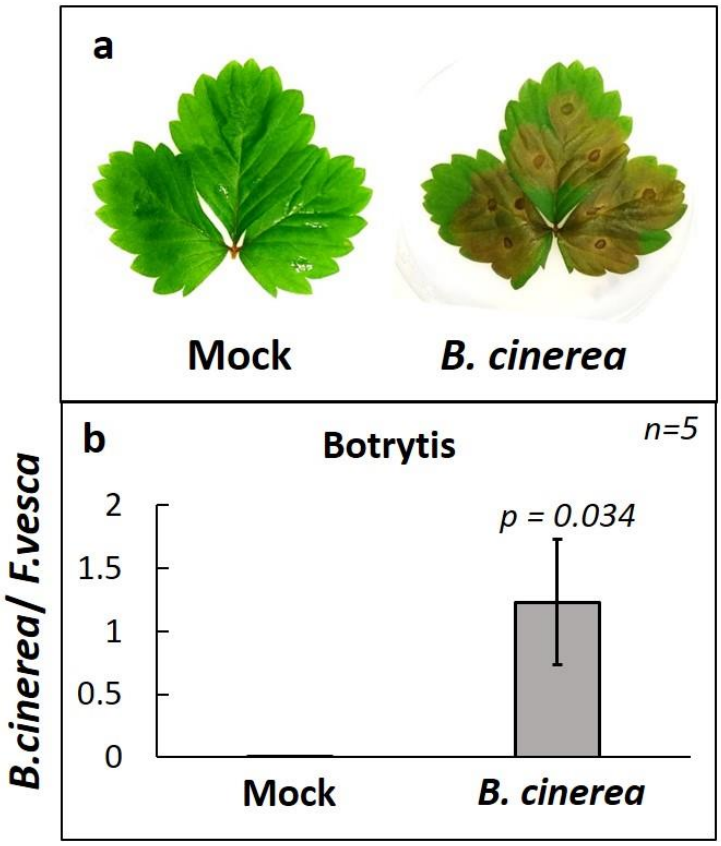
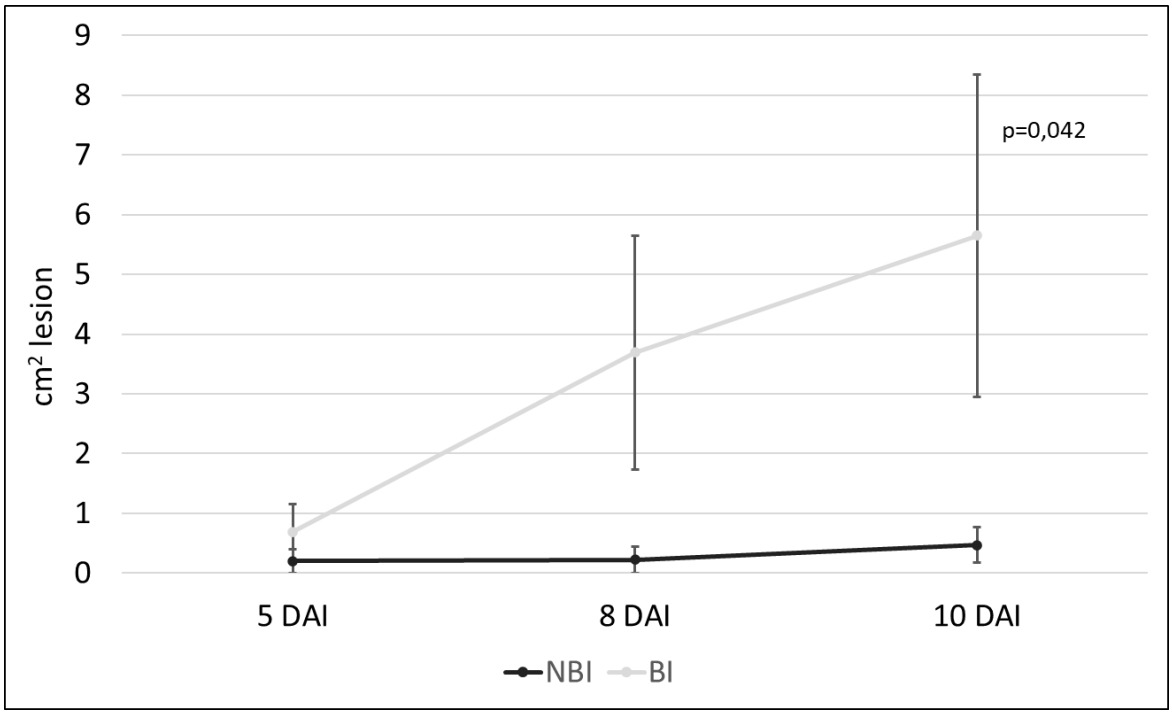
Supplementary Material

