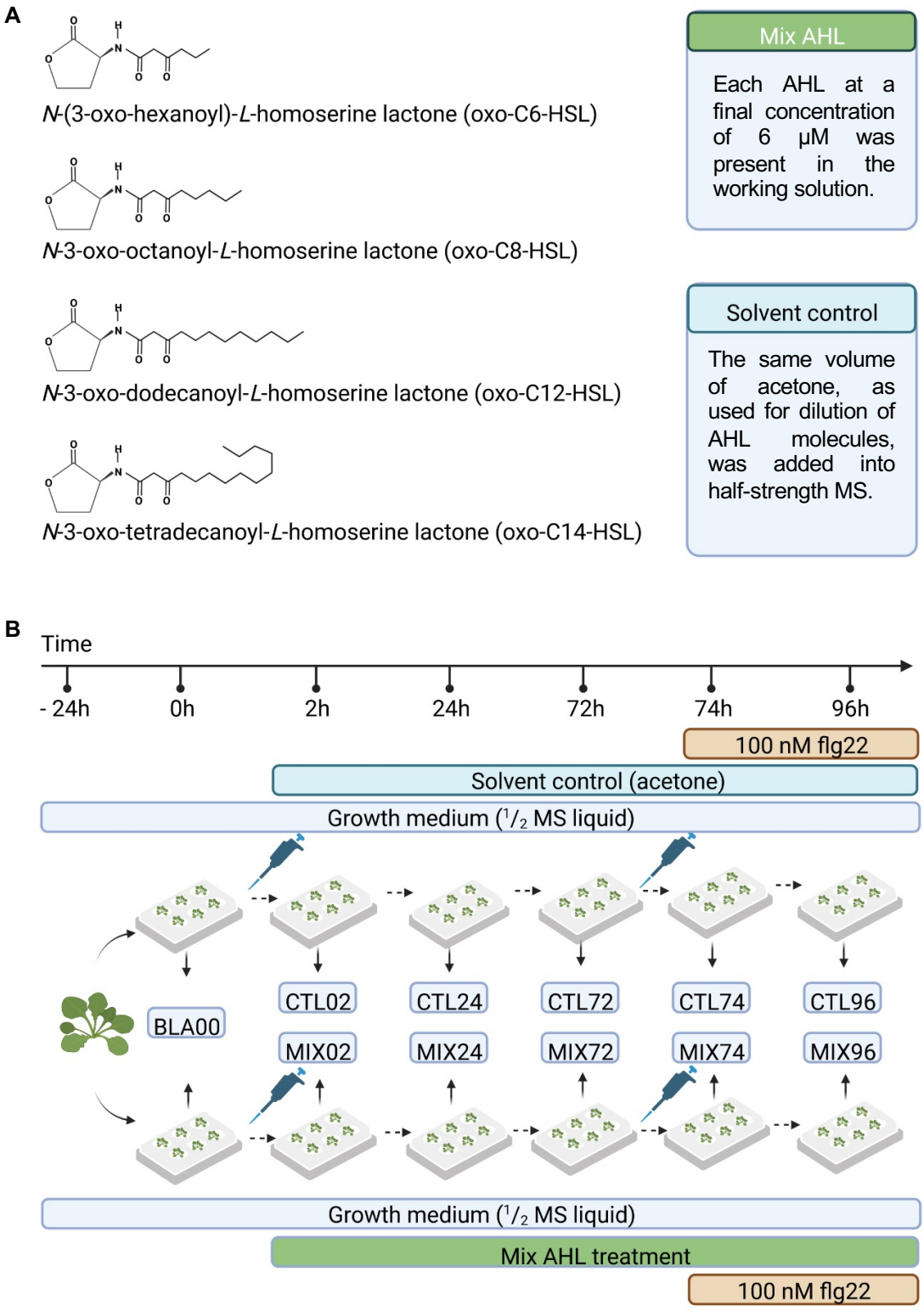
