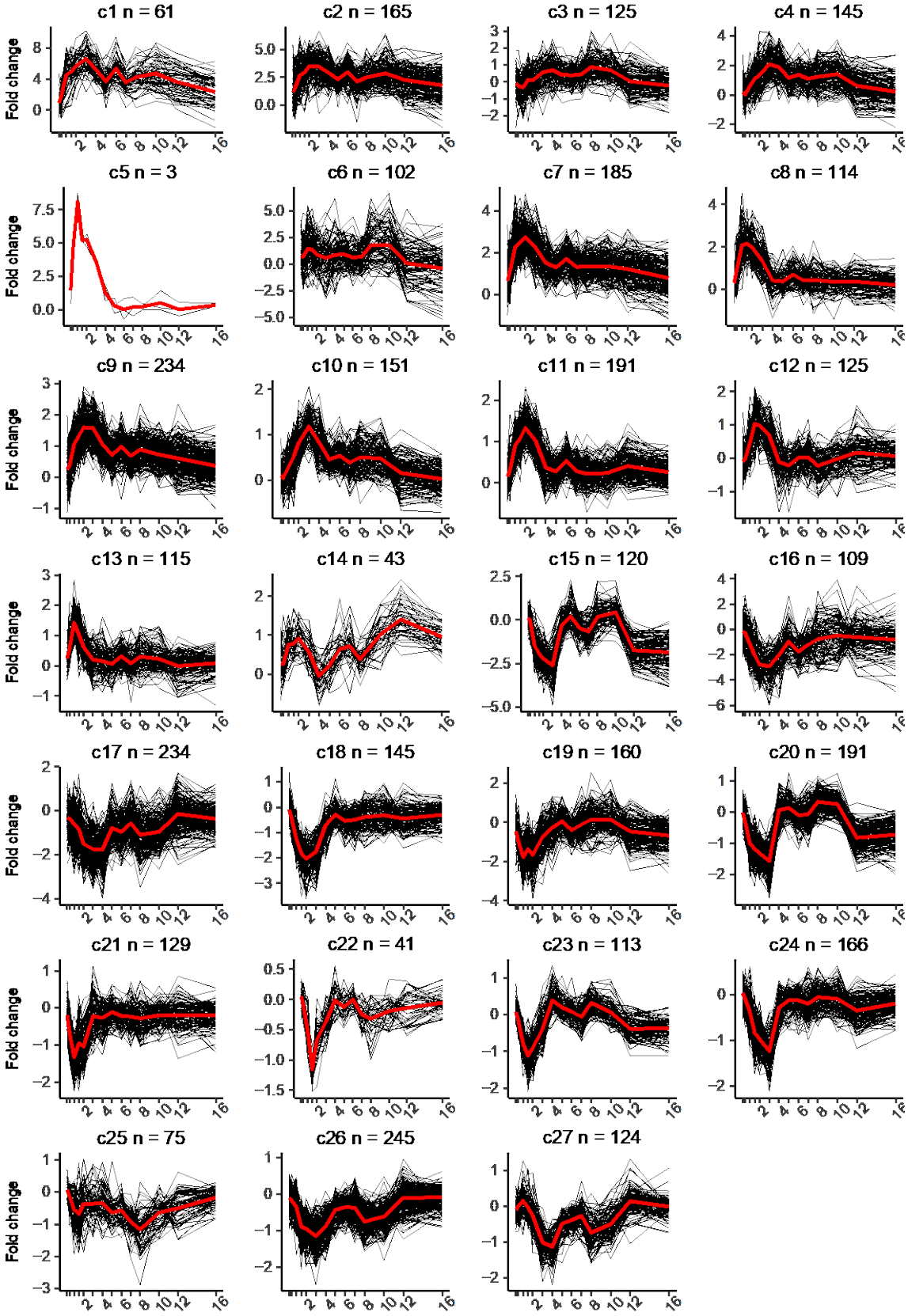
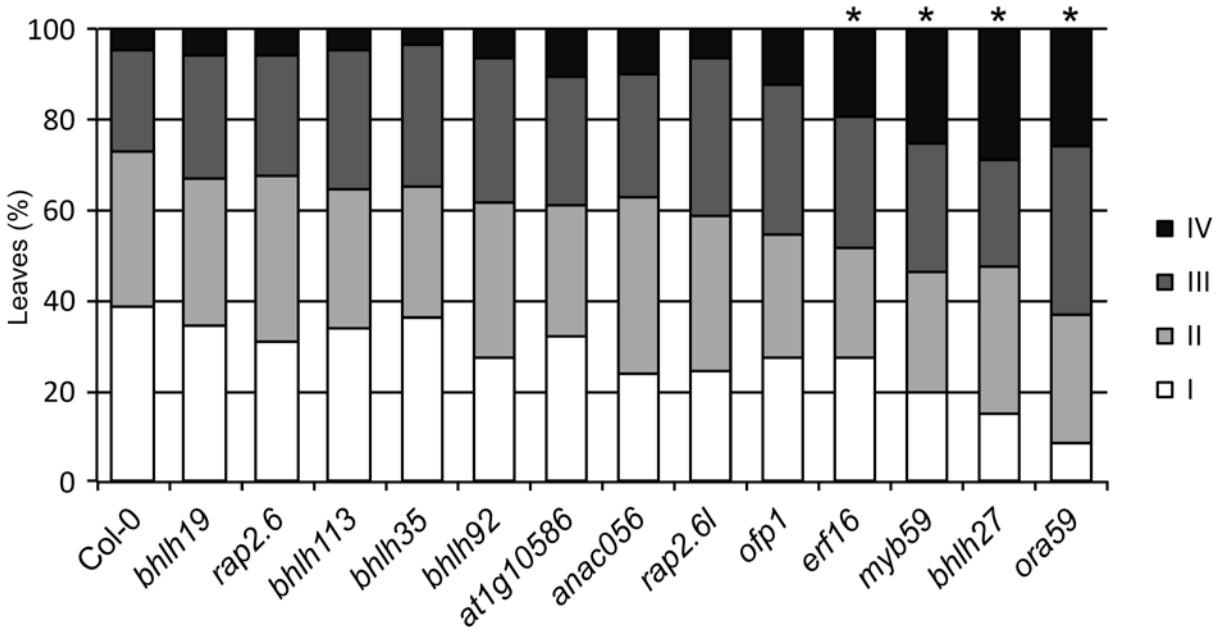
