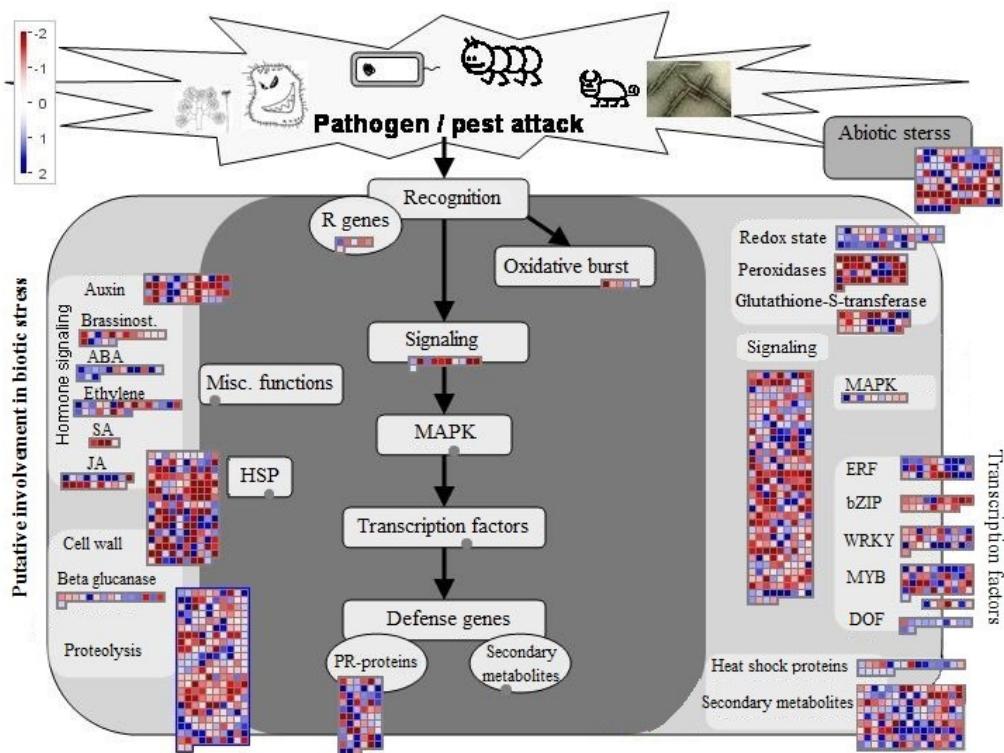
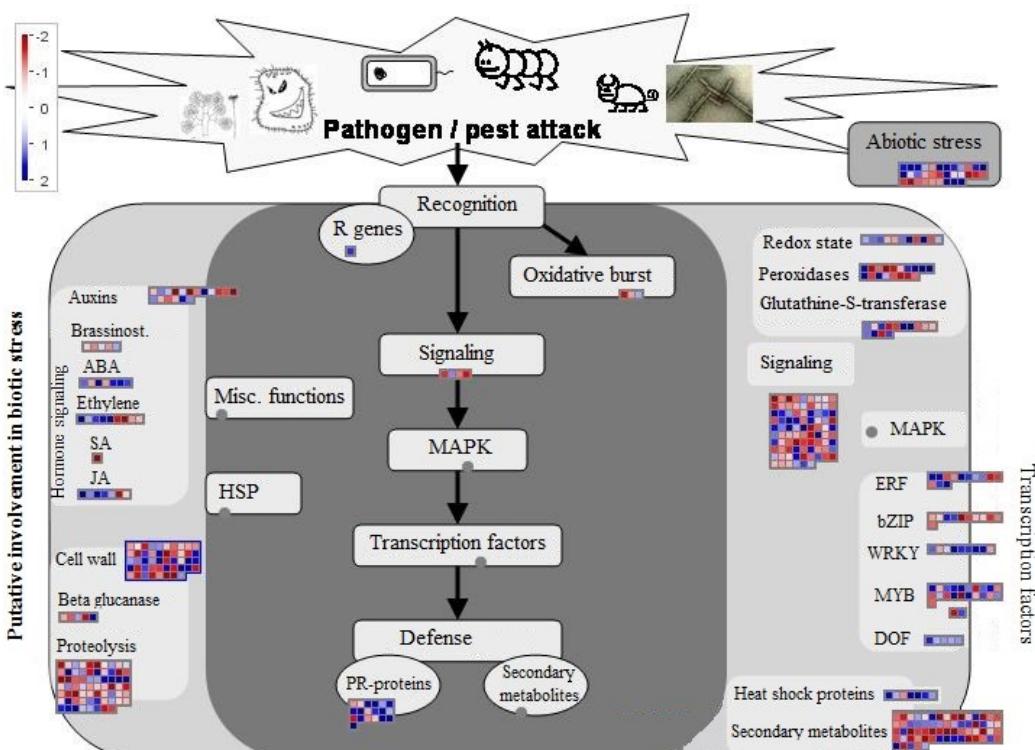


