Table S2. Genes affected by the mutation of *rpoS*

ORF	**Product**	***Gene***	**Ratio* *rpoS* E/Wt E**	**Ratio* *rpoS* PE/Wt PE**
lpg0001	chromosomal replication initiator protein DnaA	*dnaA*	0.00	2.63
lpg0003	DNA recombination and repair protein ATPase RecI	-	-2.20	-0.87
lpg0005	peptidylarginine deiminase	-	-2.11	0.65
lpg0006	biosynthetic arginine decarboxylase	*speA*	-0.12	2.79
lpg0023	transmembrane protein COG4539	-	-0.23	-3.94
lpg0026	amino acid permease COG0531	-	2.04	-1.08
lpg0028	ubiquinone biosynthesis protein COQ7, central met	-	-0.60	2.70
lpg0049	amino acid transporter, permease	-	3.35	4.00
lpg0052	carboxyphosphoenolpyruvate phosphonomutase (c	-	0.41	2.41
lpg0060	methylase	-	-4.67	-0.41
lpg0064	hypothetical	-	-3.64	-0.64
lpg0065	ORF	-	-3.12	-0.78
lpg0066	carbamoyl phosphate synthase large chain (fusion	-	-3.54	-1.52
lpg0069	tRNA-Asn	-	-0.40	-2.02
lpg0073	diguanylate cyclase/phosphodiesterase domain 2 (	-	-1.46	-4.08
lpg0074	glutamate synthase	-	0.06	-3.01
lpg0083	COG0189: glutathione synthase/ribosomal protein	-	0.61	3.81
lpg0084	hypothetical	-	-2.14	2.49
lpg0088	glutamine ABC transporter (arginine 3rd transport s	-	0.43	-4.33
lpg0100	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acylt	-	0.52	2.72
lpg0104	peptide methionine sulfoxide reductase	-	-0.53	3.34
lpg0105	(cytochrome oxidase?) (phosphatidylglycerophosph	-	0.89	2.49
lpg0107	hypothetical (membrane protein required for meiotic	-	0.21	3.20
lpg0112	hypothetical protein	-	2.95	0.06
lpg0118	glycine cleavage system T protein (aminomethyltra	*gcvT1*	2.02	2.50
lpg0124	cytochrome c4	-	1.89	2.57
lpg0126	ninein (GSK3B interacting protein)	*cegC2*	2.33	1.50
lpg0135	SdhB	*sdhB*	0.41	-2.79
lpg0137	phosphoglycerate kinase	*pgk*	-0.49	2.29
lpg0138	glyceraldehyde 3-phosphate dehydrogenase	*gap*	1.90	4.38
lpg0139	transketolase I	*tktA*	0.46	2.32
lpg0152	hypothetical (GCN5-related N-acetylase, acetyltran	-	0.74	2.87
lpg0153	small ORF (104aa)	-	-0.56	-5.31
lpg0154	ORF	-	2.34	-1.32
lpg0156	signal transduction protein (EAL/GGDEF domain pr	-	-0.20	-2.05
lpg0163	hydrolases of the alpha/beta superfamily	-	0.36	-3.40
lpg0165	conserved hypothetical protein	-	0.27	-2.46
lpg0172	ORF	-	-1.53	2.26
lpg0175	pyoverdine biosynthesis protein PvcB	-	2.10	2.76
lpg0176	FAD monooxygenase, PheA/TfdB family (phenol 2-	-	1.35	2.01
lpg0178	hypothetical	-	-1.04	2.05
lpg0187	L. pneumophila zinc metalloprotein (peptidase, M2	-	1.07	2.28
lpg0194	catalase/(hydro)peroxidase KatG	-	1.17	2.25
lpg0204	2-deoxy-D-gluconate-3-dehydrogenase (3-oxoacyl-	-	2.84	3.26
lpg0219	hypothetical	-	2.20	2.42

lpg0220	hypothetical	-	2.04	1.44
lpg0227	ORF	*ceg7*	3.15	-0.14
lpg0233	benzoylformate decarboxylase	*mdlC*	-0.55	-3.29
lpg0244	pyridine nucleotide-disulfide oxidoreductase, FAD-d	-	-0.67	-3.73
lpg0251	RNA binding protein (cold-inducible) rrm	-	-2.10	0.40
lpg0251	RNA binding protein (cold-inducible) rrm	-	-2.20	0.50
lpg0260	small ORF (132aa)	-	-0.97	2.80
lpg0266	small ORF (144aa)	-	0.21	2.13
lpg0272	cysteine transferase	-	1.30	2.31
lpg0277	sensory box protein (GGDEF family protein) LssE p	-	-1.33	-2.38
lpg0285	ORF	-	1.48	2.13
lpg0287	translation elongation factor P (EF-P)	*efp*	2.29	2.44
lpg0292	ORF	-	-0.12	2.00
lpg0295	mannose-1-phosphate guanyltransferase (sugar ph	-	1.83	2.78
lpg0296	(phosphotransferase) hypothetical	-	0.52	4.09
lpg0308	cell wall associated hydrolase, putative pseudogen	-	2.63	0.57
lpg0311	tRNA-Tyr	-	-0.14	4.29
lpg0312	tRNA-Gly	-	0.17	4.49
lpg0313	tRNA-Thr	-	0.58	3.30
lpg0314	elongation factor Tu (EF-Tu)	*tuf2*	0.54	2.53
lpg0316	preprotein translocase, SecE subunit	*secE*	-0.67	3.40
lpg0317	transcription antitermination protein NusG	*nusG*	-0.74	3.06
lpg0320	50S ribosomal protein L10	*rplJ*	0.08	3.38
lpg0321	50S ribosomal protein L7/L12	*rplL*	0.66	4.94
lpg0325	30S ribosomal protein S7	*rpS7*	-0.46	2.02
lpg0328	30S ribosomal protein S10	*rpsJ*	0.31	3.47
lpg0329	50S ribosomal protein L3	*rplC*	-0.39	2.61
lpg0335	30S ribosomal protein S3	*rpsC*	-1.48	2.34
lpg0336	50S ribosomal protein L16/(L10E)	*rplP*	-0.43	2.51
lpg0342	30S ribosomal protein S14	*rpsN*	-1.70	2.80
lpg0343	30S ribosomal protein S8	*rpsH*	-0.91	3.01
lpg0344	50S ribosomal protein L6/(L9E)	*rplF*	-0.65	3.03
lpg0345	50S ribosomal protein L18	*rplR*	-0.28	2.71
lpg0346	30S ribosomal protein S5	*rpsE*	0.14	2.35
lpg0348	50S ribosomal protein L15	*rplO*	-1.80	2.34
lpg0349	preprotein translocase (secretion protein SecY)	*secY*	-2.89	2.01
lpg0352	30S ribosomal protein S11	*rpsK*	-1.14	2.89
lpg0353	30S ribosomal protein S4	*rpsD*	-0.20	2.69
lpg0362	3-oxoacyl-[acyl-carrier protein] synthase II (beta-ke	*fabF*	-2.77	0.50
lpg0369	carboxylesterase/phospholipase	-	0.38	3.41
lpg0370	oligoketide cyclase/lipid transporter protein COG28	-	-0.29	2.82
lpg0383	small ORF (160aa) very weak IcmL homolog	-	-0.53	-2.72
lpg0385	LemA protein (cytoplasmic membrane protein)	-	-0.36	-3.71
lpg0389	ORF	-	-2.22	-1.34
lpg0392	zinc metalloprotease (metal-dependent hydrolase)	-	-2.10	-2.02
lpg0394	COG0350 methylated DNA protein cysteine S-meth	-	-2.18	1.77
lpg0395	50S ribosomal protein L19	*rplS*	-2.24	1.59
lpg0396	tRNA (guanine N1) methyltransferase	*trmD*	-2.44	2.63

