Supplemental Table 1. ArgR affected genes[†]

ORF	**Predicted Protein**	**Gene**	**Category**	**Ratio* E Phase Δ*argR*/ wild-type**	**Ratio* PE Phase Δ*argR*/ wild-type**
lpg0064	hypothetical	-	Function Unknown	0.097	-1.502
lpg0069	tRNA-Asn	-	tRNA	-0.270	-1.578
lpg0076	conserved hypothetical protein	-	Function Unknown	0.737	1.714
lpg0112	hypothetical protein	-	Function Unknown	-0.517	-1.541
lpg0154	ORF	-	Function Unknown	-0.169	-1.899
lpg0173	transcriptional regulator, LysR	-	Transcription & Signal Transductio	-0.082	-1.714
lpg0174	pyoverdine biosynthesis protein, PvcA	*pvcA*	Transport & Binding	0.557	-5.528
lpg0175	pyoverdine biosynthesis protein, PvcB	*pvcB*	Transport & Binding	0.593	-4.021
lpg0177	chloramphenicol resistance protein	-	Transport & Binding	1.200	-3.879
lpg0179	O-methyltransferase	-	Function Unknown	-1.290	-2.419
lpg0209	ORF	-	Function Unknown	0.311	1.751
lpg0218	phosphoribosylaminoimidazole carboxylase	*purE*	Nucleotide Metabolism	0.319	-1.760
lpg0227	Ceg7	*ceg7*	Icm/Dot Translocated Substrates	-0.076	-1.578
lpg0239	4-aminobutyrate aminotransferase	*gabT*	Amino Acid Metabolism	0.504	1.547
lpg0286	oxidoreductase	-	Function Unknown	0.028	1.761
lpg0438	ORF	-	Function Unknown	0.456	1.812
lpg0443	IcmR	*icmR*	Transport & Binding	0.298	1.830
lpg0444	IcmQ	*icmQ*	Transport & Binding	0.186	1.645
lpg0452	IcmG (DotF)	*icmG*	Transport & Binding	0.035	1.625
lpg0460	phosphoribosylamineimidazolecarboxamide	*purH*	Nucleotide Metabolism	0.316	1.580
lpg0463	acetyl CoA carboxylase	-	Carbohydrate Metabolism	-0.680	2.395
lpg0482	endo-1,4 beta-glucanase	-	Protein Fate	-0.025	2.344
lpg0483	ankyrin repeat protein, LegA12	*legA12*	Icm/Dot Translocated Substrates	-0.075	-1.914
lpg0491	amino acid ABC transporter, periplasmic binding protein	-	Transport & Binding	7.591	5.103
lpg0492	amino acid ABC transporter, permease	*yqiY*	Transport & Binding	7.923	5.200
lpg0493	amino acid ABC transporter, ATP binding component	-	Transport & Binding	7.291	4.744
lpg0494	argininosuccinate synthase	*argG*	Amino Acid Metabolism	7.144	3.883
lpg0495	argininosuccinate lyase	*argH*	Amino Acid Metabolism	5.494	3.907
lpg0496	ornithine carbamoyltransferase	*argF*	Amino Acid Metabolism	5.012	3.573
lpg0497	adenosine deaminase	-	Nucleotide Metabolism	-0.350	2.196
lpg0516	conserved hypothetical protein	-	Function Unknown	-0.392	-1.625

