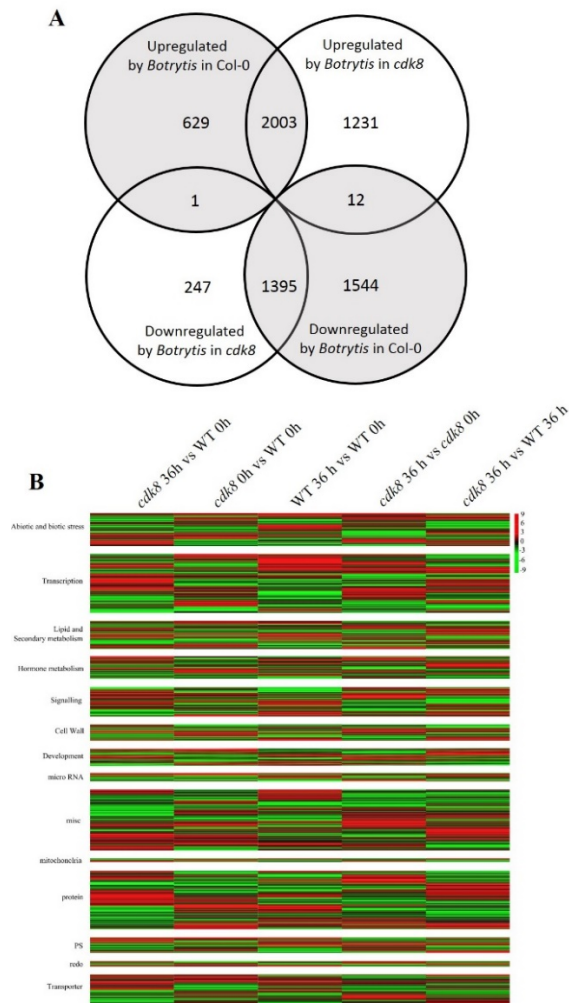
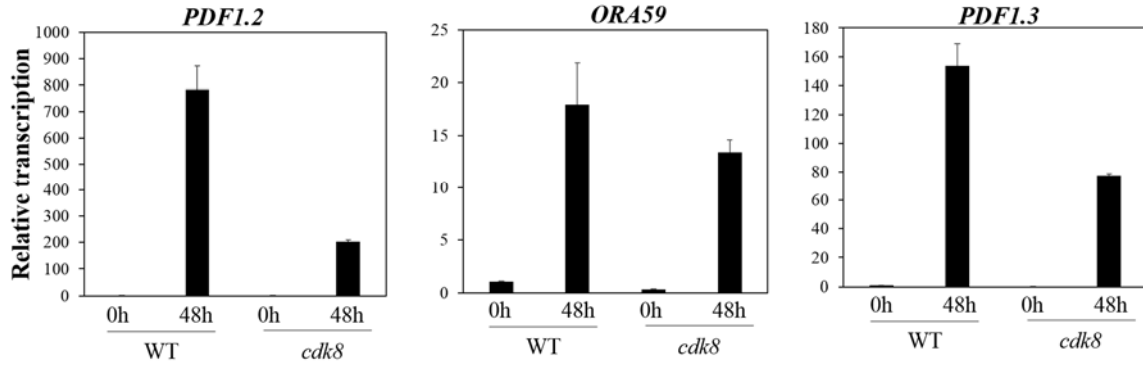


**Supplemental Figure 1. Disease symptoms and fungal growth revealed by trypan blue staining of *B. cinerea* inoculated leaves of wild type and *cdk8* mutant plants.**

