

TABLE S4. Genes differentially transcribed after 5 or 15 min. acid treatment^a in *L. monocytogenes* grown to log phase at 37 °C.

Name ^b	Description of encoded protein ^c	Fold-change ^d	
		5 min	15 min
lmo0047	unknown	1.51 *	1.63 **
lmo0111	unknown	-1.93 ***	-2.32 ***
lmo0130	similar to 5-nucleotidase, putative peptidoglycan bound protein (LPXTG motif)	1.63 **	1.65 **
lmo0135	similar to oligopeptide ABC transport system substrate-binding proteins	2.36 **	2.27 **
lmo0136	similar to oligopeptide ABC transporter, permease protein	2.27 **	2.10 **
lmo0137	similar to oligopeptide ABC transporter, permease protein	1.64 **	1.54 *
lmo0152	similar to oligopeptide ABC transporter-binding protein	2.15 **	2.36 **
lmo0180	similar to sugar ABC transporter, permease protein	1.71 *	1.80 *
lmo0181	similar to sugar ABC transporter, sugar-binding protein	1.75 *	1.87 **
lmo0200 (<i>prfA</i>)	listeriolysin positive regulatory protein	1.72 *	1.80 **
lmo0217	similar to <i>B. subtilis</i> DivIC protein	-1.56 **	-1.96 ***
lmo0230	similar to <i>B. subtilis</i> YacH protein	1.53 *	1.56 *
lmo0231	similar to arginine kinase	-	1.60 **
lmo0232 (<i>clpC</i>)	endopeptidase Clp ATP-binding chain C	1.59 **	1.67 **
lmo0238 (<i>cysE</i>)	similar to serine O-acetyltransferase	-1.52 *	-1.65 **
lmo0269	similar to transporter	-	-2.13 **
lmo0278	similar to sugar ABC transporter, ATP-binding protein	-	1.79 *
lmo0279	highly similar to anaerobic ribonucleoside-triphosphate reductase	-1.63 *	-1.64 *
lmo0304	unknown	-1.53 *	-1.61 **
lmo0307	unknown	-2.36 **	-2.04 *
lmo0354	similar to fatty-acid--CoA ligase	-2.15 **	-2.19 **
lmo0372	similar to beta-glucosidase	-	1.59 *
lmo0412	unknown	-	-2.51 *
lmo0449	unknown	-1.85 ***	-2.01 ***
lmo0455	similar to unknown proteins	-1.54 *	-1.64 **
lmo0490	similar to shikimate 5-dehydrogenase	-2.67 **	-2.96 **
lmo0496	similar to <i>B. subtilis</i> YnzC protein	-	1.52 **
lmo0533	similar to unknown proteins	-1.57 ***	-1.71 ***
lmo0573	conserved hypothetical protein	1.73 *	1.97 **
lmo0604	similar to <i>B. subtilis</i> YvlA protein	1.54 *	1.61 *
lmo0618	similar to protein kinase	-1.51 **	-1.56 **
lmo0676	similar to flagellar biosynthetic protein FlhP	-1.92 ***	-2.49 ***
lmo0680	similar to flagella-associated protein flhA	-1.59 **	-1.87 ***
lmo0681	similar to flagellar biosynthesis protein FlhF	-1.54 *	-1.84 **
lmo0683	similar to chemotactic methyltransferase CheR	-2.16 **	-2.68 **
lmo0721	putative fibronectin-binding protein	-1.56 **	-1.54 **
lmo0773	similar to alcohol dehydrogenase	-1.79 ***	-1.81 ***
lmo0800	similar to <i>B. subtilis</i> YqkB protein	-	1.52 *