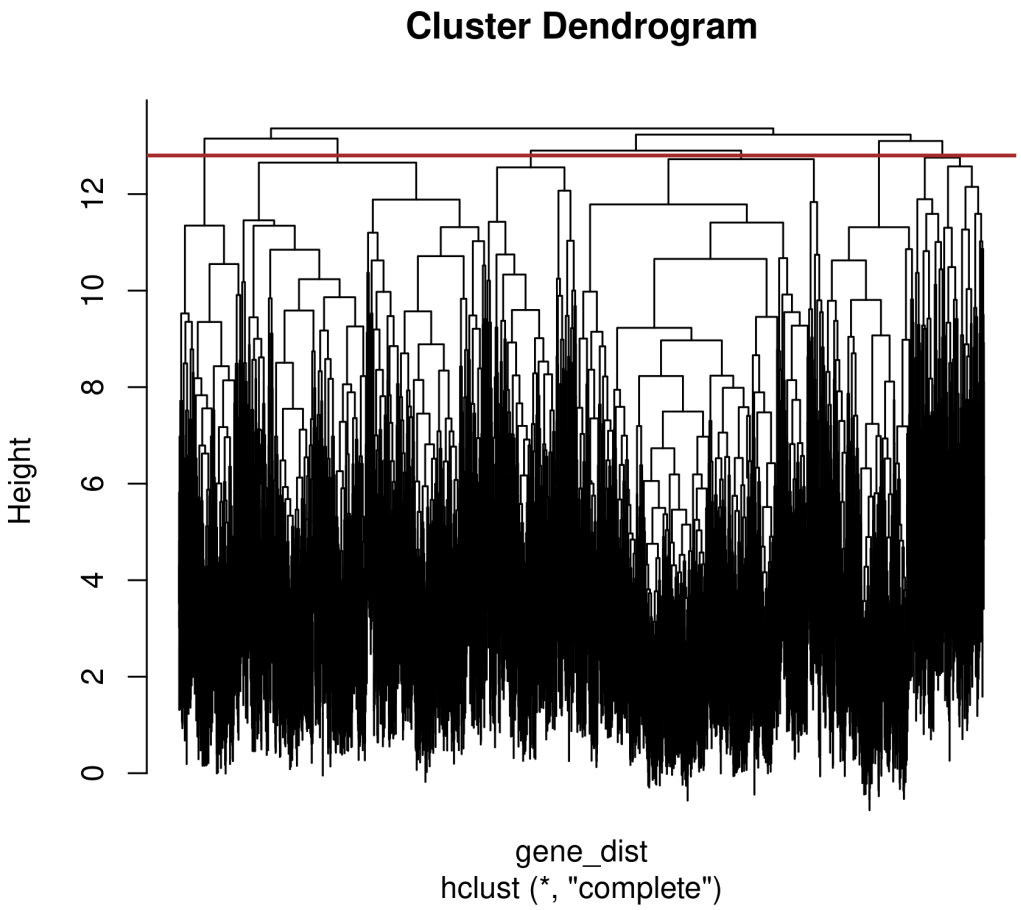
Supplementary Figure S1



