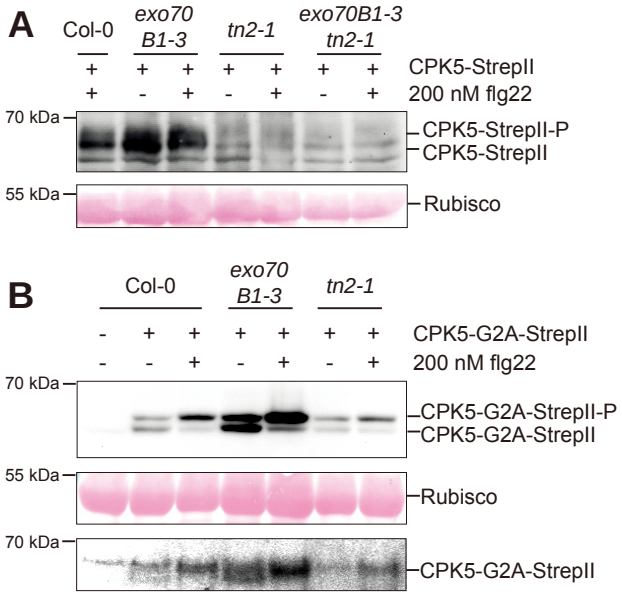

**Supplemental Figure 12. *CPK5-OE* transgenic plants display cell death and resistance to *G. cichoracearum*.**
(Supports Figure 6)

**(A)** Four-week-old plants were infected with *G. cichoracearum*. The leaves were detached and photographed at 8 dpi. Bar = 2.4 cm.
**(B)** The leaves were stained by trypan blue after infection with *G. cichoracearum* at 8 dpi. Bar = 50 μm.
**(C)** Quantification of fungal growth in plants at 5 dpi by counting the number of conidiophores per colony. Bars represent means and standard deviation ($n \geq 18$). Lower-case letters indicate statistically significant differences ($P < 0.05$, one-way ANOVA). The experiment was performed three times with similar results.




**Supplemental Figure 13. *TN2* transcript accumulates in the *CPK5* overexpression line.**
(Supports Figure 6)

*TN2* transcript levels were examined by RT-qPCR. Leaves were detached from five-week-old plants for RNA isolation. *ACT2* was used as an internal control. Bars represent mean and standard deviation of values obtained from three independent biological samples. Lower-case letters indicate statistically significant differences ($P < 0.05$, one-way ANOVA). The experiment was performed three times with similar results.




**Supplemental Figure 14. CPK5 and CPK5-G2A accumulate after ectopic expression in *exo70B1-3* but not in *tn2-1*.**
(Supports Figure 7)

**(A)** CPK5-StrepII was transiently expressed in mesoph yll protoplasts derived from six-week-old wild type, mutant lines *exo70B1-3* or *tn2-1*, or double mutant line *exo70B1-3 tn2-1*, and CPK5 protein levels were assessed by immunoblotting after treatment for 15 min with flg22 (+) or buffer (-). The experiment was performed several times with similar results.
**(B)** The CPK5-G2A-StrepII variant, which lacks plasma membrane localization, was transiently expressed in protoplasts and elicited as above, and proteins were analyzed for kinase activity via an in-gel kinase assay using MBP as substrate (autoradiography, lower panel) or visualized by immunoblot with Strep-Tactin HRP (upper panel). The experiment was performed two times with similar results.

