

TABLE S1. *Listeria monocytogenes* genes transcribed at higher levels<sup>a</sup> at 7°C compared to 37°C

Name <sup>b</sup>	Gene Function <sup>c</sup>	Fold change <sup>d</sup> (7°C/37°C)	
		Log phase	Stationary phase
lmo0005 ( <i>recF</i> )	RecF protein	2.14 ***	-
lmo0013 ( <i>qoxA</i> )	AA3-600 quinol oxidase subunit II	2.05 **	-
lmo0019	unknown	-	5.10 ***
lmo0042	similar to <i>E. coli</i> DedA protein	4.48 ***	-
lmo0047	unknown	2.99 ***	2.82 *
lmo0066	similar to toxin components	-	2.66 ***
lmo0076	similar to <i>E. coli</i> Ada protein (O6-methylguanine-DNA methyltransferase)	-	2.68 ***
lmo0114	similar to putative repressor C1 from lactococcal bacteriophage Tuc2009	-	2.02 ***
lmo0117 ( <i>lmaB</i> )	antigen B	7.36 ***	-
lmo0118 ( <i>lmaA</i> )	antigen A	5.08 ***	-
lmo0119	unknown	5.98 ***	-
lmo0120	unknown	6.12 ***	-
lmo0121	similar to bacteriophage minor tail proteins	3.47 ***	-
lmo0122	similar to phage proteins	-	2.03 ***
lmo0123	similar to protein gp18 from Bacteriophage A118	4.35 ***	-
lmo0124	unknown	3.13 ***	-
lmo0125	unknown	3.40 ***	-
lmo0126	unknown	4.81 ***	-
lmo0127	weakly similar to protein gp20 from Bacteriophage A118	3.50 ***	-
lmo0129	similar to autolysin: N-acetylmuramoyl-L-alanine amidase	4.73 ***	-
lmo0131	conserved hypothetical protein	-	2.89 ***
lmo0133	similar to <i>E. coli</i> YjdI protein	-	2.60 ***
lmo0134	similar to <i>E. coli</i> YjdJ protein	-	5.02 ***
lmo0137	similar to oligopeptide ABC transporter, permease protein	-	2.11 ***
lmo0193	unknown	4.22 ***	-
lmo0194	ABC transporter, ATP-binding protein	4.47 ***	-
lmo0195	similar to membrane protein (putative ABC transporter component)	4.20 ***	-
lmo0200 ( <i>prfA</i> )	listeriolysin positive regulatory protein	-	4.60 ***
lmo0249 ( <i>rplA</i> )	ribosomal protein L1	-	2.10 ***
lmo0250 ( <i>rplJ</i> )	ribosomal protein L10	-	2.34 ***
lmo0251 ( <i>rplL</i> )	ribosomal protein L12	-	2.54 ***
lmo0256	conserved hypothetical protein	-	2.06 ***
lmo0266	similar to transcriptional regulators	-	3.70 ***
lmo0267	similar to other proteins	-	4.63 ***
lmo0268	similar to phosphoglycerate mutase	-	3.59 ***
lmo0269	similar to transporter	2.07 ***	-
lmo0273	unknown	-	2.47 ***
lmo0283	similar to ABC transporter permease protein	2.81 ***	-
lmo0284	similar to ABC transporter (ATP-binding protein)	2.24 ***	-
lmo0285	putative lipoprotein	2.43 ***	-
lmo0312	similar to unknown proteins	2.11 *	-
lmo0321	similar to unknown proteins	2.49 ***	4.82 ***
lmo0322	similar to unknown proteins	2.06 **	-
lmo0352	highly similar to regulatory proteins (DeoR family)	2.12 ***	-
lmo0361	similar to conserved hypothetical integral membrane protein	4.67 ***	-
lmo0362	similar to conserved hypothetical protein	6.11 ***	-
lmo0365	similar to conserved hypothetical protein	6.74 ***	-
lmo0366	conserved hypothetical protein, putative lipoprotein	7.20 ***	-
lmo0367	conserved hypothetical protein similar to <i>B. subtilis</i> YwbN protein	6.08 ***	-
lmo0377	unknown	2.05 ***	-
lmo0391	unknown	-	2.19 ***
lmo0433 ( <i>inlA</i> )	Internalin A	-	2.05 ***
