TABLE S1 Categories of differentially regulated genes comparing the isogenic FabT deletion mutant to M1GAS2221 wild-type

		35°C				40°C			
		ME		Stat		ME		Stat	
		Up	Down	Up	Down	Up	Down	Up	Down
Virulence		4	4	5	4	4	6	9	4
Cell wall, membrane and envelope biogenesis		2	2	12	3	2	--	7	14
Transport		4	10	24	33	6	1	44	17
Transcription		7	7	5	21	5	--	10	43
Translation		--	6	24	12	--	--	6	59
Replication, repair and cell division		7	1	2	1	1	--	--	4
DNA processing and metabolism		--	2	5	8	3	1	4	20
General stress		3	1	1	6	--	1	2	10
Energy production and conversion		1	--	4	1	--	--	4	--
Posttranslational modification, protein turnover and chaperones		5	2	6	9	1	2	8	12
Nucleotide transport and metabolism		1	8	9	23	1	--	6	14
Amino acid transport and metabolism		1	10	6	5	--	--	--	1
Inorganic ion transport and metabolism		--	6	11	6	1	2	8	2
Metabolism	**General**	--	--	1	--	--	--	--	--
	Carbon	8	12	2	35	3	3	11	18
	Lipids	11	--	13	1	9	--	12	3
	Fermentation	1	3	1	5	2	--	2	3
	Coenzymes and cofactors	1	1	4	1	--	1	3	8
Phage proteins		33	1	18	5	--	--	--	42
Hypothetical proteins		9	15	15	31	2	9	14	56
Function unknown		6	7	11	20	2	1	12	27
Other		1	--	--	2	--	--	2	3
TOTAL		105	98	179	232	42	27	164	360

TABLE S2 Differentially-expressed genes comparing the isogenic *fabT* deletion mutant to the wild-type MGAS2221 grown at 35°C

A. Up-regulated genes during mid-exponential phase

Locus tag	Gene	Fold change	Function
Amino acid metabolism and transport			
M5005_Spy1329	*cysM*	**6.2**	Cystathionine beta-synthase (CBS) and Cysteine synthase
Cell wall, membrane, envelope biogenesis			
M5005_Spy0425		**1.9**	Glycosyltransferase involved in cell envelope biogenesis
M5005_Spy0426		**1.9**	Glycosyltransferase involved in cell envelope biogenesis
Energy production and conversion			
M5005_Spy0125		**6.3**	Hypothetical ATP synthase subunit G
Function unknown			
M5005_Spy0122		**1.6**	PAS and HTH domains containing protein
M5005_Spy0529		**1.6**	Uncharacterized Fe-S protein
M5005_Spy1197		**2.3**	Hypothetical highly conserved Streptococcal and related phage proteins
M5005_Spy1362		**2.5**	Glyco_hydro_100 superfamily; putative hydrolase
M5005_Spy1650	*degV*	**1.8**	Uncharacterized protein containing a bound fatty acid molecule
M5005_Spy1828		**39.5**	Membrane protein/Phage receptor in *L. lactis*
Hypothetical proteins			
M5005_Spy0123		**11.9**	Hypothetical protein
M5005_Spy0477		**1.7**	Hypothetical protein
M5005_Spy0754		**2.4**	Hypothetical protein
M5005_Spy0911		**1.5**	Hypothetical protein
M5005_Spy1142		**3.0**	Hypothetical protein/peptidase S11
M5005_Spy1143		**3.0**	Hypothetical protein
M5005_Spy1144		**3.3**	Hypothetical protein
M5005_Spy1730		**2.0**	DUF4298 superfamily protein. Unknown function
M5005_Spy1823		**1.5**	Predicted transmembrane protein of unknown function
Metabolism - Carbon			
M5005_Spy0528		**1.6**	Putative phosphohexomutase
M5005_Spy0751	*acoA*	**2.5**	Pyruvate dehydrogenase E1 component, alpha subunit
M5005_Spy0752	*acoB*	**2.5**	Pyruvate dehydrogenase E1 component, beta subunit
M5005_Spy0753	*acoC*	**2.4**	Pyruvate dehydrogenase, dihydrolipoamide acyltransferase (E2) component
M5005_Spy0755	*acoL*	**2.4**	Pyruvate dehydrogenase, dihydrolipoamide dehydrogenase (E3) component
M5005_Spy1538	*pmi*	**1.6**	Mannose-6-phosphate isomerase.
M5005_Spy1841	*sdhB*	**6.3**	Serine dehydratase beta chain
M5005_Spy1842	*sdhA*	**6.0**	Serine dehydratase alpha chain
Metabolism - Lipids			
M5005_Spy0879	*dgk*	**3.5**	Diacylglycerol kinase (DAG)

M5005_Spy1484	*accD*	**6.7**	Acetyl-CoA carboxylase subunit
M5005_Spy1485	*accA*	**6.5**	Acetyl-CoA carboxylase subunit
M5005_Spy1486	*accC*	**6.2**	Acetyl-CoA carboxylase subunit
M5005_Spy1487	*fabZ*	**6.3**	Beta-hydroxyacyl-ACP dehydrase
M5005_Spy1488	*accB*	**6.5**	Acetyl-CoA carboxylase subunit
M5005_Spy1489	*fabF*	**6.3**	Beta-ketoacyl-ACP synthase II (KAS II)
M5005_Spy1490	*fabG*	**6.4**	Beta-ketoacyl-ACP reductase
M5005_Spy1491	*fabD*	**6.3**	Malonyl-CoA:ACP-transacylase
M5005_Spy1492	*fabK*	**6.0**	Enoyl-ACP reductase II
M5005_Spy1496	*phaB*	**1.7**	Enoyl-CoA hydratase
Metabolism - Coenzymes and cofactors			
M5005_Spy0945	*coaA*	**1.8**	Pantothenate kinase; coenzyme A (CoA) biosynthetic pathway
Metabolism - Fermentation pathways			
M5005_Spy1569	*pfl*	**1.8**	Pyruvate formate lyase
Nucleotide metabolism and transport			
M5005_Spy0012	*hpt*	**1.6**	Hypoxanthine phosphoribosyl transferase
Other			
M5005_Spy1809	*uviB*	**1.8**	Enterocin A Immunity ; it protects from bacteriocidal activity
Phage proteins			
M5005_Spy1045		**2.8**	Phage protein
M5005_Spy1417		**3.5**	Lambdoid phage 5005.3 protein
M5005_Spy1419		**2.4**	Lambdoid phage 5005.3 protein
M5005_Spy1420		**2.7**	Lambdoid phage 5005.3 protein
M5005_Spy1422		**2.6**	Lambdoid phage 5005.3 protein
M5005_Spy1423		**2.9**	Lambdoid phage 5005.3 protein
M5005_Spy1424		**2.6**	Lambdoid phage 5005.3 protein
M5005_Spy1425		**3.0**	Lambdoid phage 5005.3 protein
M5005_Spy1426		**2.9**	Lambdoid phage 5005.3 protein
M5005_Spy1427		**2.9**	Lambdoid phage 5005.3 protein
M5005_Spy1428		**3.1**	Lambdoid phage 5005.3 protein
M5005_Spy1429		**3.2**	Lambdoid phage 5005.3 protein
M5005_Spy1430		**2.8**	Lambdoid phage 5005.3 protein
M5005_Spy1431		**2.4**	Lambdoid phage 5005.3 protein
M5005_Spy1432		**2.9**	Lambdoid phage 5005.3 protein
M5005_Spy1433		**2.6**	Lambdoid phage 5005.3 protein
M5005_Spy1434		**2.9**	Lambdoid phage 5005.3 protein
M5005_Spy1435		**2.5**	Lambdoid phage 5005.3 protein
M5005_Spy1437		**2.2**	Lambdoid phage 5005.3 protein
M5005_Spy1441		**2.6**	Lambdoid phage 5005.3 protein
M5005_Spy1445		**3.4**	Lambdoid phage 5005.3 protein
M5005_Spy1448		**3.6**	Lambdoid phage 5005.3 protein
M5005_Spy1450		**2.9**	Lambdoid phage 5005.3 protein

M5005_Spy1451		**3.2**	Lambdoid phage 5005.3 protein
M5005_Spy1452		**3.0**	Lambdoid phage 5005.3 protein
M5005_Spy1453		**3.1**	Lambdoid phage 5005.3 protein
M5005_Spy1454		**2.7**	Lambdoid phage 5005.3 protein
M5005_Spy1455		**2.0**	Lambdoid phage 5005.3 protein
M5005_Spy1456		**2.2**	Lambdoid phage 5005.3 protein
M5005_Spy1457		**2.5**	Lambdoid phage 5005.3 protein
M5005_Spy1458		**2.5**	Lambdoid phage 5005.3 protein
M5005_Spy1460		**3.2**	Lambdoid phage 5005.3 protein
M5005_Spy1461		**3.1**	Lambdoid phage 5005.3 protein
Posttranslational modification, protein turnover, chaperones			
M5005_Spy0739		**1.6**	Protein involved in chaperone, transcription, and protein transport complexes
M5005_Spy1114		**1.5**	Membrane proteinase, regulator of anti-sigma factor
M5005_Spy1356	*pepC*	**1.7**	Aminopeptidase C
M5005_Spy1577	*pepXP*	**1.6**	Aminopeptidase
M5005_Spy1782	*pepO*	**1.6**	Predicted metalloendopeptidase
Replication, repair and cell division			
M5005_Spy0011	*tilS*	**1.7**	Predicted ATPase of the PP-loop family implicated in cell cycle control
M5005_Spy0013	*ftsH*	**1.6**	ATP-dependent zinc metalloprotease
M5005_Spy0339	*exoA*	**1.6**	Exonuclease III
M5005_Spy0387		**1.6**	Uracil-DNA glycosylases (UDG); base excision repair pathway
M5005_Spy0737	*mutX*	**1.6**	MutT homolog. It might hydrolyze oxidized purine nucleoside triphosphates
M5005_Spy1075	*uvrB*	**1.5**	excinuclease ABC, B subunit
M5005_Spy1320	*recX*	**1.8**	Regulator of recombination
General stress			
M5005_Spy0386	*phoH*	**1.6**	PhoH-like protein; PhoH is induced by phosphate starvation
M5005_Spy1328		**1.5**	IMPACT family protein involved in response to stress
M5005_Spy1769	*ahpF*	**1.8**	Alkyl hydroperoxide reductase, subunit F. Role in oxidative stress defense
Transcription			
M5005_Spy0124	*sloR*	**10.2**	Transcriptional regulator. PTS EIIC superfamily
M5005_Spy0483		**2.1**	Putative stress-responsive transcriptional regulator
M5005_Spy0881		**6.4**	Transcription regulator; MerR family
M5005_Spy1576	*srv*	**1.6**	GntR family of transcriptional regulators. cAMP-binding protein
M5005_Spy1589	*crgR*	**1.6**	Transcriptional regulator, GntR family
M5005_Spy1798	*spxA*	**3.1**	Transcriptional regulator
M5005_Spy1830		**2.3**	Transcriptional regulator
Transport			
M5005_Spy0270	*atmA*	**2.0**	ABC transporter substrate binding domain
M5005_Spy0478		**1.7**	Putative permease
M5005_Spy0738		**1.6**	Putative permease; pheromone autoinducer 2 (AI-2) transporter
M5005_Spy1363		**2.8**	ABC transporter trans-membrane subunit
Virulence			

M5005_Spy0385		**5.4**	Acute rheumatic fever streptococcal myosin cross-reactive protein
M5005_Spy0880	*hlyIII*	**5.3**	Hemolysin III-related/erythrocyte lysis
M5005_Spy1106	*grab*	**1.9**	Protein G-related alpha 2 macroglobulin-binding protein (GRAB)
M5005_Spy1737	*ropB*	**1.7**	Transcriptional activator, Rgg/GadR/MutR family

B. Down-regulated genes during mid-exponential phase

Locus tag	Gene	Fold change	Function
Amino acid metabolism and transport			
M5005_Spy0014		**-1.7**	Putative amino acid transporter
M5005_Spy0659	*apbA*	**-1.7**	Putative ketopantoate reductase
M5005_Spy1270	*arcC*	**-11.5**	Carbamate kinase; arginine deiminase pathway
M5005_Spy1271		**-11.4**	Acetyl ornithine deacetylase; arginine deiminase pathway
M5005_Spy1272	*arcD*	**-11.9**	Putative permease; arginine deiminase pathway
M5005_Spy1273	*arcB*	**-10.2**	Ornithine carbamoyl transferase; arginine deiminase pathway
M5005_Spy1274		**-12.0**	Acetyl transferase; arginine deiminase pathway
M5005_Spy1275	*arcA*	**-11.3**	Arginine deiminase; arginine deiminase pathway
M5005_Spy1297	*aroA2*	**-1.8**	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase
M5005_Spy1298	*aroB*	**-1.8**	3-dehydroquinate synthetase
Cell wall, membrane, envelope biogenesis			
M5005_Spy0017	*sibA*	**-1.7**	Putative amidase
M5005_Spy0705	*amiC*	**-2.3**	Amidase
DNA processing and metabolism			
M5005_Spy1137	*coiA*	**-1.8**	Competence protein
M5005_Spy1169	*spd3*	**-1.9**	DNA/RNA non-specific endonuclease
Function unknown			
M5005_Spy0944		**-2.0**	Putative S-adenosylmethionine-dependent methyltransferase
M5005_Spy1276		**-1.7**	Putative cAMP-binding protein
M5005_Spy1387		**-1.6**	Predicted oxidoreductase
M5005_Spy1407		**-2.0**	Putative esterase/lipase
M5005_Spy1530		**-2.1**	Cell surface protein with leucine-rich repeats
M5005_Spy1691		**-2.7**	endonuclease/exonuclease/phosphatase family protein
M5005_Spy1843		**-2.5**	Putative transglycosylase
Hypothetical proteins			
M5005_Spy0015		**-3.1**	Hypothetical protein
M5005_Spy0072		**-2.8**	Hypothetical protein
M5005_Spy0073		**-1.9**	Hypothetical protein
M5005_Spy0255		**-2.7**	Hypothetical protein
M5005_Spy0651		**-1.7**	Conserved protein with leucine-rich repeats
M5005_Spy0852		**-1.5**	Hypothetical protein
M5005_Spy0904		**-2.6**	Hypothetical membrane protein

M5005_Spy1170		**-1.7**	Hypothetical membrane protein
M5005_Spy1324		**-2.5**	Hypothetical protein
M5005_Spy1413		**-1.5**	Hypothetical protein
M5005_Spy1619		**-2.7**	Hypothetical protein
M5005_Spy1714		**-1.8**	Hypothetical cell surface protein
M5005_Spy1759		**-2.3**	Hypothetical protein; member of the Nudix hydrolase family
M5005_Spy1827		**-1.9**	Hypothetical membrane protein
M5005_Spy1860		**-1.9**	Hypothetical membrane protein
Inorganic ion transport and metabolism			
M5005_Spy0653	*czcD*	**-1.8**	Co/Zn/Cd efflux system component
M5005_Spy1161	*focA*	**-1.7**	Putative formate transporter
M5005_Spy1167		**-1.9**	Putative cation transport ATPase
M5005_Spy1405	*copA*	**-3.1**	Cation transporter ATPase
M5005_Spy1406	*copY*	**-1.9**	Copper transport repressor
M5005_Spy1575	*norA*	**-2.8**	Uncharacterized MFS-type transporter
Metabolism - Carbon			
M5005_Spy0505	*ppc*	**-2.3**	PEP carboxylase
M5005_Spy0903	*oadB*	**-2.4**	Oxaloacetate decarboxylase beta subunit
M5005_Spy0908	*citX*	**-2.4**	Citrate lyase subunit
M5005_Spy1119	*gapN*	**-2.6**	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase
M5005_Spy1139	*nagB*	**-2.2**	Putative glucosamine-6-phosphate deaminase
M5005_Spy1388	*nagA*	**-1.6**	Putative N-acetylglucosamine-6-phosphate deacetylase
M5005_Spy1395	*lacD.1*	**-3.3**	Tagatose-6-phosphate aldolase; Lac.1 (cluster I) tagatose pathway
M5005_Spy1396	*lacC.1*	**-5.9**	Tagatose-6-phosphate kinase; Lac.1 (cluster I) tagatose pathway
M5005_Spy1397	*lacB.1*	**-4.8**	Galactose-6-phosphate isomerase subunit; Lac.1 (cluster I) tagatose pathway
M5005_Spy1398	*lacA.1*	**-4.3**	Galactose-6-phosphate isomerase subunit; Lac.1 (cluster I) tagatose pathway
M5005_Spy1681	*dexB*	**-2.3**	Glucan 1,6-alpha-glucosidase
M5005_Spy1783	*dexS*	**-3.7**	Putative alpha amylase/glycosidase
Metabolism - Coenzymes and cofactors			
M5005_Spy0652		**-1.8**	Pyridoxamine 5'-phosphate oxidase
Metabolism - Fermentation pathways			
M5005_Spy0039	*adh2*	**-4.3**	Acetaldehyde dehydrogenase
M5005_Spy0040	*adhA*	**-3.5**	Alcohol dehydrogenase
M5005_Spy1749	*pflC*	**-1.5**	Pyruvate formate lyase activating enzyme
Nucleotide metabolism and transport			
M5005_Spy0029	*purD*	**-1.7**	Phosphoribosylglycinamide synthetase involved in *de novo* purine synthesis
M5005_Spy0136	*purA*	**-1.6**	Adenylosuccinate synthetase involved in de novo purine synthesis
M5005_Spy0641	*pyrB*	**-2.7**	Aspartate carbamoyl transferase
M5005_Spy0642	*carA*	**-2.6**	Carbamoyl phosphate synthase small subunit
M5005_Spy0643	*carB*	**-2.5**	Carbamoyl phosphate synthase large subunit
M5005_Spy0703	*pyrF*	**-3.7**	Orotidine 5-phosphate decarboxylase
M5005_Spy0704	*pyrE*	**-3.6**	Orotate phosphoribosyltransferase

