Supplementary methods

Fungal pathogen assay and disease quantification

B. cinerea strain B05.10 and *V. dahilae* strain JR2 were cultured on Malt extract agar (2% malt extract, 1% Bacto peptone) and potato dextrose agar (PDA), respectively. The *B. cinerea* spores were diluted in 1% Sabouraud Maltose Broth buffer to a final concentration of 10^4 spores/ml for spray inoculation on tomato leaves and 10^5 spores/ml for drop inoculation on the other plant materials[1]. A 10 µl spore suspension was used for drop inoculation of all plant materials used, except tomato fruits, in which 20 µl was used. *V. dahilae* soil-inoculation assay was performed as described previously[2]. For *Arabidopsis* liquid root culture inoculation, 2-week-old *Arabidopsis* plants were grown in root culture (0.32% Murashige and Skoog salt, 2% sucrose, 0.1% MES, pH adjusted to 5.8 using KOH), and *V. dahilae* spores were added into the culture to a final concentration of 10^6 spores/ml. After 5 min inoculation, the root culture was replaced with fresh sterile medium solution. Fungal biomass quantification was performed as described previously[3]. The p values were calculated using Student's t-test for the comparison of two samples, and using one-way ANOVA for the comparison of multiple samples.

Fungal *DCL* gene transcript quantification

Infected plant tissues were collected 3 days after *B. cinerea* inoculation and 2–3 weeks after *V. dahilae* inoculation. The collected samples were subjected to RNA extraction using the Fisher BioReagents™ SurePrep™ Plant/Fungi Total RNA Purification Kit (Fisher scientific, Waltham, MA), cDNA synthesis using SuperScript III Reverse Transcriptase (Invitrogen Carlsbad, CA), and quantitative RT-PCR quantification[4]. The expression of *Bc-DCL1* and *Bc-DCL2* in *B. cinerea* after treatment of synthesized *Bc-DCL1/2*-sRNAs and -dsRNAs was measured as described previously[4].

sRNA detection methods

sRNA detection was mostly carried out by Northern blot analysis, except for Fig. 3e, in which sRNA stem-loop RT-PCR was used due to very limited amount of *B. cinerea* protoplasts that were purified from the infected tissue. The Northern blot analysis was performed as described[5-8], and sRNA stem-loop RT-PCR was done as described in Chen et al.[9].

RNA treatment using varying concentrations

The RNAs were diluted to a final concentration of 1, 5, and 10 ng/µl. 20 µl of the diluted RNAs, as well as water, were applied on the surface of rose petals and tomato fruits immediately prior to *B. cinerea* infection. The pictures were taken at 3 dpi for the rose petals, and 5 dpi for the tomato fruits.

RNA treatment of varying incubation times

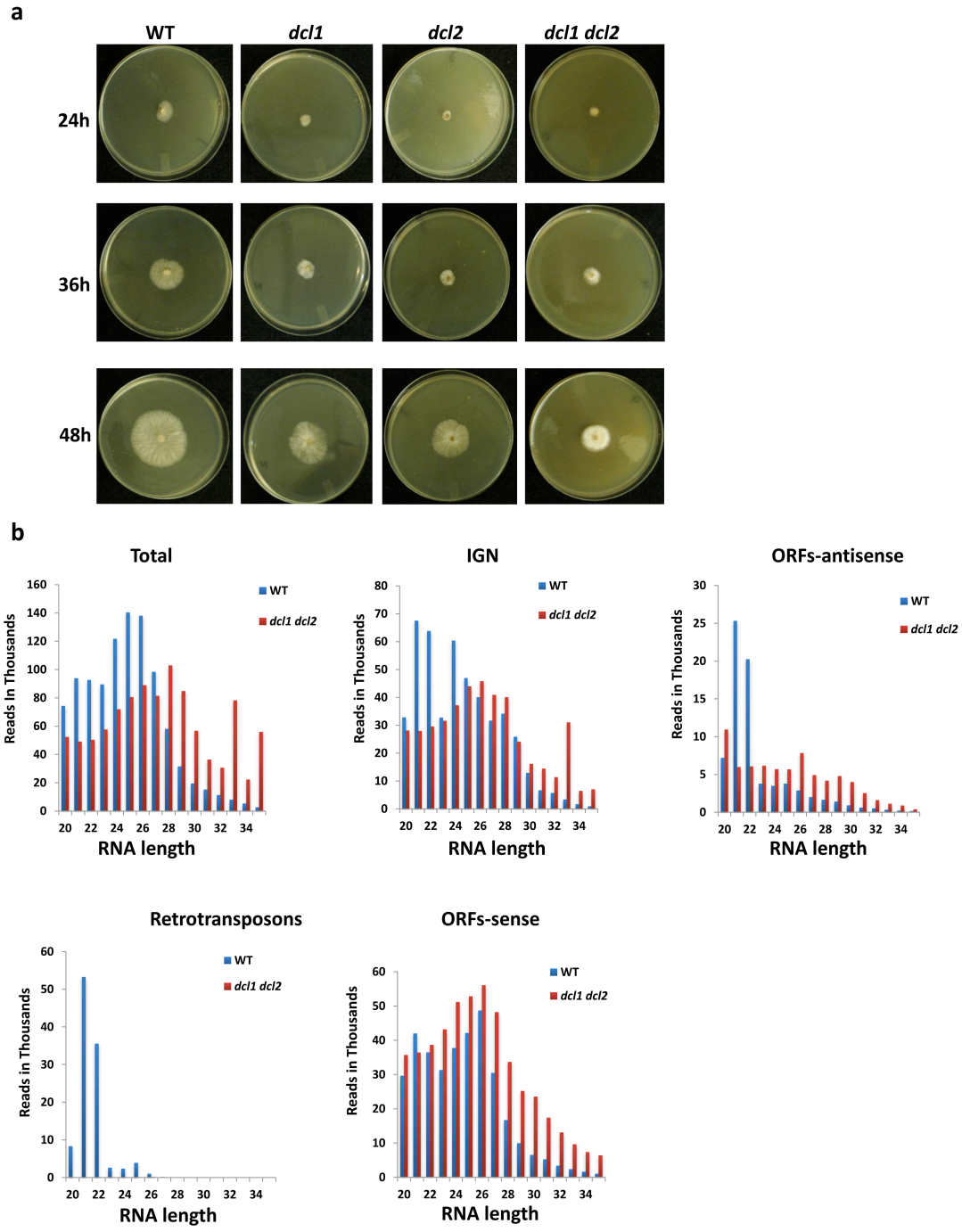
20 µl of 20 ng/µl *YFP*-dsRNAs and -sRNAs, *Bc-DCL1/2*-dsRNAs and sRNAs, and water were applied on the surface of rose petals and tomato fruits, which were then incubated in a box for 1, 3 and 5 days before *B. cinerea* infection, respectively. The pictures were taken at 3 dpi for the rose petals, and 5 dpi for the tomato fruits.