Supplementary Figure S1. Experimental setting and time schedule of the transcriptome analysis.

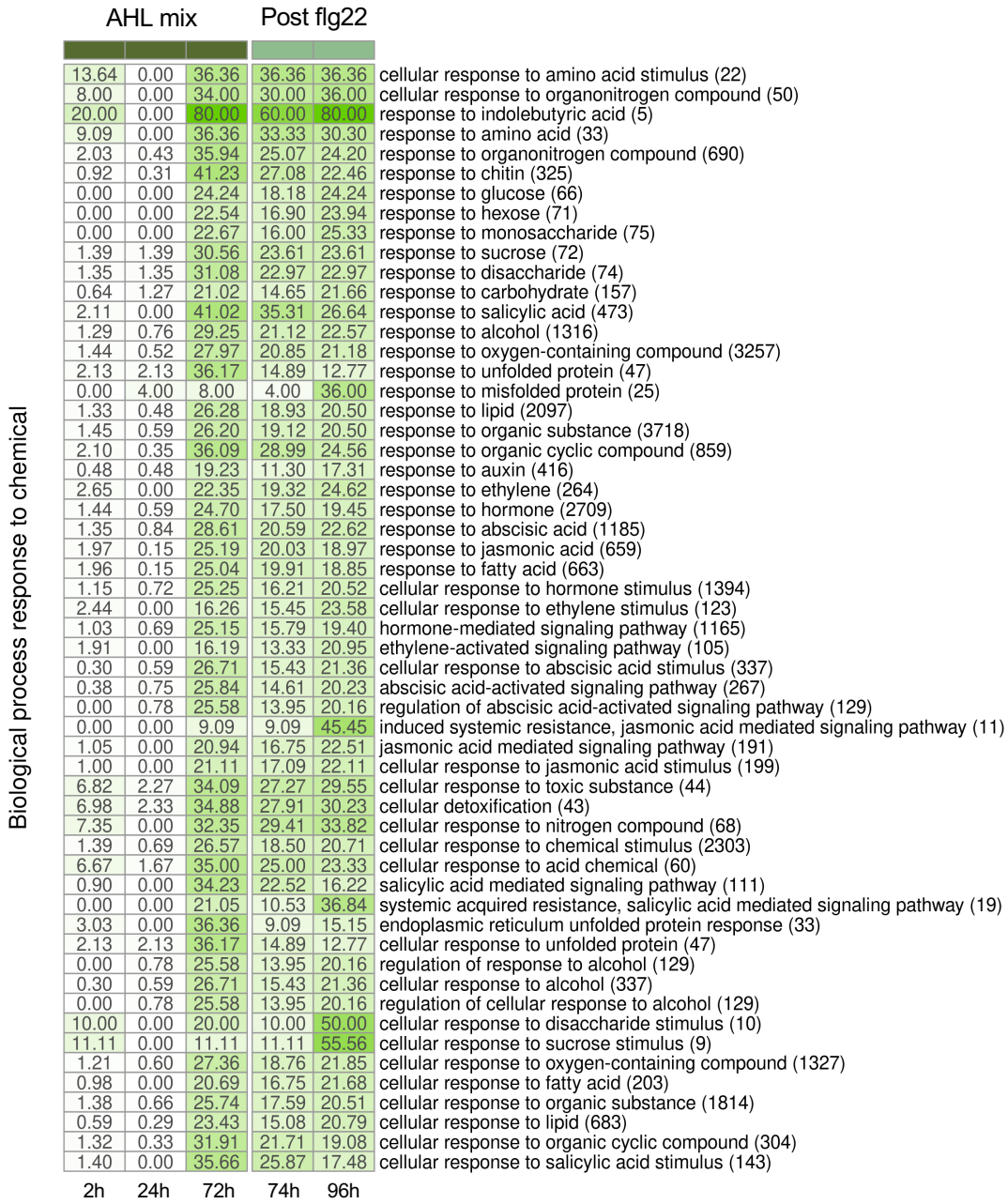
Mixed AHLs contain four AHL molecules with different acyl chain lengths, each at a final concentration of 6 µM in the working solution (A). The same volume of acetone was added to the solvent control. Two-week old sterile *Arabidopsis thaliana* Col-0 plants were transferred into six-well plates and grown for additional 24h. The blank control for the transcriptome analysis was collected before adding mixed AHL (AHL mix) or the solvent (control). The samples were collected 2h, 24h, 72h, 74h, and 96h thereafter (B).



Supplementary Figure S2. Cluster dendrogram of gene expression patterns across the experimental time course.

