Multiple hormone treatment revealed novel cooperative relationships between abscisic acid and biotic stress hormones in cultured cells [Plant Biotechnol. 29(1): 19-34 (2012)]

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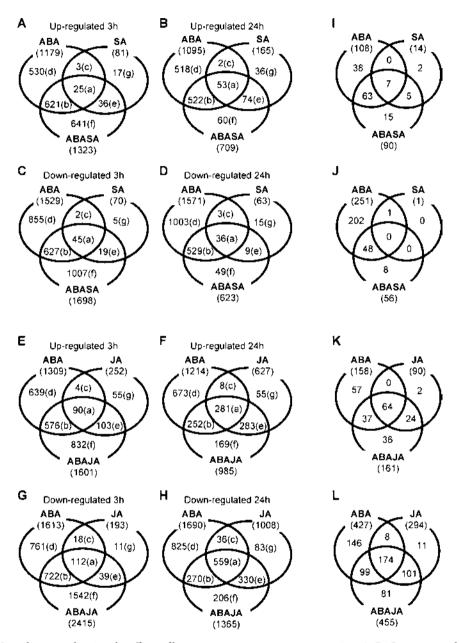


Figure S1. Venn diagrams showing the effects of hormone treatment on gene expression. A–D, Genes up- or down-regulated  $\geq 2$  fold by ABA, SA, or ABA+SA classified by expression profile. E–F, Genes up- or down-regulated  $\geq 2$  fold by ABA, MeJA, or ABA+MeJA classified by expression profile. The numbers inside the ellipses indicate the number of genes in each class. I–L, Follow-up classification of genes that were up- or down-regulated by 3 h of double hormone treatment. The classification (I–L) of these genes [A, C, E, and F, section (f), respectively] was based on their expression profile after 24 h of treatment. The numbers inside the ellipses indicate the number of genes in each class.

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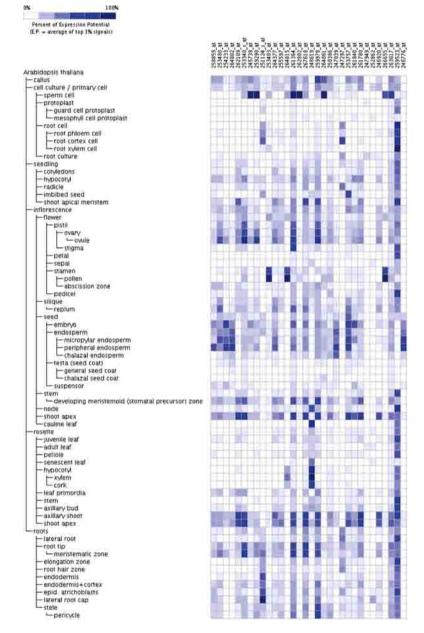


Figure S2A. Expression profiles of genes involved in cell cycle regulation in different tissues and organs. Heat maps of the expression profiles of the genes in Table 6. Genevestigator was used for data analysis and heat-map plotting.

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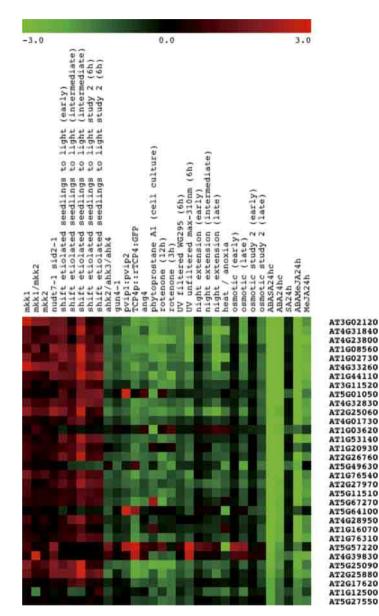


Figure S2B. Expression profiles of genes involved in cell cycle regulation in several mutants and stress-treated plants. Heat maps of the expression profiles of the genes in Table 6. The data were generated using Genevestigator; MeV (v4.3) was used to generate a heat map of our microarray data.