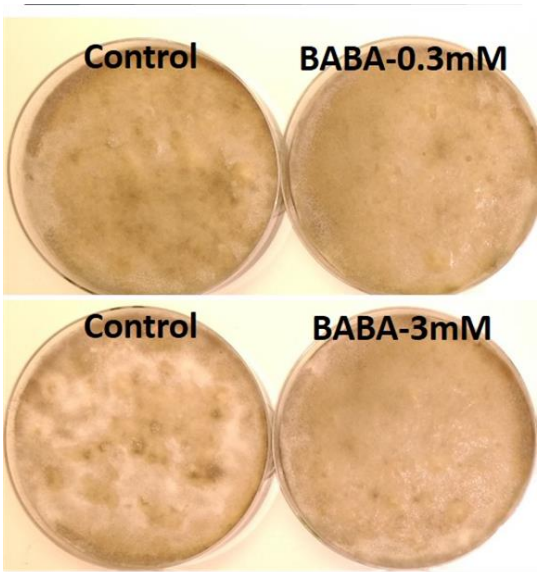
Supplementary Figures and Tables



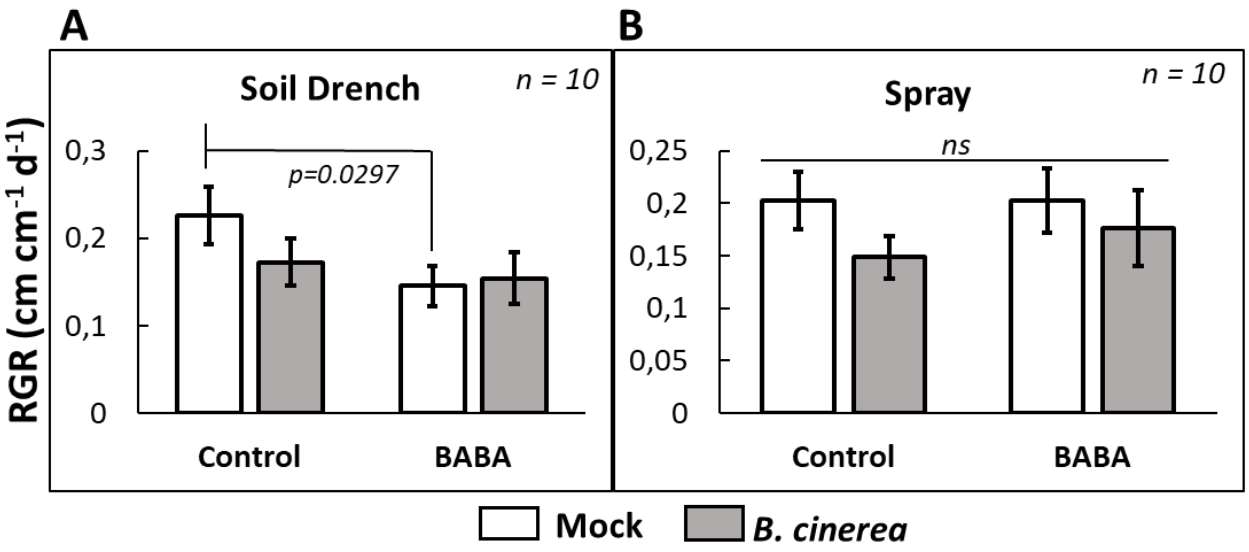
Supplementary figure S1: Quantification method for *Botrytis cinerea* infection and verification of pathogenicity in *Fragaria vesca* leaves. (a) Representative *F. vesca* 'Hawaii-4' leaves showing infection by *B. cinerea* 5 days after drop inoculation of fungal spores (right) or mock suspension (left). (b) Genomic DNA-based qPCR quantification of *B. cinerea* DNA relative to *F. vesca* DNA using genome-specific primers for *B. cinerea* (Bc3F and Bc3R) and *F. vesca* (EF1αF and EF1αR) in non-infected (Mock) and infected *(B. cinerea)* leaf samples. Y-axis values represents relative amount of *B. cinerea* DNA to *F. vesca* DNA. '*n'* = number of replicates (i.e. individual plants). Error bars show standard error (±1 SE). P-values report comparisons between infected and uninfected plants using Student's t-test.



