

Table S2. *Listeria monocytogenes* genes transcribed at lower levels^a at 7°C compared to 37°C

| Name ^b | Gene Function ^c | Fold change ^d (7°C/37°C) | |
|-------------------------|--|-------------------------------------|------------------|
| | | Log phase | Stationary phase |
| lmo0013 (<i>qoxA</i>) | AA3-600 quinol oxidase subunit II | - | -2.04 *** |
| lmo0014 (<i>qoxB</i>) | AA3-600 quinol oxidase subunit I | - | -2.05 *** |
| lmo0018 | beta-glucosidase | -2.84 ** | - |
| lmo0021 | similar to PTS system, fructose-specific IIA component | -2.14 ** | - |
| lmo0022 | similar to PTS system, fructose-specific IIB component | -4.39 * | - |
| lmo0024 | similar to PTS system, mannose-specific IID component | -4.76 ** | - |
| lmo0027 | similar to PTS system, beta-glucosides specific enzyme IABC | -6.84 * | - |
| lmo0044 (<i>rpsF</i>) | ribosomal protein S6 | - | -3.07 *** |
| lmo0045 (<i>ssb</i>) | highly similar to single-strand binding protein (SSB) | - | -3.99 *** |
| lmo0046 (<i>rpsR</i>) | ribosomal protein S18 | - | -4.16 *** |
| lmo0053 (<i>rplI</i>) | 50S ribosomal protein L9 | - | -2.44 *** |
| lmo0101 | similar to transcription regulator | - | -2.02 *** |
| lmo0104 | unknown | -2.12 *** | - |
| lmo0109 | similar to transcriptional regulatory proteins, AraC family | -4.35 ** | -2.65 *** |
| lmo0110 | similar to lipase | -5.17 ** | - |
| lmo0180 | similar to sugar ABC transporter, permease protein | -2.39 ** | - |
| lmo0181 | similar to sugar ABC transporter, sugar-binding protein | -3.50 ** | - |
| lmo0183 | similar to alpha-glucosidase | -3.64 ** | - |
| lmo0184 | similar to oligo-1,6-glucosidase | -3.11 ** | - |
| lmo0196 | similar to <i>B. subtilis</i> SpoVG protein | - | -3.29 *** |
| lmo0197 | similar to <i>B. subtilis</i> SpoVG protein | - | -2.24 *** |
| lmo0201 (<i>plcA</i>) | phosphatidylinositol-specific phospholipase c | -2.72 *** | - |
| lmo0202 (<i>hly</i>) | listeriolysin O precursor | -14.43 *** | -3.80 *** |
| lmo0204 (<i>actA</i>) | actin-assembly inducing protein precursor | -2.38 ** | - |
| lmo0205 (<i>plcB</i>) | phospholipase C | -3.12 *** | - |
| lmo0208 | conserved hypothetical protein | -2.45 *** | - |
| lmo0217 | similar to <i>B. subtilis</i> DivIC protein | - | -2.03 *** |
| lmo0238 (<i>cysE</i>) | similar to serine O-acetyltransferase | -2.65 *** | -2.23 *** |
| lmo0239 (<i>cysS</i>) | cysteinyI-tRNA synthetase | -3.24 *** | -3.23 *** |
| lmo0240 | highly similar to <i>B. subtilis</i> YazC protein | -3.21 *** | -3.20 *** |
| lmo0241 | similar to conserved hypothetical proteins like to <i>B. subtilis</i> YacO protein | -3.35 *** | - |
| lmo0242 | similar to <i>B. subtilis</i> Yacp protein | -3.61 *** | -2.06 *** |
| lmo0243 (<i>sigH</i>) | RNA polymerase sigma-30 factor (sigma-H) | -2.78 *** | - |
| lmo0244 | similar to ribosomal protein L33 type II | - | -2.03 *** |
| lmo0245 (<i>secE</i>) | highly similar to preprotein translocase subunit | - | -2.15 *** |
| lmo0258 (<i>rpoB</i>) | RNA polymerase (beta subunit) | - | -3.57 *** |
| lmo0259 (<i>rpoC</i>) | RNA polymerase (beta subunit) | - | -2.66 *** |
| lmo0291 | conserved hypothetical protein similar to <i>B. subtilis</i> YycJ protein | - | -2.38 *** |
| lmo0295 | similar to FMN-containing NADPH-linked nitro/flavin reductase | -2.93 * | - |