M5005_Spy0857	*guaC*	**-2.9**	Putative guanosine monophosphate reductase
Phage proteins			
M5005_Spy0913	*xerD*	**-1.8**	Phage integrase
Posttranslational modification, protein turnover, chaperones			
M5005_Spy0341	*prtS*	**-3.9**	Peptidase
M5005_Spy1715	*scpA*	**-2.0**	Peptidase C5
M5005_Spy1758		**-1.7**	Peptidase, C69 family
Replication, repair and cell division			
M5005_Spy1582	*dnaQ*	**-2.1**	DNA polymerase III subunit epsilon
General stress			
M5005_Spy1574		**-3.0**	Putative universal stress protein UspA
Transcription			
M5005_Spy0155		**-1.6**	Putative transcriptional antiterminator
M5005_Spy0186		**-7.2**	M trans-acting positive regulator (MGA) PRD domain protein
M5005_Spy0639	*pyrR*	**-2.8**	Transcriptional regulator of pyrimidine biosynthesis
M5005_Spy0914		**-1.6**	Putative transcriptional regulator
M5005_Spy1581		**-2.2**	Putative transcriptional regulator
M5005_Spy1747		**-1.6**	Transcriptional regulator
M5005_Spy1748		**-1.6**	DeoR family transcriptional regulator
Translation			
M5005_Spy0619	*infC*	**-1.6**	IF-3 translation initiation factor
M5005_Spy0620	*rpl36*	**-1.6**	50S ribosomal protein L35
M5005_Spy0621	*rplT*	**-1.8**	50S ribosomal protein L20
M5005_Spy0794	*thdF*	**-1.6**	Putative tRNA modification GTPase
M5005_Spy1138	*rsuA*	**-1.6**	Putative pseudouridine synthase
M5005_Spy1483	*serS*	**-2.0**	Seryl-tRNA synthetase
Transport			
M5005_Spy0137		**-1.5**	Uncharacterized ABC-type transport system membrane component
M5005_Spy0324	*fhuA*	**-1.6**	Uncharacterized ABC-type transport system
M5005_Spy0640	*pyrP*	**-2.6**	Putative uracyl permease
M5005_Spy0658		**-1.7**	Phosphotransferase system IIC component
M5005_Spy0829	*potD*	**-1.5**	Spermidine/putrescine ABC-type transport system component
M5005_Spy1058	*malE*	**-2.0**	Putative maltose/maltodetrin transporter
M5005_Spy1094		**-5.3**	Putative transport protein
M5005_Spy1399	*ptsIIc*	**-4.5**	PTS galactose-specific EIIc component; Lac.1 (cluster I) tagatose pathway
M5005_Spy1692		**-2.6**	PTS system glucose/maltose-specific transporter subunit IIC
M5005_Spy1784		**-2.7**	Phosphotransferase system IIABC component
Virulence			
M5005_Spy0182	*speG*	**-1.7**	SpeG exotoxin
M5005_Spy1415	*sdaD2*	**-2.1**	Streptodornase
M5005_Spy1718	*sic1.01*	**-1.9**	Streptococcal inhibitor of complement

C. Up-regulated genes during stationary phase

Locus tag	Gene	Fold change	Function
Amino acid metabolism and transport			
M5005_Spy0713	*bcaT*	**1.6**	Branched-chain amino acid aminotransferase
M5005_Spy1269	*asnA*	**2.2**	Asparagine synthetase A
M5005_Spy1298	*aroB*	**1.8**	3-dehydroquinate synthetase
M5005_Spy1359		**1.5**	D-alanine/D-serine/glycine permease
M5005_Spy1596	*glnA*	**1.8**	Glutamine synthetase
M5005_Spy1658	*cysE*	**2.0**	Serine acetyltransferase
Cell wall, membrane, envelope biogenesis			
M5005_Spy0247	*pbp7*	**1.6**	D-alanyl-D-alanine carboxipeptidase
M5005_Spy0384		**2.6**	Putative peptidoglycan-binding protein
M5005_Spy0510	*murN*	**1.9**	UDP-N-acetylmuramoylpentapeptide-lysine N(6)-alanyltransferase
M5005_Spy0511	*murM*	**2.0**	UDP-N-acetylmuramoylpentapeptide-lysine N(6)-alanyltransferase
M5005_Spy0607	*rgpE*	**1.6**	Putative glycosyl transferase
M5005_Spy0608	*rgpF*	**1.6**	Lipopolysaccharide biosynthesis protein
M5005_Spy0663	*mur1.1*	**1.9**	Mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase
M5005_Spy0686	*mvaA*	**2.0**	HMG-CoA reductase; mevalonate pathway
M5005_Spy0687	*mvaS.1*	**1.7**	HMG-CoA synthase; mevalonate pathway
M5005_Spy0705	*amiC*	**5.7**	Amidase
M5005_Spy1252	*murG*	**1.6**	Peptidoglycan synthesis protein
M5005_Spy1253	*murD*	**1.6**	Peptidoglycan synthesis protein
DNA processing and metabolism			
M5005_Spy0002	*dnaN*	**1.5**	DNA polymerase III beta subunit
M5005_Spy0712	*parC*	**1.6**	DNA topoisomerase IV subunit A
M5005_Spy1228	*recN*	**1.5**	DNA repair protein
M5005_Spy1232	*xseB*	**1.5**	Exonuclease VII small subunit
M5005_Spy1804	*mutL*	**1.5**	DNA mismatch repair protein
Energy production and conversion			
M5005_Spy0579	*atpA*	**2.3**	F0F1 ATP synthase alpha subunit
M5005_Spy0580	*atpG*	**2.3**	F0F1 ATP synthase gamma subunit
M5005_Spy0581	*atpD*	**2.2**	F0F1 ATP synthase beta subunit
M5005_Spy0582	*atpC*	**2.0**	F0F1 ATP synthase delta subunit
Function unknown			
M5005_Spy0080		**2.6**	Histidine triad (HIT) protein
M5005_Spy0209		**1.7**	Protein predicted to bind ssDNA or ssRNA
M5005_Spy0360		**1.5**	Predicted dehydrogenase
M5005_Spy0512		**1.9**	Putative phosphatase/hydrolase
M5005_Spy0610		**1.6**	Putative glycosyl transferase
M5005_Spy1248		**1.9**	Putative pyridoxal phosphate enzyme
M5005_Spy1362		**1.6**	Invertase; a hydrolase

M5005_Spy1601		**1.7**	Band 7-domain protein. It may cluster to form membrane micro-domains
M5005_Spy1650	*degV*	**2.8**	Uncharacterized protein containing a bound fatty acid molecule
M5005_Spy1654		**2.1**	Putative ribonuclease
M5005_Spy1828		**36.7**	Membrane protein/Phage receptor in *L. lactis*
Hypothetical proteins			
M5005_Spy0383		**2.5**	Hypothetical protein
M5005_Spy0651		**1.9**	Hypothetical protein containing leucine-rich repeats
M5005_Spy0744		**2.7**	Hypothetical protein
M5005_Spy0963		**1.7**	Putative membrane protein
M5005_Spy1095		**1.8**	Hypothetical protein
M5005_Spy1141		**2.0**	Hypothetical protein
M5005_Spy1162		**1.5**	Hypothetical membrane protein
M5005_Spy1247		**1.8**	Hypothetical protein
M5005_Spy1383		**1.6**	Hypothetical protein
M5005_Spy1517		**1.8**	Hypothetical protein
M5005_Spy1552		**2.4**	Hypothetical membrane protein
M5005_Spy1653		**1.7**	Hypothetical protein
M5005_Spy1656		**1.9**	Hypothetical protein
M5005_Spy1657		**1.8**	Hypothetical protein
M5005_Spy1659		**2.1**	Hypothetical protein
Inorganic ion transport and metabolism			
M5005_Spy0321	*fhuG*	**1.9**	Iron transporter
M5005_Spy0322	*fhuB*	**2.1**	Iron transporter
M5005_Spy0323	*fhuD*	**2.5**	Iron transporter
M5005_Spy0653	*czcD*	**1.7**	Co/Zn/Cd efflux system component
M5005_Spy0950	*phoU*	**1.6**	Putative phosphate regulatory protein
M5005_Spy0952	*pstB2*	**1.8**	ATP-binding cassette domain of the phosphate transport system
M5005_Spy0953	*pstA*	**1.8**	Phosphate transporter ATP-binding protein
M5005_Spy0954	*pstC*	**2.2**	Phosphate transporter permease subunit PstC
M5005_Spy0955	*pstS*	**1.5**	Phosphate ABC transporter substrate-binding protein PstS
M5005_Spy1094		**7.8**	Putative transporter of the Major Facilitator Superfamily (MFS)
M5005_Spy1551	*corA*	**1.8**	Membrane transporter of divalent cations, such as Mg^{2+}, Co^{2+}, and Ni^{2+}
Metabolism			
M5005_Spy0382	*msrA.2*	**2.0**	Methionine sulfoxide reductase
Metabolism - Carbon			
M5005_Spy0661	*fruB*	**3.3**	1-phosphofructokinase
M5005_Spy0938	*pgmA*	**1.6**	Phosphoglucomutase
Metabolism - Lipids			
M5005_Spy0879	*dgk*	**9.7**	Diacylglycerol (DAG) kinase
M5005_Spy1484	*accD*	**17.1**	Acetyl-CoA carboxylase subunit
M5005_Spy1485	*accA*	**18.0**	Acetyl-CoA carboxylase subunit
M5005_Spy1486	*accC*	**18.7**	Acetyl-CoA carboxylase subunit

M5005_Spy1487	*fabZ*	**18.1**	Beta-hydroxyacyl-ACP dehydrase
M5005_Spy1488	*accB*	**19.0**	Acetyl-CoA carboxylase subunit
M5005_Spy1489	*fabF*	**20.1**	Beta-ketoacyl-ACP synthase II (KAS II)
M5005_Spy1490	*fabG*	**20.0**	Beta-ketoacyl-ACP reductase
M5005_Spy1491	*fabD*	**19.5**	Malonyl-CoA:ACP-transacylase
M5005_Spy1492	*fabK*	**18.7**	Enoyl-ACP reductase II
M5005_Spy1493	*acpP*	**8.8**	Acyl carrier protein (ACP)
M5005_Spy1494	*fabH*	**9.0**	Beta-ketoacyl-ACP synthase III (KAS III)
M5005_Spy1496	*phaB*	**3.1**	Enoyl-CoA hydratase
Metabolism - Coenzymes and cofactors			
M5005_Spy0631	*thiI*	**1.5**	Thiamine biosynthesis protein
M5005_Spy0652		**2.0**	Putative pyridoxine 5'-phosphate (PNP) oxidase
M5005_Spy0960	*mreA*	**1.6**	FAD/FMN synthetase
M5005_Spy1357	*nadE*	**1.6**	NAD synthetase
Metabolism - Fermentation pathways			
M5005_Spy0873	*ldh*	**2.3**	L-Lactate dehydrogenase
Nucleotide metabolism and transport			
M5005_Spy0639	*pyrR*	**4.5**	Protein containing a phosphoribosyl transferase (PRT) domain
M5005_Spy0640	*pyrP*	**5.4**	Pyrimidine permease
M5005_Spy0641	*pyrB*	**5.9**	Aspartate/ornithine carbamoyl transferase
M5005_Spy0642	*carA*	**6.2**	Carbamoyl phosphate synthase small subunit
M5005_Spy0643	*carB*	**6.1**	Carbamoyl phosphate synthase large subunit
M5005_Spy0703	*pyrF*	**8.1**	Orotidine-5-P decarboxylase
M5005_Spy0704	*pyrE*	**8.5**	Phosphoribosyl transferase
M5005_Spy1515		**2.2**	Nucleoside Triphosphate Pyrophosphohydrolase
M5005_Spy1857	*guaB*	**1.9**	IMP dehydrogenase/GMP reductase
Phage proteins			
M5005_Spy1041		**3.9**	Hypothetical phage protein
M5005_Spy1427		**2.7**	Hypothetical phage protein
M5005_Spy1447		**2.6**	Phage protein. Superfamily II DNA/RNA helicases
M5005_Spy1448		**2.6**	Putative phage nuclease
M5005_Spy1449		**2.1**	Phage associated DNA primase
M5005_Spy1450		**2.1**	Phage associated DNA_Pol_A superfamily
M5005_Spy1451		**2.0**	Phage protein
M5005_Spy1452		**2.1**	Hypothetical phage protein
M5005_Spy1453		**2.1**	CRISPR/Cas system-associated protein Cas4
M5005_Spy1454		**2.1**	Hypothetical phage protein
M5005_Spy1455		**2.0**	Hypothetical phage protein
M5005_Spy1456		**2.4**	Hypothetical phage protein
M5005_Spy1458		**2.4**	Hypothetical phage protein
M5005_Spy1459		**2.4**	Hypothetical phage protein
M5005_Spy1460		**2.6**	Hypothetical DNA-binding phage protein

M5005_Spy1461		**2.7**	Hypothetical phage protein
M5005_Spy1462		**1.8**	Hypothetical phage protein
M5005_Spy1463		**2.6**	Hypothetical phage protein
Posttranslational modification, protein turnover, chaperones			
M5005_Spy0417	*pcp*	**1.6**	Pyrrolidone-carboxylate peptidase
M5005_Spy1133	*prsA*	**2.0**	Putative foldase
M5005_Spy1227		**1.6**	Putative peptidase
M5005_Spy1331		**1.5**	Cyclophilin-type peptidylprolyl cis- trans isomerase
M5005_Spy1577	*pepXP*	**2.2**	X-Prolyl dipeptidyl aminopeptidase
M5005_Spy1782	*pepO*	**1.7**	Predicted metalloendopeptidase
Replication, repair and cell division			
M5005_Spy0893	*gid*	**1.6**	Glucose inhibited division protein
M5005_Spy1249	*ftsZ*	**1.7**	Cell division protein
General stress			
M5005_Spy1255	*typA*	**1.7**	Predicted membrane GTPase involved in stress response
Transcription			
M5005_Spy0155		**1.9**	Transcriptional antiterminator with PTS regulation domain
M5005_Spy0660	*fruR*	**4.4**	Transcriptional regulator of sugar metabolism
M5005_Spy0881		**7.5**	MerR-type transcription regulator
M5005_Spy1229	*argR1*	**1.7**	Arginine repressor
M5005_Spy1686	*relA*	**1.7**	(p)ppGpp synthetase
Translation			
M5005_Spy0045	*rplD*	**1.6**	50S ribosomal protein L4
M5005_Spy0048	*rpsS*	**1.7**	30S ribosomal protein S19
M5005_Spy0051	*rplP*	**1.8**	50S ribosomal protein L16
M5005_Spy0052	*rpmC*	**1.8**	50S ribosomal protein L29
M5005_Spy0053	*rpsQ*	**1.7**	30S ribosomal protein S17
M5005_Spy0056	*rplE*	**1.8**	50S ribosomal protein L5
M5005_Spy0058	*rpsH*	**2.0**	30S ribosomal protein S8
M5005_Spy0081	*tyrS*	**3.2**	Tyrosyl tRNA synthetase
M5005_Spy0104		**1.7**	Putative tRNA dihydrouridine synthase-like (DUS)
M5005_Spy0147	*leuS*	**1.7**	Leucyl tRNA synthetase
M5005_Spy0232	*fus*	**1.6**	Elongation factor G
M5005_Spy0345	*metS*	**1.5**	Methionyl tRNA synthetase
M5005_Spy0427	*thrS*	**1.7**	Threonyl tRNA synthetase
M5005_Spy0588	*pheT*	**1.6**	Phenylalanyl tRNA synthetase
M5005_Spy1132	*alaS*	**1.5**	Alanyl tRNA synthetase
M5005_Spy1140	*queA*	**1.7**	Queuosine (Q) biosynthesis protein
M5005_Spy1330		**1.6**	Putative RNA binding, ribosomal protein
M5005_Spy1384	*glyS*	**1.6**	Glycyl-tRNA synthetase beta subunit
M5005_Spy1385	*glyQ*	**1.6**	Glycyl-tRNA synthetase, alpha subunit
M5005_Spy1483	*serS*	**2.9**	Seryl tRNA synthetase

M5005_Spy1655	*cysS*	**2.1**	Cysteinyl-tRNA synthetase
M5005_Spy1660	*pnpA*	**2.0**	Polynucleotide phosphorylase (PNPase)
M5005_Spy1685	*dtd*	**1.7**	D-Tyrosyl-tRNAtyr deacylase
M5005_Spy1808	*argS*	**1.7**	Arginyl tRNA synthetase
Transport			
M5005_Spy0064	*secY*	**2.0**	Preprotein translocase subunit SecY
M5005_Spy0078	*adcC*	**1.6**	ABC transporter
M5005_Spy0079	*adcB*	**1.6**	ABC transporter
M5005_Spy0103		**1.8**	Deoxynucleoside kinase
M5005_Spy0196		**1.9**	ABC transporter subunit
M5005_Spy0197		**1.9**	ABC transporter ATPase subunit
M5005_Spy0235		**1.7**	ABC transporter subunit
M5005_Spy0236		**1.7**	ABC transporter permease subunit
M5005_Spy0249	*oppA*	**1.6**	ABC transporter subunit
M5005_Spy0275		**1.8**	Serine/threonine/sodium symporter
M5005_Spy0370	*mtsC*	**1.5**	ABC transporter subunit
M5005_Spy0606	*rgpD*	**1.6**	ABC transporter subunit
M5005_Spy0706		**4.7**	ABC transporter substrate-binding protein
M5005_Spy0707		**4.6**	ABC transporter permease subunit
M5005_Spy0743		**2.7**	ABC transporter substrate binding protein
M5005_Spy0745		**2.5**	ABC transporter permease subunit
M5005_Spy0746		**3.4**	ABC transporter ATPase subunit
M5005_Spy0965		**2.6**	Predicted permease
M5005_Spy1372	*proB*	**2.4**	ABC transporter permease subunit
M5005_Spy1373		**2.1**	ABC transporter subunit
M5005_Spy1480	*manM*	**1.7**	PTS system mannose-specific transporter subunit IIC
M5005_Spy1481	*manN*	**1.7**	PTS system mannose-specific transporter subunit IID
M5005_Spy1707	*dppD*	**1.7**	ABC transporter ATP-binding subunit
M5005_Spy1708	*dppE*	**1.9**	ABC transporter ATP-binding subunit
Virulence			
M5005_Spy0385		**2.5**	Acute rheumatic fever streptococcal myosin cross-reactive protein
M5005_Spy0880	*hlyIII*	**12.5**	Putative hemolysin III-related/erythrocyte lysis
M5005_Spy1333	*yvqE*	**1.6**	Histidine kinase
M5005_Spy1599	*pgk*	**1.6**	3-phosphoglycerate kinase
M5005_Spy1720	*mga*	**1.5**	Transcriptional regulator