lpg0517	COG0656: aldo/keto reductases	*ytbE*	Function Unknown	0.467	1.696
lpg0565	spore maturation protein B	-	Motility & Cell Division	0.031	-2.327
lpg0634	ORF	-	Icm/Dot Translocated Substrates	0.016	-1.671
lpg0659	ABC transporter ElsE, ATP binding protein	-	Transport & Binding	0.596	-2.066
lpg0674	adenylate cyclase	-	Nucleotide Metabolism	-0.064	-1.612
lpg0688	Hsp60, 60K heat shock protein	*htpB*	Detoxification & Stress Adaptation	-0.235	1.595
lpg0707	membrane protein	-	Function Unknown	0.836	2.246
lpg0711	imidazolonepropionase	*hutI*	Amino Acid Metabolism	0.531	-2.468
lpg0854	ORF	-	Function Unknown	0.072	1.547
lpg0882	small ORF (144aa)	-	Function Unknown	0.045	-1.971
lpg0884	ORF hypothetical	-	Function Unknown	0.440	1.757
lpg0913	MraZ protein	*mraZ*	Motility & Cell Division	0.475	2.346
lpg0931	type IV pilus biogenesis protein, PilQ	*pilQ*	Transport & Binding	2.195	0.338
lpg0968	ORF	-	Function Unknown	-0.585	-2.380
lpg0977	single strand DNA binding protein, Ssb	*ssB*	Replication & Repair	-0.125	-1.637
lpg0984	ORF hypothetical	-	Function Unknown	1.051	1.505
lpg1035	copper efflux ATPase	*copA*	Transport & Binding	-1.189	1.772
lpg1058	polyhydroxyalkanoic synthase	*phbC*	Amino Acid Metabolism	1.545	2.908
lpg1131	cyclopropane fatty acid synthase	*cfa*	Lipid Metabolism	0.474	-1.519
lpg1156	leucine aminopeptidase	-	Protein Fate	1.312	2.687
lpg1177	riboflavin biosynthesis protein, RibD	*ribD*	Cofactor Metabolism	-1.025	-1.660
lpg1230	hypothetical	-	Function Unknown	0.923	3.941
lpg1239	TraD	-	Transport & Binding	-0.277	-1.597
lpg1247	LvhB10, type IV secretion system protein B10	*lvhB10*	Transport & Binding	0.979	1.760
lpg1249	LvhB8, conjugal transfer protein	*lvhB8*	Transport & Binding	1.043	1.714
lpg1293	intracellular septation protein A	*ispZ*	Motility & Cell Division	0.497	1.635
lpg1367	1-aminocyclopropane-1-carboxylate deaminase	-	Carbohydrate Metabolism	-0.399	-2.397
lpg1388	hypothetical	-	Function Unknown	0.396	1.652
lpg1472	biotin synthase, BioB	*bioB*	Cofactor Metabolism	0.023	-1.748
lpg1476	hypothetical COG2331	-	Function Unknown	0.051	1.701
lpg1482	ORF	-	Function Unknown	-0.480	-1.951
lpg1505	conserved hypothetical protein	-	Function Unknown	-0.053	2.007
lpg1511	lipoate-protein ligase B	-	Transport & Binding	0.293	1.562
lpg1527	small ORF (151aa)	-	Function Unknown	0.680	-1.574