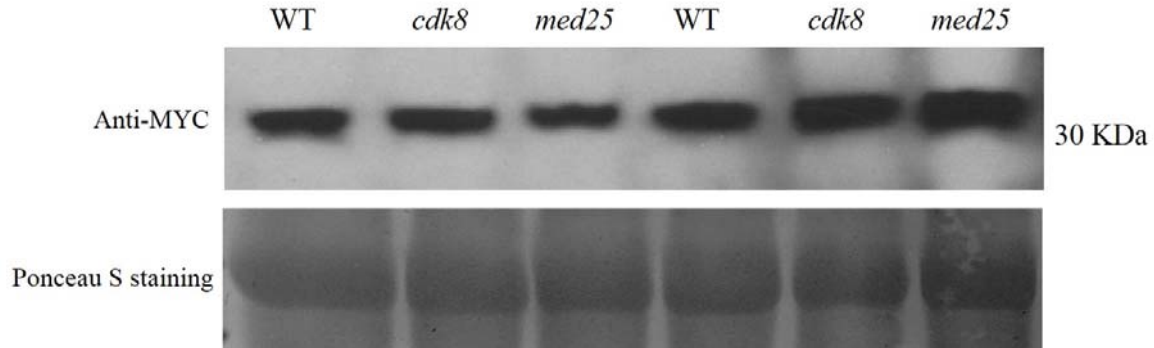
*B. cinerea* disease symptom in wild-type (Col-0) and *cdk8* mutant plants after (A) drop, and (B) spray inoculation, (C) Trypan blue staining of *B. cinerea* and (D) *A. brassicicola* inoculated leaves of wild type and *cdk8* mutant at 48 hours after inoculation. The disease assays were repeated at least three times with similar results. dai indicates days after inoculation. Scale bars indicate 100  $\mu$ m in C and D.



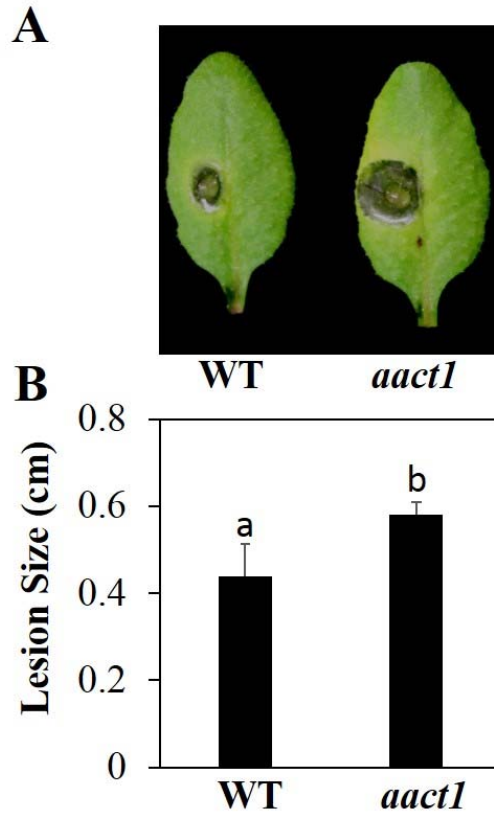
**Supplemental Figure 2. Venn diagram and heat map presenting differential expressions in wild type and *cdk8* after mock or *B. cinerea* inoculation.** (A) Venn diagram showing differential expression of genes in wild-type and *cdk8* mutant after mock treatment or *B. cinerea* inoculation. (B) Heat map presenting differential expressions by functional categories in *cdk8* and wild type plants with mock and *B. cinerea* inoculation. The heat map was generated based on 2-fold changes in gene expression on RPKM transcript counts ( $FDR \leq 0.05$ ) using wild type mock (WT 0h) as a reference. Statistically significant changes were determined by R software V3.16.5 ( $P < 0.05$ , *t* test). Misc is abbreviation of miscellaneous enzyme families and PS indicates photosynthesis.



**Supplemental Figure 3. CDK8 dependent expression of *PDF1.2*, *ORA59* and *PDF1.3* genes in response to *A. brassicicola*.** (A) qRT-PCR results demonstrated that the gene inductions of *PDF1.2*, *ORA59* and *PDF1.3* were also reduced in *cdk8* in responses to *A. brassicicola*. Relative transcript levels were normalized with Arabidopsis *Actin2* (*ACT2*). The normalized expression level of wild type was set to 1. Error bars indicate SE of mean value (n=3). Two independent biological replicates were performed.

