

1 **Supplemental Data**

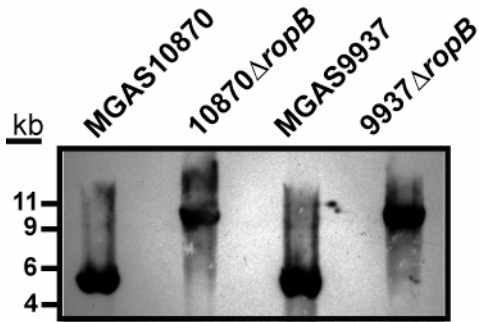
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3 **Inventory of supplemental items**

4

5 Supplemental Data include 3 supplemental figures and 3 supplemental tables

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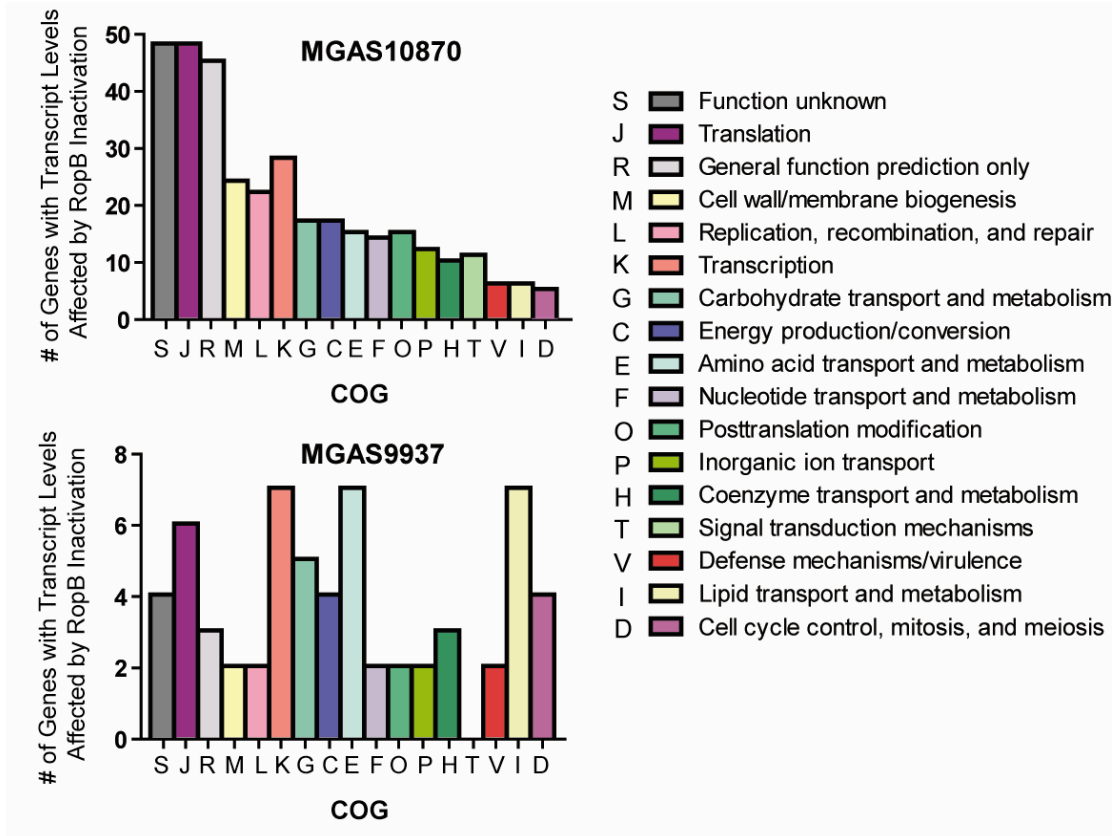
4

5 Supplemental Figure 1.

6 Southern blot of RopB-inactivated strains following digestion with *Xmn*I. Replacement
7 of *ropB* with spectinomycin resistance cassette removes an *Xmn*I cut site thereby
8 increasing fragment size by ~ 5 kb.

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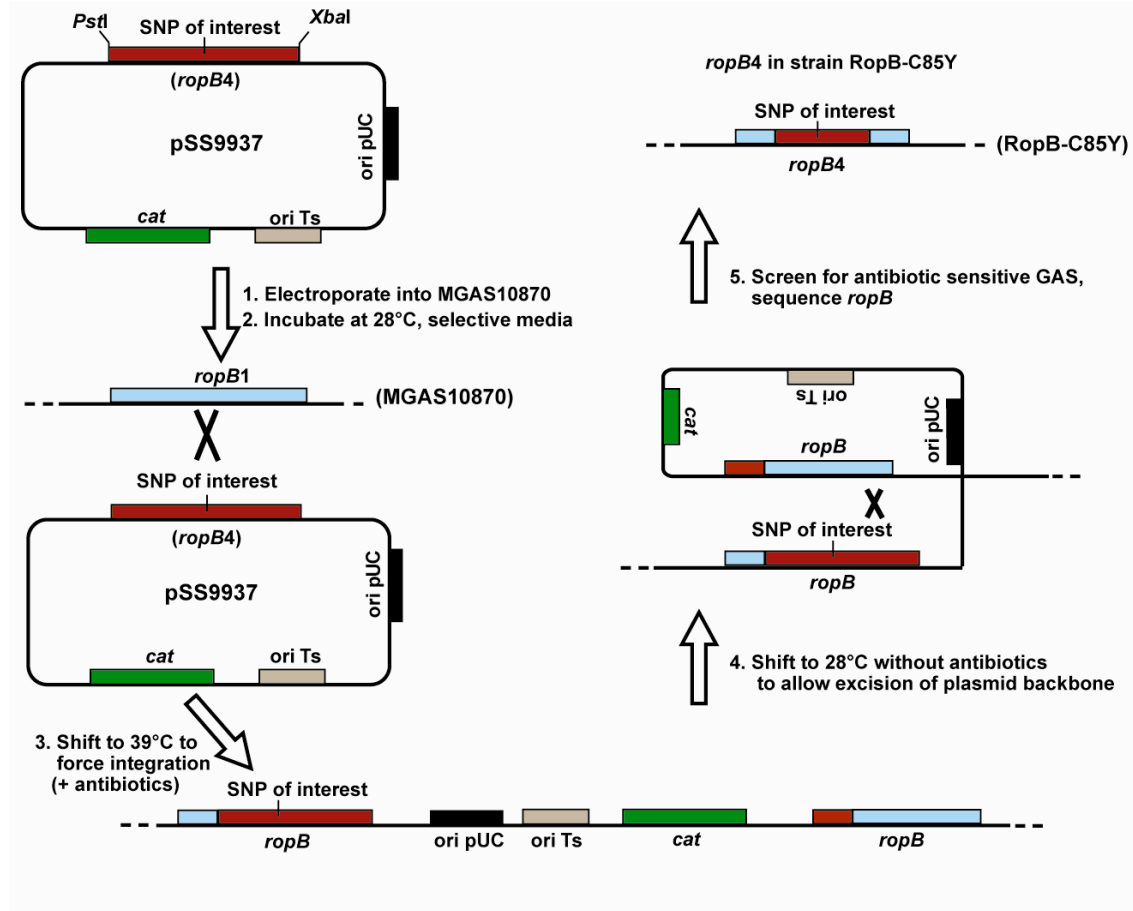


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3 Supplemental Figure 2.

4 Comparison of effects of RopB inactivation in strains MGAS10870 (*ropB1* allele) and
5 MGAS9937 (*ropB2* allele). Genes with at least two-fold difference in mean transcript
6 level between parental and RopB-inactivated strains were grouped into clusters of
7 orthologous groups (COGs) based on annotation of the serotype M3 strain MGAS315
8 genome (www.ncbi.nlm.nih.gov/sutils/coxik.cgi?gi=249). For clarity of data
9 presentation, a COG was included in the graphed data if at least four genes from that
10 category were altered in either strain MGAS10870 or MGAS9937. COGs were ordered
11 left to right based on the number of genes affected in strain MGAS10870. Note that the
12 scale for the two strains is different due to the significantly larger number of genes
13 altered by RopB inactivation in strain MGAS10870 compared to strain MGAS9937.

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4 Supplemental Figure 3.

5 Schematic of isoallelic strain creation using strain RopB-C85Y as example. *ropB* and
 6 surrounding gene region was amplified from strain MGAS9937, which contains the
 7 C85Y amino acid replacement (*ropB4*). The PCR fragment was cloned into pJL1055
 8 using *Pst*I and *Xba*I to create plasmid pSS9937. pSS9937 was electroporated into strain
 9 MGAS10870 (*ropB1*) with integration of the plasmid forced by growing cells at the non-
 10 permissive temperature in the presence of chloramphenicol (39°C). Cells were then
 11 shifted to the permissive temperature (28°C) and grown in the absence of
 12 chloramphenicol to allow for plasmid excision. Chloramphenicol-sensitive GAS strains

- 1 (i.e. strains in which the plasmid had excised) were sequenced to determine desired *ropB*
- 2 sequence. *cat*, chloramphenicol acetyl transferase; Ori Ts, temperature sensitive origin of
- 3 replication; Ori pUC, non-temperature sensitive origin of replication.

Supplemental Table 1.

ropB sequences of invasive, serotype M3 group A *Streptococcus* stains used in this study.

