

1 TABLE S1. Upregulated genes in H7858 grown on CCS as compared to it grown in MBHIB at 7°C

H7858 gene name	Gene product	FC ^a
LMOh7858_0048	Putrescine carbamoyltransferase (EC 2.1.3.6)	31.36
LMOh7858_0049	Agmatine/putrescine antiporter, associated with agmatine catabolism	19.56
LMOh7858_0050	Agmatine deiminase (EC 3.5.3.12)	13.67
LMOh7858_0051	Carbamate kinase (EC 2.7.2.2)	18.29
LMOh7858_0176	Zinc ABC transporter, periplasmic-binding protein ZnuA	7.64
LMOh7858_0221	Phosphatidylinositol-specific phospholipase C (EC 4.6.1.13)	2.83
LMOh7858_0222	Thiol-activated cytolysin	2.54
LMOh7858_0224	Actin-assembly inducing protein ActA precursor	2.86
LMOh7858_0225	Broad-substrate range phospholipase C (EC 3.1.4.3)	3.19
LMOh7858_0311	Multiple sugar ABC transporter, ATP-binding protein	2.54
LMOh7858_0382	Transketolase (EC 2.2.1.1)	3.39
LMOh7858_0383	Transaldolase (EC 2.2.1.2)	3.98
LMOh7858_0384	oxidoreductase, short-chain dehydrogenase/reductase family	3.69
LMOh7858_0385	Ribose 5-phosphate isomerase B (EC 5.3.1.6)	5.86
LMOh7858_0396	Fumarate reductase flavoprotein subunit (EC 1.3.99.1)	6.38
LMOh7858_0499	Internalin B (GW modules)	2.71
LMOh7858_0536	antigen, putative	17.50
LMOh7858_0755	Flagellin protein FlaA	3.43
LMOh7858_0840	FMN-dependent NADH-azoreductase	2.73
LMOh7858_0957	Sulfate permease	3.95
LMOh7858_1214	Cob(III)alamin reductase	3.81
LMOh7858_1215	Propanediol utilization polyhedral body protein PduT	3.72
LMOh7858_1216	Propanediol utilization polyhedral body protein PduU	4.48
LMOh7858_1217	Propanediol utilization protein PduV	6.57
LMOh7858_1217.1	Predicted alpha-ribazole-5-phosphate synthase CblS for cobalamin biosynthesis	6.36
LMOh7858_1219	Adenosylcobinamide-phosphate guanylyltransferase (EC 2.7.7.62)	5.02
LMOh7858_1220	Cobalamin synthase	6.08
LMOh7858_1221	Alpha-ribazole-5'-phosphate phosphatase (EC 3.1.3.73)	6.78
LMOh7858_1242	L-threonine 3-O-phosphate decarboxylase (EC 4.1.1.81)	2.77

