

Table S3. Unique genes of LMO referenced to L.monocytogenes EGD-e_160963

ORF_id	Sequence_id	Group_id	start	end	strand	COG_id	COG_annotation	VTDB_annotation	Uniprot_annotation
or_10	ALS19B24.1	group_1348	12918	13886	-	COG1577	I-Mevalonate kinase,ERG12,Isoprenoid bio-		Mevalonate kinase OS=Pyrococcus abyssi (strain GDS) / OX=272844 GN=pykP PE=3 Sv=1
or_19	ALS19B24.1	group_1915	23132	23953	-	COG4990	R-Predicted cysteine peptidase, C39 family,-		Uncharacterized protein YpB OS= Bacillus subtilis (strain 168) / OX=224308 GN=yvpB PE=3 Sv=1
or_20	ALS19B24.1	group_2301	24194	24934	-	COG2188	K-DNA-binding transcriptional regulator, Gr-		Probable fructosylase utilization operon transcriptional repressor OS=Escherichia coli O157:H7 OX=83334 GN=frR PE=3 Sv=2
or_21	ALS19B24.1	group_2287	24950	25351	-	COG4893	P-Tyrosine carboxypeptidase system, mannose/fr-		PTS system sorbose-specific EAIIc subunit OS=Neisseria pneumoniae OX=373 GN=psrF PE=3 Sv=1
or_23	ALS19B24.1	group_2292	25862	26665	-	COG3715	F-Phosphotransferase system, mannose/fr-		N-Acetylglucosamine permease IC component 1 OS=Escherichia coli (strain K12) / OX=83333 GN=nagC PE=1 Sv=1
or_25	ALS19B24.1	group_2294	27495	28199	-	COG4821	R-Uncharacterized conserved protein, cont-		UPF0309 protein Lmo0205 OS=Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e) / OX=169963 GN=lmo0205 PE=3 Sv=1
or_26	ALS19B24.1	group_2297	28254	28895	-	COG3142	P-Copper homeostasis protein CusC/CuCuC-		PF03932 family protein CusC OS=Enterococcus faecalis (strain ATCC 700802 / V583) OX=226185 GN=cusC PE=2 Sv=1
or_28	ALS19B24.1	group_1836	31088	31963	-	COG6119	M-Muonemyltransferase carbonoyltransferase		Probable muonemyltransferase OS= Bacillus subtilis (strain 168) / OX=224308 GN=muM PE=2 Sv=2
or_52	ALS19B24.1	group_1808	54839	56812	-	COG3887	T-Cyclic di-AMP phosphodiesterase GdpP, c-		Cyclic-di-AMP phosphodiesterase PdeA OS=Listeria monocytogenes serotype 1/2a (strain 104035) / OX=393133 GN=pdeA PE=3 Sv=1
or_78	ALS19B24.1	group_33	82599	84437	-	-	-	-	Toxin BC_0920 OS= Bacillus cereus (strain ATCC 14579 / DSM 31 / CCUG 7414 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NCT 2599 / NRRL B-3711) / OX=226900 GN=BC_0920 PE=1 Sv=1
or_85	ALS19B24.1	group_602	88888	94767	-	-	-	-	-
or_87	ALS19B24.1	group_2206	97127	97369	-	COG636	C-FoF1-type ATP synthase, membrane subu-		ATP synthase subunit c, chloroplastic OS=Plasium sativum / OX=3888 GN=atpH PE=1 Sv=1
or_94	ALS19B24.1	group_219	103204	103836	-	-	-	-	-
or_107	ALS19B24.1	group_2220	116972	117805	-	COG2207	K-AraC-type DNA-binding domain and AraC-		HTH-type transcriptional activator RhaS OS=Escherichia fergusonii (strain ATCC 33469 / DSM 13696 / CCUG 18766 / IAM 14443 / JCM 21226 / LMIG 7866 / NBRC 102419 / NCTC 12128 / CDC 0568-73) OX=585054 GN=rhaS PE=3 Sv=1
or_129	ALS19B24.1	group_2250	133951	134710	-	COG2209	T-BAL domain, c-di-GMP-specific phosphod-		Signaling protein YkwO OS=Escherichia coli (strain K12) / OX=224308 GN=ykwO PE=3 Sv=2
or_135	ALS19B24.1	group_1804	139960	140853	-	COG1173	E-ABC-type dipeptide/glycoprotein/peckel-		Oligopeptide transport system permease protein AppC OS= Bacillus subtilis (strain 168) / OX=224308 GN=appC PE=3 Sv=1
