

Table S2. Putative MogR-regulated genes defined by genome-wide search for TTTT-N₅-AAAA sites in upstream sequences.

		<u>J774, 37°C</u>		<u>BHL, 37°C</u>		<u>BHL, RT</u>		
Accession number	Position (bp)	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Gene function
<i>lmo00004</i>	140, 109	1.0	0.88908	-1.7	2.62E-06	1.6	0.07202	similar to <i>B. subtilis</i> YaaA protein
<i>lmo00010</i>	104, 74	-1.2	0.06273	-1.2	0.26415	1.7	0.05114	similar to mevalonate kinase
<i>lmo00189</i>	136, 116	-1.1	0.58281	-1.1	0.38322	1.3	0.16889	highly similar to <i>B. subtilis</i> Veg protein
<i>lmo00675</i>	150, 119	1.4	0.05607	4.5	0.00005	-1.1	0.6259	similar to flagellar switch protein FliN
<i>lmo00690</i>	132, 101, 80	84.1	0	63.2	3.36E-44	1.1	0.47534	flagellin protein (<i>flaA</i>)
<i>lmo00691</i>	124, 103, 72	9.0	4.64E-13	6.2	0.00095	3.6	4.09E-20	chemotaxis response regulator CheY (<i>cheY</i>)
<i>lmo00703</i>	117, 96	38.7	1.85E-16	50.1	6.25E-23	4.0	0.00001	unknown
<i>lmo00723</i>	98, 77, 56	9.3	6.68E-41	45.6	0	7.6	0	similar to methyl-accepting chemotaxis protein
<i>lmo01013</i>	168, 147	-1.0	0.97158	1.0	0.95848	1.2	0.14379	similar to conserved hypothetical proteins
<i>lmo01014</i>	235, 214	-1.4	0.03998	1.2	0.42587	3.0	3.73E-08	highly similar to glycine betaine ABC transporter (<i>gbuA</i>)
<i>lmo01019</i>	130, 109	-1.2	0.24261	1.3	0.39726	2.0	0.00003	similar to <i>B. subtilis</i> YitL protein
<i>lmo01074</i>	221, 201	-1.1	0.70105	1.3	0.3562	2.3	0.05055	highly similar to teichoic acid permease TagG
<i>lmo01266</i>	88, 67	-1.3	0.29896	2.5	0.10742	11.2	1.35E-22	unknown
<i>lmo01648</i>	89, 58	-1.0	0.87133	1.3	0.59553	1.8	0.07119	unknown
<i>lmo01687</i>	128, 107	-1.2	0.14102	-1.1	0.19832	1.4	0.00188	similar to hypothetical proteins
<i>lmo01948</i>	181, 150	-1.6	0.0001	-1.1	0.37668	-1.0	0.9712	similar to two-component response regulator ResD (<i>resD</i>)
<i>lmo02142</i>	84, 53	-1.2	0.44595	1.5	0.05834	-3.2	0.03729	unknown
<i>lmo02143</i>	172, 141	1.2	0.74517	2.3	0.11148	-1.9	0.09321	weakly similar to mannose-6-phosphate isomerase
<i>lmo02165</i>	142, 121	-1.9	0.00009	1.2	0.51474	2.3	0.00007	similar to transcription regulator CRP/FNR family
<i>lmo02185</i>	46, 25	-3.4	0.31371	8.3	1	2.0	0.7739	unknown
<i>lmo02191</i>	282, 252, 221	-1.4	0.00203	1.3	0.02575	1.9	0.00018	similar to unknown proteins
<i>lmo02206</i>	108, 87	-1.1	0.67469	-1.0	0.5747	1.2	0.69028	similar to endopeptidase ATP-binding chain B ClpB (<i>clpB</i>)
<i>lmo02337</i>	68, 47	-1.1	0.39406	-1.3	0.23786	-2.0	0.06151	similar to regulatory protein DeoR family
<i>lmo02338</i>	180, 160	-1.0	0.78353	-1.2	0.12752	-1.5	0.00557	aminopeptidase C
<i>lmo02378</i>	238, 218	-1.0	0.81321	1.3	0.4245	1.7	0.0002	similar to proteins involved in resistance to cholate

The ListiList server was searched for genes containing a minimum of two TTTT-N₅-AAAA sites (allowing one mismatch/site) spaced 7-9 bp or 17-19 bp apart (1 or 2 helix turns, respectively) within 300 bp of upstream sequences. Accession numbers correspond to those given by the ListiList server <http://genolist.pasteur.fr/ListiList/>. Fold expression change is given for MogR-negative *L. monocytogenes* relative to wild-type. Candidate genes that were found by microarray analysis to be MogR-regulated (>3.5-fold, P < 0.01) are underlined with the fold expression change in bold. The position refers to the location of an upstream TTTT-N₅-AAAA site relative to the translational start codon of the gene listed. The functions of the encoded proteins are indicated according to the EGD-e genome annotation where possible, and gene names with a non-*lmo* suffix are indicated in parentheses [1]. Fold change and P-values are derived from Rosetta Resolver analysis of microarray data generated under the conditions listed.

References

1. Glaser P, Frangeul L, Buchrieser C, Rusniok C, Amend A, et al. (2001) Comparative genomics of *Listeria* species. Science 294: 849-852.