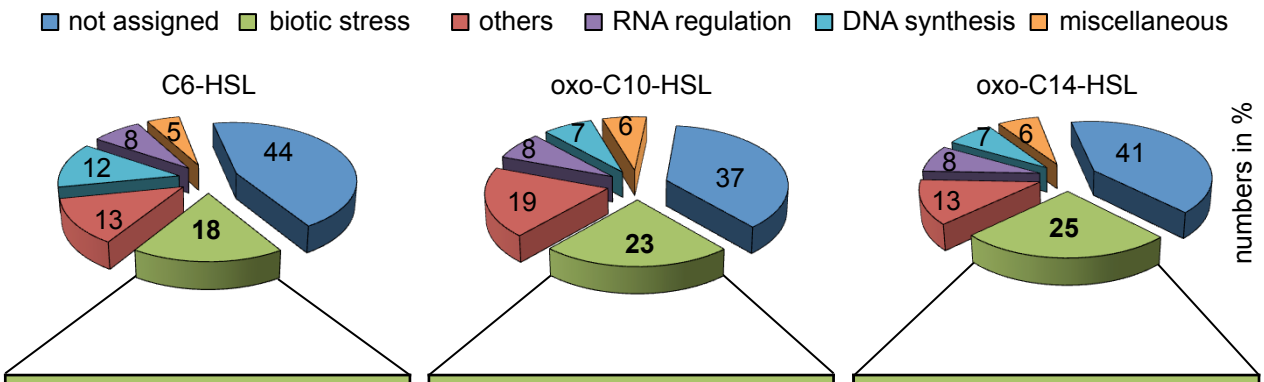
Functional Categories:



subgroup	genes	%
signaling	16	30
protein degradation	13	24
cell wall	7	13
defense proteins	6	11
transcription factors	5	9
secondary metabolism	3	6
hormone metabolism	3	6
redox	1	2

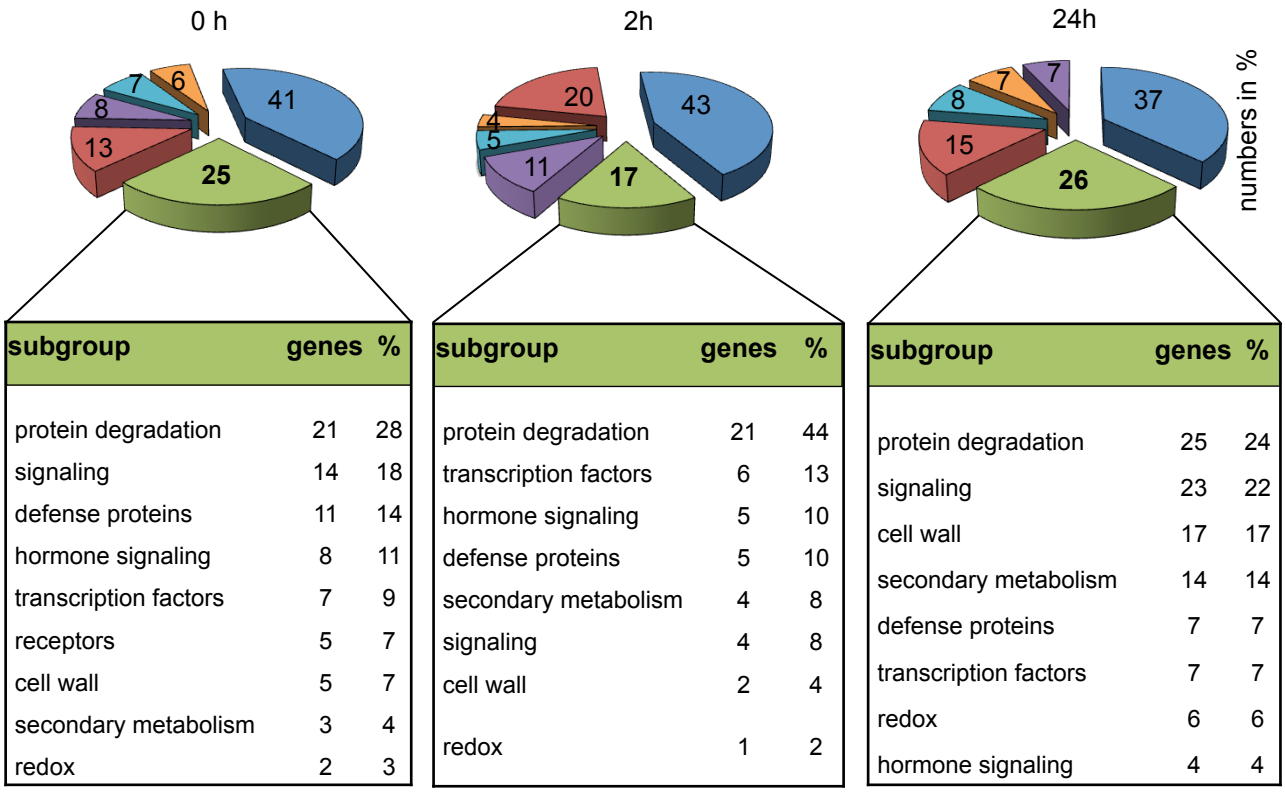
subgroup	genes	%
protein degradation	28	35
signaling	15	19
transcription factors	7	9
defense proteins	7	9
cell wall	7	9
secondary metabolism	5	6
glucan hydrolases	5	6
hormone metabolism	4	5
redox	2	3