D. Down-regulated genes during stationary phase

Locus tag	Gene	Fold change	Function
Amino acid metabolism and transport			
M5005_Spy0157	*opuAA*	**-2.5**	ABC transporter glycine betaine/L-proline ATP binding subunit
M5005_Spy0158	*opuABC*	**-1.7**	ABC transporter glycine betaine/L-proline transmembrane subunit
M5005_Spy0549		**-2.2**	Putative chorismate mutase
M5005_Spy1697	*papB*	**-1.6**	Aminodeoxychorismate synthase, component I
M5005_Spy1698	*trpG*	**-2.2**	Anthranilate/para-aminobenzoate synthases component II
Cell wall, membrane, envelope biogenesis			
M5005_Spy0017	*sibA*	**-1.8**	Protein with a CHAP domain. Putative amidase
M5005_Spy0212	*nanE*	**-3.0**	N-acetylmannosamine-6-phosphate epimerase (Sialic acid degradation)
M5005_Spy0217	*nanH*	**-2.3**	Dihydrodipicolinate synthase/N-acetylneuraminate lyase
DNA processing and metabolism			
M5005_Spy0159	*polA*	**-1.6**	DNA polymerase I
M5005_Spy0791	*uvrC*	**-1.9**	Nuclease subunit of the ABC excinuclease; subunit C
M5005_Spy1117	*deaD2*	**-1.7**	DEAD-box helicase
M5005_Spy1351		**-2.1**	Nucleic acid methyltransferase
M5005_Spy1699		**-2.0**	Recombination factor; similar to protein RarA
M5005_Spy1701	*flaR*	**-1.9**	DNA topology modulation protein FlaR-related
M5005_Spy1796		**-1.6**	Putative endonuclease involved in recombination
M5005_Spy0700	*cpsX*	**-1.5**	CRISPR-associated protein Csm6
Energy production and conversion			
M5005_Spy0319	*ppaC*	**-1.6**	Putative manganese-dependent inorganic pyrophosphatase
Function unknown			
M5005_Spy0028		**-4.8**	Surface antigen, containing a CHAP domain, and proline-recognition domain (PRD)
M5005_Spy0176		**-2.3**	Zinc finger domain containing protein
M5005_Spy0260		**-1.6**	Haloacid dehalogenase (HAD) superfamily of hydrolase proteins
M5005_Spy0296		**-1.7**	Acyl phosphatase
M5005_Spy0548	*flaV*	**-1.8**	Flavodoxin
M5005_Spy0552		**-1.5**	Haloacid dehalogenase-like hydrolase
M5005_Spy0615	*ebsA*	**-1.6**	Pore forming protein ebsA
M5005_Spy0616		**-1.7**	Ferredoxin
M5005_Spy0632	*capA*	**-1.7**	Membrane-associated metallophosphatase (MPP) superfamily
M5005_Spy0834		**-1.9**	Zn-dependent dehydrogenase
M5005_Spy0835		**-2.4**	Acid phosphatase/Haloacid dehalogenase (HAD) hydrolase
M5005_Spy0916	*ylxM*	**-1.6**	Putative DNA-binding protein
M5005_Spy0944		**-1.5**	Putative S-adenosylmethionine-dependent methyltransferase
M5005_Spy1387		**-1.8**	Predicted oxidoreductase
M5005_Spy1393		**-2.2**	Haloacid dehalogenase-like hydrolase
M5005_Spy1476		**-2.2**	Putative ATPase or kinase
M5005_Spy1503		**-1.5**	Broad specificity phosphatase

M5005_Spy1691		**-2.3**	endonuclease/exonuclease/phosphatase family protein
M5005_Spy1716		**-1.9**	Transposase domain protein
M5005_Spy1864		**-2.7**	S-adenosyl-L-methionine (AdoMet)-dependent SPOUT methyltransferase
Hypothetical proteins			
M5005_Spy0115		**-2.7**	Hypothetical protein
M5005_Spy0177		**-2.0**	Conserved hypothetical protein
M5005_Spy0216		**-2.3**	Hypothetical membrane protein
M5005_Spy0329		**-1.7**	Hypothetical protein
M5005_Spy0676		**-1.7**	Hypothetical protein
M5005_Spy0721		**-1.9**	Hypothetical protein
M5005_Spy0878		**-1.9**	Hypothetical protein
M5005_Spy0901		**-2.3**	Hypothetical protein
M5005_Spy0904		**-2.3**	Hypothetical membrane protein
M5005_Spy0994		**-1.6**	Conserved hypothetical protein
M5005_Spy1080		**-2.6**	Hypothetical protein
M5005_Spy1093		**-3.8**	Hypothetical protein
M5005_Spy1192		**-3.5**	Hypothetical protein
M5005_Spy1258		**-1.7**	Conserved hypothetical protein
M5005_Spy1350		**-1.5**	Hypothetical membrane protein
M5005_Spy1394		**-2.6**	Putative membrane protein
M5005_Spy1411		**-1.7**	Hypothetical protein
M5005_Spy1413		**-2.3**	Hypothetical protein
M5005_Spy1541		**-2.6**	Hypothetical protein
M5005_Spy1567		**-1.6**	Hypothetical membrane protein
M5005_Spy1624		**-1.9**	Hypothetical protein
M5005_Spy1667		**-2.8**	Hypothetical protein
M5005_Spy1696		**-1.8**	Hypothetical protein
M5005_Spy1714		**-1.6**	Hypothetical cell surface protein
M5005_Spy1729		**-1.8**	Hypothetical protein
M5005_Spy1755		**-1.8**	Hypothetical protein
M5005_Spy1759		**-2.1**	Hypothetical protein; member of the Nudix hydrolase family
M5005_Spy1797		**-1.7**	Hypothetical protein
M5005_Spy1859		**-2.2**	Hypothetical protein
M5005_Spy1860		**-2.8**	Hypothetical membrane protein
M5005_Spy1862		**-2.1**	Putative membrane protein
Inorganic ion transport and metabolism			
M5005_Spy0116	*atoE*	**-2.3**	Anion permease
M5005_Spy0550		**-1.8**	Voltage-gated chloride channel
M5005_Spy0598	*mscL*	**-2.9**	Large-conductance mechanosensitive channel
M5005_Spy0985	*phnA*	**-2.2**	Uncharacterized Zn-ribbon-containing protein involved in phosphonate metabolism
M5005_Spy1161	*focA*	**-1.7**	Putative formate transporter
M5005_Spy1167		**-1.7**	Putative cation transport ATPase

Metabolism - Carbon			
M5005_Spy0151	*ulaD*	**-2.6**	3-keto-L-gulonate-6-phosphate decarboxylase (L-ascorbate utilization)
M5005_Spy0152	*ulaE*	**-3.9**	putative L-xylulose 5-phosphate 3-epimerase (L-ascorbate utilization)
M5005_Spy0153	*araD/ulaF*	**-4.0**	L-ribulose-5-phosphate epimerase (L-ascorbate utilization)
M5005_Spy0156		**-1.9**	L-ascorbate-6-phosphate lactonase
M5005_Spy0218		**-2.5**	Putative sugar kinase
M5005_Spy0534		**-1.7**	Putative acetoin reductase
M5005_Spy0695	*rpiA*	**-1.7**	Ribose 5-phosphate isomerase type A
M5005_Spy0696	*deoB*	**-1.7**	Phosphopentomutase, interconverting ribose-1-p and ribose-5-P
M5005_Spy0790	*gabD*	**-2.2**	Succinate-semialdehyde dehydrogenase
M5005_Spy0833	*maeE*	**-9.9**	Malic enzyme
M5005_Spy0902		**-1.7**	Biotin carboxyl carrier protein of oxaloacetate decarboxylase
M5005_Spy0903	*oadB*	**-2.4**	Oxaloacetate decarboxylase beta subunit
M5005_Spy0905	*citD*	**-1.9**	Citrate lyase subunit gamma
M5005_Spy0906	*citE*	**-1.9**	Citrate lyase subunit beta/citryl-CoA lyase subunit
M5005_Spy0907	*citF*	**-2.0**	Citrate lyase subunit alpha/citrate CoA-transferase
M5005_Spy0908	*citX*	**-2.0**	Citrate lyase activation subunit
M5005_Spy0986	*glmS*	**-1.6**	Glucosamine-fructose-6-phosphate aminotransferase
M5005_Spy1062	*malA*	**-2.1**	Maltodextrose utilization protein
M5005_Spy1119	*gapN*	**-2.9**	Glyceraldehyde-3-P dehydrogenase (non-phosphorylating)
M5005_Spy1139	*nagB*	**-1.6**	Glucosamine-6-phosphate deaminase
M5005_Spy1376	*tal*	**-2.8**	Fructose-6-P aldolase/transaldolase
M5005_Spy1380	*glpO*	**-4.6**	Glycerol-3-phosphate dehydrogenase
M5005_Spy1381	*glpK*	**-5.5**	Glycerol kinase
M5005_Spy1395	*lacD.1*	**-4.7**	Tagatose-6-phosphate aldolase; Lac.1 (cluster I) tagatose pathway
M5005_Spy1396	*lacC.1*	**-4.7**	Tagatose-6-phosphate kinase; Lac.1 (cluster I) tagatose pathway
M5005_Spy1397	*lacB.1*	**-4.6**	Galactose-6-phosphate isomerase subunit LacB.1; Lac.1 (cluster I) tagatose pathway
M5005_Spy1398	*lacA.1*	**-4.5**	Galactose-6-phosphate isomerase subunit LacA.1; Lac.1 (cluster I) tagatose pathway
M5005_Spy1543	*scrB*	**-2.4**	Glycosyl hydrolase (sucrose utilization)
M5005_Spy1632	*lacG*	**-4.3**	Phospho-beta-galactosidase
M5005_Spy1635	*lacD.2*	**-3.5**	Tagatose-6-phosphate aldolase; Lac.2 (cluster II) tagatose pathway
M5005_Spy1636	*lacC.2*	**-3.3**	Tagatose-6-phosphate kinase; Lac.2 (cluster II) tagatose pathway
M5005_Spy1637	*lacB.2*	**-3.0**	Galactose-6-phosphate isomerase subunit LacB.2; Lac.2 (cluster II) tagatose pathway
M5005_Spy1638	*lacA.2*	**-3.2**	Galactose-6-phosphate isomerase subunit LacA.2; Lac.2 (cluster II) tagatose pathway
M5005_Spy1681	*dexB*	**-1.7**	Glucan 1,6-alpha-glucosidase
M5005_Spy1783	*dexS*	**-6.6**	Putative alpha amylase/glycosidase
Metabolism - Coenzymes and cofactors			
M5005_Spy0872	*nox*	**-1.6**	NADH oxidase
Metabolism - Lipids			
M5005_Spy1740		**-1.7**	Phosphatidylglycerophosphatase A, involved in cardiolipin synthesis
Metabolism - Fermentation pathways			
M5005_Spy0039	*adh2*	**-3.5**	Acetaldehyde dehydrogenase

M5005_Spy0040	*adhA*	**-4.9**	Alcohol dehydrogenase
M5005_Spy0094	*ackA*	**-1.6**	Acetate kinase
M5005_Spy0318	*pflC*	**-1.9**	Pyruvate formate lyase II activating enzyme
M5005_Spy0851	*pta*	**-1.6**	Phosphotransacetylase
Nucleotide metabolism and transport			
M5005_Spy0022	*purC*	**-5.5**	Phosphoribosylaminoimidazole-succinocarboxamide (SAICAR) synthase
M5005_Spy0023	*purL*	**-2.6**	PurL subunit of the formylglycinamide ribonucleotide amidotransferase
M5005_Spy0024	*purF*	**-2.7**	Protein with a phosphoribosyl transferase (PRT) domain
M5005_Spy0025	*purM*	**-2.4**	Aminoimidazole Ribonucleotide [AIR] synthetase
M5005_Spy0026	*purN*	**-2.3**	phosphoribosylglycinamide formyltransferase
M5005_Spy0027	*purH*	**-2.0**	Bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase
M5005_Spy0029	*purD*	**-2.5**	Phosphoribosylglycinamide synthetase involved in de novo purine synthesis
M5005_Spy0030	*purE*	**-2.2**	Phosphoribosylcarboxyaminoimidazole (NCAIR) mutase
M5005_Spy0031	*purK*	**-2.3**	Phosphoribosylaminoimidazole carboxylase (NCAIR synthetase)
M5005_Spy0125	*ntpG*	**-2.4**	V-type ATP synthase subunit G
M5005_Spy0126	*ntpI*	**-2.3**	V-type ATP synthase subunit I
M5005_Spy0127	*ntpK*	**-2.3**	V-type ATP synthase subunit K
M5005_Spy0128	*ntpE*	**-2.4**	V-type ATP synthase subunit E
M5005_Spy0129	*ntpC*	**-2.3**	V-type ATP synthase subunit C
M5005_Spy0130	*ntpF*	**-2.5**	V-type ATP synthase subunit F
M5005_Spy0131	*ntpA*	**-2.1**	V-type ATP synthase subunit A
M5005_Spy0132	*ntpB*	**-2.0**	V-type ATP synthase subunit B
M5005_Spy0133	*ntpD*	**-2.2**	V-type ATP synthase subunit D
M5005_Spy0698	*punA*	**-1.7**	Purine nucleoside phosphorylase (Pnp)
M5005_Spy0699	*deoD2*	**-1.6**	Purine nucleoside phosphorylase (Pnp)
M5005_Spy0774		**-1.6**	Nucleoside diphosphate kinase
M5005_Spy0775		**-2.0**	Nucleoside diphosphate kinase
M5005_Spy1789	*nrdG*	**-1.5**	Anaerobic ribonucleotide reductase-activating protein
Other			
M5005_Spy1630	*salB*	**-3.0**	Cyclase involved in the biosynthesis of class II lantibiotics
M5005_Spy1631	*salA*	**-5.1**	Type-A lantibiotic
Phage proteins			
M5005_Spy0913	*xerD*	**-1.7**	Phage integrase
M5005_Spy1052	*int.1*	**-2.2**	Phage integrase
M5005_Spy1467	*int.3*	**-1.8**	Phage integrase
M5005_Spy1193		**-2.9**	Phage protein
M5005_Spy1214		**-4.0**	Phage protein
Posttranslational modification, protein turnover, chaperones			
M5005_Spy0341	*prtS*	**-1.9**	Peptidase
M5005_Spy0593		**-1.8**	Putative zinc metallopeptidase
M5005_Spy0987	*sipC*	**-1.9**	Signal peptidase I
M5005_Spy1382		**-2.8**	Peptidase propeptide

M5005_Spy1386		**-1.6**	Isoprenylcysteine carboxyl methyltransferase
M5005_Spy1475		**-1.7**	Acetyltransferase; similar to histone acetyltransferase HPA2
M5005_Spy1700		**-2.2**	Acetyltransferase; related to histone acetyltransferases
M5005_Spy1715	*scpA*	**-1.7**	Peptidase C5
M5005_Spy1758		**-1.6**	Peptidase, C69 family
Replication, repair and cell division			
M5005_Spy1352		**-2.3**	Cell division protein GpsB
General stress			
M5005_Spy0483		**-1.7**	Putative stress responsive transcriptional regulator
M5005_Spy0697	*arsC*	**-1.7**	Arsenate reductase
M5005_Spy1259	*dpr*	**-3.3**	DNA starvation/stationary phase protection protein
M5005_Spy1378	*npx*	**-3.0**	NADH peroxidase
M5005_Spy1514		**-1.8**	Universal stress protein
M5005_Spy1765	*csp*	**-2.0**	Cold-Shock Protein (CSP)
Transcription			
M5005_Spy0034		**-3.0**	Helix-turn-helix XRE-family like protein
M5005_Spy0118		**-3.4**	Putative LysR transcriptional regulator
M5005_Spy0138	*nusG*	**-1.6**	Transcription antitermination protein NusG
M5005_Spy0186		**-12.4**	M trans-acting positive regulator (MGA) PRD domain protein
M5005_Spy0914		**-2.7**	Putative transcriptional regulator
M5005_Spy1083		**-2.3**	Transcriptional antiterminator or activator containing a PRD domain
M5005_Spy1277	*ahrC.2*	**-2.6**	Arginine repressor
M5005_Spy1377		**-2.8**	M regulator protein trans-acting positive regulator (Mga)
M5005_Spy1402	*lacR.1*	**-2.4**	Transcriptional regulator of sugar metabolism
M5005_Spy1412	*nusA*	**-1.7**	Transcription elongation factor
M5005_Spy1500	*hrcA*	**-1.9**	Heat-inducible transcription repressor
M5005_Spy1544	*scrR*	**-1.8**	Putative Transcriptional regulator (sucrose utilization)
M5005_Spy1583		**-1.5**	Putative transcriptional regulator
M5005_Spy1625	*salR*	**-1.7**	Signal transduction response regulator
M5005_Spy1626	*salK*	**-1.7**	Signal transduction histidine kinase
M5005_Spy1639	*lacR.2*	**-2.6**	Transcriptional regulator of sugar metabolism
M5005_Spy1747		**-1.7**	Transcriptional regulator
M5005_Spy1748		**-1.6**	DeoR family transcriptional regulator
M5005_Spy1760		**-1.9**	Putative transcriptional regulator
M5005_Spy1779		**-3.0**	DNA-binding transcriptional activator of the SARP family
M5005_Spy1786		**-3.8**	Putative transcriptional regulator
Translation			
M5005_Spy0207	*rnpA*	**-1.6**	Ribonuclease P protein component
M5005_Spy0597	*rpsU*	**-1.7**	30S ribosomal protein S21
M5005_Spy0619	*infC*	**-1.7**	IF-3 translation initiation factor
M5005_Spy0620	*rpl36*	**-1.6**	50S ribosomal protein L35
M5005_Spy0621	*rplT*	**-1.6**	50S ribosomal protein L20