**Supplemental Table 1. Primers used in this study**

| Primer name: 5′-3′ sequence (enzyme) |
|---|
| *cpk5-2*-dCaps-F： TATTGCTAAGCGGAGTCCCACC (XmnI cuts) |
| *cpk5-2*-dCaps-R： ACAGCATCAAATATCCCTTGAAGTGTT |
| CPK5-genomic-pEGAD-F：TGCAGAGCTCACCATGTGACTACGACAACTACT(SacI) |
| CPK5-genomic-pEGAD-R： ATGTACCGGTTGCGCGTCTCTCATGCTAATGTTT(AgeI) |
| CPK5-VKJC-AD-F： GTACCATATGATGGGCAATTCTTGCCGTGGAT(NdeI) |
| CPK5-VKJC-AD-R： AGTCGGATCCCTACGCGTCTCTCATGCTAATG(BamHI) |
| CPK5-VK-AD-F： GTACCATATGATGGGCAATTCTTGCCGTGGAT(NdeI) |
| CPK5-VK-AD-R： GCTAGGATCCCTAGATCCATGGATGACGCAAGAC (BamHI) |
| CPK5-JC-AD-F： GTACCATATGTGTGAGAATGGTGTTGCACCAG(NdeI) |
| CPK5-JC-AD-R： AGTCGGATCCCTACGCGTCTCTCATGCTAATG(BamHI) |
| CPK6-VK-AD-F： GTTCCATATGGGCAATTCATGTCGTGGTTCTTT (NdeI) |
| CPK6-VK-AD-R： TAATCCCGGGCTAGATCCATGGATGACGCAAGA (XmaI) |
| CPK4-VK-AD-F： GTAGCATATGATGGAGAAACCAAACCCTAGAAG (NdeI) |
| CPK4-VK-AD-R： ATTAGGATCCCTAAATCCAAGGGTGACACAATG (BamHI) |
| TN2-1-318-BD-F：GTCGCATATGTATTCATCATCGTCTTCTTC (NdeI) |
| TN2-1-318-BD-R：TATAGAATTCTCAAGAAGATTCAGTCCCGG (EcoRI) |
| TN2-1-160-BD-F：GTCGCATATGTATTCATCATCGTCTTCTTC (NdeI) |
| TN2-1-160-BD-R：TATACTGCAGTCAGCAATCACGAGAACAATG (PstI) |
| TN2-161-318-BD-F：GTCACATATGCTGAAGATGACTCGAAGCTA (NdeI) |
| TN2-161-318-BD-R：TATAGAATTCTCAAGAAGATTCAGTCCCGG (EcoRI) |
| TN2-1-219-BD-F：GTCGCATATGTATTCATCATCGTCTTCTTC (NdeI) |
| TN2-1-219-BD-R：TATAGAATTCTCACCAAATTCCAACCACTCTC (EcoRI) |
| TN2-220-318-BD-F：GTCGCATATGGCAAGAGGAGGTAATGGAAG (NdeI) |
| TN2-220-318-BD-R：TATAGAATTCTCAAGAAGATTCAGTCCCGG (EcoRI) |
| CPK5-VKJC-pSY738-F： GTACGTCGACATGGGCAATTCTTGCCGTGG(SalI) |
| CPK5-VKJC-pSY738-R： ATTGGCGGCCGCTTCGCGTCTCTCATGCTAAT(NotI) |
| CPK5-VK-pSY738-F： GTACGTCGACATGGGCAATTCTTGCCGTGG (SalI) |
| CPK5-VK-pSY738-R： GCTAGCGGCCGCTTGATCCATGGATGACGCAAG (NotI) |
| CPK5-VKJC-nLUC-F：GTACGGTACCATGGGCAATTCTTGCCGT(KpnI) |
| CPK5-VKJC-nLUC-R：ATTGGTCGACCGCGTCTCTCATGCTAAT(SalI) |

CPK5-VK-nLUC-F：GTACGGTACCATGGGCAATTCTTGCCGT(KpnI)

CPK5-VK-nLUC-R：TATAGTCGACGATCCATGGATGACGCAAG (SalI)

CPK6-VK-nLUC-F：GTACGGTACCATGGGCAATTCATGTCGTGGTTCT (KpnI)

CPK6-VK-nLUC-R：TAAAGTCGACGATCCATGGATGACGCAAGA (SalI)

CPK4-VK-nLUC-F：GTACGGTACCATGGAGAAACCAAACCCTAG (KpnI)

CPK4-VK-nLUC-R：GATAGTCGACAATCCAAGGGTGACACAATG (SalI)

TN2-cLUC-F：GTCGGGTACCTATTCATCATCGTCTTCTTCT (KpnI)

TN2-cLUC-R：TATACTGCAGTCAAGAAGATTCAGTCCCGG (PstI)