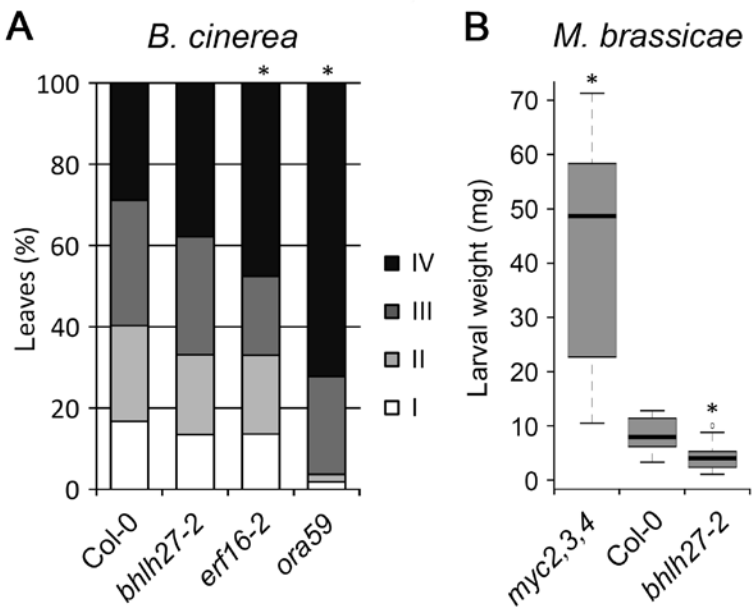