M5005_Spy1325	*raiA*	**-1.8**	RaiA ("ribosome-associated inhibitor A)
M5005_Spy1338	*fmt*	**-1.5**	Methionyl-tRNA formyltransferase
M5005_Spy1408	*rbfA*	**-1.6**	Ribosome-binding factor A
M5005_Spy1410		**-1.7**	Ribosomal protein HS6-type (S12/L30/L7a)
M5005_Spy1666	*rpsO*	**-2.0**	30S ribosomal protein S15
M5005_Spy1694		**-1.8**	Putative 16S ribosomal RNA methyltransferase RsmE
M5005_Spy1695	*prmA*	**-1.9**	Putative ribosomal protein L11 methyltransferase
Transport			
M5005_Spy0117		**-2.7**	Putative transport protein
M5005_Spy0149		**-4.0**	Phosphotransferase system, galactitol-specific IIB component
M5005_Spy0150		**-3.9**	Phosphotransferase system, IIA component
M5005_Spy0213		**-2.7**	ABC transporter for polysacharides subunit
M5005_Spy0214		**-2.4**	ABC transporter for polysacharides permease subunit
M5005_Spy0215		**-2.4**	ABC transporter for polysacharides transmembrane subunit
M5005_Spy0220	*tatD*	**-1.6**	Sec-independent protein translocase
M5005_Spy0428	*drrA*	**-1.8**	ABC transporter, ATPase subunit
M5005_Spy0430		**-1.8**	ABC transporter, permease subunit
M5005_Spy0780		**-2.0**	Phosphotransferase system, mannose/fructose-specific component IIA
M5005_Spy0782	*ptsC*	**-1.9**	Phosphotransferase system, mannose/fructose-specific component IIC
M5005_Spy0783	*ptsD*	**-1.9**	Phosphotransferase system, mannose/fructose-specific component IID
M5005_Spy0832	*maeP*	**-11.3**	Putative malate transporter
M5005_Spy1063	*malD*	**-2.1**	ABC transporter transmembrane subunit
M5005_Spy1064	*malC*	**-2.0**	Maltose/maltodextrin transporter membrane protein
M5005_Spy1067	*malX*	**-2.0**	Maltose/maltodextrin transporter subunit
M5005_Spy1079		**-2.5**	Phosphotransferase system, component IIC
M5005_Spy1081		**-2.5**	Phosphotransferase system, component IIA
M5005_Spy1082		**-2.5**	Phosphotransferase system, component IIB
M5005_Spy1121	*ptsH*	**-1.9**	Phosphotransferase System HPr (HPr)
M5005_Spy1379	*glpF*	**-4.4**	Major intrinsic protein (MIP) superfamily protein; glycerol uptake facilitator
M5005_Spy1399	*ptsIIc*	**-5.9**	PTS galactose-specific EIIc component; Lac.1 (cluster I) tagatose pathway
M5005_Spy1400	*ptsIIb*	**-6.0**	PTS galactose-specific EIIb component; Lac.1 (cluster I) tagatose pathway
M5005_Spy1401	*ptsIIa*	**-5.2**	PTS galactose-specific EIIa component; Lac.1 (cluster I) tagatose pathway
M5005_Spy1477		**-3.7**	Permease
M5005_Spy1542	*scrA*	**-2.4**	PTS system sucrose-specific transporter subunit II (sucrose utilization)
M5005_Spy1627	*salY*	**-2.5**	ABC transporter; permease component
M5005_Spy1628	*salX*	**-3.2**	ABC transporter; ATPase component
M5005_Spy1629	*salX/salT*	**-3.5**	ABC-type bacteriocin/lantibiotic exporter
M5005_Spy1633	*lacE*	**-4.6**	PTS lactose-specific EIIb component; Lac.2 (cluster II) tagatose pathway
M5005_Spy1634	*lacF*	**-3.4**	PTS lactose-specific EIIa component; Lac.2 (cluster II) tagatose pathway
M5005_Spy1692		**-2.0**	PTS system glucose/maltose-specific transporter subunit IIC
M5005_Spy1784		**-7.6**	Phosphotransferase system IIABC component
Virulence			
M5005_Spy0282	*covR*	**-1.8**	Response regulator of virulence gene expression

M5005_Spy0283	*covS*	**-1.9**	Histidine kinase of virulence gene expression
M5005_Spy1065	*amyA*	**-2.0**	Maltose/Maltodextrin glucosidase
M5005_Spy1540	*endoS*	**-2.2**	Endo-beta-N-acetylglucosaminidase

TABLE S3 Differentially-expressed genes comparing the isogenic *fabT* deletion mutant to the wild-type MGAS2221 grown at 40 °C

A. Up-regulated genes during mid-exponential phase

Locus tag	Gene	Fold change	Function
Cell wall, membrane, envelope biogenesis			
M5005_Spy0425		**1.9**	Glycosyltransferase involved in cell envelope biogenesis
M5005_Spy0426		**1.9**	Glycosyltransferase involved in cell envelope biogenesis
DNA processing and metabolism			
M5005_Spy0964		**1.6**	Type I restriction endonuclease subunit
M5005_Spy1075	*uvrB*	**1.6**	Excinuclease ABC, B subunit
M5005_Spy1228	*recN*	**1.5**	ATPase involved in DNA repair
Function unknown			
M5005_Spy1650	*degV*	**1.9**	Uncharacterized protein containing a bound fatty acid molecule
M5005_Spy1828		**30.3**	Membrane protein/Phage receptor in *L. lactis*
Hypothetical			
M5005_Spy1143		**3.2**	Hypothetical protein
M5005_Spy1144		**2.8**	Hypothetical protein
Inorganic ion transport			
M5005_Spy1152	*kup*	**1.6**	Potassium transporter
Metabolism - Carbon			
M5005_Spy0751	*acoA*	**1.7**	Pyruvate dehydrogenase E1 component, alpha subunit
M5005_Spy0752	*acoB*	**1.7**	Pyruvate dehydrogenase E1 component, beta subunit
Metabolism - Lipids			
M5005_Spy0879	*dgk*	**3.2**	Diacylglycerol kinase (DAG)
M5005_Spy1484	*accD*	**7.1**	Acetyl-CoA carboxylase subunit
M5005_Spy1485	*accA*	**7.2**	Acetyl-CoA carboxylase subunit
M5005_Spy1486	*accC*	**7.1**	Acetyl-CoA carboxylase subunit
M5005_Spy1487	*fabZ*	**6.7**	Beta-hydroxyacyl-ACP dehydrase
M5005_Spy1488	*accB*	**6.7**	Acetyl-CoA carboxylase subunit
M5005_Spy1489	*fabF*	**6.8**	Beta-ketoacyl-ACP synthase II (KAS II)
M5005_Spy1490	*fabG*	**6.3**	Beta-ketoacyl-ACP reductase
M5005_Spy1491	*fabD*	**6.0**	Malonyl-CoA:ACP-transacylase
M5005_Spy1492	*fabK*	**5.7**	Enoyl-ACP reductase II
Metabolism - Fermentation pathways			
M5005_Spy0318	*pflC*	**1.6**	Pyruvate formate lyase activating enzyme
M5005_Spy1569	*pfl*	**2.3**	Pyruvate formate lyase
Nucleotide metabolism and transport			
M5005_Spy0012	*hpt*	**1.6**	Hypoxanthine phosphoribosyl transferase
Posttranslational modification, protein turnover, chaperones			

M5005_Spy1142		**2.7**	Hypothetical protein/peptidase S11
Replication, repair and cell division			
M5005_Spy0013	*ftsH*	**1.6**	ATP-dependent zinc metalloprotease
Transcription			
M5005_Spy0483		**1.7**	Putative stress-responsive transcriptional regulator
M5005_Spy0881		**5.2**	Transcription regulator; MerR family
M5005_Spy0991		**1.7**	Transcriptional regulator, GntR family
M5005_Spy1798	*spxA*	**2.3**	Transcriptional regulator
M5005_Spy1830		**2.1**	Transcriptional regulator
Transport			
M5005_Spy0270	*atmA*	**1.6**	ABC transporter substrate binding domain
M5005_Spy0965		**1.8**	ABC-type transport system predicted permease
M5005_Spy0967		**1.8**	ABC transporter, ATP-binding domain
M5005_Spy0992		**1.7**	ABC transporter, ATPase component
M5005_Spy0993		**1.6**	ABC transporter, permease component
M5005_Spy1784		**1.7**	PTS system IIA component
Virulence			
M5005_Spy0385		**5.0**	Acute rheumatic fever streptococcal myosin cross-reactive protein
M5005_Spy0880	*hlyIII*	**4.4**	Hemolysin III-related/erythrocyte lysis
M5005_Spy1106	*grab*	**2.9**	Protein G-related alpha 2 macroglobulin-binding protein (GRAB)
M5005_Spy1720	*mga*	**1.5**	Transcriptional regulator of virulence genes

B. Down-regulated genes during mid-exponential phase

Locus tag	Gene	Fold change	Function
DNA processing and metabolism			
M5005_Spy1169	*spd3*	**-3.7**	DNA/RNA non-specific endonuclease
Function unknown			
M5005_Spy1407		**-2.1**	Putative esterase/lipase
Hypothetical proteins			
M5005_Spy0115		**-2.2**	Hypothetical protein
M5005_Spy0717		**-1.5**	Hypothetical protein
M5005_Spy0718		**-2.1**	Hypothetical protein
M5005_Spy1170		**-3.5**	Hypothetical membrane protein
M5005_Spy1205		**-2.9**	Hypothetical protein
M5005_Spy1216		**-1.8**	Hypothetical protein
M5005_Spy1382		**-2.4**	Hypothetical protein
M5005_Spy1530		**-1.9**	Cell surface protein with leucine-rich repeats
M5005_Spy1714		**-2.5**	Hypothetical cell surface protein
Inorganic ion transport and metabolism			

M5005_Spy0653	*czcD*	**-2.2**	Co/Zn/Cd efflux system component
M5005_Spy1575	*norA*	**-2.0**	Uncharacterized MFS-type transporter
Metabolism - Carbon			
M5005_Spy1119	*gapN*	**-2.7**	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase
M5005_Spy1637	*lacB.2*	**-2.7**	Galactose-6-phosphate isomerase subunit LacB.2; Lac.2 (cluster II) tagatose pathway
M5005_Spy1638	*lacA.2*	**-2.6**	Galactose-6-phosphate isomerase subunit LacA.2; Lac.2 (cluster II) tagatose pathway
Metabolism - Coenzymes and cofactors			
M5005_Spy0652		**-1.7**	Putative pyridoxamine 5'-phosphate oxidase
Posttranslational modification, protein turnover, chaperones			
M5005_Spy0114		**-2.3**	Sortase (surface protein trans-peptidase)
M5005_Spy1715	*scpA*	**-2.6**	Peptidase C5
General stress			
M5005_Spy1574		**-2.4**	Putative universal stress protein UspA
Transport			
M5005_Spy1704	*dppA*	**-1.6**	ABC transporter, substrate-binding component
Virulence			
M5005_Spy0139	*nga*	**-3.2**	Nicotine adenine dinucleotide glycohydrolase (NADase)
M5005_Spy0140	*ifs*	**-3.2**	Protein immunity factor for Nga
M5005_Spy0141	*slo*	**-3.0**	Streptolysin O (SLO), a cytolytic exotoxin
M5005_Spy1415	*sdaD2*	**-3.3**	Streptodornase
M5005_Spy1684	*ska*	**-2.4**	Staphylokinase
M5005_Spy1718	*sic1.01*	**-2.4**	Streptococcal inhibitor of complement

C. Up-regulated genes during stationary phase

Locus tag	Gene	Fold change	Function
Cell wall, membrane, envelope biogenesis			
M5005_Spy0384		**2.0**	Putative peptidoglycan-binding protein
M5005_Spy0684	*mvaK2*	**1.7**	Mevalonate kinase; mevalonate pathway
M5005_Spy0685		**1.6**	IPP isomerase; mevalonate pathway
M5005_Spy1070	*dltD*	**1.5**	Protein involved in D-alanine esterification of lipoteichoic acid
M5005_Spy1071	*dltC*	**1.8**	D-alanyl carrier protein
M5005_Spy1072	*dltB*	**1.6**	Putative membrane protein involved in D-alanine export
M5005_Spy1252	*murG*	**1.5**	Peptidoglycan synthesis protein
DNA processing and metabolism			
M5005_Spy0397		**1.8**	Transposase
M5005_Spy0557		**3.3**	Transposase IS116/IS110/IS902 family
M5005_Spy0558		**2.7**	Transposase
M5005_Spy0913	*xerD*	**1.7**	Site-specific DNA recombinase
Energy production and conversion			

M5005_Spy0579	*atpA*	**1.8**	F0F1 ATP synthase alpha subunit
M5005_Spy0580	*atpG*	**1.8**	F0F1 ATP synthase gamma subunit
M5005_Spy0581	*atpD*	**2.0**	F0F1 ATP synthase beta subunit
M5005_Spy0582	*atpC*	**2.0**	F0F1 ATP synthase delta subunit
Function unknown			
M5005_Spy0610		**1.6**	Putative glycosyl transferase
M5005_Spy0931		**1.9**	Glycine cleavage H-protein
M5005_Spy0932		**1.9**	Flavin-dependent oxidoreductase
M5005_Spy0933		**1.5**	NADH/Flavin oxidoreductase
M5005_Spy1248		**1.7**	Putative pyridoxal phosphate enzyme
M5005_Spy1311		**2.0**	Putative transcriptional regulator/sugar kinase
M5005_Spy1407		**2.6**	Esterase/lipase
M5005_Spy1523		**1.6**	Putative membrane protein
M5005_Spy1601		**1.5**	Band 7-domain protein. It may cluster to form membrane micro-domains
M5005_Spy1650	*degV*	**1.7**	Uncharacterized protein containing a bound fatty-acid molecule
M5005_Spy1654		**2.0**	Putative ribonuclease
M5005_Spy1828		**25.5**	Membrane protein/Phage receptor in *L. lactis*
Hypothetical proteins			
M5005_Spy0198		**1.6**	Hypothetical conserved protein
M5005_Spy0383		**2.1**	Hypothetical protein
M5005_Spy0399		**2.1**	Hypothetical protein
M5005_Spy0402		**2.1**	Hypothetical protein
M5005_Spy0716		**1.6**	Hypothetical protein
M5005_Spy0930		**2.0**	Hypothetical protein; putative ADP-ribose binding domain
M5005_Spy1247		**1.9**	Hypothetical protein
M5005_Spy1312		**2.4**	Hypothetical protein
M5005_Spy1316		**2.6**	Hypothetical protein
M5005_Spy1552		**1.6**	Hypothetical membrane protein
M5005_Spy1656		**1.7**	Hypothetical protein
M5005_Spy1659		**2.2**	Hypothetical protein
M5005_Spy1731		**2.1**	Hypothetical protein
M5005_Spy1788	*yaaA*	**1.5**	Hypothetical protein
Inorganic ion transport and metabolism			
M5005_Spy0321	*fhuG*	**2.6**	Iron transporter
M5005_Spy0322	*fhuB*	**2.9**	Iron transporter
M5005_Spy0323	*fhuD*	**2.1**	Iron transporter
M5005_Spy0952	*pstB2*	**2.1**	ATP-binding cassette domain of the phosphate transport system
M5005_Spy0953	*pstA*	**2.0**	Phosphate transporter ATP-binding protein
M5005_Spy0954	*pstC*	**1.9**	Phosphate transporter permease subunit PstC
M5005_Spy0978		**2.4**	Na+/alanine symporter
M5005_Spy1404	*copZ*	**3.0**	Copper chaperone
Metabolism - Carbon			