LMOh7858_1243	Threonine kinase in B12 biosynthesis	2.88
LMOh7858_1245	Alcohol dehydrogenase (EC 1.1.1.1)	4.97
LMOh7858_1249	Ethanolamine ammonia-lyase heavy chain (EC 4.3.1.7)	4.97
LMOh7858_1250	Ethanolamine ammonia-lyase light chain (EC 4.3.1.7)	5.50
LMOh7858_1253	Acetaldehyde dehydrogenase, ethanolamine utilization cluster	5.26
LMOh7858_1254	Ethanolamine utilization protein similar to PduA/PduJ	5.56
LMOh7858_1254.2	Ethanolamine utilization protein similar to PduL	5.89
LMOh7858_1258.1	Ethanolamine utilization protein similar to PduT	6.19
LMOh7858_1260	Ethanolamine permease	5.90
LMOh7858_1262.1	Substrate-specific component CblT of predicted B12-regulated ECF transporter	8.33
LMOh7858_1264	Cobyrinic acid A,C-diamide synthase	10.02
LMOh7858_1265	Adenosylcobinamide-phosphate synthase	12.88
LMOh7858_1266	Cobalt-precorrin-8x methylmutase (EC 5.4.1.2)	11.84
LMOh7858_1267	Cobalt-precorrin-6 synthase, anaerobic	11.27
LMOh7858_1268	Cobalt-precorrin-6y C5-methyltransferase (EC 2.1.1.-)	12.39
LMOh7858_1269	Cobalt-precorrin-6y C15-methyltransferase [decarboxylating] (EC 2.1.1.-)	11.32
LMOh7858_1270	Cobalt-precorrin-4 C11-methyltransferase (EC 2.1.1.133)	9.70
LMOh7858_1271	Cobalamin biosynthesis protein CbiG	11.54
LMOh7858_1272	Cobalt-precorrin-3b C17-methyltransferase	10.29
LMOh7858_1273	Cobalt-precorrin-6x reductase (EC 1.3.1.54)	10.85
LMOh7858_1274	Uroporphyrinogen-III methyltransferase (EC 2.1.1.107)	12.55
LMOh7858_1275	Sirohydrochlorin cobaltochelataase CbiK (EC 4.99.1.3)	10.40
LMOh7858_1276	Cobalt-precorrin-2 C20-methyltransferase (EC 2.1.1.130)	11.76
LMOh7858_1277	Substrate-specific component CbiM of cobalt ECF transporter	9.95
LMOh7858_1278	Additional substrate-specific component CbiN of cobalt ECF transporter	9.02
LMOh7858_1279	Transmembrane component CbiQ of energizing module of cobalt ECF transporter	7.54
LMOh7858_1280	ATPase component CbiO of energizing module of cobalt ECF transporter	5.30
LMOh7858_1281	Cobyrinic acid synthase	2.94
LMOh7858_1282	Cob(I)alamin adenosyltransferase PduO (EC 2.5.1.17)	2.66
LMOh7858_1329.1	FIG00774262: hypothetical protein	7.76

LMOh7858_1331	transporter	8.12
LMOh7858_2119	PTS system, mannose-specific IIA component (EC 2.7.1.69)	6.31
LMOh7858_2119.1	Putative glucosamine-fructose-6-phosphate aminotransferase	3.42
LMOh7858_2121	putative glucosamine-fructose-6-phosphate aminotransferase	3.99
LMOh7858_2122	PTS system, mannose-specific IID component (EC 2.7.1.69)	5.61
LMOh7858_2123	PTS system, mannose-specific IIC component (EC 2.7.1.69)	4.78
LMOh7858_2124	PTS system, mannose-specific IIB component (EC 2.7.1.69)	4.71
LMOh7858_2253	Maltose phosphorylase (EC 2.4.1.8)	3.45
LMOh7858_2253.1	Maltodextrose utilization protein MalA	5.71
LMOh7858_2255	Maltose/maltodextrin ABC transporter, permease protein MalG	6.32
LMOh7858_2256	Maltose/maltodextrin ABC transporter, permease protein MalF	7.96
LMOh7858_2257	Maltose/maltodextrin ABC transporter, substrate binding periplasmic protein	5.74
LMOh7858_2292.2	FIG00774368: hypothetical protein	5.05
LMOh7858_2292.3	Inosose dehydratase (EC 4.2.1.44)	4.27
LMOh7858_2426.4	FIG00775213: hypothetical protein	2.85
LMOh7858_2503	FIG00774521: hypothetical protein	4.96
LMOh7858_2504	Rrf2 family transcriptional regulator	4.24
LMOh7858_2903	serine/threonine protein phosphatase family protein	2.78
LMOh7858_2922	Transketolase (EC 2.2.1.1)	4.77
LMOh7858_2925	Galactitol-1-phosphate 5-dehydrogenase (EC 1.1.1.251)	7.62
LMOh7858_2926	Galactitol-1-phosphate 5-dehydrogenase (EC 1.1.1.251)	5.48
LMOh7858_2927	PTS system, galactitol-specific IIC component (EC 2.7.1.69)	4.38
LMOh7858_2928	PTS system, galactitol-specific IIB component (EC 2.7.1.69)	3.17
LMOh7858_2994	Haloacid dehalogenase-like hydrolase	5.34
LMOh7858_2995	Transcription regulator, RpiR family	3.11
LMOh7858_3062	hydrolase, haloacid dehalogenase-like family	7.97
LMOh7858_3063	PTS system, mannitol-specific IIB component (EC 2.7.1.69)	19.28
LMOh7858_3064	oxidoreductase, Gfo/Idh/MocA family	9.36
LMOh7858_3065	N-acetylmannosamine-6-phosphate 2-epimerase (EC 5.1.3.9)	13.04