^A MGAS strain	Year	Disease or source	<i>ropB</i> sequence changes	Predicted amino acid change relative to strain
	isolated		from strain MGAS10870	MGAS10870
10870	2002	Soft tissue	Reference sequence	Reference sequence
15003	2003	Pyrexia	G3A	M1I
9887	2000	Bacteremia	G19A	V7I
9893	2000	Meningitis	G19A	V7I
9908	2003	Bacteremia	G19A	V7I
9990	2001	Bacteremia	G19A	V7I
10830	2001	Upper respiratory	G19A	V7I
10834	2001	Soft tissue	G19A	V7I
10850	2001	Soft tissue	G19A	V7I
10863	2001	Arthritis	G19A	V7I
10874	2002	Blood	G19A	V7I

15001	2003	Necrotizing fasciitis	G19A	V7I
15007	2003	Peritonitis	G19A	V7I
15008	2004	Bacteremia	G19A	V7I
15009	2001	Bacteremia	G19A	V7I
15011	2001	Bacteremia	G19A	V7I
15012	2004	Arthritis	G19A	V7I
15020	2005	Necrotizing fasciitis	G19A	V7I
15021	2005	Necrotizing fasciitis	G19A	V7I
15029	2005	Soft tissue	G19A	V7I
15033	2001	Lymph node	G19A	V7I
15041	2001	Lower respiratory	G19A	V7I
15047	2001	Bacteremia	G19A	V7I
15053	2006	Arthritis	G19A	V7I
15054	2006	Bacteremia	G19A	V7I
15057	2006	Lower respiratory	G19A	V7I

15061	2006	Increased SOB	G19A	V7I
15184	2006	Necrotizing fasciitis	G19A	V7I
15189	2007	Soft tissue	G19A	V7I
15195	2007	Lower respiratory	G19A	V7I
15201	2003	Pharyngeal	G19A	V7I
15212	2003	Pharyngeal	G19A	V7I
16479	2008	Bacteremia	G19A	V7I
15043	2005	Bacteremia	G65A	C22Y
15062	2006	Peritonitis	G65A	C22Y
9897	2000	Lower respiratory	G254A	C85Y
9926	2000	Arthritis	G254A	C85Y
9937	2000	Soft tissue	G254A	C85Y
9982	1999	Necrotizing fasciitis	G254A	C85Y
10842	2001	Arthritis	G254A	C85Y
15042	2005	Decreased LOC	T281A	I94N

315	1988	Toxic shock	T307C	S103P
3397	1995	Soft tissue	A451T	N151Y
10838	2001	Soft tissue	G462A	M154I
10006	1994	Soft tissue	T552A	N182K
15000	2003	Kidney	G665A	C222Y
10041	1996	Necrotizing fasciitis	T670C	Y224H
10044	1996	Necrotizing fasciitis	T670C	Y224H
15005	2003	Bacteremia	G19A, G677A	V7I, R226Q
15006	2003	Bacteremia	G19A, G677A	V7I, R226Q
15013	2005	Lower respiratory	G19A, G677A	V7I, R226Q
15014	2005	Soft tissue	G19A, G677A	V7I, R226Q
15018	2005	Soft tissue	G19A, G677A	V7I, R226Q
15022	2005	Lower respiratory	G19A, G677A	V7I, R226Q
15026	2005	Weakness, SOB	G19A, G677A	V7I, R226Q
15032	2005	Abscess	G19A, G677A	V7I, R226Q

15040	2005	Upper respiratory	G19A, G677A	V7I, R226Q
15046	2006	Bacteremia	G19A, G677A	V7I, R226Q
15059	2006	Bacteremia	G19A, G677A	V7I, R226Q
15189	2007	Soft tissue	G19A, G677A	V7I, R226Q
15191	2007	Necrotizing fasciitis	G19A, G677A	V7I, R226Q
15209	2007	Soft tissue	G19A, G677A	V7I, R226Q
16473	2008	Abscess	G19A, G677A	V7I, R226Q
16477	2008	Soft tissue	G19A, G667A	V7I, R226Q
16478	2008	Soft tissue	G19A, G667A	V7I, R226Q
15211	2007	Unknown	G680A	C227Y
15034	2005	Lymphatic	G710T	G237V
3385	1995	Arthritis	G733A	A245T
15036	2005	Lower respiratory	C739T	Q247 ^B
15037	2005	Pre-term labor	C739T	Q247 ^B
15031	2005	Unknown	A754T	I252F

15017	2005	Toxic shock	T803G	F268C
3370	1992	Lower respiratory	None	None
3374	1994	Lower respiratory	None	None
3376	1994	Bacteremia	None	None
3378	1994	Necrotizing fasciitis	None	None
3382	1994	Necrotizing fasciitis	None	None
3392	1995	Necrotizing fasciitis	None	None
3394	1995	Necrotizing fasciitis	None	None
3452	1995	Bacteremia	None	None
3475	1995	Bacteremia	None	None
3664	1992	Lower respiratory	None	None
9881	2000	Arthritis	None	None
9884	2000	Upper respiratory	None	None
9892	2000	Soft tissue	None	None
9901	2000	Arthritis	None	None

9904	2000	Arthritis	None	None
9911	2000	Necrotizing fasciitis	None	None
9913	2000	Soft tissue	None	None
9917	2000	Soft tissue	None	None
9919	2000	Necrotizing fasciitis	None	None
9921	2000	Soft tissue	None	None
9930	2000	Necrotizing fasciitis	None	None
9934	2000	Soft tissue	None	None
9941	2000	Soft tissue	None	None
9945	2000	Soft tissue	None	None
9955	2000	Upper respiratory	None	None
9958	2000	Upper respiratory	None	None
9959	2000	Peritonitis	None	None
9967	2000	Necrotizing fasciitis	None	None
9969	2000	Bacteremia	None	None

9973	2000	Soft tissue	None	None
9978	1998	Arthritis	None	None
9983	1999	Necrotizing fasciitis	None	None
9986	1999	Soft tissue	None	None
10002	1994	Lower respiratory	None	None
10003	1994	Arthritis	None	None
10021	1995	Soft tissue	None	None
10024	1995	Arthritis	None	None
10025	1995	Arthritis	None	None
10029	1995	Necrotizing fasciitis	None	None
10048	1996	Bacteremia	None	None
10051	1993	Soft tissue	None	None
10398	2000	Adenitis	None	None
10738	1994	Bacteremia	None	None
10742	1995	Arthritis	None	None

10846	2001	Lower respiratory	None	None
10854	2001	Lower respiratory	None	None
10858	2001	Peripartum	None	None
10866	2001	Lower respiratory	None	None
15002	2003	Pneumonia	None	None
15004	2003	Soft tissue	None	None
15010	2004	Fever R/O endoc	None	None
15015	2005	Soft tissue	None	None
15016	2005	Lower respiratory	None	None
15019	2005	Bacteremia	None	None
15023	2005	Pericarditis	None	None
15024	2005	Soft tissue	None	None
15025	2005	Fever, urosepsis	None	None
15027	2005	Necrotizing fasciitis	None	None
15028	2005	Scarlet fever	None	None

15030	2005	Bacteremia	None	None
15035	2005	Soft tissue	None	None
15038	2005	Lower respiratory	None	None
15039	2005	Lower respiratory	None	None
15044	2006	Bacteremia	None	None
15045	2006	Post operative	None	None
15048	2006	Lower respiratory	None	None
15049	2006	Lower respiratory	None	None
15050	2006	Lower respiratory	None	None
15051	2006	Necrotizing fasciitis	None	None
15052	2006	Soft tissue	None	None
15055	2006	Bacteremia	None	None
15056	2006	Fascial cellulitis	None	None
15058	2006	Necrotizing fasciitis	None	None
15060	2006	Soft tissue	None	None

15063	2006	Fever, bloody stool	None	None
15064	2006	Necrotizing fasciitis	None	None
15185	2006	Soft tissue	None	None
15186	2006	Necrotizing fasciitis	None	None
15187	2007	Pyelonephritis	None	None
	2007	Bacteremia, lower	None	None
15188		respiratory		
15190	2007	Soft tissue	None	None
15192	2007	Arthritis	None	None
15193	2007	Lower respiratory	None	None
15194	2007	Necrotizing fasciitis	None	None
15196	2007	Soft tissue	None	None
15197	2007	Bacteremia	None	None
15198	2007	Soft tissue	None	None
15199	2007	SOB, pleural effusion	None	None

15200	2007	Soft tissue	None	None
15202	2007	Pyrexia	None	None
15203	2007	Upper respiratory	None	None
15210	2007	Shoulder pain	None	None
15213	2008	Soft tissue	None	None
16469	2008	Sepsis, cellulitis	None	None
16470	2007	Osteomyelitis	None	None
16471	2008	Upper respiratory	None	None
16472	2008	Soft tissue	None	None
16474	2008	Soft tissue	None	None
16475	2008	Soft tissue	None	None
16476	2008	Bacteremia	None	None

^AMGAS = Musser Group A *Streptococcus*

^BNucleotide change predicted to result in pre-mature stop codon

Supplemental Table 2

Genes influenced by RopB inactivation in serotype M3 strains MGAS10870 and MGAS9937.

MGAS315 gene number	Gene name	Putative function of encoded protein	Fold-change in MGAS10870^A	Fold-change in MGAS9937^A
<i>SpyM3_0001</i>	<i>dnaA</i>	Chromosomal replication initiator protein	2.199	—
<i>SpyM3_0002</i>	<i>dnaN</i>	DNA polymerase III, beta chain	3.792	—
<i>SpyM3_0003</i>	—	Hypothetical cytosolic protein	6.967	—
<i>SpyM3_0004</i>	—	GTP-binding protein, probable translation factor	3.099	—
<i>SpyM3_0005</i>	<i>pth</i>	Peptidyl-tRNA hydrolase	2.956	—
<i>SpyM3_0006</i>	<i>trcF</i>	Transcription-repair coupling factor	3.982	2.791
<i>SpyM3_0007</i>	—	Heat shock protein 15	4.092	2.512
<i>SpyM3_0008</i>	<i>divIC</i>	Cell division protein DIVIC	2.611	2.211
<i>SpyM3_0009</i>	—	Beta-lactamase	3.933	—
<i>SpyM3_0010</i>	<i>mesJ</i>	tRNA(Ile)-lysine synthetase Tils	4.614	2.200
<i>SpyM3_0011</i>	<i>hpt</i>	Hypoxanthine-guanine phosphoribosyltransferase	3.481	—
<i>SpyM3_0014</i>	—	Secreted protein	5.528	—
<i>SpyM3_0017</i>	<i>plsX</i>	Fatty acid phospholipid synthesis protein	2,500	—