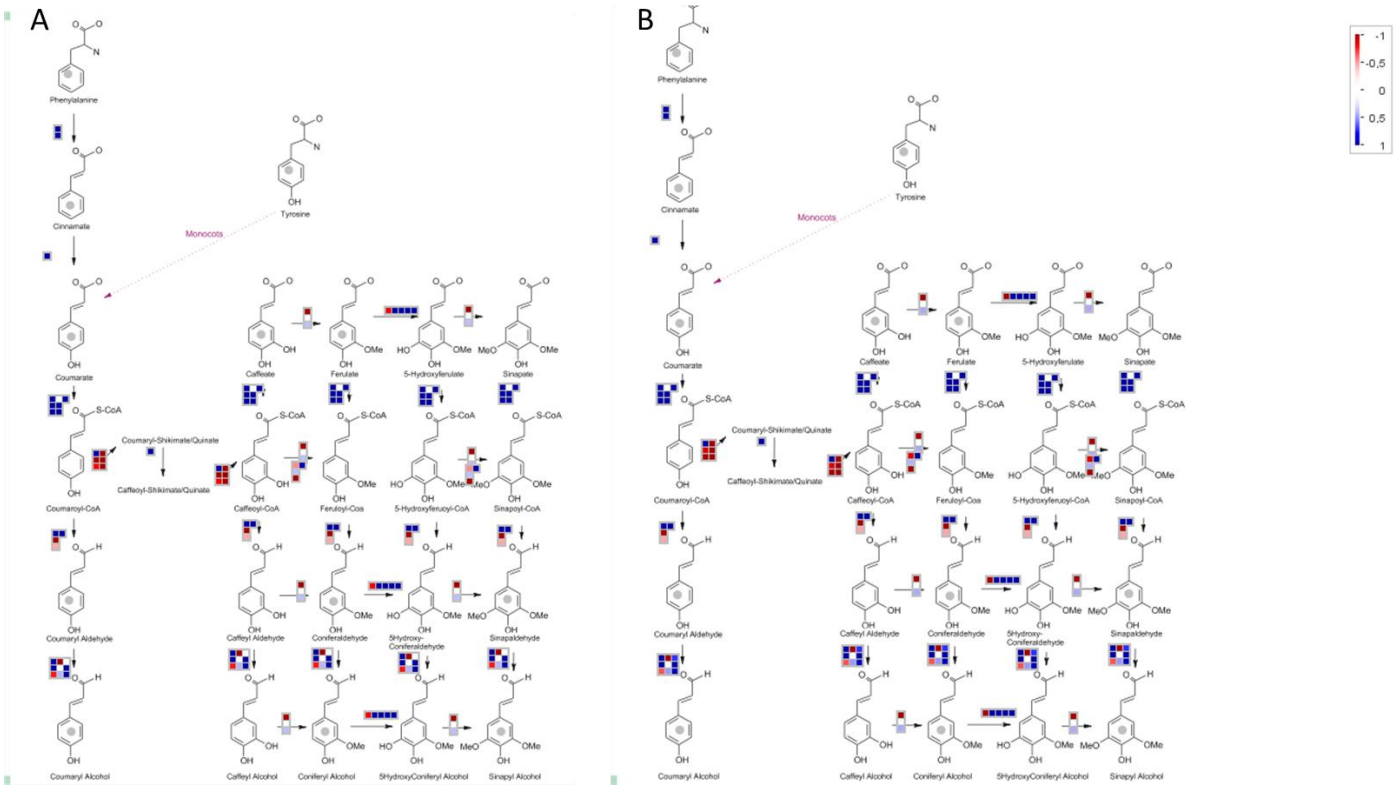
Supplementary figure S2: Effects of BABA soil drench on resistance of *Fragaria ananassa* to infection with *Botrytis cinerea*. Plants were soil drenched with water or 0.2 mM BABA 8 days prior to drop-inoculation of leaves with *B. cinerea* (No BABA and Infected (NBI) and BABA and Infected (BI), respectively). Measurement of lesion area (in cm^2) was done using ImageJ of images taken 5, 8, and 10 days after inoculation. Values show average lesion area on infected detached leaves from 16 individual plants (n = 16). Error bars show standard error (±1 SE). P-values report significant comparisons between control plants (NBI) and plants treated with BABA (BI) using Student's t-test.



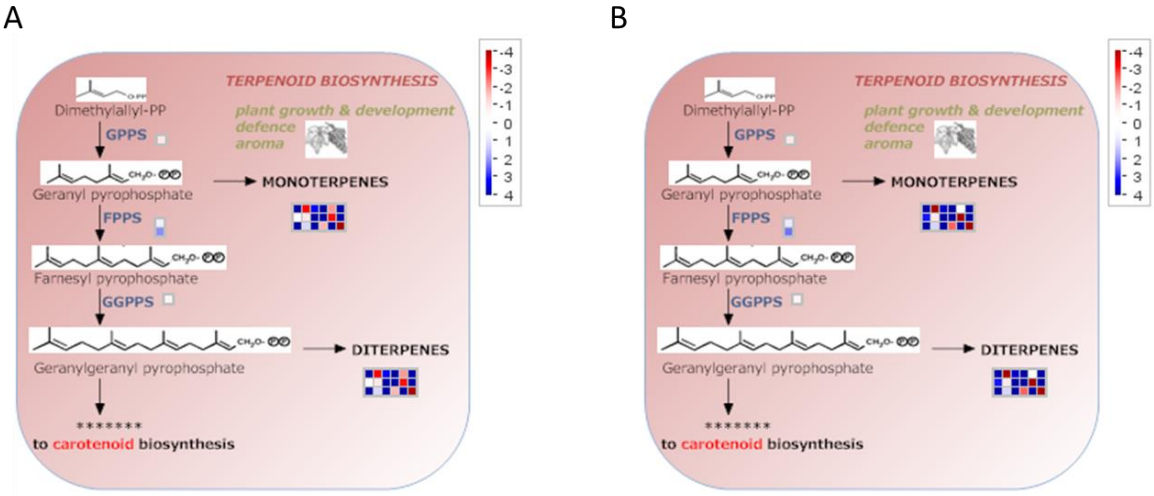
Supplementary figure S3: Direct effects of BABA on *Botrytis cinerea* growth. Growth of *B. cinerea* (brown mycelium) on potato dextrose agar amended with 0 mM, 0.3 mM, and 3 mM β-aminobutyric acid (BABA). A spore suspension of *B. cinerea* was spread on the agar and the plates were incubated in darkness for 4 weeks at room temperature.