lmo0484	unknown	4.37 ***	-
lmo0485	unknown	2.48 ***	-

lmo0515	conserved hypothetical protein	-	4.01 ***
lmo0518	similar to unknown protein	2.76 ***	-
lmo0519	similar to multidrug resistance protein	4.47 ***	-
lmo0525	unknown	3.08 ***	-
lmo0540	similar to penicillin-binding protein	-	3.48 ***
lmo0541	similar to ABC transporter (binding protein)	13.44 ***	-
lmo0553	unknown	-	2.28 ***
lmo0561	similar to phosphorybosil-AMP-cyclohydrolase (HisI2 protein)	-	2.94 ***
lmo0562	similar to phosphoribosyl-AMP cyclohydrolase (HisI1 protein)	-	4.71 ***
lmo0563	highly similar to cyclase HisF	-	3.47 ***
lmo0564	highly similar to phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase	-	3.47 ***
lmo0565	similar to amidotransferases	-	2.20 ***
lmo0570	similar histidinol phosphate phosphatase	-	2.14 ***
lmo0579	similar to unknown protein	-	2.32 ***
lmo0581	conserved hypothetical protein	2.27 ***	-
lmo0590	similar to a fusion of two types of conserved hypothetical protein	2.00 ***	-
lmo0592	unknown	2.15 **	-
lmo0593	similar to transport proteins (formate)	2.21 **	-
lmo0595	similar to O-acetylhomoserine sulphydrylase	2.31 ***	-
lmo0596	similar to unknown proteins	2.26 **	-
lmo0597	similar to transcription regulator CRP/FNR family	5.18	-
lmo0599	conserved hypothetical protein	2.86 ***	-
lmo0600	unknown	2.24 ***	-
lmo0604	similar to <i>B. subtilis</i> YvIA protein	5.22 ***	-
lmo0609	similar to <i>E. coli</i> phage shock protein E	-	2.14 ***
lmo0610	similar to internalin proteins, putative peptidoglycan bound protein (LPXTG motif)	-	4.41 ***
lmo0617	unknown	-	2.14 ***
lmo0623	unknown	-	2.92 ***
lmo0624	similar to unknown proteins	2.16 ***	3.42 ***
lmo0625	unknown	-	7.19 ***
lmo0626	similar to unknown protein	-	2.85 ***
lmo0656	conserved hypothetical protein	2.30 ***	-
lmo0661	similar to unknown proteins	-	2.28 ***
lmo0665	unknown	2.02 ***	-
lmo0666	similar to unknown protein	2.98 ***	-
lmo0669	similar to oxidoreductase	-	2.04 ***
lmo0672	similar to unknown protein	2.64 ***	-
lmo0680	similar to flagella-associated protein flhA	2.22 ***	-
lmo0681	similar to flagellar biosynthesis protein FlhF	2.20 **	-
lmo0683	similar to chemotactic methyltransferase CheR	2.37 **	-
lmo0684	unknown	2.24 **	-
lmo0685	similar to motility protein (flagellar motor rotation) MotA	2.51 **	-
lmo0686 ( <i>motB</i> )	similar to motility protein (flagellar motor rotation) MotB	2.17 ***	-
lmo0687	unknown	2.69 ***	-
lmo0688	similar to unknown protein	2.43 ***	-
lmo0689	similar to CheA activity-modulating chemotaxis protein CheV	2.49 ***	-
lmo0734	similar to transcriptional regulator (LacI family)	2.34 ***	-
lmo0753	similar to transcription regulator Crp/Fnr family	-	3.05 ***
lmo0754	weakly similar to a bile acid 7-alpha dehydratase	-	4.37 ***
lmo0757	similar to hypothetical proteins	-	2.37 ***
lmo0759	unknown	-	2.97 ***
lmo0760	unknown	-	2.53 ***
lmo0778	unknown	2.92 ***	-
lmo0780	unknown	2.68 ***	-
lmo0781	similar to mannose-specific phosphotransferase system (PTS) component IID	-	4.26 ***