<i>SpyM3_0018</i>	<i>acpP.1</i>	Acyl carrier protein	3.186	—
<i>SpyM3_0039</i>	<i>rpsJ</i>	SSU ribosomal protein S10P	2.326	2.305
<i>SpyM3_0042</i>	<i>rplW</i>	LSU ribosomal protein L23P	2.133	2.399
<i>SpyM3_0045</i>	<i>rplV</i>	LSU ribosomal protein L22P	—	2.197
<i>SpyM3_0048</i>	<i>rpmC</i>	LSU ribosomal protein L29P	—	2.056
<i>SpyM3_0057</i>	<i>rpsE</i>	SSU ribosomal protein S5P	—	2.000
<i>SpyM3_0058</i>	<i>rpmD</i>	LSU ribosomal protein L30P	—	2.770
<i>SpyM3_0060</i>	<i>secY</i>	Protein translocase subunit secY	2.199	2.287
<i>SpyM3_0061</i>	<i>adk</i>	Adenylate kinase, nucleoside-diphosphate kinase	2.354	2.815
<i>SpyM3_0062</i>	<i>infA</i>	Bacterial protein translation initiation factor 1 (IF-1)	2.781	—
<i>SpyM3_0063</i>	<i>rpmJ</i>	LSU ribosomal protein L36P	2.444	—
<i>SpyM3_0064</i>	<i>rpsM</i>	SSU ribosomal protein S13P	2.268	—
<i>SpyM3_0065</i>	<i>rpsK</i>	SSU ribosomal protein S11P	2.443	—
<i>SpyM3_0066</i>	<i>rpoA</i>	DNA-directed RNA polymerase alpha chain	2.454	—
<i>SpyM3_0067</i>	<i>rplQ</i>	LSU ribosomal protein L17P	2.420	—
<i>SpyM3_0072</i>	—	Adenosine 5-monophosphoramidase	4.779	3.654
<i>SpyM3_0073</i>	<i>tyrS</i>	Tyrosyl-tRNA synthetase	2.408	—
<i>SpyM3_0085</i>	—	Adenine-specific methyltransferase	3.289	—

<i>SpyM3_0088</i>	<i>proC</i>	Pyrroline-5-carboxylate reductase	2.575	—
<i>SpyM3_0089</i>	<i>pepA</i>	Glutamyl aminopeptidase	2.917	—
<i>SpyM3_0090</i>	—	Hypothetical membrane associated protein	3.202	—
<i>SpyM3_0091</i>	<i>trx.1</i>	Thioredoxin	11.24	—
<i>SpyM3_0092</i>	—	tRNA binding domain protein	2.608	2.092
<i>SpyM3_0097</i>	<i>nra</i>	Transcriptional factor	-2.150	—
<i>SpyM3_0098</i>	<i>cbp</i>	Fibronectin-binding protein	5.041	2.037
<i>SpyM3_0099</i>	—	Signal peptidase I	6.485	3,719
<i>SpyM3_0100</i>	—	Fibronectin-binding protein	4.895	2.712
<i>SpyM3_0101</i>	—	Sortase B family protein	4.712	2.837
<i>SpyM3_0102</i>	—	Hypothetical protein	4.274	2.558
<i>SpyM3_0104</i>	—	Fibronectin-binding protein	4.605	—
<i>SpyM3_0124</i>	—	Hypothetical membrane associated protein	2.335	—
<i>SpyM3_0128</i>	<i>nga</i>	NAD glycohydrolase	—	2.305
<i>SpyM3_0129</i>	—	Hypothetical protein	—	3.185
<i>SpyM3_0132</i>	—	Hypothetical protein	-2.604	—
<i>SpyM3_0133</i>	<i>metB</i>	Cystathionine beta-lyase	6.479	—
<i>SpyM3_0152</i>	—	Metal-dependent hydrolase	3.533	—

<i>SpyM3_0153</i>	—	tRNA-specific adenosine deaminase	4.843	—
<i>SpyM3_0156</i>	<i>pgi</i>	Glucose-6-phosphate isomerase	3.493	—
<i>SpyM3_0160</i>	<i>hasC.2</i>	UTP--glucose-1-phosphate uridylyltransferase	2.310	—
<i>SpyM3_0161</i>	<i>gpsA</i>	Glycerol-3-phosphate dehydrogenase [NAD(P)+]	3.347	—
<i>SpyM3_0172</i>	—	Sensory transduction protein kinase FasC	2.121	—
<i>SpyM3_0175</i>	<i>rnpA</i>	Ribonuclease P protein component	2.322	—
<i>SpyM3_0177</i>	—	Jag protein	2.414	—
<i>SpyM3_0178</i>	<i>rmpH</i>	LSU ribosomal protein L34P	2.124	2.182
<i>SpyM3_0187</i>	—	Transcriptional regulator, RpiR family	2.519	—
<i>SpyM3_0190</i>	<i>ksgA</i>	Dimethyladenosine transferase	2.318	—
<i>SpyM3_0196</i>	<i>purR</i>	Pur operon repressor	3.025	—
<i>SpyM3_0197</i>	<i>prgA</i>	Surface exclusion protein	3.231	—
<i>SpyM3_0198</i>	<i>rpsL</i>	SSU ribosomal protein S12P	2.519	—
<i>SpyM3_0199</i>	<i>rpsG</i>	SSU ribosomal protein S7P	3.155	—
<i>SpyM3_0206</i>	<i>mecA</i>	Negative regulator of genetic competence <i>mecA</i>	2.065	—
<i>SpyM3_0207</i>	<i>rgpG</i>	Undecaprenyl-phosphate alpha-N-acetylglucosaminephosphotransferase	2.661	2.208
<i>SpyM3_0208</i>	—	ABC transporter ATP-binding protein	2.126	—

<i>SpyM3_0209</i>	—	SufD protein	3.316	—
<i>SpyM3_0211</i>	—	IscU protein	2.117	—
<i>SpyM3_0213</i>	—	D-alanyl-D-alanine serine-type carboxypeptidase	2.787	2.399
<i>SpyM3_0214</i>	<i>dacA</i>	D-alanyl-D-alanine serine-type carboxypeptidase	2.021	—
<i>SpyM3_0215</i>	<i>oppA</i>	Oligopeptide-binding protein oppA	4.592	2.454
<i>SpyM3_0216</i>	<i>oppB</i>	Oligopeptide transport system permease protein oppB	3.801	3.528
<i>SpyM3_0217</i>	<i>oppC</i>	Oligopeptide transport system permease protein oppC	—	3.307
<i>SpyM3_0218</i>	<i>oppD</i>	Oligopeptide transport ATP-binding protein oppD	2.481	4.565
<i>SpyM3_0224</i>	—	GTP-binding protein	5.074	—
<i>SpyM3_0225</i>	—	Hypothetical RNA binding protein	5.059	—
<i>SpyM3_0226</i>	<i>nadD</i>	Nicotinate-nucleotide adenylyltransferase	2.755	—
<i>SpyM3_0227</i>	—	Hydrolase (HAD superfamily)	2.791	—
<i>SpyM3_0228</i>	—	iojap protein family	3.036	—
<i>SpyM3_0230</i>	—	Hypothetical cytosolic protein	2.430	—
<i>SpyM3_0231</i>	—	Hypothetical cytosolic protein	6.147	—
<i>SpyM3_0238</i>	—	Potassium uptake protein ktrA	4.590	—
<i>SpyM3_0239</i>	—	Potassium uptake protein ktrB	2.058	—
<i>SpyM3_0240</i>	<i>gidB</i>	Methyltransferase gidB	2.285	2.533

<i>SpyM3_0241</i>	<i>lemA</i>	LemA protein	2.418	—
<i>SpyM3_0242</i>	<i>htpX</i>	Endopeptidase htpX	2.019	—
<i>SpyM3_0243</i>	—	Hypothetical cytosolic protein	2.129	—
<i>SpyM3_0245</i>	<i>csrS</i>	Transmembrane histidine kinase CsrS	3.432	—
<i>SpyM3_0246</i>	<i>nrdR</i>	Putative regulatory protein	2.409	—
<i>SpyM3_0251</i>	—	Hypothetical cytosolic protein	2.151	—
<i>SpyM3_0252</i>	<i>murC</i>	UDP-N-acetylmuramate--alanine ligase	2.246	—
<i>SpyM3_0253</i>	—	Acetyltransferase, GNAT family	2.278	—
<i>SpyM3_0255</i>	<i>greA</i>	Transcription elongation factor greA	2.701	—
<i>SpyM3_0259</i>	—	Hydrolase (HAD superfamily)	2.111	—
<i>SpyM3_0261</i>	—	Hypothetical exported protein	2.923	—
<i>SpyM3_0262</i>	<i>glr</i>	Glutamate racemase	3.642	—
<i>SpyM3_0263</i>	—	Xanthosine triphosphate pyrophosphatase	3.259	—
<i>SpyM3_0264</i>	—	Putative phosphoesterase	3.158	—
<i>SpyM3_0265</i>	—	CBS domain containing protein	3.677	—
<i>SpyM3_0266</i>	<i>xerD</i>	DNA integration recombination inversion protein	2.598	—
<i>SpyM3_0267</i>	<i>scpA</i>	Segregation and condensation protein ScpA	3.037	—
<i>SpyM3_0268</i>	<i>scpB</i>	Segregation and condensation protein ScpB	3.005	—

<i>SpyM3_0269</i>	—	Ribosomal large subunit pseudouridine synthase B	2.728	—
<i>SpyM3_0270</i>	—	Hypothetical cytosolic protein	2.485	—
<i>SpyM3_0271</i>	—	23S rRNA methyltransferase	3.089	—
<i>SpyM3_0273</i>	—	Membrane-associated phospholipid phosphatase	2.152	—
<i>SpyM3_0276</i>	<i>hlyX</i>	Magnesium and cobalt efflux protein corC	2.820	—
<i>SpyM3_0278</i>	—	Inorganic pyrophosphatase	2.127	—
<i>SpyM3_0285</i>	—	Export protein for polysaccharides and teichoic acids	3.238	—
<i>SpyM3_0286</i>	<i>upp</i>	Uracil phosphoribosyltransferase	6.294	—
<i>SpyM3_0288</i>	—	Hypothetical cytosolic protein	2.745	—
<i>SpyM3_0289</i>	<i>tmk</i>	Thymidylate kinase	2.412	—
<i>SpyM3_0290</i>	—	DNA polymerase III, delta subunit	2.196	—
<i>SpyM3_0291</i>	—	Initiation-control protein	3.128	—
<i>SpyM3_0292</i>	—	Tetrapyrrole (Corrin Porphyrin) methylase family protein	2.471	—
<i>SpyM3_0293</i>	—	Hypothetical membrane associated protein	3.145	2.098
<i>SpyM3_0296</i>	<i>exoA</i>	Exodeoxyribonuclease III	2.751	—
<i>SpyM3_0302</i>	<i>nrdI</i>	NrdI protein	2.920	2.692
<i>SpyM3_0308</i>	—	Hypothetical protein	3.131	2.580
<i>SpyM3_0309</i>	<i>fabG</i>	Short chain dehydrogenase	2.637	2.573