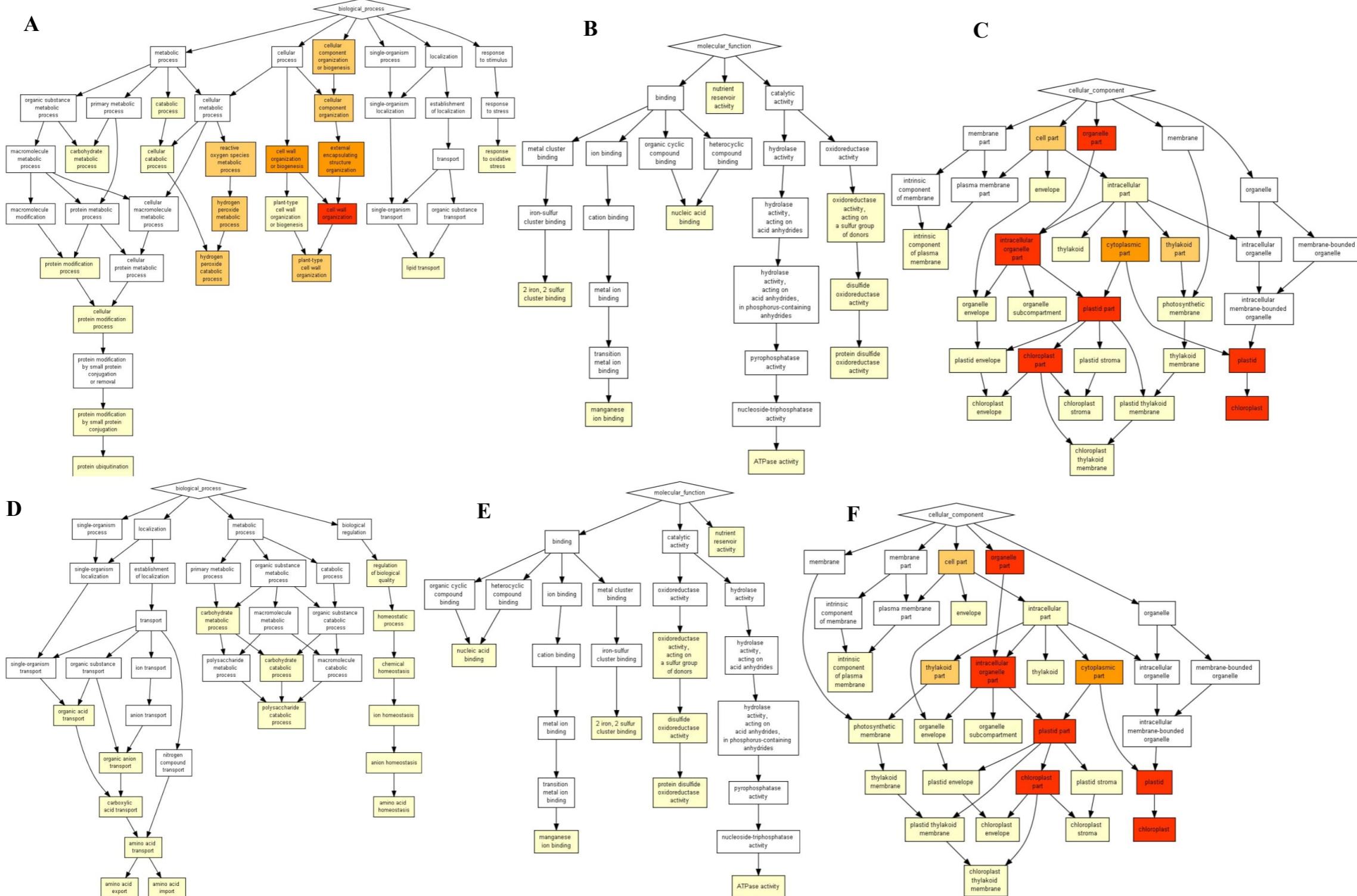
Supplementary Figure 1 – Mapman analysis on Col0 differentially expressed genes (DEGs) involved in biotic stress pathway (*Thimm et al., 2004*).