lpg0397	16S rRNA processing protein RimM	*rimM*	-2.60	4.41
lpg0399	30S ribosomal protein S16	*rpsP*	-1.41	2.99
lpg0401	ORF	-	-0.17	2.53
lpg0415	ORF	-	0.05	-2.71
lpg0416	glucose-6-phosphate-1-dehydrogenase	*zwf*	-0.99	-2.48
lpg0431	ORF	-	-2.42	1.03
lpg0436	ORF	*legA11*	2.14	-1.76
lpg0438	ORF	-	-2.36	0.68
lpg0459	IcmH (DotU)	*icmH*	-0.23	2.53
lpg0461	ribosomal protein L11 methyltransferase	*prmA*	-0.86	2.07
lpg0462	acetyl CoA carboxylase, biotin carboxylase subunit	*accC*	-0.23	3.54
lpg0463	acetyl CoA carboxylase, biotin carboxyl carrier prote	-	1.00	2.76
lpg0467	zinc metalloprotease (hemagglutinin/protease)	-	1.60	2.57
lpg0469	endonuclease/exonuclease/phosphatase family pro	-	-0.97	-2.67
lpg0470	fructose bisphosphate aldolase	-	2.03	2.47
lpg0471	phenol hydroxylase (ferredoxin-NADP reductase)	*poxF*	1.12	3.08
lpg0474	CDP-diacylglycerol-serine-O-phosphatidyltransferas	-	-0.62	2.06
lpg0476	sigma-54 modulation protein	-	-0.92	-2.86
lpg0478	50S ribosomal protein L33	*rpL33*	-0.03	4.02
lpg0479	50S ribosomal protein L28	*rpmB*	-0.04	4.51
lpg0482	endo-1,4 beta-glucanase or (deblocking) aminopep	-	2.50	2.16
lpg0483	ORF	*legA12*	2.54	0.16
lpg0484	HflK protein (phage lambda CII protease?)	*hflK*	-0.30	2.13
lpg0485	HflC protein (phage lambda CII repressor?)	*hflC*	-0.26	2.92
lpg0486	adenylosuccinate synthetase	*purA*	0.25	3.97
lpg0490	arginine repressor (transcriptional regulator)	-	3.80	-1.08
lpg0491	amino acid (glutamine) ABC transporter, periplasmi	-	6.94	1.56
lpg0492	amino acid (glutamine) ABC transporter, permease	*yqiY*	6.20	-0.87
lpg0493	amino acid (glutamine) ABC transporter, ATP bindin	-	6.17	1.17
lpg0494	argininosuccinate synthase	*argG*	6.79	0.84
lpg0495	argininosuccinate lyase	*argH*	4.82	-0.28
lpg0496	ornithine carbamoyltransferase	*argF*	3.96	0.04
lpg0497	adenosine deaminase	-	2.20	1.87
lpg0499	carboxy-terminal protease	-	0.21	-2.30
lpg0503	undecaprenyl diphosphate synthetase (undecapren	*uppS*	-0.19	2.64
lpg0506	outer membrane protein (bacterial surface antigen f	-	-0.40	3.64
lpg0507	outer membrane protein OmpH	-	-0.04	2.70
lpg0508	UDP-3-O-(3-hydroxymyristoyl) glucosamine N-aclyt	*lpxD*	1.49	6.12
lpg0517	COG0656: aldo/keto reductases, related to diketogu	*ytbE*	2.57	2.14
lpg0518	ORF	-	2.06	0.95
lpg0525	unknown virulence protein	-	-0.97	-2.16
lpg0527	signal transduction protein (possible competence pr	-	-0.70	-2.57
lpg0533	dihydrolipoamide succinyltransferase (2-oxoglutara	*sucB*	2.36	1.59
lpg0536	pyridoxamine 5'-phosphate oxidase	*pdxH*	0.93	2.87
lpg0540	major facilitator family transporter (multidrug efflux t	-	1.47	2.02
lpg0541	protein product; similar to probable membrane prote	-	0.28	2.72
lpg0542	DNA binding protein Fis (recombinational enhancer	*fis*	-0.48	2.36
lpg0543	ribose-phosphate pyrophosphokinase (phosphoribo	*prsA*	0.34	2.13

lpg0548	phosphopantetheine adenylyltransferase (lipopolysa	*kdtB*	0.18	2.88
lpg0549	gamma-glutamyltranspeptidase	-	-2.04	1.70
lpg0550	hypothetical (FAD-dependent oxidoreductase)	-	-3.70	-6.31
lpg0562	hypothetical COG5394	-	2.21	2.21
lpg0563	ORF	-	2.90	-0.03
lpg0568	tyrosyl tRNA synthetase	*tyrS*	2.22	2.42
lpg0579	ORF	-	0.14	3.89
lpg0580	adenosine deaminase	*add*	1.19	3.18
lpg0584	hypothetical (phosphate transport regulator?)	-	1.24	2.71
lpg0585	conserved hypothetical protein	-	-0.93	-2.79
lpg0586	transcriptional regulator, alginate biosynthesis?	-	-0.39	-4.10
lpg0589	small ORF (128aa)	-	-2.10	-4.91
lpg0592	nitrogen regulatory P-II transcription regulator (nitro	*glnK*	2.19	2.18
lpg0594	ORF	-	-0.10	2.53
lpg0595	4-amino-4-deoxychorismate lyase (branched chain	-	0.20	3.62
lpg0597	2-acylglycerophosphoethanolamine acyltransferase	*aas*	-2.51	-0.27
lpg0608	hypothetical (SAM-dependent methyltransferase?)	-	-0.67	3.18
lpg0609	alanyl tRNA synthetase	*alaS*	4.19	3.81
lpg0610	major facilitator family transporter (multidrug efflux t	-	2.51	0.19
lpg0620	conserved hypothetical protein	-	-0.52	-4.52
lpg0621	SidA	*sidA*	2.44	0.58
lpg0622	transmembrane protein	-	-2.36	-1.79
lpg0623	hypothetical	-	-1.12	-3.04
lpg0625	expressed protein	-	-1.37	-4.19
lpg0626	DNA uptake/competence protein ComA (DNA interr	-	1.74	-2.14
lpg0627	type IV pilin (competence and adherence associate	*pilE3*	-0.34	-3.48
lpg0628	type IV fimbrial biogenesis PilY1-related protein	-	0.04	-2.03
lpg0629	Tfp pilus assembly protein PilX?	-	0.19	-3.04
lpg0631	type IV fimbrial biogenesis protein PilV	-	-1.19	-4.32
lpg0632	type IV pre-pilin (type IV fimbrial pilin; fimbrial bioge	-	-2.18	-5.40
lpg0633	polysaccharide deacetylase (peptidoglycan N-acety	-	-2.52	-1.40
lpg0645	partial RtxA	-	-0.84	-2.13
lpg0650	50S ribosomal protein L31	*rpmE*	0.38	3.80
lpg0653	major facilitator family transporter (multidrug efflux t	-	-1.27	3.19
lpg0663	soluble lytic murein transglycosylase	-	-3.20	-2.68
lpg0665	putative transmembrane protein COG 2259	-	-0.18	-3.77
lpg0666	conserved hypothetical protein	-	-2.05	-3.98
lpg0667	conserved hypothetical protein	-	-0.57	-4.57
lpg0668	bromodomain? protein-protein interactions? [overla	-	0.64	-3.03
lpg0669	hypothetical exported protein [overlaps (different fra	-	0.72	-3.85
lpg0670	hypothetical	-	-0.51	-4.07
lpg0671	NADH dehydrogenase transmembrane protein	*ndh*	-0.88	-5.43
lpg0672	acetoacetate decarboxylase (ADC)	-	-0.46	-3.82
lpg0681	lipoprotein, putative	-	-2.40	-2.44
lpg0695	hypothetical (inversin? alpha- or delta- latroinsectot	*legA8*	-0.93	-2.06
lpg0698	hypothetical (ATPase)	-	-1.21	2.84
lpg0699	outer membrane protein TolC (outer membrane cha	-	-0.63	3.43
lpg0700	protein-L-isoaspartate-O-methyltransferase	*pcm*	0.63	2.23