| lmo0298 | similar to PTS beta-glucoside-specific enzyme IIC component | -4.38 * | - |
| lmo0299 | similar to PTS beta-glucoside-specific enzyme IIB component | -9.09 * | - |
| lmo0300 | similar to phospho-beta-glucosidase and phospho-beta-galactosidase | -6.81 * | - |

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| lmo0301 | similar to PTS beta-glucoside-specific enzyme IIA component | -2.06 ** | - |
| lmo0307 | unknown | -2.76 *** | - |
| lmo0319 | similar to phospho-beta-glucosidase | -4.41 ** | - |
| lmo0323 | similar to unknown proteins | -2.05 * | - |
| lmo0342 | similar to transketolase | -2.16 * | - |
| lmo0343 | similar to transaldolase | -3.20 * | - |
| lmo0345 | similar to sugar-phosphate isomerase | -2.90 * | -2.17 ** |
| lmo0346 | similar to triosephosphate isomerase | -3.69 ** | - |
| lmo0347 | similar to dihydroxyacetone kinase | -2.10 * | -2.68 ** |
| lmo0348 | similar to dihydroxyacetone kinase | - | -2.37 *** |
| lmo0349 | unknown | - | -4.05 ** |
| lmo0351 | similar to unknown proteins | - | -4.17 ** |
| lmo0354 | similar to fatty-acid--CoA ligase | -3.09 *** | - |
| lmo0355 | similar to Flavocytochrome C Fumarate Reductase chain A | -10.10 *** | - |
| lmo0386 | similar to <i>B. subtilis</i> IolD protein, to acetolactate synthase | -2.73 * | - |
| lmo0387 | similar to <i>B. subtilis</i> YhdG protein | - | -2.20 *** |
| lmo0388 | unknown | - | -2.06 *** |
| lmo0398 | similar to phosphotransferase system enzyme IIA | -9.25 * | - |
| lmo0399 | similar to fructose-specific phosphotransferase enzyme IIB | -3.22 * | - |
| lmo0400 | similar to fructose-specific phosphotransferase enzyme IIC | -15.17 * | - |
| lmo0401 | highly similar to <i>E. coli</i> YbgG protein, a putative sugar hydrolase | -4.82 * | - |
| lmo0402 | similar to transcriptional antiterminator (BglG family) | -3.69 * | - |
| lmo0408 | unknown | - | -2.58 *** |
| lmo0424 | similar to <i>Staphylococcus xylosus</i> glucose uptake protein | -4.27 * | - |
| lmo0425 | similar to transcription antiterminator BglG family | -15.82 ** | - |
| lmo0426 | similar to PTS fructose-specific enzyme IIA component | -25.39 ** | - |
| lmo0427 | similar to PTS fructose-specific enzyme IIB component | -19.37 ** | - |
| lmo0428 | similar to PTS fructose-specific enzyme IIC component | -12.30 ** | - |
| lmo0429 | similar to sugar hydrolase | -9.76 ** | - |
| lmo0431 | similar to acetyltransferase | -2.08 ** | - |
| lmo0443 | similar to <i>B. subtilis</i> transcription regulator LytR | - | -5.31 *** |
| lmo0471 | unknown | -5.30 * | - |
| lmo0472 | unknown | -13.43 * | - |
| lmo0493 | similar to acylase | -2.03 ** | - |
| lmo0517 | similar to phosphoglycerate mutase | -4.54 * | - |
| lmo0536 | similar to 6-phospho-beta-glucosidase | -2.67 ** | - |
| lmo0539 | similar to tagatose-1,6-diphosphate aldolase | - | -4.57 *** |
| lmo0593 | similar to transport proteins | - | -3.05 *** |
| lmo0636 | similar to unknown proteins | -2.21 *** | - |
| lmo0641 | similar to heavy metal-transporting ATPase | -2.95 ** | - |
| lmo0647 | unknown | - | -2.80 *** |
| lmo0707 | similar to flagellar hook-associated protein 2 FliD | - | -2.12 *** |
| lmo0711 | similar to flagellar basal-body rod protein flgC | - | -2.04 *** |