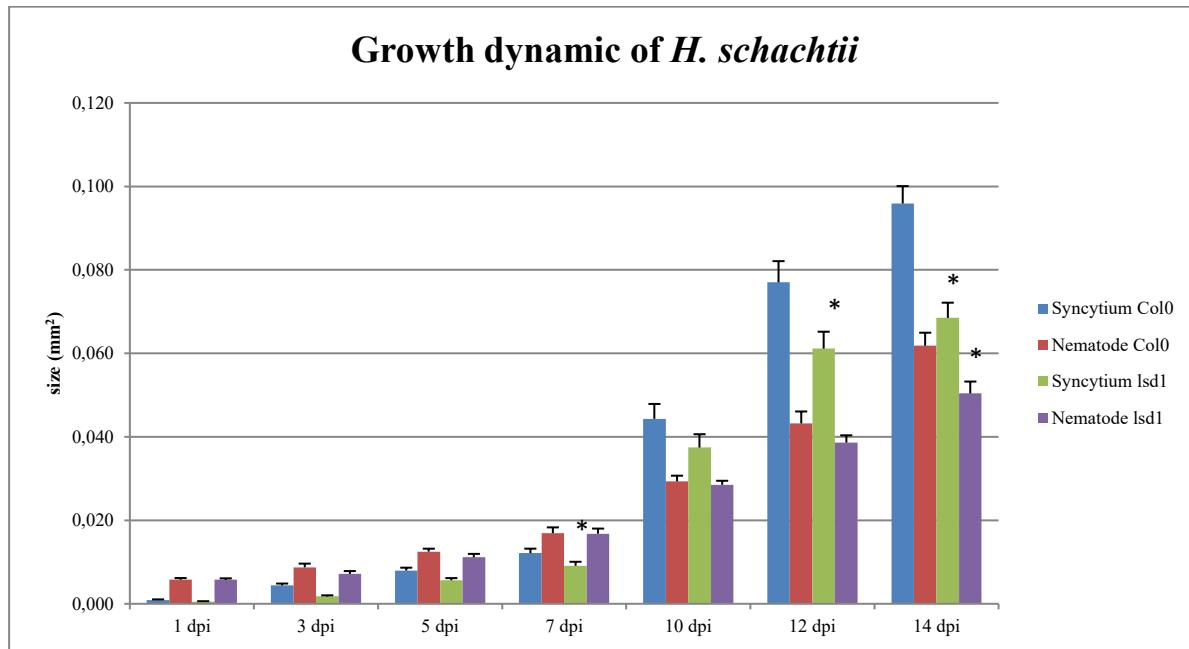
Supplementary Figure 2 – Mapman analysis on *lsd1*(Col0) differentially expressed genes (DEGs) involved in biotic stress pathway (*Thimm et al., 2004*).



Supplementary Figure 3 – Gene Ontology enRICHment anaLysis and visuaLizAtion tool (Gorilla; Eden *et al.* 2009) DEGs from Col0 involved in (A) biological processes, (B) molecular functioning, and responsible for (C) cellular components. DEGs from *lsd1*(Col0) involved in (D) biological processes, (E) molecular functioning, and responsible for (F) cellular components.