subgroup	genes	%
protein degradation	21	28
signaling	14	18
defense proteins	11	14
hormone signaling	8	11
transcription factors	7	9
receptors	5	7
cell wall	5	7
secondary metabolism	3	4
redox	2	3

Supplemental Figure 1. "Response to Biotic" Stress Is the Gene Ontology Term with the Highest Number of Genes Regulated upon AHL Treatment

Biotic stress is the functional category with the highest number of genes regulated in AHL-treated plants. The functional annotation was performed using the MapMan application software (Thimm et al., 2004). The pie charts represent the number of genes in particular functional categories among all differentially expressed genes. The tables below the pie charts present a further analysis of the differentially expressed genes belonging to the "biotic stress" category, divided into subgroups, showing the number of genes and their percentage within the "biotic stress" functional category.

response to flg22 in oxo-C14-HSL pretreated plants



subgroup	genes	%
protein degradation	21	28
signaling	14	18
defense proteins	11	14
hormone signaling	8	11
transcription factors	7	9
receptors	5	7
cell wall	5	7
secondary metabolism	3	4
redox	2	3

subgroup	genes	%
protein degradation	21	44
transcription factors	6	13
hormone signaling	5	10
defense proteins	5	10
secondary metabolism	4	8
signaling	4	8
cell wall	2	4
redox	1	2

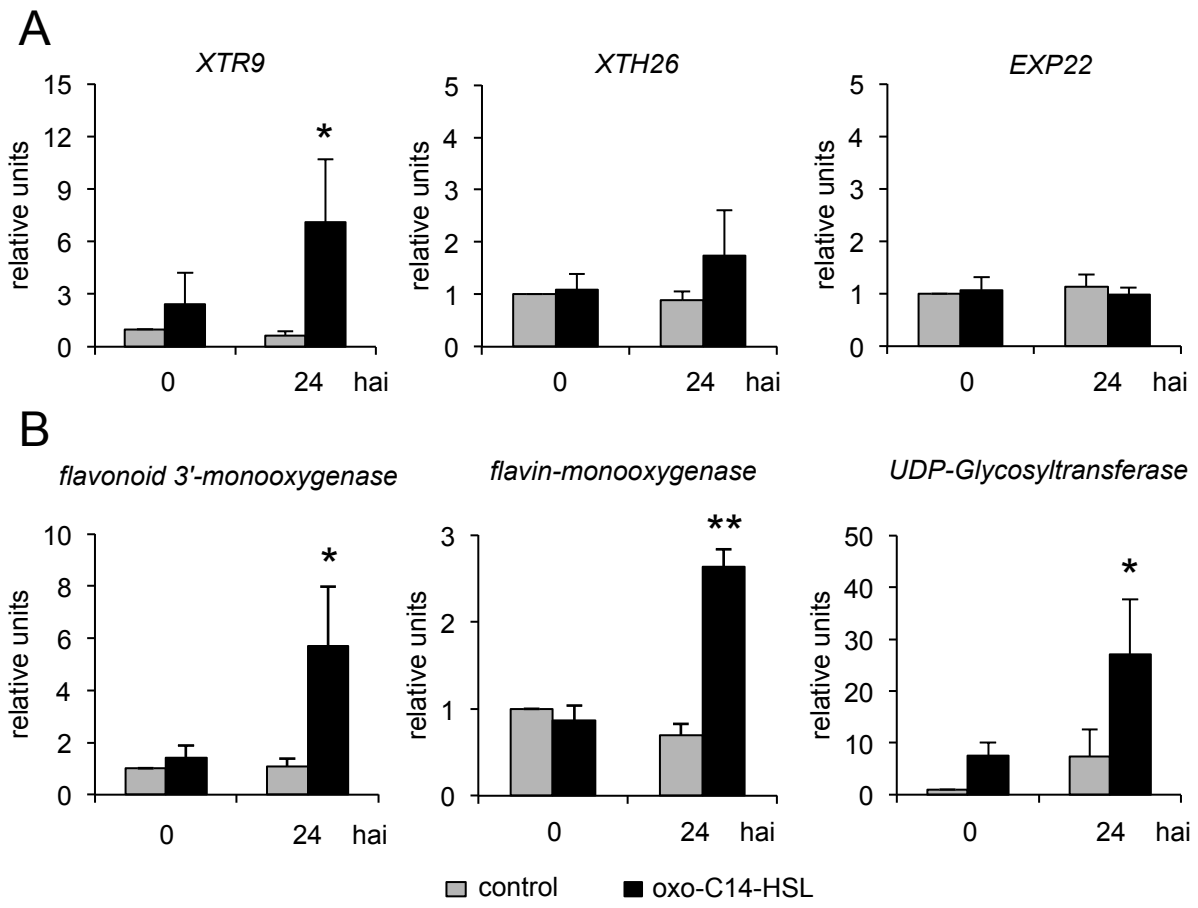
subgroup	genes	%
protein degradation	25	24
signaling	23	22
cell wall	17	17
secondary metabolism	14	14
defense proteins	7	7
transcription factors	7	7
redox	6	6
hormone signaling	4	4

