

Table S6. Unique genes of *Listeria* pathogen (UGLP) referenced to *L.monocytogenes* EGD-e_169963

ORF_id	Sequence_id	Group_id	start	end	strand	COG_id	COG_annotation	VDB_annotation	Uniprot_annotation
orf_5	ALS191824.1	group_1688	4869	5981	-	COG1195	L/Recombinational DNA repair ATPase RecF/RecF	-	DNA replication and repair protein RecF OS= <i>Listeria monocytogenes</i> serovar 1/2a (strain ATCC BAA-679 / EGD-e) OX=169963 GN=recF Pe-3 SV=1
orf_8	ALS191824.1	group_1331	10728	12242	-	COG5302	I/Phosphatidylserine/ phosphatidylglycerophosphate/cardiolipin synth	-	Cardiolipin synthase 1 OS= <i>Bacillus cereus</i> (strain ATCC 14579 / DSM 31 / CCUG 7414 / JCM 2152 / NBRC 15305 / NCIMB 9437 / NCTC 2599 / NRI 8-3711) OX=226900 GN=c1s Pe-3 SV=1
orf_9	ALS191824.1	group_1272	12250	12776	-	COG1670	R/Protein N-acetyltransferase, Bim/RimI family/BimI	-	Spermidine N(1)-acetyltransferase OS= <i>Wigglesworthia glossinidia</i> brevipalpis (strain ATCC-36870) GN=spd Pe-3 SV=1
orf_11	ALS191824.1	group_1364	13843	14814	-	COG3407	I/Mevalonate pyrophosphate decarboxylase/MVD/Lisproindole biosyn	-	-
orf_13	ALS191824.1	group_537	16219	17325	-	COG1622	C/Heme/copper-type cytochrome/quinol oxidase, subunit 2/CyoAa	-	Probable quinol oxidase subunit 2 OS=Staphylococcus epidermidis (strain ATCC 12228 / FDA P1 1200) OX=169963 GN=cyoAa Pe-3 SV=1
orf_15	ALS191824.1	group_1813	19311	19923	-	COG1845	C/Heme/copper-type cytochrome/quinol oxidase, subunit 3/CyoCb	-	Quinol oxidase subunit 3 OS= <i>Bacillus subtilis</i> (strain 168) OX=224308 GN=cyoCb Pe-1 SV=1
orf_16	ALS191824.1	group_1520	19924	20256	-	COG1325	C/Heme/copper-type cytochrome/quinol oxidase, subunit 4/CyoD	-	Quinol oxidase subunit 4 OS= <i>Bacillus subtilis</i> (strain ATCC 22029 / NRI 8-3447 / W3) OX=655816 GN=cyoD Pe-1 SV=1
orf_22	ALS191824.1	group_2197	25351	25839	-	COG3444	G/Phosphotransferase system, mannose/fructose/N-acetylglactosai-	-	PTS system sorbose-specific EIIb component OS= <i>Lactobacillus casei</i> OX=1582 GN=sorB Pe-1 SV=1
orf_24	ALS191824.1	group_20	26646	27467	-	COG3716	G/Phosphotransferase system, mannose/fructose/N-acetylglactosai-	-	-
orf_27	ALS191824.1	group_2179	29263	31004	-	COG2190	G/Phosphotransferase system IA component/NagE	-	-
orf_31	ALS191824.1	group_2241	33397	34452	-	COG1609	K/DNA-binding transcriptional regulator, LacI/PurK family/PurK	-	PTS system beta-glucoside-specific EIIBcA component OS= <i>Alkalihalobacillus halodurans</i> (strain ATCC BAA-125 / DSM 18197 / FERM 7344 / JCM 9153 / C-125) OX=272558 GN=hgP Pe-3 SV=1
orf_32	ALS191824.1	group_2260	34654	35619	-	COG1940	G/Sugar kinase of the NBD/HSP70 family, may contain an N-termin-	-	-
orf_33	ALS191824.1	group_2232	35616	38018	-	-	-	-	-
orf_35	ALS191824.1	group_2236	39885	40470	-	COG4949	M/Glucosamine 6-phosphate synthase, contains amidotransferase	-	-
orf_60	ALS191824.1	group_264	64950	66146	-	COG4499	U/ESX protein secretion system component YufK/YufK	-	-
orf_61	ALS191824.1	group_223	66160	70656	-	COG1674	D/DNA segregation ATPase FtsK/SpoIIIE or related protein/FtsK	-	-