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3 ^aFC, fold change. FC= average normalized RNA-seq coverage (NRC) (CCS) ÷ average NRC (MBHIB)

4 TABLE S2. Down regulated genes H7858 grown on CCS as compared to it grown in MBHIB at 7°C

H7858 Gene Name	Gene Product	FC ^a
LMOh7858_0107	oxidoreductase, aldo/keto reductase family Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein	0.37
LMOh7858_0175	O	0.38
LMOh7858_0246	Dihydropteroate synthase (EC 2.5.1.15)	0.16
LMOh7858_0367	Internalin-like protein (LPXTG motif) Lmo0331 homolog	0.40
LMOh7858_0506	Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129) Cell envelope-associated transcriptional attenuator LytR-CpsA-Psr,	0.32
LMOh7858_0508	subfa	0.31
LMOh7858_0625	Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19) O-acetylhomoserine sulphydrylase (EC 2.5.1.49) / O-succinylhomoserine	0.31
LMOh7858_0655	sulphydrylase	0.37
LMOh7858_0667	Transcriptional regulator, MarR family	0.38
LMOh7858_0852.2	GTP pyrophosphokinase (EC 2.7.6.5)	0.32
LMOh7858_0878	acetyltransferase, GNAT family Putative peptidoglycan bound protein (LPXTG motif) Lmo0880	0.36
LMOh7858_0940	homolog	0.30
LMOh7858_1015.1	FIG00774399: hypothetical protein	0.27
LMOh7858_1015.2	FIG00774456: hypothetical protein	0.39
LMOh7858_1066.1	FIG00774146: hypothetical protein	0.28
LMOh7858_1202.1	FIG00774448: hypothetical protein	0.00
LMOh7858_1289	N-acetylmuramoyl-L-alanine amidase, family 4	0.39
LMOh7858_1299	Transcriptional regulator, MarR family	0.38
LMOh7858_1308.2	FIG00774960: hypothetical protein	0.24
LMOh7858_1321.2	DUF1801 domain-containing protein PhnB protein; putative DNA binding 3-demethylubiquinone-9 3-	0.36
LMOh7858_1321.3	methyltransfer	0.28
LMOh7858_1339	Trehalose-6-phosphate hydrolase (EC 3.2.1.93) PTS system, trehalose-specific IIB component (EC 2.7.1.69) / PTS	0.18
LMOh7858_1340	system,	0.19