M5005_Spy0522	*ugl*	**3.6**	Unsaturated glucuronyl hydrolase
M5005_Spy0753	*acoC*	**1.7**	Pyruvate dehydrogenase, dihydrolipoamide acyltransferase (E2) component
M5005_Spy0830	*citA*	**1.9**	Response regulator of citrate/malate metabolism
M5005_Spy0831	*citB*	**1.9**	Histidine kinase of citrate/malate metabolism
M5005_Spy0898	*citG*	**2.3**	ATP:dephospho-CoA triphosphoribosyl transferase; citrate lyase prosthetic group
M5005_Spy1139	*nagB*	**1.8**	Glucosamine-6-phosphate isomerase/deaminase
M5005_Spy1313		**1.8**	Beta glucosidase/beta-galactosidase
M5005_Spy1314	*hyl*	**2.1**	Beta-N-acetylglucosaminidase/hyaluronidase
M5005_Spy1317		**2.1**	Alpha mannosidase/glycosyl hydrolase
M5005_Spy1741	*gldA*	**1.8**	Glycerol dehydrogenases; it catalyzes oxidation of glycerol to dihydroxyacetone
M5005_Spy1742	*mipB*	**1.8**	Transaldolase
Metabolism - Lipids			
M5005_Spy0879	*dgk*	**5.5**	Diacylglycerol (DAG) kinase
M5005_Spy1484	*accD*	**19.8**	Acetyl-CoA carboxylase subunit
M5005_Spy1485	*accA*	**22.0**	Acetyl-CoA carboxylase subunit
M5005_Spy1486	*accC*	**20.6**	Acetyl-CoA carboxylase subunit
M5005_Spy1487	*fabZ*	**20.4**	Beta-hydroxyacyl-ACP dehydrase
M5005_Spy1488	*accB*	**21.2**	Acetyl-CoA carboxylase subunit
M5005_Spy1489	*fabF*	**19.8**	Beta-ketoacyl-ACP synthase II (KAS II)
M5005_Spy1490	*fabG*	**18.1**	Beta-ketoacyl-ACP reductase
M5005_Spy1491	*fabD*	**17.5**	Malonyl-CoA:ACP-transacylase
M5005_Spy1492	*fabK*	**15.8**	Enoyl-ACP reductase II
M5005_Spy1493	*acpP*	**7.5**	Acyl carrier protein (ACP)
M5005_Spy1494	*fabH*	**6.6**	Beta-ketoacyl-ACP synthase III (KAS III)
Metabolism - Coenzymes and cofactors			
M5005_Spy0244	*nifS3*	**1.8**	Bi-functional selenocysteine lyase/cysteine desulfurase
M5005_Spy0245	*nifU*	**1.8**	NifU homolog involved in Fe-S cluster formation
M5005_Spy0246	*sufS*	**1.7**	FeS assembly protein SufB
Metabolism - Fermentation pathways			
M5005_Spy1743	*pflD*	**2.0**	Pyruvate formate lyase 2
M5005_Spy1749	*pflA*	**3.7**	Pyruvate formate lyase activating enzyme 1
Nucleotide transport and metabolism			
M5005_Spy1660	*pnpA*	**1.7**	Polynucleotide phosphorylase (PNPase)
M5005_Spy0348	*nrdI*	**2.3**	Ribonucleotide reductase stimulatory protein
M5005_Spy0349	*nrdE.1*	**2.3**	Ribonucleotide diphosphate reductase, alpha subunit
M5005_Spy0641	*pyrB*	**2.9**	Aspartate/ornithine carbamoyl transferase
M5005_Spy0642	*carA*	**3.0**	Carbamoyl phosphate synthase small subunit
M5005_Spy0643	*carB*	**3.4**	Carbamoyl phosphate synthase large subunit
Other			
M5005_Spy0393		**2.0**	Bacteriocin
M5005_Spy1137	*coiA*	**2.9**	Competence protein CoiA-like family
Posttranslational modification, protein turnover, chaperones			

M5005_Spy0351	*spyA*	**2.8**	ADP ribosyl transferase
M5005_Spy0382	*msrA.2*	**1.9**	Putative methionine sulfoxide reductase
M5005_Spy0416		**2.6**	Glutamine cyclotransferase
M5005_Spy0928	*lplA*	**1.9**	Lipoate protein ligase/lipoyl transferase
M5005_Spy0929		**2.0**	NAD-dependent protein deacetylase, SIR2 family
M5005_Spy1136	*pepB*	**1.8**	Peptidase family M3B Oligopeptidase F
M5005_Spy1577	*pepXP*	**1.8**	X-Prolyl dipeptidyl aminopeptidase
M5005_Spy1658	*cysE*	**1.8**	Serine acetyltransferase
General stress			
M5005_Spy0891	*satD*	**2.0**	Sat operon component, possibly involved in acid resistance
M5005_Spy0892	*satE*	**2.6**	Sat operon component, possibly involved in acid resistance
Transcription			
M5005_Spy0155		**1.6**	Transcriptional antiterminator with PTS regulation domain
M5005_Spy0195		**2.9**	Putative transcriptional regulator
M5005_Spy0559		**2.3**	M protein trans-acting positive regulator (MGA) PRD domain
M5005_Spy0560		**1.9**	Transcriptional regulator
M5005_Spy0881		**3.1**	MerR-type transcription regulator
M5005_Spy0899		**1.6**	Putative transcriptional regulator
M5005_Spy1306	*trxS*	**1.6**	Putative signal transduction histidine kinase
M5005_Spy1315		**2.6**	Putative transcriptional regulator
M5005_Spy1747		**2.5**	Putative transcriptional regulator of sugar metabolism
M5005_Spy1748		**2.4**	Putative transcriptional regulator of sugar metabolism
Translation			
M5005_Spy0071	*rplQ*	**1.6**	50S ribosomal protein L17
M5005_Spy0104		**1.5**	Putative tRNA dihydrouridine synthase-like (DUS)
M5005_Spy0414		**3.1**	Ribonuclease R
M5005_Spy0415	*smpB*	**3.2**	Small protein B (SmpB), a component of the trans-translation system
M5005_Spy1138		**2.6**	16S rRNA pseudouridine synthase, *Escherichia coli* RsuA like
M5005_Spy1655	*cysS*	**1.6**	Cysteinyl-tRNA synthetase
Transport			
M5005_Spy0078	*adcC*	**1.7**	ABC transporter
M5005_Spy0079	*adcB*	**1.6**	ABC transporter
M5005_Spy0103		**1.6**	Deoxynucleoside kinase
M5005_Spy0158	*opuABC*	**1.8**	ABC transporter transmembrane subunit
M5005_Spy0169		**2.1**	Anion permease
M5005_Spy0196		**3.5**	ABC transporter subunit
M5005_Spy0197		**3.5**	ABC transporter ATPase subunit
M5005_Spy0370	*mtsC*	**1.8**	ABC transporter subunit
M5005_Spy0475		**1.8**	Phosphotransferase system IIA component
M5005_Spy0519	*agaD*	**3.2**	PTS system mannose/fructose/sorbose family IID component
M5005_Spy0520	*agaW*	**2.8**	PTS system mannose/fructose/sorbose family IIC component
M5005_Spy0521	*agaV*	**3.3**	PTS system, mannose/fructose/sorbose family, IIB component

M5005_Spy0523		**2.9**	PTS system, mannose/fructose-specific component IIA
M5005_Spy0569	*sagH*	**1.6**	Streptolysin S biosynthesis, permease protein
M5005_Spy0570	*sagI*	**1.7**	ABC-type multidrug transport system, permease component
M5005_Spy0745		**1.5**	ABC transporter permease subunit
M5005_Spy0746		**2.0**	ABC transporter ATPase subunit
M5005_Spy0826	*potA*	**1.8**	ABC-type spermidine/putrescine transport system, ATPase component
M5005_Spy0827	*potB*	**1.9**	ABC-type spermidine/putrescine transport system, permease component I
M5005_Spy0828	*potC*	**1.5**	ABC-type spermidine/putrescine transport system, permease component II
M5005_Spy0829	*potD*	**1.8**	spermidine/putrescine ABC transporter substrate-binding protein
M5005_Spy0965		**2.1**	Predicted permease
M5005_Spy1059	*malF*	**2.0**	Maltose ABC-type transport system, permease component
M5005_Spy1086		**3.9**	Nicotinamide mononucleotide transporter
M5005_Spy1308		**1.9**	ABC sugar transporter substrate-binding subunit
M5005_Spy1309		**2.8**	ABC sugar transporter, permease component
M5005_Spy1310		**2.3**	ABC sugar transporter, permease component
M5005_Spy1372	*proB*	**2.8**	ABC transporter permease subunit
M5005_Spy1373		**1.8**	ABC transporter subunit
M5005_Spy1470	*ecsB*	**1.8**	Putative ABC-type exoprotein transport system, permease component
M5005_Spy1471		**1.7**	ABC transporter, ATPase component
M5005_Spy1481	*manN*	**1.6**	PTS system mannose-specific transporter subunit IID
M5005_Spy1521	*cbiO*	**1.8**	ABC cobalt transporter, ATP-binding subunit
M5005_Spy1522	*cbiQ*	**1.7**	ABC cobalt transporter, permease subunit
M5005_Spy1524	*cycC*	**1.8**	ABC transporter subunit
M5005_Spy1525	*cycD*	**2.8**	ABC transporter subunit
M5005_Spy1526	*fhuC*	**3.0**	ABC transporter, ATP-binding component of iron-siderophores subunit
M5005_Spy1527	*fhuB2*	**2.4**	ABC transporter cobalamin/Fe3+-siderophores transport systems, ATPase subunit
M5005_Spy1528	*fhuD2*	**2.6**	ABC heme transporter, heme-binding subunit
M5005_Spy1529	*shp*	**3.1**	Cell surface heme-binding protein Shp
M5005_Spy1530		**2.2**	Heme uptake protein
M5005_Spy1744		**2.2**	PTS system, IIC component
M5005_Spy1745		**2.1**	PTS system, IIB component
M5005_Spy1746		**1.9**	PTS system, IIA component
Virulence			
M5005_Spy0205	*fasC*	**1.7**	Histidine kinase; Fas (fibronectin/fibrinogen binding/ haemolytic activity/streptokinase regulator
M5005_Spy0206	*fasA*	**1.6**	Response regulator
M5005_Spy0385		**2.1**	Acute rheumatic fever streptococcal myosin cross-reactive protein
M5005_Spy0565	*sagD*	**1.8**	Streptolysin S biosynthesis scaffold/docking protein
M5005_Spy0566	*sagE*	**1.8**	Streptolysin S biosynthesis protease associated
M5005_Spy0567	*sagF*	**1.7**	Streptolysin S biosynthesis, SagF protein
M5005_Spy0568	*sagG*	**1.7**	Streptolysin S biosynthesis, ATP-binding export protein
M5005_Spy0571		**1.8**	Predicted extracellular nuclease
M5005_Spy0880	*hlyIII*	**4.9**	Putative hemolysin III-related/erythrocyte lysis

D. Down-regulated genes during stationary phase

Locus tag	Gene	Fold change	Function
Amino acid metabolism and transport			
M5005_Spy0014		**-1.8**	Putative amino acid transporter
Cell wall, membrane, envelope biogenesis			
M5005_Spy0010		**-1.5**	Beta lactamase
M5005_Spy0017	*sibA*	**-3.3**	Protein with a CHAP domain. Putative amidase
M5005_Spy0303	*glr*	**-1.8**	Glutamate racemase; required for peptidoglycan synthesis
M5005_Spy0425		**-1.5**	Glycosyltransferase; cell envelope biogenesis
M5005_Spy0533		**-1.6**	Metallo-beta-lactamase superfamily protein
M5005_Spy0664	*mur1.2*	**-3.6**	Mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase
M5005_Spy0687	*mvaS.1*	**-1.6**	HMG-CoA synthase; mevalonate pathway
M5005_Spy0734	*cpsFO*	**-1.5**	Glucose-1-phosphate thymidylyltransferase, short form
M5005_Spy0735	*cpsFP*	**-1.6**	dTDP-4-dehydrorhamnose 3,5-epimerase
M5005_Spy0817	*dacA1*	**-1.9**	D-alanyl-D-alanine carboxypeptidase
M5005_Spy0818		**-2.3**	Polysaccharide deacetylase
M5005_Spy0875	*srtA*	**-1.8**	Sortase; cysteine transpeptidase
M5005_Spy1160		**-1.8**	Penicillin-binding protein
M5005_Spy1753	*pbp2A*	**-1.6**	Monofunctional biosynthetic peptidoglycan transglycosylase
DNA processing and metabolism			
M5005_Spy0019	*recO*	**-2.8**	DNA repair protein RecO
M5005_Spy0093		**-3.0**	Adenine-specific DNA methylase
M5005_Spy0294		**-3.1**	Transposase
M5005_Spy0439	*smc*	**-1.6**	Structural maintenance of chromosomes (SMC) protein
M5005_Spy0457		**-1.6**	Plasmid stabilization protein
M5005_Spy0678		**-2.1**	Putative endonuclease
M5005_Spy0708	*ung*	**-1.7**	Uracil DNA glycosylase
M5005_Spy0791	*uvrC*	**-2.1**	Nuclease subunit of the ABC excinuclease; subunit C
M5005_Spy0862	*tdk2*	**-2.5**	Thymidine kinase
M5005_Spy0874	*gyrA*	**-2.2**	DNA gyrase
M5005_Spy1146	*holA*	**-2.1**	DNA polymerase III, delta subunit
M5005_Spy1159	*recR*	**-1.7**	Recombinational DNA repair protein (RecF pathway)
M5005_Spy1320	*recX*	**-2.0**	Regulator of recombination
M5005_Spy1351		**-2.2**	Nucleic acid methyltransferase
M5005_Spy1564		**-1.7**	Ribonuclease HII
M5005_Spy1719	*emm1.0*	**-1.8**	Chromosome segregation ATPase
M5005_Spy1796		**-1.8**	Putative endonuclease involved in recombination
M5005_Spy1799	*recA*	**-1.8**	DNA repair and recombination protein RecA
M5005_Spy1854		**-1.8**	Protein containing an S4 domain; it might interact with RecF
M5005_Spy1866	*parB*	**-2.6**	Chromosome partitioning protein
Function unknown			

M5005_Spy0100	*trx.1*	**-2.5**	Thioredoxin-like protein
M5005_Spy0260		**-3.1**	Haloacid dehalogenase (HAD) superfamily of hydrolase proteins
M5005_Spy0266		**-2.3**	S-adenosylmethionine-dependent methyltransferase
M5005_Spy0279	*lemA*	**-1.7**	Transmembrane protein similar to LemA
M5005_Spy0300		**-3.3**	Putative HD superfamily hydrolase
M5005_Spy0301		**-2.4**	Putative bacterial BAX inhibitor
M5005_Spy0319	*ppaC*	**-1.8**	Putative manganese-dependent inorganic pyrophosphatase
M5005_Spy0381		**-1.9**	Putative RNA-bindining protein
M5005_Spy0548	*flaV*	**-2.0**	Flavodoxin
M5005_Spy0552		**-2.0**	Haloacid dehalogenase-like hydrolase
M5005_Spy0603	*rgpAc*	**-1.7**	Putative glycosyltransferase
M5005_Spy0672		**-1.8**	Putative nucleotidyl transferase involved in tRNA repair
M5005_Spy0731		**-1.9**	Putative SAM-dependent methyltransferase
M5005_Spy0792		**-2.2**	Protein belonging to the Nitroreductase-like family
M5005_Spy0835		**-4.1**	Haloacid dehalogenase (HAD) hydrolase
M5005_Spy0861		**-4.1**	Tautomerase enzyme
M5005_Spy0876		**-2.1**	Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily
M5005_Spy0916	*ylxM*	**-3.3**	Putative DNA-binding protein
M5005_Spy0944		**-1.7**	Putative S-adenosylmethionine-dependent methyltransferase
M5005_Spy1113		**-1.6**	Signal transduction protein containing GAF and PtsI domains
M5005_Spy1163		**-1.9**	Putative small molecule binding protein (contains 3H domain)
M5005_Spy1364		**-1.5**	DEAD-box ATP-dependent RNA helicase
M5005_Spy1393		**-1.8**	Haloacid dehalogenase-like hydrolase
M5005_Spy1476		**-4.1**	Putative ATPase or kinase
M5005_Spy1478		**-1.8**	Haloacid dehalogenase-like hydrolase
M5005_Spy1608		**-1.8**	Esterase/hydrolase
M5005_Spy1864		**-2.1**	S-adenosyl-L-methionine (AdoMet)-dependent SPOUT methyltransferase
Hypothetical proteins			
M5005_Spy0003		**-2.3**	Hypothetical protein
M5005_Spy0009		**-2.1**	Hypothetical protein
M5005_Spy0099		**-3.1**	Hypothetical secreted protein
M5005_Spy0115		**-4.5**	Hypothetical protein
M5005_Spy0122		**-2.3**	PAS and HTH domains containing hypothetical protein
M5005_Spy0241	*rgpG*	**-2.4**	Hypothetical protein
M5005_Spy0267		**-2.1**	Hypothetical protein
M5005_Spy0268		**-3.6**	Hypothetical protein
M5005_Spy0281		**-1.7**	Predicted metal-binding, possibly nucleic acid-binding protein
M5005_Spy0302		**-2.4**	Hypothetical protein
M5005_Spy0329		**-1.8**	Hypothetical protein
M5005_Spy0358		**-1.7**	Hypothetical protein
M5005_Spy0458		**-1.9**	Hypothetical protein
M5005_Spy0461		**-2.4**	Hypothetical protein
M5005_Spy0479		**-2.7**	Hypothetical protein