or_137	ALS19B24.1	group_180	141337	141705	-	-	-	-	-
or_138	ALS19B24.1	group_33	141702	143006	-	-	-	-	-
or_152	ALS19B24.1	group_1788	151839	152645	-	COG1108	-ABC type Mo2+/Zn2+ transport system, I-		Toxin BC_0920 OS= Bacillus cereus (strain ATCC 14579 / DSM 31 / CCUG 7414 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NCT 2599 / NRRL B-3711) / OX=226900 GN=BC_0920 PE=1 Sv=1
or_167	ALS19B24.1	group_170	168011	169270	-	COG5361	X-Uncharacterized conserved protein;		High-affinity zinc uptake system membrane protein ZnuB OS= Bacillus subtilis (strain 168) / OX=224308 GN=znuB PE=1 Sv=1
or_174	ALS19B24.1	group_1800	175763	177760	-	COG1043	J-Methionyl-tRNA synthetase,MetG;Amino-		Methionine-tRNA ligase OS=Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e) / OX=169963 GN=metG PE=3 Sv=1
or_185	ALS19B24.1	group_1412	191296	193473	-	COG0300	J165 RNA A1518 and A1519 N6 dimethyl-		Ribosomal small subunit methyltransferase A OS=Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e) / OX=169963 GN=rsmA PE=3 Sv=1
or_197	ALS19B24.1	group_2242	205643	206473	-	COG0664	TzAMP-binding domain of CRP or a regulat-		PTS system oligo-beta-mannoside-specific EAIIc component OS= Bacillus subtilis (strain 168) / OX=224308 GN=mannP PE=3 Sv=1
or_201	ALS19B24.1	group_2382	209470	211389	-	-	(ActA) actin assembly inducing protein precursor (ActA) -Regulation		Actin assembly-inducing protein YnfA OS=Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e) / OX=169963 GN=actA PE=1 Sv=1
or_204	ALS19B24.1	group_2379	212366	212689	-	-	-	-	Uncharacterized protein Lmo0206 OS=Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e) / OX=169963 GN=lmo0206 PE=3 Sv=1
or_205	ALS19B24.1	group_2335	212824	213285	-	COG4808	S-Uncharacterized protein YehH, DUf13-		Uncharacterized lipoprotein Lmo0207 OS=Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e) / OX=169963 GN=lmo0207 PE=3 Sv=1
or_216	ALS19B24.1	group_2344	224652	226508	-	COG634	T-Hsp90alpha guanine prosthaphorin phospho-		Probable hsp90alpha guanine prosthaphorin phosphatase OS= Bacillus subtilis (strain 168) / OX=224308 GN=hsp90 PE=3 Sv=1
or_219	ALS19B24.1	group_772	229840	230724	-	COG1281	O-RexDex-regulated molecular chaperone, H-		33 kDa chaperonin OS=Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e) / OX=169963 GN=hspD PE=3 Sv=1
or_233	ALS19B24.1	group_2322	256491	256964	-	COG0245	I2C-methyl-D-erythritol 2,4-cyclodiphosph-		2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase OS=Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e) / OX=169963 GN=hspF PE=3 Sv=1
or_237	ALS19B24.1	group_1649	260896	261306	-	COG1939	J235 RNA maturation mini-RNAe III.MmC-		Mini-ribonuclease 3 OS=Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e) / OX=169963 GN=miniR PE=3 Sv=1
or_255	ALS19B24.1	group_1726	276728	280333	-	COG0086	X-DNA-directed RNA polymerase, beta' sub-		DNA-directed RNA polymerase subunit beta' OS=Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e) / OX=169963 GN=ppc PE=3 Sv=1
or_267	ALS19B24.1	group_8	293845	295281	-	COG2723	G-Beta-glucosidase BglG/Phi-Bacillus subtilis		Aryl-phospho-beta-D-glucosidase BglG OS= Bacillus subtilis (strain 168) / OX=224308 GN=bglG PE=1 Sv=1