Supplemental Figure 1. SplineCluster analysis of MeJA-responsive gene expression profiles.
(Supports Figure 2)
Shown are the 27 clusters identified by SplineCluster. The number of genes in a cluster is displayed above each plot. Individual genes are plotted in black. Red lines indicate the mean expression level (log_2-fold change (MeJA/mock)) for all genes in a cluster. The x-axis indicates time (h).



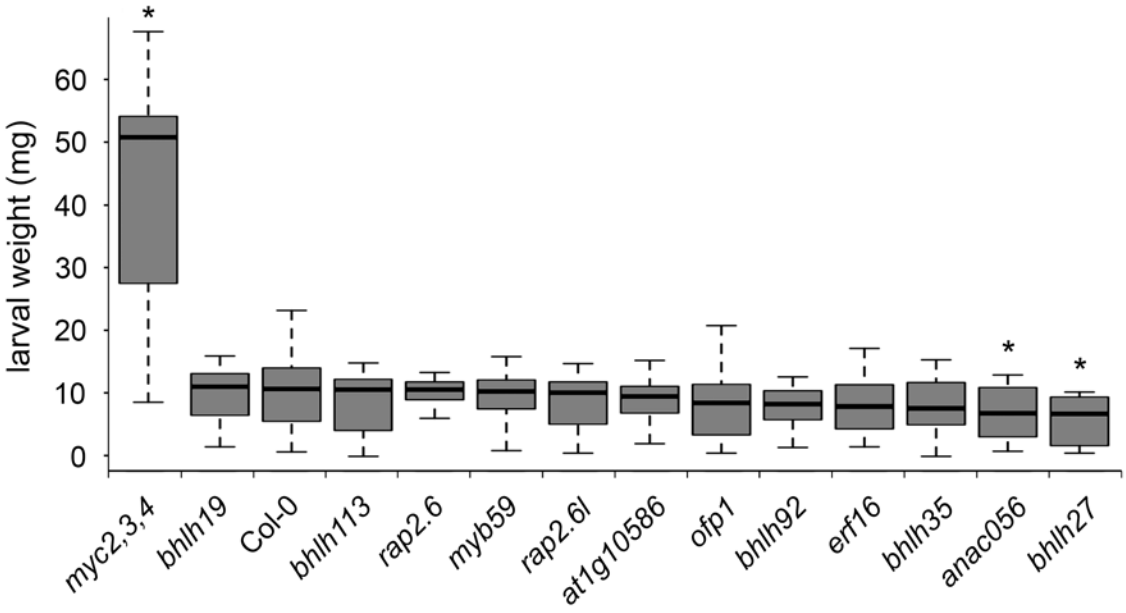
Supplemental Figure 2. *B. cinerea* disease severity assay with selected mutant lines.
(Supports Figure 2)
Quantification of *B. cinerea* disease severity at 3 days after inoculation of T-DNA insertion lines for selected genes encoding predicted early regulators of the JA pathway. *bHLH19*, *RAP2.6*, *bHLH027* belong to Cluster 1; *AT1G10586*, *RAP2.6L*, *OFP1*, *ERF16* belong to Cluster 2; *MYB59* belongs to Cluster 4; *bHLH92* belongs to Cluster 6; *bHLH35* belongs to Cluster 7; *ANAC056* belongs to Cluster 13; *bHLH113* belongs to Cluster 14. Disease severity of inoculated leaves was scored in four classes ranging from restricted lesion (class I), non-spreading lesion (class II), spreading lesion (class III), up to severely spreading lesion (class IV). The percentage of leaves in each class was calculated per plant (n=20). Asterisk indicates statistically significant difference from Col-0 (Chi-squared test; $P \leq 0.05$). Most genotypes were tested multiple times.



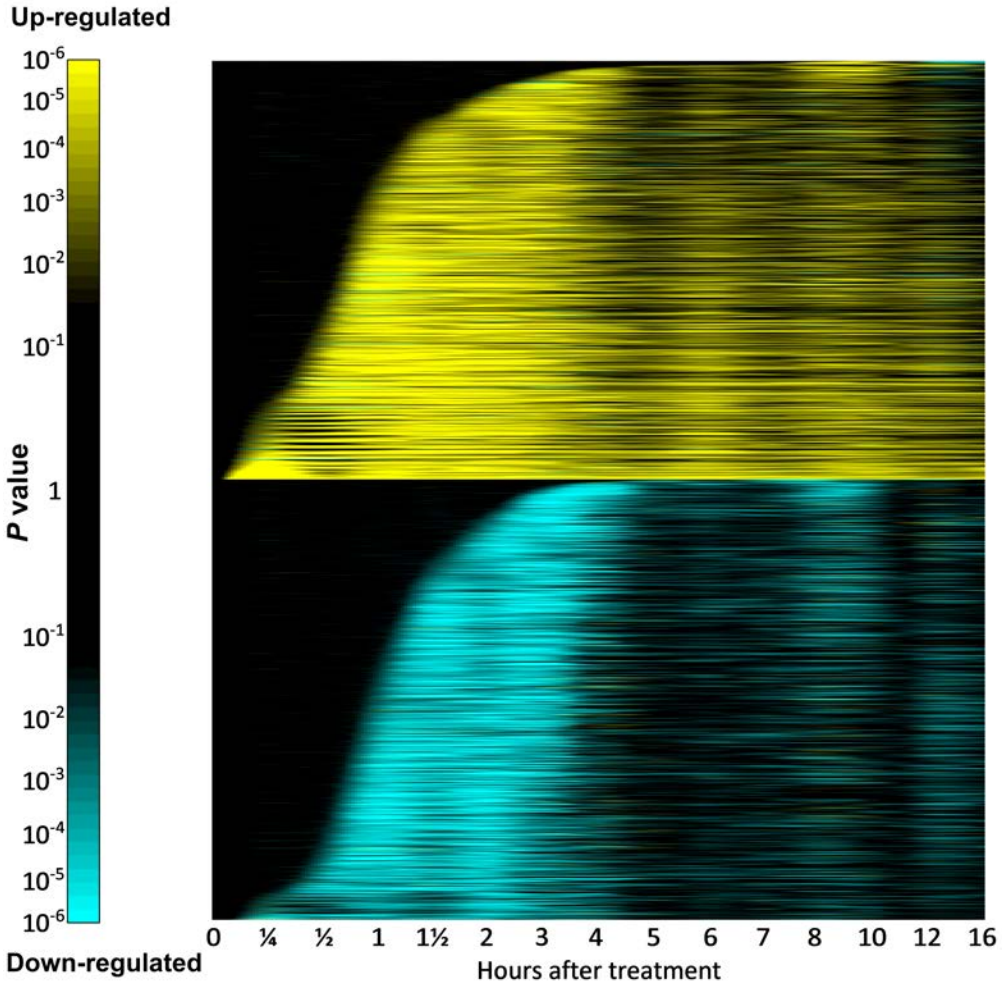
Supplemental Figure 3. *B. cinerea* disease severity and growth of *M. brassicae* larvae on additional mutant alleles.

