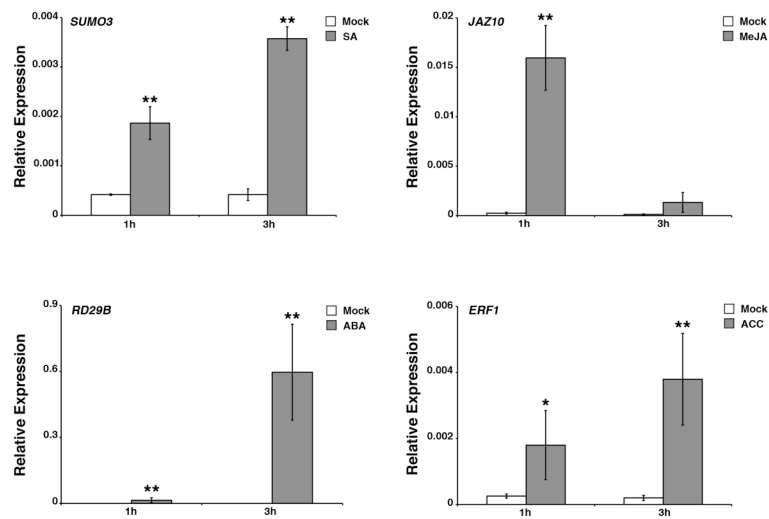


Supplemental Figure S1. Transcriptome profiling of Arabidopsis after treatment with *E*-2-hexenal.

(A) Venn diagrams showing the number of transcripts with a change in abundance of at least two-fold ($p < 0.05$; FDR 0.05) following 1h, 3h or 24h exposure of Arabidopsis leaves to *E*-2-hexenal. **(B, C)** Functional categorization of the genes differentially expressed after *E*-2-hexenal treatment using FatiGo (<http://babelomics.bioinfo.cipf.es>). Overrepresented GO terms for the genes either up regulated (B) or down regulated (C) after 1h, 1h-3h and 3h treatment with *E*-2-hexenal at biological process levels 3-9 ($p \leq 0.005$). Number of genes for each GO category is indicated as percentage of the total number of genes with an ontology at each time-point. Only categories $\geq 3\%$ of total number of genes are shown.

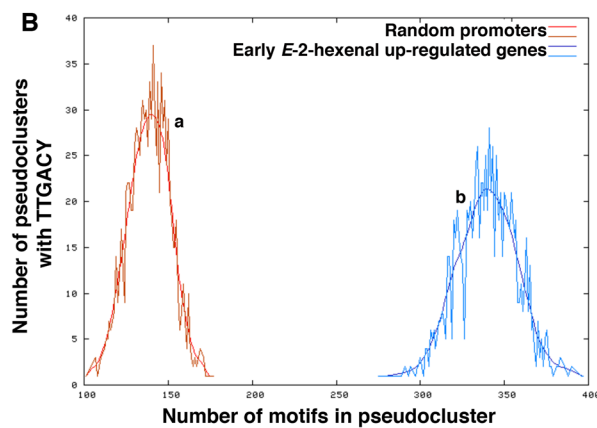
Functional categorizations at the classes Molecular Function and Cellular Compartment are shown in supplemental figure S1 and S2 online.



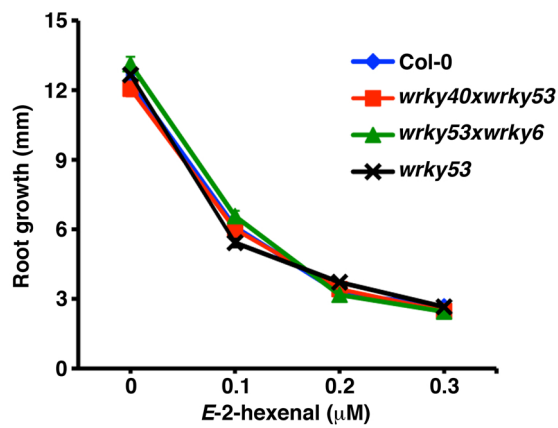
Supplemental Figure S2. Q-RT-PCR of Arabidopsis Plants Treated with SA, MeJA, ABA or ACC for control marker genes.

Arabidopsis plants were treated with 300 μ M SA, 100 μ M MeJA, 50 μ M ABA, 100 μ M ACC or mock treated for 1h and 3h and the transcript levels of *SUMO3*, *JAZ10*, *RD29B* and *ERF1*, respectively, were measured by Q-RT-PCR. Values are normalized to the expression of *SAND* and are means of three independent biological replicates. Error bars indicate SE; asterisks indicate significant differences between hormone and mock treated samples (ANOVA, ** = $p \leq 0.01$, * = $p \leq 0.05$ according to LSD post-hoc analysis).

tool	early-point induced genes (1h)	mid-point induced genes (1h and 3h)
TAIR Motif Analysis	TTGACT (7.3 E ⁻²³) TTGACC (1.7 E ⁻⁰⁹)	TTGACT (3.6 E ⁻¹⁴) TTGACC (3.7 E ⁻¹¹)
RSA-tools oligo analysis motif	TTGACT (8.3 E ⁻³²) TTGACC (6.9 E ⁻¹¹)	TTGACT (3.4 E ⁻²¹) TTGACC (1.1 E ⁻⁰⁷)
Athena	TTGACY (< 10 E ⁻¹⁰)	TTGACY (< 10 E ⁻¹⁰)
AlignACE motif finder tool	KTTGACYYK (50*)	ND



Supplemental Figure S3. Enrichment of the WRKY-box Motif in the Promoters of the Early-Point (1h) Time and Mid-Point Time (1h and 3h) Genes Up-Regulated by *E-2-hexenal*. (A) Motif analysis (The Arabidopsis Information Resource; TAIR), Regulatory Sequence Analysis Tool (RSAT; <http://rsat.ulb.ac.be>; (van Helden et al., 1998)), ATHENA (<http://www.bioinformatics2.wsu.edu/cgi-bin/Athena/cgi/home.pl>; (O'Connor et al., 2005)) and AlignACE (<http://atlas.med.harvard.edu>; (Roth et al., 1998)) identified the W-box motif (TTGACY) as the only known *cis*-element statistically enriched in the promoters of the early-point (1h) time and mid-point (1h and 3h) time genes up-regulated by *E-2-hexenal*. Numbers between brackets indicate p-values; * = MAP score, a measure of the motif significance (the higher the MAP score the more significant is the associated motif). ND, not detected; Y: C/T; K: G/T. (B) Occurrences of the TTAGACY motif in the promoter regions of the early-point time genes induced by *E-2-hexenal* (blue line) compared to a set of random Arabidopsis promoters (red line) analysed with POBO (<http://ekhidna.biocenter.helsinki.fi/pobo>; (Kankainen and Holm, 2004)). Different letters indicate statistically significant differences in occurrence of the TTAGACY motif (χ^2 test; $\alpha = 0.05$).



Supplemental Figure S4. Root Growth of Wild-Type (Col-0) and *wrky* Mutant Seedlings after Aerial Treatment with *E*-2-hexenal.

Three-day old wild-type (Col-0), *wrky40 wrky53*, *wrky53 wrky6* and *wrky53* seedlings were exposed for 24h to various concentrations of aerial *E*-2-hexenal. Root growth was measured 3 days after the treatment. Values (representative of three independent experiments) are means of ≥ 15 seedlings for each treatment/genotype combination. Error bars indicate SE.