lmo0782	similar to mannose-specific phosphotransferase system (PTS) component IIC	-	2.79 ***

lmo0783	similar to mannose-specific phosphotransferase system (PTS) component IIB	-	5.29 ***
lmo0784	similar to mannose-specific phosphotransferase system (PTS) component IIA	-	4.63 ***
lmo0795	conserved hypothetical protein	2.22 ***	-
lmo0799	unknown	2.41 ***	-
lmo0800	similar to <i>B. subtilis</i> YqkB protein	-	5.35 ***
lmo0806	similar to transcription regulator	2.89 **	-
lmo0808	similar to spermidine/putrescine ABC transporter, permease protein	2.42 **	-
lmo0809	similar to spermidine/putrescine ABC transporter, permease protein	2.25 ***	-
lmo0810	similar to spermidine/putrescine-binding protein	2.17 ***	-
lmo0811	similar to carbonic anhydrase	2.32 ***	-
lmo0818	similar to cation transporting ATPase	2.17 ***	-
lmo0823	similar to oxydoreductases	-	3.82 ***
lmo0830 ( <i>fbp</i> )	highly similar to fructose-1,6-bisphosphatase	2.30 **	-
lmo0835	putative peptidoglycan bound protein (LPXTG motif)	2.37 *	-
lmo0836	similar to <i>B. subtilis</i> YrkR protein	2.56 ***	-
lmo0843	similar to <i>B. subtilis</i> protein YsdA	-	2.46 ***
lmo0844	conserved hypothetical protein	3.61 ***	-
lmo0850	hypothetical protein	2.57 ***	3.68 ***
lmo0851	unknown	-	2.10 ***
lmo0867	unknown	3.08 ***	-
lmo0869	unknown	2.00 **	-
lmo0873	Similar to transcriptional regulator (antiterminator)	-	2.03 ***
lmo0875	similar to PTS system, beta-glucoside enzyme IIB component	-	2.03 ***
lmo0894 ( <i>rsbW</i> )	sigma-B activity negative regulator RsbW	-	2.07 ***
lmo0903	conserved hypothetical protein	4.50 ***	-
lmo0905	unknown	2.10 ***	3.08 ***
lmo0906	similar to glutathione Reductase	-	3.75 ***
lmo0907	similar to phosphoglycerate mutase	-	2.06 ***
lmo0910	unknown	-	2.22 ***
lmo0911	unknown	-	2.25 ***
lmo0912	similar to transporters (formate)	-	3.76 ***
lmo0913	similar to succinate semialdehyde dehydrogenase	-	2.70 ***
lmo0915	similar to phosphotransferase system enzyme IIC	-	2.06 ***
lmo0937	unknown	-	2.21 ***
lmo0939	unknown	-	2.47 ***
lmo0944	similar to <i>B. subtilis</i> YneR protein	2.04 ***	-
lmo0945	similar to C-terminal part of <i>B. subtilis</i> ComEC protein and to ComEA	-	2.51 ***
lmo0954	unknown	-	3.66 ***
lmo0955	unknown	-	2.13 ***
lmo0994	unknown	-	2.48 ***
lmo1000	similar to phytoene dehydrogenase	2.30 ***	-
lmo1001	similar to <i>B. subtilis</i> protein YkvS	4.41 ***	-
lmo1007	unknown	18.96 ***	-
lmo1015 ( <i>gbuB</i> )	highly similar to glycine betaine ABC transporters (permease)	4.27 ***	-
lmo1016 ( <i>gbuC</i> )	highly similar to glycine betaine ABC transporters (glycine betaine-binding protein)	3.85 ***	-
lmo1023	similar to a bacterial K(+)-uptake system	-	2.31 ***
lmo1056	unknown	2.02 ***	-
lmo1064	similar to membrane and transport proteins	2.35 ***	-
lmo1069	similar to <i>B. subtilis</i> Ylal protein	-	2.93 ***
lmo1091	similar to glycosyltransferases	-	2.39 ***
lmo1112	highly similar to TN916 ORF21	4.34 *	-
lmo1131	similar to ABC transporters, ATP-binding proteins	2.20 *	-
lmo1132	similar to ABC transporters, ATP-binding proteins	4.37 ***	-
