

**Supplementary Table S2. Differentially expressed genes in seedlings of *A. thaliana* exposed to *E. amylovora* mVOCs. Values are expressed as fold change with re-spect to unexposed plants.**

Locus tag	Gene symbol	Fold change	Gene description	Gene Ontology		
				Molecular function	Biological process	Cellular component
<b>UPREGULATED GENES</b>						
<i>AT1G03103</i>	<i>AT1G03103</i>	2.05	bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein			extracellular region
<i>AT1G06340</i>	<i>AT1G06340</i>	3.80	plant Tudor-like protein			
<i>AT1G07645</i>	<i>DSI-1VOC</i>	2.04	desiccation-induced 1VOC-like protein			extracellular region
<i>AT1G09860</i>	<i>PUP16</i>	2.27	purine permease 16	purine nucleobase transmembrane transporter activity	purine nucleobase transport	membrane
<i>AT1G09935</i>	<i>AT1G09935</i>	2.45	Phosphoglycerate mutase family protein	catalytic activity	biological process	
<i>AT1G09950</i>	<i>RAS1</i>	2.94	response to ABA and salt 1			
<i>AT1G12805</i>	<i>AT1G12805</i>	2.49	nucleotide binding protein			mitochondrion
<i>AT1G14880</i>	<i>PCR1</i>	2.47	cadmium resistance protein 1	mRNA binding	defense response to bacterium	cytoplasm
<i>AT1G15520</i>	<i>ABCG40</i>	2.57	pleiotropic drug resistance 12	efflux transmembrane transporter activity	abscisic acid transport	mitochondrion
<i>AT1G21990</i>	<i>AT1G21990</i>	4.93	F-box/RNI-like/FBD-like domains-containing protein			
<i>AT1G27461</i>	<i>AT1G27461</i>	2.88	uncharacterized protein	core promoter sequence-specific DNA binding	seed dormancy process	cytosol
<i>AT1G28260</i>	<i>AT1G28260</i>	2.10	Telomerase activating protein Est1			
<i>AT1G30950</i>	<i>UFO</i>	2.41	UNUSUAL FLORAL ORGANS F-box family protein	transcription factor binding	SCF-dependent proteasomal ubiquitin-	part of ubiquitin ligase complex



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				Molecular function	Biological process	Cellular component
					dependent protein catabolic process	
<i>AT1G50060</i>	<i>AT1G50060</i>	2.80	CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein			extracellular region
<i>AT1G54020</i>	<i>AT1G54020</i>	2.60	GDSL-like Lipase/Acyl hydrolase superfamily protein			
<i>AT1G57943</i>	<i>PUP17</i>	4.38	purine permease 17	purine nucleobase transmembrane transporter activity	purine nucleobase transport	membrane
<i>AT1G60570</i>	<i>AT1G60570</i>	2.06	Galactose oxidase/kelch repeat superfamily protein			cytoplasm
<i>AT1G64130</i>	<i>AT1G64130</i>	2.23	polyketide cyclase/dehydrase and lipid transport superfamily protein		macromolecule biosynthetic process	
<i>AT1G64160</i>	<i>DIR5</i>	4.24	Disease resistance-responsive (dirigent-like protein) family protein	guiding stereospecific synthesis activity	(-)-pinorexinol biosynthetic process	extracellular region
<i>AT1G65570</i>	<i>AT1G65570</i>	2.14	Pectin lyase-like superfamily protein	polygalacturonase activity	carbohydrate metabolic process	apoplast
<i>AT1G69818</i>	<i>AT1G69818</i>	2.05	defensin-like protein			extracellular region
<i>AT1G69920</i>	<i>GSTU12</i>	2.08	glutathione S-transferase TAU 12	glutathione transferase activity	toxin catabolic process	cytoplasm
<i>AT1G72260</i>	<i>THI2.1</i>	4.35	thionin 2.1	toxin activity	jasmonic acid mediated signaling pathway	extracellular region
<i>AT1G77655</i>	<i>AT1G77655</i>	2.55	uncharacterized protein		cellular component assembly	mitochondrion