<i>SpyM3_0318</i>	<i>mtsA</i>	Manganese-binding protein	2.152	—
<i>SpyM3_0321</i>	<i>cypB</i>	Peptidyl-prolyl cis-trans isomerase	2.606	—
<i>SpyM3_0324</i>	<i>rplK</i>	LSU ribosomal protein L11P	2.674	—
<i>SpyM3_0325</i>	<i>rplA</i>	LSU ribosomal protein L1P	3.952	—
<i>SpyM3_0326</i>	<i>pyrH</i>	Uridylate kinase	3.813	—
<i>SpyM3_0329</i>	<i>msrA.2</i>	Peptide methionine sulfoxide reductase msrA	3.457	—
<i>SpyM3_0333</i>	<i>phoH</i>	PhoH protein	2.478	—
<i>SpyM3_0334</i>	—	Uracil DNA glycosylase superfamily protein	2.532	—
<i>SpyM3_0335</i>	—	Hypothetical metal-binding protein	2.607	—
<i>SpyM3_0336</i>	<i>dgk</i>	Diacylglycerol kinase	3.996	—
<i>SpyM3_0337</i>	<i>era</i>	GTP-binding protein era	3.300	—
<i>SpyM3_0338</i>	—	Phosphohydrolase (MutT nudix family protein)	3.549	2.197
<i>SpyM3_0342</i>	—	Hypothetical protein	2.488	—
<i>SpyM3_0355</i>	<i>pcp</i>	Pyrrolidone-carboxylate peptidase	2.210	2.223
<i>SpyM3_0357</i>	—	Permease	5.389	—
<i>SpyM3_0358</i>	—	Bactoprenol glucosyl transferase	3.111	—
<i>SpyM3_0362</i>	<i>ccpA</i>	Catabolite control protein A	3.613	—
<i>SpyM3_0371</i>	—	Hypothetical cytosolic protein	2.124	—

<i>SpyM3_0372</i>	<i>vicR</i>	Two-component response regulator VicR	2,100	—
<i>SpyM3_0374</i>	<i>vicX</i>	Zn-dependent hydrolase (beta-lactamase superfamily)	2.056	—
<i>SpyM3_0375</i>	<i>rnc</i>	Ribonuclease III	4.664	—
<i>SpyM3_0376</i>	<i>smc</i>	Chromosome partition protein smc	—	3.550
<i>SpyM3_0385</i>	—	UDP-glucose 6-dehydrogenase	2.054	—
<i>SpyM3_0393</i>	—	Plasmid stabilization system antitoxin protein	2.320	—
<i>SpyM3_0394</i>	—	Plasmid stabilization system toxin protein	2.150	—
<i>SpyM3_0399</i>	—	Hydrolase (HAD superfamily)	2.586	—
<i>SpyM3_0406</i>	—	Hypothetical membrane spanning protein	2.804	3.217
<i>SpyM3_0407</i>	—	Hypothetical membrane spanning protein	3.091	2.881
<i>SpyM3_0416</i>	—	Hypothetical protein	2.887	—
<i>SpyM3_0420</i>	<i>lysS</i>	Lysyl-tRNA synthetase	2.472	—
<i>SpyM3_0421</i>	—	Hydrolase (HAD superfamily)	5.238	—
<i>SpyM3_0422</i>	—	Phosphoglycerate mutase family protein	5.802	—
<i>SpyM3_0423</i>	—	Transcriptional regulator	3.889	—
<i>SpyM3_0425</i>	—	N-acetylmuramoyl-L-alanine amidase	—	-2.288
<i>SpyM3_0427</i>	—	Hypothetical exported protein	2.650	—
<i>SpyM3_0429</i>	<i>pepF</i>	Oligoendopeptidase F	2.873	2.103

<i>SpyM3_0434</i>	<i>murN</i>	Factor essential for expression of methicillin resistance	2.558	2.196
		UDP-N-acetylmuramoylpentapeptide-lysine N(6)-		
<i>SpyM3_0435</i>	<i>murM.1</i>	alanyltransferase,	2.328	—
		UDP-N-acetylmuramoylpentapeptide-lysine N(6)-seryltransferase		
<i>SpyM3_0436</i>	—	Hydrolase (HAD superfamily)	2.715	—
<i>SpyM3_0440</i>	<i>pacL</i>	Calcium-transporting ATPase	2.996	—
<i>SpyM3_0454</i>	<i>prfB</i>	Bacterial peptide chain release factor 2 (RF-2)	2.401	—
<i>SpyM3_0455</i>	<i>ftsE</i>	Cell division ATP-binding protein ftsE	2.104	—
<i>SpyM3_0459</i>	<i>dinG</i>	ATP-dependent helicase, DinG family	2.540	—
<i>SpyM3_0461</i>	<i>asnC</i>	Asparaginyl-tRNA synthetase	2.116	—
<i>SpyM3_0465</i>	<i>pepD</i>	Dipeptidase A	—	2.409
<i>SpyM3_0466</i>	<i>adcA</i>	High-affinity zinc uptake system protein znuA precursor	—	2.493
<i>SpyM3_0467</i>	—	Transcriptional regulator, GntR family	2.060	—
<i>SpyM3_0471</i>	<i>flaV</i>	Flavodoxin	2.907	—
<i>SpyM3_0474</i>	<i>rplS</i>	LSU ribosomal protein L19P	2.486	—
<i>SpyM3_0477</i>	—	Septation ring formation regulator	2.258	—
<i>SpyM3_0478</i>	—	Hypothetical cytosolic protein	5.385	5.097
<i>SpyM3_0493</i>	—	ATP synthase C chain	3.335	—

<i>SpyM3_0494</i>	—	ATP synthase A chain	2.512	—
<i>SpyM3_0495</i>	—	ATP synthase B chain	2.903	—
<i>SpyM3_0496</i>	—	ATP synthase delta chain	2.581	—
<i>SpyM3_0497</i>	—	ATP synthase alpha chain	2.088	—
<i>SpyM3_0500</i>	<i>atpC</i>	ATP synthase epsilon chain	2.102	—
<i>SpyM3_0513</i>	<i>rexB</i>	ATP-dependent nuclease subunit B	2.405	—
<i>SpyM3_0514</i>	<i>rexA</i>	ATP-dependent nuclease subunit A	2.082	—
<i>SpyM3_0515</i>	—	Arginine-binding protein	3.151	—
<i>SpyM3_0521</i>	<i>rmlD</i>	dTDP-4-dehydrorhamnose reductase	4.188	—
<i>SpyM3_0522</i>	<i>rgpAc</i>	alpha-(1,2)-rhamnosyltransferase	2.189	—
<i>SpyM3_0524</i>	<i>rgpCc</i>	Polysaccharide export ABC transporter permease protein	2.046	—
<i>SpyM3_0528</i>	—	Phosphoglycerol transferase	2.129	2.616
<i>SpyM3_0529</i>	—	Glycosyltransferase involved in cell wall biogenesis	—	2.120
<i>SpyM3_0530</i>	—	Hypothetical protein	2.206	2.018
<i>SpyM3_0531</i>	—	Transcriptional activator amrA	2.098	—
<i>SpyM3_0532</i>	—	Hypothetical membrane spanning protein	2.404	—
<i>SpyM3_0538</i>	<i>infC</i>	Bacterial protein translation initiation factor 3 (IF-3)	2.208	—
<i>SpyM3_0541</i>	—	Sulfatase family protein	2.458	2.216

<i>SpyM3_0542</i>	—	Methyltransferase	2.037	—
<i>SpyM3_0543</i>	<i>aroD</i>	3-dehydroquinate dehydratase	2.255	—
<i>SpyM3_0545</i>	—	Hypothetical cytosolic protein	2.712	—
<i>SpyM3_0550</i>	<i>thil</i>	Thiamine biosynthesis protein thil	2.414	—
<i>SpyM3_0558</i>	<i>pyrR</i>	Pyrimidine operon regulatory protein pyrR	2.595	—
<i>SpyM3_0567</i>	<i>rpsP</i>	SSU ribosomal protein S16P	2.384	—
<i>SpyM3_0568</i>	—	RNA binding protein	2.309	—
<i>SpyM3_0570</i>	—	Hypothetical cytosolic protein	—	2.082
<i>SpyM3_0576</i>	—	Hypothetical membrane spanning protein	2.443	—
<i>SpyM3_0577</i>	<i>apbA</i>	Ketopantoate reductase PanE ApbA family protein	2.524	—
<i>SpyM3_0578</i>	<i>fruR</i>	Fructose repressor	2.139	—
<i>SpyM3_0579</i>	<i>fruK</i>	1-phosphofructokinase	—	-2.586
<i>SpyM3_0580</i>	<i>fruA</i>	PTS system, fructose-specific IIABC component	—	-2.547
<i>SpyM3_0582</i>	—	N-acetylmuramidase	2.024	—
<i>SpyM3_0586</i>	—	DegV family protein	2.421	—
<i>SpyM3_0592</i>	—	GTP pyrophosphokinase	2.111	—
<i>SpyM3_0593</i>	—	Two-component response regulator	2.325	—
<i>SpyM3_0600</i>	<i>mvaS.2</i>	Hydroxymethylglutaryl-CoA synthase	4.331	4.532

<i>SpyM3_0601</i>	<i>thyA</i>	Thymidylate synthase	2.124	—
<i>SpyM3_0602</i>	<i>dys</i>	Dihydrofolate reductase	2.017	—
<i>SpyM3_0603</i>	—	Hypothetical membrane associated protein	3.271	—
<i>SpyM3_0604</i>	<i>clpX</i>	ATP-dependent endopeptidase clp ATP-binding subunit clpX	2.908	—
<i>SpyM3_0605</i>	<i>engB</i>	GTP-binding protein YihA	3.005	2.542
<i>SpyM3_0606</i>	—	Hypothetical protein	2.498	—
<i>SpyM3_0620</i>	—	Cystine transport system permease protein	—	3.638
<i>SpyM3_0627</i>	—	Hypothetical cytosolic protein	3.866	—
<i>SpyM3_0628</i>	<i>rpsA</i>	SSU ribosomal protein S1P	3.633	—
<i>SpyM3_0629</i>	—	Hypothetical protein	2.023	—
<i>SpyM3_0630</i>	—	Rhodanese-related sulfurtransferases	2.294	—
<i>SpyM3_0632</i>	—	Transporter	2.304	—
<i>SpyM3_0635</i>	<i>hflX</i>	GTP-binding protein hflX	2.408	—
<i>SpyM3_0636</i>	—	Cystathionine beta-lyase, cystathionine gamma-lyase	3.052	—
<i>SpyM3_0640</i>	<i>apt</i>	Adenine phosphoribosyltransferase	2.216	—
<i>SpyM3_0641</i>	—	DNA replication protein dnaD	2.470	—
<i>SpyM3_0644</i>	—	NIF3-related protein	—	2.888
<i>SpyM3_0645</i>	—	Glycine D-amino acid oxidases family	—	2.737