lpg0702	threonine(-3-)dehydrogenase	*tdh*	2.45	2.22
lpg0709	formiminoglutamase (arginase family protein)	-	0.49	2.14
lpg0713	oligopeptide transporter	-	-2.03	0.45
lpg0717	small ORF (153aa)	-	-0.56	-3.26
lpg0719	valyl tRNA synthase	*valS*	1.62	4.30
lpg0721	RND efflux membrane fusion protein (acriflavin resi	-	0.92	2.35
lpg0722	ORF hypothetical?	-	1.74	4.06
lpg0727	transcription termination factor NusB (nitrogen utiliz	*nusB*	-1.14	2.44
lpg0729	phosphatidylglycerophosphatase A (PgpA)	*pgpA*	0.66	-2.45
lpg0731	hypothetical protein	-	0.86	3.63
lpg0732	hypothetical protein	-	2.24	2.35
lpg0740	17kDa common antigen (17kDa surface antigen pre	*omp*	2.22	-0.50
lpg0741	inosine-5'-monophosphate dehydrogenase (IMP de	-	-0.91	-2.33
lpg0749	imidazole glycerol phosphate synthase, cyclase su	*hisF*	2.36	3.22
lpg0752	N-acetylneuraminic acid synthetase (N-acylneuram	*nnaB1*	-2.18	1.45
lpg0754	acetyltransferase (hexapeptide transferase) (serine	-	0.95	2.44
lpg0755	COG0399: Predicted pyridoxal phosphate-depende	*yvfE*	1.14	3.48
lpg0756	RmlC protein (dTDP-6-deoxy-D-glucose-3,5-epime	-	-2.14	0.12
lpg0758	dTDP-glucose 4,6-dehydratase RmlB	*rfbB*	-2.58	1.08
lpg0759	glucose-6-phosphate isomerase	*pgi*	-0.69	2.72
lpg0761	NAD dependent epimerase/dehydratase; UDP-gluc	-	-2.54	0.32
lpg0762	O-antigen initiating glycosyl transferase group 4-UD	-	-2.11	0.76
lpg0767	hypothetical	-	-2.59	-0.50
lpg0773	polysaccharide ABC transporter, ATP binding protei	-	-2.65	-0.42
lpg0774	hypothetical (Legionella pneumophila)	-	-2.75	-0.18
lpg0779	glycosyltransferase	-	-0.21	3.62
lpg0782	O-antigen acetylase (lipopolysaccharide modificatio	-	-2.16	-0.51
lpg0788	ORF	-	-2.09	1.58
lpg0790	L-serine dehydratase (iron, sulfur-dependent) (L-se	*sda-2*	2.06	1.29
lpg0792	beta lactamase induction signal transducer AmpG	*ampG*	-2.85	-0.81
lpg0797	tRNA-Met	-	-2.31	-0.29
lpg0801	adenylsuccinate lyase	-	0.34	3.23
lpg0810	small ORF (105aa) competence protein ComEA (D	-	0.27	2.91
lpg0821	lipopolysaccharide biosynthesis glycosyltransferase	-	1.54	5.20
lpg0827	agglutination protein, COG1538: membrane protein	*tolC*	0.65	2.62
lpg0831	flavin containing monooxygenae (dimethylaniline m	-	-0.02	2.93
lpg0841	toluene tolerance ABC transporter, ATP binding pro	-	-0.93	-2.60
lpg0843	toluene tolerance protein Ttg2C (mce related protei	-	-0.52	-2.99
lpg0847	UDP-N-acetylglucosamine 1-carboxyvinyltransferas	*murA*	-0.65	-2.02
lpg0848	conserved hypothetical protein TIGR00486	-	-1.24	-2.73
lpg0853	transcriptional regulator FleQ (polar flagellar protein	*fleQ*	-1.75	-2.81
lpg0854	ORF	-	-0.58	-2.58
lpg0855	signal peptide peptidase SppA (protease IV) (SohB	-	-0.94	2.72
lpg0858	heme exporter protein CcmC	*ccmC*	0.87	2.90
lpg0864	cytochrome c type biogenesis protein CcmH	*cycH*	3.81	4.41
lpg0869	3-hydroxyisobutyryl Coenzyme A hydrolase (croton	-	2.11	2.69
lpg0872	peptide chain release factor 3	*prfC*	-0.84	2.06
lpg0874	NAD(P) transhydrogenase (beta subunit)	*pntB*	0.01	-2.14

lpg0875	transmembrane NAD(P) transhydrogenase (alpha s	*pntAb2*	-0.33	-2.92
lpg0877	hypothetical transporter	-	2.99	2.09
lpg0878	small ORF (99aa)	-	-1.42	-5.48
lpg0891	sensory box protein/GGDEF/EAL domains	-	3.90	2.44
lpg0892	kynurenine 3-monooxygenase (kynurenine 3-hydro:	-	-0.46	-3.02
lpg0893	hypothetical	-	-2.74	-4.85
lpg0896	lipoprotein (enhanced entry protein EnhC?) COG07	-	2.10	2.44
lpg0901	hypothetical protein NMA0899	-	-1.87	-4.72
lpg0902	ORF	-	0.17	-4.71
lpg0906	hypothetical?	-	-0.13	-2.88
lpg0908	flagella basal body P-ring formation protein FlgA	-	-0.48	-2.41
lpg0922	electron transfer flavoprotein, beta subunit	*etfB*	-0.31	2.66
lpg0935	universal stress protein A (UspA)	-	-0.85	-3.26
lpg0940	LidA (translocated substrate of Dot/Icm system) (Us	*lidA*	0.99	-2.13
lpg0941	ORF	-	0.86	2.77
lpg0946	pyridoxal phosphate biosynthetic protein PdxJ (pyri	*pdxJ*	1.90	2.91
lpg0953	AMP-binding protein (long chain fatty acid-CoA liga:	-	-1.22	-3.40
lpg0963	ORF	-	2.09	-1.73
lpg0967	ORF	-	0.61	-2.87
lpg0968	ORF	-	2.66	-2.65
lpg0969	ORF	-	3.76	-2.06
lpg0976	antirestriction protein	-	2.42	0.64
lpg0977	single strand DNA binding protein (ssb)	-	0.79	2.54
lpg0987	membrane protein?	-	-0.35	-2.16
lpg1007	cation efflux system HelB (HlyD family secretion pro	-	-0.73	-2.62
lpg1011	uncharacterized conserved protein	-	-0.61	-4.54
lpg1012	small ORF (65aa)	-	0.39	-3.22
lpg1032	conserved hypothetical protein	-	-0.82	-2.99
lpg1035	copper efflux ATPase (copper resistance protein A)	*pcoA*	2.63	3.84
lpg1048	ATP synthase F1, subunit alpha (F0F1-type ATP sy	-	2.61	-0.76
lpg1055	hypothetical protein	-	-0.37	-2.31
lpg1060	cold shock domain family protein, COG1278: cold s	-	2.16	2.05
lpg1067	small ORF (85aa)	-	-0.09	-3.75
lpg1070	integrase (phage related)	*int*	2.14	2.40
lpg1080	deoxyguanosine triphosphate triphosphohydrolase	-	1.73	-3.53
lpg1084	hypothetical (cytosolic protein)	-	2.12	0.42
lpg1094	chemiosmotic efflux system B protein C (outer mem	-	-1.14	-2.90
lpg1098	small ORF (63aa)?	-	-0.32	-4.57
lpg1112	small ORF (127aa)	-	0.86	-3.97
lpg1113	hypothetical	-	-0.77	-3.39
lpg1115	DNA integration/recombination/inversion protein (ci	*kaiC2*	1.74	-3.11
lpg1116	chitinase (exochitinase) aminosugars metabolism?	-	2.40	-0.94
lpg1117	small ORF (157aa) transcriptional repressor of spor	*paiA*	0.83	-2.50
lpg1118	serine-type D-Ala-D-Ala carboxypeptidase (D-alany	-	1.49	-2.45
lpg1120	hypothetical protein	-	-0.54	3.04
lpg1127	acyl CoA synthetase, long chain fatty acid:CoA ligas	-	-1.68	-4.20
lpg1131	cyclopropane fatty acid synthase (cyclopropane fatt	*cfa*	0.03	-2.06
lpg1134	nitropropane dioxygenase/(trans-enoyl-CoA reducta	-	0.12	-2.97