LMOh7858_1511	FIG00774487: hypothetical protein	0.30
LMOh7858_1614	Iron-sulfur cluster regulator IscR	0.38
LMOh7858_1812.1	Hypothetical protein SAV1869	0.38
LMOh7858_1858	Glutamate synthase [NADPH] small chain (EC 1.4.1.13)	0.30
LMOh7858_1859	Glutamate synthase [NADPH] large chain (EC 1.4.1.13)	0.29
LMOh7858_1956	Orotate phosphoribosyltransferase (EC 2.4.2.10)	0.26
LMOh7858_1957	Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23)	0.27
LMOh7858_1958	Dihydroorotate dehydrogenase, catalytic subunit (EC 1.3.3.1)	0.29
LMOh7858_1959	Dihydroorotate dehydrogenase electron transfer subunit (EC 1.3.3.1)	0.22
LMOh7858_1960	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)	0.21
LMOh7858_1961	Carbamoyl-phosphate synthase small chain (EC 6.3.5.5)	0.22
LMOh7858_1965.1	FIG00774989: hypothetical protein	0.37
LMOh7858_1977	Copper chaperone	0.38
LMOh7858_2167	Cell division protein FtsL	0.37
LMOh7858_2179	Excinuclease ABC subunit A paralog of unknown function	0.38
LMOh7858_2262.2	FIG00774113: hypothetical protein	0.37
LMOh7858_2337	N-acetylmuramoyl-L-alanine amidase, family 4	0.31
LMOh7858_2343.1	FIG00774091: hypothetical protein	0.18
LMOh7858_2490	L-Cystine ABC transporter, permease protein TcyM	0.18
LMOh7858_2491	L-Cystine ABC transporter, permease protein TcyL	0.12
LMOh7858_2492	L-Cystine ABC transporter, periplasmic cystine-binding protein TcyK	0.31
LMOh7858_2495	HTH-type transcriptional regulator YtlI, LysR family	0.26
LMOh7858_2521	PTS system, IIB component	0.38
LMOh7858_2566.1	FIG00774101: hypothetical protein	0.23
LMOh7858_2584.1	FIG00774650: hypothetical protein	0.40
LMOh7858_2635	FIG00774998: hypothetical protein	0.25
LMOh7858_2635.1	Hypothetical protein, homolog of fig 393130.3.peg.2627	0.20
LMOh7858_2717.1	FIG00774295: hypothetical protein	0.13
LMOh7858_2717.2	FIG00774092: hypothetical protein	0.19
LMOh7858_2752	lipoprotein, putative	0.30
LMOh7858_2951	Mg(2+) transport ATPase, P-type (EC 3.6.3.2)	0.27

LMOh7858_3026.1	hypothetical protein	0.31
	Beta-glucosidase (EC 3.2.1.21); 6-phospho-beta-glucosidase (EC	
LMOh7858_3027	3.2.1.86)	0.24
LMOh7858_3028	PTS system, cellobiose-specific IIB component (EC 2.7.1.69)	0.12
LMOh7858_3066.6	hypothetical secreted protein	0.30
LMOh7858_3076	D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)	0.24
LMOh7858_3082	transporter	0.27
LMOh7858_3083	Catalyzes the cleavage of p-aminobenzoyl-glutamate to p-aminobenzoate and glutamate	0.29

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6 ^aFC, fold change. FC= average normalized RNA-seq coverage (NRC) (CCS) ÷ average NRC (MBHIB)

