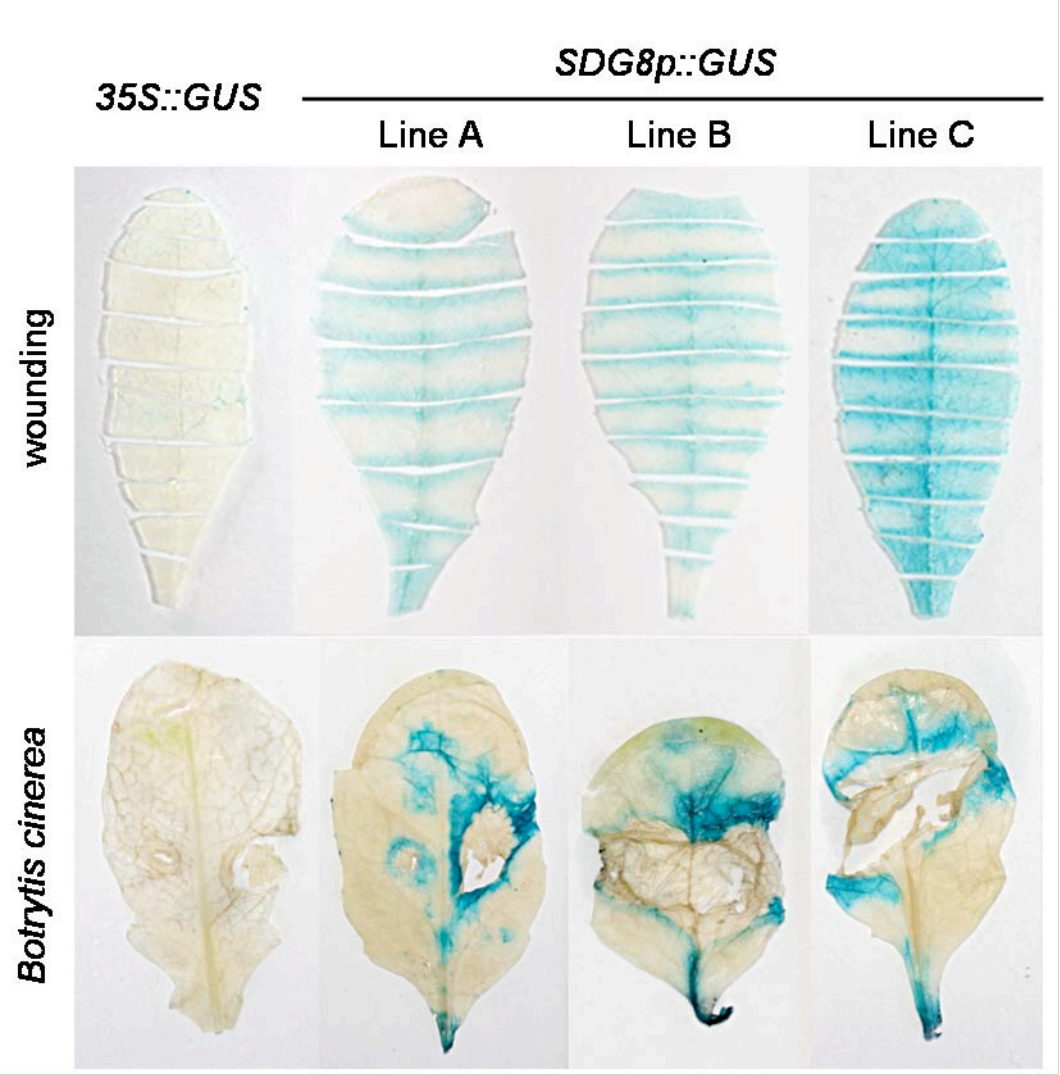
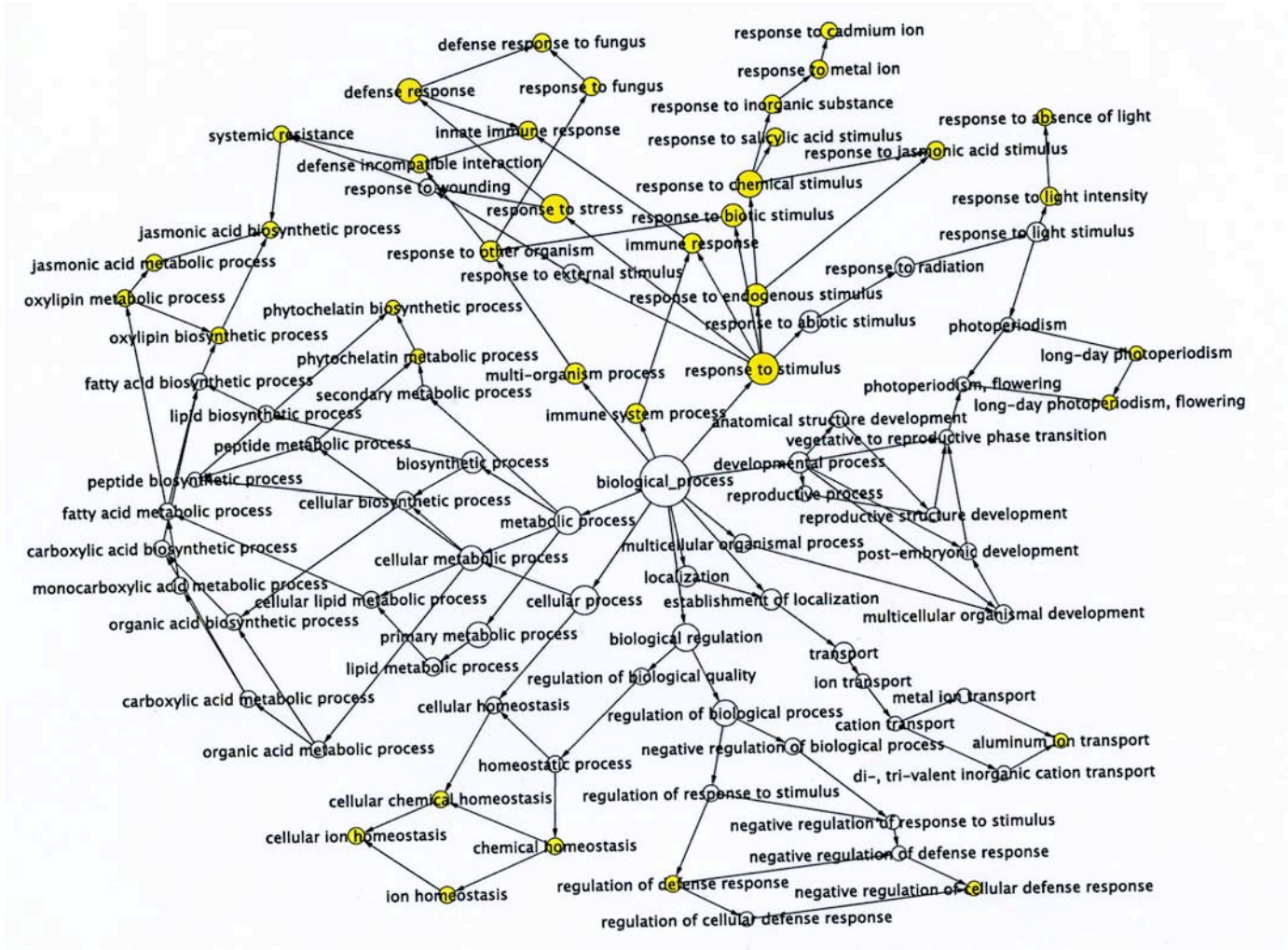
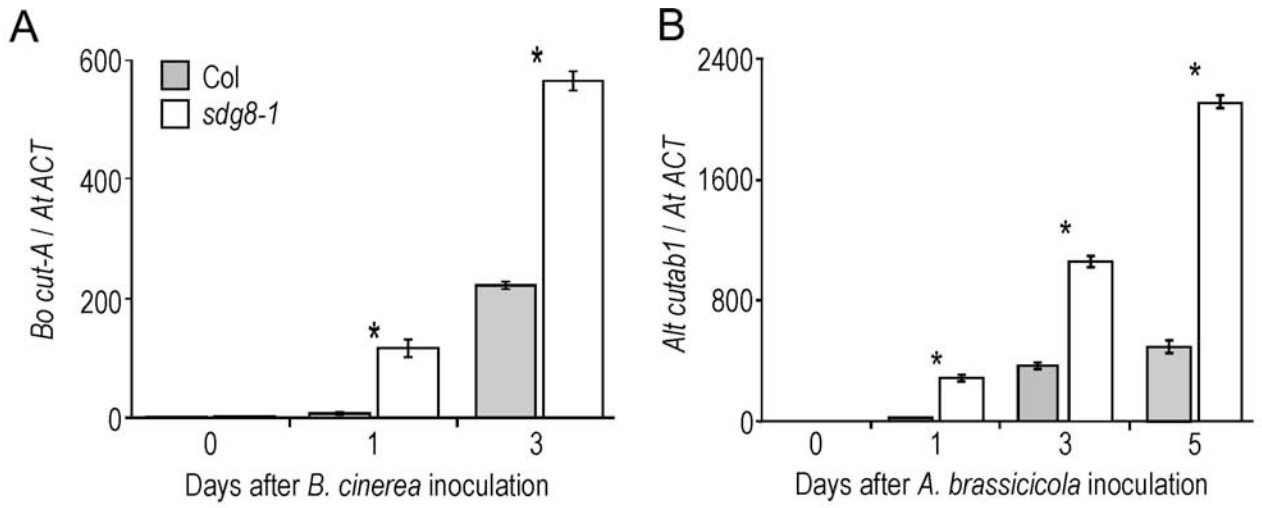


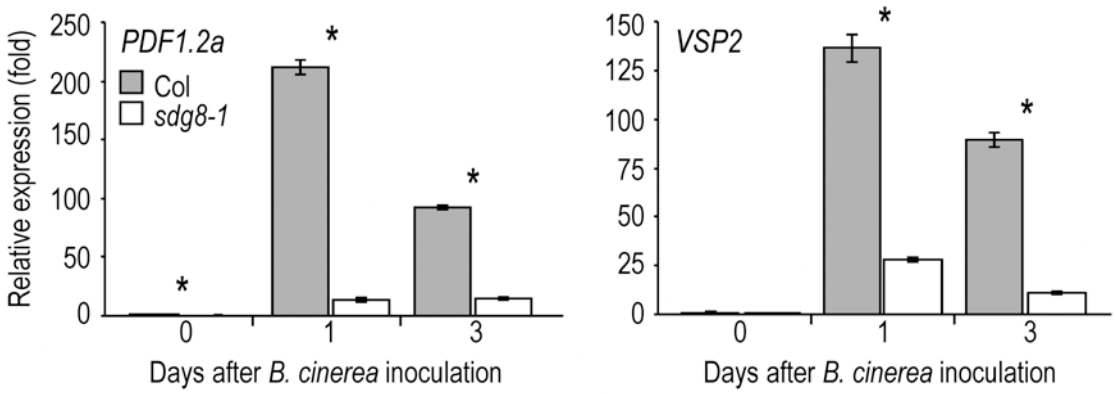
Supplemental Figure S1. Stress-induced expression of *SDG8p::GUS* in independent transgenic lines. Images show leaves wounded by slicing or inoculated with *B. cinerea* at 3 days post-inoculation from transgenic *Arabidopsis* plants containing the *35S::GUS* (control) or the *SDG8p::GUS* construct. Three independent transgenic lines are shown for *SDG8p::GUS.* Blue staining indicates GUS activity.



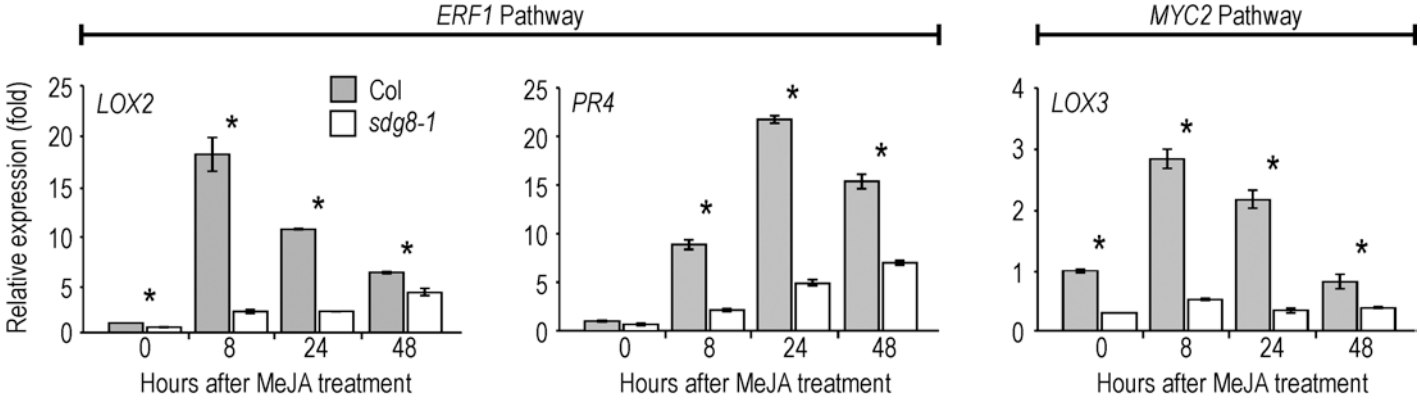
Supplemental Figure S2. Gene ontology analysis of differentially expressed genes in *sdg8-1* seedlings. Genes were identified by microarray analysis previously reported in Xu et al. (2008). Color of the circles corresponds to the level of significance of the overrepresented GO category from $P \leq 0.05$ and below, according to a multiple *t*-test with false discovery rate-corrected *p*-value. Yellow tones denote decreasing *P* values, and the size of the circle is proportional to the number of genes in each category.