Functional categories:

not assigned | biotic stress | others | RNA regulation | DNA synthesis | miscellaneous

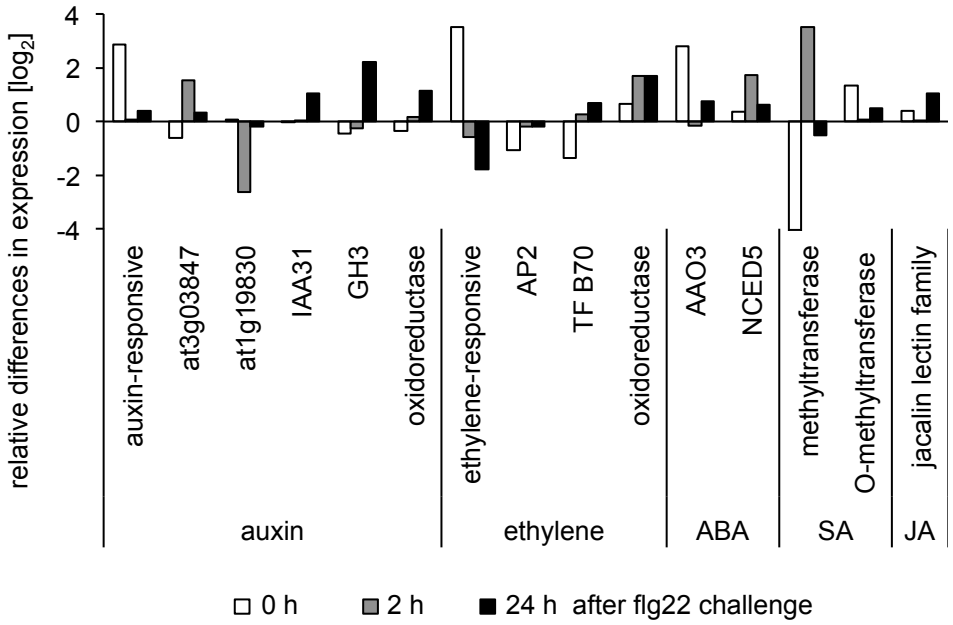
Supplemental Figure 2. Response to a Secondary Challenge in Oxo-C14-HSL-Pretreated Plants Varies from the Response in Non-Pretreated Plants

Two-week-old *Arabidopsis* seedlings were pretreated with 6 µM oxo-C14-HSL. After 3 days seedlings were inoculated with 100 nM flg22 in order to trigger the defense mechanisms. Response to biotic stress is the major functional category from which genes are differentially regulated in AHL-primed plants upon treatment with 100 nM flg22. The functional annotation was performed using the MapMan software (Thimm et al., 2004). The tables below the pie charts present a further analysis of the differentially expressed genes belonging to the “biotic stress” category, divided into subgroups, showing the number of genes and their percentage within the “biotic stress” functional category.