7 TABLE S3. Genes involved in cobalamin biosynthesis upregulated in H7858 grown on CSS compared to in MBHIB at 7°C

H7858	Gene name in		H7858 gene product	FC ^b
	EGD-e ^a	10403S ^a		
LMOh7858_1214	lmo1142	LMRG_00585	Cob(III)alamin reductase	3.81
LMOh7858_1217.1	lmo1146	LMRG_00589	Predicted alpha-ribazole-5-phosphate synthase CblS for cobalamin biosynthesis	6.36
LMOh7858_1219	lmo1147	LMRG_00590	Adenosylcobinamide-phosphate guanylyltransferase (EC 2.7.7.62)	5.02
LMOh7858_1220	lmo1148 (<i>cobS</i>)	LMRG_00591	Cobalamin synthase	6.08
LMOh7858_1221	lmo1149	LMRG_00592	Alpha-ribazole-5'-phosphate phosphatase (EC 3.1.3.73)	6.78
LMOh7858_1242	lmo1169 (<i>cobD</i>)	LMRG_00612	L-threonine 3-O-phosphate decarboxylase (EC 4.1.1.81)	2.77
LMOh7858_1262.1	lmo1190	LMRG_00636	Substrate-specific component CblT of predicted B12-regulated ECF transporter	8.33
LMOh7858_1264	lmo1191 (<i>cobB</i>)	LMRG_00637	Cobyric acid A,C-diamide synthase	10.02
LMOh7858_1265	lmo1192 (<i>cobD</i>)	LMRG_00638	Adenosylcobinamide-phosphate synthase	12.88
LMOh7858_1266	lmo1193	LMRG_00639	Cobalt-precorrin-8x methylmutase (EC 5.4.1.2)	11.84
LMOh7858_1267	lmo1194 (<i>cbiD</i>)	LMRG_00640	Cobalt-precorrin-6 synthase, anaerobic	11.27
LMOh7858_1268	lmo1195 (<i>cbiE</i>)	LMRG_00641	Cobalt-precorrin-6y C5-methyltransferase (EC 2.1.1.-)	12.39
LMOh7858_1269	lmo1196	LMRG_00642	Cobalt-precorrin-6y C15-methyltransferase [decarboxylating] (EC 2.1.1.-)	11.32
LMOh7858_1270	lmo1197 (<i>cbiF</i>)	LMRG_00643	Cobalt-precorrin-4 C11-methyltransferase (EC 2.1.1.133)	9.70
LMOh7858_1271	lmo1198 (<i>cbiG</i>)	LMRG_00644	Cobalamin biosynthesis protein CbiG	11.54
LMOh7858_1272	lmo1199 (<i>cbiH</i>)	LMRG_00645	Cobalt-precorrin-3b C17-methyltransferase	10.29
LMOh7858_1273	lmo1200	LMRG_00646	Cobalt-precorrin-6x reductase (EC 1.3.1.54)	10.85
LMOh7858_1274	lmo1201	LMRG_00647	Uroporphyrinogen-III methyltransferase (EC 2.1.1.107) / Uroporphyrinogen	12.55
LMOh7858_1275	lmo1202 (<i>cbiK</i>)	LMRG_00648	Sirohydrochlorin cobaltochelataase CbiK (EC 4.99.1.3)	10.40
LMOh7858_1276	lmo1203 (<i>cbiL</i>)	LMRG_00649	Cobalt-precorrin-2 C20-methyltransferase (EC 2.1.1.130)	11.76
LMOh7858_1277	lmo1204	LMRG_00650	Substrate-specific component CbiM of cobalt ECF transporter	9.95
LMOh7858_1278	lmo1205	LMRG_00651	Additional substrate-specific component CbiN of cobalt ECF transporter	9.02
LMOh7858_1279	lmo1206 (<i>cbiQ</i>)	LMRG_00652	Transmembrane component CbiQ of energizing module of cobalt ECF transporter	7.54
LMOh7858_1280	lmo1207	LMRG_00653	ATPase component CbiO of energizing module of cobalt ECF transporter	5.30
LMOh7858_1281	lmo1208 (<i>cobQ</i>)	LMRG_00654	Cobyric acid synthase	2.94

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9 ^aStrain EGD-e (GenBank accession no.: [NC_003210](#)) and 10403S (GenBank accession no.: [NC_017544](#)) are *L. monocytogenes*;

10 ^bFC, fold change, FC = average NRC(CSS) ÷ average NRC(MBHIB); only genes with FDR < 0.05 are listed.

11 TABLE S4. Upregulated genes involved in ethanolamine and 1,2-propanediol utilization in H7858 grown on CSS compared to in
 12 MBHIB at 7°C