<i>SpyM3_0646</i>	<i>rmlA</i>	Glucose-1-phosphate thymidyltransferase	2.374	—
<i>SpyM3_0647</i>	<i>rmlC</i>	dTDP-4-dehydrorhamnose 3,5-epimerase	2.652	—
<i>SpyM3_0648</i>	<i>rmlB</i>	dTDP-glucose 4,6-dehydratase	2.716	—
<i>SpyM3_0649</i>	<i>mutX</i>	7,8-dihydro-8-oxoguanine-triphosphatase	2.048	—
<i>SpyM3_0666</i>	—	Lipoate-protein ligase A	2.500	—
<i>SpyM3_0669</i>	—	Hypothetical membrane spanning protein	3.180	—
<i>SpyM3_0670</i>	—	Hypothetical membrane associated protein	2.579	—
<i>SpyM3_0672</i>	—	Hypothetical protein	—	2.347
<i>SpyM3_0673</i>	<i>hemN</i>	Oxygen-independent coproporphyrinogen-III oxidase	5.547	2.513
<i>SpyM3_0674</i>	—	Acyl-[acyl-carrier-protein] hydrolase	2.931	—
<i>SpyM3_0675</i>	—	Hydrolase (HAD superfamily)	2.477	2.568
<i>SpyM3_0676</i>	—	Hypothetical membrane spanning protein	4.611	—
<i>SpyM3_0725</i>	<i>hylP.1</i>	Hyaluronoglucosaminidase	-2.337	—
<i>SpyM3_0738</i>	<i>scIB</i>	Collagen-like surface protein	2.007	—
<i>SpyM3_0741</i>	—	PTS system, mannose fructose family IIA component	2.034	—
<i>SpyM3_0748</i>	—	Succinate-semialdehyde dehydrogenase [NADP+]	3.040	—
<i>SpyM3_0749</i>	<i>uvrC</i>	Excinuclease ABC subunit C	2.597	—
<i>SpyM3_0750</i>	—	NAD(P)H-dependent quinone reductase	3.042	—

<i>SpyM3_0751</i>	—	Xaa-His dipeptidase	2.133	—
<i>SpyM3_0756</i>	—	Polysaccharide deacetylase	5.028	2.350
<i>SpyM3_0763</i>	<i>murB</i>	UDP-N-acetylenolpyruvoylglucosamine reductase	2.413	—
<i>SpyM3_0765</i>	<i>potB</i>	Spermidine putrescine transport system permease protein potB	2.071	—
<i>SpyM3_0770</i>	<i>malP</i>	Malate-sodium symport	4.865	—
<i>SpyM3_0773</i>	<i>aphA</i>	Class B acid phosphatase	2.509	—
<i>SpyM3_0775</i>	—	Lipase acylhydrolase family protein	2.086	—
<i>SpyM3_0776</i>	—	Hypothetical membrane spanning protein	2.000	—
<i>SpyM3_0779</i>	—	Redox-sensitive transcriptional regulator Rex	2.584	—
<i>SpyM3_0780</i>	—	Hypothetical cytosolic protein	3.730	—
<i>SpyM3_0781</i>	—	Cysteine desulfurase, selenocysteine lyase	3.106	—
<i>SpyM3_0782</i>	<i>prs</i>	Ribose-phosphate pyrophosphokinase	2.759	—
<i>SpyM3_0783</i>	—	Organic phosphate binding CYTH family protein	4.020	—
<i>SpyM3_0784</i>	—	GTP pyrophosphokinase homolog	3.994	2.716
<i>SpyM3_0785</i>	<i>ppnK</i>	ATP-NAD kinase	3.744	2.527
<i>SpyM3_0786</i>	<i>rluD</i>	Ribosomal large subunit pseudouridine synthase D	3.247	3.599
<i>SpyM3_0788</i>	—	Short chain dehydrogenase	2.051	—
<i>SpyM3_0791</i>	—	Glycine betaine transport ATP-binding protein	2.288	—

<i>SpyM3_0792</i>	—	Glycine betaine transport system permease protein, glycine betaine-binding protein	2.319	—
<i>SpyM3_0799</i>	<i>prfA</i>	Bacterial peptide chain release factor 1 (RF-1)	3.321	2.358
<i>SpyM3_0809</i>	<i>ldh</i>	L-lactate dehydrogenase	2.545	—
<i>SpyM3_0810</i>	<i>gyrA</i>	DNA gyrase subunit A	2.734	—
<i>SpyM3_0811</i>	—	Sortase	2.122	—
<i>SpyM3_0812</i>	—	Glyoxalase family protein	2.219	3.063
<i>SpyM3_0823</i>	—	Hypothetical membrane associated protein	—	6.653
<i>SpyM3_0828</i>	—	Mg ²⁺ citrate complex secondary transporter	—	3.919
<i>SpyM3_0829</i>	—	Hypothetical protein	—	5.167
<i>SpyM3_0831</i>	—	Na ⁺ transporting oxaloacetate decarboxylase beta chain	—	6.820
<i>SpyM3_0832</i>	<i>citD</i>	Citrate lyase acyl carrier protein	2.723	—
<i>SpyM3_0833</i>	<i>citE</i>	Citrate lyase beta chain, citryl-CoA lyase subunit	—	5.785
<i>SpyM3_0834</i>	<i>citF</i>	Citrate lyase alpha chain, citrate CoA-transferase	—	7.442
<i>SpyM3_0835</i>	<i>citX</i>	Apo-citrate lyase phosphoribosyl-dephospho-CoA transferase	—	4.540
<i>SpyM3_0368</i>	<i>oadA</i>	Na ⁺ transporting oxaloacetate decarboxylase alpha chain	—	7.266
<i>SpyM3_0837</i>	<i>citC</i>	[Citrate [pro-3S]-lyase] ligase	2.030	2.298
<i>SpyM3_0838</i>	—	Hypothetical protein	2.261	2.188

<i>SpyM3_0842</i>	<i>ylxM</i>	Signal recognition particle associated protein	2.380	—
<i>SpyM3_0843</i>	—	Transcriptional regulator, GntR family	4.623	—
<i>SpyM3_0845</i>	<i>guaA</i>	GMP synthase [glutamine-hydrolyzing]	2.544	—
<i>SpyM3_0850</i>	—	Transcriptional regulator, GntR family /aminotransferase Class I	—	2.567
<i>SpyM3_0854</i>	<i>lplA</i>	Lipoate-protein ligase A	—	2.169
<i>SpyM3_0855</i>	—	SIR2 family protein	—	2.457
<i>SpyM3_0856</i>	—	ATPase associated with chromosome architecture replication	—	2.394
<i>SpyM3_0857</i>	—	Glycine cleavage system H protein	2.636	—
<i>SpyM3_0858</i>	—	Luciferase-like monooxygenase	2.124	2.187
<i>SpyM3_0859</i>	—	Probable NADH-dependent flavin oxidoreductase yqiG	2.134	—
<i>SpyM3_0861</i>	<i>dpfB</i>	Phosphopantothenate--cysteine ligase	2.066	—
<i>SpyM3_0866</i>	—	Nucleoside transport system permease protein	2.737	—
<i>SpyM3_0868</i>	—	Nucleoside-binding protein	2.593	—
<i>SpyM3_0871</i>	<i>coaA</i>	Pantothenate kinase	3.583	—
<i>SpyM3_0872</i>	<i>rpsT</i>	SSU ribosomal protein S20P	3.087	—
<i>SpyM3_0876</i>	<i>phoU</i>	Phosphate transport system protein phoU	2.106	2.143
<i>SpyM3_0877</i>	<i>pstB</i>	Phosphate transport ATP-binding protein pstB	2.330	—
<i>SpyM3_0878</i>	<i>pstB2</i>	Phosphate transport ATP-binding protein pstB	2.080	—

<i>SpyM3_0882</i>	—	Putative 23S rRNA m(5)C methyltransferase	2.157	—
<i>SpyM3_0884</i>	—	Hypothetical cytosolic protein	2.556	—
<i>SpyM3_0885</i>	<i>spxA</i>	Arsenate reductase family protein	2.336	—
<i>SpyM3_0886</i>	<i>mreA</i>	Riboflavin kinase FMN adenylyltransferase	2.177	—
<i>SpyM3_0888</i>	—	Hypothetical protein	2.601	—
<i>SpyM3_0905</i>	<i>cfa</i>	cAMP factor	3.057	2.314
<i>SpyM3_0913</i>	<i>pfkA</i>	6-phosphofructokinase	2.854	—
<i>SpyM3_0914</i>	<i>dnaE</i>	DNA polymerase III alpha subunit	3.078	2.052
<i>SpyM3_0915</i>	—	Transcriptional regulator, GntR family	—	18.20
<i>SpyM3_0916</i>	—	ABC transporter ATP-binding protein	—	12.08
<i>SpyM3_0917</i>	—	ABC transporter permease protein	—	16.54
<i>SpyM3_0918</i>	—	Putative membrane-associated alkaline phosphatase	2.368	—
<i>SpyM3_0963</i>	—	Phage protein	-2.183	—
<i>SpyM3_0964</i>	—	Transcriptional regulator, Cro C1 family	-2.391	—
<i>SpyM3_0980</i>	<i>glgP</i>	Maltodextrin phosphorylase	—	2.340
<i>SpyM3_0982</i>	<i>malR</i>	Transcriptional regulator, LacI family	2.622	—
<i>SpyM3_0984</i>	<i>malF</i>	Maltodextrin transport system permease protein malC	—	2.119
<i>SpyM3_1009</i>	—	Hypothetical cytosolic protein	—	2.311

