

**Table S4.** Potato sprouts' metabolites with the highest fluctuation 72 h after infection by *Rhizoctonia solani* as revealed performing metabolomics analyses.

The connections between those metabolites with enzymes catalyzing their biosynthesis and corresponding encoding genes were based on information retrieved from the databases PotatoCyc and KEGG. In cases where no hits were found in these databases, searches were performed in the PlantCyc database, and results are displayed for other plant species. Linking to the associated on-line sources is provided by clicking on the bold highlighted codes/words holding the shift button.

Metabolite(s)	Catalyzing enzyme(s)	Biosynthetic pathway(s)	Accession number		Organism <sup>a</sup>
			PotatoCyc	PlantCyc	
$\beta$ -alanine	glutamate decarboxylase (E.C. 4.1.1.15)	$\beta$ -alanine metabolism [ <b>rn00410</b> ]	<b>SGNU-269741</b> , <b>SGNU-274223</b> ,		<i>S. tuberosum</i>
		pantothenate and CoA biosynthesis [ <b>ec00770</b> ]	<b>SGNU-277090</b> , <b>SGNU-287538</b> <b>SGNU-287539</b> , <b>SGNU-287540</b> , <b>SGNU-293317</b>		
	aspartate 1-decarboxylase (E.C. 4.1.1.11)				
	aldehyde dehydrogenase (NAD <sup>+</sup> ) (E.C. 1.2.1.3)	$\beta$ -alanine metabolism [ <b>rn00410</b> ]	<b>SGNU-270085</b>		<i>S. tuberosum</i>
	aminobutyraldehyde dehydrogenase (E.C. 1.2.1.19)				
beta-ureidopropionase (E.C. 3.5.1.6)		pyrimidine metabolism [ <b>ec00240</b> ],	<b>JGI-819740</b>		<i>P. trichocarpa</i>
		$\beta$ -alanine metabolism [ <b>rn00410</b> ],	<b>LOC_Os07g30170.1</b>		<i>O. sativa</i>
		pantothenate and CoA biosynthesis	<b>PYD3</b>		<i>A. thaliana</i>
		[ <b>ec00770</b> ]	<b>TC100937</b> , <b>TC100938</b> , <b>TC108524</b>		<i>M. truncatula</i>
$\beta$ -alanine aminotransferase (E.C. 2.6.1.18)		$\beta$ -alanine metabolism [ <b>rn00410</b> ], propanoate metabolism [ <b>rn00640</b> ]	<b>AT-3G08860.1</b>		<i>A. thaliana</i>
N-acetyl-beta-alanine deacetylase (E.C. 3.5.1.21)		$\beta$ -alanine metabolism [ <b>rn00410</b> ]			
aminoacyl-lysine dipeptidase (E.C. 3.4.13.4)					

carnosine synthase (E.C. 6.3.2.11)

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guanidinopropionase (E.C. 3.5.3.17)

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aminoacylhistidine dipeptidase

(E.C. 3.4.13.3)

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pantothenate amidohydrolase

pantothenate and CoA biosynthesis

(E.C. 3.5.1.22)

[**rn00770**]

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anserinase (E.C. 3.4.13.5)

$\beta$ -alanine metabolism [**rn00410**]

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4-aminobutanoic acid (GABA)

glutamate decarboxylase (E.C. 4.1.1.15)

alanine, aspartate and glutamate metabolism

[**rn00250**]

**SGN-U269741**, **SGN-U274223**,  
**SGN-U277090**, **SGNU-287538**,  
**SGNU-287539**, **SGNU-287540**  
**SGNU-293317**

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*S. tuberosum*

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aldehyde dehydrogenase (NAD+)

arginine and proline metabolism [**rn00330**]

**SGNU-270085**

*S. tuberosum*

(E.C. 1.2.1.3)

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guanidinobutyrase (E.C. 3.5.3.7)

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aminoacylhistidine dipeptidase

(E.C. 3.4.13.3)