lmo0806	similar to transcription regulator	-	2.03 *
lmo0808	similar to spermidine/putrescine ABC transporter, permease protein	1.87 *	2.08 *
lmo0809	similar to spermidine/putrescine ABC transporter, permease protein	1.90 **	2.07 **
lmo0810	similar to spermidine/putrescine-binding	2.27 **	2.25 ***
lmo0811	similar to carbonic anhydrase	2.55 **	2.78 **
lmo0814	similar to oxidoreductases	-1.97 **	-1.78 *
lmo0847	similar to Glutamine ABC transporter (binding and transport protein)	2.27 **	2.29 **
lmo0848	similar to amino acid ABC transporter, ATP-binding protein	1.82 **	1.91 **
lmo0883	similar to B. subtilis YbtB protein	-2.22 ***	-2.81 ***
lmo0903	conserved hypothetical protein	2.61 **	2.65 **
lmo0912	similar to transporters (formate)	-3.98 **	-4.14 ***
lmo0952	unknown	-1.56 ***	-1.75 ***
lmo0960	similar to proteases	-2.37 ***	-2.10 **
lmo0997 (<i>clpE</i>)	ATP-dependent protease	2.01 **	1.83 *
lmo0998	similar to hypothetical protein	-1.48 **	-1.89 ***
lmo1066	similar to extragenic suppressor protein SuhB and to myo-inositol-1(or 4)-monophosphatase	-1.64 **	-1.69 **
lmo1089 (<i>tagD</i>)	highly similar to glycerol-3-phosphate cytidyltransferase (<i>gct</i>), CDP-glycerol pyrophosphorylase (teichoic acid biosynthesis protein D)	-1.86 ***	-2.03 ***
lmo1090	similar to glycosyltransferases	-1.51 **	-1.64 ***
lmo1120	unknown	-	-1.90 *
lmo1138	similar to ATP-dependent Clp protease proteolytic component	1.63 **	1.61 **
lmo1257	unknown	-5.50 *	-4.50 *
lmo1266	unknown	-2.04 *	-2.17 *
lmo1294 (<i>miaA</i>)	similar to tRNA isopentenylpyrophosphate transferase	-	-1.67 ***
lmo1360 (<i>folD</i>)	highly similar to methylenetetrahydrofolate dehydrogenase and methenyltetrahydrofolate cyclohydrolase	-1.81 ***	-2.02 ***
lmo1369	similar to phosphotransbutyrylase	-1.80 **	-1.67 **
lmo1406 (<i>pflB</i>)	pyruvate formate-lyase	-4.03 *	-4.30 *
lmo1407 (<i>pflC</i>)	pyruvate-formate lyase activating enzyme	-2.86 *	-2.72 *
lmo1441	similar to putative peptidoglycan acetylation protein	-	-1.86 **
lmo1474 (<i>grpE</i>)	heat shock protein GrpE	1.84 **	1.71 **
lmo1475 (<i>hrcA</i>)	transcription repressor of class I heat-shock gene HrcA	1.83 **	1.76 **
lmo1500	similar to unknown proteins	-	-1.70 ***
lmo1544 (<i>minD</i>)	highly similar to cell division inhibitor (septum placement) protein MinD	-	-1.52 ***
lmo1556 (<i>hemC</i>)	highly similar to porphobilinogen deaminases (hydroxymethylbilane synthase)	-	-1.59 *
lmo1557 (<i>hemA</i>)	highly similar to glutamyl-tRNA reductase	-1.72 ***	-1.87 ***
lmo1589 (<i>argB</i>)	highly similar to N-acetylglutamate 5-phosphotransferase	-	-4.37 *
lmo1590 (<i>argJ</i>)	highly similar to ornithine acetyltransferase and amino-acid acetyltransferases	-6.76 *	-4.84 *

lmo1591 (<i>argC</i>)	similar to N-acetylglutamate gamma-semialdehyde dehydrogenases	-25.44 *	-11.04 *
lmo1597	unknown	-2.69 ***	-3.04 ***
lmo1625	similar to putative transporters	-	-1.53 ***
lmo1634	similar to Alcohol-acetaldehyde dehydrogenase	-6.66 *	-6.24 *
lmo1639	similar to dna-3-methyladenine glycosidase	-1.54 **	-1.71 **
lmo1696	similar to unknown proteins	-	-1.50 **
lmo1710	similar to putative flavodoxin	-	-1.60 ***
lmo1744	similar to unknown proteins	-1.81 **	-2.18 ***
lmo1749	similar to shikimate kinase	-2.46 ***	-2.88 ***
lmo1750	similar to unknown protein	-1.66 *	-1.61 *
lmo1752	unknown	-	1.55 **
lmo1803	similar to FtsY of E. coli and SRP receptor alpha-subunit	1.67 **	1.70 **
lmo1828	similar to conserved hypothetical protein	-1.50 **	-1.91 ***
lmo1833 (<i>pyrD</i>)	highly similar to dihydroorotase	-	1.57 **
lmo1835 (<i>pyrAB</i>)	highly similar to carbamoyl-phosphate synthetase (catalytic subunit)	1.83 *	1.91 **
lmo1840 (<i>pyrR</i>)	highly similar to pyrimidine operon regulatory protein	-	1.57 *
lmo1856 (<i>deoD</i>)	purine nucleoside phosphorylase	-	-1.59 ***
lmo1857	similar to hypothetical protein	-	-1.70 ***
lmo1867	similar to pyruvate phosphate dikinase	-	1.53 **
lmo1884	similar to xanthine permeases	1.54 *	1.53 *
lmo1917 (<i>pflA</i>)	similar to pyruvate formate-lyase	-4.54 *	-
lmo1926	similar to chorismate mutase	-1.93 **	-2.52 ***
lmo1943	similar to unknown proteins	-1.52 **	-1.57 **
lmo1965	similar to unknown proteins	-	-2.52 *
lmo1977	similar to unknown proteins	-	-1.78 ***
lmo1992	similar to alpha-acetolactate decarboxylase	1.68 ***	1.65 ***
lmo2006 (<i>alsS</i>)	similar to alpha-acetolactate synthase protein, AlsS	-	1.52 **
lmo2040 (<i>ftsL</i>)	similar to cell-division protein FtsL	-	-1.51 ***
lmo2041	similar to unknown proteins	-	-1.68 ***
lmo2057 (<i>ctaB</i>)	highly similar to heme A farnesyltransferase	1.60 **	1.61 ***
lmo2063	unknown	-1.78 ***	-1.83 ***
lmo2090 (<i>argG</i>)	similar to argininosuccinate synthase	-8.74 *	-10.59 *
lmo2100	similar to transcriptional regulator (GntR family) and to aminotransferase (MocR-like)	1.61 *	-2.79 **
lmo2114	similar to ABC transporter (ATP-binding protein)	2.28 **	2.25 **
lmo2115	similar to ABC transporter (permease)	2.23 **	2.16 **
lmo2152	similar to thioredoxin	1.52 **	1.49 **
lmo2156	unknown	1.94 ***	1.89 ***
lmo2173	similar to sigma-54-dependent transcriptional activator	-3.11 *	-3.23 *
lmo2184	similar to ferrichrome ABC transporter (binding protein)	-	1.50 **
lmo2190 (<i>mecA</i>)	competence negative regulator mecA	-	1.52 **
lmo2200	similar to transcription regulator	1.51 *	1.49 *
lmo2238	similar to transport system permease protein	-3.46 *	-3.75 **