<i>SpyM3_1019</i>	—	Hypothetical protein	3.112	2.417
<i>SpyM3_1021</i>	—	Hypothetical cytosolic protein	2.474	—
<i>SpyM3_1023</i>	—	Phosphorylase, Pnp Udp family	—	2.794
<i>SpyM3_1025</i>	<i>psr</i>	Transcriptional regulator, LytR family	2.654	—
<i>SpyM3_1026</i>	<i>aroK</i>	Shikimate kinase	2.385	—
<i>SpyM3_1027</i>	<i>aroA.1</i>	3-phosphoshikimate 1-carboxyvinyltransferase	2.038	—
<i>SpyM3_1028</i>	—	Ribonuclease BN	2.906	—
<i>SpyM3_1029</i>	<i>map</i>	Methionine aminopeptidase	2.475	—
<i>SpyM3_1031</i>	—	Ribosomal-protein-S5-alanine acetyltransferase	4.127	—
<i>SpyM3_1037</i>	—	Hypothetical protein	2.260	2.187
<i>SpyM3_1040</i>	—	Hypothetical membrane spanning protein	5.737	—
<i>SpyM3_1042</i>	<i>udk</i>	Uridine kinase	3.073	—
<i>SpyM3_1044</i>	—	Peptidoglycan N-acetylglucosamine deacetylase	2.121	—
<i>SpyM3_1045</i>	<i>gapN</i>	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	3.669	—
<i>SpyM3_1048</i>	<i>nrdH</i>	Glutaredoxin	5.382	—
<i>SpyM3_1049</i>	<i>nrdE.1</i>	Ribonucleoside-diphosphate reductase alpha chain	3.857	3.107
<i>SpyM3_1050</i>	<i>nrdF</i>	Ribonucleoside-diphosphate reductase beta chain	4.429	4.666
<i>SpyM3_1059</i>	<i>prsA</i>	Peptidyl-prolyl cis-trans isomerase	2.026	—

<i>SpyM3_1072</i>	<i>holA</i>	DNA polymerase III, delta subunit	4.862	—
<i>SpyM3_1076</i>	—	Methyltransferase	2.950	—
<i>SpyM3_1082</i>	—	Hypothetical membrane spanning protein	2.430	—
<i>SpyM3_1083</i>	<i>murF</i>	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	2.397	—
<i>SpyM3_1084</i>	<i>ddl</i>	D-alanine--D-alanine ligase	2.922	—
<i>SpyM3_1086</i>	—	Penicillin-binding protein	3.055	—
<i>SpyM3_1087</i>	<i>fdhC</i>	Formate transporter	2.204	—
<i>SpyM3_1091</i>	<i>pyrD</i>	Dihydroorotate dehydrogenase	2.549	—
<i>SpyM3_1094</i>	—	Phage protein	-2.389	—
<i>SpyM3_1109</i>	—	Phage protein	-2.060	—
<i>SpyM3_1124</i>	—	Phage protein	-2.515	—
<i>SpyM3_1137</i>	—	Phage protein	-2.283	—
<i>SpyM3_1150</i>	—	Hypothetical protein	2.598	—
<i>SpyM3_1151</i>	<i>recN</i>	DNA repair protein recN	2.751	—
<i>SpyM3_1154</i>	<i>fps</i>	Dimethylallyltransferase, geranyltranstransferase	2.232	—
<i>SpyM3_1155</i>	<i>xseB</i>	Exodeoxyribonuclease VII small subunit	2.639	—
<i>SpyM3_1159</i>	<i>phr</i>	Deoxyribodipyrimidine photolyase	7.367	—
<i>SpyM3_1162</i>	—	Hypothetical cytosolic protein	2.364	—

<i>SpyM3_1167</i>	<i>divIVA</i>	Cell division initiation protein DivIVA	2.197	—
<i>SpyM3_1169</i>	—	Integral membrane protein	2.148	—
<i>SpyM3_1174</i>	<i>divIB</i>	Cell division initiation protein DivIB	2.120	—
<i>SpyM3_1178</i>	—	GTP-binding protein TypA BipA	2.653	—
<i>SpyM3_1179</i>	—	Rhodanese-related sulfurtransferases	2.684	—
<i>SpyM3_1181</i>	—	Hypothetical cytosolic protein	3.474	—
<i>SpyM3_1185</i>	—	Transcriptional regulator	3.345	—
<i>SpyM3_1186</i>	—	Ribose operon repressor	2.527	2.082
<i>SpyM3_1187</i>	—	ATP-dependent endopeptidase Lon	2.164	—
<i>SpyM3_1198</i>	<i>argR</i>	Arginine repressor, argR	4.145	2.449
<i>SpyM3_1199</i>	—	Hypothetical protein	2.362	—
<i>SpyM3_1205</i>	<i>speK</i>	Exotoxin type C precursor	2.928	4.526
<i>SpyM3_1226</i>	—	Phage protein	-2.047	—
<i>SpyM3_1248</i>	—	Phage protein	-3.767	—
<i>SpyM3_1250</i>	—	Phage single-strand DNA binding protein	-2.029	—
<i>SpyM3_1265</i>	—	Phage protein	2.264	—
<i>SpyM3_1277</i>	—	Hypothetical cytosolic protein	2.716	—
<i>SpyM3_1278</i>	—	Hypothetical protein	4.043	—

<i>SpyM3_1353</i>	—	Phage protein	2.080	—
<i>SpyM3_1364</i>	—	S1-type RNA-binding domain	2.462	—
<i>SpyM3_1365</i>	—	Peptidyl-prolyl cis-trans isomerase	2.373	—
<i>SpyM3_1367</i>	—	Two-component sensor protein yvqE	2.534	—
<i>SpyM3_1368</i>	—	Transporter yvqF	2.570	—
<i>SpyM3_1373</i>	<i>priA</i>	Primosomal protein N	—	2.517
<i>SpyM3_1374</i>	—	DNA-directed RNA polymerase omega chain	2.041	—
<i>SpyM3_1375</i>	<i>gmk</i>	Guanylate kinase	4.130	—
<i>SpyM3_1376</i>	—	Hydrolase (HAD superfamily)	2.180	—
<i>SpyM3_1387</i>	—	Cell division initiation protein DivIVA	2.804	—
<i>SpyM3_1388</i>	—	Hypothetical cytosolic protein	4.688	—
<i>SpyM3_1391</i>	<i>pepC</i>	Aminopeptidase C	5.668	2.536
<i>SpyM3_1392</i>	<i>nadE</i>	NH(3)-dependent NAD(+) synthetase	2.883	2.641
<i>SpyM3_1393</i>	—	Nicotinate phosphoribosyltransferase	2.254	—
<i>SpyM3_1395</i>	<i>nox.2</i>	Thioredoxin reductase	—	2.166
<i>SpyM3_1397</i>	—	Amino acid transport ATP-binding protein	6.172	—
<i>SpyM3_1398</i>	—	Amino acid ABC transporter permease protein	2.162	—
<i>SpyM3_1402</i>	<i>ftsL</i>	Cell division protein ftsL	2.923	—

<i>SpyM3_1403</i>	<i>mraW</i>	S-adenosyl-methyltransferase <i>mraW</i>	2.247	—
<i>SpyM3_1404</i>	—	Hypothetical protein	2.578	—
<i>SpyM3_1415</i>	—	Phage protein	-2.101	—
<i>SpyM3_1417</i>	—	Phage infection protein	—	-2.039
<i>SpyM3_1427</i>	—	Phage protein	-2.022	—
<i>SpyM3_1444</i>	—	Phage protein	—	-2.201
<i>SpyM3_1447</i>	—	Phage protein	-2.106	—
<i>SpyM3_1449</i>	—	Phage protein	-2.269	—
<i>SpyM3_1453</i>	—	Phage protein	—	-2.435
<i>SpyM3_1461</i>	—	Hypothetical protein	2.228	—
<i>SpyM3_1462</i>	<i>tkt</i>	Transketolase	2.410	—
<i>SpyM3_1463</i>	<i>tal</i>	Transaldolase	2.421	—
<i>SpyM3_1465</i>	<i>npx</i>	NADH peroxidase	2.149	—
<i>SpyM3_1474</i>	—	Aldo keto reductase family	2.339	—
<i>SpyM3_1477</i>	—	Hypothetical protein	2.172	—
<i>SpyM3_1479</i>	—	Transcriptional regulator, TetR family	3.070	—
<i>SpyM3_1487</i>	—	PTS system, galactose-specific IIB component	-2.076	—
<i>SpyM3_1488</i>	—	PTS system, galactose-specific IIA component	-2.578	—

<i>SpyM3_1489</i>	<i>lacR.1</i>	Lactose phosphotransferase system repressor	-2.665	—
<i>SpyM3_1496</i>	—	LSU ribosomal protein L7AE	—	-2.053
<i>SpyM3_1497</i>	—	Hypothetical cytosolic protein	—	-2.104
<i>SpyM3_1498</i>	<i>nusA</i>	N utilization substance protein A	—	-2.281
<i>SpyM3_1499</i>	—	Hypothetical cytosolic protein	—	-2.574
<i>SpyM3_1500</i>	<i>trmB</i>	tRNA (m(7)G46) methyltransferase	2.940	—
<i>SpyM3_1501</i>	—	Phosphotransferase enzyme family	3.367	—
<i>SpyM3_1502</i>	—	Protein ecsB	2.395	—
<i>SpyM3_1503</i>	—	ABC-type transporter ATP-binding protein ecsA	2.106	—
<i>SpyM3_1507</i>	—	Acetyltransferase	2.522	—
<i>SpyM3_1510</i>	—	Hydrolase (HAD superfamily)	2.954	—
<i>SpyM3_1511</i>	<i>manL</i>	PTS system, mannose-specific IIB component	3.385	—
<i>SpyM3_1512</i>	<i>manM</i>	PTS system, mannose-specific IIC component	2.753	—
<i>SpyM3_1514</i>	—	Hypothetical cytosolic protein	5.753	—
<i>SpyM3_1516</i>	<i>serS</i>	Seryl-tRNA synthetase	—	-2.005
<i>SpyM3_1517</i>	<i>accA</i>	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	—	2.806
<i>SpyM3_1518</i>	<i>accD</i>	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	—	3.021