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aminobutyraldehyde dehydrogenase (E.C. 1.2.1.19)

arginine and proline metabolism [**rn00330**]

$\beta$ -alanine metabolism [**rn00410**]

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feruloyl esterase (E.C. 3.1.1.73)

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gamma-glutamyl-gamma-aminobutyrate

arginine and proline metabolism [**rn00330**]

hydrolase (E.C. 3.5.1.94)

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$\gamma$ -chaconine

UDP-glucose glucotransferase St-SGT2

steroidal glycoalkaloid biosynthesis

**SGNU293662**, **SGNU283603**

*S. tuberosum*

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(E.C. 2.4.1.-)

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cinnamic acid

phenylalanine ammonia-lyase

phenylalanine metabolism [**rn00360**]

**SGN-U312619**, **SGN-U312620**,

*S. lycopersicum*

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(E.C. 4.3.1.24)

nitrogen metabolism [**rn00910**]

**SGN-U312621**, **SGN-U333748**,

phenylpropanoid biosynthesis [**ko00940**]

**SGN-U333750**, **SGN-U312617**,

**SGN-U312618**, **SGN-U325698**,

**SGN-U330655**, **SGN-U333749**,

**SGN-U333751**, **SGN-U341447**,

*A. thaliana*

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	phenylalanine/tyrosine ammonia-lyase; PTAL (E.C. 4.3.1.25)	phenylalanine metabolism [ <b>rn00360</b> ] nitrogen metabolism [ <b>rn00910</b> ] phenylpropanoid biosynthesis [ <b>ko00940</b> ]		
	2-enoate reductase (E.C. 1.3.1.31)	phenylalanine metabolism [ <b>rn00360</b> ]		
	cinnamoyl-CoA:phenyllactate CoA- transferase (E.C. 2.8.3.17) FldA	tropane, piperidine and pyridine alkaloid biosynthesis [ <b>rn00960</b> ]		
colneleic acid	9-divinyl ether synthase (St), St-StDES	<b>divinyl ether biosynthesis I (9-LOX)</b>	G-9759	<i>S. tuberosum</i>
colnelenic acid	9-divinyl ether synthase (St), St-StDES	<b>divinyl ether biosynthesis I (9-LOX)</b>	G-9759	<i>S. tuberosum</i>
ferulic acid	4-coumarate--CoA ligase (E.C. 6.2.1.12)	phenylpropanoid biosynthesis [ <b>rn00940</b> ]	<b>SGNU269219, SGNU269220</b> <b>SGNU269221, SGNU269458,</b> <b>SGNU269459, SGNU271690,</b> <b>SGNU273689, SGNU276387,</b> <b>SGNU279444, SGNU281563,</b> <b>SGNU281995, SGNU287264,</b> <b>SGNU287264, SGNU287265,</b> <b>SGNU287266, SGNU292841,</b> <b>SGNU293253, SGNU294251</b> <b>SGNU296205, SGNU297674</b>	<i>S. tuberosum</i>
	caffeic acid 3-O-methyltransferase (E.C. 2.1.1.68)	phenylpropanoid biosynthesis [ <b>ko00940</b> ]	<b>1481.m00053, BE319602</b> <b>BG646036, BI311272,</b> <b>OMT1, TC100776,</b> <b>TC100776, TC102340,</b> <b>TC98964</b>	<i>M. truncatula</i>
	feruloyl esterase (E.C. 3.1.1.73)	phenylpropanoid biosynthesis [ <b>ko00940</b> ]		
	deacylase (E.C. 3.5.1.71)	phenylpropanoid biosynthesis [ <b>ko00940</b> ]		
	caffeic acid 3-O-methyltransferase (E.C. 2.1.1.68)	phenylpropanoid biosynthesis [ <b>rn00940</b> ]/Suberin biosynthesis	<b>1481.m00053</b> <b>BE319602</b> <b>BG646036</b> <b>BI311272</b>	<i>M. truncatula</i>