lmo1137	unknown	5.23 **	-
lmo1145	similar to <i>Salmonella enterica</i> PduV protein	2.23 **	-
lmo1151	similar to <i>Salmonella</i> Typhimurium PduA protein	-	2.38 ***
lmo1172	similar to similar to two-component response regulator	2.22 ***	3.84 ***
lmo1173	similar to two-component sensor histidine kinase	2.13 **	3.75 ***

lmo1175 ( <i>eutB</i> )	similar to ethanolamine ammonia-lyase, heavy chain	-	2.18 ***
lmo1176 ( <i>eutC</i> )	similar to ethanolamine ammonia-lyase, light chain	-	2.39 ***
lmo1177	similar to putative carboxysome structural protein ( <i>eutL</i> )	3.23 ***	-
lmo1179	similar to acetaldehyde dehydrogenase / alcohol dehydrogenase	-	4.19 ***
lmo1180	similar to putative carboxysome structural protein	-	3.90 ***
lmo1181	similar to cobalamin adenosyl transferase	5.08 **	2.10 **
lmo1182	similar to <i>Salmonella enterica</i> PduL protein	5.82 **	2.38 **
lmo1183	unknown	9.23 ***	2.10 **
lmo1184	similar to carbon dioxide concentrating mechanism protein	6.31 **	3.17 **
lmo1185	similar to <i>Salmonella enterica</i> PduT protein	5.68 ***	-
lmo1186	similar to ethanolamine utilization protein EutH - <i>E. coli</i>	2.70 **	2.02 **
lmo1231	similar to DNA polymerase beta, to <i>B. subtilis</i> YshC protein	-	2.38 ***
lmo1232	similar to MutS protein (MutS2)	-	2.17 ***
lmo1245	unknown	7.80 ***	-
lmo1246	similar to ATP-dependent RNA helicase (DEAD motif)	2.27 ***	-
lmo1249	unknown	2.65 *	-
lmo1252	similar to <i>B. subtilis</i> YxkD protein	3.15 ***	-
lmo1257	unknown	-	2.11 ***
lmo1340	similar to <i>B. subtilis</i> YqgU protein	-	7.34 ***
lmo1428 ( <i>opuCA</i> )	similar to glycine betaine/carnitine/choline ABC transporter (ATP-binding protein)	2.16 ***	-
lmo1431	similar to ABC transporter (ATP-binding protein)	2.15 ***	-
lmo1450	similar to ATP-dependent RNA helicase, DEAD-box family ( <i>deaD</i> )	2.03 ***	-
lmo1479 ( <i>lepA</i> )	highly similar to GTP-binding protein <i>LepA</i>	2.39 ***	-
lmo1485	similar to unknown proteins	2.05 ***	-
lmo1486	unknown	2.02 **	-
lmo1498	similar to O-methyltransferase	-	2.28 *
lmo1499	similar to unknown proteins	-	3.89 **
lmo1512	similar to putative tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	-	2.28 ***
lmo1513	similar to iron-sulfur cofactor synthesis protein	-	2.54 ***
lmo1518	unknown	-	2.37 ***
lmo1519 ( <i>aspS</i> )	aspartyl-tRNA synthetase	-	3.78 ***
lmo1526	similar to unknown proteins	2.62 ***	-
lmo1537	conserved GTP binding protein	2.01 ***	-
lmo1558	similar to hypothetical GTP binding protein	2.02 **	-
lmo1567 ( <i>citZ</i> )	highly similar to citrate synthase subunit II	2.15 ***	-
lmo1568	similar to unknown proteins	2.08 ***	-
lmo1583	similar to thiol peroxidases	2.14 ***	-
lmo1617	similar to multidrug-efflux transporter	2.98 ***	-
lmo1618	similar to transcription regulator MarR family	2.32 **	-
lmo1649	unknown	-	2.44 ***
lmo1650	similar to hypothetical proteins	-	2.50 ***
lmo1690	similar to hypothetical proteins	-	2.19 ***
lmo1692	unknown	-	2.66 ***
lmo1713	similar to cell-shape determining proteins	2.31 ***	-