lpg1138	spermidine/putrescine-binding periplasmic protein F	-	-3.15	-0.75
lpg1141	spermidine/putrescine ABC transporter, ATP-bindin	-	-5.45	0.40
lpg1143	short chain type dehydrogenase/reductase (retinol	-	-1.17	-4.54
lpg1144	ORF	*cegC3*	2.07	0.11
lpg1145	ORF	-	0.54	-4.32
lpg1148	ORF	-	1.15	-2.31
lpg1151	ORF	-	-1.27	-2.47
lpg1154	ORF	-	1.29	-5.34
lpg1157	lipase B (conserved hypothetical protein-putative AT	-	-2.54	-2.45
lpg1161	phosphoribosyltransferase	-	-0.87	-3.23
lpg1167	hypothetical (cytoplasmic protein)	-	-2.49	1.23
lpg1177	riboflavin biosynthesis protein RibD	*ribD*	1.37	3.60
lpg1183	ORF	-	1.75	-2.29
lpg1186	competence lipoprotein ComL	-	1.12	2.37
lpg1188	Kup system potassium uptake protein	*kup2*	0.51	2.81
lpg1193	phosphoribosyl-ATP pyrophosphatase/phosphoribo	*hisI*	0.94	2.44
lpg1194	imidazoleglycerol-phosphate synthase, cyclase sub	-	2.46	2.59
lpg1204	orotate phosphoribosyltransferase	*pyrE*	1.21	2.14
lpg1206	sigma 54 modulation protein YhbH	-	0.64	-5.04
lpg1207	conserved hypothetical protein COG2606	-	-0.37	-4.69
lpg1210	acetyltransferase (ribosomal-protein alanine acetylt	-	-0.10	2.37
lpg1218	flagellar basal body rod modification protein FlgD	*flgD*	0.73	-3.47
lpg1221	flagellar basal body rod protein FlgG	*flgG*	0.04	-3.10
lpg1223	flagellar P-ring protein (precursor) FlgI	*flgI*	-0.28	-2.12
lpg1226	flagellar hook associated protein type 3 FlgL	*flgL*	-0.52	-3.13
lpg1228	hypothetical COG4804	-	0.17	2.11
lpg1230	hypothetical	-	3.64	1.24
lpg1234	hypothetical	-	-0.61	-2.87
lpg1237	type II restriction enzyme (Eco47II, Sau96I)	-	1.16	4.59
lpg1249	LvhB8 (conjugal transfer protein)	*virB8*	2.21	-1.18
lpg1258	LvrB	*lvrB*	4.38	2.93
lpg1260	phage repressor (putative repressor protein of prop	*prpA*	1.77	3.64
lpg1270	small ORF (152aa)	-	0.59	3.91
lpg1274	hypothetical	-	-3.31	-6.60
lpg1279	small ORF (123aa) hypothetical	-	-0.43	-2.49
lpg1280	malate oxidoreductase (NAD linked malic enzyme)	*sfcA*	0.67	2.98
lpg1285	homogentisate 1,2-dioxygenase (homogentisicase)	-	1.57	2.46
lpg1290	hypothetical protein	-	-0.45	-3.65
lpg1292	DNA-binding response regulator (two component)	-	-0.94	-2.14
lpg1293	intracellular septation protein A	*ispZ*	-1.85	-2.60
lpg1298	small ORF (65aa) weak eukaryotic hits?	-	-0.80	-3.83
lpg1303	phosphoribosyl anthranilate isomerase (N-5'-phosp	*trpF*	-0.25	2.31
lpg1305	tryptophan synthetase (alpha chain) TrpA	*trpA*	-0.84	3.10
lpg1307	cysteinyl-tRNA synthetase	*cysS*	-0.66	2.22
lpg1309	small ORF (104aa)	-	2.25	0.79
lpg1318	ORF	-	-1.07	-6.10
lpg1338	flagellar hook associated protein 2 (flagellar cap pr	*fliD*	-0.07	-3.83
lpg1346	DNA polymerase III, delta subunit	*holA*	0.18	3.02

lpg1348	leucyl tRNA synthetase	*leuS*	-0.04	3.34
lpg1355	SidG, LepC, Vng0394c	*sidG*	-1.70	-5.52
lpg1356	TPR repeat protein (enhanced entry protein EnhC)	-	0.08	-2.82
lpg1363	type II protein secretion LspF (general secretion pat	*gspF*	0.49	2.00
lpg1364	glutamine synthetase, type I (glutamate-ammonia l	*glnA*	2.54	2.50
lpg1368	ORF	-	0.13	-5.27
lpg1370	small ORF (98aa) DNA binding protein Fis (recomb	*fis*	-0.98	-2.76
lpg1374	rod shape determining protein RodA	*rodA*	-0.70	-2.67
lpg1376	hypothetical COG1576	-	-2.18	-0.60
lpg1377	hypothetical COG0799	-	-1.29	-2.92
lpg1385	small ORF (125aa)	-	-0.33	-5.23
lpg1386	enhanced entry protein EnhA (ErfK/YbiS/YcfS/Ynh	-	-0.89	-4.98
lpg1387	ORF	-	-0.50	-4.33
lpg1391	50S ribosomal protein L32	*rpmF*	0.32	2.13
lpg1396	acyl carrier protein (ACP)	*acpP*	0.07	2.50
lpg1398	aminodeoxychorismate lyase (thymidylate kinase?)	-	-3.93	-1.64
lpg1401	type 4 fimbrial biogenesis protein PilZ	*pilZ*	-1.44	-2.07
lpg1406	glycosyltransferase (dolichol phosphate mannosyltr	-	-3.31	-1.52
lpg1418	3-phosphoserine aminotransferase (phosphoserine	*serC*	-2.58	-0.66
lpg1419	3-phosphoshikimate 1-carboxyvinyltransferase (5-e	-	-2.04	1.86
lpg1420	cytidylate kinase	*cmk*	-0.93	3.74
lpg1425	orotidine 5'-phosphate decarboxylase PyrF	*pyrF*	-2.33	1.74
lpg1426	hypothetical (serine protease?)	*vpdC*	-2.62	-1.07
lpg1427	short chain dehydrogenase (3-oxoacyl [acyl carrier	-	-2.40	-2.36
lpg1428	competence comG operon protein?, type 4 fimbrial	-	-2.08	-2.82
lpg1438	transcriptional regulatory protein CpxR (DNA bindin	*cpxR*	-2.43	-2.57
lpg1439	Mg2+ and Co2+ transporter CorC (metal ion transp	-	-2.94	-4.11
lpg1440	metal dependent hydrolase	-	-2.10	-1.57
lpg1441	phosphate starvation-inducible protein PhoH (ATP	-	-1.33	-2.14
lpg1442	metal dependent phosphoesterase (PHP family)	-	-0.40	2.44
lpg1446	hypothetical (transcriptional regulator) TIGR00281	-	-2.10	-1.27
lpg1455	phospholipase C (phosphatidylcholine hydrolyzing)	-	-1.14	-4.27
lpg1460	conserved hypothetical protein	-	-1.07	2.37
lpg1464	NTP pyrophosphohydrolase (mutator protein MutT)	-	-2.02	-0.57
lpg1468	small ORF (157aa)	-	2.06	-0.97
lpg1476	hypothetical (type I antifreeze protein?) COG2331	-	1.30	2.07
lpg1482	ORF	-	2.27	1.00
lpg1484	ORF	-	2.44	2.05
lpg1490	adenylate cyclase PLUS two component hybrid sen	*cyaA*	-1.28	-5.06
lpg1491	ORF	-	0.14	-3.11
lpg1495	small ORF (97aa)	-	2.26	-2.04
lpg1496	ORF	-	-0.36	-5.65
lpg1497	aminopeptidase N	*pepN*	-0.99	-4.10
lpg1501	GCN5-related N-acetyltransferase (ribosomal prote	-	-2.15	-1.75
lpg1510	D-alanine-aminotransferase (D-aspartate aminotran	-	-2.91	1.15
lpg1512	DedA/PAP2 domain protein (integral membrane pro	-	-2.75	-0.44
lpg1515	toxin secretion ATP binding protein (ABC-type bact	-	-2.01	-3.99
lpg1516	ABC transporter, ATP binding/permease fusion prot	-	-2.72	-2.82