Cloning and data analysis of *Arabidopsis* AGO1- and AGO2-associated sRNAs

V. dahilae infected *Arabidopsis* prepared in liquid root culture were collected at 2 and 4 dpi. *At*-AGO1 and *At*-AGO2 immunoprecipitations were performed in parallel as previously described[10]. *At*-AGO1- and *At*-AGO2-associated RNAs were extracted and used for sRNA library construction and Illumina HiSeq 2000 deep sequencing[11]. The read number of *Vd-sRNAs* in *At*-

AGO1 and *At*-AGO2 IP libraries were normalized with total *V. dahilae* sRNAs after removing tRNAs, rRNAs, snoRNAs, and snRNAs, etc. The *Vd*-sRNAs that had a higher read number than 100 RPM after normalization and also had host target genes in *Arabidopsis* were selected. *At*-AGO1-enriched *Vd*-sRNA effectors were defined as the selected *Vd*-sRNAs with a 10 times greater read number in the *At*-AGO1 IP library compared to the *At*-AGO2 IP library. *At*-AGO2 enriched *Vd*-sRNAs were defined as the selected *Vd*-sRNAs with a 10 times greater read number in the *At*-AGO2 IP library compared to the *At*-AGO1 IP library.

Supplementary Figures



Supplementary Fig 1. *B. cinerea dcl1* and *dcl2* single mutants and the *dcl1 dcl2* double mutant attenuate fungal growth and development, and most of the retrotransposon-derived Bc-sRNAs were dependent on both Bc-DCL1 and Bc-DCL2. (a) *B. cinerea* WT, *dcl1* and *dcl2* single mutants, and the *dcl1 dcl2* double mutant were grown in ME medium, and pictures were taken after 24, 36, and 48 hours. (b) sRNA libraries were constructed from WT *B. cinerea* and the *dcl1 dcl2* double mutant and sequenced using Illumina deep sequencing. The normalized Bc-sRNAs were mapped to the whole genome (total), IGN, ORFs-antisense, retrotransposons, and ORFs-sense. The production of Bc-sRNAs from retrotransposon regions, as well as the ORFs-antisense and IGN regions, was largely impaired in the *dcl1 dcl2* double mutant.