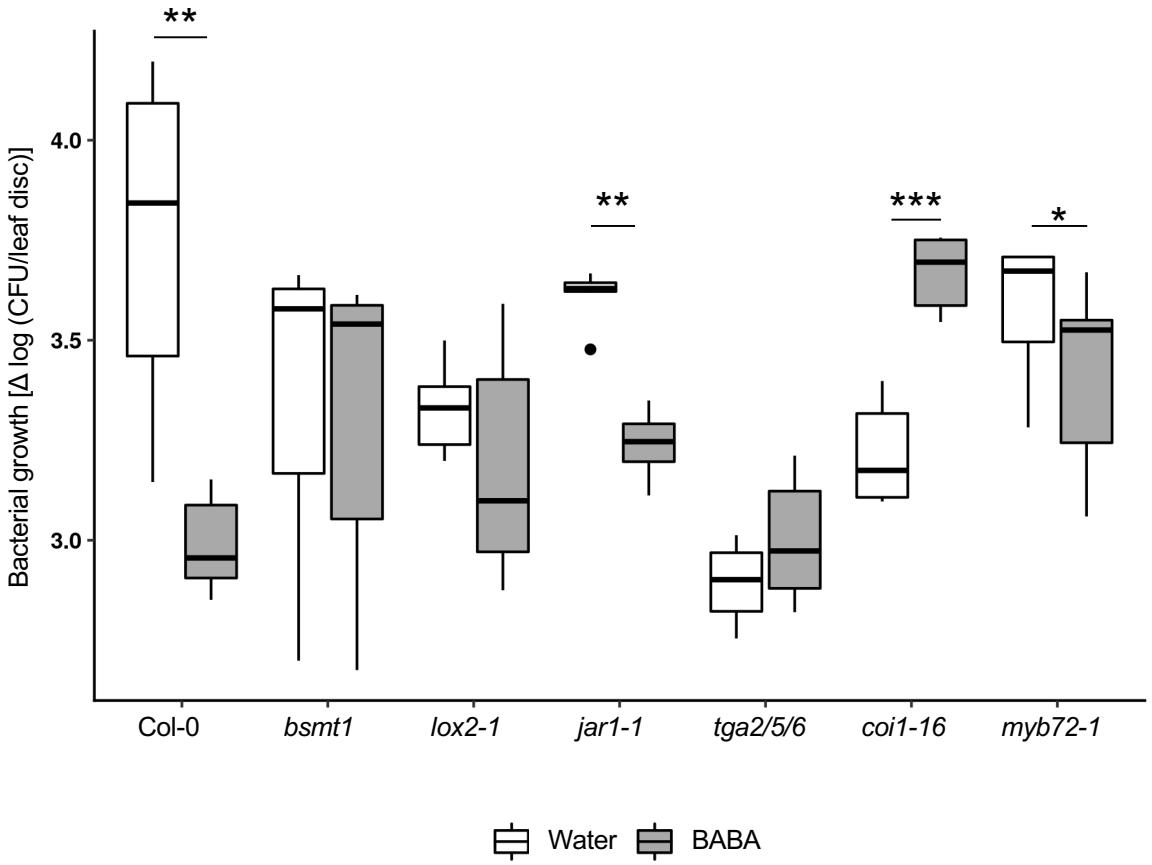
Gene expression over time was analyzed using R package DESeq2 (Love et al., 2014) with the default setting in the comparison between gene expression full model (time + treat + treat: time) and gene expression reduced model (time + treat). Patterns of differentially expressed genes were identified by threshold (*p* adjusted < 0.05) in comparisons between control (acetone) and AHL mix-treated samples across the experimental time course. The method (termed Complete) was used to calculate the gene distance in the genes which have differential expression patterns. Six groups of gene expression patterns were identified. The brown line in the plot represented the gene distance of 12.5.

Supplementary Figure S3



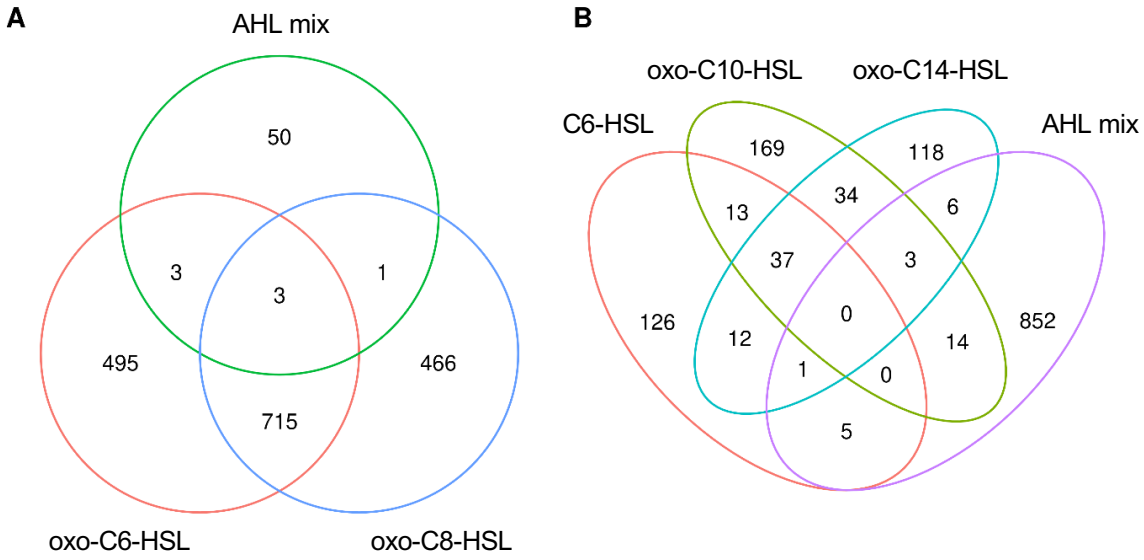
Supplementary Figure S3. Changes in the GO term "biological process response to chemical" during the experimental time course.