lpg1517	HlyD family secretion protein (hemoloysin) (type I se	-	-2.38	-2.73
lpg1518	sensory box protein/GGDEF domain/EAL domain (t	-	-1.22	-3.77
lpg1520	uncharacterized conserved hypothetical protein CO	-	-0.56	2.17
lpg1522	(type IV) pilus assembly protein PilB	*pilB*	-1.22	-4.13
lpg1523	(type IV) pilus assembly protein PilC (bacterial type	*pilC*	-1.12	-3.52
lpg1524	type 4 (IV) prepilin-like protein leader peptide proce	*pilD*	-1.63	-2.27
lpg1526	ORF	-	-1.45	-2.65
lpg1529	2-methylcitrate dehydratase PrpD	*prpD*	2.93	3.77
lpg1538	poly(A) polymerase I (tRNA nucleotidyltransferase/p	*pcnB*	-4.52	-0.99
lpg1541	GTP-binding protein EngA	*engA*	0.10	2.94
lpg1548	nucleoside diphosphate kinase	*ndk*	0.70	3.75
lpg1551	ORF	-	0.77	-2.90
lpg1552	UDP-2,3-diacylglucosamine hydrolase	-	-2.18	0.82
lpg1564	membrane protein (nodulin 21?)	-	-1.30	-2.64
lpg1577	RNA polymerase sigma E factor RpoE (RNA polym	*rpoE*	-1.50	-4.93
lpg1578	small ORF (149aa)	-	-2.78	-0.55
lpg1580	cytochrome b-561 transmembrane protein	-	-2.21	-2.72
lpg1586	small ORF (125aa)	-	-2.07	-2.29
lpg1591	30S ribosomal protein S18	*rpsR*	-0.49	2.47
lpg1592	30S ribosomal protein S6	*rpsF*	-0.19	3.49
lpg1605	hypothetical	-	3.33	1.05
lpg1613	acetyltransferase, GNAT family	-	2.35	1.96
lpg1614	glutamate rich protein GrpB	*yqkA*	2.16	-0.72
lpg1622	ORF	-	-1.12	-2.13
lpg1623	hydrogenase	-	1.58	3.36
lpg1631	chalcone and stilbene synthases (3-oxoacyl[ACP]sy	-	2.35	0.57
lpg1635	dienelactone hydrolase	-	-1.64	-4.48
lpg1636	acetyltransferase, GNAT family (GCN5-related N-ac	-	-0.51	-3.51
lpg1637	polysaccharide deacetylase (chitooligosaccharide d	-	0.99	-2.10
lpg1639	ORF	-	-1.12	-4.71
lpg1644	ORF	-	-1.02	-2.47
lpg1646	cytochrome b561 transmembrane protein (secretory	-	-0.69	-2.58
lpg1647	hypothetical (exported protein)	-	-1.64	-3.39
lpg1648	signal peptide protein (integral membrane or export	-	-1.12	-4.23
lpg1655	class 4 metalloprotease (zinc metalloprotease) (viru	*lasB*	-1.45	-2.10
lpg1659	membrane protein	-	-1.20	-3.03
lpg1664	penicillin binding protein 1C, peptidoglycan biosynth	-	1.56	2.51
lpg1667	conserved hypothetical protein	-	-1.06	-2.92
lpg1669	alpha-amylase, putative	-	1.27	-5.30
lpg1670	ORF	-	1.52	-3.21
lpg1672	phosphoribosylglycinamide formyltransferase (phos	-	-2.14	-1.75
lpg1673	phosphoribosylamine-glycine ligase (GARS) (glycin	-	-1.11	-2.30
lpg1675	phosphoribosylimidazole-succinocarboxamide synth	-	-2.04	-1.18
lpg1680	thiol:disulfide interchange protein DsbD	*dsbD*	0.97	-2.48
lpg1684	ORF	-	2.60	-0.70
lpg1695	transposase IS630 family	-	1.20	2.57
lpg1698	(ProQ, activator of ProP osmoprotectant transporte	-	1.45	2.32
lpg1699	3-demethylubiquinone-9 3-methyltransferase UbiG	*ubiG*	0.81	2.43

lpg1702	Tpr	-	2.04	-2.27
lpg1713	translation elongation factor Ts (EF-Ts) (ubiquitin as	*tsf*	-0.44	2.50
lpg1714	30S ribosomal protein S2	*rpsB*	0.36	3.59
lpg1718	huntingtin interacting protein B	*legAS4*	2.16	-0.96
lpg1719	methionine aminopeptidase	*map*	-0.27	2.75
lpg1721	deaminase (zinc binding protein) (zinc binding hydr	*yfhC*	-0.59	-2.14
lpg1726	oxidoreductase, acyl CoA dehydrogenase family (a	*yafH*	-0.23	-2.15
lpg1727	hydrolase	-	-2.11	0.86
lpg1738	ORF	-	-0.26	2.29
lpg1743	Fis transcriptional activator (factor for inversion stim	*fis*	2.55	1.49
lpg1751	ORF	-	3.05	1.54
lpg1755	transmembrane protein (protease?)	-	-2.57	0.75
lpg1765	outer membrane lipoprotein carrier protein (periplas	*lolA*	0.17	-2.69
lpg1778	peptide chain release factor 2 (RF-2)	*prfB*	0.63	2.40
lpg1779	hypothetical	-	-0.92	-2.43
lpg1781	flagellar motor protein MotA (chemotaxis MotA prote	*motA*	-0.82	-4.33
lpg1782	flagellar biosynthesis sigma factor FliA (motility sign	*fliA*	-0.27	-4.95
lpg1783	flagellar biosynthesis MinD (septum-site determinin	-	-0.30	-2.27
lpg1784	flagellar GTP-binding protein FlhF (flagellar biosynt	-	-0.05	-4.24
lpg1787	flagellar biosynthetic protein FliR	*fliR*	-0.38	-3.23
lpg1796	transcriptional regulator, LysR family	-	-1.86	-3.19
lpg1811	aspartokinase (aspartate kinase, lysine sensitive)	*lysC*	1.73	3.48
lpg1812	ATP-dependent DNA helicase (UvrD/Rep helicase)	-	-2.31	0.63
lpg1819	ABC transporter, ATP binding/permease protein Ms	-	-2.31	1.43
lpg1836	coiled coil domain protein	*ceg25*	2.21	0.72
lpg1839	glycyl tRNA synthetase, beta subunit	*glyS*	-1.00	2.55
lpg1840	glycyl tRNA synthetase, alpha subunit	*glyQ*	-0.38	2.46
lpg1845	lipoprotein VacJ, peptidoglycan stabilization, virulen	*vacJ*	-0.27	2.07
lpg1852	alkaline phosphatase (alkaline phosphomonoestera	-	1.44	4.07
lpg1853	uridine kinase (uridine/cytidine kinase)	*udk*	-0.54	3.52
lpg1862	trigger factor TF (FKBP-type peptidyl prolyl cis-trans	*tig*	-0.41	2.20
lpg1865	tRNA-Arg	-	-2.88	-0.12
lpg1869	ribonuclease III (dsRNA-specific ribonuclease) (RN	*rnc*	-2.83	-0.47
lpg1876	ORF	-	-0.82	-5.65
lpg1884	Microtubule binding protein, putative	*legC2/ylfB*	-1.57	-2.20
lpg1887	ORF	-	0.58	-3.10
lpg1889	lipase (triacyglycerol lipase)	-	-0.19	-4.00
lpg1890	galA protein 1	*legLC8*	3.45	0.45
lpg1891	hypothetical protein HI1736	-	-0.13	-2.14
lpg1893	major facilitator family transporter (multidrug efflux t	-	0.50	2.56
lpg1898	methanol dehydrogenase regulatory protein (MoxR	-	-1.22	-2.99
lpg1899	transmembrane protein	-	-0.49	-3.03
lpg1901	conserved hypothetical protein	-	0.54	2.37
lpg1903	hydrolase (esterase/lipase/thioesterase)	-	0.74	-4.76
lpg1905	ectonucleoside triphosphate diphosphohydrolase I (	-	2.19	2.93
lpg1911	glutamate tRNA synthetase catalytic subunit (glutan	*gltX*	-0.14	2.53
lpg1914	fimbrial protein, type IV pilin, PilE	*pilE*	-0.71	-4.22
lpg1915	Tfp pilus assembly protein, major type IV pilin class	*pilE*	-0.16	-3.98