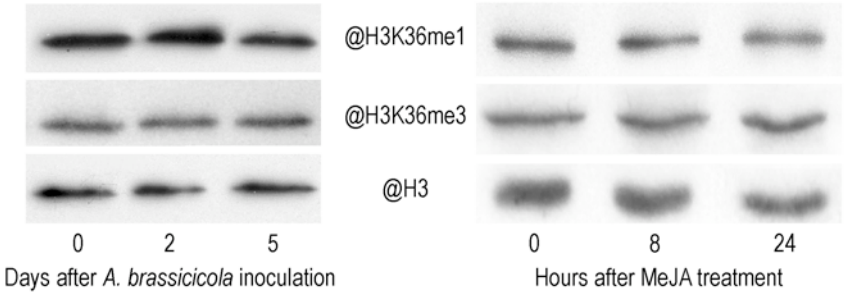
Supplemental Figure S3. Comparison of fungal pathogen growth in infected leaves of mutant *sdg8-1* and wild-type Col plants. Results from an independent experiment are shown, which confirms that *B. cinerea* (A) and *A. brassicicola* (B) multiplication is enhanced in *sdg8-1* compared to Col, as described in Figure 2. Data represent the mean ± SD of triplicates. Asterisks indicate significance at $P<0.05$ using *t*-test.



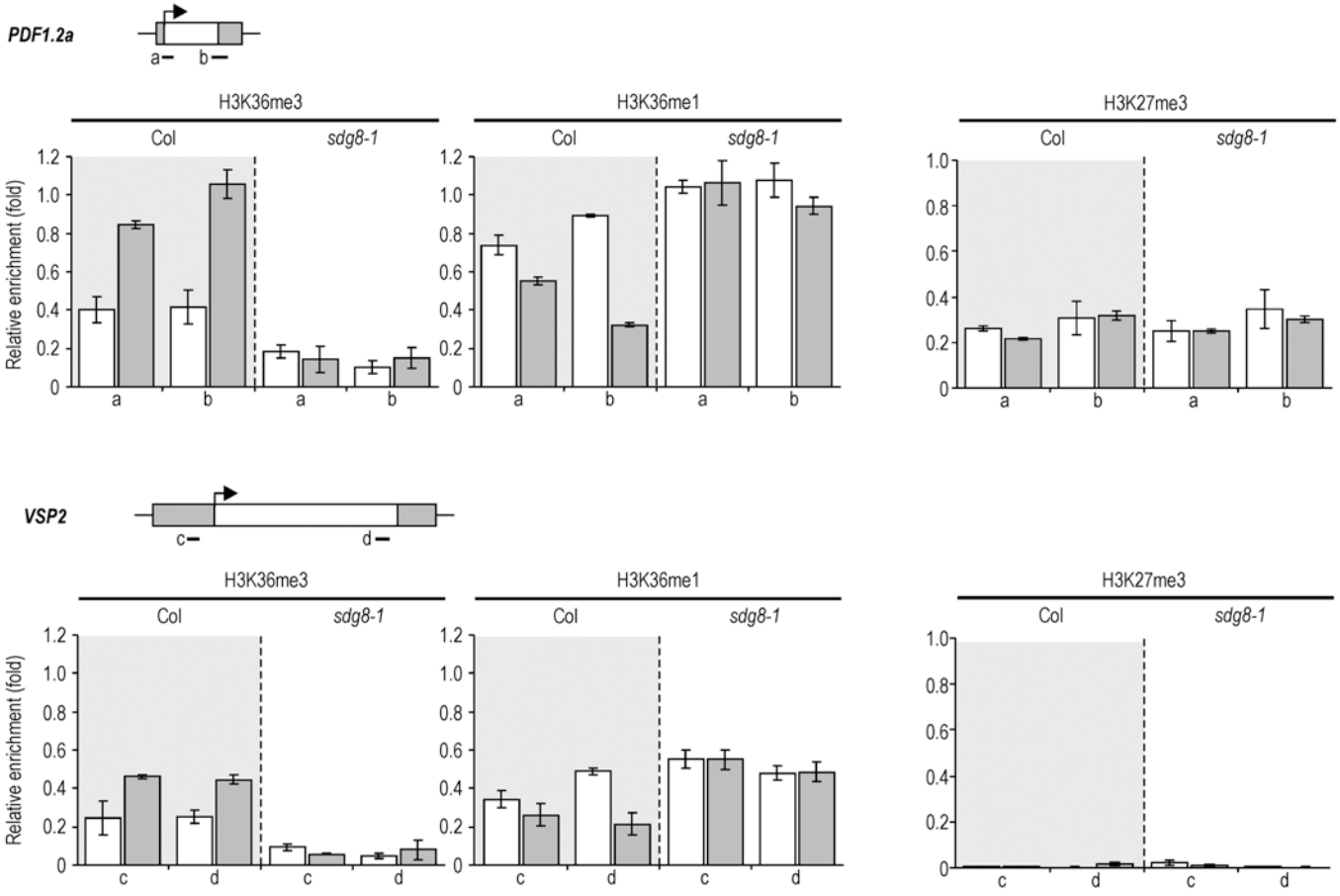
Supplemental Figure S4. Comparison of defense gene expression in response to *B. cinerea* infection in mutant *sdg8-1* and wild-type Col plants. Expression levels of *PDF1.2a* (left) and *VSP2* (right) in *sdg8-1* and Col leaves after *B. cinerea* inoculation are presented relative to average wild-type levels at time point 0 (set as 1). Data represents the mean ± SD of triplicates. Similar results were obtained in two independent experiments (refer to Supplemental Table S3). Differences in fold induction of defense marker genes in *sdg8-1* and Col are listed in Table S3. Asterisks indicate a significant difference between Col and *sdg8-1* at $P<0.05$ (two sided *t*-test).



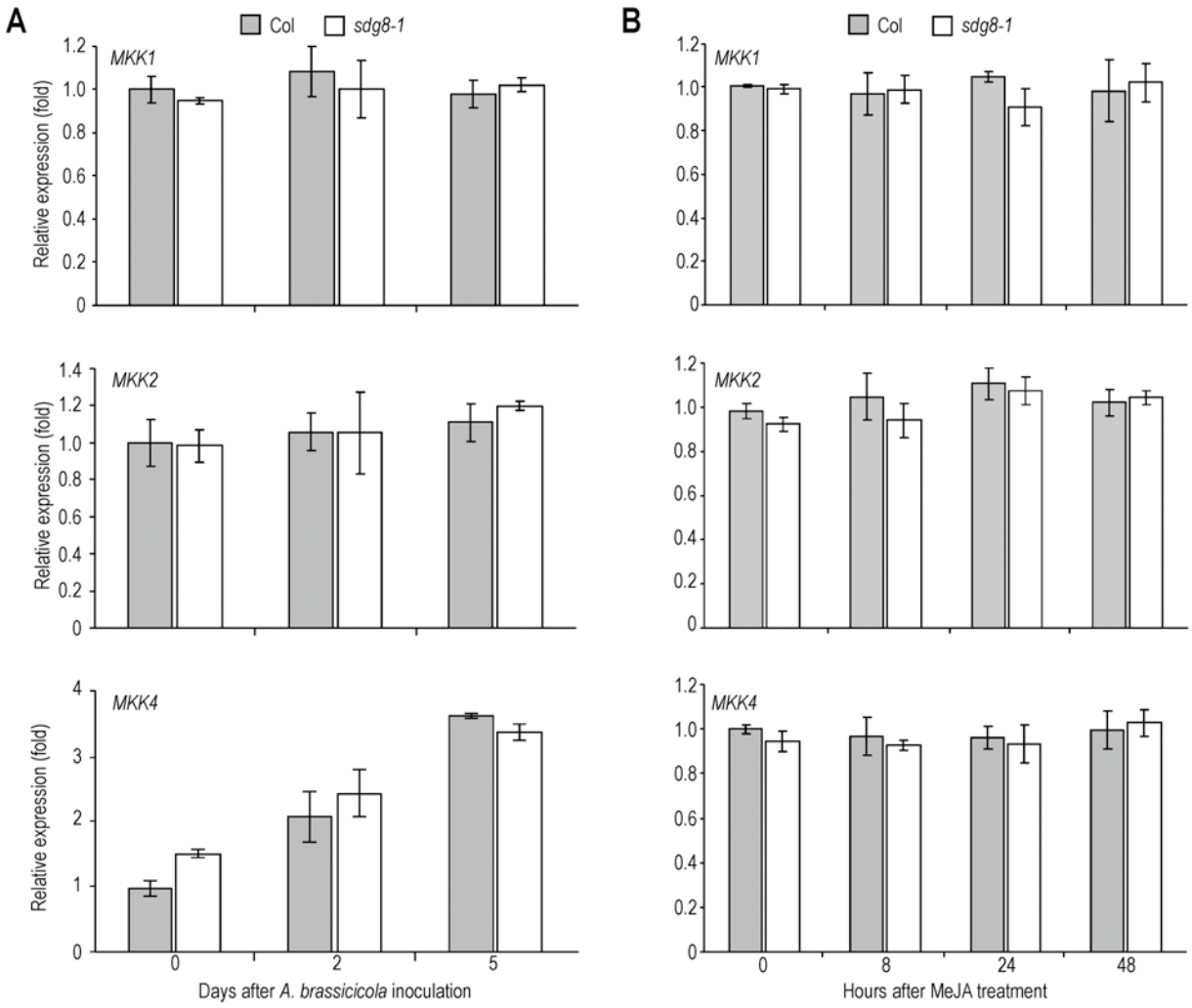