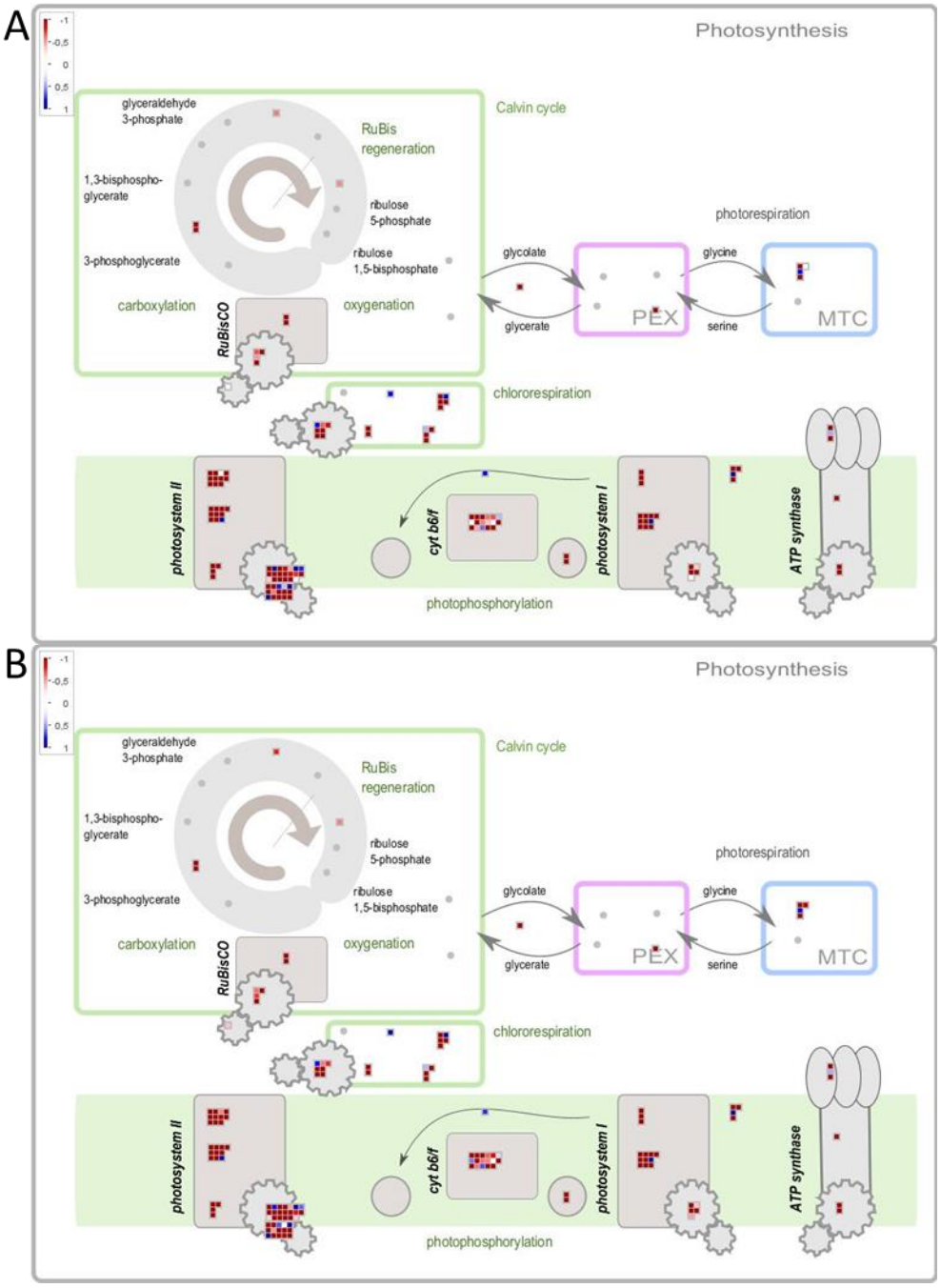
Supplementary figure S4: Effect of BABA on relative growth rate (RGR) of *Fragaria vesca* 'Hawaii-4' plants. RGR of plants that were (A) soil-drenched with 0.2 mM or (b) spray-treated with 0.3 mM β-aminobutyric acid (BABA). Control plants were treated with a suspension without BABA. All plants were subsequently infected with *Botrytis cinerea* spores or mock-infected. '*n'* = number of replicates (i.e. individual plants). Error bars show standard error (±1 SE). P-values report comparisons between treatment combinations using Student's t-test. '*ns*' = not statistically significant.