or_293	ALS19B24.1	group_2318	321234	324005	-	COG3711	K-Transcriptional antitermimator,BglG;		Probable hKAB operon regulator OS= Bacillus subtilis (strain 168) / OX=224308 GN=hK PE=1 Sv=1
or_296	ALS19B24.1	group_8	325729	327120	-	COG2723	G-Beta-glucosidase/Phi-Bacillus beta-glucos-		6-phospho-beta-galactosidase OS=Clostridium acetobutylicum (strain ATCC 25424 / DSM 752 / JCM 1419 / LMIG 5710 / VMH B-1787) / OX=272562 GN=hacG PE=3 Sv=1
or_297	ALS19B24.1	group_2314	327113	327454	-	COG1447	G-Phosphotransferase system, cellobiose/Phi-		PTS system oligo-beta-mannoside-specific EAIIc component OS= Bacillus subtilis (strain 168) / OX=224308 GN=mannP PE=3 Sv=1
or_301	ALS19B24.1	group_2244	329923	330999	-	COG2008	E-Threonine aldolase,GLY1;		Low-specificity L-threonine aldolase 1 OS=Arabidopsis thaliana OX=3702 GN=TLA1 PE=1 Sv=1
or_311	ALS19B24.1	group_2027	340278	340952	-	COG0819	H-Aminopyrimidine aminohydrolase TenA (-		Aminopyrimidine aminohydrolase OS= Bacillus subtilis (strain 168) / OX=224308 GN=tenA PE=1 Sv=1
or_312	ALS19B24.1	group_2115	340945	341754	-	COG2145	E-Hydroxyphenylhydrolase YnfH (-) sugar kinase		Mannosylglycerate hydrolase OS=Escherichia coli (strain K12) / OX=83333 GN=hmg PE=1 Sv=2
or_314	ALS19B24.1	group_2226	342551	343195	-	COG3352	H-Thiamine monophosphate synthase,THE-		Thiamine-phosphate synthase OS=Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e) / OX=169963 GN=hmg PE=3 Sv=1
or_317	ALS19B24.1	group_2249	346377	347036	-	-	-	-	-
or_321	ALS19B24.1	group_23	349326	350228	-	-	-	-	HTH-type transcriptional regulator rgg OS=Streptococcus gordonii (strain Challis / ATCC 35105 / BCR 15272 / CH1 / DLI / V288) / OX=467705 GN=rgg PE=4 Sv=1
or_336	ALS19B24.1	group_2334	370445	370534	-	-	-	-	-
or_340	ALS19B24.1	group_2243	373832	374596	-	COG1028	I-NAD(P)-dependent dehydrogenase, short-		NAD-dependent glycerol dehydrogenase OS=Listeria innocua serovar 6a (strain ATCC BAA-680 / CLIP 11262) / OX=272626 GN=goD PE=1 Sv=1
or_341	ALS19B24.1	group_2295	374621	375067	-	COG0698	G-Ribose 5-phosphate isomerase RpiB/RpiB-		Ribose-5-P isomerase B OS=Listeria innocua serovar 6a (strain ATCC BAA-680 / CLIP 11262) / OX=272626 GN=rpiB PE=1 Sv=1
or_343	ALS19B24.1	group_2299	375842	376492	-	COG376	G-Dihydroxyacetone kinase,DAK3;Isopreno-		PF-dependent dihydroxyacetone kinase 2, ADP-binding subunit DhaL OS=Listeria innocua serovar 6a (strain ATCC BAA-680 / CLIP 11262) / OX=272626 GN=dhaL PE=2 Sv=1
or_345	ALS19B24.1	group_2302	377631	377872	-	COG0599	R-Uncharacterized conserved protein YnfZ,-		Putative glycerol transporter Lmo067 OS=Listeria innocua serovar 6a (strain ATCC BAA-680 / CLIP 11262) / OX=272626 GN=lmo067 PE=2 Sv=1
or_346	ALS19B24.1	group_2293	377888	378319	-	-	-	-	Putative glycerol transporter Lmo068 OS=Listeria innocua serovar 6a (strain ATCC BAA-680 / CLIP 11262) / OX=272626 GN=lmo068 PE=2 Sv=1
or_347	ALS19B24.1	group_2300	378404	378781	-	COG3412	T-Phosphotransferase subunit DhaM of the-		Putative dihydroxyacetone kinase 2, phosphoryl donor subunit DhaM OS=Listeria innocua serovar 6a (strain ATCC BAA-680 / CLIP 11262) / OX=272626 GN=dhaM2 PE=1 Sv=1
or_348	ALS19B24.1	group_2217	378964	379728	-	COG1349	K-GNA-binding transcriptional regulator o-		HTH-type transcriptional regulator GmrR OS=Listeria innocua serovar 6a (strain ATCC BAA-680 / CLIP 11262) / OX=272626 GN=gmrR PE=4 Sv=1