lmo1722	similar to ATP-dependent RNA helicases	2.24 ***	2.46 ***
lmo1762	unknown	2.71 ***	-
lmo1791	unknown	-	2.79 ***
lmo1826	unknown	2.07 ***	-
lmo1828	similar to conserved hypothetical protein	2.06 ***	-
lmo1829	similar to fibronectin binding proteins	2.23 ***	-
lmo1832 ( <i>pyrF</i> )	highly similar to orotidine 5-phosphate decarboxylases	-	2.55 **
lmo1835 ( <i>pyrAB</i> )	highly similar to carbamoyl-phosphate synthetase (catalytic subunit)	2.17 **	-
lmo1836 ( <i>pyrAa</i> )	highly similar to carbamoyl-phosphate synthetase (glutaminase subunit)	2.39 **	-
lmo1838 ( <i>pyrB</i> )	highly similar to aspartate carbamoyltransferase	2.36 **	-
lmo1840 ( <i>pyrR</i> )	highly similar to pyrimidine operon regulatory protein	2.28 **	-

lmo1843	similar to conserved hypothetical proteins	2.66 ***	-
lmo1844 ( <i>lsp</i> )	highly similar to signal peptidase II	2.30 ***	-
lmo1845	similar to conserved hypothetical proteins	-	4.95 ***
lmo1864	similar to hemolysinIII proteins, putative integral membrane protein	2.76 ***	3.29 ***
lmo1865	similar to conserved hypothetical proteins	2.41 ***	-
lmo1868	similar to conserved hypothetical proteins	-	2.74 ***
lmo1870	similar to alkaline phosphatase	2.80 ***	-
lmo1887	similar to conserved hypothetical proteins	2.09 ***	-
lmo1891 ( <i>recU</i> )	similar to DNA repair and homologous recombination protein	2.31 ***	-
lmo1936 ( <i>gpsA</i> )	similar to NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	2.23 **	2.64 ***
lmo1937	similar to unknown protein	2.24 **	-
lmo1951	similar to unknown proteins	-	2.22 ***
lmo1957 ( <i>fhuG</i> )	similar to ferrichrome ABC transporter (permease)	2.29 ***	-
lmo1958 ( <i>fhuB</i> )	similar to ferrichrome ABC transporter (permease)	3.11 ***	-
lmo1960 ( <i>fhuC</i> )	similar to ferrichrome ABC transporter (ATP-binding protein)	3.84 ***	-
lmo1961	similar to oxidoreductases	2.25 ***	-
lmo1962	similar to transcription regulators (TetR family)	-	2.49 ***
lmo1963	similar to unknown proteins	-	2.78 ***
lmo1964	similar to ABC transporter, ATP-binding protein	-	2.68 ***
lmo1972	similar to pentitol PTS system enzyme II B component	-	2.50 ***
lmo1978	similar to glucose-6-phosphate 1-dehydrogenase	-	4.19 ***
lmo1984 ( <i>ilvB</i> )	similar to acetolactate synthase (acetohydroxy-acid synthase) (large subunit)	2.02 **	-
lmo1985 ( <i>ilvN</i> )	similar to acetolactate synthase (acetohydroxy-acid synthase) (small subunit)	3.13 ***	-
lmo1986 ( <i>ilvC</i> )	similar to ketol-acid reductoisomerase (acetohydroxy-acid isomeroreductase)	2.63 **	-
lmo1988 ( <i>leuB</i> )	similar to 3-isopropylmalate dehydrogenase	2.69 *	-
lmo1990 ( <i>leuD</i> )	similar to 3-isopropylmalate dehydratase (small subunit)	2.31 *	-
lmo1991 ( <i>ilvA</i> )	similar to threonine dehydratase	2.31 **	-
lmo1992	similar to alpha-acetolactate decarboxylase	4.22 ***	5.73 ***
lmo1997	similar to PTS mannose-specific enzyme IIA component	-	3.42 ***
lmo1998	similar to opine catabolism protein	-	2.20 ***
lmo2006 ( <i>alsS</i> )	similar to alpha-acetolactate synthase protein, AlsS	3.20 ***	-