Supplemental Figure S5. Comparison of JA/ET pathway gene expression in response to MeJA treatment in mutant *sdg8-1* and wild-type Col plants. Expression levels of JA/ET-responsive genes (*LOX2*, *PR4* and *LOX3*) in *sdg8-1* and Col leaves after treatment with exogenously applied MeJA are presented relative to average wild-type levels at time point 0 (set as 1). Data represents the mean ± SD of triplicates. Similar results were obtained in two independent experiments (refer to Supplemental Table S4). Differences in fold induction of defense marker genes in *sdg8-1* and Col are listed in Table S4. Asterisks indicate a significant difference between Col and *sdg8-1* at $P<0.05$ (two sided *t*-test).



Supplemental Figure S6. Western blot analysis of global H3K36 methylation in response to *A. brassicicola* inoculation or MeJA treatment. Histone-enriched protein extracts of wild-type Col leaves inoculated with *A. brassicicola* (left) or treated with exogenous MeJA (right) were immunoblotted using antibodies that specifically recognize the indicated histone forms. Histone H3 total protein was used as a loading control.



Supplemental Figure S7. Histone methylation at ET/JA pathway defense genes in response to MeJA treatment in mutant *sdg8-1* and wild-type Col plants. Chromatin immunoprecipitation analysis was used to determine the relative levels of H3K36me3, H3K36me1 and H3K27me3 before (white bar) and 8 h after (black bar) exogenous MeJA treatment of 6-week-old Col and *sdg8-1* plants at indicated regions of *PDF1.2a* and *VSP2*. Data represents the mean ± SD of triplicates. Similar results were obtained in two independent experiments (refer to Supplemental Table S7). Amplified regions (named a to d) are indicated below each gene, which is represented by a white box for the coding region and grey boxes for the 5' and 3' untranslated regions.



Supplemental Figure S8. Expression of *MKK* genes in response to *A. brassicicola* inoculation and MeJA treatment in mutant *sdg8-1* and wild-type Col plants. Expression levels of *MKK1*, *MKK2* and *MKK4* after *A. brassicicola* inoculation and exogenous MeJA treatment are presented relative to average wild-type levels at time point 0 (set as 1). Data represents the mean ± SD of triplicates. Similar results were obtained in two independent experiments (refer to Supplemental Tables S2 and S4). Note that no significant difference was observed between Col and *sdg8-1*.