| lmo0721 | putative fibronectin-binding protein | -2.73 *** | - |
| lmo0726 | Hypothetical CDS | - | -3.26 *** |
| lmo0727 | similar to L-glutamine-D-fructose-6-phosphate amidotransferase | - | -3.09 *** |
| lmo0735 | similar to Ribulose-5-Phosphate 3-Epimerase | - | -2.31 *** |
| lmo0736 | similar to ribose 5-phosphate isomerase | - | -2.71 *** |
| lmo0737 | unknown | - | -2.54 *** |
| lmo0738 | similar to phosphotransferase system (PTS) beta-glucoside-specific enzyme IABC component | - | -3.38 *** |

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| lmo0739 | similar to 6-phospho-beta-glucosidase | - | -7.74 *** |
| lmo0781 | similar to mannose-specific phosphotransferase system (PTS) component IID | -2.04 * | - |
| lmo0782 | similar to mannose-specific phosphotransferase system (PTS) component IIC | -2.47 ** | - |
| lmo0788 | unknown | -3.67 ** | - |
| lmo0792 | similar to conserved hypothetical protein | - | -2.04 *** |
| lmo0794 | similar to <i>B. subtilis</i> YwnB protein | - | -2.60 *** |
| lmo0796 | conserved hypothetical protein | - | -3.71 *** |
| lmo0813 | similar to fructokinases | -3.31 *** | - |
| lmo0814 | similar to oxidoreductases | -2.36 *** | - |
| lmo0822 | similar to transcriptional regulators | - | -2.09 *** |
| lmo0829 (<i>nifJ</i>) | highly similar to pyruvate-flavodoxin oxidoreductase | -3.11 *** | - |
| lmo0864 | unknown | -2.86 * | - |
| lmo0865 | similar to phosphomannomutase | -2.18 * | - |
| lmo0912 | similar to transporters (formate) | -4.23 *** | - |
| lmo0914 | similar to PTS system, IIB component | -2.99 * | - |
| lmo0916 | similar to phosphotransferase system enzyme IIA | -12.87 ** | - |
| lmo0917 | similar to beta-glucosidase | -6.00 * | - |
| lmo0931 | similar to lipoate protein ligase A | - | -2.55 *** |
| lmo0940 | unknown | -2.68 *** | - |
| lmo0941 | unknown | -2.47 *** | - |
| lmo0942 | similar to heat shock protein HtpG | -2.27 *** | - |
| lmo0943 (<i>fri</i>) | non-heme iron-binding ferritin | - | -2.08 *** |
| lmo0944 | similar to <i>B. subtilis</i> YneR protein | - | -4.57 *** |
| lmo0953 | unknown | - | -2.28 *** |
| lmo0956 | similar to N-acetylglucosamine-6P-phosphate deacetylase (EC 3.5.1.25) | -2.73 ** | - |
| lmo0957 | similar to glucosamine-6-Phosphate isomerase (EC 5.3.1.10) | - | -2.91 *** |
| lmo0960 | similar to proteases | -2.28 * | - |
| lmo0961 | similar to proteases | -2.20 * | - |
| lmo0971 (<i>dltD</i>) | DltD protein for D-alanine esterification of lipoteichoic acid and wall teichoic acid | -2.20 *** | - |
| lmo0972 (<i>dltC</i>) | D-alanyl carrier protein | -2.02 ** | - |
| lmo0973 (<i>dltB</i>) | DltB protein for D-alanine esterification of lipoteichoic acid and wall teichoic acid | -2.13 *** | - |
| lmo0974 (<i>dltA</i>) | D-alanine-activating enzyme (<i>dae</i>), D-alanine-D-alanyl carrier protein ligase (<i>dcl</i>) | -2.13 ** | - |
| lmo1002 (<i>ptsH</i>) | PTS phosphocarrier protein Hpr (histidine containing protein) | - | -3.44 *** |
| lmo1013 | similar to conserved hypothetical proteins like to <i>B. subtilis</i> YkuT protein | -3.00 *** | - |
| lmo1043 | similar to molybdopterin-guanine dinucleotide biosynthesis MobB | -2.31 * | - |
| lmo1046 | similar to molybdenum cofactor biosynthesis protein C | -2.37 * | - |