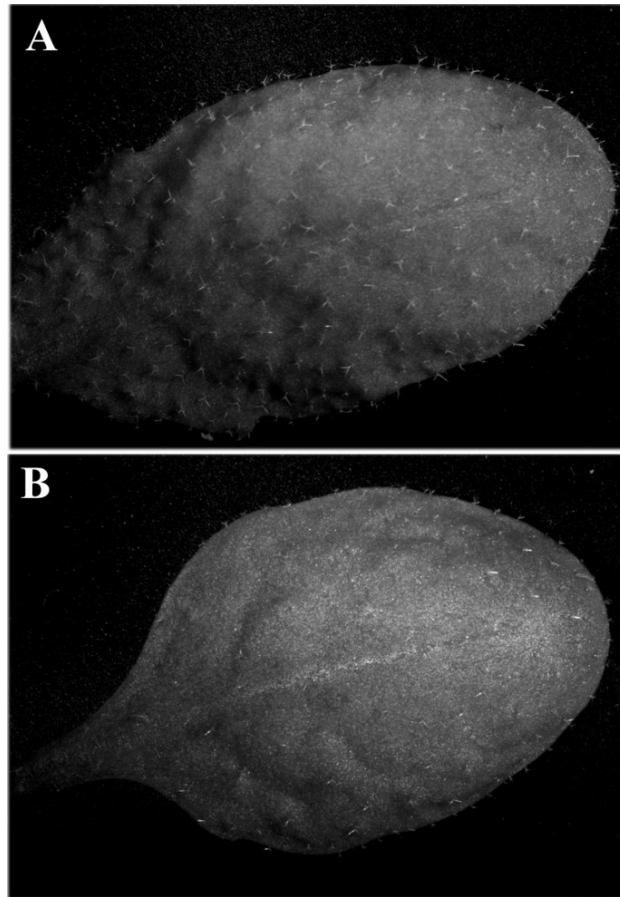


**Supplemental Figure 4. Western blot confirming equal protein amounts used in wild type and mutant protoplasts for activation assays.** Western blots show comparable protein levels of transcription factor 35S:ERF1-MYC in wild type, *cdk8* and *med25* protoplasts. The protein was extracted from protoplasts transformed with 35S:ERF1-MYC and *PDF1.2pro*-GUS as well as 35S:FLuc.