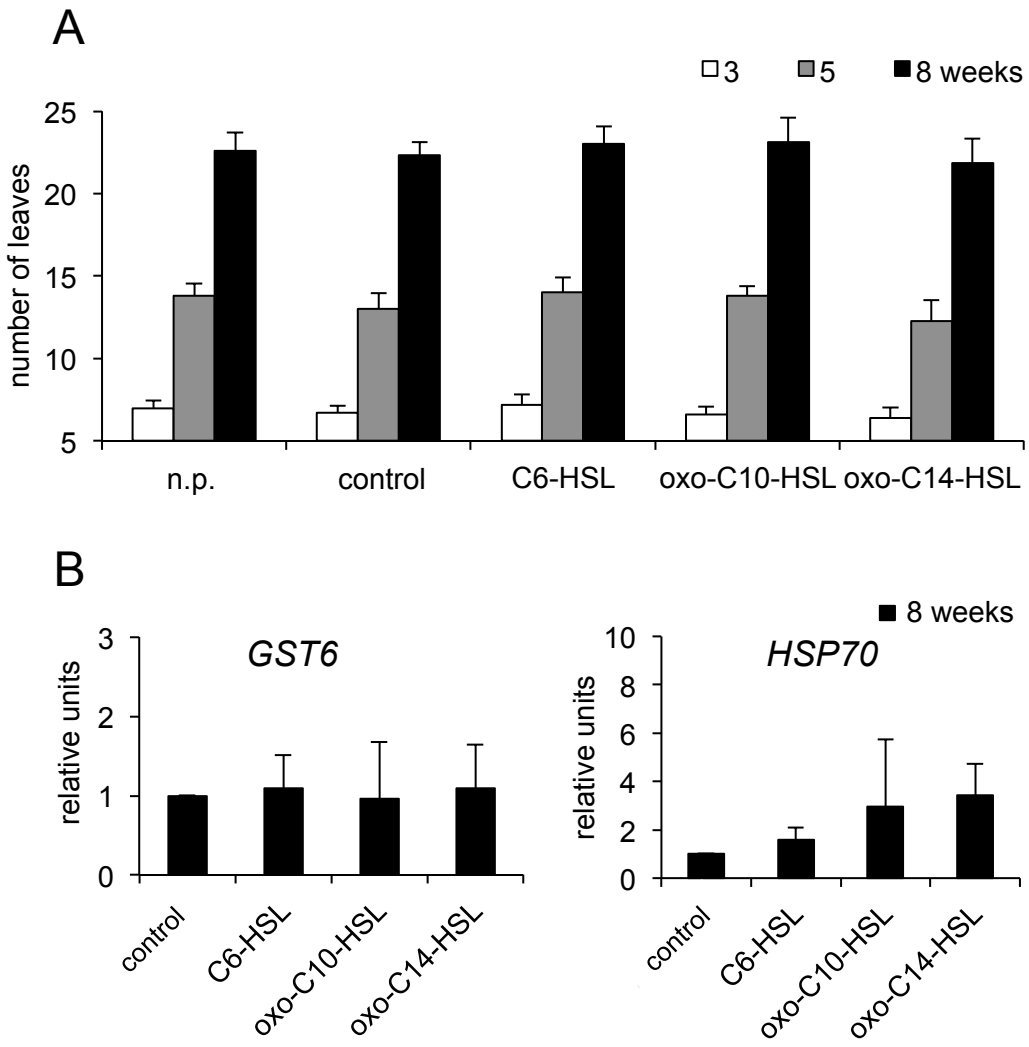
Supplemental Figure 3. Expression of Cell Wall-Related Genes, which Were Locally Regulated in Oxo-C14-HSL-Primed Plants after Flg22 Challenge, in Systemic Tissues of Oxo-C14-HSL-Pretreated Plants Challenged with *Pst*

The expression profiles of three cell wall-related genes: *xyloglucosyl transferase* (*XTR9*), *endo-xyloglucan transferase* (*XTH26*) and *expansin22* (*EXP22*) (**A**) and three genes related to secondary metabolism: *flavonoid 3'-monooxygenase*, *flavin-monooxygenase,* and *UDP-Glcosyltransferase* (**B**). Plants were grown in the sterile systemic hydroponic system, pretreated with 6 µM oxo-C14-HSL or acetone (control) for 3 days and subsequently challenged with *Pst* for the number of hours as indicated, hours after inoculation (hai). The level of respective mRNA is presented in relation to the expression of the ubiquitin ligase and the 0 hai time point. Graphs present a mean of three independent biological repetitions. Error bars represent standard error. * represents $p < 0.05$, ** $p < 0.005$ in Student's *t*-test.