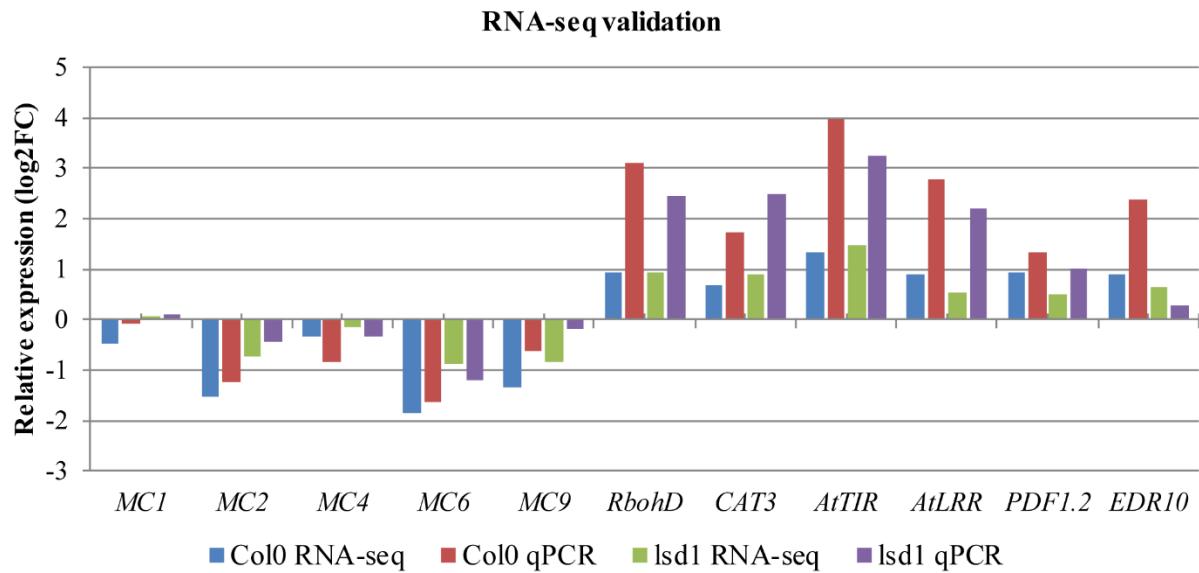
Supplementary Figure 4 – Growth dynamic of *H. schachtii* on Col0 and *lsd1*(Col0). Data represent 2 independent experiments – 10 plants per genotype (means \pm SEM). Data were analyzed using t-test ($p < 0,05$). Asterisks indicate $p < 0,05$ compared to wild-type.



Supplementary Figure 5 – List of primers used in this study

Primer list		
LP lol2	<i>Forward</i>	TGGAACAAATCTTGAATGCTC
RP lol2	<i>Reverse</i>	TGACAAGTTGGTCTTCACCC
Sail LB3	<i>Forward</i>	TAGCATCTGAATTTCATAACCAATCTCGATACA
Act2.Fwd	<i>Forward</i>	TTCACCACAAACAGCAGAGCGGG
Act2.Rev	<i>Reverse</i>	CGTGATGACTGCCATCGGGT
RbohD_Fw	<i>Forward</i>	CGATGAAAATGAGACGAGGCA
RbohD_Rev	<i>Reverse</i>	TCGTCGGCGAATCTTGCCTT
MC1_Fwd	<i>Forward</i>	TCCACATGGTGTCAAGCTCC
MC1_Rev	<i>Reverse</i>	TGCCAGCTCTGTTCATTC
MC2_Fwd	<i>Forward</i>	CAGAACGAGCGGTGATAGT
MC2_Rev	<i>Reverse</i>	TCCGCTTCTTCTCGGTGAG
MC4_Fwd	<i>Forward</i>	GCGACATGAATCTGATTACTGATGA
MC4_Rev	<i>Reverse</i>	ATCTGCTCCTGGCTTCGTC
MC6_Fwd	<i>Forward</i>	TGAACCGGCTAAATCGGGTG
MC6_Rev	<i>Reverse</i>	CAAGATCCCTGAAATCATCATCGGT
MC9_Fwd	<i>Forward</i>	TCCAGCAACATATCTCCGGC
MC9_Rev	<i>Reverse</i>	TCAAGTGGTCAAGGACTGCC
AtTIR_Fwd	<i>Forward</i>	AAAGTTCTTAAATGGAGGCAAGCA
AtTIR_Rev	<i>Reverse</i>	AGCTTCGAGTCATCATCACCTGA
AtLRR_Fwd	<i>Forward</i>	CTGCTCTCTTAAATTGTTAGTTGTCTC
AtLRR_Rev	<i>Reverse</i>	GCTTATTAGCCTCATGCTTAAAATCTTGA
CAT3_Fwd	<i>Forward</i>	ACACCAGAGAGGGAAACTTGATCT
CAT3_Rev	<i>Reverse</i>	TCCCACGGATGAAGAACAA
EDR10_Fwd	<i>Forward</i>	AGCTCTTCTTCCTTCGAGTGATG
EDR10_Rev	<i>Reverse</i>	CCACTGTTTCACATGATCTCCTTC
PDF1.2_Fwd	<i>Forward</i>	CGGCAATGGTGGAAAGCACAGAA
PDF1.2_Rev	<i>Reverse</i>	TGCATGATCCATGTTGGCTCC