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				Molecular function	Biological process	Cellular component
AT1G79800	ENODL7	3.58	early nodulin-like protein 7	electron transfer activity		membrane
AT2G02620	AT2G02620	2.80	cysteine/histidine-rich C1 domain-containing protein			nucleus
AT2G03460	AT2G03460	2.97	Galactose oxidase/kelch repeat superfamily protein			
AT2G04045	AT2G04045	2.71	Defensin-like (DEFL) family protein			extracellular region
AT2G11005	AT2G11005	2.02	glycine-rich protein			nucleus
AT2G14378	AT2G14378	2.48	egg cell-secreted-like protein (DUF1278)			
AT2G14610	PR1	2.10	pathogenesis-related protein 1		defense response	extracellular region
AT2G19550	AT2G19550	2.30	alpha/beta-Hydrolases superfamily protein			membrane
AT2G22060	AT2G22060	2.62	galactose oxidase/kelch repeat protein			mitochondrion
AT2G22460	AT2G22460	2.03	MIZU-KUSSEI-like protein		hydrotropism	nucleus
AT2G25685	SCRL17	2.15	SCR-like protein 17			
AT2G25890	AT2G25890	2.06	Oleosin-like protein			mitochondrion
AT2G26130	RSL1	2.46	RING/U-box protein with C6HC-type zinc finger	RNA-DNA hybrid ribonuclease activity	gibberellin mediated signaling pathway	nucleus
AT2G26450	AT2G26450	2.06	Plant invertase/pectin methylesterase inhibitor superfamily		cell differentiation	
AT2G29470	GSTU3	5.19	glutathione S-transferase TAU 3		toxin catabolic process	cytoplasm
AT2G30770	CYP71A13	4.16	cytochrome P450, family 71, subfamily A, polypeptide 13	indoleacetaldoxime dehydratase activity	camalexin biosynthetic process	endoplasmic reticulum lumen



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				Molecular function	Biological process	Cellular component
AT2G32275	AT2G32275	2.07	uncharacterized protein			nucleus
AT2G33720	AT2G33720	5.77	AP2/B3-like transcriptional factor family protein	DNA-binding transcription factor activity	response to lipid	nucleus
AT2G34090	MEE18	2.02	maternal effect embryo arrest 18 protein	LPPG:FO 2-phospho-L-lactate transferase activity	embryo development ending in seed dormancy	mitochondrion
AT2G38240	JAO4	2.61	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein	jasmonic acid hydrolase	defense response to fungus	cytoplasm
AT2G44240	AT2G44240	4.85	NEP-interacting protein (DUF239)		response to oxidative stress	extracellular region
AT3G10300	AT3G10300	2.06	Calcium-binding EF-hand family protein	calcium ion binding	hormone-mediated signaling pathway	nucleus
AT3G14415	GOX2	2.61	Aldolase-type TIM barrel family protein	(S)-2-hydroxy-acid oxidase activity	defense response to bacterium	apoplast
AT3G21500	DXS2	3.31	1-deoxy-D-xylulose 5-phosphate synthase 1	NOT 1-deoxy-D-xylulose-5-phosphate synthase activity	terpenoid biosynthetic process	chloroplast
AT3G23420	AT3G23420	3.12	F-box and associated interaction domain-containing protein			
AT3G27503	SCRL19	2.24	SCR-like 19		signal transduction	extracellular region
AT3G28220	AT3G28220	2.97	TRAF-like family protein		alpha-amino acid metabolic process	chloroplast envelope
AT3G30720	QQS	2.56	qua-quine starch	protein binding	negative regulation of starch metabolic process	cytosol
AT3G43572	AT3G43572	2.42	uncharacterized protein			
AT3G43850	AT3G43850	3.05	uncharacterized protein		defense response to bacterium	nucleus