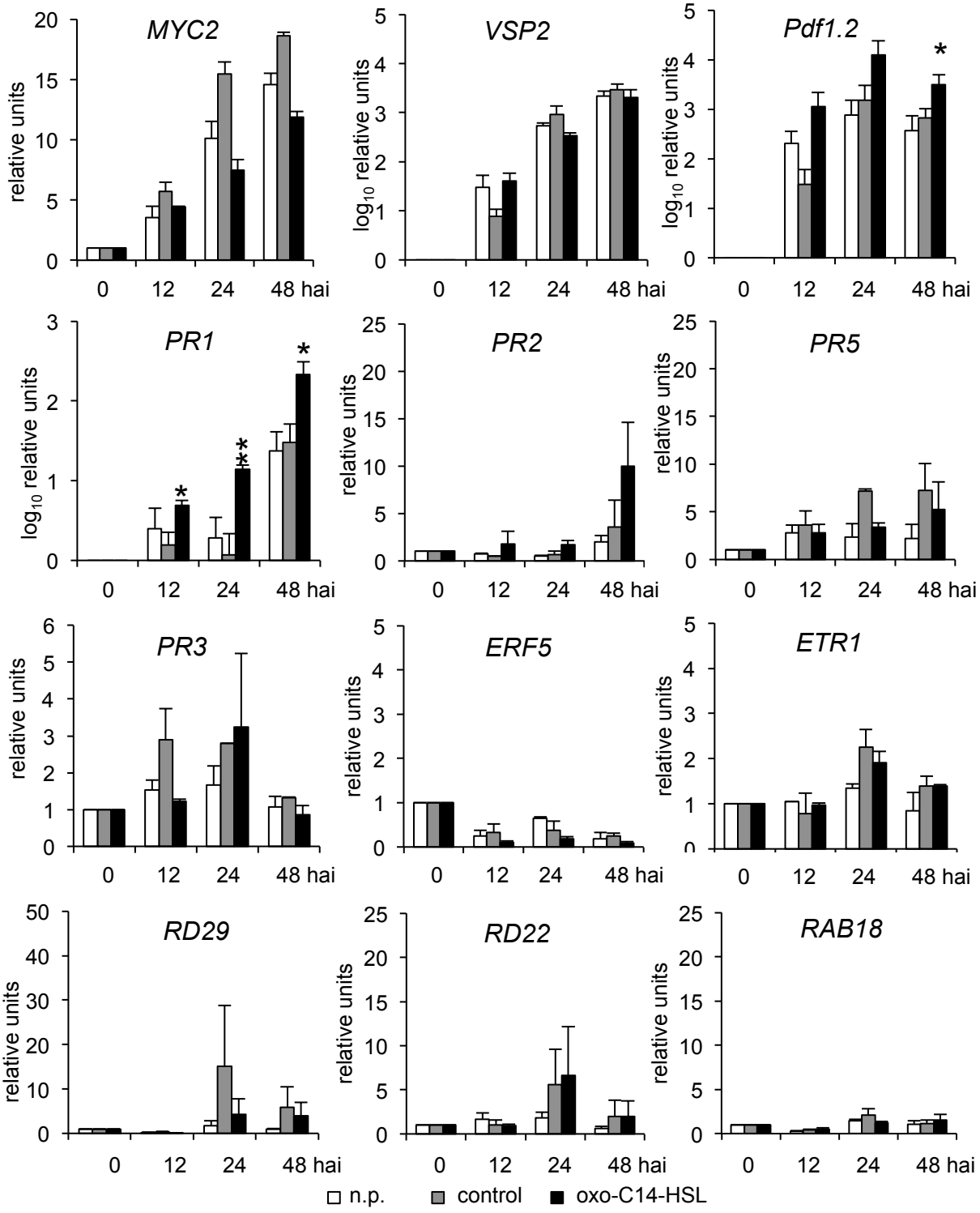
Supplemental Figure 4. Hormones-Associated Gene Ontology Terms Are not Enriched within the Differentially Expressed Gene Groups

Differentially regulated genes related to hormone signaling as revealed by the microarray experiment. Note: there is no enrichment in genes related to hormones upon pretreatment with the tested AHLs. The numbers represent the $\log_2$ fold change relative to the solvent control.



