

**Table S1. Microarray analysis of MogR-negative *L. monocytogenes* relative to wild-type during growth in different conditions.**

	37°C	37°C	RT	
	J774	BHI	BHI	
<i>lmo0019</i>	*-1.1	<b>3.7</b>	3.2	unknown
<i>lmo0036</i>	*2.1	*1.8	<b>-9.5</b>	similar to ornithine carbamoyltransferase
<i>lmo0043</i>	*-1.1	2.1	<b>5.5</b>	similar to arginine deiminase
<i>lmo0093</i>	*1.2	*-1.3	<b>4.8</b>	similar to ATP synthase epsilon chain
<i>lmo0157</i>	*-1.5	<b>-9.9</b>	*1.3	similar to ATP dependent helicase
<i>lmo0178</i>	*-1.1	<b>-3.6</b>	<b>-4.9</b>	similar to xylose repressor
<i>lmo0179</i>	*-1.1	<b>-4.1</b>	<b>-5.0</b>	similar to sugar ABC transporters, permease proteins
<i>lmo0181</i>	*1.6	<b>-4.9</b>	-3.2	similar to sugar ABC transporter, sugar-binding protein
<i>lmo0202</i>	*1.1	*1.8	<b>-7.3</b>	listeriolysin O precursor
<i>lmo0254</i>	*1.2	*1.2	<b>-4.7</b>	unknown
<i>lmo0262</i>	*-1.5	<b>4.0</b>	*1.1	internalin G
<i>lmo0278</i>	*1.1	*-1.3	<b>-4.4</b>	similar to sugar ABC transporter, ATP-binding protein
<i>lmo0279</i>	*-1.3	<b>-4.0</b>	*-1.2	highly similar to anaerobic ribonucleoside-triphosphate reductase
<i>lmo0280</i>	*-1.1	<b>-3.8</b>	-2.1	highly similar to anaerobic ribonucleotide reductase activator protein
<i>lmo0300</i>	*1.3	*-1.5	<b>-3.8</b>	similar to phospho-beta-glucosidase and phospho-beta-galactosidase
<i>lmo0321</i>	*1.2	*-1.1	<b>5.0</b>	similar to unknown proteins
<i>lmo0322</i>	*1.3	*2.3	<b>4.0</b>	similar to unknown proteins
<i>lmo0327</i>	*1.1	*-1.1	<b>-7.1</b>	similar to cell surface proteins (LPXTG motif)
<i>lmo0343</i>	*1.4	*-1.5	<b>-7.8</b>	similar to transaldolase
<i>lmo0344</i>	*1.3	*-1.3	<b>-12.1</b>	similar to dehydrogenase/reductase
<i>lmo0345</i>	*1.1	*-2.0	<b>-4.1</b>	similar to sugar-phosphate isomerase
<i>lmo0347</i>	*1.5	*1.1	<b>-11.2</b>	similar to dihydroxyacetone kinase
<i>lmo0372</i>	*-1.2	*-1.3	<b>-4.1</b>	similar to beta-glucosidase
<i>lmo0377</i>	*1.2	*-1.1	<b>-3.7</b>	unknown
<i>lmo0393</i>	*-1.1	-2.2	<b>-4.1</b>	unknown
<i>lmo0398</i>	*1.6	<b>9.9</b>	<b>-8.2</b>	similar to phosphotransferase system enzyme IIA
<i>lmo0399</i>	*1.3	*2.4	<b>-7.4</b>	similar to fructose-specific phosphotransferase enzyme IIB
<i>lmo0400</i>	*1.2	<b>14.5</b>	<b>-8.7</b>	similar to fructose-specific phosphotransferase enzyme IIC
<i>lmo0401</i>	*1.5	*1.8	<b>-7.0</b>	highly similar to <i>E. coli</i> YbgG protein, a putative sugar hydrolase
<i>lmo0406</i>	*-1.1	2.8	<b>4.4</b>	similar to <i>B. subtilis</i> YyaH protein
<i>lmo0444</i>	*1.1	<b>-3.6</b>	-2.3	conserved hypothetical protein
<i>lmo0469</i>	*-1.5	*1.0	<b>3.7</b>	unknown
<i>lmo0495</i>	*1.1	<b>-7.3</b>	*-1.4	similar to transmembrane protein
<i>lmo0498</i>	*1.2	*-1.4	<b>-10.9</b>	similar to ribose 5-phosphate isomerase
<i>lmo0536</i>	*1.2	*-1.6	<b>-3.9</b>	similar to 6-phospho-beta-glucosidase