CPK5-genomic-G2A-F： TCCCATTGTTTCATGGCCAATTCTTGCCGTGGA

CPK5-genomic-G2A-R： TCCACGGCAAGAATTGGCCATGAAACAATGGGA

CPK5-genomic-K126M-F： GTTGACTACGCTTGTATGTCAATATCCAAGAGG

CPK5-genomic-K126M-R： CCTCTTGGATATTGACATACAAGCGTAGTCAAC

CPK5-VK-K126M-F： GTTGACTACGCTTGTATGTCAATATCCAAGAGG

CPK5-VK-K126M-R： CCTCTTGGATATTGACATACAAGCGTAGTCAAC

CPK5-VK-D221A-F： GGTGTGATGCATAGAGCCTTGAAGCCTGAGAAT

CPK5-VK-D221A-R： ATTCTCAGGCTTCAAGGCTCTATGCATCACACC

CPK5-genomic-attB-pDONR207-F：

GGGGACAAGTTTGTACAAAAAAGCAGGCTTCACCATGTGACTACGACAACTACT

CPK5-genomic-attB-pDONR207-R：

GGGGACCACTTTGTACAAGAAAGCTGGGTCCGCGTCTCTCATGCTAATGTTTAG

CPK5-CDS-attB-pDONR207-F：

GGGGACAAGTTTGTACAAAAAAGCAGGCTTCGAAGGAGATAGAACCATGGTCATGGGCAA
TTCTTGCCGTGGAT

YC-attB-pDONR207-R：

GGGGACCACTTTGTACAAGAAAGCTGGGTCCTAGTACAGCTCGTCCATGCCGAGAG

**Supplemental Table 2.** ANOVA tables for statistical analyses.

For Figure 1 D

| | Samples | N | alpha = 0.05 | | |
|---|---|---|---|---|---|
| | | | 1 | 2 | 3 |
| Duncan[a,b] | *exo70b1-3* | 18 | 17.9444 | | |
| | Col-0 | 14 | | 46.0000 | |
| | *cpk5-2* *exo70b1-3* | 14 | | | 70.2857 |
| | Significance | | 1.000 | 1.000 | 1.000 |

For Figure 2 D

| | Samples | N | alpha = 0.05 | | |
|---|---|---|---|---|---|
| | | | 1 | 2 | 3 |
| Duncan[a,b] | *exo70b1-3 cpk11* | 26 | 14.1538 | | |
| | *exo70b1-3* | 30 | 15.1000 | | |
| | *exo70b1-3 cpk6* | 30 | 15.6333 | | |
| | *exo70b1-3 cpk4* | 28 | 15.7500 | | |
| | *cpk6* | 37 | | 33.6486 | |
| | *cpk11* | 33 | | 34.7273 | |
| | *cpk4* | 41 | | 35.3415 | |
| | Col-0 | 37 | | 39.1351 | |
| | *cpk5-1* | 28 | | | 51.6786 |
| | *exo70b1-3 cpk5-1* | 29 | | | 56.2069 |
| | Significance | | .650 | .112 | .150 |

For Figure 3 A

| | Samples | N | alpha = 0.05 | | |
|---|---|---|---|---|---|
| | | | 1 | 2 | 3 |
| Duncan[a] | Col-0 | 14 | 43.7857 | | |
| | *cpk5-2* | 14 | | 76.8571 | |
| | *cpk5-1* | 14 | | 82.1429 | |
| | *pad4* | 14 | | | 125.7143 |
| | Significance | | 1.000 | .363 | 1.000 |

For Figure 3 B

| 0 dpi | Samples | N | alpha = 0.05 |
|---|---|---|---|
| | | | 1 |
| Duncan[a] | *pad4* | 3 | 3.3998 |
| | *cpk5-1* | 3 | 3.4066 |
| | *cpk5-2* | 3 | 3.4424 |
| | Col-0 | 3 | 3.6213 |
| | Significance | | .229 |

| 3 dpi | Samples | N | alpha = 0.05 | |
|---|---|---|---|---|
| | | | 1 | 2 |
| Duncan[a] | *cpk5-2* | 3 | 5.7609 | |
| | *cpk5-1* | 3 | 6.2109 | |
| | Col-0 | 3 | 6.3532 | |
| | *pad4* | 3 | | 7.6971 |
| | Significance | | .079 | 1.000 |