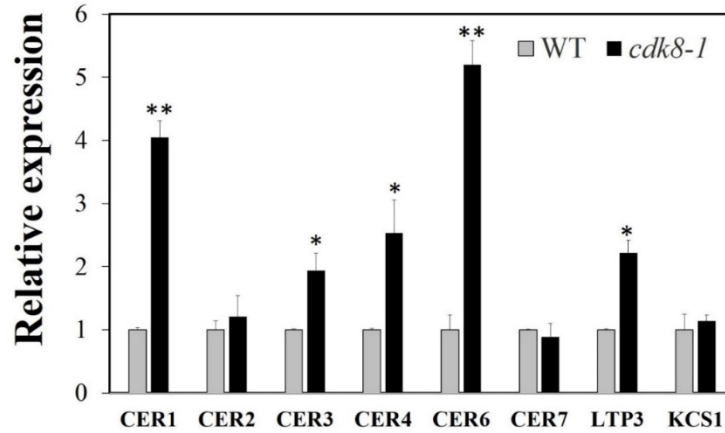


**Supplemental Figure 5. The CDK8 target gene *AACT1* is required for resistance to *B. cinerea*.**

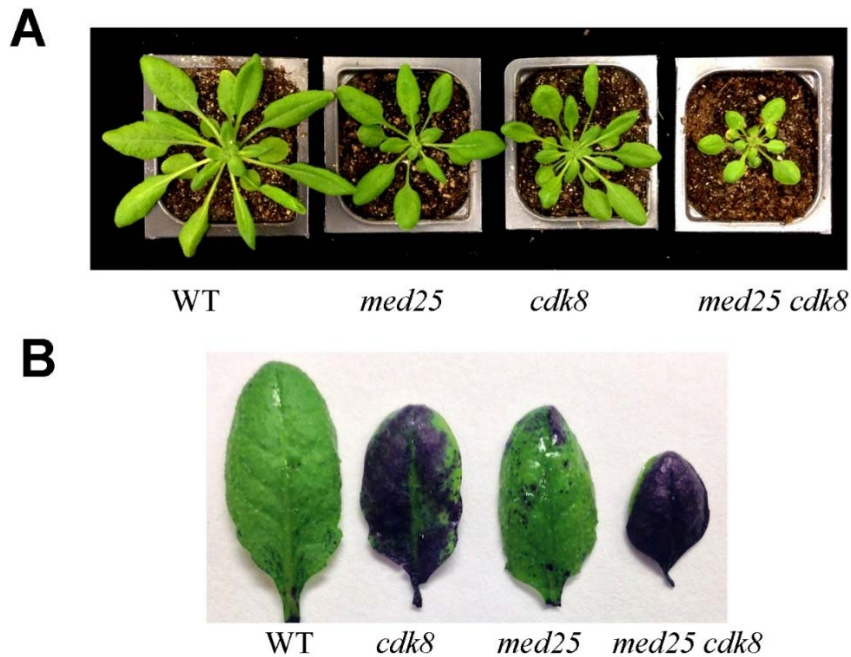
(A) Diseases symptom and (B) Disease lesion sizes in wild type (Col-0) and *aact1* mutants at 3 day after drop inoculation with *B. cinerea*. The means marked with a and b are significantly different from each other (Student's *t* test,  $P < 0.01$ ). Error bars indicate mean values  $\pm$ SE from at least 12 disease lesions.



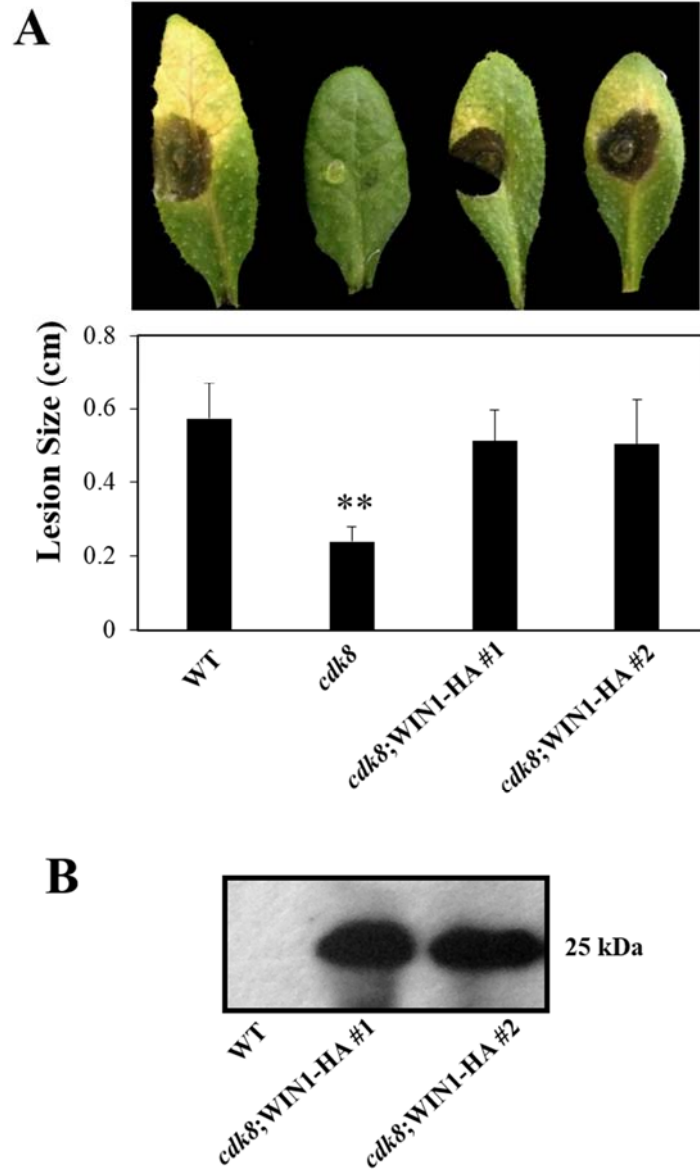
**Supplemental Figure 6. The leaf surface phenotypes of *cdk8* and wild type plants.**  
(A) Wild type plants, (B) The glossy leaf surface of *cdk8* mutant.