a **Alignment of selected *Bc-DCL1* and *Bc-DCL2* RNAi fragments with the four *Arabidopsis DCLs***

```
Bc-DCL1   ----A---CCG---------GTAGATGCTAGAGATAATGTCAAGAAAGCTGCGGAAGAAC
At-DCL3   --------------------------------CACCATTGGGGTGTATTTGCCGCAAGATG
At-DCL1   AATGTGAGCTTCTGGAAGGCGCTGCTGCTGAAAAAGTCGCGGCGGAAGTTGGCAAACCAG
At-DCL2   ----T---------------GATGCTTCACAGGAGTTTTTGGCTGAGATACCTCAAGGTC
At-DCL4   ----T---------------ATGGCTGCTGAGGCCCTCTCTTCTGGTGTTGCTAAAGATG
                                                                **

Bc-DCL1   TTGAAGGTTTGCTACACAGTCAAATATGTACTGCAGAAGATCCCAGCTTGCTGCAGTACT
At-DCL3   ATAAG-------------------------------------------------AGTCTGGT
At-DCL1   AAAATGGTAATGC-ACATGACGAGATGGAGGAGGGAGAGCTCCCT-GATGATCCTGTGGT
At-DCL2   TTAATTGGAGTGT-TGCAAACATAAATGGAAATG--------------------------
At-DCL4   AGAATGCATCTGA-CCTCCTCAGCTTAGCGGCGT-------------------------
             *

Bc-DCL1   CAATCAAAGGTAAACCTGAG-------ACTCTTGCCTACTATGATCCCTTGGGCCCGAAA
At-DCL3   AGATTTGCAGCAAAA------------CCATCTGTCAGCAGTAATTTCTGGGCATGTATC
At-DCL1   CTCGGGAGGGGAGCACGTTGATGAAGTAATAGGCGCCGCAGTGGCTGATGGGAAAGTTAC
At-DCL2   ----------------------------------------CGGAGGCAGGTCTCCTAAC
At-DCL4   ----------------------------------------TGAAGGAACCATTATTCTC

Bc-DCL1   TTCAATACTCCTCTTTATCTTCAAATGCTCCCGCTTCT-AAAAGACAATCCTATCTTTCG
At-DCL3   TCCAAAGCTAAAAGAACTCTTCCATCTATTGGATTCCTTTAGAGGTGACAAGCAAAAGCA
At-DCL1   TCCAAAAGTACAATCATTGATCAAACTACTCCTCAAATATCAGCACACAGCTGATTTTCG
At-DCL2   TTTAAAAACTGTCTGCCTCATTGAGACTCTTCTTGGTTATAGCTCCTTGGAGAACATACG
At-DCL4   TAGAAAGCTAGTTCAATTGATTAAGATCCTTTCGGTATTCAGGCTAGAGCCACACATGAA
          *  **           *  *  *         *

Bc-DCL1   GAAGCCATTTGTATTTG---GGACAGAAGCCAGTAGAACTCTAGGATCTTGGTGTGTTGA
At-DCL3   GTGCCTTATTTTAGTTGAGAGAATTATAACTGCGAAAGTGATCGAAAGATTCGTTAAGAA
At-DCL1   AGCTATTGTTTTCGTTGAGAGGGTGGTTGCTGCTTTGGTTCTTCCTAAGGTTTTTGCGGA
At-DCL2   GTGCATCATTTTTGTGGATAGGGTGATAACAGCCATCGTTCTGGAATCCCTTTTGGCTGA
At-DCL4   ATGTATAATATTTGTCAATCGGATTGTGACTGCAAGAACATTGTCATGCATACTAAATAA
                *  *  *     *         *           *                 *

Bc-DCL1   CCAGATCTGGACTTTCTGTCTTCAAGAAGAAGAGTCTAAGAAACTACAAGCAAGGACGGA
At-DCL3   AGAA-GCCTCTTTGGCTTACCTTAATGTCTTGTATTTAA----CCGAAAACAACCCCTCC
At-DCL1   GCTG-CCTT----CGCTTAGTTTTATACGGTGTGCCAGCATGATTGGACACAATAACAGC
At-DCL2   GATT-CTTCCAAACTGTAA-TAACTGGAAAACCAAGTACGTTGCAGGAAATAACTCTGGT
At-DCL4   CT-----TGGAACTGCTACGGTCTTGGAAGTCTGATTTCCTTGTTGGACTTAGTTCTGGA
                        *                       *  *

Bc-DCL2   GGATGCCATTTGCTGCACGCCAAAAATACATCGAG-------CAGATCTTCGCCTTCGAG
At-DCL3   GGACTCAAAGATTTTTAATCCTGAAGAGCGTGAAGGAGTGGAAAAGTTTGCTACAACGGT
At-DCL1   GGATTCTACGGTTTGTACTATAAAAGATCGAAAAGAATTAGAGAAAACATGTGCCTATGCC
At-DCL2   GAATTCAAAGGTCTATACCTGTGAGAATGAGTCTGTGCTGGCTGGGTTTGTCCCCTTTTC
At-DCL4   CAATGCCAAGGTTTATTCAGTGGAAAGCAATGTCCAGCTGGATGGTTTTGTTTCATCTCC
            *  * *     *         *                         *    *

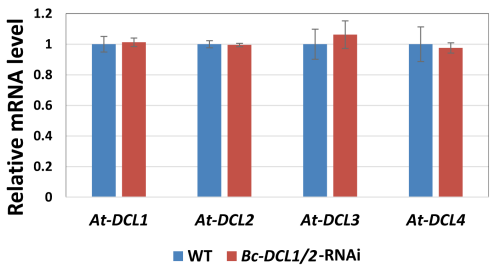
Bc-DCL2   TAAAGCTACCACTTCTATCTATTATCTACTATACCCCAGAGTCAAATATCATCGTG----
At-DCL3   TAAAGAAGG---TCCAATATTGTATAACCCATCACCAT-CCTGTAGTTTGGAATTG----
At-DCL1   TTCAGAGAT---AGTCGTCGAGTATGACAAAGCTGCTACTATGTGGTCTCTTCATGAGAC
At-DCL2   TACACCAAG---CTTCAAGTATTACCAGCAC-ATAAAAATACCAAGTCCCAAAC------
At-DCL4   TTTAGTCAA---AGTATATTATTATCGGTCAGCTTTAAGTGATGCATCTCAATC------
          *  *                **                  *

Bc-DCL2   ------------------------ACGAAAACTGTGGCGAGCCTGAGAAAGATTGTGCAA
At-DCL3   ----AAAGAAAAGTTAGAAACTTCACAC-------CTCAAGTTTGATGCTTCTCTTAGAA
At-DCL1   AATAAAGCAAATGATTGCAGCTGTTGAAGAAGCGGCACAAGCAAGTTCAAGGAAAAGCAA
At-DCL2   ----GAGC------------------------------AAGCTTGGTAGAGAAGCTAGAA
At-DCL4   ----GACCATCAGATA-------------------TGAAAACATGCTGGAGGACATCAAA
                                            *   *              **

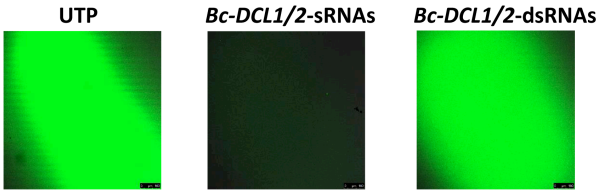
Bc-DCL2   AGTCTCAACATTTTCGAAGACCCCTACGTTTTGACACTAAAAAGGAGTGATAGCGAAAAA
At-DCL3   GGCTTCAAGAGTTGGGAAAAGAC---AGTTTTC----------------TGAATATGGA
At-DCL1   GTGGCAATTTATGGGGGCTAGGG---ATGCTGGAGCAAAGGATGAATTGAGACAGGTTTA
At-DCL2   AGACTAACGATAA------AGCA---TCGCTTATCCCTTGGAACCT----TGGATCTC-A
At-DCL4   CAGCG--GTGCTT------GGCA---TCACTTAAGCTGCTGATTGA----TACTCATCAA
                                  *                       *

Bc-DCL2   AGTCAACGTGAGCTGGCGAAAGTACTCAAGAGTTTTAAGACATATAGTCAAACCCAATTA
At-DCL3   T---------------AATAAGTTT-GAGACATATCAAAAGA--G---------ATTGTC
At-DCL1   T---------------GGCGTCTCTGAAAGAACGGAGAGCGA--TGGTGCTGCCAATTTG
At-DCL2   A---------------CTCCTCTACTGTTGATTCTGTAGAGA--AG--------AGACTG
At-DCL4   A---------------CACAAACCCTCCTAAGTATGAAAAG----G--------CTTCTC
                                              *                   *
```