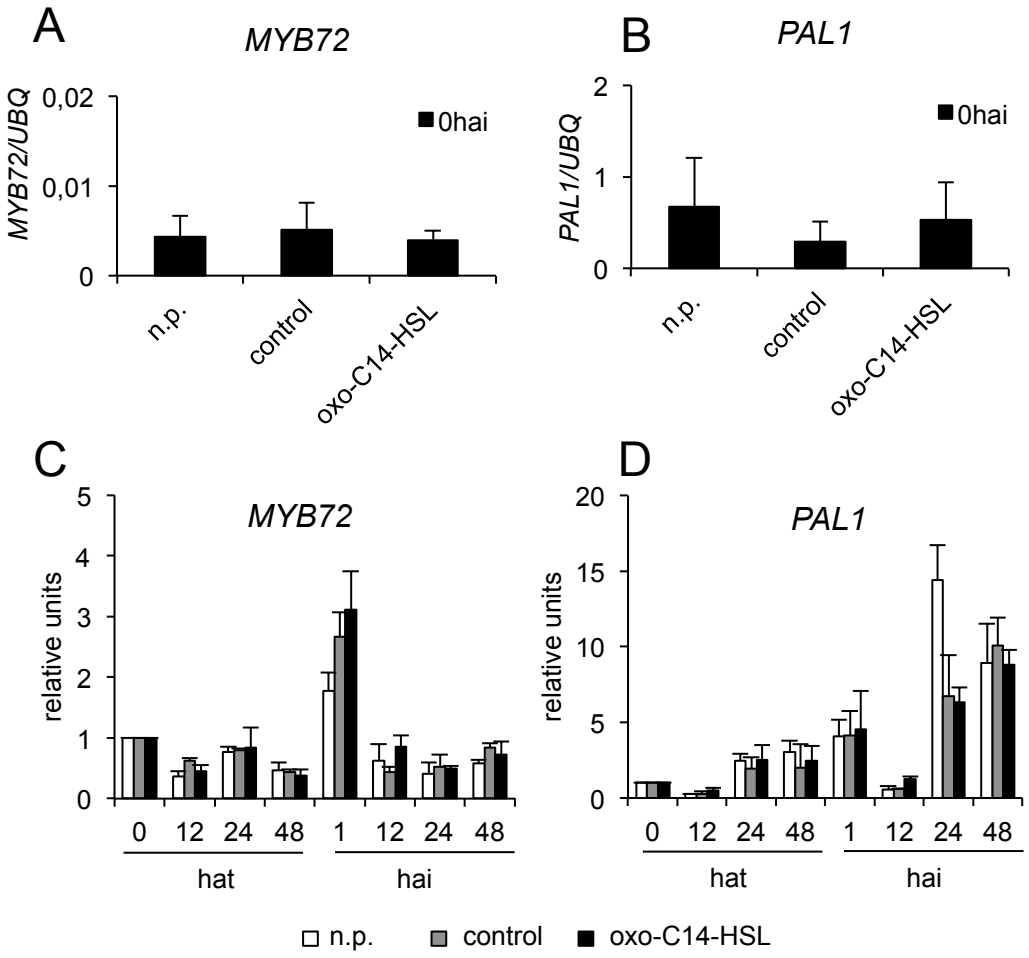
Supplemental Figure 5. Long-Term Observation of the Influence of AHLs on Plant Development and Plant's Defense System

A. *Arabidopsis* plants were cultivated for 8 weeks in the sterile systemic hydroponic system. The 1/2x MS medium was changed every week and supplied with 6 µM AHLs every fourth day. Number of developed leaves was assessed after 3, 5, and 8 weeks.
B. After 8 weeks plants were harvested for RNA extraction and transcriptional analysis of the OPDA-regulated genes (lower panels). The level of respective mRNA was determined *via* quantitative RT-PCR using the expression of ubiquitin ligase and the respective mRNA level in control plants for normalization. Error bars represent standard error, n = 30 per treatment.



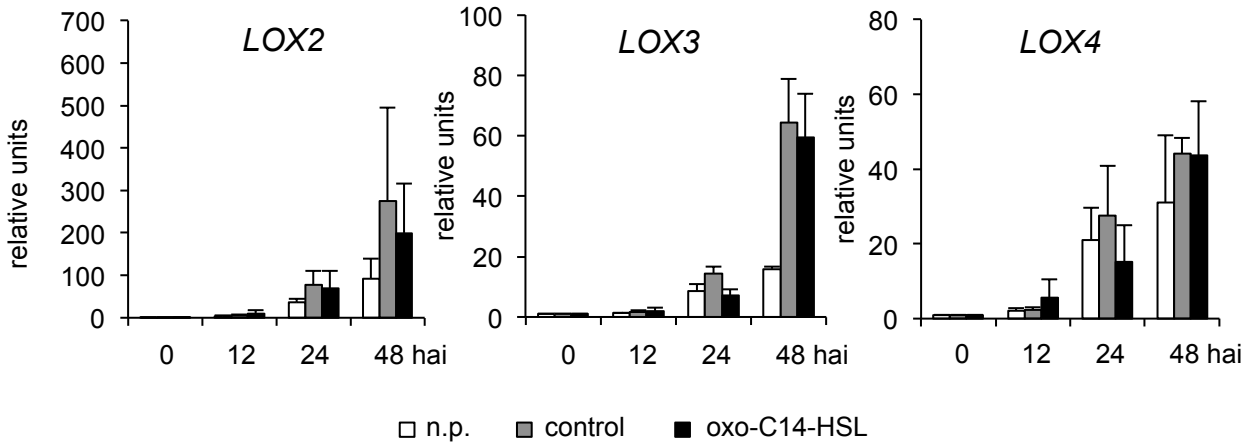
Supplemental Figure 6. Pretreatment with Oxo-C14-HSL Has No Impact on the Expression of JA-, SA-, ET-, and ABA-Regulated Genes