**Supplemental Table 2.** ANOVA tables for statistical analyses. (Continued)

For Figure 3 C

| 0 dpi | Samples | N | alpha = 0.05 | |
|---|---|---|---|---|
| | | | 1 | 2 |
| Duncan[a] | Col-0 | 3 | 2.9566 | |
| | *cpk5-1* | 3 | 3.1181 | 3.1181 |
| | *rps2* | 3 | 3.2671 | 3.2671 |
| | *cpk5-2* | 3 | | 3.3474 |
| | Significance | | .080 | .178 |

| 3 dpi | Samples | N | alpha = 0.05 | |
|---|---|---|---|---|
| | | | 1 | 2 |
| Duncan[a] | Col-0 | 3 | 5.7112 | |
| | *cpk5-1* | 3 | 5.7511 | |
| | *cpk5-2* | 3 | 5.9642 | |
| | *rps2* | 3 | | 6.7020 |
| | Significance | | .168 | 1.000 |

For Figure 3 D

| 0 dpi | Samples | N | alpha = 0.05 |
|---|---|---|---|
| | | | 1 |
| Duncan[a] | *cpk5-1* | 3 | 3.4945 |
| | *cpk5-2* | 3 | 3.5816 |
| | Col-0 | 3 | 3.6565 |
| | *pad4* | 3 | 3.6666 |
| | Significance | | .344 |

| 3 dpi | Samples | N | alpha = 0.05 | |
|---|---|---|---|---|
| | | | 1 | 2 |
| Duncan[a] | Col-0 | 3 | 5.1142 | |
| | *cpk5-2* | 3 | 5.2038 | |
| | *cpk5-1* | 3 | 5.4460 | 5.4460 |
| | *pad4* | 3 | | 6.1056 |
| | Significance | | .361 | .080 |

For Supplemental Figure 1 *PR1*

| 0 dpi | Samples | N | alpha = 0.05 | |
|---|---|---|---|---|
| | | | 1 | 2 |
| Duncan[a] | Col-0 | 3 | .0065870 | |
| | *cpk5-2* | 3 | .2868027 | .2868027 |
| | *exo70b1-3* | | | |
| | *exo70b1-3* | 3 | | .8618200 |
| | Significance | | .415 | .123 |

| 3 dpi | Samples | N | alpha = 0.05 | |
|---|---|---|---|---|
| | | | 1 | 2 |
| Duncan[a] | *cpk5-2* | 3 | .0998923 | |
| | *exo70b1-3* | | | |
| | Col-0 | 3 | .2785110 | |
| | *exo70b1-3* | 3 | | 6.6409353 |
| | Significance | | .616 | 1.000 |

| 5 dpi | Samples | N | alpha = 0.05 | |
|---|---|---|---|---|
| | | | 1 | 2 |
| Duncan[a] | *cpk5-2* | 3 | .4858990 | |
| | *exo70b1-3* | | | |
| | Col-0 | 3 | 1.2701640 | |
| | *exo70b1-3* | 3 | | 7.0522263 |
| | Significance | | .543 | 1.000 |

For Supplemental Figure 1 *PR2*

| 0 dpi | Samples | N | alpha = 0.05 | |
|---|---|---|---|---|
| | | | 1 | 2 |
| Duncan[a] | Col-0 | 3 | .0067653 | |
| | *cpk5-2* | 3 | .0101274 | |
| | *exo70b1-3* | | | |
| | *exo70b1-3* | 3 | | .1423141 |
| | Significance | | .692 | 1.000 |

| 3 dpi | Samples | N | alpha = 0.05 | |
|---|---|---|---|---|
| | | | 1 | 2 |
| Duncan[a] | *cpk5-2* | 3 | .4465329 | |
| | *exo70b1-3* | | | |
| | Col-0 | 3 | .4809249 | |
| | *exo70b1-3* | 3 | | 2.0618184 |
| | Significance | | .455 | 1.000 |

| 5 dpi | Samples | N | alpha = 0.05 | |
|---|---|---|---|---|
| | | | 1 | 2 |
| Duncan[a] | Col-0 | 3 | 1.4502477 | |
| | *cpk5-2* | 3 | 1.4803887 | |
| | *exo70b1-3* | | | |
| | *exo70b1-3* | 3 | | 2.9485384 |
| | Significance | | .549 | 1.000 |