**Supplemental Figure 7. The expression of cuticle wax biosynthesis genes in wild type and *cdk8* mutant.** Relative transcript levels were normalized with Arabidopsis *Actin2* (*ACT2*). The normalized expression level of wild type was set to 1. Error bars indicate SE of mean value (n=3). Three independent biological replicates were performed. Significance between the mean values were analyzed statistically (Student's *t* test, \*\* P< 0.01).



**Supplemental Figure 8. Growth and cuticle permeability of *cdk8* and *med25* single and double mutants.** (A) Five-week-old wild-type (Col-0), *med25*, *cdk8* and *med25 cdk8* double mutant. (B) Cuticle permeability as revealed by toluidine-blue staining. At least 10 leaves for each genotypes were stained at room temperature for 1 h for each staining experiment.



**Supplemental Figure 9. Disease symptoms of *cdk8*;WIN1-HA plants to *B. cinerea*.**

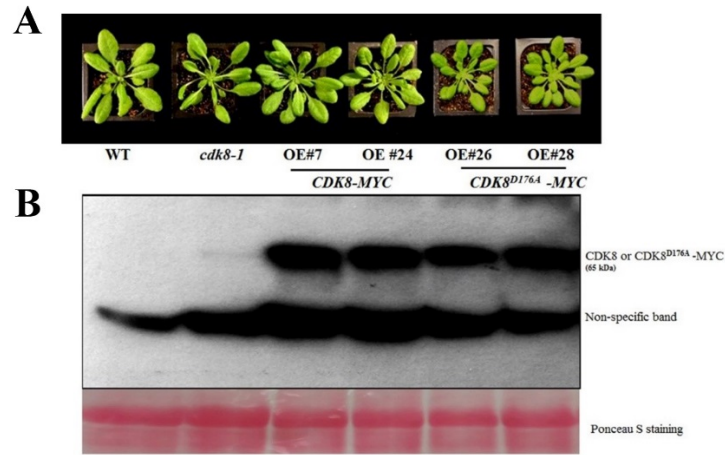
(A) The *cdk8*;WIN1-HA plants exhibit WT level of resistance to *B. cinerea* and (B) Western Blots demonstrate the WIN1-HA expressions. In A, the error bars indicate the mean  $\pm$  SE from at least 20 disease lesions. Significance between the mean values were analyzed statistically (Student's *t* test, \*\*  $P < 0.01$ ).