lpg1918	ORF	-	2.59	-1.21
lpg1922	ATP dependent DNA helicase (DEAD box family) R	-	2.64	1.57
lpg1926	hypothetical protein	-	-0.40	-4.44
lpg1948	FLJ00180 protein	*legLC4*	3.29	-0.56
lpg1949	hypothetical protein	-	-1.43	-2.85
lpg1950	guanine nucleotide exchange protein (RalF) (ADP r	*ralF*	-0.29	-2.96
lpg1955	hypothetical (gluconate permease?) (transport prote	-	1.40	2.93
lpg1956	chloromuconate cycloisomerase (mandelate racem	-	1.56	3.43
lpg1960	ORF	-	0.91	-4.15
lpg1963	hypothetical protein	-	-1.56	-5.22
lpg1972	small ORF (125aa)	-	3.08	-0.32
lpg1976	UVB-resistance protein UVR8	*legG1*	3.77	0.43
lpg1981	small ORF (98aa)	-	2.05	2.37
lpg1988	dihydrofolate reductase	-	0.82	2.46
lpg1993	polysaccharide deacetylase	-	-1.52	-4.13
lpg1997	small ORF (104aa)	-	-0.85	2.54
lpg2001	protein export protein SecD (preprotein translocase	*secD*	-0.67	3.33
lpg2002	transmembrane protein YajC, preprotein translocas	*yajC*	-0.22	2.09
lpg2006	ABC transporter ATP binding protein	*uup-A*	0.65	2.07
lpg2012	ribonuclease PH (RNAse PH)	*rph*	0.76	2.23
lpg2016	hypothetical (YGGT family protein) (transmembrane	-	0.52	2.54
lpg2017	ORF	-	-0.18	-2.26
lpg2018	hypothetical protein	-	-1.59	-2.14
lpg2029	dihydroneopterin aldolase FolB, kinase? COG1539	-	2.03	0.93
lpg2031	arginyl tRNA synthetase	*argS*	0.91	2.84
lpg2036	Maf-like protein (septum formation) (nucleotide binc	-	-3.02	0.55
lpg2046	ABC transporter, ATP binding protein	-	0.61	2.14
lpg2051	isopentenyl-diphosphate delta-isomerase (IPP isom	-	0.91	2.70
lpg2054	tRNA-Lys	-	-0.15	2.52
lpg2057	Prophage dlp12 integrase (prophage qsr' integrase)	*intD*	-0.91	-2.12
lpg2106	conserved hypothetical protein	-	-2.81	0.74
lpg2113	ATP dependent DNA helicase?	*recG*	-0.57	-2.87
lpg2121	cold shock DNA binding domain protein (cold shock	-	-4.92	-2.31
lpg2123	cobalt zinc cadmium cation transporter (membrane	-	-1.19	-2.80
lpg2125	small ORF (153aa) transmembrane transport protei	-	-0.25	-2.13
lpg2127	hypothetical COG3034	-	2.69	-1.78
lpg2128	ORF	-	0.56	3.85
lpg2138	transcriptional regulator, LysR family	-	-0.41	-2.75
lpg2143	ORF	-	-0.81	-2.92
lpg2144	F-box protein?	*legAU13*	0.53	-3.11
lpg2147	ORF	-	-0.68	-3.56
lpg2149	ORF	-	1.32	-2.84
lpg2153	SdeC, SdeB, AliA, SdeA, SdeD homology	*sdeC*	0.76	-2.90
lpg2154	SdeC, SdeB, AliA, SdeA, SdeD homology	-	4.48	0.45
lpg2155	ORF	*sidJ*	-0.80	-2.84
lpg2157	SdeA, IMH1; Encodes a protein implicated in protei	*sdeA*	0.17	-3.27
lpg2160	ORF	-	2.28	2.44
lpg2166	hypothetical protein	-	1.67	3.47

lpg2171	hypothetical conserved protein	-	2.71	1.37
lpg2174	tRNA-Lys	-	1.59	3.60
lpg2175	(2-pyrone-4,6-)dicarboxylic acid hydrolase	-	0.08	-2.97
lpg2176	sphingosine-1-phosphate lyase I (group II decarbox	*legS2*	-1.18	3.77
lpg2177	HlyD family secretion protein (RND multidfug efflux	-	-0.93	-3.14
lpg2180	sensory box histidine kinase/response regulator (ae	-	-0.64	-3.20
lpg2181	sensory box sensor histidine kinase/response regul	-	0.15	-5.60
lpg2185	small ORF (102aa)	-	2.16	1.14
lpg2187	small ORF (133aa)	-	-0.08	-3.44
lpg2191	global stress protein GspA (heat shock protein 16 k	*ib*	0.40	-2.29
lpg2199	ORF	-	2.72	1.03
lpg2201	replication factor C subunit (activator I)	-	-0.42	-2.49
lpg2209	hypothetical (phosphatidylethanolamine-binding prc	-	-1.07	-5.52
lpg2213	hemin binding protein Hbp	-	0.69	2.84
lpg2216	purine NTPase, putative	-	0.20	-2.38
lpg2222	TPR repeat protein, protein-protein interaction	-	2.28	-3.97
lpg2233	acyl carrier protein	-	0.43	2.10
lpg2239	ORF	-	-2.72	-4.28
lpg2245	C4-dicarboxylate transport protein (Na+/H+ dicarbo	*dctA*	2.27	-1.28
lpg2246	ORF	-	2.46	-4.96
lpg2255	ORF	-	-0.34	-2.80
lpg2258	small ORF (96aa) hypothetical	-	-0.87	-2.66
lpg2268	ORF	-	-0.59	-3.99
lpg2277	O-methyltransferase, SAM-dependent	-	0.90	2.22
lpg2282	asparaginyl tRNA synthetase	*asnS*	-0.09	3.16
lpg2284	ABC transporter, ATP binding protein (lipoprotein re	-	1.37	3.30
lpg2285	lipoprotein ABC transporter (permease) (lipoprotein	-	1.14	2.78
lpg2292	tRNA-Gly	-	-2.73	-0.25
lpg2296	ORF	-	-2.53	3.08
lpg2297	ribonuclease E	*rne*	2.32	0.05
lpg2298	inclusion membrane protein A	*legC7/yifA*	-0.50	3.00
lpg2302	aspartate semialdehyde dehydrogenase	*asd*	2.38	1.09
lpg2304	adenine specific methylase	-	1.74	3.54
lpg2310	glutamate racemase	*murI*	-0.43	-3.33
lpg2312	small ORF (100aa)	-	1.00	-3.50
lpg2316	3-hydroxybutyrate dehydrogenase (D-beta hydroxyl	*bdhA*	0.01	-3.44
lpg2317	transmembrane protein	-	-0.44	-3.89
lpg2318	chemotaxis (motility protein A) transmembrane (pro	*motA*	-1.02	-2.62
lpg2321	serine transporter	*sdaC*	1.96	2.26
lpg2323	type II secretion system protein (twitching motility pı	*uptC*	-0.07	-4.38
lpg2327	CG18304 gene product	-	1.53	-4.36
lpg2330	geranyltranstransferase (farnesyl-diphosphate syntl	*ispA*	-0.40	3.27
lpg2334	ORF	-	-0.30	-3.81
lpg2339	ORF	-	-2.54	0.17
lpg2344	ORF	-	4.00	6.78
lpg2348	superoxide dismutase (copper-zinc)	*sodC*	-0.14	-2.86
lpg2351	ORF	-	-0.93	-4.23
lpg2358	30S ribosomal protein S21	*rpsU*	-0.77	3.68