(Supports Figure 2)

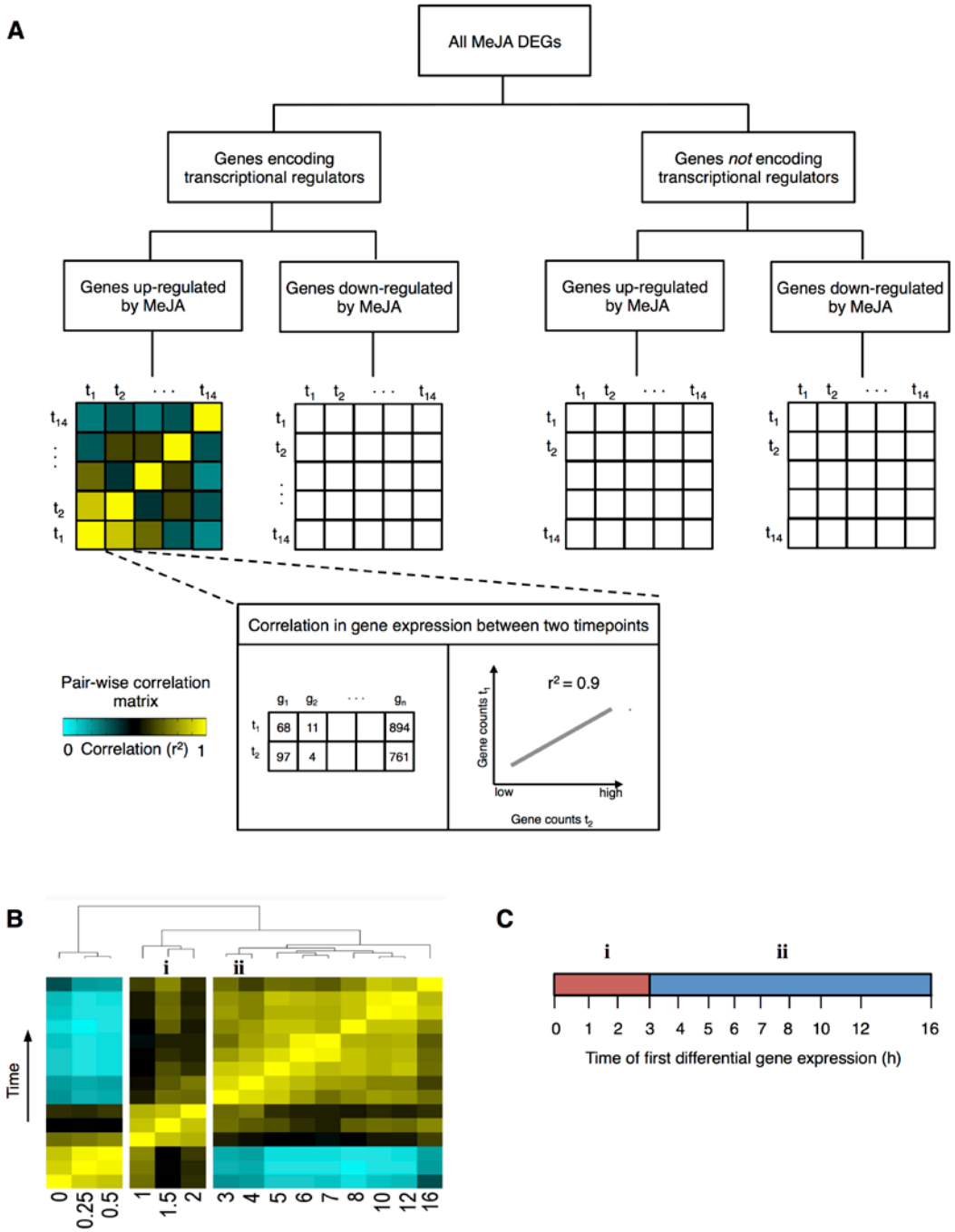
(A) Quantification of *B. cinerea* disease severity at 3 days after inoculation of T-DNA insertion lines harboring an *bHLH27* or *ERF16* mutation (*bhlh27-2*, *erf16-2*) different from that in the mutant lines tested in main Figure 2 (and Supplemental Figures 3 and 5). Disease severity of inoculated leaves was scored in four classes ranging from restricted lesion (class I), non-spreading lesion (class II), spreading lesion (class III), up to severely spreading lesion (class IV). The percentage of leaves in each class was calculated per plant (n=20). Asterisk indicates statistically significant difference from Col-0 (Chi-squared test; $P \leq 0.05$). **(B)** Larval fresh weight of *M*. *brassicae* was determined after 8 days of feeding on *bhlh27-2*. Asterisk indicates statistically significant difference from Col-0 (two-tailed Student's *t* test for pairwise comparisons; $P \leq 0.05$; $n > 10$; error bars are SE).