| lmo1047 | similar to molybdenum cofactor biosynthesis protein A | -2.04 ** | - |
| lmo1051 | similar to formylmethionine deformylase and to <i>B. subtilis</i> YkrB protein | - | -2.32 *** |
| lmo1057 | similar to L-lactate dehydrogenase | - | -3.93 *** |
| lmo1058 | similar to <i>B. subtilis</i> YktA protein | - | -4.23 *** |
| lmo1059 | unknown | - | -4.42 *** |
| lmo1086 | similar to CDP-ribitol pyrophosphorylase | - | -2.44 *** |
| lmo1087 | similar to glucitol dehydrogenase | - | -2.20 * |
| lmo1120 | unknown | -2.11 * | - |
| lmo1121 | unknown | -2.56 ** | - |

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| lmo1123 | unknown | -2.96 ** | - |
| lmo1124 | unknown | -2.40 * | - |
| lmo1140 | unknown | -2.66 ** | -2.62 *** |
| lmo1253 | similar to transcription regulator GntR family | - | -2.66 *** |
| lmo1254 | similar to alpha,alpha-phosphotrehalase | -9.60 *** | - |
| lmo1255 | similar to PTS system trehalose specific enzyme IIBC | -5.19 ** | - |
| lmo1257 | unknown | -36.15 *** | - |
| lmo1261 | unknown | - | -2.98 *** |
| lmo1293 (<i>glpD</i>) | similar to glycerol 3 phosphate dehydrogenase | -5.25 ** | - |
| lmo1303 | similar to <i>B. subtilis</i> YneA protein | -2.12 *** | - |
| lmo1348 | similar to aminomethyltransferase | -3.32 * | -2.37 *** |
| lmo1349 | similar to glycine dehydrogenase (decarboxylating) subunit 1 | -4.62 ** | -3.93 *** |
| lmo1350 | similar to glycine dehydrogenase (decarboxylating) subunit 2 | -5.26 ** | -4.74 *** |
| lmo1369 | similar to phosphotransbutyrylase | -3.36 ** | - |
| lmo1371 | similar to branched-chain alpha-keto acid dehydrogenase E3 subunit | -2.05 *** | -2.09 *** |
| lmo1372 | similar to branched-chain alpha-keto acid dehydrogenase E1 subunit (2-oxoisovalerate dehydrogenase alpha subunit) | -2.33 *** | - |
| lmo1373 | similar to branched-chain alpha-keto acid dehydrogenase E1 subunit (2-oxoisovalerate dehydrogenase beta subunit) | -2.29 *** | - |
| lmo1380 | unknown | - | -2.44 *** |
| lmo1388 (<i>tcsA</i>) | CD4+ T cell-stimulating antigen, lipoprotein | - | -2.70 ** |
| lmo1389 | similar to sugar ABC transporter, ATP-binding protein | -2.02 ** | - |
| lmo1391 | similar to sugar ABC transporter, permease protein | -2.07 ** | - |
| lmo1399 | similar to unknown protein | - | -2.13 *** |
| lmo1406 (<i>pflB</i>) | pyruvate formate-lyase | -2.48 *** | - |
| lmo1413 | putative peptidoglycan bound protein (LPXTG motif) | -2.02 ** | - |
| lmo1423 | unknown | - | -2.35 *** |
| lmo1424 | similar to manganese transport proteins NRAMP | -2.26 *** | -5.39 *** |
| lmo1460 | similar to <i>B. subtilis</i> RecO protein involved in DNA repair and homologous recombination | -2.55 *** | -3.41 *** |
| lmo1463 | similar to cytidine deaminase | - | -2.57 *** |
| lmo1464 | similar to diacylglycerol kinase | - | -2.35 *** |
| lmo1465 | similar to unknown proteins | - | -2.19 *** |
| lmo1466 | similar to unknown proteins | - | -2.33 *** |
| lmo1522 | similar to unknown proteins | - | -2.82 *** |
| lmo1535 | similar to unknown proteins | - | -2.28 ** |
| lmo1538 | similar to glycerol kinase | -3.62 ** | - |
| lmo1539 | similar to glycerol uptake facilitator | -4.65 ** | - |
| lmo1570 (<i>pykA</i>) | highly similar to pyruvate kinases | - | -3.26 *** |