	Gene name in			H7858 gene product	FC ^b
	H7858	EGD-e ^a	10403S ^a		
Ethanolamine utilization					
	LMOh7858_1245	lmo1171 (<i>pduQ</i>) ^c	LMRG_00617	Alcohol dehydrogenase (EC 1.1.1.1)	4.97
	LMOh7858_1249	lmo1175 (<i>eutB</i>)	LMRG_00621	Ethanolamine ammonia-lyase heavy chain (EC 4.3.1.7)	4.97
	LMOh7858_1250	lmo1176 (<i>eutC</i>)	LMRG_00622	Ethanolamine ammonia-lyase light chain (EC 4.3.1.7)	5.50
	LMOh7858_1253	lmo1179	LMRG_00625	Acetaldehyde dehydrogenase, ethanolamine utilization cluster	5.26
	LMOh7858_1254	lmo1180	LMRG_00626	Ethanolamine utilization protein similar to PduA/PduJ	5.56
	LMOh7858_1254.2	lmo1182	LMRG_00628	Ethanolamine utilization protein similar to PduL	5.89
	LMOh7858_1258.1	lmo1185	LMRG_00631	Ethanolamine utilization protein similar to PduT	6.19
	LMOh7858_1260	lmo1186	LMRG_00632	Ethanolamine permease	5.90
1,2-propanediol utilization					
	LMOh7858_1214	lmo1142	LMRG_00585	Cob(III)alamin reductase	3.81
	LMOh7858_1215	lmo1143	LMRG_00586	Propanediol utilization polyhedral body protein PduT	3.72
	LMOh7858_1216	lmo1144	LMRG_00587	Propanediol utilization polyhedral body protein PduU	4.48
	LMOh7858_1217	lmo1145	LMRG_00588	Propanediol utilization protein PduV	6.57
	LMOh7858_1243	lmo1170	LMRG_00613	Threonine kinase in B12 biosynthesis	2.88
	LMOh7858_1245	lmo1171 (<i>pduQ</i>) ^c	LMRG_00617	Alcohol dehydrogenase (EC 1.1.1.1)	4.97
	LMOh7858_1282	lmo1209	LMRG_00655	Cob(I)alamin adenosyltransferase PduO (EC 2.5.1.17)	2.66

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14 ^aStrain EGD-e (GenBank accession no.: [NC_003210](https://www.ncbi.nlm.nih.gov/nuccore/NC_003210)) and 10403S (GenBank accession no.: [NC_017544](https://www.ncbi.nlm.nih.gov/nuccore/NC_017544)) are *L. monocytogenes*;

15 ^bFC, fold change, FC= average NRC(CSS) ÷ average NRC(MBHIB); only genes with FDR <0.05 are listed;

16 °As the gene product Alcohol dehydrogenase of the gene LMOh7858_1245 may participate in both of the ethanolamine utilization and
17 the 1,2-propanediol utilization pathways, this gene was listed under both categories.

18 TABLE S5. Upregulated genes involved in carbohydrate transport and utilization in H7858 grown on CSS compared to in MBHIB at
 19 7°C

	Gene name in			H7858 gene product	FC ^b
	H7858	EGD-e ^a	10403S ^a		
Mannose					
LMOh7858_2119	lmo1997	LMRG_01145	PTS system, mannose-specific IIA component (EC 2.7.1.69)		6.31
LMOh7858_2122	lmo2000	LMRG_01148	PTS system, mannose-specific IID component (EC 2.7.1.69)		5.61
LMOh7858_2123	lmo2001	LMRG_01149	PTS system, mannose-specific IIC component (EC 2.7.1.69)		4.78
LMOh7858_2124	lmo2002	LMRG_01150	PTS system, mannose-specific IIB component (EC 2.7.1.69)		4.71
Galactitol					
LMOh7858_2925	lmo2663	LMRG_02208	Galactitol-1-phosphate 5-dehydrogenase (EC 1.1.1.251)		7.62
LMOh7858_2926	lmo2664	LMRG_02209	Galactitol-1-phosphate 5-dehydrogenase (EC 1.1.1.251)		5.48
LMOh7858_2927	lmo2665	LMRG_02210	PTS system, galactitol-specific IIC component (EC 2.7.1.69)		4.38
LMOh7858_2928	lmo2666	LMRG_02211	PTS system, galactitol-specific IIB component (EC 2.7.1.69)		3.17
Mannitol					
LMOh7858_3063	lmo2799	LMRG_01898	PTS system, mannitol-specific IIB component (EC 2.7.1.69)		19.28
Maltose					
LMOh7858_2253	lmo2121	LMRG_01275	Maltose phosphorylase (EC 2.4.1.8)		3.45
LMOh7858_2253.1	lmo2122	LMRG_01276	Maltodextrose utilization protein MalA		5.71
LMOh7858_2255	lmo2123	LMRG_01277	Maltose/maltodextrin ABC transporter, permease protein MalG		6.32
LMOh7858_2256	lmo2124	LMRG_01278	Maltose/maltodextrin ABC transporter, permease protein MalF		7.96
LMOh7858_2257	lmo2125	LMRG_01279	Maltose/maltodextrin ABC transporter, substrate binding periplasmic protein		5.74
Pentose phosphate pathway					
LMOh7858_2922	lmo2660	LMRG_02205	Transketolase (EC 2.2.1.1)		4.77
LMOh7858_0382	lmo0342	LMRG_00033	Transketolase (EC 2.2.1.1)		3.39
LMOh7858_0383	lmo0343 (<i>tal2</i>)	LMRG_00034	Transaldolase (EC 2.2.1.2)		3.98
LMOh7858_0384	lmo0344	LMRG_00035	oxidoreductase, short-chain dehydrogenase/reductase family		3.69
LMOh7858_0385	lmo0345	LMRG_00036	Ribose 5-phosphate isomerase B (EC 5.3.1.6)		5.86