Supplemental Figure 4. Growth of *M. brassicae* larvae on selected mutant lines.
(Supports Figure 2)
T-DNA insertion lines were chosen based on the MeJA-induced expression of the TF genes they are mutated in. See for information on which co-expression gene cluster the genes belong to the Legend to Supplemental Figure 3. Larval fresh weight was determined after 8 days of feeding on T-DNA insertion lines for selected genes encoding predicted regulators of the JA pathway. Values represent mean weight (±SE) of the larvae. Asterisk indicates statistically significant difference from Col-0 (two-tailed Student's *t* test for pairwise comparisons; $P \leq 0.05$; n=30; error bars are SE). Most genotypes were tested multiple times.



Supplemental Figure 5. Timing of differential expression for all differentially expressed genes.
(Supports Figure 4)
All differentially expressed genes were divided in two groups, dependent on whether they were up- or down-regulated over time by MeJA treatment. Estimated *z* scores reflect significance of differential expression over time and were used to order genes according to their time of first differential expression. Shown are *z* scores converted to *P* values.

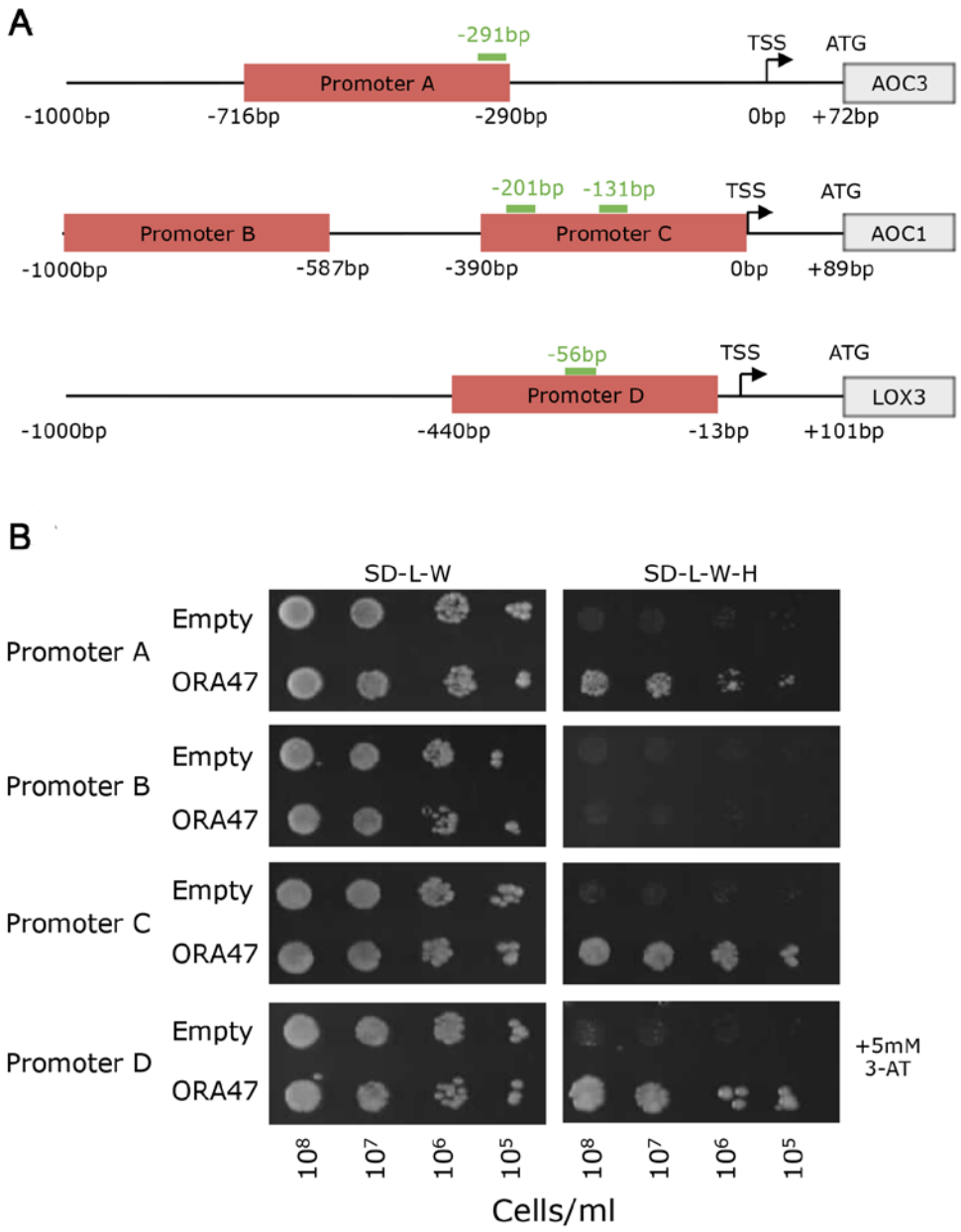


Supplemental Figure 6. Identification of transcriptional phases induced in response to MeJA treatment.