TC100776

TC102340

TC98964

OMT1

*A. thaliana*

N-feruloylglycine deacylase

(E.C. 3.5.1.71)

coniferyl-aldehyde dehydrogenase

phenylpropanoid biosynthesis [rn00940]

(E.C. 1.2.1.68)

trans-feruloyl-CoA synthase

(E.C. 6.2.1.34)

feruloyl esterase (E.C. 3.1.1.73)

ferulate-5-hydroxylase (E.C. 1.14.-.-)

sinapate 1-glucosyltransferase

AT3G21560, AT4G15480,

*A. thaliana*

(E.C. 2.4.1.120)

AT4G15490, AT4G15500,

SGT1

*B. napus**R. sativus*

hydroxycinnamate 4-beta-

glucosyltransferase (E.C. 2.4.1.126)

feruloyltyramine

tyramine N-feruloyltransferase

suberin biosynthesis

SGNU269846, SGNU269847,

*S. tuberosum*

(E.C. 2.3.1.110)

SGNU283523, SGNU287587,

SGNU287588

fumaric acid

**fumarate hydratase** (E.C. 4.2.1.2)

phenylalanine degradation I Citrate cycle

SGNU273248

*S. tuberosum*

(TCA cycle) [ko00020]

**fumarylacetoacetase** (E.C. 3.7.1.2)

phenylalanine degradation I

SGNU290011, SGNU290010,

*S. tuberosum*

SGNU290009, SGNU278057,

SGNU271822

**succinate dehydrogenase** (E.C. 1.3.99.1)

citrate cycle (TCA cycle) [ko00020],

butanoate metabolism [rn00650], reductive

carboxylate cycle (CO<sub>2</sub> fixation) [rn00720],

benzoate degradation via CoA ligation

[rn00632]

fumarate reductase (NADH)

(E.C. 1.3.1.6)

aspartate ammonia-lyase (E.C. 4.3.1.1)	alanine, aspartate and glutamate metabolism [rn00250], nitrogen metabolism [rn00910]	<b>SGNU269166, SGNU274897</b>	<i>S. tuberosum</i>
glutamin-(asparagin)-ase (E.C. 3.5.1.38)			
adenylosuccinate lyase (E.C. 4.3.2.2)	purine metabolism [rn00230] alanine, aspartate and glutamate metabolism [rn00250]	<b>SGNU284950, SGNU290676</b>	<i>S. tuberosum</i>
acylpyruvate hydrolase (E.C. 3.7.1.5)	tyrosine metabolism [rn00350]		
argininosuccinate lyase (E.C. 4.3.2.1)	alanine, aspartate and glutamate metabolism [rn00250], arginine and proline metabolism [rn00330]	<b>SGNU280046, SGNU280873</b>	<i>S. tuberosum</i>
maleate isomerase (E.C. 5.2.1.1)	butanoate metabolism [rn00650], nicotinate and nicotinamide metabolism [rn00760]		
carboxymethyloxysuccinate lyase (E.C. 4.2.99.12)			
fumarylacetoacetase (E.C. 3.7.1.2)	tyrosine metabolism [rn00350], styrene degradation [rn00643]	<b>SGNU271822, SGNU278057, SGNU290009, SGNU290010, SGNU290011</b>	<i>S. tuberosum</i>
fumaric acid	succinate dehydrogenase (E.C. 1.3.5.1)	citrate cycle (TCA cycle) [rn00020]	<b>AT2G18450, AT3G27380, AT5G65165 BQ138479 JGI-219180, JGI-593943 LOC_Os07g04240.1, LOC_Os09g20440.1</b> <i>A. thaliana</i> <i>M. truncatula</i> <i>P. trichocarpa</i> <i>O. sativa</i>
adenylosuccinate lyase (E.C. 4.3.2.2)	purine metabolism [rn00230]	<b>SGNU284950, SGNU290676</b>	<i>S. tuberosum</i>
benzylsuccinate synthase (E.C. 4.1.99.11)	benzoate degradation via CoA ligation [rn00632]		
2-hydroxy-6-ketono-2,4-dienedioic acid hydrolase (E.C. 3.7.1.-)	phenylalanine metabolism [rn00360]		
lyases (E.C. 4.1.99.-)	1- and 2-Methylnaphthalene degradation		