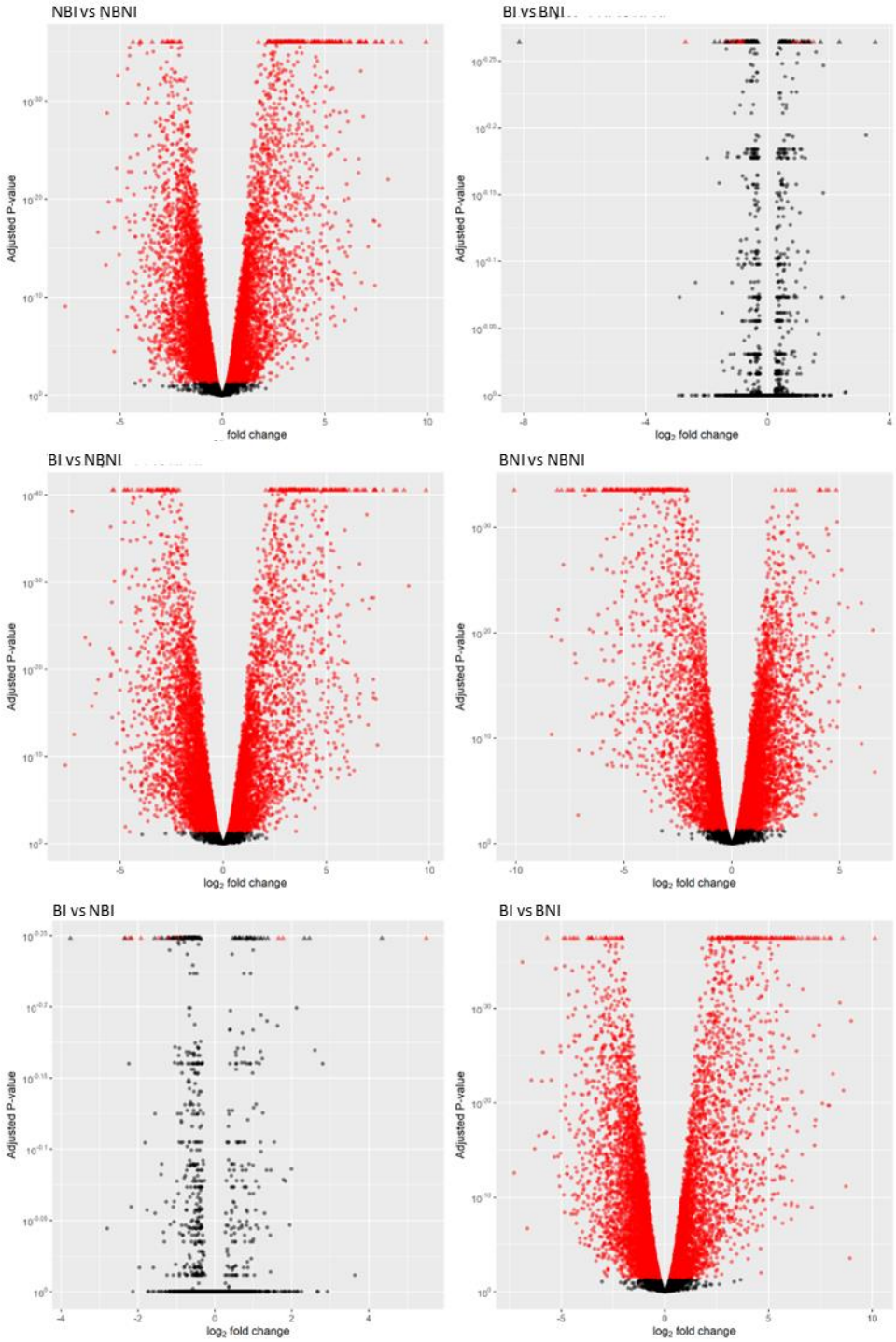
Supplementary figure S5. Visualization of DEGs in the phenylpropanoid pathway in *Fragaria vesca* leaves after β-aminobutyric acid (BABA) treatment and *Botrytis cinerea* infection.
Differentially expressed genes (DEGs) were displayed onto metabolic pathways using the MAPMAN software. (A) *B. cinerea*-infected vs. mock-infected plants (No BABA and infected (NBI) vs. No BABA and non-infected (NBNI)). (B) BABA-treated and *B. cinerea*-infected plants vs. mock-infected plants (BABA and infected (BI) vs. NBNI). Blue cells: upregulation compared to NBNI; red cells: downregulation compared to NBNI.