| lmo1589 (<i>argB</i>) | highly similar to N-acetylglutamate 5-phosphotransferase | -2.72 * | - |
| lmo1590 (<i>argJ</i>) | highly similar to ornithine acetyltransferase and amino-acid acetyltransferases | -3.31 * | - |
| lmo1591 (<i>argC</i>) | similar to N-acetylglutamate gamma-semialdehyde dehydrogenases | -9.92 ** | - |
| lmo1604 | similar to 2-cys peroxiredoxin | - | -2.31 *** |
| lmo1605 (<i>murC</i>) | similar to UDP-N-acetyl muramate-alanine ligases | -2.22 *** | - |
| lmo1606 | similar to DNA translocase | -2.47 *** | - |
| lmo1608 | similar to unknown proteins | - | -2.18 *** |
| lmo1614 | similar to unknown proteins | -2.13 *** | - |
| lmo1626 | unknown | -2.29 *** | - |
| lmo1627 (<i>trpA</i>) | highly similar to tryptophan synthase (alpha subunit) | -3.70 *** | - |

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| lmo1628 (<i>trpB</i>) | highly similar to tryptophan synthase (beta subunit) | -3.28 *** | - |
| lmo1630 (<i>trpC</i>) | highly similar to indol-3-glycerol phosphate synthases | -2.66 ** | - |
| lmo1631 (<i>trpD</i>) | highly similar to anthranilate phosphoribosyltransferase | -3.16 *** | - |
| lmo1632 (<i>trpG</i>) | highly similar to anthranilate synthase beta subunit | -4.31 *** | - |
| lmo1634 | similar to Alcohol-acetaldehyde dehydrogenase | -24.49 *** | - |
| lmo1657 (<i>tsf</i>) | translation elongation factor | - | -2.07 *** |
| lmo1658 (<i>rpsB</i>) | 30S ribosomal protein S2 | - | -2.07 *** |
| lmo1683 | similar to transcription regulators (Fur family), PerR in <i>B. subtilis</i> | - | -2.65 *** |
| lmo1687 | similar to hypothetical proteins | - | -6.32 *** |
| lmo1703 | similar to similar to RNA methyltransferases | - | -3.14 *** |
| lmo1727 | similar to transcription regulators (LacI family) | -2.94 ** | - |
| lmo1728 | some similarities to cellobiose-phosphorylase | -2.41 * | - |
| lmo1730 | similar to sugar ABC transporter binding protein | -3.37 * | -2.16 ** |
| lmo1731 | similar to sugar ABC transporter, permease protein | -2.21 * | - |
| lmo1768 (<i>purF</i>) | glutamine phosphoribosylpyrophosphate amidotransferase | -2.07 * | - |
| lmo1793 | similar to putative 16S rRNA processing protein RimM | - | -2.35 *** |
| lmo1825 | similar to pantothenate metabolism flavoprotein homolog | - | -2.09 *** |
| lmo1848 | similar metal cations ABC transporter (permease protein) | - | -2.48 *** |
| lmo1849 | similar to metal cations ABC transporter, ATP-binding proteins | - | -2.42 *** |
| lmo1862 | similar to hypothetical proteins | - | -2.47 *** |
| lmo1863 | similar to hypothetical proteins | - | -2.88 *** |
| lmo1865 | similar to conserved hypothetical proteins | - | -8.51 *** |
| lmo1866 | similar to conserved hypothetical proteins | - | -3.82 *** |
| lmo1867 | similar to pyruvate phosphate dikinase | - | -10.04 *** |
| lmo1879 (<i>cspD</i>) | similar to cold shock protein | -8.15 ** | - |
| lmo1883 | similar to chitinases | -9.03 ** | -5.16 *** |
| lmo1893 | unknown | - | -2.21 *** |
| lmo1917 (<i>pflA</i>) | similar to pyruvate formate-lyase | -2.78 * | - |
| lmo1941 | similar to unknown proteins | - | -2.48 *** |
| lmo1956 (<i>fur</i>) | similar to transcriptional regulator (Fur family) | - | -3.01 *** |
| lmo1975 | similar to <i>E. coli</i> DNA-damage-inducible protein dinP | -2.88 *** | - |