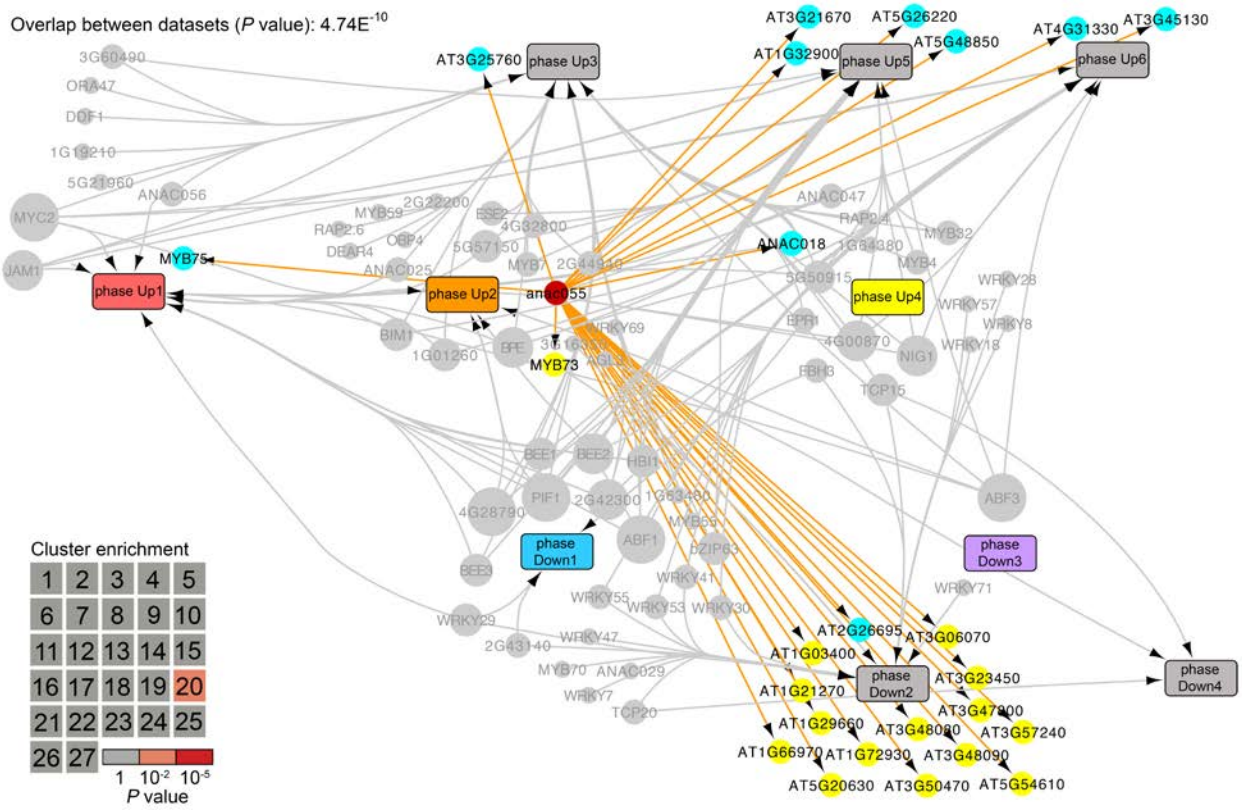
(Supports Figure 4)

(A) Generating correlation matrices for different sets of MeJA-induced genes. The complete list of MeJA-responsive DEGs is progressively filtered into four sets of genes according to two binary criteria: 1) Gene encodes a transcriptional regulator (true or false); 2) Direction of change in expression (up-regulated or down-regulated). For each of the four mutually exclusive gene sets, a correlation matrix of gene transcription counts between all pairs of time points is computed. Inset, an example illustrating how the squared Pearson correlation coefficient (r^2) is computed between one pair of time points. **(B)** The dendrogram obtained by hierarchical clustering of the transcriptome correlation matrix of each of the four gene sets reveals that there are groups of time points showing highly correlated levels of gene expression within that group, but displaying reduced correlation levels with the time points belonging to other groups. A relatively weak correlation between a pair of adjacent time points signifies a coordinated switch in transcriptional activity of a fraction of the genes. In this example, two phases are identified; the first begins