orf_75	ALS191824.1	group_1268	79817	80869	-	COG2169	L/Methylphosphotriester-DNA-protein-cysteine methyltransferase (-	-	-
orf_76	ALS191824.1	group_2078	80881	81330	-	COG1353	S/Uncharacterized conserved protein YhmI, contains pentapeptide res-	-	-
orf_77	ALS191824.1	group_450	81661	82617	-	COG1052	CH/Lactate dehydrogenase or related 2-hydroxyacid dehydrogenase	-	Putative 2-hydroxyacid dehydrogenase SH0752 OS=Staphylococcus haemolyticus (strain JCS1435) OX=279808 GN=SH0752 Pe-3 SV=1
orf_82	ALS191824.1	group_42	86323	86691	-	COG0789	K/DNA-binding transcriptional regulator, MerR family/SoxR	-	HTH-type transcriptional regulator HmrR OS= <i>Rhizobium leguminosarum</i> bv. viciae OX=387 GN=hmrR Pe-4 SV=1
orf_84	ALS191824.1	group_2070	88121	88810	-	COG0664	T;cAMP-binding domain of CRP or a regulatory subunit of cAMP-dep-	-	-
orf_86	ALS191824.1	group_1611	94764	97070	-	-	-	-	-
orf_88	ALS191824.1	group_1918	97366	98412	-	-	-	-	-
orf_90	ALS191824.1	group_2084	99902	100771	-	COG0224	C/FoF1-type ATP synthase, gamma subunit;AtpG;FoF1-type ATP synt-	-	-
orf_92	ALS191824.1	group_1947	102155	102478	-	COG3555	C/FoF1-type ATP synthase, epsilon subunit;AtpE;FoF1-type ATP synt-	-	-
orf_93	ALS191824.1	group_1919	102466	103028	-	-	-	-	-
orf_96	ALS191824.1	group_114	105123	105929	-	COG3715	G/Phosphotransferase system, mannose/fructose/N-acetylglactosai-	-	PTS system sorbose-specific EIIC component OS= <i>Klebsiella pneumoniae</i> OX=573 GN=sorA Pe-2 SV=1
orf_99	ALS191824.1	group_2097	107499	107849	-	COG4898	S/Uncharacterized conserved protein	-	-
orf_102	ALS191824.1	group_2046	109349	109720	-	COG1747	G/Chitodextrinase;	-	-
orf_103	ALS191824.1	group_1371	110013	112283	-	COG3979	G/Chitodextrinase;	-	-
orf_106	ALS191824.1	group_2083	115087	116829	-	COG1132	V;ABC-type multidrug transport system, ATPase and permease comp-	-	-
orf_108	ALS191824.1	group_2262	117841	118956	-	COG0657	L/acetyl esterase/lipase/Aes;	-	-
orf_109	ALS191824.1	group_1984	119060	119770	-	COG2200	T;EAL domain, c-di-GMP-specific phosphodiesterase class I (or its em-	-	-
orf_113	ALS191824.1	group_185	121664	122092	-	-	-	-	-
orf_114	ALS191824.1	group_144	122104	122520	-	-	-	-	-
orf_126	ALS191824.1	group_221	130249	130671	-	COG4824	X/Phage-related holin (Lysis protein)	-	Uncharacterized protein Lmo0128 OS= <i>Listeria monocytogenes</i> serovar 1/2a (strain ATCC BAA-679 / EGD-e) OX=169963 GN=lmo0128 Pe-3 SV=1
orf_127	ALS191824.1	group_1849	130653	131380	-	COG0860	N;N-acetylglucosyl-L-alanine amidase/AmeC;	-	Sporulation-specific N-acetylglucosyl-L-alanine amidase OS= <i>Bacillus subtilis</i> (strain 168) OX=224308 GN=ameC Pe-1 SV=1
orf_128	ALS191824.1	group_1295	131419	133767	-	COG0737	PV;2',3'-cyclic-nucleotide 2'-phosphodiesterase/5'- or 3'-nucleotidase	-	Cell wall protein Lmo0130 OS= <i>Listeria monocytogenes</i> serovar 1/2a (strain ATCC BAA-679 / EGD-e) OX=169963 GN=lmo0130 Pe-1 SV=1
orf_130	ALS191824.1	group_562	134782	136290	-	COG4109	K/Predicted transcriptional regulator containing CBS domains/Tol	-	Inosine 5'-monophosphate dehydrogenase OS= <i>Trichomonas foetus</i> OX=56690 GN=IMPDH Pe-1 SV=1