		<b>[rn00624]</b>		
D-galactaric acid	uronate dehydrogenase (E.C. 1.1.1.203)	ascorbate and aldarate metabolism		
	galactarate dehydratase (E.C. 4.2.1.42)	<b>[ko00053]</b>		
gluconic acid	gluconolactonase (E.C. 3.1.1.17.)	pentose phosphate pathway		
		<b>[ko00030]</b>		
	gluconate 2-dehydrogenase (E.C. 1.1.1.215.)			
glyceric acid	glycerate dehydrogenase (E.C. 1.1.1.29)	glycine, serine and threonine metabolism <b>[rn00260]</b>	<b>SGNU272307, SGNU288419</b>	<i>S. tuberosum</i>
		glyoxylate and dicarboxylate metabolism <b>[rn00630]</b>		
	hydroxypyruvate reductase (E.C. 1.1.1.81)		<b>SGNU283355, SGNU286066</b>	<i>S. tuberosum</i>
	glyoxylate/hydroxypyruvate reductase A (E.C. 1.1.1.79)			
	glyoxylate reductase (E.C. 1.1.1.26)			
	glyoxylate reductase (NADP+) (E.C. 1.1.1.79)			
	3-phosphoglycerate phosphatase (E.C. 3.1.3.38)	glycine, serine and threonine metabolism <b>[rn00260]</b>		
	glycerate kinase (E.C. 2.7.1.31)	glycine, serine and threonine metabolism <b>[rn00260]</b> , glycerolipid metabolism <b>[rn00561]</b> , glyoxylate and dicarboxylate metabolism <b>[rn00630]</b>	<b>AT1G80380</b> <b>JGI-415047, JGI-829520</b>	<i>A. thaliana</i> <i>P. trichocarpa</i>
	2-hydroxy-3-oxopropionate reductase (E.C. 1.1.1.60)	glyoxylate and dicarboxylate metabolism <b>[rn00630]</b>	<b>SGNU278460, SGNU285986</b>	<i>S. tuberosum</i>
	phosphoglycerate phosphatase (E.C. 3.1.3.20)			
	oxaloglycolate reductase (decarboxylating) (E.C. 1.1.1.92)	glyoxylate and dicarboxylate metabolism <b>[rn00630]</b>		
	tartrate decarboxylase (E.C. 4.1.1.73)			

	aldehyde dehydrogenase (NAD+) (E.C. 1.2.1.3)	glycerolipid metabolism [rn00561]	SGNU270085	<i>S. tuberosum</i>
	kinases (E.C. 2.7.1.-)		SGNU271185, SGNU274832, SGNU276713, SGNU276826, SGNU277635, SGNU277961, SGNU281005, SGNU281971, SGNU282732, SGNU284158, SGNU286178, SGNU288877, SGNU292150, SGNU295240	<i>S. tuberosum</i>
linoleic acid	lipoxygenase (E.C. 1.13.11.12)	linoleic acid metabolism [rn00591]	SGNU268108, SGNU268109, SGNU268110, SGNU269397, SGNU275813, SGNU283623, SGNU285664, SGNU286657, SGNU286658, SGNU286659, SGNU291453, SGNU294974, SGNU296125	<i>S. tuberosum</i>
	arachidonate 15-lipoxygenase (E.C. 1.13.11.33)			
	linoleate isomerase (E.C. 5.2.1.5)			
	linoleate 11-lipoxygenase (E.C. 1.13.11.45)			
	cytochrome P450 1.14.14.1)		SGNU276200, SGNU291486	<i>S. tuberosum</i>
	arachidonate 5-lipoxygenase (E.C. 1.13.11.34)			
	linoleate (8R)-dioxygenase (E.C. 1.13.11.44)			
	linoleoyl-CoA desaturase (E.C. 1.14.19.3)			
	phospholipase A (E.C. 3.1.1.4)		SGNU278771, GNU278772, SGNU278773, SGNU278774, SGNU278776, SGNU278777,	<i>S. tuberosum</i>

