TABLE S5. Genes differentially transcribed after 5 or 15 min. acid treatment[a] in *L. monocytogenes* grown to stationary phase at 37 °C

Name[b]	Gene Function[c]	Fold change[d]	
		5 min	15 min
lmo0104	unknown	-	-1.64 *
lmo0113	similar to protein gp35 from Bacteriophage A118	-	-1.81 *
lmo0114	similar to putative repressor C1 from lactococcal bacteriophage Tuc2009	-	-1.57 *
lmo0189	highly similar to B. subtilis Veg protein	-	1.66 **
lmo0217	similar to B. subtilis DivIC protein	-2.37 *	-3.03 ***
lmo0321	similar to unknown proteins	-	-2.13 **
lmo0351	similar to unknown proteins	-1.60 *	-1.85 **
lmo0523	similar to B. subtilis YybC protein	-	6.34 *
lmo0524	similar to putative sulfate transporter	-	-1.72 *
lmo0578	putative conserved membrane protein	-	-2.15 **
lmo0648	similar to membrane proteins	-	-1.83 **
lmo0770	similar to transcriptional regulator (LacI family)	-	-1.68 *
lmo0904	unknown	-	-1.67 *
lmo0998	similar to hypothetical protein	-1.63 *	-1.60 *
lmo1041	similar to molybdate ABC transporter binding protein	-	-1.66 *
lmo1046	molybdenum cofactor biosynthesis protein C	-	-1.58 *
lmo1049	similar to molybdopterin biosynthesis protein MoeB	-	-1.75 **
lmo1166	similar to NADPH-dependent butanol dehydrogenase	-	-1.84 **
lmo1219	unknown	-	-1.66 *
lmo1227	similar to uracil-DNA glycosylase	-	-1.55 **
lmo1261	unknown	-2.89 *	-4.46 ***
lmo1348	similar to aminomethyltransferase	-	-2.62 *
lmo1397 (*cinA*)	similar to competence-damage inducible protein CinA	-	-1.54 *
lmo1411	unknown	-	-1.66 *
lmo1453	conserved hypothetical protein	-	-2.77 **
lmo1541	similar to unknown protein	1.60 *	1.57 **
lmo1542 (*rplU*)	ribosomal protein L21	1.51 *	1.69 ***
lmo1597	unknown	-	-1.75 *
lmo1604	2-cys peroxiredoxin	-	-1.51 *
lmo1605 (*murC*)	UDP-N-acetyl muramate-alanine ligases	-	-1.63 *
lmo1614	similar to unknown proteins	-	3.99 *
lmo1639	similar to dna-3-methyladenine glycosidase	-2.06 *	-1.83 *
lmo1828	similar to conserved hypothetical protein	-2.42 ***	-2.07 **
lmo1856 (*deoD*)	purine nucleoside phosphorylase	-1.59 *	-1.65 **
lmo1857	similar to hypoyhetical protein	-	-1.57 **
lmo1929 (*ndk*)	similar to nucleoside diphosphate kinase	-	-1.73 ***

Gene	Function		
lmo1932	heptaprenyl diphosphate synthase component I	-	-1.51 *
lmo1939 (*cmk*)	similar to cytidylate kinase	-	-1.62 *
lmo1965	similar to unknown proteins	-	-1.90 *
lmo2020 (*divIVA*)	similar to cell-division initiation protein (septum placement)	-	-1.93 **
lmo2113	similar to unknown proteins	-	-1.58 **
lmo2129	unknown	-	-1.94 *
lmo2139	similar to ABC transporter (ATP-binding protein)	-	-1.54 **
lmo2176	similar to transcriptional regulator (tetR family)	-1.68 *	-1.91 **
lmo2207	similar to unknown protein	-	-1.68 **
lmo2210	unknown	-	2.73 *
lmo2248	similar to unknown proteins	-	-1.57 **
lmo2255	unknown	-	-1.63 *
lmo2293	Protein gp10 [Bacteriophage A118]	-	4.28 *
lmo2304	Bacteriophage A118 gp65 protein	-	3.03 *
lmo2334	similar to transcriptional regulator	-	-1.84 *
lmo2362	similar to amino acid antiporter (acid resistance)	-	1.85 *
lmo2378	similar to proteins involved in resistance to cholate and to NA(+) and in pH homeostasis	-	-1.56 *
lmo2448	conserved hypothetical protein	-	-1.84 ***
lmo2536 (*atpI*)	highly similar to ATP synthase subunit i	-	-1.56 ***
lmo2586	similar to formate dehydrogenase alpha chain	-	-1.79 *
lmo2625 (*rplP*)	ribosomal protein L16	-	1.69 *
lmo2630 (*rplW*)	ribosomal protein L23	-	1.50 *
lmo2632 (*rplC*)	ribosomal protein L3	-	1.50 *
lmo2633 (*rpsJ*)	ribosomal protein S10	-	1.64 *
lmo2658	similar to spermidine/spermine N1-acetyl transferase	-	-1.65 **
lmo2741	similar to drug-efflux transporters	-	-2.62 **
lmo2773	similar to transcription antiterminator	1.53 *	1.72 ***

[a]Acid treatment was BHI-MOPS adjusted to pH 3.5 with HCl followed by incubation at 37°C

[b]Gene names are from ListiList (http://genolist.pasteur.fr/ListiList). Predicted operons are boxed. Operon predictions are from ListiList and Toledo-Arana et al., Nature 459:950-956, 2009.

[c]gene functions were based on annotation provided by ListiList

[d]Superscripts are adjusted p values: "***" (< 0.001), "**" (< 0.01), "*" ($\leq$ 0.05)