Relative expression of JA-regulated genes; *MYC2*, *VSP2,* and *Pdf1.2;* SA-regulated genes: *PR1*, *PR2, and PR5*; ET-regulated genes; *PR3*, *ERF5*, and *ETR1;* ABA-regulated genes: *RD29*, *RD22*, and *RAB18. Arabidopsis* plants were grown in the sterile systemic hydroponic system for 5 weeks, pretreated with 6 µM oxo-C14-HSL, its solvent acetone (control) for 3 days or not pretreated (n.p.), and challenged with *Pst* for the number of hours as indicated. The level of respective mRNA was determined *via* quantitative RT-PCR using the expression of ubiquitin ligase *At5g25760* for normalization. Graphs present a mean from three independent biological repetitions. Error bars represent standard error. hai; hours after inoculation. * represents $p < 0.05$, ** $p < 0.005$ in Student's *t*-test.



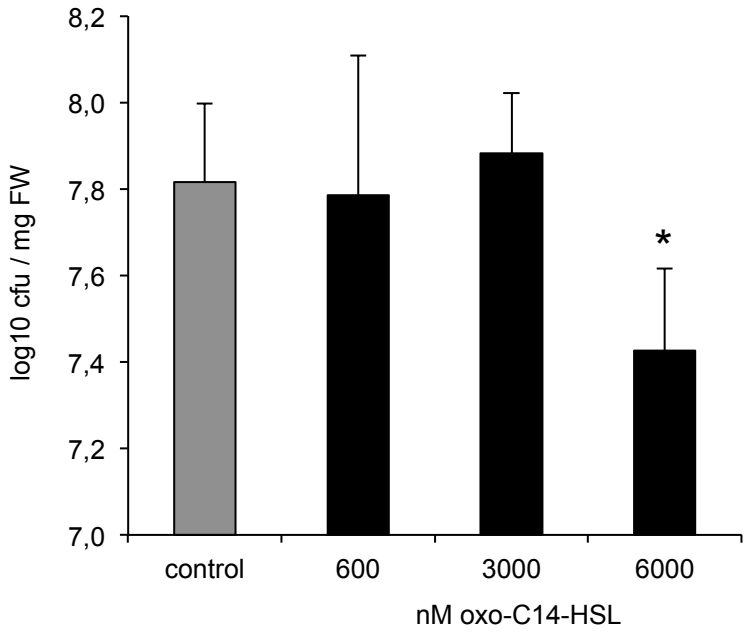
Supplemental Figure 7. Neither the *MYB72* Nor the *PAL1* Gene Was Induced upon AHL Priming

Expression profile of the *MYB72* transcription factor upregulated upon ISR (**A**, **C**) and the SAR-regulated *PAL* gene (**B**, **D**) encoding for phenylalanine-ammonia lyase in *Arabidopsis* plants grown in the sterile systemic hydroponic system and pretreated with 6 µM oxo-C14-HLS for 3 days (hat; hours after treatment) prior to challenge with *Pst* bacteria for the number of hours as indicated, hai (hours after inoculation). Quantitative RT-PCR was performed using the expression of the housekeeping gene ubiquitin ligase for normalization. Data represent a mean from three independent biological replications. Values in **C** and **D** were normalized to the 0 hat time point. Error bars represent standard error.



Supplemental Figure 8. Expression of *LOX* Genes

The expression profiles of three cytosolic lipoxygenases (*LOX2*, *LOX3*, and *LOX4*) in plants grown in the sterile systemic hydroponic system and subsequently challenged with *Pst* bacteria for the number of hours as indicated do not differ in plants pretreated with 6 µM oxo-C14-HSL, its solvent acetone (control) for 3 days or not pretreated (n.p.). Total RNA was extracted and the level of respective mRNA was determined *via* quantitative RT-PCR using the expression of ubiquitin ligase *At5g25760* for normalization. Graphs present a mean of three independent biological repetitions. Error bars represent standard error. hai; hours after inoculation.