SGNU278781, SGNU283241,

SGNU283241, SGNU289839,

SGNU289846

	palmitoyl-CoA hydrolase (E.C. 3.1.2.2)		<b>JGI-663966, JGI-675790</b>	<i>P. trichocarpa</i>
oxalic acid	<b>oxalate oxidase</b> (E.C. 1.2.3.4)	glyoxylate and dicarboxylate metabolism [ko00630]		
	oxaloacetase (E.C. 3.7.1.1)			
	glyoxylate oxidase (E.C. 1.2.3.5)			
	oxalate decarboxylase (E.C. 4.1.1.2)			
	ascorbate 2,3-dioxygenase (E.C. 1.13.11.13)			
	oxalyl coenzyme A synthetase (E.C. 6.2.1.8)			
	oxalate coenzyme A-transferase (E.C. 2.8.3.2)			
	formyl-CoA transferase (E.C. 2.8.3.16)			
pipecolic acid	saccharopine dehydrogenase (NAD+, L- glutamate forming) (E.C. 1.5.1.9)	tropane, piperidine and pyridine alkaloid biosynthesis [rn00960]	<b>JGI-739274, JGI-739281</b>	<i>P. trichocarpa</i>
	saccharopine dehydrogenase (NAD+, L- lysine forming) (E.C. 1.5.1.7)			
	lysine 6-dehydrogenase (E.C. 1.4.1.18)			
pyroglutamic acid	aminoacyltransferase (E.C. 2.3.2.-)	glutathione metabolism [rn00480], butirosin and neomycin biosynthesis [rn00524]	<b>SGNU278180, SGNU279602, SGNU293093</b>	<i>S. tuberosum</i>
sesquiterpenoid phytoalexins	vetispiradiene synthase, VS1 (E.C. 4.2.3.21)	biosynthesis of alkaloids derived from terpenoid and polyketide [map01066]/sesquiterpenoid phytoalexins biosynthesis	<b>VS1</b>	<i>H. muticus</i>
sesquiterpenoid phytoalexins & steroidal glycoalkaloids	3-hydroxy-3-methylglutaryl-CoA reductase, HMG1 (E.C. 1.1.1.34)	terpenoid backbone biosynthesis [map00900], biosynthesis of alkaloids derived from terpenoid and polyketide [map01066]	<b>AW687494, BE124699, BG644380, BQ140041, CB892390, TC102857, TC106632</b>	<i>M. truncatula</i>



			HMG1	<i>A. thaliana</i>
			JGI-595031, JGI-798252,	<i>P. trichocarpa</i>
			JGI-820962, JGI-829982,	
			JGI-831722, JGI-834149	
			LOC_Os01g31610.1,	<i>O. sativa</i>
			LOC_Os01g34270.1,	
			LOC_Os02g48330.1,	
			LOC_Os03g38870.1,	
			LOC_Os05g02990.1,	
			LOC_Os05g38960.1,	
			LOC_Os08g40180.1,	
			LOC_Os09g31970.1	
sesquiterpenoid	1-deoxy-D-xylulose-5-phosphate	terpenoid backbone biosynthesis [ko00900],	SGNU270961, SGNU270962,	<i>S. tuberosum</i>
phytoalexins & steroidal glycoalkaloids	reductoisomerase, dxr (E.C. 1.1.1.267)	biosynthesis of alkaloids derived from terpenoid and polyketide [map01066]	SGNU270963	
sesquiterpenoid	farnesyl diphosphate synthase, ispA	terpenoid backbone biosynthesis [ko00900],	SGNU269148, SGNU269149,	<i>S. tuberosum</i>
phytoalexins & steroidal glycoalkaloids	(E.C. 2.5.1.1 2.5.1.10)	biosynthesis of alkaloids derived from terpenoid and polyketide [map01066]	SGNU287228, SGNU287229	
$\gamma$ -solanine	UDP-galactose galactosyltransferase St- SGT1 (E.C. 2.4.1.-)	biosynthesis of alkaloids derived from terpenoid and polyketide [map01066]	SGNU269176, SGNU270492, SGNU270493, SGNU275270, SGNU275759, SGNU277244, SGNU278383, SGNU279601, SGNU280444, SGNU283603, SGNU287245, SGNU289954, SGNU290507, SGNU293303 SGNU293662, SGNU298857	<i>S. tuberosum</i>
steroidal glycoalkaloids	farnesyl-diphosphate farnesyltransferase, FDFT1 (E.C. 2.5.1.21)	steroid biosynthesis [ko00100], biosynthesis of alkaloids derived from terpenoid and polyketide [map01066]	SGNU270583, SGNU287853	<i>S. tuberosum</i>