Supplementary Figure 6 – Comparison of expression levels of differentially expressed genes quantified by qRT-PCR and RNA-seq analysis. The genes *metacaspases (MC1, MC2, MC4, MC6 and MC9)*, ROS signaling *respiratory burst oxidase homolog D (RBOH D)*, *catalase 3 (CAT3)*, two R-genes *AtTIR* and *AtLRR* and stress related markers *PDF1.2* and *ERD10* were selected for analysis.



Supplementary Figure 7 – The nematode induced changes in jasmonic acid (JA), salicylic acid (SA), ethylene (ET) related genes in 12 dpi syncytia of Col0 and *lsd1*(Col0) plants. Genes were divided into three functional groups: marker genes, signaling, biosynthesis. Genes differentially expressed in transcriptome data present bolded.

Function	Gene	Accession no.	Log2FC		Log2FC	
			Col0	p-value	<i>lsd1</i> (Col0)	p-value
Jasmonic acid (JA)						
Marker	<i>PDF1.2</i>	At5g44420	0,933	0,1308422	0,522	0,2412968
	<i>PDF2.1</i>	At2g02120	0,639	0,0183975	1,232	4,06E-05
	<i>PR3</i>	At3g12500	-0,200	0,345067	0,699	0,0014728
	<i>PR4/HEL</i>	At3g04720	-0,128	0,5965495	0,234	0,2527143
	<i>THI2.1</i>	At1g72260	0,216	0,4981015	0,495	0,2065587
Signalling	<i>COII</i>	At2g39940	-0,247	0,2438883	-0,264	0,2063272
	<i>JAR1</i>	At2g46370	-0,192	0,3980509	0,144	0,7027459
	<i>JAZ1</i>	At1g19180	0,966	0,0018641	0,62	0,1137719
	<i>JAZ5</i>	At1g17380	2,209	3,19E-20	1,351	0,0038343
	<i>JAZ6</i>	At1g72450	1,550	1,21E-09	1,351	0,0038343
	<i>JAZ8</i>	At1g30135	1,435	0,0002534	1,422	0,0080657
	<i>JAZ10</i>	At5g13220	3,621	3,45E-29	2,455	2,34E-16
Biosynthesis	<i>AOC1</i>	At3g25760	3,143	8,92E-13	0,842	0,1126373
	<i>AOC3</i>	At3g25780	1,765	2,65E-11	1,487	4,69E-06
	<i>AOC4</i>	At1g13280	-0,112	0,6237259	-0,361	0,1612409
	<i>DDE2</i>	At5g42650	0,818	0,0022679	0,301	0,3296245
	<i>LOX2</i>	At3g45140	0,753	0,1130193	0,402	0,3595181
	<i>LOX3</i>	At1g17420	2,641	2,96E-24	2,738	5,45E-10
	<i>LOX4</i>	At1g72520	2,766	1,88E-37	1,818	5,07E-05
	<i>LOX5</i>	At3g22400	-0,426	0,0812774	-0,504	0,1028233
	<i>LOX6</i>	At1g67560	0,956	1,90E-05	1,123	0,0007534
Salicylic acid (SA)						
Marker	<i>PR1</i>	At2g14610	-0,740	0,2004696	1,629	2,51E-05
	<i>PR2</i>	At3g57260	0,661	0,1685574	1,969	0,0002115
	<i>PR5</i>	At1g75040	1,290	0,0026548	2,394	7,20E-06
Signalling	<i>EDS1</i>	At3g48090	-0,235	0,281574	0,105	0,6852671
	<i>EDS5</i>	At4g39030	1,182	2,99E-06	0,725	0,008045
	<i>NPR1</i>	At4g26120	-0,060	0,8440157	0,003	0,9940736
	<i>NPR3</i>	At5g45110	0,644	0,0214997	0,452	0,2426548
	<i>NPR4</i>	At4g19660	-0,425	0,0663996	-0,283	0,2569571
	<i>PBS3</i>	At5g13320	0,315	0,4254392	0,791	0,1242446
Biosynthesis	<i>EPS1</i>	At5g67160	0,788	0,0054264	0,303	0,3189124
	<i>ICSI/EDS16</i>	At1g74710	-0,315	0,36478	0,456	0,1233578
	<i>ICS2</i>	At1g18870	-0,818	0,0060831	-1,796	8,40E-05
	<i>PAL1</i>	At2g37040	0,899	5,99E-05	1,32	0,0024843
	<i>PAL2</i>	At3g53260	0,472	0,0408146	1,248	0,0028396
	<i>PAL3</i>	At5g04230	-0,265	0,5967316	-0,25	0,6329567