M5005_Spy0493		**-2.2**	Hypothetical protein
M5005_Spy0515		**-2.5**	Hypothetical protein
M5005_Spy0671		**-2.0**	Hypothetical protein
M5005_Spy0676		**-4.5**	Hypothetical protein
M5005_Spy0690		**-2.1**	Hypothetical protein
M5005_Spy0702		**-1.9**	Hypothetical protein
M5005_Spy0714		**-2.1**	Hypothetical protein
M5005_Spy0721		**-2.4**	Hypothetical protein
M5005_Spy0761		**-1.6**	Hypothetical protein
M5005_Spy0846		**-3.2**	Hypothetical protein
M5005_Spy0877		**-2.2**	Hypothetical protein
M5005_Spy0922		**-2.0**	Hypothetical protein
M5005_Spy0962		**-2.7**	Hypothetical protein
M5005_Spy0994		**-1.9**	Conserved hypothetical protein
M5005_Spy1053		**-2.9**	Hypothetical protein
M5005_Spy1054		**-2.2**	Hypothetical protein
M5005_Spy1089		**-3.5**	Hypothetical protein
M5005_Spy1093		**-3.7**	Hypothetical protein
M5005_Spy1144		**-2.4**	Hypothetical protein
M5005_Spy1192		**-1.7**	Hypothetical protein
M5005_Spy1239		**-3.0**	Hypothetical protein
M5005_Spy1258		**-2.4**	Conserved hypothetical protein
M5005_Spy1293		**-1.9**	Hypothetical protein
M5005_Spy1295		**-3.2**	Hypothetical protein
M5005_Spy1296		**-4.1**	Hypothetical protein
M5005_Spy1321		**-1.8**	Hypothetical protein
M5005_Spy1353		**-1.8**	Hypothetical protein
M5005_Spy1361	*aapA*	**-2.1**	Hypothetical protein
M5005_Spy1390		**-1.5**	Hypothetical protein
M5005_Spy1394		**-2.0**	Hypothetical protein
M5005_Spy1411		**-1.7**	Hypothetical protein
M5005_Spy1413		**-2.4**	Hypothetical protein
M5005_Spy1567		**-1.8**	Hypothetical membrane protein
M5005_Spy1594		**-2.7**	Hypothetical protein
M5005_Spy1598		**-1.5**	Hypothetical membrane protein
M5005_Spy1729		**-3.0**	Hypothetical protein
M5005_Spy1730		**-2.5**	DUF4298 superfamily. Unknown function
M5005_Spy1757		**-1.8**	Hypothetical protein
M5005_Spy1794		**-1.6**	Hypothetical membrane protein
M5005_Spy1797		**-2.0**	Hypothetical protein
M5005_Spy1859		**-4.4**	Hypothetical protein
Inorganic ion transport and metabolism			
M5005_Spy0598	*mscL*	**-2.1**	Large-conductance mechanosensitive channel

M5005_Spy0985	*phnA*	**-1.8**	Uncharacterized Zn-ribbon-containing protein involved in phosphonate metabolism
Metabolism - Carbon			
M5005_Spy0194	*gpsA*	**-1.6**	Glycerol-3-phosphate dehydrogenase
M5005_Spy0233	*plr*	**-2.2**	Glyceraldehyde 3-phosphate dehydrogenase
M5005_Spy0790	*gabD*	**-2.4**	Succinate-semialdehyde dehydrogenase
M5005_Spy1056	*malM*	**-1.8**	4-alpha-glucanotransferase
M5005_Spy1119	*gapN*	**-5.9**	Putative aldehyde dehydrogenase
M5005_Spy1376	*tal*	**-2.5**	Fructose-6-P aldolase/transaldolase
M5005_Spy1395	*lacD.1*	**-4.0**	Tagatose-6-phosphate aldolase; Lac.1 (cluster I) tagatose pathway
M5005_Spy1396	*lacC.1*	**-4.4**	Tagatose-6-phosphate kinase; Lac.1 (cluster I) tagatose pathway
M5005_Spy1397	*lacB.1*	**-3.6**	Galactose-6-phosphate isomerase subunit LacB.1; Lac.1 (cluster I) tagatose pathway
M5005_Spy1398	*lacA.1*	**-3.3**	Galactose-6-phosphate isomerase subunit LacA.1; Lac.1 (cluster I) tagatose pathway
M5005_Spy1602		**-1.7**	Dihydroxyacetone kinase family
M5005_Spy1632	*lacG*	**-5.4**	Phospho-beta-galactosidase
M5005_Spy1636	*lacC.2*	**-2.8**	Tagatose-6-phosphate kinase; Lac.2 (cluster II) tagatose pathway
M5005_Spy1637	*lacB.2*	**-3.3**	Galactose-6-phosphate isomerase subunit LacB.2; Lac.2 (cluster II) tagatose pathway
M5005_Spy1638	*lacA.2*	**-4.1**	Galactose-6-phosphate isomerase subunit LacA.2; Lac.2 (cluster II) tagatose pathway
M5005_Spy1681	*dexB*	**-1.8**	Glucan 1,6-alpha-glucosidase
M5005_Spy1783	*dexS*	**-3.2**	Putative alpha amylase/glycosidase
M5005_Spy1843		**-2.7**	Transclycosylase
Metabolism - Lipids			
M5005_Spy0020	*plsX*	**-2.2**	Putative glycerol-3-phosphate acyltransferase PlsX
M5005_Spy1740		**-1.7**	Phosphatidylglycerophosphatase A, involved in cardiolipin synthesis
M5005_Spy1847	*pgsA*	**-1.9**	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase; cardiolipin synthase
Metabolism - Coenzymes and cofactors			
M5005_Spy0264		**-1.7**	Predicted HD superfamily hydrolase involved in NAD metabolism
M5005_Spy0292		**-1.8**	Aminodeoxychorismate lyase
M5005_Spy0689	*dyr*	**-2.6**	Dihydrofolate reductase (DHFR)
M5005_Spy0848	*ppnK*	**-1.7**	Polyphosphate/ATP-dependent NAD kinase
M5005_Spy0872	*nox*	**-2.0**	NADH oxidase
M5005_Spy0923	*pdxK*	**-2.0**	Pyridoxamine kinase
M5005_Spy0945	*coaA*	**-2.3**	Pantothenate kinase, coenzyme A (CoA) biosynthetic pathway
M5005_Spy1108	*metK2*	**-1.9**	S-adenosylmethionine synthetase
Metabolism - Fermentation pathways			
M5005_Spy0040	*adhA*	**-2.9**	Alcohol dehydrogenase
M5005_Spy0094	*ackA*	**-2.7**	Acetate kinase
M5005_Spy0851	*pta*	**-1.6**	Phosphotransacetylase
Nucleotide metabolism and transport			
M5005_Spy0012	*hpt*	**-2.6**	Hypoxanthine phosphoribosyl transferase
M5005_Spy0199		**-2.1**	deoxyuridine 5'-triphosphate nucleotidohydrolase (dut)
M5005_Spy0263	*nadD*	**-1.8**	Nicotinate (nicotinamide) nucleotide adenylyltransferase
M5005_Spy0327	*upp*	**-2.9**	Uracil phosphoribosyltransferase

M5005_Spy0330	*tmk*	**-1.5**	Thymidylate kinase
M5005_Spy0377	*pyrH*	**-2.5**	Uridylate (UMP) kinase
M5005_Spy0688	*thyA*	**-2.1**	Thymidylate synthase
M5005_Spy0857	*guaC*	**-2.6**	Putative guanosine monophosphate reductase
M5005_Spy0925	*rnhB*	**-1.7**	Anaerobic ribonucleoside triphosphate reductase
M5005_Spy1116	*udk*	**-2.6**	Uridine monophosphate kinase
M5005_Spy1124	*nrdF.2*	**-1.7**	Ribonucleotide reductase, beta subunit
M5005_Spy0919	*guaA*	**-1.9**	GMP synthase
M5005_Spy1341	*gmk*	**-2.3**	Guanylate kinase
M5005_Spy1587	*udp*	**-1.7**	Uridine phosphorylase
Other			
M5005_Spy1326	*comFC*	**-2.4**	ComF-family protein involved in competence
M5005_Spy1631	*salA*	**-3.4**	Type-A lantibiotic
M5005_Spy1809	*uviB*	**-2.6**	Enterocin A Immunity
Phage proteins			
M5005_Spy1052	*int.1*	**-2.0**	Phage integrase
M5005_Spy1193		**-1.6**	Lambdoid phage 5005.2 protein
M5005_Spy1197		**-3.8**	Lambdoid phage 5005.2 protein
M5005_Spy1202		**-2.7**	Lambdoid phage 5005.2 protein
M5005_Spy1203		**-2.4**	Lambdoid phage 5005.2 protein
M5005_Spy1204		**-2.2**	Lambdoid phage 5005.2 protein
M5005_Spy1206		**-2.7**	Lambdoid phage 5005.2 protein
M5005_Spy1209		**-2.7**	Lambdoid phage 5005.2 protein
M5005_Spy1214		**-2.1**	Lambdoid phage 5005.2 protein
M5005_Spy1215		**-1.8**	Lambdoid phage 5005.2 protein
M5005_Spy1416		**-2.7**	Lambdoid phage 5005.3 protein
M5005_Spy1417		**-3.5**	Conserved hypothetical membrane phage 5005.3 protein
M5005_Spy1418		**-2.8**	Lambdoid phage 5005.3 protein
M5005_Spy1419		**-3.4**	Lambdoid phage 5005.3 protein
M5005_Spy1420		**-2.8**	Lambdoid phage 5005.3 protein
M5005_Spy1421		**-3.0**	Lambdoid phage 5005.3 protein
M5005_Spy1422		**-2.4**	Lambdoid phage 5005.3 protein
M5005_Spy1423		**-2.2**	Lambdoid phage 5005.3 protein
M5005_Spy1424		**-2.4**	Lambdoid phage 5005.3 protein
M5005_Spy1426		**-2.2**	Lambdoid phage 5005.3 protein
M5005_Spy1428		**-2.4**	Lambdoid phage 5005.3 protein
M5005_Spy1429		**-2.9**	Lambdoid phage 5005.3 protein
M5005_Spy1430		**-2.5**	Lambdoid phage 5005.3 protein
M5005_Spy1431		**-2.6**	Lambdoid phage 5005.3 protein
M5005_Spy1432		**-2.5**	Lambdoid phage 5005.3 protein
M5005_Spy1433		**-2.8**	Lambdoid phage 5005.3 protein
M5005_Spy1434		**-3.0**	Lambdoid phage 5005.3 protein
M5005_Spy1435		**-3.0**	Lambdoid phage 5005.3 protein

M5005_Spy1437		**-3.0**	Lambdoid phage 5005.3 protein
M5005_Spy1438		**-2.7**	Lambdoid phage 5005.3 protein
M5005_Spy1439		**-2.4**	Lambdoid phage 5005.3 protein
M5005_Spy1440		**-2.7**	Lambdoid phage 5005.3 protein
M5005_Spy1441		**-3.0**	Lambdoid phage 5005.3 protein
M5005_Spy1443		**-2.1**	Lambdoid phage 5005.3 protein
M5005_Spy1444		**-2.5**	Lambdoid phage 5005.3 protein
M5005_Spy1447		**-2.1**	Lambdoid phage 5005.3 protein. Superfamily II DNA/RNA helicases
M5005_Spy1448		**-2.3**	Putative lambdoid phage 5005.3 nuclease
M5005_Spy1449		**-1.8**	Lambdoid phage 5005.3 associated DNA primase
M5005_Spy1450		**-1.7**	Lambdoid phage 5005.3 associated DNA_Pol_A superfamily
M5005_Spy1451		**-1.7**	Lambdoid phage 5005.3 protein
M5005_Spy1452		**-2.1**	Lambdoid phage 5005.3 protein
M5005_Spy1454		**-1.8**	Lambdoid phage 5005.3 protein
Posttranslational modification, protein turnover, chaperones			
M5005_Spy0114		**-3.4**	Sortase (surface protein transpeptidase)
M5005_Spy0371	*cypB*	**-2.7**	Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family
M5005_Spy0866		**-1.7**	Acetyltransferase
M5005_Spy1122	*nrdH*	**-3.3**	Glutaredoxin/thioredoxin; it might be associated with class Ib ribonucleotide reductase
M5005_Spy1240	*clpE*	**-1.6**	Clp protease subunit
M5005_Spy1382		**-3.2**	Peptidase propeptide
M5005_Spy1475		**-2.7**	Acetyltransferase; similar to histone acetyltransferase HPA2
M5005_Spy1593		**-1.5**	Metal-dependent protease; putative molecular chaperone
M5005_Spy1762	*groES*	**-2.0**	Co-chaperonin GroES (HSP10)
M5005_Spy1782	*pepO*	**-1.9**	Predicted metalloendopeptidase
M5005_Spy1850		**-2.0**	Putative Zn-dependent peptidase
M5005_Spy1865	*htrA*	**-3.0**	Trypsin-like serine protease
Replication, repair and cell division			
M5005_Spy0008	*divIC*	**-1.8**	Septum formation initiation protein
M5005_Spy0011	*tilS*	**-2.3**	Predicted ATPase of the PP-loop faimly implicated in cell cycle control
M5005_Spy0506	*ftsW*	**-1.7**	Cell division protein FtsW
M5005_Spy1352		**-4.8**	Cell division protein GpsB
General stress			
M5005_Spy0483		**-2.6**	Putative stress responsive transcriptional regulator
M5005_Spy0778	*msrB*	**-2.0**	Peptide methionine sulfoxide reductase MsrB
M5005_Spy1241	*mutT*	**-1.6**	Mutator mutT protein
M5005_Spy1259	*dpr*	**-3.3**	DNA starvation/stationary phase protection protein
M5005_Spy1328		**-2.2**	IMPACT family protein involved in response to stress
M5005_Spy1378	*npx*	**-2.2**	NADH peroxidase
M5005_Spy1514		**-2.2**	Universal stress protein
M5005_Spy1559	*trx*	**-2.1**	Thioredoxin
M5005_Spy1603	*asp*	**-2.1**	Putative alkaline shock protein

M5005_Spy1765	*csp*	**-1.7**	Cold-Shock Protein (CSP)
Transcription			
M5005_Spy0118		**-3.4**	Putative LysR transcriptional regulator
M5005_Spy0138	*nusG*	**-1.9**	Transcription antitermination protein NusG
M5005_Spy0186		**-2.1**	M trans-acting positive regulator (MGA) PRD domain protein
M5005_Spy0239	*mecA*	**-1.7**	Negative regulator of genetic competence, sporulation and motility
M5005_Spy0269		**-2.7**	Putative transcriptional regulator
M5005_Spy0284	*nrdR*	**-1.7**	transcriptional regulator NrdR for ribonucleotide reductase genes
M5005_Spy0293	*greA*	**-2.8**	Transcription elongation factor
M5005_Spy0367	*scaR*	**-1.9**	Putative transcriptional regulator
M5005_Spy0517	*regR*	**-1.6**	Putative transcriptional regulator
M5005_Spy0654		**-2.0**	Putative transcriptional regulator
M5005_Spy0679		**-2.9**	Putative RelA / SpoT
M5005_Spy0680		**-2.3**	Response regulator
M5005_Spy0681		**-2.2**	Histidine kinase
M5005_Spy0701	*cpsY*	**-1.6**	Putative transcriptional regulator
M5005_Spy0804	*srtR*	**-2.0**	Response regulator
M5005_Spy0805	*srtK*	**-1.7**	Histidine kinase
M5005_Spy0847		**-2.2**	Putative RelA / SpoT
M5005_Spy0917		**-2.3**	Putative transcriptional regulator
M5005_Spy0924		**-2.0**	Putative transcriptional regulator
M5005_Spy0947	*ciaH*	**-2.3**	Histidine kinase
M5005_Spy0948	*ciaR*	**-3.0**	Response regulator
M5005_Spy0959	*spxA*	**-1.5**	Transcriptional regulator SpxA
M5005_Spy0991		**-1.9**	Putative transcriptional regulator
M5005_Spy1057	*malR*	**-2.0**	Putative transcriptional regulator
M5005_Spy1223		**-2.2**	HU/IHF-like transcriptional protein
M5005_Spy1277	*ahrC.2*	**-3.3**	Arginine repressor
M5005_Spy1340		**-1.6**	DNA-directed RNA polymerase, omega subunit
M5005_Spy1377		**-2.0**	M regulator protein trans-acting positive regulator
M5005_Spy1402	*lacR.1*	**-3.2**	Transcriptional regulator of sugar metabolism
M5005_Spy1412	*nusA*	**-1.8**	Transcription elongation factor
M5005_Spy1474	*lytR*	**-1.7**	Transcriptional regulator
M5005_Spy1583		**-2.1**	Putative transcriptional regulator
M5005_Spy1611	*rpoE*	**-3.4**	DNA-directed RNA polymerase, delta subunit
M5005_Spy1625	*salR*	**-1.5**	Signal transduction response regulator
M5005_Spy1626	*salK*	**-1.6**	Signal transduction histidine kinase
M5005_Spy1639	*lacR.2*	**-4.5**	Transcriptional regulator of sugar metabolism
M5005_Spy1640		**-1.7**	Putative transcriptional regulator
M5005_Spy1764	*ctsR*	**-1.7**	Transcriptional repressor of stress genes
M5005_Spy1779		**-1.6**	DNA-binding transcriptional activator of the SARP family
M5005_Spy1785		**-2.5**	Putative transcriptional regulator
M5005_Spy1798	*spxA*	**-2.3**	Transcriptional regulator