Analysis of the enriched GO terms among differentially expressed genes across the experimental time course, was performed using the R package ViSEAGO with default setting (Brionne et al., 2019). The GO term "biological process response to the chemical" was shown with the percentage of participating genes for different processes. The percentage was highlighted in green color in the plot. Total gene number of each process was indicted at the end of the process name (in brackets). Compared to others, response to jasmonic acid was very prominent among the enriched GO terms.



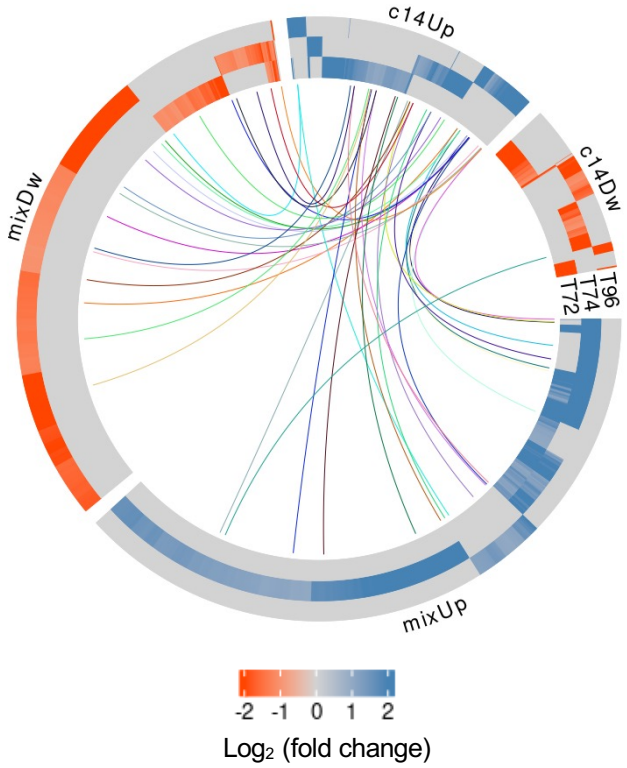
Supplementary Figure S4. BABA induces enhanced resistance in plants grown in a jar hydroponic system.

Three-week old Col-0 plant and several mutants deficient in jasmonate homeostasis were transferred to a sterile hydroponic system, based on glass jars, perlite, and ¼ MS medium. Plants were grown in a growth chamber for another 3-4 weeks. During the growth process, fresh ¼ MS was added weekly into the jars according to plants' requirement. Roots were pretreated with a final concentration of 250 µM β-aminobutyric acid (BABA) or water (control) for 72h and subsequently leaves were inoculated with the plant pathogens *Pseudomonas syringae* pv. *tomato* (*Pst*), OD_{600nm} = 0.01 (10^7 CFU/mL) in 10 mM $MgCl_2$. Bacterial proliferation was used to assess plant resistance and is expressed as difference in the number of Colony Forming Unit (CFU) in leaf discs between 96h and 2h time points (Δlog (CFU/leaf disc)). Boxes represent the interquartile range between the first and the third quartile and the middle line marks the median, whiskers indicate 1.5× interquartile range, points indicate outliers. Statistical analysis was performed by Student's *t*-test, * $p < 0.05$, ** $p < 0.005$, *** $p < 0.001$, $n \geq 3$. The results demonstrated that BABA-priming may be established in jar-grown plants and is independent of JAR1 and the MYB72 transcription factor however, requires LOX2, COI1, TGA2/5/6 transcription factors as well as BSMT1.



Supplementary Figure S5. Gene expression in response to AHL mix differs from that of response to single AHL molecules.