Supplemental Figure 9. Effect of Different Concentrations of Oxo-C14-HSL on Induced Resistance

Pathogenicity assay with *Pseudomonas syringae* DC3000 pathovar *tomato* (*Pst*) on *Arabidopsis Col*-0 wild type plants grown for 5-weeks in the sterile systemic hydroponic system. Plant roots were pretreated with different concentrations of oxo-C14-HSL or its solvent acetone (control) for 3 days, and leaves were subsequently spray-inoculated with *Pst* ($OD_{600\ nm}$ = 0.1). The colony forming units (cfu) were counted after 48 hours. * represents $p < 0.05$ in Student's *t*-test.

Supplemental Table 1. List of Primers Used in Quantitative RT-PCR

Annealing temperature for all primers was set to 60°C

gene	primer sequence
PR1	TCG GAG CTA CGC AGA ACA ACT
	TCT CGC TAA CCC ACA TGT TCA
Pdf1.2	GTT TGC TTC CAT CAT CAC CC
	GGG ACG TAA CAG ATA CAC TTG
GST6	GCA TGT TCG GCA TGA CCA CTG
	GCA CCT TGG AGT CAG TAC CC
HSP70	CGC CAA CGA TCA AGG CAA CC
	GCT TCT CAC CTG GAC CGG AA
VSP2	CAA ACT AAA CAA TAA ACC ATA CCA TAA
	GCC AAG AGC AAG AGA AGT GA
MYC2	GGT TGG GAC GCA ATG ATT AGA GT
	CCA TCT TCA CCG TCG CTT GTT G
PR2	TCT TGA ACC CAC TTG TCG GC
	GGC TCT GAC ATC GAG CTC ATC
PR5	TCC TTG ACC GGC GAG AGT T
	AGG AAC AAT TGC CCT ACC ACC
RD29	GAG GAA GTG AAA GGA GGA GGA GG
	CAG TGG AGC CAA GTG ATT GTG G
RAB18	TCG GTC GTT GTA TTG TGC TTT TT
	CCA GAT GCT CAT TAC ACA CTC ATG
RD22	GCG AGC TAA AGC AGT TGC GGT ATG
	GGG AGG AAG TGG CAG ACC GGA AC
PR3	GAC GCC GAC CGT GCC GCC GGG
	CGG CGA CTC TCC CGT CTT GGC C
ERF5	GAC GAA GCA GCG TTT AGA CTA CGA GG
	GGA GAT AAC GGC GAC AGA AGC GG
ETR1	CGA GAA GCT CGG GTG GTA GT
	GCC GTG CAT CCT TTT CC
MYB72	TCA TGA TCT GCT TTT GTG CTT TG
	ACG AGA TCA AAA ACG TGT GGA AC

PAL1	AAC GGA GGA GGA GTG GAC G
	CTT TTC ATT TGC TCC GCT GC
LOX2	GTA GCC CCA GTT CTC ATT AAC AGG G
	CGG GTC TAG TTT GCT TAT TAA CGG C
LOX3	TAT GGA TTT GCG GCA GAG ATC GGA
	AGG CTC AGA ACT CGG AAC CAA CAA
LOX4	GGG ATC AAC CCG GTC AAC ATA GAA C
	GTC CAC CAT AAA CAA ACG GTT CGT C
XTR9	GGA GCA ACG CAC CAT TCA AGG
	CGT ACT GGG CAG GAT TGA GAG
XTH26	GGA AGG GAT CAG TCA GCA TCA AG
	GTG CTA TGA TTG CCG GAG CC
EXP22	TAA AGG AAA CAA GAC CGG GTG G
	CCT GAA CGA TAA ACC TTG GCC G
At5g07990	GCT GGG AGG AGA ATC TGT GC
	GGA TGT ACC ACC AAA GGA ACC G
At1g12140	AAC TTC GGA GAG AGC ATT CGT C
	GCT GTT GAA GAG GCA GAG AAG A
At3g29630	GCG GGT TCG GTT CAA TGT G
	GAC CGT ATC CCT CAA GCT CTC C
Actin 2	GGA AGG ATC TGT ACG GTA AC
	TGT GAA CGA TTC CTG GAC CT
At5g25760	GCT TGG AGT CCT GCT TGG ACG
	CGC AGT TAA GAG GAC TGT CCG GC