or_349	ALS19B24.1	group_2353	379794	380027	-	COG0456	J-Ribosomal protein S18 acetylase RlmA and		Uncharacterized N-acetyltransferase ynfJ2 OS=Neisseria meningitidis OX=2788 GN=ynfJ2 PE=2 Sv=1
or_386	ALS19B24.1	group_2214	412457	412825	-	-	-	-	-
or_396	ALS19B24.1	group_2341	419544	420002	-	COG1762	GT-Phosphotransferase system, mannitol/fr-		PTS system 2-O-alpha-mannosyl-D-glycerate-specific EIIBC component OS=Escherichia coli (strain K12) / OX=83333 GN=hmgA PE=1 Sv=1
or_398	ALS19B24.1	group_26	420335	421447	-	COG1299	G-Phosphotransferase system, fructose/sp-		PTS system fructose-specific EIIBC component OS=Vibrio cholerae serotype O1 (strain ATCC 39315 / El Tor Inaba 16966) / OX=243277 GN=fruA PE=2 Sv=1
or_399	ALS19B24.1	group_22	421460	424206	-	COG0383	E-Alpha-mannosidase,MngB;		Probable alpha-mannosidase OS=Escherichia coli (strain K12) / OX=83333 GN=hmg PE=1 Sv=2
or_403	ALS19B24.1	group_904	427104	428111	-	COG3036	P-Phosphate/sulfate permease,PIA;		Probable low-affinity inorganic phosphate transporter OS= Bacillus subtilis (strain 168) / OX=224308 GN=piP PE=3 Sv=2
or_423	ALS19B24.1	group_2288	445049	447010	-	COG3711	K-Transcriptional antitermimator,BglG;		Probable hKAB operon regulator OS= Bacillus subtilis (strain 168) / OX=224308 GN=hK PE=1 Sv=1
or_426	ALS19B24.1	group_26	447804	448010	-	COG1299	G-Phosphotransferase system, fructose/sp-		PTS system fructose-specific EIIBC component OS=Rhodococcus capsulatus OX=1261 GN=fruA PE=3 Sv=1
or_427	ALS19B24.1	group_22	448956	451508	-	COG0383	E-Alpha-mannosidase,MngB;		Mannosylglycerate hydrolase OS=Escherichia coli (strain K12) / OX=83333 GN=hmgB PE=1 Sv=2
or_435	ALS19B24.1	group_2257	466517	467362	-	COG7002	R-Uncharacterized conserved protein YnfJ,-		Quinone oxidoreductase 2 OS=Escherichia coli (strain K12) / OX=83333 GN=qrnB PE=1 Sv=1
or_440	ALS19B24.1	group_2077	472330	472644	-	-	-	-	-
or_442	ALS19B24.1	group_2352	473936	476716	-	COG1511	S-Uncharacterized membrane protein YnfH,-		Uncharacterized protein YnfH OS= Bacillus subtilis (strain 168) / OX=224308 GN=ynfH PE=4 Sv=2
or_449	ALS19B24.1	group_2352	483934	484599	-	COG3619	S-Uncharacterized membrane protein YnfK,-		UPF0700 transmembrane protein YnfK OS= Bacillus subtilis (strain 168) / OX=224308 GN=ynfK PE=3 Sv=1
or_450	ALS19B24.1	group_2343	484620	485375	-	-	-	-	-
or_456	ALS19B24.1	group_2222	492918	494018	-	COG3535	S-Uncharacterized conserved protein, DUf1-		Uncharacterized protein YnfM OS= Bacillus subtilis (strain 168) / OX=224308 GN=ynfM PE=3 Sv=1
or_457	ALS19B24.1	group_1395	494011	495561	-	COG0145	E-DNA-methyltransferase XosA/xosA/methyl-		Putative D-/L-hydantoinase subunit A OS=Pseudomonas sp. (strain K5671) / OX=29441 GN=hyuA PE=3 Sv=1
or_463	ALS19B24.1	group_19	501693	501959	-	COG2963	X-Transposase InsE and inactivated derivat-		-
or_480	ALS19B24.1	group_2235	516076	516636	-	COG1309	K-DNA-binding protein, AcrR family, includ-		HTH-type dhaKLM operon transcriptional activator DhaS OS=Lactococcus lactis subsp. lactis (strain IL14003) / OX=272623 GN=dhaS PE=1 Sv=1