Information on differentially expressed genes (DEGs) after exposure to single AHL molecules including 6 μM C6-HSL, 1 μM oxo-C6-HSL, 10 μM oxo-C8-HSL, 6 μM oxo-C10-HSL and 6 μM oxo-C14-HSL were extracted from previous studies (Zhao et al.2016; Liu et al.2022; Schenk et al. 2014). DEGs induced by AHL mix, compared to solvent control, were obtained in this study. The comparison of genes differentially regulated 24h post AHL treatment is presented in (A), and the comparison at 72h post AHL treatment is presented in (B). Many genes responded specifically to AHL mix, indicating that the response of plants exposed to AHL mix differs from that exposed to single AHL molecules.



Supplementary Figure S6. Responses to the flg22 challenge differs between plants primed with AHL mix and oxo-C14-HSL.

Information on gene expression upon response to 100 nM flg22 in oxo-C14-HSL (C14)-primed plants was extracted from Schenk *et al.* (2014). Information on gene expression of AHL mix-primed plants response to flg22 was obtained in this study. Data were collected for the 72h (T72) time point: 72h post AHL-priming and prior the flg22 challenge; 74h (T74): 2h post flg22 challenge); and 96h (T96): 24h post the flg22 challenge. The up-regulated genes were indicated in green and down-regulated were marked in red. The gaps in the gene list were marked with light gray. Differentially expressed genes (DEGs) were identified by threshold (p adjusted < 0.05) and the absolute $\log_2$ value of fold change > 1. DEGs common in oxo-C14-HSL- and AHL mix-primed plants are indicated by lines inside the plot.

Supplementary Table S1. Jasmonic acid (JA)-related gene expression in a single AHL treatment.

GeneID	Log_2(FC)	AHLs	Time	Category	Gene_description	Gene_name
AT2G06050	-1.10	oxo-C6-HSL	24h	Biosynthesis	oxophytodienoate-reductase 3	OPR3
AT3G25760	-1.17	oxo-C6-HSL	24h	Biosynthesis	allene oxide cyclase 1	AOC1
AT3G45140	-2.16	oxo-C6-HSL	24h	Biosynthesis	lipoxygenase 2	LOX2
AT1G20510	-1.08	oxo-C8-HSL	24h	Biosynthesis	OPC-8 coenzyme A ligase1 (OPCL1)	OPCL1
AT2G06050	-1.38	oxo-C8-HSL	24h	Biosynthesis	oxophytodienoate-reductase 3	OPR3
AT3G25760	-1.14	oxo-C8-HSL	24h	Biosynthesis	allene oxide cyclase 1	AOC1
AT3G45140	-2.28	oxo-C8-HSL	24h	Biosynthesis	lipoxygenase 2	LOX2
AT3G53510	-1.05	oxo-C8-HSL	24h	Metabolism	ABC-2 type transporter family protein	JAT4

Note: data on Arabidopsis treated with *N*-(3-oxo-hexanoyl)-L-homoserine lactone (oxo-C6-HSL) and *N*-3-oxo-octanoyl-L-homoserine lactone (oxo-C8-HSL) at 24h, were extracted from previous studies (Zhao et al., 2016; Liu et al., 2022).

Supplementary Table S2. List of oligonucleotides used in this study.