M5005_Spy1807	*argR2*	**-1.9**	Arginine repressor
M5005_Spy1848		**-1.5**	Putative transcriptional regulator
Translation			
M5005_Spy0005	*pth*	**-1.8**	Peptidyl-tRNA hydrolase
M5005_Spy0007	*hsp15*	**-2.2**	Ribosome-associated heat shock protein (Hsp15)
M5005_Spy0043	*rpsJ*	**-3.0**	30S ribosomal protein S10
M5005_Spy0044	*rplC*	**-2.3**	50S ribosomal protein L3
M5005_Spy0101		**-1.6**	Putative tRNA binding domain-containing protein
M5005_Spy0207	*rnpA*	**-2.0**	Ribonuclease P protein component
M5005_Spy0211	*rpmH*	**-2.9**	50S ribosomal protein L34
M5005_Spy0261		**-2.4**	Ribosome biogenesis GTPase
M5005_Spy0262		**-2.5**	Predicted RNA-binding protein, possibly ribosomal protein
M5005_Spy0265		**-1.9**	Putative ribosome-associated protein
M5005_Spy0278	*gidB*	**-2.4**	16S rRNA methyltransferase GidB
M5005_Spy0312		**-1.8**	23S rRNA methyltransferase
M5005_Spy0375	*rplA*	**-1.7**	50S ribosomal protein L1
M5005_Spy0380	*rrf*	**-1.9**	Ribosome recycling factor (RRF)
M5005_Spy0438	*rnc*	**-2.4**	Ribonuclease III
M5005_Spy0456	*relB*	**-2.0**	RelB antitoxin
M5005_Spy0462	*asnS*	**-1.9**	Asparaginyl-tRNA synthetase
M5005_Spy0495	*lysS*	**-1.5**	Lys_tRNA synthetase
M5005_Spy0498		**-2.1**	tRNA deacylase; it deacylates mischarged tRNAs
M5005_Spy0530	*prfB*	**-1.6**	Peptide chain release factor 2
M5005_Spy0546	*rpmE*	**-2.2**	50S ribosomal protein L31 type B
M5005_Spy0551	*rplS*	**-2.2**	50S ribosomal protein L19
M5005_Spy0587	*pheS*	**-1.8**	Phenylalanyl-tRNA synthetase
M5005_Spy0619	*infC*	**-2.9**	IF-3 translation initiation factor
M5005_Spy0620	*rpl36*	**-2.6**	50S ribosomal protein L35
M5005_Spy0621	*rplT*	**-2.0**	50S ribosomal protein L20
M5005_Spy0655	*rimM*	**-2.3**	16S rRNA-processing protein RimM
M5005_Spy0677	*fms*	**-3.6**	Polypeptide deformylase
M5005_Spy0715	*rpsA*	**-3.0**	30S ribosomal protein S1
M5005_Spy0776	*lepA*	**-1.5**	Elongation Factor 4 (EF4)
M5005_Spy0795	*rplJ*	**-3.1**	50S ribosomal protein L10
M5005_Spy0863	*prfA*	**-1.7**	Peptide chain release factor
M5005_Spy0864	*hemK*	**-1.6**	S-adenosylmethionine-dependent methyltransferase of polypeptide chain release factors
M5005_Spy0865		**-1.7**	Putative translation factor
M5005_Spy0915	*ffh*	**-1.6**	Signal recognition particle GTPase
M5005_Spy0921		**-2.9**	Elongation factor 3 (EF-3)
M5005_Spy0946	*rpsT*	**-2.6**	30S ribosomal protein S20
M5005_Spy1105		**-1.8**	Acetyltransferase, including N-acetylases of ribosomal proteins
M5005_Spy1134		**-1.7**	Methylase of polypeptide chain release factors
M5005_Spy1140	*queA*	**-1.6**	Queuosine (Q) biosynthesis protein

M5005_Spy1294		**-1.8**	Acetyltransferase, including N-acetylases of ribosomal proteins
M5005_Spy1325	*raiA*	**-1.9**	Ribosome-associated inhibitor A (RaiA)
M5005_Spy1410		**-1.6**	Ribosomal protein HS6-type (S12/L30/L7a)
M5005_Spy1468	*trmB*	**-1.5**	tRNA (guanine-N(7)-)-methyltransferase
M5005_Spy1547	*efp*	**-1.6**	Elongation factor P
M5005_Spy1555	*rpsF*	**-1.8**	30S ribosomal protein S6
M5005_Spy1612	*ropA*	**-2.7**	Trigger factor (TF) protein; molecular chaperone
M5005_Spy1646	*rpsI*	**-1.8**	30S ribosomal protein S9/S16
M5005_Spy1647	*rplM*	**-2.8**	50S ribosomal protein L13
M5005_Spy1652		**-1.6**	rRNA methylase
M5005_Spy1666	*rpsO*	**-2.5**	30S ribosomal protein S15
M5005_Spy1669	*def*	**-2.4**	Polypeptide deformylase
M5005_Spy1780	*rpsB*	**-2.3**	30S ribosomal protein S2
M5005_Spy1781	*tsf*	**-1.7**	Translation elongation factor Ts
M5005_Spy1814	*hisS*	**-1.9**	Histidyl-tRNA synthetase
M5005_Spy1815	*rpmF*	**-3.6**	50S ribosomal protein L32
M5005_Spy1816	*rpmG*	**-2.4**	50S ribosomal protein L33
M5005_Spy1831	*rpsD*	**-1.8**	30S ribosomal protein S4
M5005_Spy1858	*trsA*	**-1.9**	Tryptophanyl-tRNA synthetase
Transport			
M5005_Spy0117		**-2.2**	Putative transport protein
M5005_Spy0220	*tatD*	**-2.0**	Sec-independent protein translocase
M5005_Spy0368	*mtsA*	**-2.0**	ABC transporter, manganese-binding protein
M5005_Spy0662	*fruA*	**-2.0**	Phosphotransferase system, fructose-specific IIC component
M5005_Spy0806	*srtA*	**-2.3**	Multidrug resistance protein (MRP)-like transporter
M5005_Spy1067	*malX*	**-2.1**	Maltose/maltodextrin transporter subunit
M5005_Spy1167		**-1.7**	Putative cation transport ATPase
M5005_Spy1379	*glpF*	**-1.9**	Major intrinsic protein (MIP) superfamily protein; glycerol uptake facilitator
M5005_Spy1399	*pstIIc*	**-3.3**	PTS galactose-specific EIIc component; Lac.1 (cluster I) tagatose pathway
M5005_Spy1400	*pstIIb*	**-3.9**	PTS galactose-specific EIIb component; Lac.1 (cluster I) tagatose pathway
M5005_Spy1401	*pstIIa*	**-3.3**	PTS galactose-specific EIIa component; Lac.1 (cluster I) tagatose pathway
M5005_Spy1628	*salX*	**-2.1**	ABC transporter; ATPase component
M5005_Spy1633	*lacE*	**-4.3**	PTS lactose-specific EIIb component; Lac.2 (cluster II) tagatose pathway
M5005_Spy1634	*lacF*	**-3.0**	PTS lactose-specific EIIa component; Lac.2 (cluster II) tagatose pathway
M5005_Spy1728		**-1.8**	ABC transporter ATP-binding protein
M5005_Spy1784		**-1.9**	Phosphotransferase system IIABC component
M5005_Spy1846	*cbiO1*	**-1.6**	ABC-type cobalt transport system, ATPase component
Virulence			
M5005_Spy0283	*covS*	**-2.5**	Histidine kinase of virulence gene expression
M5005_Spy0668	*mac*	**-3.3**	Bacterial protein Mac1
M5005_Spy0777	*sclB*	**-1.7**	Adhesion protein belonging to the collagen superfamily
M5005_Spy1415	*sdaD2*	**-2.8**	Streptodornase

TABLE S4 Differentially-expressed genes common to the isogenic *fabT* deletion mutant and the wild-type MGAS2221 grown at 35°C and 40°C

A. Up-regulated at 35°C during mid-exponential phase

Locus tag	Feature ID	FC[a]-WT	FC[b]-FabT	Function
M5005_Spy0780	*ptsA*	**2.7**	**2.2**	PTS system mannose/sorbose-specific IIa component
M5005_Spy0781	*ptsB*	**2.7**	**2.2**	PTS system mannose/sorbose-specific IIb component
M5005_Spy0783	*ptsD*	**2.7**	**2.2**	PTS system mannose/sorbose-specific IId component
M5005_Spy1106	*grab*	**2.9**	**2.0**	Gram positive anchor
M5005_Spy1587	*udp*	**1.5**	**1.9**	Uridine phosphorylase
M5005_Spy1733	M5005_Spy1733	**28.5**	**12.2**	Hypothetical protein
M5005_Spy1734	*spi_2*	**41.2**	**11.1**	Spi_2; peptidase C10 family protein
M5005_Spy1735	*speB*	**42.0**	**16.3**	SpeB; peptidase C10 family protein
M5005_Spy1736	M5005_Spy1736	**18.3**	**9.6**	Hypothetical protein
M5005_Spy1765	*csp*	**2.7**	**2.7**	Cold-shock protein
M5005_Spy1860	M5005_Spy1860	**1.9**	**1.5**	Uncharacterized conserved protein

[a] **FC-WT** refers to fold-change in wild-type MGAS2221 when comparing gene expression at 35°C to gene expression at 40°C

[b] **FC-FabT** refers to fold-change in the *fabT* deletion mutant MGAS2221D*fabT* when comparing gene expression at 35°C to gene expression at 40°C

B. Up-regulated at 40°C during mid-exponential phase

Locus tag	Feature ID	FC-WT	FC-FabT	Function
M5005_Spy0346	M5005_Spy0346	**1.9**	**2.0**	Hypothetical protein
M5005_Spy0347	*nrdF.1*	**2.3**	**1.9**	Class I ribonucleotide reductase, subunit beta
M5005_Spy0348	*nrdI*	**2.4**	**1.8**	Class I ribonucleotide reductase, subunit alpha
M5005_Spy0349	*nrdE.1*	**2.3**	**2.0**	Class I ribonucleotide reductase
M5005_Spy1052	*int.1*	**2.3**	**2.0**	ϕ 5005.1 protein
M5005_Spy1416	M5005_Spy1416	**8.4**	**2.8**	ϕ 5005.3 protein
M5005_Spy1418	M5005_Spy1418	**9.3**	**2.7**	ϕ 5005.3 protein
M5005_Spy1419	M5005_Spy1419	**9.9**	**2.9**	ϕ 5005.3 protein
M5005_Spy1420	M5005_Spy1420	**11.5**	**2.8**	ϕ 5005.3 protein
M5005_Spy1421	M5005_Spy1421	**9.5**	**2.9**	ϕ 5005.3 protein
M5005_Spy1422	M5005_Spy1422	**10.3**	**3.0**	ϕ 5005.3 protein
M5005_Spy1423	M5005_Spy1423	**10.6**	**2.9**	ϕ 5005.3 protein
M5005_Spy1424	M5005_Spy1424	**10.0**	**3.0**	ϕ 5005.3 protein
M5005_Spy1425	M5005_Spy1425	**10.3**	**2.7**	ϕ 5005.3 protein
M5005_Spy1426	M5005_Spy1426	**9.3**	**2.6**	ϕ 5005.3 protein
M5005_Spy1427	M5005_Spy1427	**10.6**	**2.8**	ϕ 5005.3 protein
M5005_Spy1428	M5005_Spy1428	**11.2**	**2.7**	ϕ 5005.3 protein

M5005_Spy1429	M5005_Spy1429	**10.9**	**2.4**	ϕ 5005.3 protein
M5005_Spy1430	M5005_Spy1430	**10.9**	**2.7**	ϕ 5005.3 protein
M5005_Spy1431	M5005_Spy1431	**8.3**	**2.6**	ϕ 5005.3 protein
M5005_Spy1432	M5005_Spy1432	**11.0**	**2.7**	ϕ 5005.3 protein
M5005_Spy1433	M5005_Spy1433	**9.8**	**2.5**	ϕ 5005.3 protein
M5005_Spy1435	M5005_Spy1435	**9.3**	**2.6**	ϕ 5005.3 protein
M5005_Spy1436	M5005_Spy1436	**10.4**	**2.8**	ϕ 5005.3 protein
M5005_Spy1437	M5005_Spy1437	**13.0**	**3.6**	ϕ 5005.3 protein
M5005_Spy1438	M5005_Spy1438	**9.7**	**2.6**	ϕ 5005.3 protein
M5005_Spy1439	M5005_Spy1439	**9.9**	**2.6**	ϕ 5005.3 protein
M5005_Spy1440	M5005_Spy1440	**9.2**	**3.1**	ϕ 5005.3 protein
M5005_Spy1441	M5005_Spy1441	**10.6**	**2.8**	ϕ 5005.3 protein
M5005_Spy1793	*nrdD*	**1.7**	**1.7**	Class III ribonucleotide reductase
M5005_Spy1840	*trmU*	**2.0**	**1.7**	tRNA methyl transferase

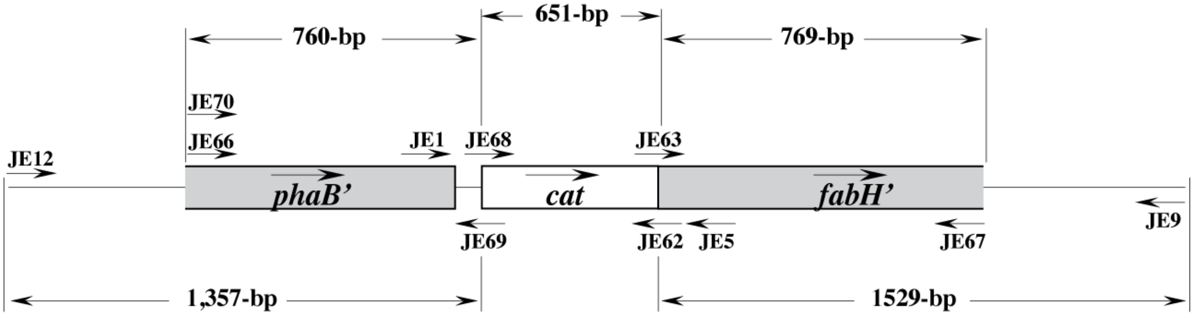
C. Up-regulated at 35°C during stationary phase

Locus tag	Feature ID	FC-WT	FC-FabT	Function
M5005_Spy0032	M5005_Spy0032	**1.6**	**1.6**	Putative chromosome segregation protein
M5005_Spy0360	M5005_Spy0360	**1.6**	**2.0**	Predicted dehydrogenase
M5005_Spy0614	*pepT*	**1.7**	**1.6**	Peptidase T
M5005_Spy0616	M5005_Spy0616	**2.1**	**1.5**	Ferredoxin
M5005_Spy0617	M5005_Spy0617	**1.7**	**1.5**	Cytidine monophosphate kinase
M5005_Spy0780	*ptsA*	**3.6**	**3.1**	PTS system mannose/sorbose-specific IIa component
M5005_Spy0781	*ptsB*	**3.7**	**1.9**	PTS system mannose/sorbose-specific IIb component
M5005_Spy0784	M5005_Spy0784	**3.5**	**2.1**	Putative histidine kinase
M5005_Spy0785	M5005_Spy0785	**3.2**	**2.0**	Putative response regulator
M5005_Spy0786	M5005_Spy0786	**2.9**	**1.7**	Substrate binding domain of LysR transcriptional regulators
M5005_Spy0790	*gabD*	**1.5**	**1.6**	Succinate-semialdehyde dehydrogenase
M5005_Spy0872	*nox*	**1.5**	**1.7**	NADH oxidase
M5005_Spy0877	M5005_Spy0877	**2.1**	**2.6**	Hypothetical protein
M5005_Spy0878	M5005_Spy0878	**1.9**	**1.9**	Hypothetical protein
M5005_Spy1325	*raiA*	**1.9**	**1.8**	RaiA ("ribosome-associated inhibitor A)
M5005_Spy1351	M5005_Spy1351	**1.8**	**1.6**	Nucleic acid methyltransferase
M5005_Spy1411	M5005_Spy1411	**1.7**	**1.6**	Hypothetical protein
M5005_Spy1413	M5005_Spy1413	**1.6**	**1.6**	Hypothetical protein
M5005_Spy1601	M5005_Spy1601	**1.5**	**2.4**	Band 7 domain protein. It may cluster to form membrane microdomains
M5005_Spy1711	*lmb*	**2.1**	**1.5**	Metal-binding protein AcdA
M5005_Spy1860	M5005_Spy1860	**4.6**	**1.5**	Hypothetical membrane protein

D. Up-regulated at 40°C during the stationary phase

Locus tag	Feature ID	FC-WT	FC-FabT	Function
M5005_Spy0308	M5005_Spy0308	**1.7**	**1.5**	Structural maintenance of chromosome (SMC) protein
M5005_Spy0347	*nrdF.1*	**1.9**	**3.3**	Class I ribonucleotide reductase, subunit beta
M5005_Spy0348	*nrdI*	**1.8**	**5.0**	Class I ribonucleotide reductase, subunit alpha
M5005_Spy0349	*nrdE.1*	**2.0**	**4.3**	Class I ribonucleotide reductase
M5005_Spy0869	M5005_Spy0869	**2.2**	**1.7**	Lysozyme-like protein
M5005_Spy0921	M5005_Spy0921	**4.8**	**1.7**	EF-3 elongation factor
M5005_Spy0922	*pdxK*	**5.9**	**2.5**	Unknown function protein
M5005_Spy0923	M5005_Spy0923	**5.0**	**2.2**	Pyridoxal kinase
M5005_Spy0924	M5005_Spy0924	**6.0**	**2.6**	HTH and aminotransferase domain protein
M5005_Spy1026	M5005_Spy1026	**6.9**	**2.5**	ϕ 5005.1 protein
M5005_Spy1027	M5005_Spy1027	**4.8**	**2.2**	ϕ 5005.1 protein
M5005_Spy1029	M5005_Spy1029	**4.8**	**2.5**	ϕ 5005.1 protein
M5005_Spy1030	M5005_Spy1030	**5.4**	**2.1**	ϕ 5005.1 protein
M5005_Spy1031	M5005_Spy1031	**5.6**	**2.4**	ϕ 5005.1 protein
M5005_Spy1032	M5005_Spy1032	**4.7**	**2.0**	ϕ 5005.1 protein
M5005_Spy1033	M5005_Spy1033	**4.7**	**2.0**	ϕ 5005.1 protein
M5005_Spy1035	M5005_Spy1035	**3.6**	**2.2**	ϕ 5005.1 protein
M5005_Spy1039	M5005_Spy1039	**4.8**	**2.7**	ϕ 5005.1 protein
M5005_Spy1041	M5005_Spy1041	**9.2**	**2.1**	ϕ 5005.1 protein
M5005_Spy1042	M5005_Spy1042	**5.3**	**2.0**	ϕ 5005.1 protein
M5005_Spy1043	M5005_Spy1043	**5.5**	**2.2**	ϕ 5005.1 protein
M5005_Spy1045	M5005_Spy1045	**3.0**	**2.1**	ϕ 5005.1 protein
M5005_Spy1049	M5005_Spy1049	**3.1**	**1.9**	ϕ 5005.1 protein
M5005_Spy1222	*int.2*	**2.9**	**4.7**	ϕ 5005.2 protein
M5005_Spy1316	M5005_Spy1316	**2.0**	**4.2**	Uncharacterized conserved protein
M5005_Spy1317	M5005_Spy1317	**2.1**	**3.7**	Alpha-mannosidase
M5005_Spy1327	*comFA*	**4.5**	**2.7**	DNA uptake protein
M5005_Spy1367	*ftsL*	**1.6**	**1.6**	Septum formation initiator
M5005_Spy1414	M5005_Spy1414	**8.5**	**3.0**	ϕ 5005.3 protein
M5005_Spy1420	M5005_Spy1420	**15.4**	**3.4**	ϕ 5005.3 protein
M5005_Spy1432	M5005_Spy1432	**9.0**	**2.1**	ϕ 5005.3 protein
M5005_Spy1437	M5005_Spy1437	**12.9**	**2.5**	ϕ 5005.3 protein
M5005_Spy1459	M5005_Spy1459	**4.5**	**1.8**	ϕ 5005.3 protein
M5005_Spy1467	*int.3*	**2.2**	**6.5**	ϕ 5005.3 protein
M5005_Spy1656	M5005_Spy1656	**1.6**	**1.5**	Hypothetical protein
M5005_Spy1793	*nrdD*	**1.8**	**1.9**	Class III ribonucleotide reductase
M5005_Spy1822	M5005_Spy1822	**2.0**	**1.9**	Putative transcriptional regulator