| lmo1994 | similar to transcription regulators (LacI family) | -2.39 *** | - |
| lmo1995 (<i>dra</i>) | similar to deoxyribose-phosphate aldolase | -2.68 *** | - |
| lmo1997 | similar to PTS mannose-specific enzyme IIA component | -12.64 ** | - |
| lmo1998 | similar to opine catabolism protein | -12.57 ** | - |
| lmo1999 | weakly similar to glucosamine-fructose-6-phosphate | -7.81 ** | - |
| lmo2000 | similar to PTS mannose-specific enzyme IID component | -36.08 ** | - |
| lmo2001 | similar to PTS mannose-specific enzyme IIC component | -16.00 ** | - |
| lmo2002 | similar to PTS mannose-specific enzyme IIB component | -3.76 ** | - |
| lmo2003 | similar to transcription regulator GntR family | -12.52 ** | - |
| lmo2004 | similar to transcription regulator GntR family | -7.72 ** | - |
| lmo2016 (<i>cspB</i>) | similar to major cold-shock protein | -2.28 ** | -15.39 *** |
| lmo2039 (<i>pbpB</i>) | similar to penicillin-binding protein 2B | -2.03 *** | - |
| lmo2046 | weakly similar to ketopantoate reductase involved in thiamin biosynthesis | - | -2.06 *** |
| lmo2063 | unknown | -2.57 *** | - |
| lmo2068 (<i>groEL</i>) | class I heat-shock protein (chaperonin) GroEL | - | -2.02 *** |
| lmo2083 | unknown | -2.08 ** | - |
| lmo2090 (<i>argG</i>) | similar to argininosuccinate synthase | -4.80 * | - |
| lmo2091 (<i>argH</i>) | similar to argininosuccinate lyase | -2.04 ** | - |
| lmo2099 | similar to transcription antiterminator | -2.51 * | - |

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|-------------------------|--|------------|-----------|
| lmo2105 | similar to ferrous iron transport protein B | -2.36 * | - |
| lmo2119 | similar to unknown proteins | - | -2.72 *** |
| lmo2125 | similar to maltose/maltodextrin ABC-transporter (binding protein) | -2.23 * | - |
| lmo2132 | unknown | - | -2.26 *** |
| lmo2159 | similar to oxidoreductase | -9.05 ** | - |
| lmo2160 | similar to unknown proteins | -8.43 ** | - |
| lmo2161 | unknown | -7.33 * | - |
| lmo2162 | similar to unknown proteins | -5.39 ** | - |
| lmo2163 | similar to oxidoreductase | -6.22 * | - |
| lmo2173 | similar to sigma-54-dependent transcriptional activator | -3.93 *** | - |
| lmo2175 | similar to dehydrogenase | -6.32 ** | - |
| lmo2213 | similar to unknown protein | -2.03 * | - |
| lmo2225 (<i>citG</i>) | similar to fumarate hydratase | - | -2.09 *** |
| lmo2238 | similar to transport system permease protein | -3.16 ** | - |
| lmo2251 | similar to amino acid ABC transporter (ATP-binding protein) | -2.76 * | - |
| lmo2332 (<i>int</i>) | putative integrase [Bacteriophage A118] | -2.08 *** | - |
| lmo2335 (<i>fruA</i>) | highly similar to phosphotransferase system (PTS) fructose-specific enzyme IIA component | - | -2.78 *** |
| lmo2340 | similar to <i>Erwinia chrysanthemi</i> IndA protein | -2.35 ** | -2.94 *** |
| lmo2362 | similar to amino acid antiporter (acid resistance) | -7.78 ** | -8.17 *** |
| lmo2363 | similar to glutamate decarboxylase | -5.95 *** | -7.59 *** |
| lmo2385 | similar to <i>B. subtilis</i> YuxO protein | - | -2.00 ** |
| lmo2391 | conserved hypothetical protein similar to <i>B. subtilis</i> YhFK protein | - | -2.12 *** |
| lmo2406 | similar to <i>B. subtilis</i> YunF protein | - | -2.72 *** |