<i>lmo0554</i>	*1.3	*-1.2	<b>5.3</b>	similar to NADH-dependent butanol dehydrogenase
<i>lmo0589</i>	*-1.1	*1.5	<b>4.1</b>	unknown
<i>lmo0611</i>	*-1.0	*1.2	<b>3.6</b>	similar to acyl-carrier protein phosphodiesterase and NAD(P)H dehydrogenase
<i>lmo0643</i>	*-1.1	*1.1	<b>-3.8</b>	similar to putative transaldolase
<i>lmo0655</i>	*-1.2	*1.2	<b>4.2</b>	similar to phosphoprotein phosphatases
<i>lmo0670</i>	*-1.6	<b>5.7</b>	-1.2	unknown

<i>lmo0672</i>	*1.2	*1.7	<b>4.0</b>	similar to unknown protein
<i>lmo0673</i>	<b>4.3</b>	<b>4.4</b>	<b>5.8</b>	unknown
<i>lmo0675</i>	*1.4	<b>4.5</b>	*-1.1	similar to flagellar switch protein FliN
<i>lmo0677</i>	*1.7	<b>5.1</b>	2.9	similar to flagellar biosynthesis protein FliQ
<i>lmo0678</i>	2.5	*6.9	<b>6.7</b>	similar to flagellar biosynthetic protein FliR
<i>lmo0679</i>	<b>8.4</b>	<b>100.0</b>	<b>4.5</b>	similar to flagellar biosynthetic protein FlhB
<i>lmo0680</i>	<b>5.8</b>	<b>5.8</b>	*1.3	similar to flagella-associated protein FlhA
<i>lmo0682</i>	2.5	<b>9.6</b>	*-1.2	similar to flagellar hook-basal body protein FlgG
<i>motA</i>	<b>3.8</b>	<b>4.4</b>	2.0	similar to motility protein (flagellar motor rotation) MotA
<i>motB</i>	*4.7	<b>6.4</b>	*-1.3	similar to motility protein (flagellar motor rotation) MotB
<i>lmo0687</i>	<b>5.6</b>	<b>10.3</b>	*-1.2	unknown
<i>lmo0688</i>	<b>15.8</b>	1.3	2.4	similar to unknown protein
<i>lmo0689</i>	<b>5.5</b>	<b>13.1</b>	-2.1	similar to CheA activity-modulating chemotaxis protein CheV
<i>flaA</i>	<b>84.1</b>	<b>63.2</b>	*1.1	flagellin protein
<i>cheY</i>	<b>9.0</b>	<b>6.2</b>	<b>3.6</b>	chemotaxis response regulator CheY
<i>cheA</i>	<b>17.5</b>	<b>14.0</b>	2.0	two-component sensor histidine kinase CheA
<i>lmo0693</i>	<b>23.2</b>	<b>100.0</b>	2.0	similar to flagellar motor switch protein FliY C-terminal part
<i>lmo0694</i>	<b>14.5</b>	<b>25.5</b>	2.9	unknown
<i>lmo0695</i>	<b>20.0</b>	<b>16.7</b>	*2.1	unknown
<i>lmo0696</i>	<b>12.9</b>	<b>25.2</b>	3.2	similar to flagellar hook assembly protein
<i>lmo0697</i>	<b>30.9</b>	<b>29.7</b>	2.1	similar to flagellar hook protein FlgE
<i>lmo0698</i>	<b>19.8</b>	<b>26.3</b>	*1.2	weakly similar to flagellar switch protein
<i>lmo0699</i>	<b>100.0</b>	<b>100.0</b>	1.6	similar to flagellar switch protein FliM
<i>lmo0700</i>	<b>12.4</b>	<b>18.8</b>	1.9	similar to flagellar motor switch protein FliY
<i>lmo0701</i>	<b>5.8</b>	*4.5	3.1	unknown
<i>lmo0702</i>	<b>11.9</b>	<b>81.0</b>	3.3	unknown
<i>lmo0703</i>	<b>38.7</b>	<b>50.1</b>	<b>4.0</b>	unknown
<i>lmo0704</i>	<b>9.1</b>	<b>67.3</b>	2.2	unknown
<i>lmo0705</i>	<b>50.2</b>	<b>58.6</b>	<b>5.6</b>	similar to flagellar hook-associated protein FlgK
<i>lmo0706</i>	<b>14.3</b>	<b>34.7</b>	*1.8	similar to flagellar hook-associated protein 3 FlgL
<i>lmo0707</i>	<b>53.9</b>	<b>100.0</b>	<b>7.1</b>	similar to flagellar hook-associated protein 2 FliD