For Supplemental Figure 1 *SID2*

| 0 dpi | Samples | N | alpha = 0.05 | |
|---|---|---|---|---|
| | | | 1 | 2 |
| Duncan[a] | Col-0 | 3 | .0127833 | |
| | *cpk5-2* | 3 | .0200796 | |
| | *exo70b1-3* | | | |
| | *exo70b1-3* | 3 | | .0555138 |
| | Significance | | .122 | 1.000 |

| 3 dpi | Samples | N | alpha = 0.05 | |
|---|---|---|---|---|
| | | | 1 | 2 |
| Duncan[a] | *cpk5-2* | 3 | .0261251 | |
| | *exo70b1-3* | | | |
| | Col-0 | 3 | .0269666 | |
| | *exo70b1-3* | 3 | | .1569492 |
| | Significance | | .981 | 1.000 |

| 5 dpi | Samples | N | alpha = 0.05 | |
|---|---|---|---|---|
| | | | 1 | 2 |
| Duncan[a] | *cpk5-2* | 3 | .0916237 | |
| | *exo70b1-3* | | | |
| | Col-0 | 3 | .1348391 | |
| | *exo70b1-3* | 3 | | .3717127 |
| | Significance | | .254 | 1.000 |

**Supplemental Table 2.** ANOVA tables for statistical analyses. (Continued)

For Supplemental Figure 1 *PAD4*

| 0 dpi | Samples | N | alpha = 0.05 | |
|---|---|---|---|---|
| | | | 1 | 2 |
| Duncan[a] | Col-0 | 3 | .0011683 | |
| | *cpk5-2 exo70b1-3* | 3 | .0046389 | |
| | *exo70b1-3* | 3 | | .0552615 |
| | Significance | | .757 | 1.000 |

| 3 dpi | Samples | N | alpha = 0.05 | |
|---|---|---|---|---|
| | | | 1 | 2 |
| Duncan[a] | Col-0 | 3 | .0043106 | |
| | *cpk5-2 exo70b1-3* | 3 | .0068724 | |
| | *exo70b1-3* | 3 | | .0753591 |
| | Significance | | .850 | 1.000 |

| 5 dpi | Samples | N | alpha = 0.05 | |
|---|---|---|---|---|
| | | | 1 | 2 |
| Duncan[a] | *cpk5-2 exo70b1-3* | 3 | .0116196 | |
| | Col-0 | 3 | .0225771 | |
| | *exo70b1-3* | 3 | | .1090998 |
| | Significance | | .486 | 1.000 |

For Supplemental Figure 2

| 0 dpi | Samples | N | alpha = 0.05 |
|---|---|---|---|
| | | | 1 |
| Duncan[a] | Col-0 | 3 | .05644650 |
| | *sid2* | 3 | .06373000 |
| | *cpk5-2 exo70b1-3* | 3 | .06537550 |
| | *exo70b1-3* | 3 | .08417600 |
| | Significance | | .074 |

| 3 dpi | Samples | N | alpha = 0.05 | | |
|---|---|---|---|---|---|
| | | | 1 | 2 | 3 |
| Duncan[a] | *sid2* | 3 | .04454650 | | |
| | Col-0 | 3 | | .31236950 | |
| | *cpk5-2 exo70b1-3* | 3 | | .36756500 | |
| | *exo70b1-3* | 3 | | | .89499900 |
| | Significance | | 1.000 | .089 | 1.000 |

For Supplemental Figure 3

| 0 dpi | Samples | N | alpha = 0.05 |
|---|---|---|---|
| | | | 1 |
| Duncan[a] | *exo70b1-3* | 3 | 3.090638 |
| | *cpk5-2 exo70b1-3* | 3 | 3.151615 |
| | Col-0 | 3 | 3.264296 |
| | Significance | | .397 |

| 3 dpi | Samples | N | alpha = 0.05 | |
|---|---|---|---|---|
| | | | 1 | 2 |
| Duncan[a] | *exo70b1-3* | 3 | 5.556497 | |
| | *cpk5-2 exo70b1-3* | 3 | | 6.193469 |
| | Col-0 | 3 | | 6.273091 |
| | Significance | | 1.000 | .469 |

For Supplemental Figure 5 D

| | Samples | N | alpha = 0.05 | | |
|---|---|---|---|---|---|
| | | | 1 | 2 | 3 |
| Duncan[a,b] | *exo70b1-3* | 26 | 13.5385 | | |
| | Col-0 | 27 | | 35.1852 | |
| | *cpk5-6 exo70b1-3* | 29 | | 39.3103 | |
| | *cpk5-5 exo70b1-3* | 27 | | | 64.6667 |
| | *cpk5-3 exo70b1-3* | 32 | | | 67.7188 |
| | *cpk5-4 exo70b1-3* | 32 | | | 70.5000 |
| | Significance | | 1.000 | .253 | .128 |