| lmo2410 | unknown | -2.42 *** | - |
| lmo2451 | similar to preprotein translocase subunit SecG | - | -2.78 *** |
| lmo2452 | similar to carboxylesterase | - | -2.90 *** |
| lmo2453 | similar to lipolytic enzyme | - | -4.28 *** |
| lmo2484 | similar to <i>B. subtilis</i> YvID protein | - | -2.26 ** |
| lmo2539 (<i>glyA</i>) | highly similar to glycine hydroxymethyltransferase | - | -2.11 *** |
| lmo2540 | similar to phosphatases | - | -2.17 *** |
| lmo2579 | conserved hypothetical protein | -2.46 *** | - |
| lmo2584 | similar to formate dehydrogenase associated protein | -2.83 * | - |
| lmo2585 | similar to <i>B. subtilis</i> YrhD protein | -4.45 * | - |
| lmo2586 | similar to formate dehydrogenase alpha chain | -2.05 ** | - |
| lmo2596 (<i>rpsI</i>) | ribosomal protein S9 | - | -2.11 *** |
| lmo2646 | unknown | -71.90 *** | - |
| lmo2647 | similar to creatinine amidohydrolase | -14.48 ** | - |
| lmo2648 | similar to Phosphotriesterase | -21.38 ** | - |
| lmo2649 | similar to hypothetical PTS enzyme IIC component | -23.67 ** | - |
| lmo2650 | similar to hypothetical PTS enzyme IIB component | -51.77 * | - |
| lmo2651 | similar to mannitol-specific PTS enzyme IIA component | -28.46 ** | - |
| lmo2652 | similar to transcriptional antiterminator | -3.39 *** | - |
| lmo2666 | similar to PTS system galactitol-specific enzyme IIB component | -2.03 * | - |
| lmo2667 | similar to PTS system galactitol-specific enzyme IIA component | -2.02 * | - |
| lmo2675 | unknown | -4.51 *** | -2.18 *** |
| lmo2676 | similar to UV-damage repair protein | -3.79 *** | -2.45 *** |
| lmo2695 | similar to dihydroxyacetone kinase | -3.20 * | - |
| lmo2696 | similar to hypothetical dihydroxyacetone kinase | -3.85 * | - |

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|-------------------------|--|-----------|-----------|
| lmo2697 | unknown | -2.83 * | - |
| lmo2730 | similar to phosphatase | -2.02 *** | - |
| lmo2731 | similar to transcription regulator (RpiR family) | -2.39 *** | - |
| lmo2771 | similar to beta-glucosidase | -2.42 ** | - |
| lmo2772 | similar to beta-glucoside-specific enzyme IIABC | -2.14 * | - |
| lmo2773 | similar to transcription antiterminator | -2.77 *** | - |
| lmo2785 (<i>kat</i>) | catalase | - | -3.72 *** |
| lmo2788 (<i>bvrA</i>) | transcription antiterminator | -2.10 *** | - |
| lmo2795 | similar to <i>E. coli</i> RpiR transcription regulator | -3.38 ** | - |
| lmo2796 | similar to transcription regulator | -2.46 * | - |
| lmo2797 | similar to phosphotransferase system mannitol-specific enzyme IIA | -2.06 * | - |
| lmo2799 | similar to phosphotransferase system mannitol-specific enzyme IIBC | -10.46 * | - |
| lmo2800 | similar to dehydrogenase | -7.41 * | - |
| lmo2809 | hypothetical secreted protein | -2.71 * | - |
| lmo2820 | amino-terminal domain similar to transcription regulators | -2.04 *** | - |
| lmo2828 | unknown | -2.24 *** | -2.87 *** |
| lmo2851 | similar to AraC-type regulatory protein | - | -2.63 *** |

^aGenes were considered to be up-regulated at 7°C if the fold change compared to 37°C was ≥ 2.0 with an adjusted p-value ≤ 0.05

^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 are based on annotation provided by ListiList.

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