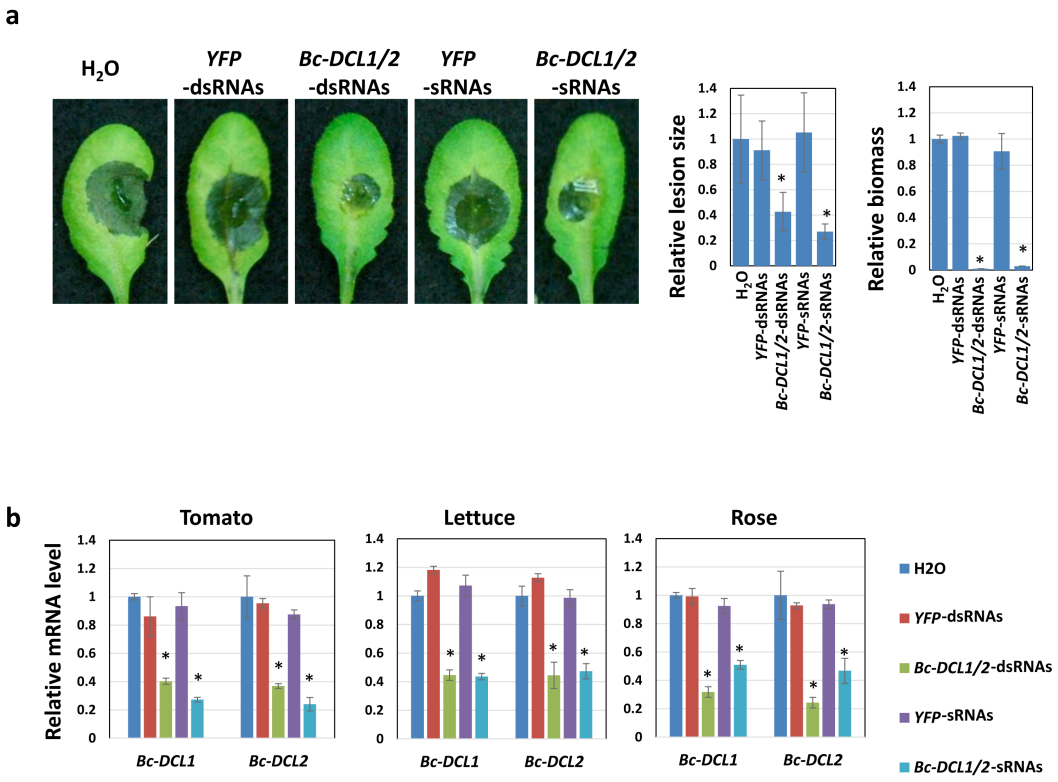
b



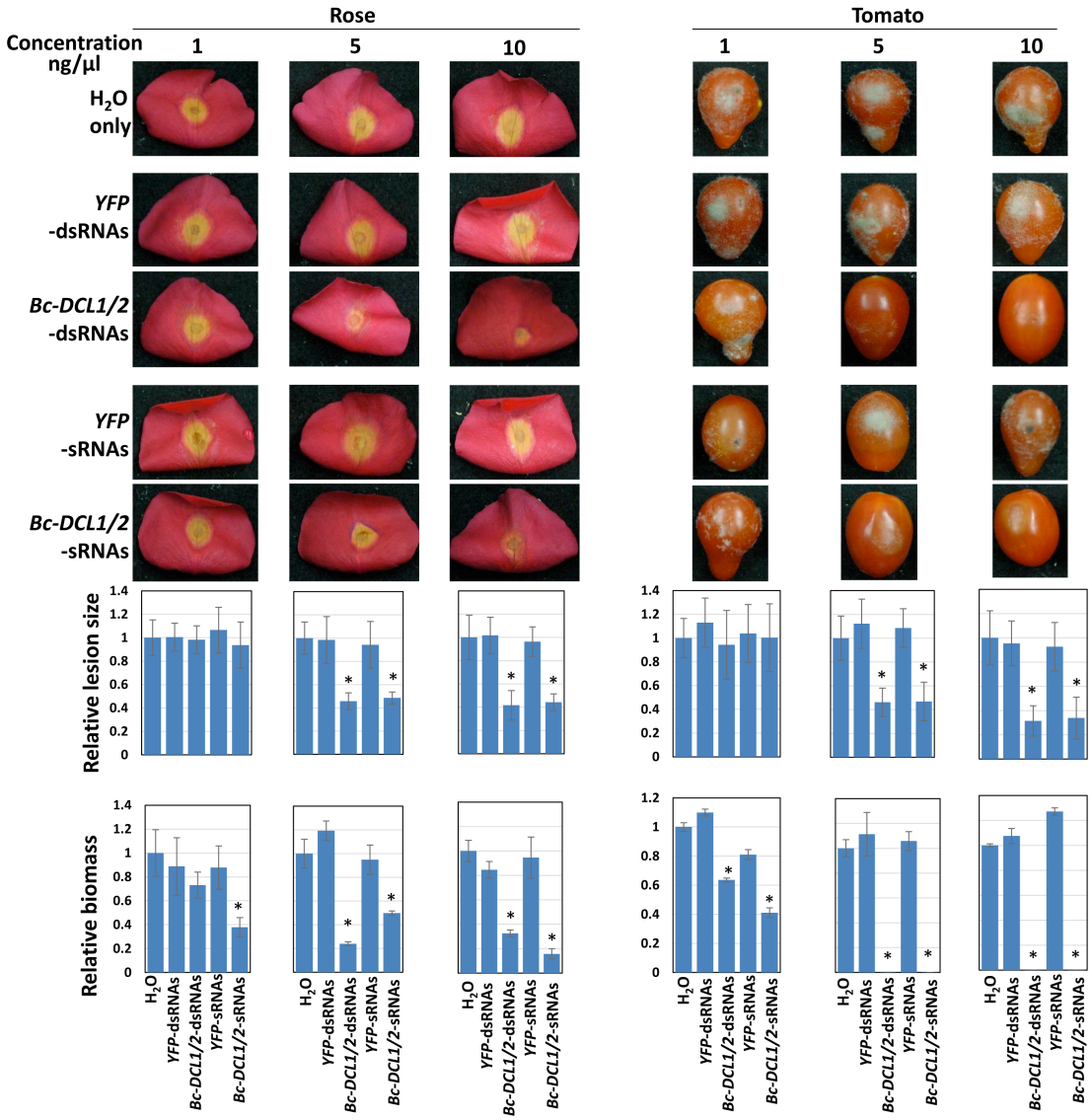
Supplementary Fig 2. Selected *Bc-DCL1* and *Bc-DCL2* RNAi fragments did not target *Arabidopsis DCLs*. (a) The selected RNAi fragments from *Bc-DCL1* (252 bp) and *Bc-DCL2* (238 bp) were aligned with 4 *Arabidopsis DCL* genes. The selected RNAi fragments are highlighted (yellow), and asterisks represent the conserved area among these genes. (b) The relative expression levels of four *Arabidopsis DCL* genes (*At-DCL1*, *At-DCL2*, *At-DCL3*, and *At-DCL4*) were measured by quantitative RT-PCR in *Arabidopsis Bc-DCL1/2*-RNAi plants. *Arabidopsis* WT was used as a control.