Accession number / Gene	Name	Sequence (5' -> 3')	Reference
AT3G25760 AOC1	RT-qAtAOC1-F	TCAGAACTTGGGAAATACCGAA	(Huang et al., 2021)
	RT-qAtAOC1-R	TAAGAATTTTTGGGCTGTGTCG	
AT5G42650 AOS	RT-qAtAOS-F	AACACCAGCTCCAGCTCTATTCTT	(Huang et al., 2021)
	RT-qAtAOS-R	TTGACTCTGTACACCGTGGAGTT	
AT3G45140 LOX2	RT-qAtLOX2-F	ATGAGCCTGTTATCAATGCTGC	(Hu et al., 2013)
	RT-qAtLOX2-R	AACACCAGCTCCAGCTCTATTCTT	
AT1G17420 LOX3	RT-qAtLOX3-F	TATGGATTTGCGGCAGAGATCGGA	(Schenk et al., 2014)
	RT-qAtLOX3-R	AGGCTCAGAACTCGGAACCAACAA	
AT1G72520 LOX4	RT-qAtLOX4-F	GGGATCAACCCGGTCAACATAGAAC	(Schenk et al., 2014)
	RT-qAtLOX4-R	GTCCACCATAAACAAACGGTTCGTC	
AT1G76690 OPR2	RT-qAtOPR2-F	CCAGAAGCATTAGGGCTG	(Beynon et al., 2009)
	RT-qAtOPR2-R	GGCTTCCCTCATTGGCAT	
AT2G06050 OPR3	RT-qAtOPR3-F	ATTATGGCATGTTGGACGTG	(Huang et al., 2021)
	RT-qAtOPR3-R	AACAAAACTCGCCACCTGTT	
AT3G48520 CYP94B3	RT-CYP94B3-F	TGGCTTACACGAAGGCTTGTC	(Heitz et al., 2012)
	RT-CYP94B3-R	AGTCCCACGAAACTGGAGGAT	
AT2G27690 CYP94C1	RT-CYP94C1-F	GGCCCGGATTACGAAGAGTTT	(Heitz et al., 2012)
	RT-CYP94C1-R	GGCCGGAACTTACCTTCGTT	
AT1G51760 IAR3	RT-qAtIAR3-F	TCGGATTAAGCAAGTGAAGGA	(Smirnova et al., 2017)
	RT-qAtIAR3-R	TTGCTTCTTGTACCCCTGCT	
AT1G44350 ILL6	RT-qAtIAR3-F	GTGTCCCATATCCATCCAACGG	(Smirnova et al., 2017)
	RT-qAtIAR3-R	AGACTAATGACCGCGGAAGAAG	
AT5G05600 JAO2-2	RT-qAtJAO2_2-F	CCTCCTTTATACCCTCCCATGAC	(Smirnova et al., 2017)
	RT-qAtJAO2_2-R	TTTGCCTTGTGGACCTTGAGTTC	
AT3G55970 JAO3-1	RT-qAtJAO3_1-F	AGCTCCTCATGCTTTCATCGTT	(Smirnova et al., 2017)
	RT-qAtJAO3_1-R	CGATCACTCTGTGTTCTACGCT	
AT2G38240 JAO4-1	RT-qAtJAO4_1-F	GGAATTTACAAAAGCGTGGAACA	(Smirnova et al., 2017)
	RT-qAtJAO4_1-R	CGGGATATCACTTCTCGGGT	
AT2G46370 JAR1	RT-qAtJAR1-F	AACGCTACTGACCCTGAAGAAGC	(Hu et al., 2013)
	RT-qAtJAR1-R	GGTGAAGTGTCACCATCAACCA	
AT1G19640 JMT	RT-qAtJMT-F	ATGTCCATGGCCAAAGAGGG	(Li et al., 2017)
	RT-qAtJMT-R	CGGAGCTCGCAGCATAGTAA	
AT3G55090 JAT1	RT-qAtJAT1-F	TGGTTCTTCACTTGACGGAGAT	(Li et al., 2017)
	RT-qAtJAT1-R	AAGAGTCTTGGTCTTGGAGA	
AT1G32640 MYC2	RT-qAtMYC2-F	GGTTGGGACGCAATGATTAGAGT	(Schenk et al., 2014)
	RT-qAtMYC2-R	CCATCTTCACCGTCGCTTGTTG	
AT1G74930 ORA47	RT-qAtORA47-F	TCCACCGTCGATCTCCGTAGAAAA	(Hickman et al., 2017)
	RT-qAtORA47-R	GCGAATCTAGCAGCAGCTTCCTGA	
AT4G01250 WRKY22	RT-qAtWRKY22-F	ATCTCCGACGACCACTATTG	(Schikora et al., 2011)
	RT-qAtWRKY22-R	TCATCGCTAACCACCGTATC	
AT4G23550 WRKY29	RT-qAtWRKY29-F	TCCGGTACGTTTTCACCTTC	(Schikora et al., 2011)
	RT-qAtWRKY29-R	AGAGACCGAGCTTGTGAGGA	
AT5G25760 UBQ4	RT-qAtUBQ4-F	GCTTGGAGTCCTGCTTGGACG	(Schikora et al., 2011)
	RT-qAtUBQ4-R	CGCAGTTAAGAGGACTGTCCGGC	