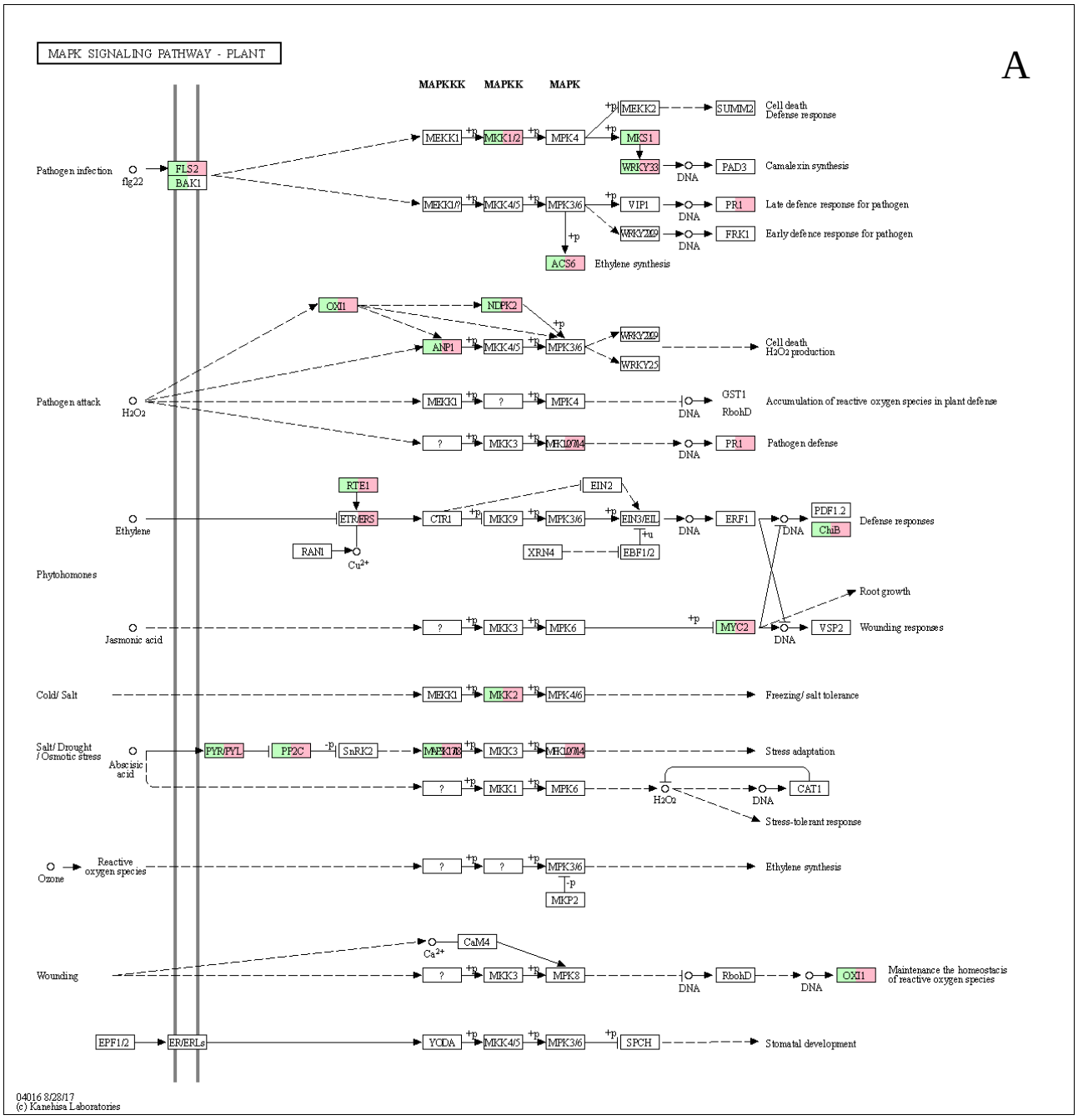
Supplementary figure S6. Visualization of DEGs in the terpenoid biosynthesis pathway in *Fragaria vesca* leaves after β-aminobutyric acid (BABA) treatment and *Botrytis cinerea* infection. Differentially expressed genes (DEGs) were displayed onto metabolic pathways using the MAPMAN software. (A) *B. cinerea*-infected vs. mock-infected plants (No BABA and infected (NBI) vs. No BABA and non-infected (NBNI)). (B) BABA-treated and *B. cinerea*-infected plants vs. mock-infected plants (BABA and infected (BI) vs. NBNI). Blue cells: upregulation compared to NBNI; red cells: downregulation compared to NBNI.