or_481	ALS19B24.1	group_1802	517646	518446	-	COG1763	S-Myo-inositol cross-reactive antigen (function U-		Oleate hydratase OS=Elaeobacter kriegia meningoseptica OX=238 GN=hyaA PE=1 Sv=1
or_495	ALS19B24.1	group_2346	531294	532233	-	COG0697	E-RibP permease of the drp12 transporter		Putative drp12 transporter YnfM OS= Bacillus subtilis (strain 168) / OX=224308 GN=ynfM PE=3 Sv=1
or_506	ALS19B24.1	group_133	534021	534167	-	COG0166	ER-Threonine dehydrogenase or related Zn-		Galactol 1-phosphatase 5 OS=Escherichia coli (strain K12) / OX=83333 GN=gatD PE=1 Sv=1
or_511	ALS19B24.1	group_1745	545609	546289	-	COG0518	F-GMP synthase, glutamine amidotransfer-		Putative glutamine amidotransferase-like protein YnfE OS=Salmonella typhimurium (strain LT / SGSC1412 / ATCC 700702) / OX=99287 GN=ynfE PE=3 Sv=2
or_516	ALS19B24.1	group_2363	549916	551346	-	COG2843	M-Poly gamma glutamate biosynthesis pro-		Capsule biosynthesis protein CapA OS= Bacillus anthracis OX=1392 GN=capA PE=2 Sv=2
or_525	ALS19B24.1	group_170	560443	561174	-	COG0361	X-Uncharacterized conserved protein;		-
or_528	ALS19B24.1	group_2225	564257	565753	-	COG2598	R-Predicted metal-dependent carbohydrate-		-
or_529	ALS19B24.1	group_2221	565764	567014	-	COG1215	N-Glycosyltransferase, catalytic subunit of (-		Uncharacterized glycosyltransferase YnfM OS= Bacillus subtilis (strain 168) / OX=224308 GN=ynfM PE=3 Sv=1
or_530	ALS19B24.1	group_2128	567030	569081	-	-	-	-	Uncharacterized protein YnfN OS= Bacillus subtilis (strain 168) / OX=224308 GN=ynfN PE=3 Sv=1
or_531	ALS19B24.1	group_2218	569094	569948	-	COG2199	T-TGGDEF domain, diguanylate cyclase (c-di-		ATP phosphoribosyltransferase OS=Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e) / OX=169963 GN=hmg PE=3 Sv=1
or_558	ALS19B24.1	group_1667	605401	606042	-	COG0040	E-ATP phosphoribosyltransferase,HistH;Hist-		Homoserine O-acetyltransferase OS=Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e) / OX=169963 GN=hmgA PE=3 Sv=1
or_594	ALS19B24.1	group_1783	635317	636423	-	COG0021	E-Homoserine O-acetyltransferase,METZ-M-		-
or_597	ALS19B24.1	group_2305	638781	639482	-	COG0664	TzAMP-binding domain of CRP or a regulat-		-
or_627	ALS19B24.1	group_2320	664242	668990	-	-	-	-	Collagen adhesin OS=Staphylococcus aureus OX=1280 GN=cna PE=1 Sv=1
or_628	ALS19B24.1	group_2324	669086	669361	-	-	-	-	-
or_629	ALS19B24.1	group_2254	669623	669950	-	COG1335	HR-Nicotinamidase-related amidase,PhnA/F-		Uncharacterized isochromanase family protein HVO_2328 OS=Halobacter volcanii (strain ATCC 29605 / DSM 3757 / JCM 8879 / NBRC 14742 / NCIMB 2012 / VKM B-1768 / DS2) / OX=309890 GN=HVO_2328 PE=1 Sv=1
or_635	ALS19B24.1	group_2319	670876	671855	-	COG1299	G-Phosphotransferase system, fructose/sp-		Fructose-1,6-bisphosphate lyase component 1 OS=Escherichia coli (strain K12) / OX=83333 GN=hmg PE=3 Sv=1
or_660	ALS19B24.1	group_2344	698785	699420	-	COG2231	L3-Methyladenine DNA glycosylase, HHM-C-		Putative DNA repair glycosylase MJI34.8 OS=Methanocaldococcus jannaschii (strain ATCC 43007 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 100440) / OX=243232 GN=MJI34.8 PE=1 Sv=1
or_661	ALS19B24.1	group_23	699410	700306	-	-	-	-	HTH-type transcriptional regulator rgg OS=Streptococcus gordonii (strain Challis / ATCC 35105 / BCR 15272 / CH