

Table S3: Strain-specific proteins of *L. monocytogenes* QOC2 compared with *L. monocytogenes* QOC1

Locus_tag	Length [bp]	Description	Best Blast hit	Amino acid identity to best hit
LMQOC2_40206	360	Putative lipoprotein	<i>LMLG_1212 L. monocytogenes</i> Finland 1998 (YP_005972342)	99%
LMQOC2_40207	123	Protein of unknown function	No hits	
LMQOC2_40208	870	Putative lipoprotein	<i>lmo2595 L. monocytogenes</i> EGDe (NP_466118.1)	100%
LMQOC2_40270	1392	Putative dntp triphosphohydrolase	<i>LMOG_01851 L. monocytogenes</i> J0161 (YP_005966720)	100%
LMQOC2_40537	318	Conserved protein of unknown function	<i>LMRG_02492 L. monocytogenes</i> 10403S (YP_005961215)	99%
LMQOC2_40538	435	Conserved protein of unknown function	<i>LMOh7858_0077 L. monocytogenes</i> H7858 (EAL10133)	99%
LMQOC2_40539	309	Conserved protein of unknown function	<i>LMRG_02494 L. monocytogenes</i> 10403S (YP_005961217)	100%
LMQOC2_40542	276	Conserved protein of unknown function	<i>LMOh7858_0087 L. monocytogenes</i> H7858 (EAL10143)	100%
LMQOC2_40543	714	Conserved protein of unknown function	<i>LMOh7858_0088 L. monocytogenes</i> H7858 (EAL10144)	100%
LMQOC2_40547	408	Conserved protein of unknown function	<i>BN424_1238 Carnobacterium maltaromaticum</i> LMA28 (CCO10735)	49%
LMQOC2_40550	294	Conserved protein of unknown function	<i>lmo0069 L. monocytogenes</i> EGDe (NP_463602)	98%
LMQOC2_40603*	204	Protein of unknown function	<i>LMHCC_2507 L. monocytogenes</i> HCC23 (ACK40842))	100%
LMQOC2_40604*	1077	Protein of unknown function	<i>LMHCC_2507 L. monocytogenes</i> HCC23 (ACK40842))	99%
LMQOC2_20106	387	Transcriptional repressor, blai/meci family	<i>lmo0252 L. monocytogenes</i> EGDe (NP_463783.1)	99%
LMQOC2_20107	1041	Regulatory sensor-transducer, blar1/mecr1 family	<i>lmo0253 L. monocytogenes</i> EGDe (NP_463784.1)	99%
LMQOC2_20108	663	Hypothetical protein	<i>lmo0254 L. monocytogenes</i> EGDe (NP_463785.1)	100%
LMQOC2_20128	2955	Hypothetical protein, putative ntpase (NACHT family)	<i>LMOSLCC2376_0245 L. monocytogenes</i> SLCC2376 (YP_006689443.1)	98%
LMQOC2_20152	1407	Conserved hypothetical protein, AAA-type atpase	<i>UKC_01057 Enterococcus gilvus</i> ATCC BAA-350 (EOI56872.1)	37%
LMQOC2_20153	519	Protein of unknown function	<i>HMPREF9282_00162 Veillonella ratti</i> ACS-216-V-Col6b (EKU79354.1)	23%
LMQOC2_20154	876	Conserved hypothetical protein protein	<i>HPL003_07175 Paenibacillus terrae</i> HPL-003 (YP_005074421.1)	27%
LMQOC2_20155	126	Hypothetical protein	<i>HMPREF9519_01901 Enterococcus faecalis</i> TX1346 (EFU17174.1)	71%
LMQOC2_20156	1239	Hypothetical protein	<i>lse_0277 L. seeligeri</i> SLCC3954 (YP_003463516.1)	59%
LMQOC2_20157	810	Hypothetical protein	<i>HMPREF9505_00770 Enterococcus faecalis</i> TX0109 (EFM70909.1)	39%
LMQOC2_20165	2652	Putative DNA/RNA helicase	<i>LMOSLCC7179_0296 L. monocytogenes</i> SLCC7179 (YP_006697989.1)	99%
LMQOC2_20166	933	5'-nucleotidase	<i>LMFG_00788 L. monocytogenes</i> FSL J2-071 (EFD91373.1))	100%

LMQOC2_20176	1200	Cell wall surface anchor family protein	<i>lmo0320 (vip) L. monocytogenes</i> EGDe (NP_463850.1)	99%
LMQOC2_20229	1188	Membrane protein of unknown function	<i>Enterococcus faecalis</i> (WP_010709719.1)	30%
LMQOC2_20238	456	Hypothetical protein	<i>LMRG_00071 L. monocytogenes</i> 10403S (AEO05392.1)	99%
LMQOC2_20302	549	Hypothetical protein	<i>LMOSLCC7179_0432 L. monocytogenes</i> SLCC7179 (CBY59638.1)	99%
LMQOC2_20314	210	Hypothetical protein	<i>LMRG_02887 L. monocytogenes</i> 10403S (AEO05470.1)	100%
LMQOC2_20315	546	Hypothetical protein	<i>LMRG_00151 L. monocytogenes</i> 10403S (AEO05471.1)	99%
LMQOC2_20366	489	CRISPR-associated recb family exonuclease Cas4a	<i>M642_15185 L. monocytogenes</i> C1-387 (AGR03388)	99%
LMQOC2_20468	534	Acetyltransferase, GNAT family	<i>lmo0614 L. monocytogenes</i> EGDe (NP_464141.1)	99%
LMQOC2_20645	1974	Cell wall surface anchor family protein (LPXTG motif)	<i>LMOF6854_0833 L. monocytogenes</i> F6854 (WP_003723802.1)	99%
LMQOC2_20962	678	Hypothetical protein, putative transcriptional regulator	<i>LMOSLCC2376_1068 L. monocytogenes</i> SLCC2376 (CBY63100.1)	96%
LMQOC2_20963	702	Hypothetical protein, putative DNA binding protein	<i>LMOSLCC2376_1069 L. monocytogenes</i> SLCC2376 (CBY63101.1)	96%
LMQOC2_20964	810	Hypothetical protein	<i>LMBG_00132 L. monocytogenes</i> FSL J1-194 (EFG00615)	99%
LMQOC2_20971	504	Hypothetical protein	<i>LMHCC_1530 L. monocytogenes</i> HCC23 (YP_002350488.1)	99%
LMQOC2_20972	306	Hypothetical protein	<i>LMOF6854_1160 L. monocytogenes</i> F6854 (EAL07611.1)	100%
LMQOC2_20973	474	Hypothetical protein	<i>LMOF6854_1159 L. monocytogenes</i> F6854 (EAL07501)	97%
LMQOC2_20974	426	Hypothetical protein	<i>LMOF6854_1161 L. monocytogenes</i> F6854 (EAL07502)	96%
LMQOC2_21040	153	Hypothetical protein	<i>HMPREF0557_01844 L. innocua</i> ATCC 33091 (EHN61104.1)	76%
LMQOC2_30208	105	Hypothetical protein	<i>LMOSLCC2372_2071 L. monocytogenes</i> SLCC2372 (YP_006685398.1)	97%
LMQOC2_30306	441	Hypothetical protein	<i>LMRG_01254 L. monocytogenes</i> 10403S (YP_005963216)	100%
LMQOC2_30307	672	Hypothetical protein	<i>LMRG_01255 L. monocytogenes</i> 10403S (YP_005963217)	100%

* putative pseudogenes, probable split gene