orf_132	ALS191824.1	group_1396	136714	136992	-	COG2388	R/Predicted acetyltransferase, GNAT superfamily/YidJ	-	Uncharacterized protein YidJ OS= <i>Escherichia coli</i> (strain K12) OX=83333 GN=yidJ Pe-1 SV=1
orf_133	ALS191824.1	group_1692	137323	138897	-	COG1747	E;ABC-type transport system, periplasmic component/DppA	-	-
orf_153	ALS191824.1	group_2238	152648	153328	-	COG0664	T;cAMP-binding domain of CRP or a regulatory subunit of cAMP-dep-	-	-
orf_154	ALS191824.1	group_1863	153608	155947	-	COG1199	L/Rad3-related DNA helicase DmgD/DmgD	-	-
orf_155	ALS191824.1	group_81	155993	156805	-	COG0561	HR;Hydroxymethylpyrimidine pyrophosphatase and other HAD fami-	-	Putative phosphatase YaeH OS= <i>Bacillus subtilis</i> (strain 168) OX=224308 GN=yaeH Pe-3 SV=1
orf_156	ALS191824.1	group_125	157089	159470	-	COG4932	M/Clumping factor A-related surface protein, MSCRAMM (microbial-	-	-
orf_157	ALS191824.1	group_125	159663	161378	-	COG4932	M/Clumping factor A-related surface protein, MSCRAMM (microbial-	-	-
orf_158	ALS191824.1	group_1449	161420	162250	-	COG1363	T;Anti-anti-sigma regulatory factor (antagonist of anti-sigma factor);J	-	-
orf_160	ALS191824.1	group_1817	163665	164298	-	COG1774	T;Cell fate regulator YnfT, FSP1 superfamily (containing sporulation, co-	-	Stage 0 sporulation protein YnfT OS= <i>Bacillus subtilis</i> (strain 168) OX=224308 GN=ynfT Pe-4 SV=1
orf_162	ALS191824.1	group_1328	164735	165508	-	COG2126	J;RNALysal Val 437 N6-methyltransferase TrmM6;TrmM6;RNA modification	-	Protein RNALysal Val 437 N6-methyltransferase YacO OS= <i>Bacillus subtilis</i> (strain 168) OX=224308 GN=yacO Pe-3 SV=1
orf_163	ALS191824.1	group_1334	165492	165764	-	COG2827	L/Predicted endonuclease, GII-Y/GII superfamily/YnQd	-	UF0213 protein lmo0166 OS= <i>Listeria monocytogenes</i> serovar 1/2a (strain ATCC BAA-679 / EGD-e) OX=169963 GN=lmo0166 Pe-3 SV=1
orf_192	ALS191824.1	group_160	198201	199409	-	COG0577	V;ABC-type antimicrobial peptide transport system, permease comp-	-	Macrolide export ATP-binding/permease protein MacB OS= <i>Bdellovibrio bacteriovorus</i> (strain ATCC 15356 / DSM 50701 / NCIMB 9529 / HD100) OX=264462 GN=macB Pe-3 SV=1
orf_198	ALS191824.1	group_2119	202641	203597	-	COG0462	F;Phosphoribosylpyrophosphate synthetase/PraS;Histidine biosynth-	-	Ribose-phosphate pyrophosphokinase 1 OS= <i>Listeria monocytogenes</i> serovar 1/2a (strain ATCC BAA-679 / EGD-e) OX=169963 GN=prs1 Pe-3 SV=1
orf_199	ALS191824.1	group_2339	204624	205577	-	-	-	-	-
orf_199	ALS191824.1	group_2330	205819	207408	-	-	-	-	-
orf_200	ALS191824.1	group_2323	207739	209271	-	COG3227	O;Zn-dependent metalloprotease (Neutral protease B);LasB	-	-
orf_202	ALS191824.1	group_1543	215721	216344	-	COG0185	J;Ribosomal protein L25 (general stress protein C23);RplJ/Ribosome 5-	-	-
orf_209	ALS191824.1	group_1276	216434	217018	-	COG0456	J;Ribosomal protein S18 acetylase Rimi and related acetyltransferase	-	-
orf_212	ALS191824.1	group_484	221370	222569	-	COG5841	D;Stage V sporulation protein SpoVb/SpoIif, required for spore cort-	-	-