lpg2359	conserved hypothetical protein	-	-0.68	2.74
lpg2376	transcriptional regulator, LysR family	-	-0.76	-3.02
lpg2385	hypothetical protein	-	-0.19	-3.13
lpg2393	bacterioferritin (cytochrome b1)	-	-1.55	-3.79
lpg2395	ORF	-	2.36	-4.95
lpg2398	aminoglycoside 6'-N-acetyltransferase	-	-2.18	-2.52
lpg2399	unknown virulence protein	-	-0.61	-4.51
lpg2409	ORF	*ceg29*	2.99	1.38
lpg2410	hypothetical (serine protease?) (membrane spannir	*vpdA*	1.76	-2.33
lpg2411	ORF	-	3.51	2.76
lpg2413	small ORF (145aa)	-	1.20	-2.90
lpg2415	transmembrane protein	-	-0.41	-4.21
lpg2416	ankyrin repeat containing protein?	*legA1*	-0.58	-2.11
lpg2417	ORF	-	-2.63	1.39
lpg2420	ORF	-	0.28	2.03
lpg2424	ORF	-	1.65	-2.43
lpg2427	acetyl coenzyme A carboxylase, carboxyltransferas	*mdcB*	-0.61	-3.13
lpg2428	malonate decarboxylase gamma subunit	*mdcC*	-1.04	-4.21
lpg2429	ORF (MdcE? malonate decarboxylase?)	*mdcG*	-0.11	-3.98
lpg2430	2-(5-triphosphoribosyl)-3'-dephosphocoenzyme A sy	*mdcB*	-2.52	-2.99
lpg2435	ORF	-	-0.81	-2.41
lpg2436	small ORF (126aa)	-	-1.58	-2.07
lpg2441	DNA binding protein (3-demethylubiquinone-9 3-me	-	-1.17	-2.56
lpg2444	ORF	-	2.11	-3.05
lpg2445	161aa ORF (serpentine receptor Sre?)	-	-2.35	0.16
lpg2451	putative N-hydroxyarylamine O-acetyltransferase	-	2.23	2.00
lpg2455	ORF	-	2.08	2.37
lpg2458	sensory box histidine kinase (two-component senso	-	-0.20	-2.11
lpg2460	hypothetical	-	2.45	-0.39
lpg2464	ORF	*sidM/drrA*	1.67	-2.42
lpg2465	SidD	*sidD*	3.61	-0.47
lpg2466	hydrogenase expression/formation protein (F420-no	*vhtD*	-0.72	-2.83
lpg2472	hydrogenase expression/formation protein HypD	*hypD*	-2.19	2.72
lpg2476	hydrogenase nickel incorporation protein HypA	*hypA*	0.80	2.58
lpg2486	phosphomannomutase	-	-0.35	3.96
lpg2488	phosphopantothenoylcysteine decarboxylase/phosp	-	2.04	1.72
lpg2490	LepB, non-muscle myosin heavy chain B (endosom	*lepB*	0.57	2.39
lpg2492	alcohol dehydrogenase	-	-1.48	-3.31
lpg2493	small heat shock protein HspC2 (molecular chapero	-	0.34	-6.53
lpg2499	lysine decarboxylase	-	-0.98	-2.13
lpg2500	carbonic anhydrase Mig5	-	0.18	-3.59
lpg2508	ORF	*sdjA*	3.11	-1.08
lpg2509	SdeD	*sdeA*	4.95	-0.24
lpg2510	SdcA	*sdcA*	1.46	-3.13
lpg2511	SidC, interaptin	*sidC*	2.30	-4.51
lpg2516	major facilitator family transporter (sugar transport,	-	2.26	1.28
lpg2525	ORF	-	-2.08	-0.92
lpg2526	ORF	-	2.36	0.07

lpg2527	contains coiled coil domain	-	0.56	-5.07
lpg2528	alpha-amylase, putative	-	0.70	-2.95
lpg2530	3-deoxy-D-arabino-heptulosonate 7-phosphate (DA	*aroF*	4.00	1.17
lpg2531	chorismate mutase/prephenate dehydratase (P-pro	-	5.00	1.29
lpg2532	aspartate aminotransferase (PLP-dependent amino	-	5.11	1.72
lpg2537	5-carboxyvanillate decarboxylase (2-amino-3-carbo	-	-0.09	-2.45
lpg2538	ORF	-	-0.10	2.06
lpg2545	small ORF (96aa)	-	-1.11	-2.37
lpg2552	ORF	-	-0.11	2.17
lpg2559	ATP-dependent DNA helicase	*recG*	-2.47	-0.60
lpg2568	hypothetical	-	0.77	-2.09
lpg2572	ORF	-	-2.14	-2.96
lpg2576	uroporphyrin-III C-methyltransferase?	-	-2.33	-1.14
lpg2578	hypothetical? (84aa ORF)	-	-1.06	-2.41
lpg2582	conserved hypothetical protein	-	-1.22	-2.30
lpg2586	cysteine protease (papain C1 family)	-	2.40	-0.29
lpg2587	probable thermolabile hemolysin	-	1.05	-3.14
lpg2589	D-alanyl-D-alanine carboxypeptidase, fraction B; pe	*dacB*	-0.07	2.46
lpg2593	rRNA methyltransferase (SUN protein)	-	-2.29	0.12
lpg2594	methionyl tRNA formyltransferase	*fmt*	-1.41	2.46
lpg2597	DNA processing enzyme DprA (SMF family) (Rossn	-	-1.22	-2.50
lpg2598	small ORF (138aa)	-	0.22	2.55
lpg2603	ORF	-	0.98	-4.41
lpg2605	conserved hypothetical protein	-	-1.17	-2.27
lpg2606	glutamine amidotransferase	-	-0.26	-2.24
lpg2618	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diam	*murF*	0.28	2.65
lpg2621	acid phosphatase, class B (vegetative storage prote	-	1.98	2.59
lpg2626	ORF	-	-0.48	-3.03
lpg2631	aminopeptidase A/I (leucine aminopeptidase)	*pepA*	0.29	3.41
lpg2633	hypothetical protein	-	1.49	2.38
lpg2637	ORF	-	0.96	2.60
lpg2639	enhanced entry protein EnhC	*enhC*	0.28	-2.67
lpg2640	enhanced entry protein EnhB	*enhB*	0.74	-3.52
lpg2641	enhanced entry protein EnhA	*enhA*	0.67	-3.07
lpg2644	tail fiber protein (collagen-like protein SclB)	*sclB*	0.57	2.49
lpg2645	excinuclease ABC subunit	*uvrC*	-2.12	-0.11
lpg2650	50S ribosomal protein L27	*rpmA*	0.32	3.18
lpg2651	50S ribosomal protein L21	*rplU*	0.22	4.65
lpg2655	sensory box protein (cGMP turnover?)	-	-0.67	-2.26
lpg2659	ATPase N2B (nucleotide (GTP) binding protein), CC	-	0.17	2.06
lpg2661	3-methyl-2-oxobutanoate hydroxymethyltransferase	*panB*	-0.81	2.84
lpg2662	pantoate-beta-alanine ligase (pantothenate synthet	*panC*	-0.58	3.08
lpg2666	probable hydrolase	-	0.32	-3.11
lpg2677	5'-nucleotidase	-	-2.02	-0.87
lpg2693	hypothetical (SmtA SAM-dependent methyltransfera	-	-1.45	-2.30
lpg2701	stringent starvation protein B COG2969	*sspB*	-0.24	2.82
lpg2702	stringent starvation protein A (transcription activator	*sspA*	0.77	3.74
lpg2713	translational initiation factor IF-3	*infC*	0.47	2.27

