

Additional file 1. Table S1. *Lactobacillus plantarum* WCFS1 genes with differential expression in presence of gallic acid.

Locus Tag	Locus	Description	COG main functional category	Fold Change ^{a,b}		Subcellular Localization Prediction ^c	Pathway Prediction ^c
				1.5 mM	15 mM		
<i>lp_0226</i>	<i>nagB</i>	glucosamine-6-phosphate isomerase/deaminase	Carbohydrate transport and metabolism		2.03	Intracellular	
<i>lp_0250</i>	-	dihydroorotase	General function prediction only	2.06			
<i>lp_0271</i>	<i>lpdB</i>	aromatic acid carboxylase, subunit B	Coenzyme transport and metabolism	19.61	26.30	Intracellular	
<i>lp_0272</i>	<i>lpdD</i>	aromatic acid carboxylase, subunit D		18.84	23.98	Intracellular	
<i>lp_0274</i>	-	TetR family transcriptional regulator	Transcription	4.43	4.15	Intracellular	
<i>lp_0349</i>	<i>amtB</i>	ammonium transport protein	Inorganic ion transport and metabolism	-3.14	-7.02	Multi-transmembrane	Sec-(SPI)
<i>lp_0728</i>	<i>groEL</i>	GroEL chaperonine	Post-translational modification, protein turnover, and chaperones	-2.14		Intracellular	
<i>lp_0747</i>	<i>pstD</i>	phosphate ABC transporter permease	Inorganic ion transport and metabolism		-2.16	Multi-transmembrane	Sec-(SPI)
<i>lp_0748</i>	<i>pstC</i>	phosphate ABC transporter permease	Inorganic ion transport and metabolism		-2.16	Multi-transmembrane	Sec-(SPI)
<i>lp_0802</i>	<i>glnPH1</i>	glutamine ABC transporter, substrate binding and permease protein	Amino acid transport and metabolism		-3.13	Multi-transmembrane	Sec-(SPI)
<i>lp_0803</i>	<i>glnQ1</i>	glutamine ABC transporter, ATP-binding	Amino acid transport and metabolism	-2.26	-2.20	Intracellular	
<i>lp_0822</i>	<i>glmS1</i>	glutamine-fructose-6-phosphate transaminase	Cell wall/membrane biogenesis		-3.47	Intracellular	
<i>lp_1061</i>	<i>rpsK</i>	30S ribosomal protein S11	Translation		-2.16	Intracellular	
<i>lp_1424</i>	-	oxidoreductase (putative)	General function prediction only		3.44	Intracellular	
<i>lp_1425</i>	-	fumarate reductase, flavoprotein subunit precursor	Energy production and conversion		3.11	Intracellular	
<i>lp_1580</i>	<i>glnR</i>	glutamine synthetase repressor	Transcription		-2.10	Intracellular	
<i>lp_1581</i>	<i>glnA</i>	glutamate--ammonia ligase	Amino acid transport and metabolism		-2.45	Intracellular	
<i>lp_1590</i>	-	integral membrane protein			2.70	Intracellular/TMH start after 60	Possibly Sec-
<i>lp_1948</i>	-	transcription regulator	Transcription		2.90	Intracellular	
<i>lp_1949</i>	-	integral membrane protein			2.78	Multi-transmembrane	Sec-(SPI)
<i>lp_2105</i>	<i>cps4D</i>	UDP N-acetyl glucosamine 4-epimerase, NAD dependent	Multifunctional: Cell envelope biogenesis, outer membrane Carbohydrate transport and metabolism		-2.37	Intracellular	
<i>lp_2229</i>	-	beta-lactamase superfamily metal-dependent hydrolase	General function prediction only		-4.13	Intracellular	
<i>lp_2312</i>	<i>glnH2</i>	glutamine/histidine ABC transporter,	Amino acid transport and metabolism		2.34	Lipid anchored	Sec-(SPII)

		substrate binding protein					
<i>lp_2363</i>	<i>atpC</i>	H(+)-transporting two-sector ATPase, epsilon subunit	Energy production and conversion		-2.90	Intracellular	
<i>lp_2659</i>	<i>xpkA</i>	xylulose-5-P phosphoketolase / fructose-6-P phosphoketolase	Carbohydrate transport and metabolism		-2.35	Intracellular	
<i>lp_2739</i>	-	ABC transporter, ATP-binding protein	Defense mechanisms		-7.25	Intracellular	
<i>lp_2740</i>	-	ABC transporter, permease protein	Secondary metabolites biosynthesis, transport and catabolism		-6.71	Multi-transmembrane	Sec-(SPI)
<i>lp_2741</i>	-	membrane protein			-2.62	Multi-transmembrane	Sec-(SPI)
<i>lp_2742</i>	-	GntR family transcriptional regulator	Transcription		-3.37	Intracellular	
<i>lp_2743</i>	-	ABC transporter ATP-binding protein	Inorganic ion transport and metabolism / Defense mechanisms		-2.67	Intracellular	
<i>lp_2744</i>	-	ABC transporter permease			-2.14	Multi-transmembrane	Sec-(SPI)
<i>lp_2776</i>	<i>dsdA</i>	D-serine dehydratase	Amino acid transport and metabolism	-2.08		Intracellular	
<i>lp_2830</i>	<i>aspA</i>	aspartate ammonia-lyase	Amino acid transport and metabolism		-2.12	Intracellular	
<i>lp_2940</i>	-	cell surface protein precursor, LPXTG-motif cell wall anchor		10.09	14.33	LPxTG Cell-wall anchored	Sec-(SPI)
<i>lp_2943</i>	-	cation transport protein	Inorganic ion transport and metabolism	51.95	73.41	Multi-transmembrane	Sec-(SPI)
<i>lp_2945</i>	<i>lpdC</i>	aromatic acid carboxylase, subunit C	Coenzyme transport and metabolism	108.47	272.09	Intracellular	
<i>lp_2949</i>	-	integral membrane protein		2.03		Multi-transmembrane	Sec-(SPI)
<i>lp_2954</i>	-	membrane protein			2.92	Multi-transmembrane	Sec-(SPI)
<i>lp_2956</i>	<i>tanLpl</i>	tannase (tannin acylhydrolase)	Lipid transport and metabolism	4.24	10.34	Intracellular	
<i>lp_3012</i>	-	oxidoreductase (putative)	Cell wall/membrane/envelope biogenesis / Carbohydrate transport and metabolism	2.49		Intracellular	
<i>lp_3015</i>	-	extracellular protein	Cell wall/membrane biogenesis		-3.43	Secretory(released) (with CS)	Sec-(SPI)
<i>lp_3270</i>	<i>purA</i>	adenylosuccinate synthase	Nucleotide transport and metabolism		-2.96	Intracellular	
<i>lp_3271</i>	<i>guaC</i>	GMP reductase	Nucleotide transport and metabolism		-3.00	Intracellular	
<i>lp_3659</i>	<i>rbsD</i>	D-ribose mutarotase	Carbohydrate transport and metabolism		-2.18	Intracellular	
<i>lp_3660</i>	<i>rbsK1</i>	ribokinase	Carbohydrate transport and metabolism		-2.08	Intracellular	

^a Fold change refers to growth in MRS supplemented with gallic acid 1.5 or 15 mM relative to growth in MRS without supplement

^b FDR $\leq$ 0.05; p<0.05

^c LocateP DataBase (<http://www.cmbi.ru.nl/locatep-db/cgi-bin/locatepdb.py>) CS: CleavageSite; Sec-(SPI): Secretory Pathway I; Sec-(SPII): Secretory Pathway II.