orf_213	ALS191824.1	group_1495	222981	223261	-	COG0188	R;Ribosomal S05 subunit-recycling heat shock protein, contains 54 do-	-	-
orf_217	ALS191824.1	group_240	226854	228929	-	COG0465	O;ATP-dependent Zn proteases/HflB;	-	-
orf_220	ALS191824.1	group_365	230840	231766	-	COG0031	E;Cysteine synthase;CysK/Cysteine biosynthesis	-	-
orf_221	ALS191824.1	group_1333	231692	233477	-	COG0024	H;Dihydroxypropanate synthase;FolP;Folate biosynthesis	-	-
orf_223	ALS191824.1	group_1603	233855	234337	-	COG0813	7-8-dihydro-6-hydroxymethylpterin pyrophosphokinase (folate bio-	-	-
orf_224	ALS191824.1	group_1687	234414	235409	-	COG0942	J;RNA-dihydrouridine synthase;DusA;RNA modification	-	-
orf_225	ALS191824.1	group_1471	235524	237020	-	COG1190	J;Lysyl-tRNA synthetase (class II);LysU;Aminoacyl-tRNA synthetases -	-	-
orf_232	ALS191824.1	group_1422	255794	256498	-	COG2111	L;2'-methyl-2'-erythritol 4-phosphate cytidyllyltransferase/igbJ/igpJ	-	-
orf_236	ALS191824.1	group_1469	261380	262061	-	COG0566	J;RNALys G18 (ribosome 2'-O)-methylase SpoI1/SpoI1;RNA modifica-	-	-
orf_240	ALS191824.1	group_1675	262657	263262	-	COG5595	K/DNA-directed RNA polymerase specialized sigma subunit, sigma24	-	-
orf_241	ALS191824.1	group_1527	263535	263714	-	COG0690	U;Preprotein translocase subunit SecE;SecE	-	-
orf_243	ALS191824.1	group_1830	264432	264802	-	-	-	-	-
orf_244	ALS191824.1	group_1731	265029	265454	-	COG0080	J;Ribosomal protein L11;RplK;Ribosome S05 subunit	-	50S ribosomal protein L11 OS= <i>Listeria welshimeri</i> serovar 6b (strain ATCC 35897 / DSM 20650 / CP 8149 / NCTC 11857 / SLCC 5334 / V8) OX=386043 GN=rplK Pe-3 SV=1
orf_252	ALS191824.1	group_1331	270372	270977	-	COG2813	J;L16S rRNA G1207 methylase RsmC/RsmC;L16S RNA modification	-	Uncharacterized protein YhmB OS= <i>Bacillus subtilis</i> (strain 168) OX=224308 GN=yhmB Pe-3 SV=1
orf_256	ALS191824.1	group_2118	280410	280955	-	COG1011	H;FMN and 5-amino-6-[5-phospho-D-ribitylamino]uracil phosphatase	-	-
orf_258	ALS191824.1	group_2	282755	284227	-	COG4886	K;Leucine-rich repeat (LRR) protein/LRR	-	Internalin H OS= <i>Listeria monocytogenes</i> serovar 1/2a (strain ATCC BAA-679 / EGD-e) OX=169963 GN=ihH Pe-1 SV=1
orf_259	ALS191824.1	group_2	284365	286011	-	COG4886	K;Leucine-rich repeat (LRR) protein/LRR	-	Internalin H OS= <i>Listeria monocytogenes</i> serovar 1/2a (strain ATCC BAA-679 / EGD-e) OX=169963 GN=ihH Pe-1 SV=1
orf_260	ALS191824.1	group_2	286219	287718	-	COG4886	K;Leucine-rich repeat (LRR) protein/LRR	-	Internalin H OS= <i>Listeria monocytogenes</i> serovar 1/2a (strain ATCC BAA-679 / EGD-e) OX=169963 GN=ihH Pe-1 SV=1
orf_261	ALS191824.1	group_1840	287853	288992	-	COG0624	E;Acetylornithine decarboxylase/Succinyl-diaminopimelate desuccinyla-	-	Probable succinyl-diaminopimelate desuccinylase OS=Staphylococcus aureus (strain SMS252) OX=282458 GN=dapE Pe-3 SV=1
orf_264	ALS191824.1	group_488	295923	295928	-	COG0408	G;Broad specificity phosphatase PhdE/PhdE	-	-