<i>lmo0708</i>	<b>28.3</b>	<b>34.0</b>	*1.4	similar to hypothetical flagellar protein
<i>lmo0709</i>	<b>28.1</b>	<b>37.2</b>	1.6	unknown
<i>lmo0710</i>	<b>20.7</b>	<b>12.0</b>	1.7	similar to flagellar basal-body rod protein FlgB
<i>lmo0711</i>	<b>18.7</b>	<b>9.0</b>	1.7	similar to flagellar basal-body rod protein FlgC
<i>lmo0712</i>	<b>18.7</b>	<b>43.4</b>	1.7	similar to flagellar hook-basal body complex protein FliE
<i>lmo0713</i>	<b>27.9</b>	<b>5.2</b>	2.9	similar to flagellar basal-body M-ring protein FliF
<i>lmo0714</i>	<b>15.5</b>	<b>13.5</b>	1.9	similar to flagellar motor switch protein FliG
<i>lmo0715</i>	<b>7.2</b>	3.2	*1.3	unknown
<i>lmo0716</i>	<b>11.1</b>	<b>3.7</b>	*1.7	similar to H <sup>+</sup> -transporting ATP synthase alpha chain FliI, flagellar-specific
<i>lmo0717</i>	<b>9.0</b>	*3.1	3.2	similar to transglycosylase
<i>lmo0723</i>	<b>9.3</b>	<b>45.6</b>	<b>7.6</b>	similar to methyl-accepting chemotaxis protein
<i>lmo0724</i>	<b>13.1</b>	<b>36.8</b>	<b>5.6</b>	similar to <i>B. subtilis</i> YvpB protein
<i>lmo0736</i>	*-1.0	*1.2	<b>-18.4</b>	similar to ribose 5-phosphate isomerase
<i>lmo0813</i>	*1.1	*-1.4	<b>-3.6</b>	similar to fructokinases
<i>lmo0852</i>	*1.4	*-1.5	<b>5.9</b>	similar to transcription regulator TetR/AcrR family

<i>lmo0869</i>	*1.1	<b>3.6</b>	*-8.7	unknown
<i>lmo0903</i>	*-1.2	1.2	<b>4.2</b>	conserved hypothetical protein
<i>lmo0914</i>	*1.4	<b>4.2</b>	*3.4	similar to PTS system, IIB component
<i>lmo1042</i>	*1.2	*1.4	<b>-5.9</b>	similar to molybdopterin biosynthesis protein MoeA
<i>lmo1043</i>	*1.1	*1.4	<b>-4.7</b>	similar to molybdopterin-guanine dinucleotide biosynthesis MobB
<i>lmo1044</i>	*1.5	1.9	<b>-4.2</b>	similar to molybdopterin converting factor, subunit 2
<i>lmo1064</i>	-1.8	*1.4	<b>3.7</b>	similar to membrane and transport proteins
<i>lmo1123</i>	*-1.3	*1.0	<b>3.9</b>	unknown
<i>lmo1129</i>	*-1.2	*-1.0	<b>-18.5</b>	similar to unknown proteins
<i>lmo1150</i>	*-1.1	2.1	<b>-5.1</b>	similar to <i>S. typhimurium</i> regulatory protein PocR
<i>lmo1186</i>	*-100	*-1.8	<b>-7.8</b>	similar to <i>E. coli</i> ethanolamine utilization protein EutH
<i>lmo1202</i>	*1.5	*1.1	<b>-3.7</b>	similar to anaerobic cobalt chelatase in cobalamin biosynthesis
<i>lmo1254</i>	*-1.1	*1.2	<b>-4.5</b>	similar to alpha, alpha-phosphotrehalase
<i>lmo1256</i>	*1.1	*1.2	<b>-5.1</b>	unknown
<i>lmo1261</i>	*-1.2	*1.1	<b>6.4</b>	unknown
<i>lmo1266</i>	*-1.3	*2.5	<b>11.2</b>	unknown
<i>lmo1298</i>	1.2	*-1.4	<b>4.1</b>	similar to glutamine synthetase repressor
<i>lmo1310</i>	*-1.2	*-1.6	<b>5.7</b>	similar to <i>E. coli</i> YbdN protein
<i>lmo1369</i>	*-1.2	*-1.0	<b>3.7</b>	similar to phosphotransbutyrylase
<i>lmo1395</i>	*-1.1	*1.3	<b>3.6</b>	similar to unknown protein
<i>lmo1424</i>	*-1.1	*1.4	<b>4.2</b>	similar to manganese transport proteins NRAMP