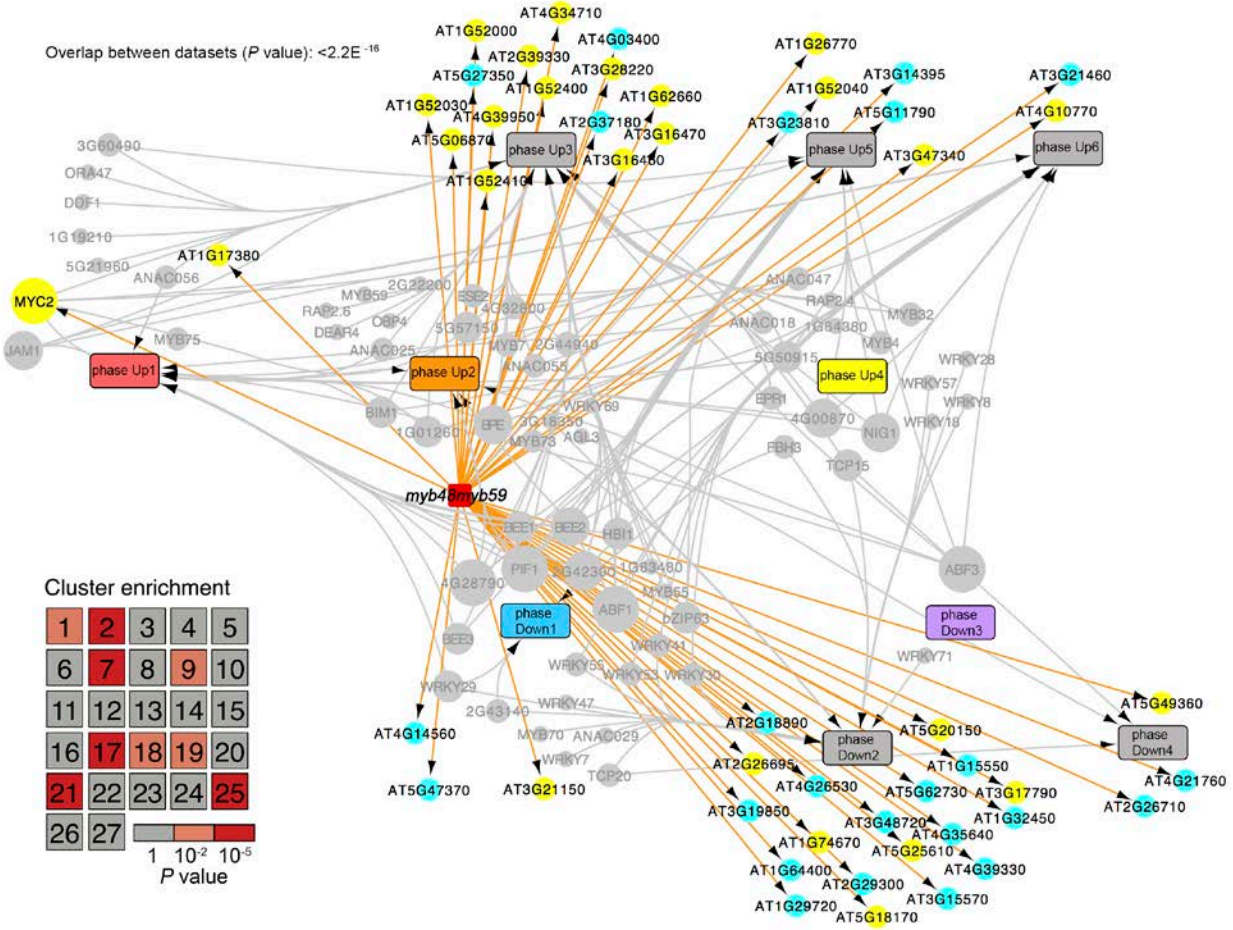
at 1 h (i) and the second at 3 h (ii). **(C)** Each gene present in one of the four final gene sets is assigned to a transcriptional phase based on its time point of first differential expression. All genes that are for the first time differentially expressed before, or equal to, the final time point in a given phase (clustered group of time points), and after the final time point of a preceding phase, are assigned to that transcriptional phase. Moreover, if a group of clustered time points includes the 0 time point, then all genes assigned to this group are combined with the genes of the adjacent group of time points, which is numbered as the first transcriptional phase. Red and blue bars indicate time intervals used for assignment of genes to phases i and ii, respectively.



Supplemental Figure 7. ORA47 can bind to the promoters of multiple *Arabidopsis* genes encoding JA biosynthesis enzymes in yeast.
(Supports Figure 6)
(A) Schematic of promoters for JA biosynthesis genes *AOC1*, *AOC3* and *LOX3*. The locations of fragments used for Y1H assays are shown in red. Occurrences of ORA47 DNA-binding motif are shown in green. Numbers are relative to transcription start site (TSS). **(B)** Interaction between ORA47 and promoter fragments A, C and D was confirmed by growth on SD-Leu-Trp-His (SD-L-W-H) media. Yeast transformed with plasmids containing promoter construct D were grown on SD-L-W-H supplemented with 5 mM 3-AT. Yeast transformed with promoter fragment B (which does not contain a significant match for the ORA47 motif) did not grow on selective media, indicating no interaction between ORA47 and this DNA sequence.



Supplemental Figure 8. Projection of ANAC055 target genes on the JA network model.
(Supports Figure 6)
Genes that are differentially expressed in the *anac055* mutant were overlaid on the network described in Figure 5. DEGs are indicated by nodes and positioned according to phase membership. Direction of misregulation in the *anac055* mutant is indicated by color; yellow, up-regulated; cyan, down-regulated. The gene encoding ANAC055 is shown as a red-colored node. Inset: heatmap indicating hypergeometric enrichment *P* value of ANAC055 target genes in each MeJA-induced co-expression cluster.