Arabidopsis CDK8	MGDGSSSRNSN...STSEKPEMLQQYNLVGRKIGGTYGVFLRARKTFPKR...PLAIKRFKQSKDGGVSPTRREIMLRRETSHEENVVVLVNH	93
Human CDK8	MDYDFKVLSS.....ERERVELDFEYEGG.KVGRGTYGVVYKRRDGDGDD....KDYALKQIEGCGSMSAGREITLRLRKLKHNVISLQKQVFL	86
Drosophila melanogaster	MDYDFKMKAI.....ERTNVELDFEYEGG.KVGRGTYGVVYKRRDGDGDD....KEYALKQIDGCGSMSAGREITLRLRKLKHNVISLQKQVFL	86
Mus musculus	MDYDFKVLSS.....ERERVELDFEYEGG.KVGRGTYGVVYKRRDGDGDD....KDYALKQIEGCGSMSAGREITLRLRKLKHNVISLQKQVFL	86
Medicago truncatula	MADG.....NR.....SNSNKEPEMLQQYNLVGRKIGGTYGVFLRARKSTTNRGKSTAIKRFKQSKDGGVSPTRREIMLRRETSHEENVVVLVNH	88
Vitis vinifera	MGDTTATSNRGGGGNGSGSNKFAIQQYDLIGRHGEGTYGVFLRARKSFSNRRGKSTAIKRFKQSKDGGVSPTRREIMLRRETSHEENVVVLVNH	100
Consensus	m 1 y k g gtyg v a k g g s a rei l re h nv l v	
Arabidopsis CDK8	NFDMSLYLAFDYAEFLDYETIIRHHRDRVGH...LNTYTVKSLIQCLINGLYLSNWIHRDLKSNILVMGADDFGVKADGFAIRIVQPLPK	189
Human CDK8	SHDRKVVLLFDYAEFLDYETIIRHHRDRVGH...LNTYTVKSLIQCLINGLYLSNWIHRDLKSNILVMGADDFGVKADGFAIRIVQPLPK	186
Drosophila melanogaster	SHDRKVVLLFDYAEFLDYETIIRHHRDRVGH...LNTYTVKSLIQCLINGLYLSNWIHRDLKSNILVMGADDFGVKADGFAIRIVQPLPK	186
Mus musculus	SHDRKVVLLFDYAEFLDYETIIRHHRDRVGH...LNTYTVKSLIQCLINGLYLSNWIHRDLKSNILVMGADDFGVKADGFAIRIVQPLPK	186
Medicago truncatula	NHTDMSLYLAFDYAEFLDYETIIRHHRDRVGH...LNTYTVKSLIQCLINGLYLSNWIHRDLKSNILVMGADDFGVKADGFAIRIVQPLPK	184
Vitis vinifera	NHTDMSLYLAFDYAEFLDYETIIRHHRDRVGH...LNTYTVKSLIQCLINGLYLSNWIHRDLKSNILVMGADDFGVKADGFAIRIVQPLPK	196
Consensus	d l dyae dl ii hr vks l q l g ylh nw hrdlkp nilvmg e g vk ad g ar plkp	
Arabidopsis CDK8	LSLNG.VVVVWYRAPELLLGRHYTSKAWDVAWGCIFAELLTLRFFQG.FEAKSSQNFQIDQLDRIEKLIGHTMDRPTLVNIFHWQNDVQHIQAH	287
Human CDK8	LAIDLDFVVVWYRAPELLLGRHYTSKAWDVAWGCIFAELLTLRFFQHCRQDDIKTSNPFYHEDQLDRIEKLIGHTMDRPTLVNIFHWQNDVQHIQAH	286
Drosophila melanogaster	LAIDLDFVVVWYRAPELLLGRHYTSKAWDVAWGCIFAELLTLRFFQHCRQDDIKTSNPFYHEDQLDRIEKLIGHTMDRPTLVNIFHWQNDVQHIQAH	286