lmo2241	similar to transcriptional regulators (GntR family)	-	-1.60 **
lmo2250 (<i>arpJ</i>)	similar to amino acid ABC transporter, permease protein	-3.89 *	-3.53 *
lmo2258	unknown	1.56 *	1.69 **
lmo2260	similar to unknown proteins	1.87 *	1.78 *
lmo2261	similar to unknown proteins	1.63 *	-
lmo2293	Protein gp10 [Bacteriophage A118]	-2.34 *	-
lmo2295	Protein gp8 [Bacteriophage A118]	-2.88 *	-2.39 *
lmo2296	similar to coat protein [Bacteriophage SPP1]	-2.32 *	-
lmo2352	similar to LysR family transcription regulator	-	1.51 *
lmo2362	similar to amino acid antiporter (acid)	-2.97 **	-2.80 **
lmo2363	similar to glutamate decarboxylase	-2.59 *	-2.28 *
lmo2380	similar to proteins involved in resistance to cholate and to NA(+) and in pH homeostasis	-	1.51 *
lmo2393	similar to B. subtilis YuzD protein	1.71 **	1.68 **
lmo2408	similar to repressor protein	-1.61 ***	-1.94 ***
lmo2409	unknown	-3.28 **	-4.21 ***
lmo2416	unknown	-1.78 **	-1.68 **
lmo2420	unknown	-1.73 ***	-2.00 ***
lmo2433	similar to acetyltransferase	1.98 *	2.10 **
lmo2439	unknown	1.63 **	1.61 **
lmo2468 (<i>clpP</i>)	ATP-dependent Clp protease proteolytic	1.58 ***	1.64 ***
lmo2484	similar to B. subtilis YviD protein	-	2.11 *
lmo2487	similar to B. subtilis YviB protein	1.56 *	1.74 **
lmo2569	similar to dipeptide ABC transporter (dipeptide-binding protein)	1.74 **	1.78 **
lmo2587	conserved hypothetical proteins	-	-1.61 **
lmo2591	surface protein (GW repeat) similar to N-acetylmuramidase	1.58 **	1.53 **
lmo2642	unknown	-1.89 *	-2.03 **
lmo2690	similar to transcription regulator, TetR family	-	1.54 **
lmo2718 (<i>cydA</i>)	highly similar to cytochrome D ubiquinol oxidase subunit I	-1.59 *	-
lmo2720	similar to acetate-CoA ligase	-2.07 **	-1.79 **
lmo2769	similar to ABC transporter, ATP-binding	-2.55 **	-3.28 ***
lmo2827	similar to transcriptional regulator (MarR)	1.50 *	-
lmo2829	similar to yeast protein Frm2p involved in fatty acid signaling	-	1.60 *
lmo2851	similar to AraC-type regulatory protein	1.73 *	-

^aAcid treatment was BHI-MOPS adjusted to pH 3.5 with HCl followed by incubation at 37°C

^bGene 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.

^cgene functions were based on annotation provided by ListiList

^dSuperscripts are adjusted p values: "****" (< 0.001), "***" (< 0.01), "**" (≤ 0.05)