20 ^aStrain EGD-e (GenBank accession no.: [NC_003210](https://ncbi.nlm.nih.gov/nuccore/NC_003210)) and 10403S (GenBank accession no.: [NC_017544](https://ncbi.nlm.nih.gov/nuccore/NC_017544)) are *L. monocytogenes*;

21 ^bFC, fold change, FC= average NRC(CSS) ÷ average NRC(MBHIB); only genes with FDR <0.05 are listed.

22 TABLE S6. Upregulated genes involved in agmatine deiminase in H7858 grown on CSS compared to in MBHIB at 7°C

Gene name in			H7858 gene product	FC ^b
H7858	EGD-e ^a	10403S ^a		
LMOh7858_0048	lmo0036 (<i>arcB</i>)	LMRG_02465 (<i>arcB</i>)	Putrescine carbamoyltransferase (EC 2.1.3.6)	31.36
LMOh7858_0049	lmo0037	LMRG_02466	Agmatine/putrescine antiporter, associated with agmatine catabolism	19.56
LMOh7858_0050	lmo0038 (<i>aguAI</i>)	LMRG_02467	Agmatine deiminase (EC 3.5.3.12)	13.67
LMOh7858_0051	lmo0039	LMRG_02468	Carbamate kinase (EC 2.7.2.2)	18.29

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24 ^aStrain EGD-e (GenBank accession no.: [NC_003210](#)) and 10403S (GenBank accession no.: [NC_017544](#)) are *L. monocytogenes*;

25 ^bFC, fold change, FC= average NRC(CSS) ÷ average NRC(MBHIB); only genes with FDR <0.05 are listed.

26 TABLE S7. Upregulated genes that are regulated by PrfA in H7858 grown on CSS compared to in MBHIB at 7°C

H7858	Gene name in		H7858 gene product	FC ^b
	EGD-e ^a	10403S ^a		
LMOh7858_0499	lmo0434 (<i>inlB</i>)	LMRG_00127	Internalin B (GW modules)	2.71
LMOh7858_0221	lmo0201 (<i>plcA</i>)	LMRG_02623	Phosphatidylinositol-specific phospholipase C (EC 4.6.1.13)	2.83
LMOh7858_0222	lmo0202 (<i>hly</i>)	LMRG_02624	Thiol-activated cytolysin	2.54
LMOh7858_0224	lmo0204 (<i>actA</i>)	LMRG_02626	Actin-assembly inducing protein ActA precursor	2.86
LMOh7858_0225	lmo0205 (<i>plcB</i>)	LMRG_02627	Broad-substrate range phospholipase C (EC 3.1.4.3)	3.19

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28 ^aStrain EGD-e (GenBank accession no.: [NC_003210](#)) and 10403S (GenBank accession no.: [NC_017544](#)) are *L. monocytogenes*;

29 ^bFC, fold change, FC= average NRC(CSS) ÷ average NRC(MBHIB); only genes with FDR <0.05 are listed;