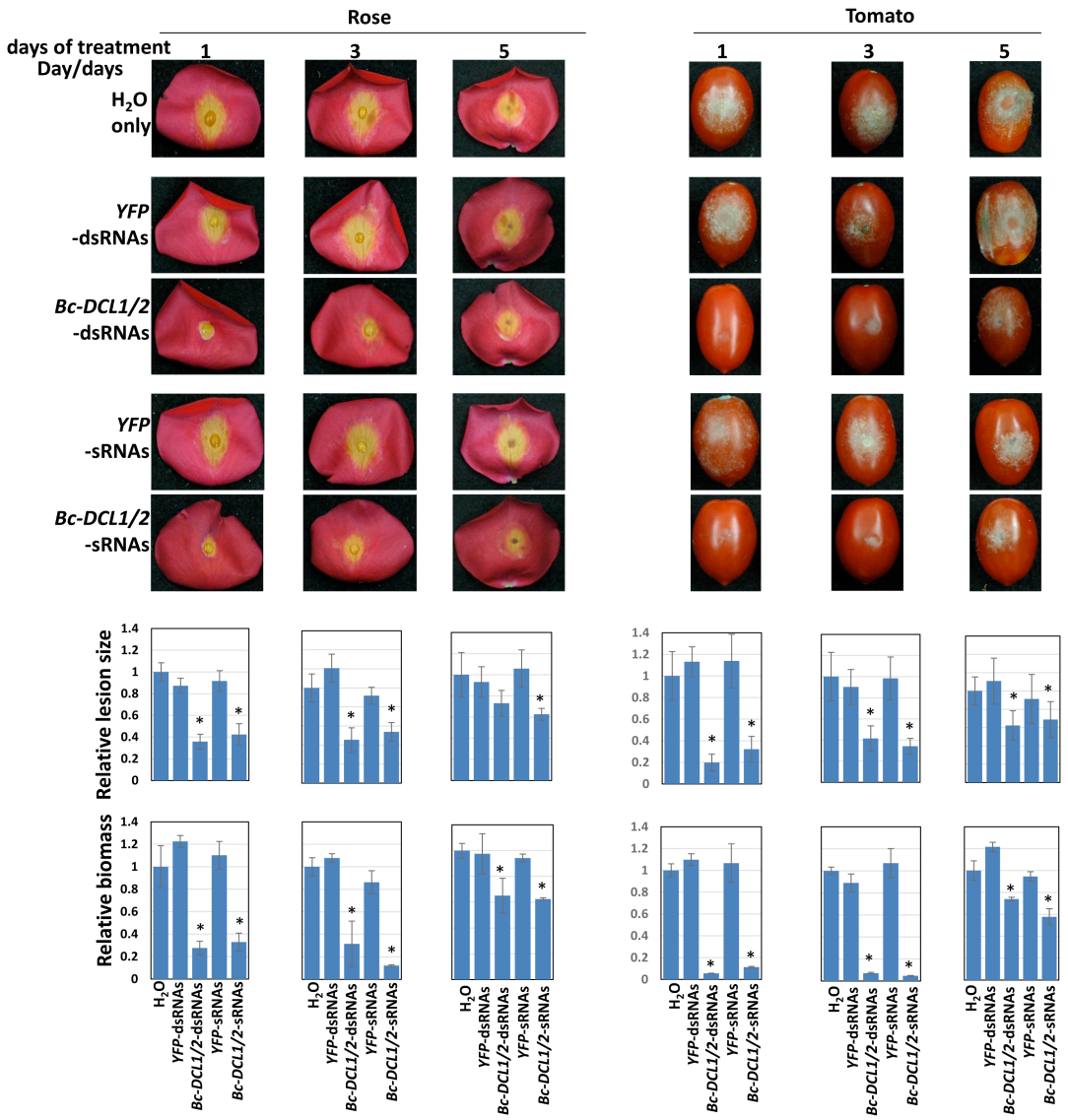
Supplementary Fig 3. The fluorescence intensity of *in vitro* transcribed *Bc-DCL1/2*-dsRNAs is stronger than that of *Bc-DCL1/2*-sRNAs. 300 ng of fluorescent *Bc-DCL1/2*-sRNAs and -dsRNAs, as well as the same amount of Fluorescein-12-UTP, were applied on microscope glass slides, and the fluorescence intensity were examined using a confocal microscope.