SUPPLEMENTAL FIGURES



JE1: 5'- GGAAGATTTTAAAGAAGGTGTCATAGC - 3'

JE5: 5'- CCACTCATGACTAGTGTCCATTATGCTAG -3'

JE9: 5'- CCCAAGCCATTCCTCCTTGAAAAATGGGGTAATC -3'

JE12: 5'- CCAACGGTTCATGGCGATGTTGAGATGGC - 3'

JE62: 5'- ATTTTAGAAAAAATCATTTATAAAAGCCAGTCATTAGGCCTATCTGAC - 3'

JE63: 5'- GACTGGCTTTTATAAATGATTTTTTCTAAAATCAGTCAGGTAGCCC - 3'

JE66: 5'- CTGGTAGCATTAGCAGAAGTTAAACGCG -3'

JE67: 5'- CAAGTATACGACGATTAGCTTGATGCAATAAAC -3'

JE68: 5'- GCTAGGAGGTGTTTACATGAACTTTAATAAAATTGATTTAGACAATTGGAAGAG -3'

JE69: 5'- CAATTTTATTAAAGTTCATGTAAACACCTCCTAGCAATAAACTTTGACAATC -3'

JE70: 5'- CGCGGATCCCTGGTAGCATTAGCAGAAGTTAAACGCG -3'

FIG S1 Strategy to replace *fabT* with *cat*. Top. Schematic representing the replacement of *fabT* with *cat*. The upstream gene, *phaB*, and downstream gene, *fabH* are shown; arrows indicate the direction of transcription. Primers used to amplify the respective fragments and the sizes of the corresponding PCR fragments are shown. **Bottom**. DNA sequences of the primers used for PCR reactions.

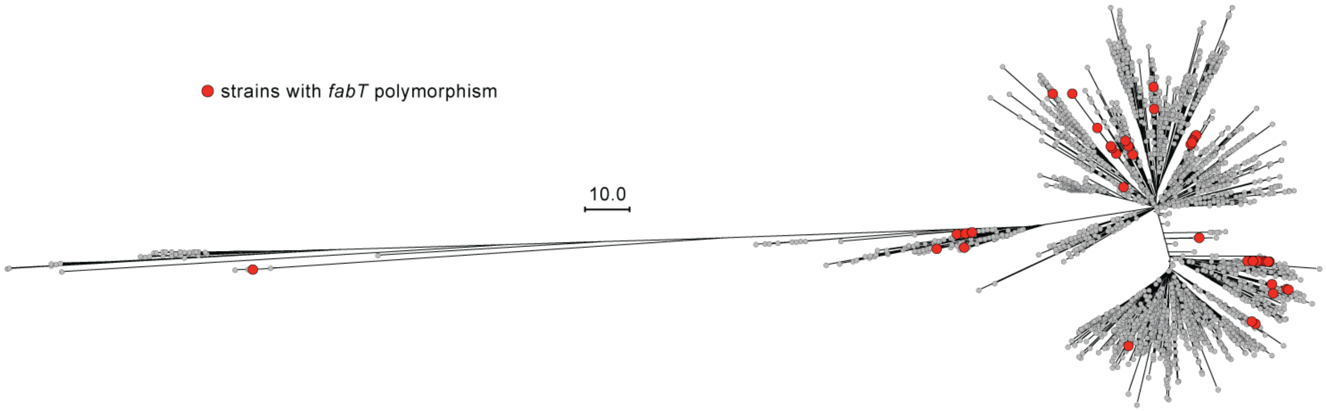


FIG S2 Neighbor-joining radial phylogram for serotype M1 strains isolated from human epidemics. Phylogenetic tree showing genetic relationships among 3,615 serotype M1 strains on two continents spanning from 1969 through 2013. This phylogram is based on 12,355 core chromosomal SNPs after excluding SNPs in the 36-kb *purA*-to-*nadC* region of recombination (12). Strains containing polymorphisms in the *fabT* gene or *fabT* promoter sequence are shown in red. They are distributed among different branches of pre- and post-epidemic isolates and have different alleles of the *fabT* gene, indicating that the polymorphism in *fabT* gene arose independently in the human host.

Figure S3

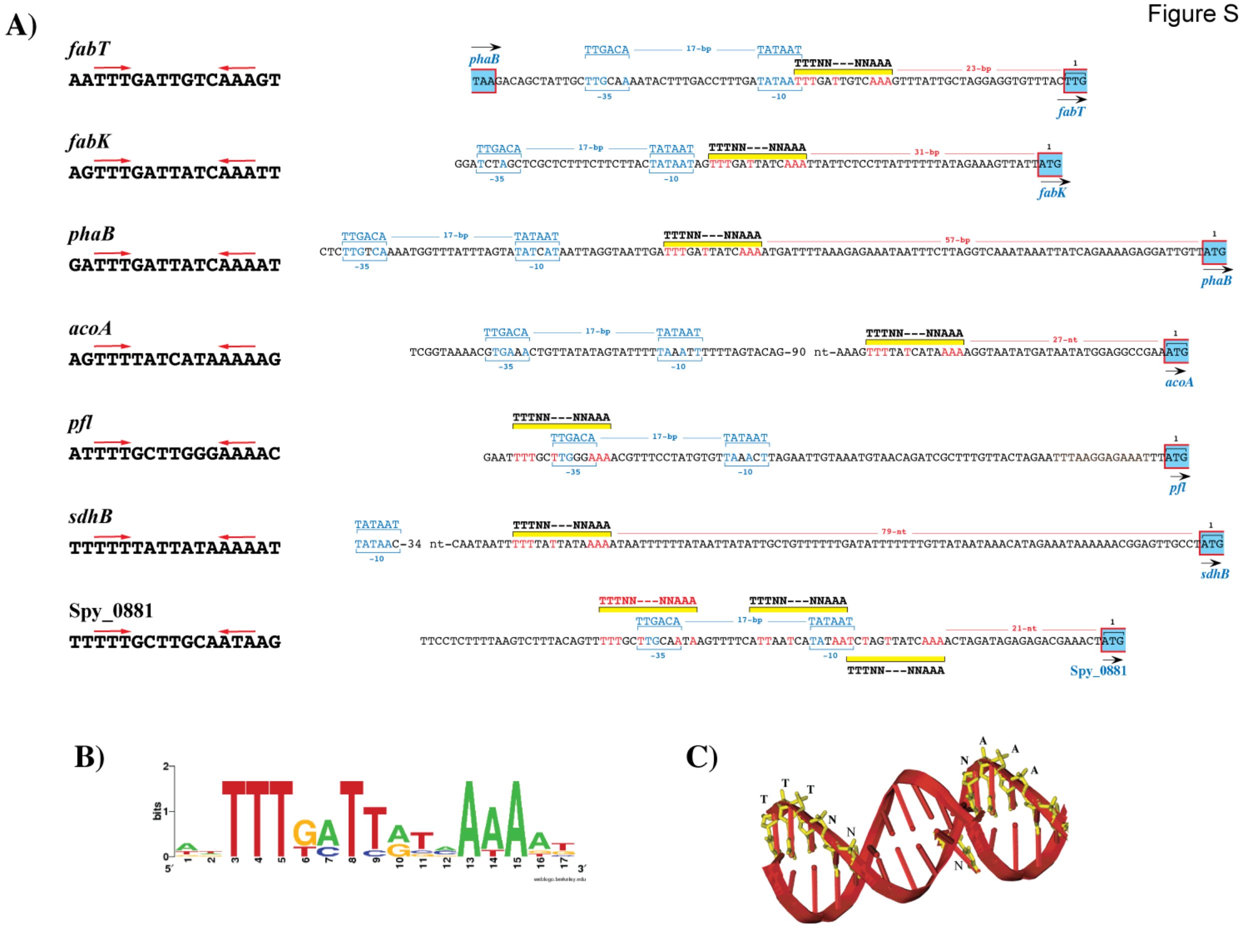


FIG S3 Consensus binding sequence for FabT in M1GAS. **(A)** Putative FabT-binding DNA sequences found upstream of *fabT*, *fabK*, *phaB*, *acoA*, *pfl*, *sdhB*, and Spy_0881. The position of the putative FabT sites within the DNA sequence is indicated. Spy_0881 contains more than one putative FabT-binding sequence. The selected FabT site for WebLogo is depicted in red. Matches to the FabT consensus sequence in the respective DNA sequences are indicated in red. Promoter sequences are depicted in blue. **(B)** FabT consensus derived from the above DNA sequences using WebLogo. **(C)** Position of the inverted repeats constituting the consensus **TTTNN**NNN**NNAAA** on DNA.

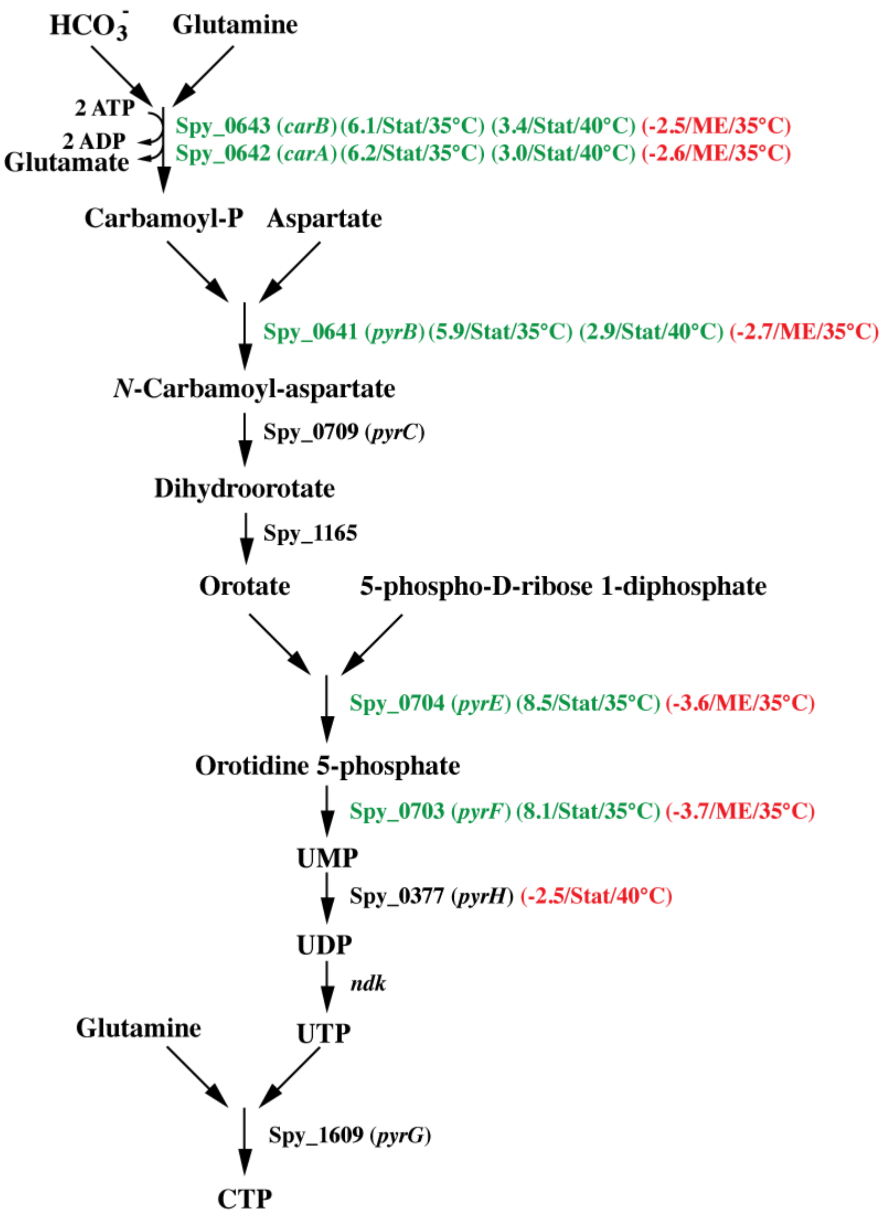


FIG S4 FabT regulation of *de novo* pyrimidine synthesis. Differentially regulated genes in the pyrimidine *de novo* biosynthesis pathway are represented either in green (upregulated in the FabT mutant), or red (downregulated). The fold-expression values are positive for upregulated genes, and negative for downregulated genes. The phases of growth are either mid-exponential (ME), or stationary (Stat). Fold expression values and growth phase are denoted in parentheses, immediately after the gene designations.

35^{o} and 40^{o}C refer to the two growth temperatures.

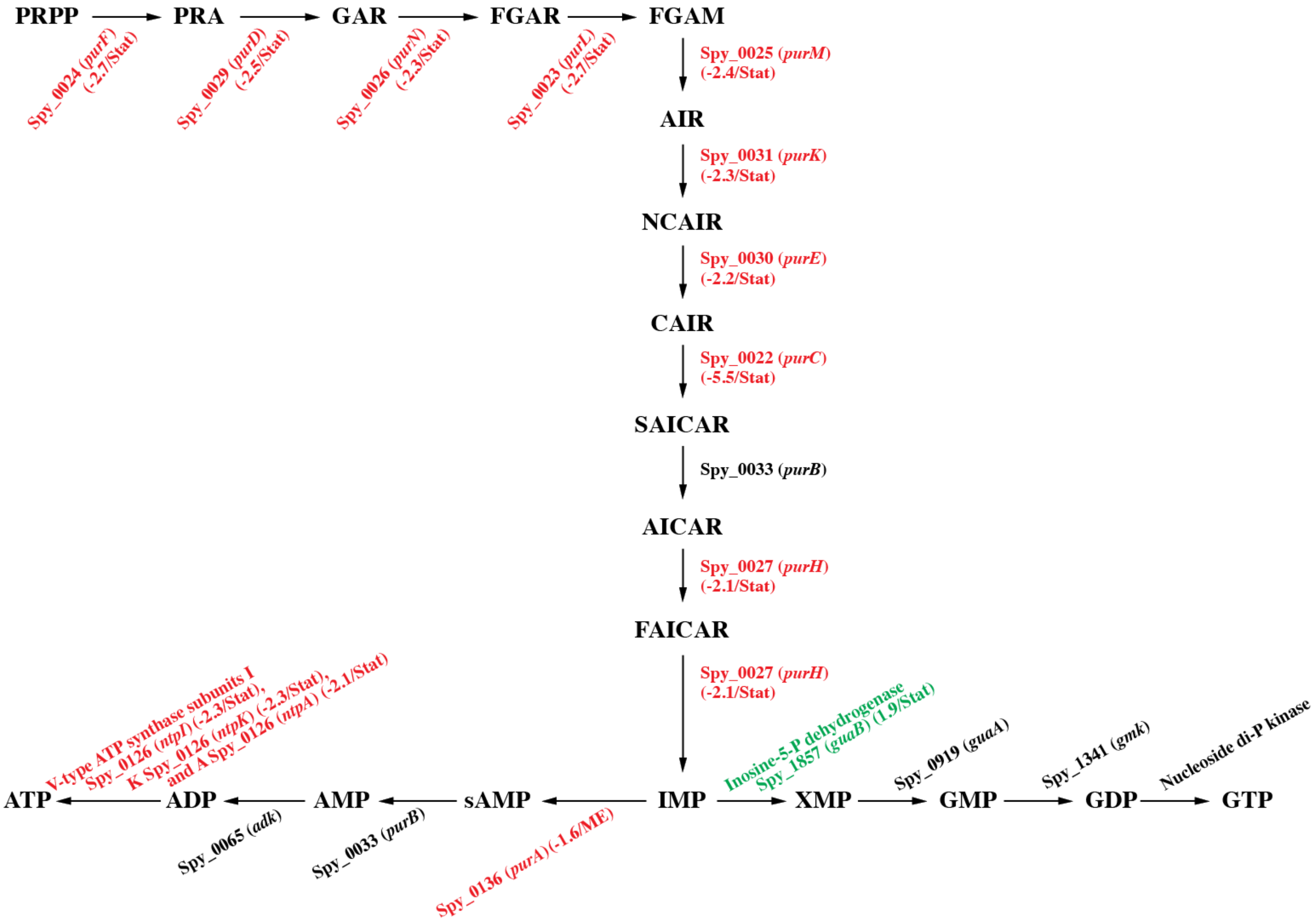


FIG S5 FabT regulation of *de novo* purine synthesis. Differentially regulated genes in the purine *de novo* biosynthesis pathway are represented either in green (upregulated in the FabT mutant), or red (downregulated). The fold expression values are positive for upregulated genes, and negative for downregulated genes. The phases of growth are either mid-exponential (ME), or stationary (Stat). Fold-expression values and growth phase are denoted in parentheses, immediately after the gene designations.