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				Molecular function	Biological process	Cellular component
<i>AT3G49840</i>	<i>AT3G49840</i>	3.15	uncharacterized transmembrane protein		chromatin organization	nuclear membrane
<i>AT3G55970</i>	<i>JOX3</i>	3.72	jasmonate-regulated protein JRG21	jasmonic acid hydrolase	defense response to fungus	cytoplasm
<i>AT3G60120</i>	<i>BGLU27</i>	2.93	beta glucosidase 27	scopolin beta-glucosidase activity	carbohydrate metabolic process	nucleus
<i>AT3G62950</i>	<i>AT3G62950</i>	2.61	Thioredoxin superfamily protein	protein binding	negative regulation of transcription by RNA polymerase II	cytoplasm
<i>AT4G10265</i>	<i>AT4G10265</i>	4.76	Wound-responsive family protein		cellular response to hypoxia	nucleus
<i>AT4G11911</i>	<i>AT4G11911</i>	2.53	STAY-GREEN-like protein			
<i>AT4G14315</i>	<i>AT4G14315</i>	3.35	uncharacterized protein		regulation of developmental process	
<i>AT4G16590</i>	<i>CSLA01</i>	3.37	cellulose synthase-like A01	glycosyltransferase activity	anthocyanin-containing compound metabolic process	Golgi apparatus
<i>AT4G22650</i>	<i>AT4G22650</i>	4.88	lipid transfer protein			extracellular region
<i>AT4G23520</i>	<i>AT4G23520</i>	3.30	Cysteine proteinases superfamily protein			
<i>AT4G26390</i>	<i>AT4G26390</i>	2.20	Pyruvate kinase family protein	magnesium ion binding	glycolytic process	cytoplasm
<i>AT4G26880</i>	<i>AT4G26880</i>	2.41	Stigma-specific Stig1 family protein		tissue development	extracellular region
<i>AT4G30064</i>	<i>LCR61</i>	2.25	low-molecular-weight cysteine-rich 61		defense response to bacterium	extracellular region
<i>AT4G33230</i>	<i>AT4G33230</i>	2.43	Plant invertase/pectin methylesterase inhibitor superfamily		cell wall modification	



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				Molecular function	Biological process	Cellular component
<i>AT1G03880</i>	<i>CRU2</i>	0.20	cruciferin 2	nutrient reservoir activity	cellular response to abscisic acid stimulus	
<i>AT1G06280</i>	<i>LBD2</i>	0.34	LOB domain-containing protein 2			nucleus
<i>AT1G07430</i>	<i>HAI2</i>	0.49	highly ABA-induced PP2C protein 2	myosin phosphatase activity	negative regulation of abscisic acid-activated signaling pathway	chloroplast
<i>AT1G09080</i>	<i>BIP3</i>	0.49	Heat shock protein 70 (Hsp 70) family protein	ATP-dependent protein folding chaperone	pollen tube growth	chloroplast
<i>AT1G09510</i>	<i>AT1G09510</i>	0.15	NAD(P)-binding Rossmann-fold superfamily protein	alcohol dehydrogenase (NAD+) activity		
<i>AT1G18350</i>	<i>MKK7</i>	0.45	MAP kinase kinase 7	kinase activity	auxin polar transport	
<i>AT1G43890</i>	<i>RAB18</i>	0.23	RAB GTPASE HOMOLOG B18			
<i>AT1G45223</i>	<i>AT1G45223</i>	0.35	ECA1 gametogenesis related family protein			extracellular region
<i>AT1G52690</i>	<i>LEA7</i>	0.31	Late embryogenesis abundant protein (LEA) family protein		protein stabilization	cytosol
<i>AT1G57760</i>	<i>AT1G57760</i>	0.31	ECA1 gametogenesis related family protein			extracellular region
<i>AT1G60190</i>	<i>PUB19</i>	0.27	ARM repeat superfamily protein	ubiquitin-protein transferase activity	regulation of seed germination	chloroplast
<i>AT1G68250</i>	<i>AT1G68250</i>	0.18	uncharacterized protein			
<i>AT1G71000</i>	<i>AT1G71000</i>	0.44	Chaperone DnaJ-domain superfamily protein		defense response to fungus	cytoplasm
<i>AT1G72980</i>	<i>LBD7</i>	0.50	LOB domain-containing protein 7			nucleus