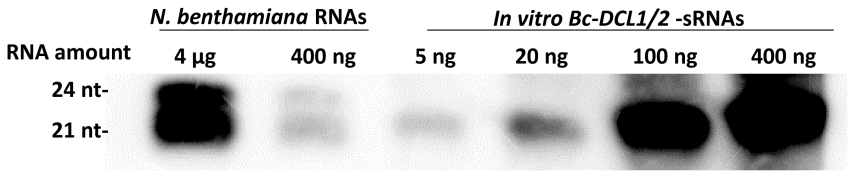
Supplementary Fig 4. *Bc-DCL1/2*-sRNAs and -dsRNAs treatment attenuated gray mold disease on *Arabidopsis* leaves, and silenced both *Bc-DCL1* and *Bc-DCL2* in various plants (a) *Arabidopsis* leaves were treated with *Bc-DCL1/2*-sRNAs and -dsRNAs, and the leaves were more resistant to *B. cinerea*, when compared with water, *YFP*-sRNAs and -dsRNAs treatments (controls). The relative lesion sizes were measured using imageJ, and the error bars indicate the standard deviation (SD) of 10 plant samples. The fungal relative DNA content (relative biomass) was measured using quantitative PCR, and error bars represent the SD of three technical replicates. (b) Both *Bc-DCL1* and *Bc-DCL2* were suppressed in the *B. cinerea* infected plant samples (tomato fruit, lettuce, and rose petal) that were pre-treated with *Bc-DCL1/2*-sRNAs and -dsRNAs, when compared with pre-treatment with water, *YFP*-sRNAs and -dsRNAs (controls). Asterisks in (a) and (b) indicate statistically significant differences ($P < 0.01$).



Supplementary Fig 5. *Bc-DCL1/2*-sRNAs and -dsRNAs remained functional when the concentration was as low as 5 ng/µl, but not at 1 ng/µl. The tomato fruits and rose petals were treated with various concentrations of *Bc-DCL1/2* and *YFP*-RNAs (1, 5 and, 10 ng/µl), and the protection *against B. cinerea* was observed with the 5 and 10 ng/µl, but not the 1 ng/µl treatment. Pictures were taken at 3 dpi for rose petals and 5 dpi for tomato fruits. The relative lesion sizes were measured using imageJ, and the error bars indicate the SD of 10 plant samples. The fungal relative biomass was measured by quantitative PCR, and error bars represent the SD of three technical replicates. Asterisks indicate statistically significant differences ($P < 0.01$).



Supplementary Fig 6. Treatment with *Bc-DCL1/2*-sRNAs and -dsRNAs protected plant samples from *B. cinerea* up to 8–10 days. The tomato fruits and rose petals were pre-treated with *Bc-DCL1/2*-sRNAs and -dsRNAs, *YFP*-sRNAs and -dsRNAs, and water for 1, 3, and 5 days, respectively, before *B. cinerea* infection. The pictures were taken at 3 dpi (up to 6–8 days after RNA pre-treatment) for rose petals and 5 dpi (up to 8–10 days after RNA pre-treatment) for tomato fruits. The relative lesion sizes were measured using software imageJ, and error bars indicate the SD of 10 plant samples. The relative biomass was measured by quantitative PCR, and error bars represent SD of three technical replicates. Asterisks indicate statistically significant differences ($P < 0.01$).



Supplementary Fig 7. A large amount of *Bc-DCL1/2*-sRNAs were produced in *N. benthamiana* plants transiently expressing the Bc-DCL1/2-RNAi construct. The level of *Bc-DCL1/2*-sRNA in 4 µg (half of the amount applied in Fig. 5) and 400 ng of total RNAs from *N. benthamiana* plants expressing the Bc-DCL1/2-RNAi construct were examined by Northern blot analysis. 5 ng, 20 ng, 100 ng, and 400 ng (the amount applied in Fig. 4) of *in vitro synthesized Bc-DCL1/2*-sRNAs were used as controls.