steroidal	squalene monooxygenase, SQLE (E.C.	steroid biosynthesis [ <b>ko00100</b> ],	<b>SGNU291972, SGNU269909</b>	<i>S. tuberosum</i>
glycoalkaloids	1.14.99.7)	biosynthesis of alkaloids derived from terpenoid and polyketide [ <b>map01066</b> ]		
succinic acid	succinyl-CoA synthetase alpha subunit, LSC1 (E.C. 6.2.1.5)	citrate cycle (TCA cycle) [ <b>ko00020</b> ], propanoate metabolism [ <b>ko00640</b> ], C5-branched dibasic acid metabolism [ <b>ko00660</b> ], reductive carboxylate cycle (CO <sub>2</sub> fixation) [ <b>ko00720</b> ]	<b>SGNU268134, SGNU270065,</b> <b>SGNU287678, SGNU287677,</b> <b>SGNU270066</b>	<i>S. tuberosum</i>
succinate dehydrogenase (ubiquinone) flavoprotein subunit (E.C. 1.3.5.1)	flavoprotein	citrate cycle (TCA cycle) [ <b>ko00020</b> ], oxidative phosphorylation [ <b>ko00190</b> ]	<b>AT2G18450, AT3G27380,</b> <b>AT5G65165</b> <b>BQ138479</b> <b>JGI-219180, JGI-593943</b> <b>LOC_Os07g04240.1</b> <b>LOC_Os09g20440.1</b>	<i>A. thaliana</i> <i>M. truncatula</i> <i>P. trichocarpa</i> <i>O. sativa</i>
succinate dehydrogenase subunit, sdhA (E.C. 1.3.99.1)	flavoprotein	citrate cycle (TCA cycle) [ <b>ko00020</b> ], oxidative phosphorylation [ <b>ko00190</b> ] benzoate degradation via CoA ligation [ <b>ko00632</b> ], butanoate metabolism [ <b>ko00650</b> ], reductive carboxylate cycle (CO <sub>2</sub> fixation) [ <b>ko00720</b> ]		
succinyl-CoA synthetase alpha subunit, LSC1 (E.C. 6.2.1.4 6.2.1.5)	flavoprotein	citrate cycle (TCA cycle) [ <b>ko00020</b> ], propanoate metabolism [ <b>ko00640</b> ]	<b>SGNU283178, SGNU-268134,</b> <b>SGNU270065, SGNU287678,</b> <b>SGNU-287677, SGNU-270066</b>	<i>S. tuberosum</i>

<sup>a</sup> *A. thaliana*; *Arabidopsis thaliana* (Arabidopsis), *B. napus*; *Brassica napus* (rapeseed), *H. muticus*; *Hyoscyamus muticus* (henbane), *M. truncatula*; *Medicago truncatula* (barrel clover), *O. sativa*; *Oryza sativa* (rice), *P. trichocarpa*; *Populus trichocarpa* (black cottonwood), *R. sativus*; *Raphanus sativus* (radish), *S. lycopersicum*; *Solanum lycopersicum* (tomato), *S. tuberosum*; *Solanum tuberosum* (potato).