Supplemental Figure 9. Projection of MYB48/MYB59 target genes on the JA network model.
(Supports Figure 6)
Genes that are differentially expressed in the *myb48myb59* double mutant line were overlaid on the network described in Figure 5. Due to space limitations, shown are the top 50 most significant differentially expressed overlapping genes. DEGs are indicated by nodes and positioned according to phase membership. Direction of misregulation in *myb48myb59* is indicated by color; yellow, up-regulated; cyan, down-regulated. Edges are drawn out from a red-colored square node, representing the double mutant, situated between MYB59 in phase Up2 and MYB48 in Phase Down1. Inset: heatmap indicating hypergeometric enrichment *P* value of MYB48/59 target genes in each MeJA-induced co-expression cluster.

Supplemental Table 1. List of primers used for genotyping of T-DNA mutants, qRT-PCR analysis and promoter cloning for Y1H assays.

Primers used for genotyping T-DNA mutants		
T-DNA line	Forward primer (5'-3')	Reverse primer (5'-3')
SALK_111492C	ATTGGGCCGAAAACATATAGG	CGACCGCATTCTAAGTCTCAC
GK-627C09	AAGAGGAATGCCATAGGTTCC	AGTGGGTGGTGATTTTTGATG
SALK_137131C	GGCACTGCGTCGTTATATAGG	AGACTCCACCATTGATGCAAC
SALK_051006C	TTCGGTTCGTGTGTTTTTCA	TATGCTGATCGGTGGTTCAA
SAIL_1225G09	TCAATCAACGTGTCATGAAGG	TCAGACTGAAGTTGTATTGGGAG
SALK_053563C	GCCACGGCTCATTTATTTTAAG	CGGCTCTTTACTGTCTTCGTG
SALK_027725C	GATGAATGTCCTTGCTATCGC	TTTATTGGCACCAACAGTTGC
GABI_461E05	ATCAAATGCATTTTGAGTGCC	CACGAAACGATTGTGTCAATG
SALK_049808C	AAACAAAAATTGCTGGTGACG	GGCCATAATCATTACGTACGC
SALK_100300C	CCAAGAAAAAGTAAAAGGGAACC	TAGCAATTGCAATCTGCTGC
SALK_033657C	AAATTTTGTTGCCAAGACACG	AATCTCATCCACGGCTTTTTC
GK_892H04	CCCCTCTAAAAAGGTACACATTG	AAGGAGTAACGAGCTTCTCCG
Primers used for qRT-PCR		
Gene	Forward primer (5'-3')	Reverse primer (5'-3')
ORA47	TCCACCGTCGATCTCCGTAGAAAA	GCGAATCTAGCAGCAGCTTCCTGA
LOX2	ACAGCCAAGGGCACTTCATT	TGATTCTGGGGAGCAGAGGT
LOX3	AACACAACCACATGGTCTTAAACTC	GGAGCTCAGAGTCTGTTTTGATAAG
AOS	TCCGATTTCTCTCCACCCAAA	TGACCCGGAAGCTTTGATCG
AOC1	CTCTCAGAACTTGGGAAATAC	GATCTCCGAGACCAAAACCTA
AOC2	ATCGAAAACCCTAGACCAAGC	CGAGACCGAACATTAAGCTGA
AOC3	CGAAGGAGATAGAAACAGTCCAGC	CCGAGACAAAGCTCTGTTGGTT
OPR3	CCGGCGGTTTTCTCATCTC	GCTTCCATGCTTCTACTTGT
JAR1	GGGTTGTATCGATACCGGCTTGG	CTTCTGAGAGTCTCTTTGCAGCCG
Primers used for cloning of promoters for Y1H assay		
Promoter	Primer (5'-3')	
A (*AOC3*) - F	AAAAAAGCAGGCTTCGAGTTGCTGATAAAAAAAAAAAGAGTGG	
A (*AOC3*) - R	CAAGAAAGCTGGGTCCTTGGTCGGTTCGGTTGTGTCAATTTG	
B (*AOC1*) - F	AAAAAAGCAGGCTTCGAAGATTTAGATTTCGAACCTATTTG	
B (*AOC1*) - R	CAAGAAAGCTGGGTCCAAGAAAACATATAAAACTCCAAAAC	
C (*AOC1*) - F	AAAAAAGCAGGCTTCGTTCATCTAACAAAACTATTATC	
C (*AOC1*) - R	CAAGAAAGCTGGGTCGAGTTTTACGAAATGTCTATGTG	
D (*LOX3*) - F	AAAAAAGCAGGCTTCGACAACTAACTTTATTTTATCCAATCAGC	
D (*LOX3*) - R	CAAGAAAGCTGGGTCCGGCGAGTGAGAGATATAAATAGAGAGAG	