orf_268	ALS191824.1	group_81	295401	296213	-	COG0561	HR;Hydroxymethylpyrimidine pyrophosphatase and other HAD fami-	-	Putative phosphatase YaeH OS= <i>Bacillus subtilis</i> (strain 168) OX=224308 GN=yaeH Pe-3 SV=1
orf_269	ALS191824.1	group_1299	296349	296852	-	-	-	-	-
orf_270	ALS191824.1	group_2327	296889	297551	-	COG0664	T;cAMP-binding domain of CRP or a regulatory subunit of cAMP-dep-	-	-
orf_271	ALS191824.1	group_2062	297810	298652	-	COG2333	C/DNA uptake channel protein CmtC/C-terminal domain of cAMP-dep-	-	-
orf_273	ALS191824.1	group_2048	299604	300578	-	COG0673	R/Predicted dehydrogenase;MvM	-	-
orf_274	ALS191824.1	group_1516	300617	301717	-	COG3839	G;ABC-type sugar transport system, ATPase component MalK/MalK	-	Oligosaccharides import ATP-binding protein MsmX OS= <i>Bacillus subtilis</i> (strain 168) OX=224308 GN=msmX Pe-1 SV=1
orf_276	ALS191824.1	group_489	304133	304684	-	COG0602	H;Organic radical activating enzyme NrdY/QaeE;QueE;RNA modifica-	-	Anaerobic ribonucleoside-triphosphate reductase-activating protein OS= <i>Salmonella typhi</i> OX=90370 GN=nrdG Pe-3 SV=1
orf_277	ALS191824.1	group_1893	304942	305613	-	COG0664	T;cAMP-binding domain of CRP or a regulatory subunit of cAMP-dep-	-	-
orf_279	ALS191824.1	group_571	306644	307306	-	COG2011	E;ABC-type methionine transport system, permease component;MetI	-	Probable D-methionine transport system permease protein MetI OS= <i>Vibrio cholerae</i> serotype O1 (strain ATCC 39315 / E1 Tor Inaba N16961) OX=243277 GN=metI Pe-3 SV=1
orf_280	ALS191824.1	group_1490	307303	308319	-	COG1135	E;ABC-type methionine transport system, ATPase component;AboC	-	Methionine import ATP-binding protein MetN OS= <i>Listeria monocytogenes</i> serovar 1/2a (strain ATCC BAA-679 / EGD-e) OX=169963 GN=metN Pe-3 SV=1
orf_281	ALS191824.1	group_1595	308334	309155	-	COG0464	T;ABC-type metal ion transport system, periplasmic component/YnfA	-	D-methionine-binding lipoprotein MetQ OS= <i>Salmonella typhi</i> OX=90370 GN=metQ Pe-3 SV=1
orf_285	ALS191824.1	group_530	313659	314981	-	COG4863	T;YnfC protein, regulator of the YnfHr two-component signal transd-	-	-
orf_287	ALS191824.1	group_222	315945	316775	-	COG1235	P/Phosphoribosyl 1,2-cyclic phosphate phosphodiesterase;PhpP	-	Putative metallo-hydrolase YnfC OS= <i>Bacillus subtilis</i> (strain 168) OX=224308 GN=ynfC Pe-2 SV=1
orf_288	ALS191824.1	group_1404	316873	318375	-	COG0265	O;Peptidic serum protease, S1-C subfamily, contain C-terminal PC-	-	Uncharacterized serine protease YnfA OS= <i>Bacillus subtilis</i> (strain 168) OX=224308 GN=ynfA Pe-3 SV=2
orf_292	ALS191824.1	group_1595	321490	322128	-	COG4886	K;Leucine-rich repeat (LRR) protein/LRR	-	Internalin I OS= <i>Listeria monocytogenes</i> serovar 1/2a (strain ATCC BAA-679 / EGD-e) OX=169963 GN=ihI Pe-2 SV=1
orf_298	ALS191824.1	group_28	360936	366272	-	COG0673	R/Predicted dehydrogenase;MvM	-	Uncharacterized oxidoreductase YnfX OS= <i>Escherichia coli</i> (strain K12) OX=83333 GN=ynfX Pe-1 SV=1
orf_368	ALS191824.1	group_1483	397340	398053	-	COG2188	K/DNA-binding transcriptional regulator, GntR family/MngR	-	-