TABLE S7. Genes differentially transcribed after 5 or 15 min. acid treatment[a] in *L. monocytogenes* grown to stationary phase at 7 °C

Name[b]	Gene Function[c]	Fold-change[d]	
		5 min	15 min
lmo0049	unknown	-	-1.56 *
lmo0115 (*lmaD*)	similar to Antigen D	1.99 ***	2.13 ***
lmo0117 (*lmaB*)	antigen B	5.12 ***	5.32 ***
lmo0118 (*lmaA*)	antigen A	5.02 ***	5.05 ***
lmo0119	unknown	3.75 ***	4.04 ***
lmo0120	unknown	3.80 ***	4.09 ***
lmo0121	similar to bacteriophage minor tail proteins	4.56 **	3.88 **
lmo0122	similar to phage proteins	3.84 ***	3.73 ***
lmo0123	similar to protein gp18 from Bacteriophage A118	4.86 ***	4.51 ***
lmo0124	unknown	4.02 ***	4.12 ***
lmo0125	unknown	4.20 ***	4.12 ***
lmo0126	unknown	4.99 ***	5.10 ***
lmo0127	weakly similar to protein gp20 from Bacteriophage A118	5.21 ***	5.09 ***
lmo0128	similar to a protein from Bacteriophage phi-105 (ORF 45)	4.20 ***	4.89 ***
lmo0129	similar to autolysin: N-acetylmuramoyl-L-alanine amidase	3.47 ***	3.94 ***
lmo0217	similar to *B. subtilis* DivIC protein	-	-1.65 *
lmo0328	unknown	-	-2.07 *
lmo0728	similar to riboflavin kinase / FAD synthase	-	-1.81 ***
lmo0883	similar to *B. subtilis* YbtB protein	-1.83 *	-
lmo0903	conserved hypothetical protein	2.35 ***	3.15 ***
lmo1049	similar to molybdopterin biosynthesis protein MoeB	-	-1.59 ***
lmo1631 (*trpD*)	highly similar to anthranilate phosphoribosyltransferase	-	3.09 **
lmo1828	similar to conserved hypothetical protein	-	-1.53 *
lmo1856 (*deoD*)	purine nucleoside phosphorylase	-	-1.63 *
lmo1926	similar to chorismate mutase	-	-1.61 *
lmo2191	similar to unknown proteins	-	-1.55 ***
lmo2210	unknown	-	-1.53 *
lmo2278 (*lysA*)	L-alanoyl-D-glutamate peptidase	-	1.72 **
lmo2279	holin [Bacteriophage A118]	-	1.74 *
lmo2282	protein gp21 [Bacteriophage A118]	-	1.75 *
lmo2283	protein gp20 [Bacteriophage A118]	-	2.07 **
lmo2286	protein gp17 [Bacteriophage A118]	1.68 **	1.64 *
lmo2288	protein gp15 [Bacteriophage A118]	2.83 ***	2.61 **
lmo2290	portein gp13 [Bacteriophage A118]	3.22 **	3.14 **
lmo2291	major tail shaft protein [Bacteriophage A118]	4.05 ***	5.26 ***
lmo2292	protein gp11 [Bacteriophage A118]	4.04 ***	3.42 ***
lmo2293	protein gp10 [Bacteriophage A118]	2.89 ***	2.70 ***
lmo2295	protein gp8 [Bacteriophage A118]	2.41 ***	2.35 ***
lmo2297	putative scaffolding protein [Bacteriophage A118]	3.23 ***	2.98 ***
lmo2299	putative portal protein [Bacteriophage A118]	-	1.69 *
lmo2303	protein gp66 [Bacteriophage A118]	2.08 **	2.02 ***
lmo2317	similar to protein gp49 [Bacteriophage A118]	-	2.01 **
lmo2322	gp44 [Bacteriophage A118]	1.98 *	-
lmo2326	similar to protein gp41 [Bacteriophage A118]	2.18 *	2.27 *
lmo2445	similar to internalin	-	-2.75 *
lmo2536 (*atpI*)	highly similar to ATP synthase subunit i	-	-1.66 ***

[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), "*" (≤ 0.05)