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				Molecular function	Biological process	Cellular component
<i>AT1G80260</i>	<i>emb1427</i>	0.49	Spc97 / Spc98 family of spindle pole body (SBP) component	gamma-tubulin binding	embryo development ending in seed dormancy	microtubule organizing center
<i>AT2G02700</i>	<i>AT2G02700</i>	0.30	cysteine/histidine-rich C1 domain-containing protein			nucleus
<i>AT2G03090</i>	<i>EXPA15</i>	0.40	expansin A15		plant-type cell wall loosening	extracellular region
<i>AT2G15010</i>	<i>AT2G15010</i>	0.24	Plant thionin		defense response	extracellular region
<i>AT2G18340</i>	<i>AT2G18340</i>	0.44	late embryogenesis abundant domain-containing protein		response to water deprivation	endoplasmic reticulum
<i>AT2G26150</i>	<i>HSFA2</i>	0.48	heat stress transcription factor A2	DNA-binding transcription factor activity	cellular response to hypoxia	nucleus
<i>AT2G28090</i>	<i>AT2G28090</i>	0.48	Heavy metal transport/detoxification superfamily protein			nucleus
<i>AT2G28860</i>	<i>CYP710A4</i>	0.32	cytochrome P450 710A4	C-22 sterol desaturase activity	sterol biosynthetic process	extracellular region
<i>AT2G29380</i>	<i>HAI3</i>	0.42	highly ABA-induced PP2C protein 3	myosin phosphatase activity		nucleus
<i>AT2G34370</i>	<i>AT2G34370</i>	0.38	Pentatricopeptide repeat (PPR) superfamily protein	zinc ion binding		mitochondrion
<i>AT2G42000</i>	<i>AtMT4a</i>	0.29	plant EC metallothionein family protein	zinc ion binding	zinc ion transport	cytoplasm
<i>AT2G42560</i>	<i>AT2G42560</i>	0.24	late embryogenesis abundant domain-containing protein		cold acclimation	cytosol
<i>AT2G47770</i>	<i>TSPO</i>	0.46	outer membrane tryptophan-rich sensory protein-like protein	heme binding	response to abscisic acid	Golgi apparatus
<i>AT3G01326</i>	<i>AT3G01326</i>	0.39	ECA1 gametogenesis related family protein			



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				Molecular function	Biological process	Cellular component
<i>AT3G02480</i>	<i>AT3G02480</i>	0.35	Late embryogenesis abundant protein (LEA) family protein		negative regulation of leaf senescence	cytosol
<i>AT3G11480</i>	<i>BSMT1</i>	0.30	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	S-adenosyl-L-methionine:benzoic acid carboxyl methyl transferase activity	defense response	nucleus
<i>AT3G14440</i>	<i>NCED3</i>	0.49	9-cis-epoxycarotenoid dioxygenase 3	9-cis-epoxycarotenoid dioxygenase activity	abscisic acid biosynthetic process	chloroplast
<i>AT3G17520</i>	<i>AT3G17520</i>	0.42	late embryogenesis abundant protein (LEA) family protein		acquisition of seed longevity	endoplasmic reticulum
<i>AT3G20160</i>	<i>GGPPS8</i>	0.40	Terpenoid synthases superfamily protein	dimethylallyltranstransferase activity	farnesyl diphosphate biosynthetic process	chloroplast
<i>AT3G22640</i>	<i>PAP85</i>	0.37	cupin family protein		response to virus	extracellular region
<i>AT3G25810</i>	<i>AT3G25810</i>	0.39	Terpenoid cyclases/Protein prenyltransferases superfamily protein	(4S)-limonene synthase activity	monoterpene biosynthetic process	chloroplast
<i>AT3G27025</i>	<i>AT3G27025</i>	0.48	uncharacterized protein		regulation of auxin polar transport	chloroplast
<i>AT3G49620</i>	<i>DIN11</i>	0.47	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein		cellular response to starvation	cytoplasm
<i>AT3G54490</i>	<i>RPB5E</i>	0.34	RNA polymerase II fifth largest subunit, E	DNA binding	DNA-templated transcription	nucleus
<i>AT3G58390</i>	<i>AT3G58390</i>	0.26	Eukaryotic release factor 1 (eRF1) family protein	protein binding	nuclear-transcribed mRNA catabolic process	nucleus