a

Alignment of selected *Vd-DCL1* and *Vd-DCL2* RNAi fragments with the four *Arabidopsis DCLs*

```
Vd-DCL1   TGCTCATGACCACAGTC-ATGAGTTCTCACCGAATGAAGACCCAGGGTCACTGATCGACT
At-DCL3   TAGCTTCGAGTGCGACAATTGATTGGTCAGCT-ATCAA--CTCCT--GTGCCTCAATAGT
At-DCL1   TGCTTTCA-AGGGATCACTTGATATTACAGAA-AACCA--GCTATCATCTCTAAAAAAGT
At-DCL2   TGGATTGCATCTCAGAG-ATGGGGTGGCAC----------TTGAT----TATCTACTAGT
At-DCL4   TCCCTTGGAACTGCAAGACTCTTCTAGAACAA-GCAAA--TCCACCTTCTACCTTCTTCT
          *           *       *                                  *

Vd-DCL1   GGAGCCATCTGCTGTCGACCAAAGAGGTTGAGTACTTGCCTTGGGATGAAGATCACAGTC
At-DCL3   TGAGTTCTTGAAGAAAAATTCTCTTCTTGATCTTCGGGATAGTGATGG--G-AATCAGTG
At-DCL1   TTCAT---GTGAGGTTAATGAGTAT---CGTGTTGGATGTTGATGTTG--A---ACCCTC
At-DCL2   TCCATCCACTCATTCACATGAAACA---TCTCTTATTGATTGGGAAGT--GATCA-GATC
At-DCL4   TCCACTCTGTCTGCATGATGGAGAA---AGTGTTATATCTGTAGATTG--GGTGACTATC
                    *           *                          *

Vd-DCL1   CCAGCTT----------CTATCAAAGCAAGT----------TTGT
At-DCL3   CAATACCTCATCCGGTCAGGAAGTCTTACTAGACGATAAAATGGAAGAAACGAATCTGAT
At-DCL1   CACGACA--------CCATGGGA-TCCTGCAAAGGCCTACCT--GTTTGT----------
At-DCL2   CGTGAATCTAACTTCTCATGAGGTTTTGGAAAAACACGAAAA----------
At-DCL4   AGAAACT---GCTTGTCATCACCAATCTTTAAGACTCCATCTGTTTTAGTGGAA----GA
                                  *       *

Vd-DCL1   GATTGATCCATACACGGGATCGCGCAAG----------CTGTTTCTCAGAGGTATT
At-DCL3   TCATTTTGCCAATGCTTCGTCTGATAAAA--ATAGTCTCGAAGAACTTGTGG--------
At-DCL1   CCCTGTTACTGACAATACGTC---TATGGAACCCATAAAAGGGATCAACTGGGAATTGGT
At-DCL2   TTGTTCTACCAACGGTGCTTCTCGCATTCTACACACAAAAGACGGCTTGTTT--------
At-DCL4   TATATTTCCTCCTTCGGGCTCTCATTTAAAGCTAGCAA---ATGGCTGCTGG--------
          * *         **                          *

Vd-DCL2   AGA--AGGTCAACG---------ATCTACTGCCACAGGCGACAAACAAGAAGCCATATGC
At-DCL3   AAAACATGACTATCAAAATAGGCAAGTCTTGCGACATGGGTCATAGA-TGGGTAGTTTCA
At-DCL1   AAATTTGATTAGTT---------AT------------------CCT-ATTCCCACATCA
At-DCL2   ATACGTTGCTAGTA---------GGAGGA--------------------ATCTGAAACGC
At-DCL4   ATACTGGTGAAATC---------AGATGTAG---CAAAGGCCATCAT-TGGTTGTACAAG
                                  * *

Vd-DCL2   TAGGGTTTATCCGGCAC-----CGTGGGCGAAAGTCGACACGATTCCATTAGATCATGCT
At-DCL3   AAATCTGTATCAGATTGCG---CTGAGGCCCTGATTGGTGCCTATTATGTAAGCGGTGGA
At-DCL1   AAGATTCTTGAAGCCTTGACTGCCGCCTCGTGCCAGGAAACGTTCTGCTACGAGAGAGCT
At-DCL2   AAGAGTGTGGCCGATGTTG---TAGAATCATTAATTGGAGCATATCTCAGCGAGGGAGGT
At-DCL4   AAAACAATTGCTGATGTGG---TTGAGGCTCTTGTGGGAGCTTTCTTAGTTGACAGTGGC
          *    *   *              *      *   *              *

Vd-DCL2   TACTT----------TGGGGCGTTGATCCCTTTCATTTCACA-CATTG
At-DCL3   TTGTCTGCTTCTCTCCATATGATGAAATGGCTCGGTATTGACGTCGATTTTGACCCAAAC
At-DCL1   GAGCTTTTAGGAGATGCGTATCTAAAATGGGTTGTTAGTCGTTTTCTGTTTCTCAAGTAT
At-DCL2   GAACTTGCAGCTTTGATGTTCATGAATTGGGTTGGAATAAAGGTCGACTTTACA---ACT
At-DCL4   TTCAAAGGTGCTGTGAAATTTCTGAAGTGGATTGGTGTAAATGTTGATTTTGAA---TCC
                                  ***  *       *   **

Vd-DCL2   TCG--AGGTTCGACTGGTTGCAGAACAGC-----TTTCCTCGAGC---------------
At-DCL3   CTAGTCGTTGA---AGCCATCAATAGAGT---TTCTCTACGGTGTTACATTCCTAAAGAA
At-DCL1   CCTCAAAAGCACGAGGGTCAGCTTACAAGGATGAGGCAACAAATGGTTAGTAATATGGTT
At-DCL2   ACGAAGATCCAGAGAGATTCCCCAATACA------AGCAGAGAAGCTTGTGAATGTAGGT
At-DCL4   TTGCAAGTACAAGATGCTTGTATTGCAAGCAGGCGCTACTTGCCCCTCACTACTCGCAAT
                                  *       *
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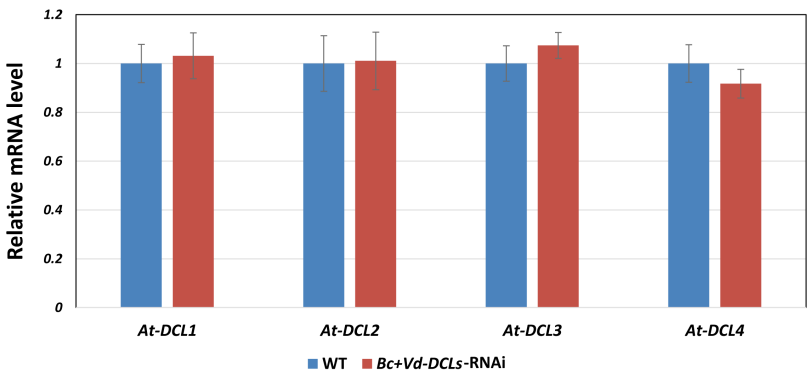
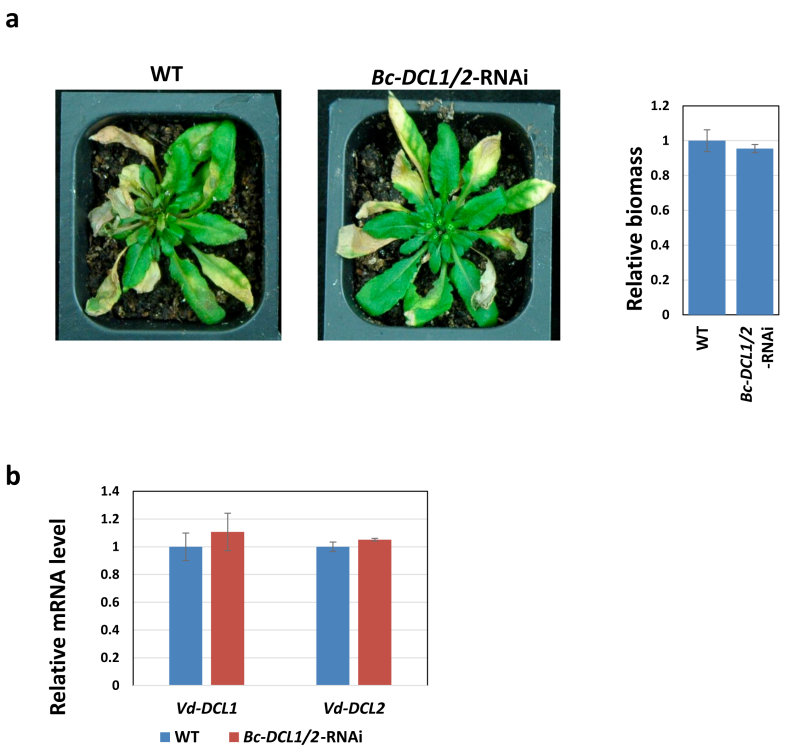
b