<i>lmo1428</i>	*-1.3	*-1.2	<b>3.5</b>	similar to glycine betaine/carnitine/choline ABC transporter (ATP-binding protein)
<i>lmo1527</i>	*-1.3	*-1.5	<b>3.9</b>	similar to protein-export membrane protein SecDF
<i>lmo1536</i>	*1.0	*1.1	<b>3.7</b>	similar to prephenate dehydratase PheA
<i>lmo1545</i>	*-1.3	*1.1	<b>4.5</b>	similar to cell-division inhibition (septum placement) protein MinC
<i>comC</i>	<b>-100.0</b>	<b>-100.0</b>	*7.1	similar to <i>B. subtilis</i> late competence protein ComC (type IV prepilin peptidase)
<i>lmo1556</i>	*-1.1	*-1.1	<b>3.6</b>	highly similar to porphobilinogen deaminases (hydroxymethylbilane synthase)
<i>lmo1557</i>	-1.3	*-1.2	<b>3.8</b>	highly similar to glutamyl-tRNA reductase
<i>lmo1685</i>	*-1.1	*1.1	<b>-4.3</b>	glutamate-1-semialdehyde aminotransferase
<i>lmo1699</i>	<b>3.7</b>	<b>36.3</b>	<b>6.9</b>	some similarities to methyl-accepting chemotaxis proteins
<i>lmo1700</i>	2.7	<b>4.1</b>	<b>9.7</b>	unknown
<i>lmo1715</i>	1.4	*1.5	<b>-4.0</b>	similar to hypothetical proteins
<i>lmo1718</i>	*1.1	*-1.1	<b>-3.9</b>	similar to putative outer surface protein
<i>lmo1730</i>	*-1.1	*1.7	<b>-8.3</b>	similar to sugar ABC transporter binding protein
<i>lmo1732</i>	*1.1	*1.4	<b>-3.7</b>	similar to sugar ABC transporter, permease protein
<i>lmo1749</i>	*-1.2	*-1.3	<b>8.5</b>	similar to shikimate kinase
<i>lmo1755</i>	*-1.1	*-1.3	<b>3.5</b>	glutamyl-tRNA(Gln) amidotransferase (subunit A)
<i>lmo1790</i>	*1.0	<b>5.7</b>	*1.9	similar to unknown proteins
<i>lmo1810</i>	*-1.1	*1.2	<b>4.8</b>	similar to unknown proteins
<i>lmo1815</i>	*-1.2	*1.1	<b>4.3</b>	similar to unknown protein
<i>lmo1838</i>	*-1.1	*-1.3	<b>4.0</b>	highly similar to aspartate carbamoyltransferase
<i>lmo1852</i>	*-1.1	-1.6	<b>-4.1</b>	similar to putative mercuric ion binding proteins
<i>lmo1883</i>	*1.0	-1.4	<b>-3.7</b>	similar to chitinases
<i>lmo1912</i>	*-1.3	*1.8	<b>5.6</b>	similar to unknown proteins (hypothetical sensory transduction histidine kinase)
<i>lmo1931</i>	*1.4	*1.4	<b>4.4</b>	similar to 2-heptaprenyl-1,4-naphthoquinone methyltransferase
<i>lmo1933</i>	*-1.1	*1.1	<b>4.0</b>	similar to GTP cyclohydrolase I

<i>lmo1999</i>	*1.1	*-1.5	<b>-35.8</b>	weakly similar to glucosamine-fructose-6-phosphate aminotransferase
<i>lmo2001</i>	*-1.7	*1.3	<b>-5.4</b>	similar to PTS mannose-specific enzyme IIC component
<i>lmo2002</i>	*1.3	*-1.2	<b>-8.1</b>	similar to PTS mannose-specific enzyme IIB component
<i>lmo2004</i>	*1.1	*-1.1	<b>-5.2</b>	similar to transcription regulator GntR family
<i>lmo2046</i>	*1.4	*-1.0	<b>4.1</b>	weakly similar to ketopantoate reductase involved in thiamin biosynthesis
<i>lmo2058</i>	*-1.1	*1.3	<b>7.1</b>	similar to heme O oxygenase
<i>lmo2066</i>	*-1.5	*1.3	<b>-4.2</b>	unknown
<i>lmo2080</i>	*-1.3	<b>-4.3</b>	*1.1	unknown