lpg2715	tRNA-Val	-	-3.11	-0.73
lpg2719	conserved hypothetical protein	-	-1.00	-3.89
lpg2720	hypothetical protein	-	-1.18	-6.16
lpg2723	transcriptional regulator (ArsR family)	-	-2.45	-0.71
lpg2725	inner membrane protein	-	3.64	2.84
lpg2726	peptidylprolyl cis-trans isomerase B (cyclophilin-typ	*ppiB*	-2.41	-0.43
lpg2733	hypothetical (transmembrane protein)	-	0.30	-2.41
lpg2735	porphobilinogen deaminase (hydroxymethylbilane s	-	0.46	2.10
lpg2764	inorganic pyrophosphatase	*ppa*	0.52	3.04
lpg2765	HIT family hydrolase (e.g., diadenosine tetraphosph	*hit*	0.27	3.27
lpg2768	polyribonucleotide nucleotidyltransferase (polynucle	*PNP*	-2.08	3.86
lpg2770	tRNA pseudouridine synthase B	-	-2.14	0.40
lpg2778	NADH dehydrogenase I, L subunit (NADH-ubiquino	*nuoL*	-2.01	1.06
lpg2786	NADH dehydrogenase I, D subunit (NADH-ubiquin	*nuoD*	-0.65	2.45
lpg2792	triosephosphate isomerase (TIM)	*tpiA*	0.41	3.90
lpg2793	LepA, interaptin	*lepA*	2.10	-0.75
lpg2795	7,8-dihydropteroate synthase	-	-2.65	-0.20
lpg2803	ORF	-	-1.62	-5.14
lpg2809	aminopeptidase N	*pepN*	1.08	2.22
lpg2815	ORF	-	0.66	2.67
lpg2818	conserved hypothetical protein	-	-0.38	-2.78
lpg2820	aldo/keto reductase (oxidoreductase)	-	-0.10	-2.08
lpg2822	virulence regulator BipA (GTP binding protein type	*bipA*	0.56	2.02
lpg2823	sugar kinase (inorganic polyphosphate/ATP-NAD ki	-	-0.30	2.53
lpg2829	SidH (myosin-like protein)	*sidH*	-3.07	-5.16
lpg2832	hypothetical	-	-3.56	-0.77
lpg2837	lysophospholipase A (GDSL-motif lipase/hydrolase	-	-1.13	-3.49
lpg2839	SsrA (tmRNA) binding protein (small protein B), pro	*smpB*	-0.92	2.69
lpg2840	AhpC/TSA family protein (bacterioferritin comigrato	-	0.19	2.03
lpg2844	proteophosphoglycan, membrane associated (muci	-	0.20	-2.30
lpg2849	hypothetical (bacteriophage glycoprotein?)	-	-0.76	-2.45
lpg2852	amidase (6-aminohexanoate-cyclic dimer hydrolase	*amic*	-1.33	-2.48
lpg2855	TPR (repeat) domain protein, protein-protein interac	-	-2.04	0.26
lpg2862	ORF	*legC8*	1.14	-5.63
lpg2864	conserved hypothetical protein	-	-0.27	2.64
lpg2876	arsenite efflux protein (arsenite permease, arsenite	-	0.03	2.47
lpg2882	methionyl tRNA synthetase	*metG_1*	-0.89	2.72
lpg2888	ORF	-	1.08	-2.51
lpg2900	CapM protein, capsular polysaccharide biosynthesi	*capM2*	-0.24	2.82
lpg2907	ORF	-	1.53	-2.06
lpg2918	lytic murein transglycosylase (membrane bound)	-	0.97	-2.10
lpg2919	(serine-type) D-alanyl-D-alanine carboxypeptidase	-	-0.77	-3.76
lpg2929	aspartate-1-decarboxylase (L-aspartate-alpha-deca	*panD*	1.63	2.50
lpg2930	sec-independent (periplasmic) protein translocase	*tatC*	-2.15	-0.53
lpg2931	conserved hypothetical protein, COG3785	-	0.05	-2.87
lpg2934	transcription termination factor rho	-	-0.07	2.09
lpg2943	UDP-N-acetylglucosamine acyltransferase, acyl-[ac	-	0.21	3.43
lpg2949	asparagine synthetase (B) (glutamine hydrolyzing)	*wbmI*	0.37	2.95

lpg2950	hypothetical protein	-	-2.53	-0.23
lpg2953	ORF	-	-0.86	-2.73
lpg2956	deoxycytidine triphosphate deaminase	*dcd*	0.12	2.81
lpg2957	stomatin like transmembrane protein	-	0.41	-3.21
lpg2958	transmembrane protein (nodulation competitiveness	-	-0.37	-2.58
lpg2959	conserved hypothetical protein	-	1.36	2.67
lpg2962	sodium-type flagellar protein (lateral flagellar MotY-	-	1.12	-3.64
lpg2967	superoxide dismutase	*sodB*	1.62	2.55
lpg2968	N-acetylornithine aminotransferase ArgD	*argD*	1.08	3.02
lpg2981	ATP synthase epsilon chain, ATP synthase F1 epsil	*atpC*	-1.28	2.10
lpg2982	H+-transporting two-sector ATPase, ATP synthase	*atpD*	-1.26	3.58
lpg2983	ATP synthase gamma chain, ATP synthase F1 gam	*atpG*	-1.59	4.03
lpg2984	F0F1-ATPase subunit alpha, ATP synthase alpha c	-	-1.02	3.17
lpg2985	ATP synthase F1, delta subunit (F0F1 ATPase subu	*atpH*	-2.15	2.39
lpg2986	ATP synthase F0, B subunit	*atpF*	-0.77	2.80
lpg2987	ATP synthase F0, C subunit	*atpE*	-0.10	2.23
lpg2989	ATP synthase protein I (ATP synthase F0, I subunit	*atpI*	-0.64	3.24
lpg2990	ORF	-	-2.76	1.58
lpg2995	lipoprotein (exported protein)	-	0.65	2.65
lpg3000	ORF	-	2.83	1.73
lpg3003	conserved hypothetical protein TIGR00278, COG07	-	-2.73	2.50
lpg3004	ribonuclease P protein component	*rnpA*	-3.30	3.03

* Log2 Ratio