For Supplemental Figure 5 E

| 0 dpi | Samples | N | alpha = 0.05 | |
|---|---|---|---|---|
| | | | 1 | 2 |
| Duncan[a,b] | Col-0 | 4 | .00179348 | |
| | *cpk5-5 exo70b1-3* | 4 | .00330734 | |
| | *cpk5-3 exo70b1-3* | 4 | .00759653 | |
| | *cpk5-6 exo70b1-3* | 4 | .01925924 | |
| | *cpk5-4 exo70b1-3* | 4 | .05559451 | |
| | *exo70b1-3* | 3 | | 3.43180783 |
| | Significance | | .970 | 1.000 |

| 5 dpi | Samples | N | alpha = 0.05 | | |
|---|---|---|---|---|---|
| | | | 1 | 2 | 3 |
| Duncan[a,b] | *cpk5-6 exo70b1-3* | 4 | 6.56568214 | | |
| | Col-0 | 4 | 8.42062563 | | |
| | *cpk5-5 exo70b1-3* | 4 | 9.64448648 | 9.64448648 | |
| | *cpk5-3 exo70b1-3* | 4 | 11.15078572 | 11.15078572 | |
| | *cpk5-4 exo70b1-3* | 4 | | 16.48335879 | |
| | *exo70b1-3* | 3 | | | 35.20505582 |
| | Significance | | .240 | .078 | 1.000 |

**Supplemental Table 2.** ANOVA tables for statistical analyses. (Continued)

For Supplemental Figure 6 D

| | Samples | N | alpha = 0.05 | | |
|---|---|---|---|---|---|
| | | | 1 | 2 | 3 |
| Duncan[a,b] | *exo70b1-3* | 26 | 13.5385 | | |
| | *ProCPK5:gCPK5* in *cpk5-2 exo70b1-3* | 24 | 15.0833 | | |
| | Col-0 | 27 | | 35.1852 | |
| | *cpk5-2 exo70b1-3* | 26 | | | 64.6538 |
| | Significance | | .585 | 1.000 | 1.000 |

For Supplemental Figure 6 E

| | Samples | N | alpha = 0.05 | |
|---|---|---|---|---|
| | | | 1 | 2 |
| Duncan[a,b] | *cpk5-2 exo70b1-3-105* | 4 | .03355315 | |
| | *ProCPK5:gCPK5* in *cpk5-2 exo70b1-3* | 3 | | .15990554 |
| | Col-0 | 4 | | .19125525 |
| | *exo70b1-3* | 3 | | .21282497 |
| | Significance | | 1.000 | .114 |

For Supplemental Figure 7 C

| | Samples | N | alpha = 0.05 | | | |
|---|---|---|---|---|---|---|
| | | | 1 | 2 | 3 | 4 |
| Duncan[a,b] | *cpk5-2 pmr4-1* | 29 | 5.3793 | | | |
| | *pmr4-1* | 31 | 5.5806 | | | |
| | *cpk5-2 acd5* | 33 | | 13.5455 | | |
| | *edr2* | 33 | | 15.3030 | | |
| | *acd5* | 36 | | 16.3056 | | |
| | *cpk5-2 edr2* | 38 | | 19.6579 | | |
| | Col-0 | 29 | | | 46.4138 | |
| | *cpk5-2* | 29 | | | | 57.8621 |
| | Significance | | .947 | .065 | 1.000 | 1.000 |

For Supplemental Figure 12 C

| | Samples | N | alpha = 0.05 | |
|---|---|---|---|---|
| | | | 1 | 2 |
| Duncan[a,b] | CPK5-OE-#7 | 23 | 20.8261 | |
| | *exo70B1-3* | 18 | 22.0000 | |
| | CPK5m-OE-#15 | 28 | | 51.0714 |
| | Col-0 | 23 | | 54.3913 |
| | Significance | | .718 | .308 |

For Supplemental Figure 13

| | Samples | N | alpha = 0.05 | |
|---|---|---|---|---|
| | | | 1 | 2 |
| Duncan[a] | Col-0 | 4 | .00009425 | |
| | CPK5-OE-#15 | 4 | .00459800 | |
| | CPK5m-OE-#7 | 4 | | .07316925 |
| | *exo70B1-3* | 4 | | .08081900 |
| | Significance | | .579 | .351 |