<i>lmo2098</i>	*1.1	-2.2	<b>-5.4</b>	similar to PTS system galactitol-specific enzyme IIA component
<i>lmo2121</i>	*-100	*-1.1	<b>-7.1</b>	similar to maltosephosphorylase
<i>lmo2124</i>	*1.0	*1.4	<b>-7.2</b>	similar to maltodextrin ABC-transport system (permease)
<i>lmo2125</i>	*1.1	*4.0	<b>-37.7</b>	similar to maltose/maltodextrin ABC-transporter (binding protein)
<i>lmo2130</i>	*-1.3	2.2	<b>4.1</b>	similar to unknown protein
<i>lmo2135</i>	*1.2	*1.2	<b>-4.1</b>	similar to PTS system, fructose-specific enzyme IIC component
<i>lmo2137</i>	*1.2	*-1.7	<b>-3.8</b>	similar to PTS system, fructose-specific enzyme IIA component
<i>lmo2174</i>	*-1.3	*3.8	<b>5.2</b>	similar to unknown proteins
<i>lmo2212</i>	*-1.4	*-1.1	<b>3.6</b>	similar to uroporphyrinogen III decarboxylase
<i>lmo2232</i>	-1.4	*-1.1	<b>3.5</b>	similar to unknown proteins
<i>lmo2256</i>	*1.1	*-1.2	<b>-4.0</b>	similar to unknown proteins
<i>lmo2279</i>	*-100	*-2.4	<b>-4.7</b>	holin [Bacteriophage A118]
<i>lmo2280</i>	*1.1	*-1.1	<b>-4.9</b>	protein gp23 [Bacteriophage A118]
<i>lmo2281</i>	*1.4	*-2.1	<b>-4.5</b>	protein gp22 [Bacteriophage A118]
<i>lmo2282</i>	1.3	*-1.7	<b>-5.9</b>	protein gp21 [Bacteriophage A118]
<i>lmo2283</i>	*-5.0	*-1.1	<b>-4.4</b>	protein gp20 [Bacteriophage A118]
<i>lmo2284</i>	*1.8	*1.1	<b>-5.1</b>	Protein gp19 [Bacteriophage A118]
<i>lmo2285</i>	*1.0	*-24.5	<b>-5.8</b>	Protein gp18 [Bacteriophage A118]
<i>lmo2286</i>	*-1.5	*1.1	<b>-3.8</b>	Protein gp17 [Bacteriophage A118]
<i>lmo2288</i>	*2.2	*1.8	<b>-3.6</b>	Protein gp15 [Bacteriophage A118]
<i>lmo2290</i>	1.3	*-1.1	<b>-4.4</b>	Protein gp13 [Bacteriophage A118]
<i>lmo2291</i>	*1.3	*1.3	<b>-4.3</b>	major tail shaft protein [Bacteriophage A118]
<i>lmo2295</i>	1.4	*-1.5	<b>-4.1</b>	protein gp8 [Bacteriophage A118]
<i>lmo2297</i>	*1.2	*-1.7	<b>-3.6</b>	putative scaffolding protein [Bacteriophage A118]
<i>lmo2298</i>	*-2.1	*-2.1	<b>-4.7</b>	protein gp4 [Bacteriophage A118]
<i>lmo2299</i>	*1.1	*-1.5	<b>-4.4</b>	putative portal protein [Bacteriophage A118]
<i>lmo2300</i>	*-1.5	*-1.2	<b>-7.5</b>	putative terminase large subunit from Bacteriophage A118
<i>lmo2304</i>	-2.1	*1.5	<b>-3.6</b>	bacteriophage A118 gp65 protein
<i>lmo2314</i>	*-1.2	*3.1	<b>-3.5</b>	unknown
<i>lmo2324</i>	*-1.5	*1.4	<b>-5.9</b>	similar to anti-repressor [Bacteriophage A118]
<i>lmo2326</i>	*-1.3	*-1.0	<b>-4.7</b>	similar to protein gp41 [Bacteriophage A118]
<i>lmo2352</i>	*-2.5	*-1.7	<b>5.5</b>	similar to LysR family transcription regulator
<i>lmo2494</i>	-1.7	<b>4.8</b>	*1.4	similar to negative regulator of phosphate regulon
<i>lmo2585</i>	1.3	*-1.2	<b>-3.7</b>	similar to <i>B. subtilis</i> YrhD protein
<i>lmo2586</i>	1.5	*1.4	<b>-3.7</b>	similar to formate dehydrogenase alpha chain
<i>lmo2646</i>	*-1.0	<b>4.3</b>	<b>-28.9</b>	unknown
<i>lmo2647</i>	*-1.2	<b>5.6</b>	<b>-17.1</b>	similar to creatinine amidohydrolase
