TABLE S6. Genes differentially transcribed after 5 or 15 min. acid treatment[a] in *L. monocytogenes* grown to log phase at 7 °C

Name[b]	Description of encoded protein[c]	Fold change[d]	
		5 min.	15 min.
lmo0066	similar to toxin components	1.51 ***	-
lmo0071	unknown	-	-7.13 *
lmo0111	unknown	-1.57 ***	-1.62 ***
lmo0133	similar to *E. coli* YjdI protein	-	1.50 *
lmo0299	similar to PTS beta-glucoside-specific enzyme IIB component	-	-2.24 *
lmo0306	unknown	-1.60 **	-1.55 *
lmo0320	similar to surface protein (peptidoglycan bound, LPXTG motif)	-	3.64 *
lmo0326	similar to transcriptional regulators	-	2.87 **
lmo0418	unknown	2.63 ***	2.14 ***
lmo0669	similar to oxidoreductase	1.35 ***	1.55 ***
lmo0735	similar to Ribulose-5-Phosphate 3-Epimerase	-	-3.57 **
lmo0875	similar to PTS system, beta-glucoside enzyme IIB component	1.61 ***	-
lmo0883	similar to *B. subtilis* YbtB protein	-1.41 **	-1.72 ***
lmo0952	unknown	-1.56 ***	-1.61 **
lmo1114	highly similar to TN916 ORF23	-	-2.02 *
lmo1151	similar to Salmonella typhimurium PduA protein	1.57 **	-
lmo1266	unknown	-1.66 ***	-1.80 ***
lmo1639	similar to dna-3-methyladenine glycosidase	-1.49 ***	-1.55 ***
lmo1749	similar to shikimate kinase	-1.67 ***	-1.93 ***
lmo1883	similar to chitinases	1.52 *	-
lmo1972	similar to pentitol PTS system enzyme II B component	-	1.62 *
lmo2009	similar to putative transport system integral membrane protein	-	1.63 *
lmo2290	Portein gp13 [Bacteriophage A118]	1.53 ***	-
lmo2291	major tail shaft protein [Bacteriophage A118]	1.70 ***	-
lmo2292	Portein gp11 [Bacteriophage A118]	1.65 ***	1.54 ***
lmo2300	putative terminase large subunit from Bacteriophage A118	-	4.32 *
lmo2408	similar to repressor protein	-	-1.64 ***
lmo2409	unknown	-	-2.26 ***
lmo2836	similar to alcohol dehydrogenase	-	2.00 **

[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 (http://genolist.pasteur.fr/ListiList).

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