lmo2057 ( <i>ctaB</i> )	highly similar to heme A farnesyltransferase	2.17 ***	-
lmo2058 ( <i>ctaA</i> )	similar to heme O oxygenase	2.23 ***	-
lmo2065	unknown	2.31 ***	-
lmo2071	unknown	2.22 ***	-
lmo2087	similar to unknown proteins	2.26 ***	-
lmo2114	similar to ABC transporter (ATP-binding protein)	2.06 ***	-
lmo2181	similar to unknown protein	2.73 **	-
lmo2185	unknown	4.63 ***	-
lmo2186	unknown	8.36 ***	-
lmo2191	similar to unknown proteins	2.46 ***	-
lmo2197	unknown	2.16 ***	-
lmo2199	similar to unknown protein	5.95 ***	-
lmo2200	similar to transcription regulator	7.03 ***	-
lmo2210	unknown	5.07 ***	-
lmo2220	similar to S. aureus Cbf1 protein	-	2.08 ***
lmo2232	similar to unknown proteins	-	2.69 ***
lmo2256	similar to unknown proteins	-	5.75 ***
lmo2258	unknown	2.05 **	-
lmo2263	similar to unknown proteins	-	2.03 ***
lmo2269	unknown	-	8.56 ***
lmo2289	Protein gp14 [Bacteriophage A118]	-	2.19 ***
lmo2291	major tail shaft protein [Bacteriophage A118]	2.62 **	-
lmo2292	Protein gp11 [Bacteriophage A118]	2.10 *	-
lmo2301	similar to putative terminase small subunit from Bacteriophage A118	-	2.21 ***
lmo2303	Protein gp66 [Bacteriophage A118]	2.33 **	-

lmo2304	Bacteriophage A118 gp65 protein	2.34 **	-
lmo2323	gp43 [Bacteriophage A118]	6.68 **	-
lmo2324	similar to anti-repressor [Bacteriophage A118]	2.69 *	-
lmo2335 ( <i>fruA</i> )	highly similar to phosphotransferase system (PTS) fructose-specific enzyme IIABC component	12.35 **	-
lmo2336 ( <i>fruB</i> )	fructose-1-phosphate kinase	21.42 ***	-
lmo2337	similar to regulatory protein DeoR family	20.71 ***	-
lmo2338 ( <i>pepC</i> )	aminopeptidase C	-	3.20 ***
lmo2345	conserved hypothetical protein	2.36 **	-
lmo2347	similar to amino acid ABC transporter (permease)	2.64 **	-
lmo2348	similar to amino acid ABC-transporter (permease)	2.32 ***	-
lmo2349	similar to amino acid ABC transporter (binding protein)	3.58 ***	-
lmo2350	similar to <i>B. subtilis</i> YtmI protein	2.09 **	-
lmo2352	similar to LysR family transcription regulator	4.04 ***	-
lmo2357	similar to unknown protein	-	2.14 ***
lmo2358	similar to N-acetylglucosamine-6-phosphate isomerase	-	2.62 ***
lmo2360	transmembrane protein	3.47 ***	-
lmo2361	conserved hypothetical protein	3.01 ***	-
lmo2372	similar to ABC-transporter ATP binding proteins	2.36 ***	-
lmo2375	unknown	3.70 ***	-
lmo2378	similar to proteins involved in resistance to cholate and to NA(+) and in pH homeostasis	2.40 ***	-
lmo2379	similar to proteins involved in resistance to cholate and to NA(+) and in pH homeostasis	2.17 ***	-
lmo2380	similar to proteins involved in resistance to cholate and to NA(+) and in pH homeostasis	2.14 ***	-
lmo2409	unknown	2.05 ***	-
lmo2432	unknown	-	2.25 ***
lmo2454	unknown	-	3.56 ***
lmo2462	similar to dipeptidases	-	2.68 ***
lmo2463	similar to transport protein	-	2.18 ***
lmo2468 ( <i>clpP</i> )	ATP-dependent Clp protease proteolytic subunit	2.87 ***	-
lmo2480	similar to acetyltransferase	2.00 ***	-
lmo2486	unknown	3.06 *	-
lmo2487	similar to <i>B. subtilis</i> YvlB protein	3.03 ***	4.71 ***