	<i>PAL4</i>	At3g10340	-0,442	0,0409101	-0,006	0,9855601
Ethylene (ET)						
Marker	<i>PDF1.2</i>	At5g44420	0,933	0,1308422	0,522	0,2412968
	<i>PR3</i>	At3g12500	-0,200	0,345067	0,699	0,0014728
	<i>PR4/HEL</i>	At3g04720	-0,128	0,5965495	0,234	0,2527143
Signalling	<i>EIL1</i>	At2g27050	-0,188	0,4376982	-0,32	0,1774092
	<i>EIN2</i>	At5g03280	-0,176	0,4708317	-0,471	0,0466092
	<i>EIN3</i>	At3g20770	-0,025	0,9019934	-0,042	0,857345
	<i>EER4</i>	At1g17440	0,204	0,4140033	0,227	0,3418443
	<i>EER5</i>	At2g19560	-0,336	0,1376128	-0,179	0,4661075
	<i>ERF1</i>	At3g23240	1,688	2,98E-06	0,49	0,2641865
	<i>ERF3</i>	At1g50640	-0,146	0,511132	0,01	0,9622668
	<i>ERF4</i>	At3g15210	0,037	0,8889884	-0,095	0,7634813
	<i>ERF5</i>	At5g47230	-0,338	0,3029006	-0,705	0,0568453
	<i>ERF6</i>	At4g17490	-0,340	0,340005	-0,893	0,0490702
	<i>ERF7</i>	At3g20310	-0,364	0,1259982	-0,078	0,7271611
	<i>ERF13</i>	At2g44840	1,159	0,0010723	0,153	0,7477557
Biosynthesis	<i>ACS2</i>	At1g01480	0,573	0,0927995	1,475	0,0003515
	<i>ACS4</i>	At2g22810	1,229	0,0478245	0,5	0,1905501
	<i>ACS6</i>	At4g11280	-0,067	0,9095863	-0,211	0,6874027
	<i>ACS7</i>	At4g26200	0,581	0,0920129	1,704	1,47E-09
	<i>ACS8</i>	At4g37770	1,776	0,0042864	2,219	1,55E-05
	<i>ACS9/ETO3</i>	At3g49700	-0,586	0,2164371	-0,15	0,5209781
	<i>ACS11</i>	At4g08040	-1,223	0,0223648	-0,687	0,1989541
	<i>ETO1</i>	At3g51770	-0,212	0,355245	0,013	0,9511515
	<i>ETO2/ACS5</i>	At5g65800	-2,110	1,37E-07	-0,449	0,3273597

Supplementary Figure 8 – Anatomy of syncytia induced in wild-type (Col0) and *lsd1* (Col0) mutant roots. Light microscopy images of cross-sections of syncytia at 12 dpi induced in Col0 (A-C) and *lsd1* (Col0) (D-E). Cross-sections are taken through the widest part of syncytia, remote from the nematode head. Scalebars - 20 μ m.