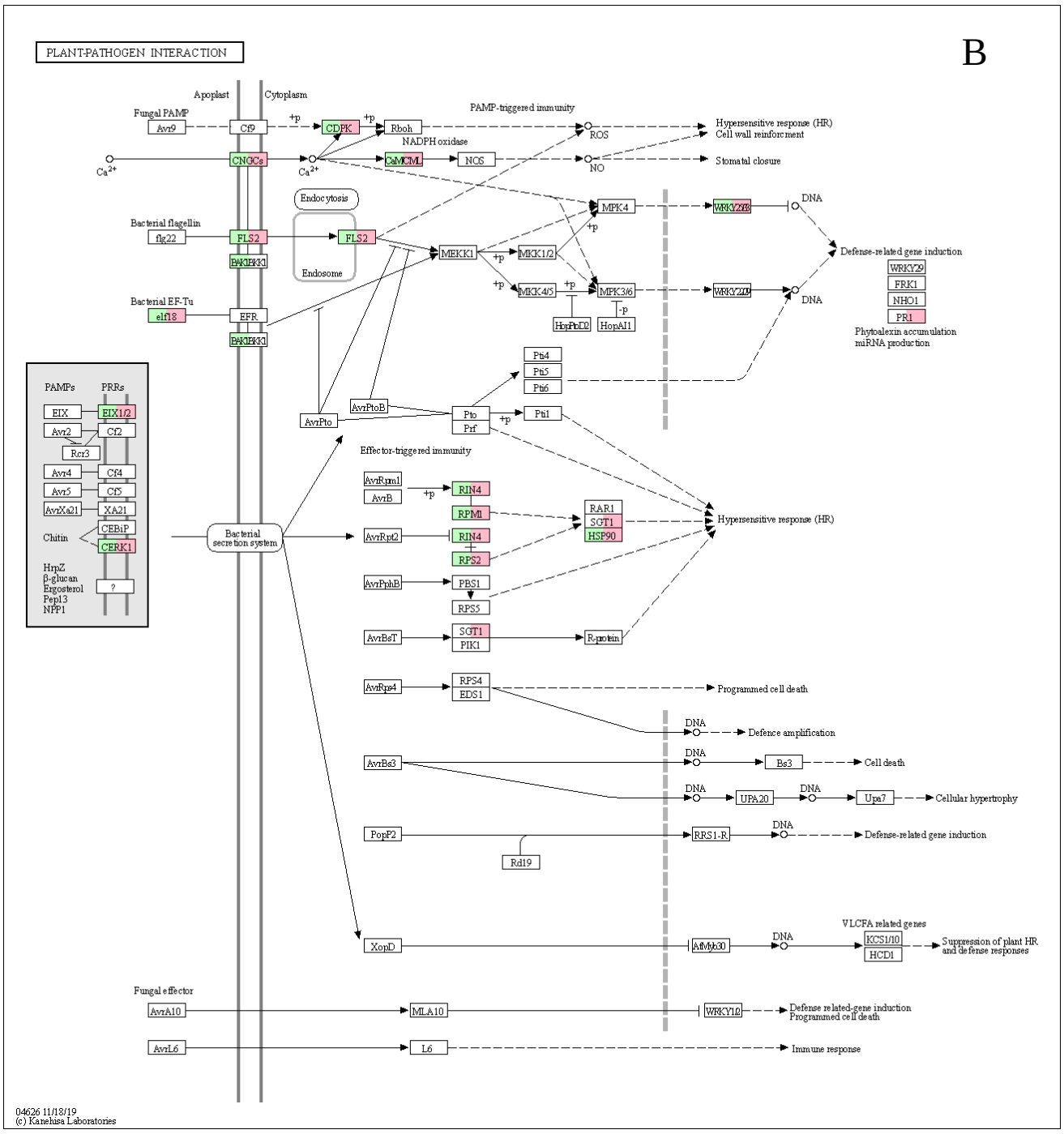


Supplementary figure S7. Visualization of enriched DEGs in photosynthesis in *Fragaria vesca* leaves after β-aminobutyric acid (BABA) treatment and *Botrytis cinerea* infection. Differentially expressed genes (DEGs) were displayed onto metabolic pathways using the MAPMAN software. (A) *B. cinerea*-infected vs. mock-infected plants (No BABA and infected (NBI) vs. No BABA and non-infected (NBNI)). (B) BABA-treated and *B. cinerea*-infected plants vs. mock-infected plants (BABA and infected (BI) vs. NBNI). Blue cells: upregulation compared to NBNI; red cells: downregulation compared to NBNI.


NBI vs NBNI
BI vs BNI
BI vs NBNI
BNI vs NBNI
BI vs NBI
BI vs BNI
Adjusted P-value
log2 fold change

Supplementary figure S8. Volcano plot (adjusted p-values versus log2 fold-change based on edgeR data) of transcripts in leaves of *Fragaria vesca* Hawaii-4 plants following BABA treatment and infection with *Botrytis cinerea*. Plants were treated with different combinations of 0.2 mM β-aminobutyric acid (BABA) as a soil drench and spray-inoculation of leaves with *B. cinerea* two days later. Transcripts with p-values < 0.05 are shown in red. (A) *Botrytis cinerea*-infected plants (No BABA and infected; NBI) vs. mock-infected plants (No BABA and non-infected; NBNI). (B) BABA-treated and mock-infected plants (BABA and non-infected; BNI) vs. NBNI. (C) BABA-treated and infected plants (BABA and infected; BI) vs. NBNI. (D) BNI vs. NBI. (E) BI vs. NBI. (F) BI vs. BNI.


MAPK SIGNALING PATHWAY - PLANT
A
MAPKKK
MAPKK
MAPK
Pathogen infection
flg22
FLS2
BAK1
MEKK1
MKK1/2
MPK4
MEKK2
SUMM2
Cell death
Defense response
MKS1
WRKY33
DNA
PAD3
Camalexin synthesis
MEKK1/2
MKK4/5
MPK3/6
VIP1
PR1
Late defence response for pathogen
WRKY29
FRK1
Early defence response for pathogen
ACS6
Ethylene synthesis
OXI1
NDPK2
ANP1
WRKY22
WRKY25
Cell death
H2O2 production
Pathogen attack
H2O2
MEKK1
?
MPK4
GST1
RbohD
Accumulation of reactive oxygen species in plant defense
MKK3
MPK1/2/7/14
PR1
Pathogen defense
RTE1
EIN2
Ethylene
ETR/ERS
CTR1
MKK9
EIN3/EIL
ERF1
PDF1.2
ChiB
Defense responses
RAN1
Cu2+
XRN4
EBF1/2
Phytohomones
Root growth
Jasmonic acid
MPK6
MYC2
VSP2
Wounding responses
Cold/ Salt
MKK2
MPK4/6
Freezing/ salt tolerance
Salt/ Drought
/ Osmotic stress
Abscisic acid
PYR/PYL
PP2C
SnRK2
MPK1/2/7/8
Stress adaptation
CAT1
Stress-tolerant response
Ozone
Reactive oxygen species
Ethylene synthesis
MKP2
Wounding
Ca2+
CaM4
MPK8
Maintenance the homeostacis of reactive oxygen species
EPF1/2
ER/ERLs
YODA
SPCH
Stomatal development
04016 8/28/17
(c) Kanehisa Laboratories



Supplementary figure S9. KEGG pathway analysis. Sequence data from the different treatments were assigned KO-numbers and mapped onto the MAPK signaling pathway - plant - Reference pathway (A) and the Plant-pathogen interaction - Reference pathway (B) to highlight similarities and differences between upregulated genes for the NBI vs NBNI (green) and the BI vs NBNI treatments.

Supplementary Table S6: List of *Fragaria vesca* and *Botrytis cinerea* primers used in this study.