Mus musculus	LAIDLDFVVVWYRAPELLLGRHYTSKAWDVAWGCIFAELLTLRFFQHCRQDDIKTSNPFYHEDQLDRIEKLIGHTMDRPTLVNIFHWQNDVQHIQAH	286
Medicago truncatula	LSLNG.VVVVWYRAPELLLGRHYTSKAWDVAWGCIFAELLTLRFFQG.FEVKATENEFQIDQLDRIEKLIGHTMDRPTLVNIFHWQNDVQHIQAH	282
Vitis vinifera	LSLNG.VVVVWYRAPELLLGRHYTSKAWDVAWGCIFAELLTLRFFQG.FEVKATENEFQIDQLDRIEKLIGHTMDRPTLVNIFHWQNDVQHIQAH	294
Consensus	l vvvv wyrapelllg hyt a d w a gcifeallt p f e np dqld if g p w p	
Arabidopsis CDK8	KYDSVGLHNVVHLNQS...AYLLSRWLEYDRKRITAAQALDHRYSRPELGRNALVPSGAGAEKVMNVPVDTTDFEGTNSLQTSFVSSGN	382
Human CDK8	TYNCSLIRYMEKHKVKPDSKAFHLLCRILTMDFIKRITSEQAMQDQYFLELPHITSDVFAGCQIP.....YFRRELEEEEPDDRDKKNCQQQGGNN	380
Drosophila melanogaster	TYNCSLIRYMEKHKVKPDSKAFHLLCRILTMDFIKRITSEQAMQDQYFLELPHITSDVFAGCQIP.....YFRRELEEEEPDDRDKKNCQQQGGNN	380
Mus musculus	TYNCSLIRYMEKHKVKPDSKAFHLLCRILTMDFIKRITSEQAMQDQYFLELPHITSDVFAGCQIP.....YFRRELEEEEPDDRDKKNCQQQGGNN	380
Medicago truncatula	KYDNASVNSVHLSKSP...AYLLSRWLEYDRKRITAAQALDHRYSRPELGRNALVPSGAGAEKVMNVPVDTTDFEGTNSLQTSFVSSGN	378
Vitis vinifera	KYDNASVNSVHLSKSP...AYLLSRWLEYDRKRITAAQALDHRYSRPELGRNALVPSGAGAEKVMNVPVDTTDFEGTNSLQTSFVSSGN	391
Consensus	y l a ll k l dp rit qa yf p p y p r t q	
Arabidopsis CDK8	NVAGNMGAGHGMGSRSMFRPMVAHNMQRMQSQGMMAYNFPAGAGLNPVFP...LQQQRGMAQFHQ.CCLRRKDPGMGMSGYAFPNKSRRL.....	470
Human CDK8	HTNGTGHFGNCDSSHTGPPFLKVVVVVFTT...TSGGLIMTSYQRSNF...HAAYNPFGEISTEFCSSMGYSATSCQPFQYSHQTHRY.....	464
Drosophila melanogaster	HTNGTGHFGNCDSSHTGPPFLKVVVVVFTT...TSGGLIMTSYQRSNF...HAAYNPFGEISTEFCSSMGYSATSCQPFQYSHQTHRY.....	454
Mus musculus	HTNGTGHFGNCDSSHTGPPFLKVVVVVFTT...TSGGLIMTSYQRSNF...HAAYNPFGEISTEFCSSMGYSATSCQPFQYSHQTHRY.....	464
Medicago truncatula	AIAGNMFGHSA.NRSVFRFIN.VGMQRHQ...LQAYNLTSQAMSSGINPAGIPMQRGVFQQAHCCLRRKDP.MGMFGYFPQCKSRRLMLNWKRLIV	472
Vitis vinifera	AVSGSMAAGHVFNRSVFRFIN.VGMQRHQ...LQAYNLTSQAMSSGINPAGIPMQRGVFQQAHCCLRRKDP.MGMFGYFPQCKSRRLMLNWKRLIV	481
Consensus	q q	