lmo2494	similar to negative regulator of phosphate regulon	3.05 ***	-
lmo2495	similar to phosphate ABC transporter (ATP-binding protein)	4.10 ***	-
lmo2498	similar to phosphate ABC transporter (permease protein)	2.63 *	-
lmo2522	similar to hypothetical cell wall binding protein from <i>B. subtilis</i>	-	2.31 ***
lmo2535 ( <i>atpB</i> )	highly similar to H <sup>+</sup> -transporting ATP synthase chain a	-	2.11 ***
lmo2557	conserved hypothetical protein	2.54 ***	-
lmo2567	unknown	4.57 ***	-
lmo2568	unknown	3.02 **	-
lmo2569	similar to dipeptide ABC transporter (dipeptide-binding protein)	2.60 ***	-
lmo2588	similar to drug-export proteins	2.23 **	-
lmo2602	conserved hypothetical protein	-	2.87 ***
lmo2603	unknown	-	2.28 ***
lmo2613 ( <i>rplO</i> )	ribosomal protein L15	-	2.41 ***
lmo2614 ( <i>rpmD</i> )	ribosomal protein L30	-	2.92 ***
lmo2615 ( <i>rpsE</i> )	ribosomal protein S5	-	3.08 ***
lmo2616 ( <i>rplR</i> )	ribosomal protein L18	-	3.09 ***
lmo2617 ( <i>rplF</i> )	ribosomal protein L6	-	2.88 ***
lmo2618 ( <i>rpsH</i> )	ribosomal protein S8	-	3.09 ***
lmo2619 ( <i>rpsN</i> )	ribosomal protein S14	-	3.10 ***
lmo2620 ( <i>rplE</i> )	ribosomal protein L5	-	3.14 ***
lmo2621 ( <i>rplX</i> )	ribosomal protein L24	-	2.73 ***
lmo2622 ( <i>rplN</i> )	ribosomal protein L14	-	2.81 ***
lmo2623 ( <i>rpsQ</i> )	ribosomal protein S17	-	2.27 ***
lmo2624 ( <i>rpmC</i> )	ribosomal protein L29	-	2.42 ***
lmo2625 ( <i>rplP</i> )	ribosomal protein L16	-	2.06 ***
lmo2626 ( <i>rpsC</i> )	ribosomal protein S3	-	2.03 ***
lmo2628 ( <i>rplY</i> )	ribosomal protein S19	-	2.01 ***

lmo2648	similar to Phosphotriesterase	-	2.34 ***
lmo2649	similar to hypothetical PTS enzyme IIC component	-	2.33 ***
lmo2650	similar to hypothetical PTS enzyme IIB component	-	2.52 ***
lmo2669	unknown	-	4.25 ***
lmo2673	conserved hypothetical protein	-	2.72 ***
lmo2674	similar to ribose 5-phosphate epimerase	-	4.30 ***
lmo2683	similar to cellobiose phosphotransferase enzyme IIB component	2.22 **	-
lmo2689	highly similar to Mg <sup>2+</sup> transport ATPase	2.15 ***	-
lmo2694	similar to lysine decarboxylase	-	2.35 ***
lmo2745	similar to ABC transporter (ATP-binding protein)	-	2.10 ***
lmo2761	similar to beta-glucosidase	2.18 **	-
lmo2766	similar to hypothetical transcriptional regulator	3.01 ***	-
lmo2784	similar to lichenan operon transcription antiterminator licR	-	2.45 ***
lmo2786 ( <i>bvrC</i> )	bvrC	-	5.27 ***
lmo2787 ( <i>bvrB</i> )	beta-glucoside-specific phosphotransferase enzyme II ABC component	-	2.74 **
lmo2811	similar to GTPase	2.28 ***	-
lmo2830	similar to thioredoxin	-	5.56 ***
lmo2852	unknown	4.15 ***	-

<sup>a</sup>Genes were considered to be up-regulated at 7°C if the fold change compared to 37°C was  $\geq 2.0$  with an adjusted p-value  $\leq 0.05$

<sup>b</sup>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.

<sup>c</sup>gene functions were based on annotation provided by ListiList

<sup>d</sup>Superscripts are adjusted p values: "\*\*\*\*" (< 0.001), "\*\*\*" (< 0.01), "\*\*" ( $\leq 0.05$ )