Sl No	Primer Name	Primer Sequence (5'-3')	Gene IDs	Purpose
1	FvEF1aRTwF	GCCCATGGTTGTTGAAACTTT	FvH4_7g20050	qPCR
2	FvEF1aRTR	GGCGCATGTCCCTCACA		
3	FvPR1.1-RTF	CGGCGACTTATCAGGCACA	FvH4_2g02920	
4	FvPR1.1-RTR	CCACAAACCCTGCCAGAAGC		
5	FvPR5.3F	ACCTCCTAATGACACTCCCGAAACA	FvH4_6g16950	
6	FvPR5.3R	CGTAGTTAGGTCCACCGAAGCATGTA		
7	FvPR4-RTF	GCAGGACAACAACTGGGATTTG	FvH4_3g26010	
8	FvPR4-RTR	GTCACTAGCAGACATTTTCCACAGG		
9	FvBG2-1RTF	CCATATTGCTGCTCCTTGTTCTG	FvH4_3g28370	
10	FvBG2-1RTR	CCTTCCAATTCCATTGCTTTTGTAC		
11	FvBG2-3RTF	CCCTAATAAACAGCCAAAGTATCAGC	FvH4_4g19500	
12	FvBG2-3RTR	CGTATCACTCTTGAGAGAAGTGG		
13	FvPGIP1-RTF	CCTAGTTCATACGGGAAATTCGTTG	FvH4_6g22790	
14	FvPGIP1-RTR	TTCATGTTAGCAAATGAGGTTGGG		
15	FvLr10-JRTF	AACTCCTGCAGAGTATGCCAACTG	FvH4_4g26920	
16	FvLr10-RTR	GCGTTGCATGTGACCTCAAAC		

17	FvWRKY75-JRTF	CCCAGAAGCTACTATCGATGCAC	FvH4_6g53770	
18	FvWRKY75-RTR	AGGCTTGTCGATTGGATGAGAGTG		
19	FvCPK1-JRTF	TATGTCACCCTTGGGTTCAGGTTG	FvH4_6g20840	
20	FvCPK1-JRTR	GTGTTCAGCAATGACTCTAAGAGCC		
21	FvPecLy1-JRTF	GACATGAGTATCCGCAACAGCAC	FvH4_4g05760	
22	FvPecLy1-RTR	CACAACGCCAGCAATCATCAATG		
23	FvSLP3-JRTF	CTAGTGAATCAGTCACGTCCTATGC	FvH4_4g07370	
24	FvSLP3-JRTR	TTTCTGCCTGCTCGTGAGAAATG		
25	FvARR3-JRTF	GAATCTCCTCTTGCAAAGTGACCG	FvH4_4g35230	
26	FvARR3-JRTR	CCATCAAAACCAACTGAGGTGCTC		
27	FvPHOT2-JRTF	GAAACTGTCGGTTTCTTCAGGGAC	FvH4_2g17220	
28	FvPHOT2-JRTR	GTGAGAAGATTCCAGAAAGGAGTGC		
29	FvDSLPR-JRTF	GGCGGAGGATTTTAGTGACACATTG	FvH4_2g20290	
30	FvDSLPR-JRTR	CTATGCTTGCCTTGTGCTTGAGA		
31	FvPAL2-RTF	GAGGGCAGAGCTAGTAGAACATG	FvH4_7g19130	
32	FvPAL2-RTR	TTAGGCAAGACACTCTTCAGTTCC		
33	Fv4CL7-RTF	CAAAGACGACGTCGTCCTTATCC	FvH4_6g16460	
34	Fv4CL7-RTR	GATGACGAGCTTAGGGTTACAGTC		
35	FvGDS-RTF	AATGGTTGTAGTTAACGAGCCTGC		

36	FvGDS-RTR	GCAGTAGTGTAAAGGTCACCATCC	FvH4_4g27940	
37	FvBAS-RTF	AGCACAAACAACTTCGTCGGAAG	FvH4_2g08040	
38	FvBAS-RTR	GAACTGAAGACGAGCCTCTTCAAC		
39	FvSCMT-RTF	GAGAACCAGAGAGCTGTGATTTCG	FvH4_3g03130	
40	FvSCMT-RTR	TTCAGACACTCTGGGAAGAGAGTG		
41	Fv12OR2-RTF	GCATGGAAACCCATTGTCAATGC	FvH4_5g32630	
42	Fv12OR2-RTR	TCGGTACAAGAAATTGGAGCCTG		
43	FvACCOX1-RTF	GAGGTTCCAACCAACTATGACAGG	FvH4_5g19290	
44	FvACCOX1-RTR	CAGTTACTCCAGCATCAACAAGACC		
45	FvECDS-RTF	TTCTTCCCTCAATCTGCAATGCG	FvH4_2g23440	
46	FvECDS-RTR	TCCTTGGTAGGAAGAGCCTCTTC		
47	FvRe1 RTF	TGAATATGAAGAGGCTTGCAAAGACTC		
48	FvRe1 RTR	TCTTCTCCATCCTAATCCCATTCTCTG		
49	Bc3F	GCTGTAATTTCAATGTGCAGAATCC	(Diguta et al., 2010) For *B. cinerea* quantification	
50	Bc3R	GGAGCAACAATTAATCGCATTTC		