<i>SpyM3_1519</i>	<i>accC</i>	Biotin carboxylase	—	3.917
<i>SpyM3_1520</i>	<i>fabZ</i>	(3R)-hydroxyacyl-[acyl carrier protein] dehydratase	—	4.846
<i>SpyM3_1521</i>	<i>accB</i>	Biotin carboxyl carrier protein of acetyl-CoA carboxylase	—	4.478
<i>SpyM3_1522</i>	<i>fabF</i>	3-oxoacyl-[acyl-carrier-protein] synthase	—	4.209
<i>SpyM3_1523</i>	<i>fabG</i>	3-oxoacyl-[acyl-carrier-protein] reductase	2.120	5.311
<i>SpyM3_1524</i>	<i>fabD</i>	Malonyl-CoA-[acyl-carrier-protein] transacylase	—	5.915
<i>SpyM3_1526</i>	<i>acpP</i>	Acyl carrier protein	3.454	—
<i>SpyM3_1534</i>	—	N-acetylmuramoyl-L-alanine amidase	2.375	—
<i>SpyM3_1535</i>	—	D-alanyl-D-alanine metallocarboxypeptidase	2.036	—
<i>SpyM3_1536</i>	—	Phosphoglycerate mutase family protein	2.645	—
<i>SpyM3_1539</i>	<i>gatB</i>	Aspartyl glutamyl-tRNA (Asn Gln) amidotransferase subunit B	2.093	—
<i>SpyM3_1540</i>	<i>gatA</i>	Aspartyl glutamyl-tRNA (Asn Gln) amidotransferase subunit A	2.953	2.094
<i>SpyM3_1541</i>	<i>gatC</i>	Glutamyl-tRNA(Gln) amidotransferase subunit C	2.644	—
<i>SpyM3_1544</i>	<i>codY</i>	Transcription pleiotropic repressor codY	2.47	—
<i>SpyM3_1545</i>	—	Aspartate aminotransferase	2.294	—
<i>SpyM3_1547</i>	—	Hydrolase (HAD superfamily)	2.305	3.178
<i>SpyM3_1548</i>	<i>asnB</i>	L-asparaginase	2.172	—
<i>SpyM3_1550</i>	—	ABC transporter ATP-binding protein	—	2.141

<i>SpyM3_1552</i>	—	Cobalt transport ATP-binding protein <i>cbiO</i>	2.028	—
<i>SpyM3_1564</i>	<i>acpS</i>	Holo-[acyl-carrier protein] synthase	2.332	—
<i>SpyM3_1566</i>	<i>pmi</i>	Mannose-6-phosphate isomerase	3.619	2.943
<i>SpyM3_1568</i>	<i>ndoS</i>	Endo-beta-N-acetylglucosaminidase F2 precursor	3.435	—
<i>SpyM3_1572</i>	<i>nusB</i>	N utilization substance protein B	2.167	—
<i>SpyM3_1573</i>	—	General stress protein, Gls24 family	2.540	—
<i>SpyM3_1578</i>	—	Magnesium and cobalt transport protein <i>corA</i>	2.973	—
<i>SpyM3_1579</i>	—	Hypothetical membrane spanning protein	3.335	—
<i>SpyM3_1581</i>	<i>ssb.2</i>	Single strand binding protein	2.422	—
<i>SpyM3_1582</i>	<i>rpsF</i>	SSU ribosomal protein S6P	2.285	—
<i>SpyM3_1584</i>	<i>mutY</i>	A G-specific adenine DNA glycosylase	2.345	2.365
<i>SpyM3_1585</i>	—	Transcriptional regulator	—	2.079
<i>SpyM3_1586</i>	<i>trx.2</i>	Thioredoxin	3.229	—
<i>SpyM3_1587</i>	—	Phosphatidylglycerophosphatase B	2.762	2.410
<i>SpyM3_1589</i>	—	CvpA family membrane protein	2.170	—
<i>SpyM3_1591</i>	—	Ribonuclease HIII	3.192	—
<i>SpyM3_1594</i>	—	Hypothetical protein	3.073	—
<i>SpyM3_1597</i>	—	Beta-lactamase family protein	2.231	—

<i>SpyM3_1606</i>	—	Hypothetical cytosolic protein	2.617	—
<i>SpyM3_1607</i>	—	Transcriptional regulator, MerR family	3.374	—
<i>SpyM3_1609</i>	—	Hypothetical cytosolic protein	2.398	—
<i>SpyM3_1617</i>	—	Ribosomal-protein-S18-alanine acetyltransferase	5.328	—
<i>SpyM3_1618</i>	—	Non-proteolytic protein, peptidase family M22	4.768	—
<i>SpyM3_1620</i>	—	Zn-dependent hydrolase	2.740	—
<i>SpyM3_1624</i>	<i>pgk</i>	Phosphoglycerate kinase	2.350	—
<i>SpyM3_1625</i>	<i>lppC</i>	Acid phosphatase	2.677	—
<i>SpyM3_1628</i>	<i>asp</i>	General stress protein, Gls24 family	2.268	—
<i>SpyM3_1631</i>	—	Alpha beta hydrolase	4.311	—
<i>SpyM3_1633</i>	<i>rpoE</i>	DNA-directed RNA polymerase delta chain	2.183	—
<i>SpyM3_1634</i>	<i>tig</i>	Trigger factor, ppiase	2.077	—
<i>SpyM3_1642</i>	<i>hsdR</i>	Type I restriction-modification system restriction subunit	2.530	—
<i>SpyM3_1643</i>	<i>hsdS</i>	Type I restriction-modification system specificity subunit	2.880	2.683
<i>SpyM3_1644</i>	<i>hsdM</i>	Type I restriction-modification system methylation subunit	2.811	3.101
<i>SpyM3_1645</i>	<i>salR</i>	Transcriptional regulatory protein degU	2.139	—
<i>SpyM3_1646</i>	<i>salk</i>	Sensory transduction protein kinase	2.033	—
<i>SpyM3_1660</i>	<i>lacR.2</i>	Lactose phosphotransferase system repressor	2.548	—

<i>SpyM3_1661</i>	—	DNA-damage-inducible protein J	3.329	—
<i>SpyM3_1662</i>	—	Hypothetical cytosolic protein	3.901	—
<i>SpyM3_1663</i>	<i>rpsI</i>	SSU ribosomal protein S9P	3.131	—
<i>SpyM3_1664</i>	<i>rplM</i>	LSU ribosomal protein L13P	2.977	—
<i>SpyM3_1667</i>	—	Fatty acid-binding protein, DegV family	2.213	—
<i>SpyM3_1671</i>	—	Hypothetical protein	—	2.618
<i>SpyM3_1673</i>	—	Hypothetical protein	2.443	4.737
<i>SpyM3_1674</i>	<i>cysE</i>	Serine acetyltransferase	—	2.678
<i>SpyM3_1675</i>	—	Hypothetical protein	—	2.483
<i>SpyM3_1684</i>	<i>def</i>	Peptide deformylase	2.183	—
<i>SpyM3_1686</i>	—	Transcriptional regulator, MarR family	—	2.458
<i>SpyM3_1689</i>	<i>eep</i>	Membrane endopeptidase, M50 family	2.945	—
<i>SpyM3_1692</i>	<i>yajC</i>	Protein translocase subunit YajC	2.124	—
<i>SpyM3_1694</i>	<i>pulA</i>	Pullulanase	-2.318	—
<i>SpyM3_1718</i>	<i>dppA</i>	Dipeptide-binding protein	2.912	2.478
<i>SpyM3_1719</i>	<i>dppB</i>	Dipeptide transport system permease protein dppB	—	2.848
<i>SpyM3_1728</i>	<i>mga</i>	Trans-acting positive regulator Mry	2.620	—
<i>SpyM3_1732</i>	—	Two component system histidine kinase	-2.096	—

<i>SpyM3_1733</i>	—	Two component response regulator	-2.456	—
<i>SpyM3_1734</i>	—	ABC transporter permease protein	3.704	—
<i>SpyM3_1735</i>	—	ABC transporter ATP-binding protein	6.514	3.382
<i>SpyM3_1736</i>	—	HlyD family secretion protein	7.196	3.662
<i>SpyM3_1737</i>	—	Hypothetical protein	-6.047	—
<i>SpyM3_1738</i>	—	Hypothetical protein	2.828	—
<i>SpyM3_1739</i>	—	Hypothetical cytosolic protein	—	2.568
<i>SpyM3_1740</i>	<i>prsA</i>	Peptidyl-prolyl cis-trans isomerase	-3.376	—
<i>SpyM3_1741</i>	<i>spi</i>	Streptopain precursor fragment	-46.08	-44.60
<i>SpyM3_1742</i>	<i>speB</i>	Streptopain precursor	-56.26	-61.37
<i>SpyM3_1743</i>	—	Hypothetical protein	-516.1	-437.5
<i>SpyM3_1759</i>	—	Translation initiation inhibitor	2.577	—
<i>SpyM3_1760</i>	—	Hypothetical cytosolic protein	2.354	—
<i>SpyM3_1761</i>	—	Ribosomal large subunit pseudouridine synthase D	2.897	—
<i>SpyM3_1762</i>	—	Hypothetical protein	2.115	—
<i>SpyM3_1767</i>	<i>clpC</i>	Negative regulator of genetic competence <i>clpC</i> <i>mecB</i>	—	2.789
<i>SpyM3_1777</i>	—	Hypothetical cytosolic protein	—	-2.446
<i>SpyM3_1778</i>	—	Amino acid permease	—	-2.736

<i>SpyM3_1782</i>	<i>rpsB</i>	SSU ribosomal protein S2P	2.018	—
<i>SpyM3_1783</i>	<i>tsf</i>	Protein translation elongation factor Ts (EF-Ts)	2.506	—
<i>SpyM3_1784</i>	<i>pepO</i>	Oligoendopeptidase O	3.041	—
<i>SpyM3_1785</i>	<i>dexS</i>	Trehalose-6-phosphate hydrolase	2.408	—
<i>SpyM3_1786</i>	—	PTS system, trehalose-specific IIBC and IIA components	2.486	—
<i>SpyM3_1790</i>	—	Hypothetical cytosolic protein	2.320	—
<i>SpyM3_1795</i>	—	Hypothetical membrane spanning protein	2.884	—
<i>SpyM3_1796</i>	—	Hypothetical cytosolic protein	2.274	—
<i>SpyM3_1798</i>	—	Hypothetical cytosolic protein	2.108	—
<i>SpyM3_1799</i>	<i>spxA</i>	Arsenate reductase family protein	2.566	—
<i>SpyM3_1800</i>	<i>recA</i>	RecA protein	2.060	—
<i>SpyM3_1801</i>	<i>cinA</i>	Colligrin	2.431	—
<i>SpyM3_1802</i>	<i>tag</i>	DNA-3-methyladenine glycosylase	—	2.250
<i>SpyM3_1803</i>	<i>ruvA</i>	Holliday junction DNA helicase ruvA	2.229	—
<i>SpyM3_1804</i>	<i>ImrP</i>	Multidrug resistance protein imrP	—	2.401
<i>SpyM3_1805</i>	<i>mutL</i>	DNA mismatch repair protein mutL	3.154	2.241
<i>SpyM3_1807</i>	—	Hypothetical cytosolic protein	2.379	—
<i>SpyM3_1809</i>	<i>argS</i>	Arginyl-tRNA synthetase	3.391	—