**Supplemental Figure 10. Amino acid sequence comparisons between full length Arabidopsis, human, Drosophila, mouse and plant CDK8 proteins.**

The highly conserved domains are in blue. The protein sequence were aligned by DNAMAN8 software with default setting.

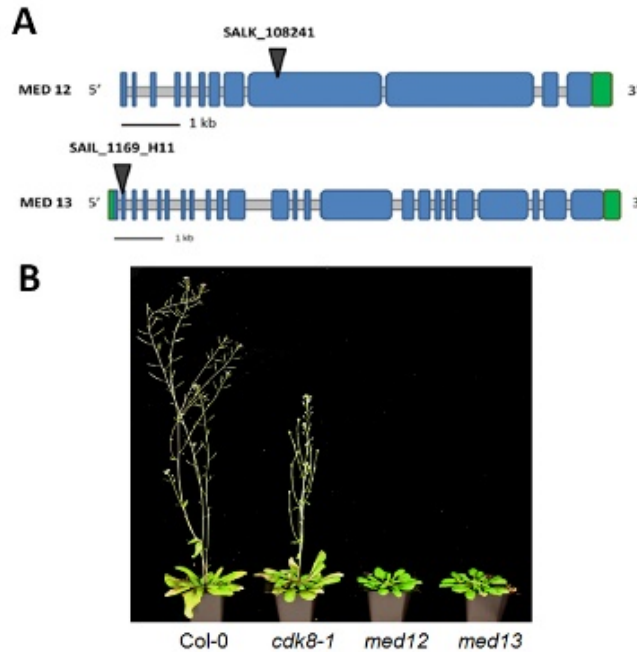




**Supplemental Figure 11. Western blot showing plants expressing wild type CDK8 and the kinase-dead CDK8 driven by the CaMV 35S promoter.**

(A) Morphology of five-week-old wild-type (Col-0), *cdk8-1*, and *35S:CDK8-MYC* overexpression lines #7 and #24, and *35S:CDK8<sup>D176A</sup>-MYC* overexpression lines #26 and #28. OE, overexpression.

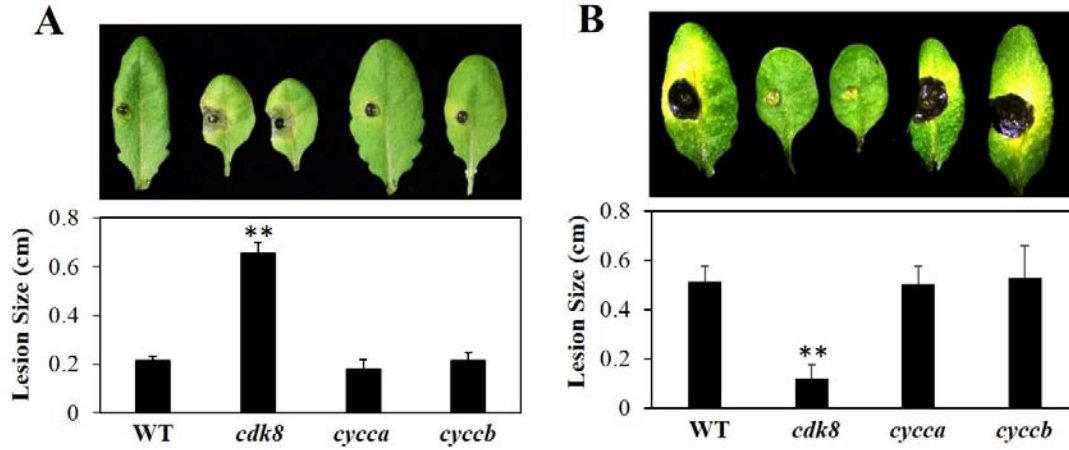
(B) Western blot analysis of CDK8 or CDK8<sup>D176A</sup>-MYC protein expressions in transgenic plants. The western blot was probed with polyclonal anti-MYC antibody and equal loading was confirmed by Ponceau S staining.



**Supplemental Figure 12. Arabidopsis mutants *med12* and *med13* in CDK8 kinase-module have altered growth responses.**

(A) Diagram showing positions of T-DNA insertion in *MED12* and *MED13* genes.

(B) Delayed flowering in *med12* and *med13*. Pictures were taken at 50 days after sowing seeds on soil.



**Supplemental Figure 13. Disease symptoms in *cycca* and *cyccb* single mutants after inoculation with *B. cinerea* and *A. brassicicola*.**

Disease symptom and lesion size in wild-type (Col-0), *cdk8* mutant, *cycca* and *cyccb* plants inoculated with (A) *A. brassicicola*, and (B) *B. cinerea* at 4 days after drop inoculation. The lesion sizes are mean of values  $\pm$ SE from at least 20 disease lesions and the double asterisk indicate that  $P < 0.01$  using Student's *t* test compared to WT.