Supplementary Fig 8. Selected *Vd-DCL1 and Vd-DCL2* RNAi fragments did not target any *Arabidopsis DCLs*. (a) The selected RNAi fragments from *Vd-DCL1* (156 bp) and *Vd-DCL2* (156 bp) were aligned against the four *Arabidopsis DCL* genes. The selected RNAi fragments were marked (yellow), and asterisks represent the conserved area among these 5 genes. (b) The relative expression levels of *Arabidopsis DCL* genes (*At-DCL1*, *At-DCL2*, *At-DCL3*, and *At-DCL4*) were measured by quantitative RT-PCR in *Arabidopsis Bc+Vd-DCLs*-RNAi plants. *Arabidopsis* WT was used as a control.



Supplementary Fig 9. *Arabidopsis Bc-DCL1/2*-RNAi plants were not resistant to *V. dahlia*. (a) 2-week-old *Arabidopsis Bc-DCL1/2*-RNAi transgenic plants and WT plants were infected with *V. dahilae*, and the disease symptoms were recorded 3-week post-inoculation. The relative biomass was measured by quantitative PCR, and error bars indicate the standard deviation SD of three technical replicates. (b) The relative mRNA levels of *Vd-DCL1* and *Vd-DCL2* in the *V. dahliae* infected *Bc-DCL1/2*-RNAi plants and WT plants were measured by quantitative RT-PCR.

Supplementary Table legends:

Supplementary Table 1: The normalized read counts of previously predicted Bc-sRNA effector candidates in *B. cinerea* WT and *dcl1 dcl2* strains.

Supplementary Table 2: At-AGO1-associated *Vd*-sRNA effector candidates and their targets.

Supplementary Table 3: At-AGO2-associated *Vd*-sRNAs and their targets.

Supplementary Table 4: The list of primers and oligoes used in the manuscript.

References

1 Mengiste, T., Chen, X., Salmeron, J. & Dietrich, R. The BOTRYTIS SUSCEPTIBLE1 gene encodes an R2R3MYB transcription factor protein that is required for biotic and abiotic stress responses in Arabidopsis. *Plant Cell* **15**, 2551-2565 (2003).

2 Ellendorff, U., Fradin, E. F., de Jonge, R. & Thomma, B. P. H. J. RNA silencing is required for Arabidopsis defence against Verticillium wilt disease. *J. Exp. Bot.* **60**, 591-602 (2009).

3 Gachon, C. & Saindrenan, P. Real-time PCR monitoring of fungal development in Arabidopsis thaliana infected by Alternaria brassicicola and Botrytis cinerea. *Plant Physiol. Biochem.* **42**, 367-371 (2004).

4 Koch, A. *et al.* Host-induced gene silencing of cytochrome P450 lanosterol C14 alpha-demethylase-encoding genes confers strong resistance to Fusarium species. *Proc. Natl. Acad. Sci. USA* **110**, 19324-19329 (2013).

5 Katiyar-Agarwal, S. & Jin, H. Discovery of pathogen-regulated small RNAs in plants. *Methods Enzymol.* **427**, 215-227 (2007).

6 Katiyar-Agarwal, S. *et al.* A pathogen-inducible endogenous siRNA in plant immunity. *Proc. Natl. Acad. Sci. U. S. A.* **103**, 18002-18007 (2006).

7 Katiyar-Agarwal, S., Gao, S., Vivian-Smith, A. & Jin, H. A novel class of bacteria-induced small RNAs in Arabidopsis. *Genes Dev.* **21**, 3123-3134 (2007).

8 Niu, D. D. *et al.* miRNA863-3p sequentially targets negative immune regulator ARLPKs and positive regulator SERRATE upon bacterial infection. *Nat. Commun.* **7** (2016).

9 Chen, C. *et al.* Real-time quantification of microRNAs by stem-loop RT-PCR. *Nucleic Acids Res.* **33**, e179 (2005).

10 Zhang, X. *et al.* Arabidopsis Argonaute 2 regulates innate immunity via miRNA393(*)-mediated silencing of a Golgi-localized SNARE gene, MEMB12. *Mol. Cell* **42**, 356-366 (2011).

11 Weiberg, A. *et al.* Fungal Small RNAs Suppress Plant Immunity by Hijacking Host RNA Interference Pathways. *Science* **342**, 118-123 (2013).