<i>SpyM3_1810</i>	—	Bacteriocin uviB	4.681	6.492
<i>SpyM3_1816</i>	<i>rpmF</i>	LSU ribosomal protein L32P	3.477	—
<i>SpyM3_1817</i>	<i>rpmG</i>	LSU ribosomal protein L33P	2.884	—
<i>SpyM3_1821</i>	—	FtsK SpoIIIE family	—	2.033
<i>SpyM3_1825</i>	—	Integral membrane protein	3.369	—
<i>SpyM3_1833</i>	<i>rpsD</i>	SSU ribosomal protein S4P	3.057	—
<i>SpyM3_1834</i>	—	Hypothetical protein	3.672	2.171
<i>SpyM3_1835</i>	<i>dnaC</i>	Replicative DNA helicase	2.778	—
<i>SpyM3_1836</i>	<i>rplI</i>	LSU ribosomal protein L9P	2.054	—
<i>SpyM3_1838</i>	<i>gidA</i>	Putative tRNA (5-carboxymethylaminomethyl-2-thiouridylate) synthase subunit GidA	—	3.182
<i>SpyM3_1839</i>	—	Phosphohydrolase (MutT nudix family protein)	—	3.469
<i>SpyM3_1840</i>	<i>mnmA</i>	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	3.023	—
<i>SpyM3_1843</i>	—	Transglycosylase SLT domain family protein	—	2.380
<i>SpyM3_1845</i>	<i>cbiO</i>	Hyaluronan ABC exporter ATP-binding protein	—	2.301
<i>SpyM3_1846</i>	<i>cbiO</i>	Hyaluronan ABC exporter ATP-binding protein	—	2.671
<i>SpyM3_1847</i>	<i>pgsA</i>	CDP-diacylglycerol--glycerol-3-phosphate 3- phosphatidyltransferase	3.292	—

<i>SpyM3_1848</i>	—	Hypothetical membrane associated protein	4.432	—
<i>SpyM3_1849</i>	—	Peptidase, M16 family	3.563	—
<i>SpyM3_1850</i>	—	Non-proteolytic protein, peptidase family M16	2.454	—
<i>SpyM3_1858</i>	<i>trsA</i>	Tryptophanyl-tRNA synthetase	5.072	—
<i>SpyM3_1860</i>	—	ABC transporter ATP-binding protein	4.291	2.358
<i>SpyM3_1864</i>	<i>degP</i>	Endopeptidase degP	2.319	—
<i>SpyM3_1865</i>	<i>spoJ</i>	Chromosome partitioning protein parB	2.643	—

^APositive numbers indicated increased transcript levels in mutant strain, whereas negative numbers indicate higher transcript levels in wild-type strain

Supplemental Table 3.

Primers and probes used in this study.

Primer	Sequence (5'→3')	Target
ropB-A	GAC GCT ATG AGT CGT TGC AC	5' primer for 5' region of <i>ropB</i>
ropB-B	GTT ATA GTT ATT ATA ACA TGT ATT TGA ATT CAA CGG TTT CAC CA	3' primer for 5' region of <i>ropB</i> with <i>spc</i> sequence overlap
ropB-C	CTA TTT AAA TAA CAG ATT AAA AAA ATT ATA ACA TTA AAC ATA AAC TGT CCT GAG GC	5' primer for 3' region of <i>ropB</i> with <i>spc</i> sequence overlap
ropB-D	TTG CAG ATA GTC TCG GTG GA	3' primer for 3' region of <i>ropB</i>
ropB-spcF	CTT ATA AGT TAT TAA CGA AAA GTG CTG AAT ACA TGT TAT AAT AAC TAT AAC	5' primer for <i>spc</i> along with <i>ropB</i> overlap sequence
ropB-spcR	TGG TGA AAC CGT TGA ATT CAA ATA CAT GTT ATA ATA ACT ATA AC	3' primer for <i>spc</i> along with <i>ropB</i> overlap sequence
ropB-SouthF	CCA AGC TAA TGC TTC GTT TAG G	5' primer for Southern blot
ropB-SouthR	CAA TTC CTG GTT TTG TCT TGT CC	3' primer for Southern blot

ropB 3' QRT	CAG CAG CAT AAG CTG GAT CAA G	5' primer for <i>ropB</i> QRT-PCR
ropB QRT probe	CAG CCT TTA TCG ATG CCG AGC ATG C	Probe for <i>ropB</i> QRT-PCR
speB QRT 5'	CGC ACT AAA CCC TTC AGC TCT T	5' primer for <i>speB</i> QRT-PCR
speB QRT 3'	ACA GCA CTT TGG TAA CCG TTG A	3' primer for <i>speB</i> QRT-PCR
speB probe	GCC TGC GCC GCC ACC AGT A	Probe for <i>speB</i> QRT-PCR
tufA QRT 5'	CAA CTC GTC ACT ATG CGC ACA T	5' primer for <i>tufA</i> QRT-PCR
tufA QRT 3'	GAG CGG CAC CAG TGA TCA T	5' primer for <i>tufA</i> QRT-PCR
tufA-probe	CTC CAG GAC ACG CGG ACT ACG TTA AAA A	Probe for <i>tufA</i> QRT-PCR
speK QRT 5'	GAA AAG TTT GAT GGG GGA CA	5' primer for <i>speK</i> QRT-PCR
speK QRT 3'	TGT GTC TAA TGC CAC CGT CT	5' primer for <i>speK</i> QRT-PCR
speK-probe	TGA ATA TCC CAA AAC CCT TTT T	Probe for <i>speK</i> QRT-PCR
M3_100 QRT-5'	AAT AAG CGT GAC ACT CAA GTT CCA	5' M3_spy0100 primer for QRT-PCR
M3_100 QRT-3'	AGC CAC AAT GCT AAG AAC TGC AA	5' M3_spy0100 primer for QRT-PCR

M3_100 probe	ACT GGT GTT GTA GGC ACC CTT GCT	Probe for 5' M3_spy0100 QRT-PCR
<i>cfa</i> QRT 5'	TCC ATT TGC ATC TGT TGA CG	5' <i>cfa</i> primer for QRT-PCR
<i>cfa</i> QRT 3'	CAC GGT CTG TTG GCT GTA AA	3' <i>cfa</i> primer for QRT-PCR
<i>cfa</i> QRT probe	TTC CTC AAG TGC TTT AAT TTC TTG	Probe for <i>cfa</i> QRT-PCR
<i>sagA</i> QRT 5'	TTG CTC CTG GAG GCT GCT	5' primer for <i>sagA</i> QRT-PCR
<i>sagA</i> QRT 3'	CTT CCG CTA CCA CCT TGA GAA T	3' primer for <i>sagA</i> QRT-PCR
<i>sagA</i> QRT probe	ACC ACT TCC AGT AGC AAT TGA GAA GCA ACA AG	Probe for <i>sagA</i> QRT-PCR
<i>slo</i> QRT 5'	GAA ATA TCC GTA TCA TGG CTA GAG AGT	5' primer for <i>slo</i> QRT-PCR
<i>slo</i> QRT 3'	CAC ATC TCT TTC GTC GAT CAC TTT	3' primer for <i>slo</i> QRT-PCR
<i>slo</i> QRT probe	GCC ACC ATT CCC AAG CTA AGC CAG TG	Probe for <i>slo</i> QRT-PCR
<i>Emm</i> QRT 5'	AGA CAG TTA CCA TCA ACA GGT GAA AC	5' primer for <i>emm</i> QRT-PCR
<i>Emm</i> QRT 3'	TAA CCC ATT CTT CAC AGC GGC AGC C	3' primer for <i>emm</i> QRT-PCR
<i>Emm</i> QRT probe	TAC TCC AGC TGT TGC CAT AAC AG	Probe for <i>emm</i> QRT-PCR
<i>ropB</i> down pJL	ACTGTCTAGAAAATTGGTGAAACCGTTG	5' primer for cloning <i>ropB</i> from strains MGAS10041,

5'		MGAS15000, MGAS15005, and MGAS15211 into pJL1055
ropB down pJL	CTG ACT GCA GTA GGA GGT CGT GAC CAA	3' primer for cloning ropB from strains MGAS10041, MGAS15000, MGAS15005, and MGAS15211 into pJL1055
3'	AAA	
ropB up pJL 5'	GTT CCT GCA GTT GGT TGA TCT CTT ATC T	5' primer for cloning ropB from strains MGAS15001 and MGAS15043 into pJL1055
ropB up pJL 3'	CAG TTC TAG AAT ATG ATG GAT CGT TTT G	3' primer for cloning ropB from strains MGAS15001 and MGAS15043 into pJL1055
ropB 9937 pJL	GTT CCT GCA GAT TAG TTG ACT CGT AGG CTT	5' primer for cloning ropB from strain MGAS9937 into pJL1055
5'	T	
ropB 9937 pJL	TGA CTC TAG AGA CCT CTG CTC ACT AGG C	3' primer for cloning ropB from strain MGAS9937 into pJL1055
3'		
5' <i>covRS</i> PCR	GAC CAT AGA GGG CAG AGA AGG	5' primer for PCR for <i>covRS</i> operon sequencing
3' <i>covRS</i> PCR	CAG TTG TGG CAA AAG ACT GC	3' primer for PCR for <i>covRS</i> operon sequencing

<i>covRS</i> seq1	AAA ATT TGT GGG CTA TGT TCA AGT	<i>covRS</i> sequencing primer
<i>covRS</i> seq2	GTC AGA AAA TCC AAA AAC GAT AGC	<i>covRS</i> sequencing primer
<i>covRS</i> seq3	AAT ATC ACT GTC ATC TTT ACC CCA A	<i>covRS</i> sequencing primer
<i>covRS</i> seq4	TAG AGT ATT TGT GAT ATC GCG CTC	<i>covRS</i> sequencing primer