<i>lmo2648</i>	*1.0	*-1.3	<b>-13.9</b>	similar to phosphotriesterase

<i>lmo2650</i>	*1.4	*3.9	<b>-11.7</b>	similar to hypothetical PTS enzyme IIB component
<i>lmo2651</i>	*1.2	<b>3.9</b>	<b>-10.2</b>	similar to mannitol-specific PTS enzyme IIA component
<i>lmo2659</i>	*1.4	<b>-5.7</b>	<b>-7.6</b>	similar to ribulose-phosphate 3-epimerase
<i>lmo2660</i>	*1.3	-1.9	<b>-7.1</b>	similar to transketolase
<i>lmo2661</i>	1.5	*-1.4	<b>-41.7</b>	similar to ribulose-5-phosphate 3-epimerase
<i>lmo2662</i>	*1.1	*-2.9	<b>-17.3</b>	similar to ribose 5-phosphate epimerase
<i>lmo2663</i>	*1.0	*1.2	<b>-33.9</b>	similar to polyol dehydrogenase
<i>lmo2664</i>	*-1.0	*-1.5	<b>-26.8</b>	similar to sorbitol dehydrogenase
<i>lmo2665</i>	*-1.1	*1.3	<b>-23.0</b>	similar to PTS system galactitol-specific enzyme IIC component
<i>lmo2666</i>	*3.7	*-1.0	<b>-20.5</b>	similar to PTS system galactitol-specific enzyme IIB component
<i>lmo2667</i>	*1.5	2.8	<b>-11.6</b>	similar to PTS system galactitol-specific enzyme IIA component
<i>lmo2668</i>	*-1.3	-2.0	<b>-13.2</b>	similar to transcriptional antiterminator (BglG family)
<i>lmo2684</i>	3.2	<b>47.2</b>	*-1.3	similar to cellobiose phosphotransferase enzyme IIC component
<i>lmo2730</i>	*-1.2	-2.4	<b>-3.6</b>	similar to phosphatase
<i>lmo2731</i>	*1.1	-2.3	<b>-4.2</b>	similar to transcription regulator (RpiR family)
<i>lmo2742</i>	*-1.0	-1.2	<b>-3.9</b>	unknown
<i>lmo2752</i>	*-1.3	<b>-4.1</b>	-1.6	similar to ABC transporter, ATP-binding protein
<i>lmo2763</i>	*-1.0	-6.2	<b>-3.9</b>	similar to PTS cellobiose-specific enzyme IIC
<i>lmo2764</i>	*1.3	<b>-6.0</b>	*-3.0	similar to xylose operon regulatory protein and to glucose kinase
<i>lmo2773</i>	*-1.3	-3.4	<b>-4.1</b>	similar to transcription antiterminator
<i>lmo2818</i>	*1.2	*-1.3	<b>-3.6</b>	similar to transmembrane efflux protein
<i>lmo2848</i>	*1.4	-2.2	<b>-3.9</b>	highly similar to L-rhamnose isomerase

\* P-value greater than 0.01; bold-type indicates expression change greater than 3.5-fold with a P-value less than 0.01. Gene names correspond to the gene names on the ListiList server <http://genolist.pasteur.fr/ListiList/>. The functions of the encoded proteins are indicated according to the EGD-e genome annotation where possible [1]. Rosetta Resolver software analysis sets the maximal fold-change possible as 100 [2]. Only genes which yielded an expression change greater than 3.5-fold with a P-value less than 0.01 in at least one of the growth conditions are listed in the table.

## References

1. Glaser P, Frangeul L, Buchrieser C, Rusniok C, Amend A, et al. (2001) Comparative genomics of *Listeria* species. *Science* 294: 849-852.
2. Hughes TR, Marton MJ, Jones AR, Roberts CJ, Stoughton R, et al. (2000) Functional discovery via a compendium of expression profiles. *Cell* 102: 109-126.