lpg1588	Coiled coils, LegC6	*legC6*	Icm/Dot Translocated Substrates	-0.288	-1.527
lpg1622	ORF	-	Function Unknown	-0.057	-1.995
lpg1641	acylaminoacyl peptidase	-	Protein Fate	-0.448	-1.753
lpg1667	conserved hypothetical protein	-	Function Unknown	-0.990	-1.532
lpg1678	phosphoribosylformylglycinamidine synthase II	*purL2*	Nucleotide Metabolism	0.482	1.952
lpg1687	ORF	-	Function Unknown	-0.575	3.308
lpg1702	Coiled coils, PpeB	*ppeB*	Icm/Dot Translocated Substrates	-0.419	-2.369
lpg1772	hypothetical	-	Function Unknown	0.809	1.547
lpg1774	ribonucleoside-diphosphate reductase	*nrdA*	Nucleotide Metabolism	0.040	1.624
lpg1851	ORF	*lem14*	Icm/Dot Translocated Substrates	-0.174	-2.104
lpg1905	ectonucleoside triphosphate diphosphohydrolase I	-	Nucleotide Metabolism	1.110	1.713
lpg1948	leucine-rich repeat, coiled-coil	*legLC4*	Icm/Dot Translocated Substrates	0.483	-2.459
lpg1986	ORF	-	Function Unknown	-0.803	-1.843
lpg2031	arginyl tRNA synthetase	*argS*	Amino Acid Metabolism	0.357	1.505
lpg2135	chemiosmotic efflux system protein B	-	Transport & Binding	0.931	-1.954
lpg2137	Serine/Threonine Kinase, LegK2	*legK2*	Icm/Dot Translocated Substrates	0.486	-1.530
lpg2191	global stress protein, GspA	*ibpA*	Detoxification & Stress Adaptation	2.618	-0.398
lpg2200	CegC4	*cegC4*	Icm/Dot Translocated Substrates	0.055	-1.675
lpg2221	ORF	-	Function Unknown	1.028	2.895
lpg2229	saframycin Mx1 synthetase B	-	Secondary Metabolites	0.170	1.566
lpg2246	ORF	-	Function Unknown	-1.195	-1.669
lpg2305	Smr domain protein	-	Protein Fate	2.206	1.433
lpg2327	CG18304 gene product	-	Icm/Dot Translocated Substrates	0.746	-2.301
lpg2391	Rtx toxin/lipase	*sdbC*	Icm/Dot Translocated Substrates	0.308	-1.564
lpg2409	Ceg29	*ceg29*	Icm/Dot Translocated Substrates	0.128	-1.704
lpg2410	patatin-like phospolipase	*vpdA*	Icm/Dot Translocated Substrates	-0.484	-1.692
lpg2424	ORF	-	Function Unknown	0.109	-1.614
lpg2445	161aa ORF, serpentine receptor	-	Function Unknown	1.510	-1.632
lpg2493	small heat shock protein, HspC2	*hspC2*	Detoxification & Stress Adaptation	0.497	-2.428
lpg2510	SdcA	*sdcA*	Icm/Dot Translocated Substrates	-0.385	-1.665
lpg2511	PI(4)P binding, SidC	*sidC*	Icm/Dot Translocated Substrates	0.524	-1.703
lpg2532	aspartate aminotransferase	-	Amino Acid Metabolism	-0.475	-2.339
lpg2579	small ORF (137aa)	-	Function Unknown	-0.418	1.612
lpg2587	probable thermolabile hemolysin	-	Pathogenic functions	-1.105	-1.910

lpg2603	ORF	*lem28*	Icm/Dot Translocated Substrates	-0.506	-1.769
lpg2626	ORF	-	Function Unknown	-3.843	0.940
lpg2662	pantoate-beta-alanine ligase	*panC*	Amino Acid Metabolism	-0.129	-2.167
lpg2665	dienelactone hydrolase family protein	-	Function Unknown	-0.425	-1.589
lpg2681	4-hydroxy-2-oxovalerate aldolase	-	Carbohydrate Metabolism	0.624	1.765
lpg2728	ORF	-	Function Unknown	0.486	-1.933
lpg2734	sensor histidine kinase, LuxN	*luxN*	Transcription & Signal Transductio	0.291	-1.536
lpg2744	ORF	-	Function Unknown	3.378	1.750
lpg2792	triosephosphate isomerase	*tpiA*	Carbohydrate Metabolism	-0.651	-1.839
lpg2808	shikimate-5-dehydrogenase	*aroE*	Amino Acid Metabolism	0.561	2.100
lpg2827	conserved hypothetical protein	-	Function Unknown	0.970	2.899
lpg2862	Coiled coils, LegC8	*legC8*	Icm/Dot Translocated Substrates	0.541	-3.252
lpg2902	conserved hypothetical protein	-	Function Unknown	0.035	2.146
lpg2924	lipoprotein	-	Transport & Binding	-0.020	4.856
lpg2933	oxidoreductase	*yigC*	Cofactor Metabolism	-0.163	-2.327
lpg2967	superoxide dismutase	*sodB*	Detoxification & Stress Adaptation	-0.534	-1.634
lpg2986	ATP synthase F0, B subunit	*atpF*	Energy Metabolism	-0.462	2.392

† affected genes defined as $\log_2$ ratio +/- 1.5 (3-fold or greater) and pval$\leq$0.005

* $\log_2$ ratio Δ*argR* (GAH280) / Wt (KS79)