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AT4G03480	AT4G03480	0.31	Ankyrin repeat family protein		defense response to bacterium	chloroplast
AT4G09600	GASA3	0.32	GAST1 protein homolog 3		response to gibberellin	extracellular region
AT4G10250	ATHSP22.0	0.40	HSP20-like chaperones superfamily protein		cellular response to hypoxia	chloroplast
AT4G27140	SESA1	0.07	seed storage albumin 1		defense response	extracellular region
AT4G27150	SESA2	0.12	seed storage albumin 2			extracellular region
AT4G27160	SESA3	0.30	seed storage albumin 3	protein histidine kinase binding	seed maturation	extracellular region
AT4G28520	CRU3	0.09	cruciferin 3	nutrient reservoir activity	cellular response to abscisic acid stimulus	protein body
AT4G33467	AT4G33467	0.20	uncharacterized protein		response to abscisic acid	nucleus
AT4G33905	AT4G33905	0.47	Peroxisomal membrane 22 kDa		response to abscisic acid	mitochondrion
AT4G37990	ELI3-2	0.47	cinnamyl alcohol dehydrogenase 8	aryl-alcohol dehydrogenase (NADP+) activity	lignin biosynthetic process	cytoplasm
AT5G03210	DIP2	0.42	E3 ubiquitin-protein ligase		defense response to virus	nucleus
AT5G04120	AT5G04120	0.41	Phosphoglycerate mutase family protein	L-phosphoserine phosphatase activity	D-serine biosynthetic process	cytoplasm
AT5G04380	AT5G04380	0.17	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein			nucleus



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AT5G05220	AT5G05220	0.15	uncharacterized protein		abscisic acid-activated signaling pathway	chloroplast
AT5G06760	LEA4-5	0.23	late embryogenesis abundant protein 4-5	osmosensor activity	response to osmotic stress	cytosol
AT5G07260	AT5G07260	0.48	START (StAR-related lipid-transfer) lipid-binding domain-containing protein	lipid binding	somatic embryogenesis	nucleus
AT5G24080	AT5G24080	0.49	Protein kinase superfamily protein	protein serine/threonine kinase activity	response to abscisic acid	extracellular region
AT5G27260	AT5G27260	0.47	Myb/SANT-like DNA-binding domain protein			nucleus
AT5G34905	AT5G34905	0.41	ECA1 gametogenesis family protein			chloroplast
AT5G35660	AT5G35660	0.39	glycine-rich protein			
AT5G40790	AT5G40790	0.35	uncharacterized protein		negative regulation of DNA-templated transcription initiation	nucleus
AT5G42797	LCR28	0.39	low-molecular-weight cysteine-rich 28			
AT5G43840	HSFA6A	0.48	heat stress transcription factor A6A	DNA-binding transcription factor activity	regulation of DNA-templated transcription	nucleus
AT5G45630	AT5G45630	0.40	senescence regulator		response to abscisic acid	cytoplasm
AT5G50360	AT5G50360	0.27	von Willebrand factor A domain protein		negative regulation of DNA-templated transcription initiation	nucleus



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<i>AT5G50600</i>	<i>HSD1</i>	0.28	hydroxysteroid dehydrogenase 1	11-beta-hydroxysteroid dehydrogenase (NADP+) activity	response to abscisic acid	chloroplast
<i>AT5G52300</i>	<i>LTl65</i>	0.36	low-temperature-induced 65		response to abscisic acid	cytoplasm
<i>AT5G53710</i>	<i>AT5G53710</i>	0.49	uncharacterized protein		response to abscisic acid	mitochondrion
<i>AT5G53905</i>	<i>AT5G53905</i>	0.43	prolamin-like protein		macromolecule biosynthetic process	nucleus
<i>AT5G54740</i>	<i>SESA5</i>	0.02	seed storage albumin 5		pollen development	extracellular region
<i>AT5G65800</i>	<i>ACS5</i>	0.43	1-aminocyclopropane-1-carboxylate synthase 5	1-aminocyclopropane-1-carboxylate synthase activity	ethylene biosynthetic process	cytoplasm