S4 Table (Part A)

Locus tag	Counts (RPKM)		Fold ch.	Gene name and function	Pathway
	Dark	Light	($\log_2$)		
**** Uninfected: 0.5 h post-inoculation (spent medium) ****					
No differentially expressed genes detected above thresholds					
**** Uninfected: 1.5 h post-inoculation (spent medium) ****					
PMM0356	10999	2995	1.877 ↑	Proline iminopeptidase (EC 3.4.11.5)	Arginine and proline metabolism
**** Uninfected: 2.5 h post-inoculation (spent medium) ****					
PMM0356	14094	1490	3.242 ↑	Proline iminopeptidase (EC 3.4.11.5)	Arginine and proline metabolism
PMM1176	1696	550	1.626 ↑	Possible Helix-turn-helix protein, CopG family	Transcriptional regulation
PMM1289	214	640	–1.582 ↓	Cyanobacteria-specific RpoD-like sigma factor, type-12	RNA polymerase
**** Uninfected: 4.5 h post-inoculation (spent medium) ****					
PMM0356	11503	1484	2.955 ↑	Proline iminopeptidase (EC 3.4.11.5)	Arginine and proline metabolism
PMM1176	2387	370	2.691 ↑	Possible Helix-turn-helix protein, CopG family	Transcriptional regulation
PMM1058	490	94	2.379 ↑	*petG*, Cytochrome b6-f complex subunit V (PetG)	Photosynthesis
PMM1400	3777	1174	1.686 ↑	Possible hemagglutinin-neuraminidase	Viral proteins
PMM1179	386	123	1.649 ↑	Permease of the drug/metabolite transporter (DMT) superfamily	Transport
PMM1289	86	682	–2.993 ↓	Cyanobacteria-specific RpoD-like sigma factor, type-12	RNA polymerase
PMM1309	164	749	–2.192 ↓	*ftsZ*, Cell division protein FtsZ (EC 3.4.24.-)	Cell division
PMM0502	158	626	–1.984 ↓	Single-stranded DNA-binding protein	Replication
PMM0577	271	974	–1.844 ↓	Cyanobacteria-specific RpoD-like sigma factor, type-14	Transcriptional regulation
PMM0244	315	1074	–1.768 ↓	*dcd*, Deoxycytidine triphosphate deaminase (EC 3.5.4.13)	Pyrimidine metabolism
PMM1711	292	902	–1.629 ↓	*sps*, Sucrose phosphate synthase(EC:2.4.1.14)	Starch and sucrose metabolism
PMM0245	276	832	–1.594 ↓	cob(I)alamin adenosyltransferase	Porphyrin and chlorophyll metabolism
PMM1697	462	1367	–1.565 ↓	Cyanobacteria-specific RpoD-like sigma factor, type-13	RNA polymerase
PMM0243	226	663	–1.549 ↓	*thyX*, Thymidylate synthase thyX (EC 2.1.1.-)	Pyrimidine metabolism
**** Uninfected: 8.5 h post-inoculation (spent medium) ****					
PMM0356	14936	1565	3.255 ↑	Proline iminopeptidase (EC 3.4.11.5)	Arginine and proline metabolism
PMM1176	2905	391	2.893 ↑	Possible Helix-turn-helix protein, CopG family	Transcriptional regulation
PMM1058	1619	229	2.82 ↑	*petG*, Ribosomal RNA small subunit methyltransferase D (EC 2.1.1.-)	Photosynthesis
PMM1179	498	151	1.722 ↑	Permease of the drug/metabolite transporter (DMT) superfamily	Transport
PMM0747	489	170	1.52 ↑	*pcyA*, Phycocyanobilin:ferredoxin oxidoreductase (EC 1.3.7.5)	Porphyrin and chlorophyll metabolism
PMM1289	72	809	–3.487 ↓	Cyanobacteria-specific RpoD-like sigma factor, type-12	RNA polymerase
PMM1309	62	637	–3.355 ↓	*ftsZ*, Cell division protein FtsZ (EC 3.4.24.-)	Cell division
PMM0577	122	1109	–3.18 ↓	Cyanobacteria-specific RpoD-like sigma factor, type-14	Transcriptional regulation
PMM0245	112	846	–2.917 ↓	cob(I)alamin adenosyltransferase	Porphyrin and chlorophyll metabolism
PMM1711	159	1051	–2.724 ↓	*sps*, Sucrose phosphate synthase(EC:2.4.1.14)	Starch and sucrose metabolism
PMM0244	154	1010	–2.711 ↓	*dcd*, Deoxycytidine triphosphate deaminase (EC 3.5.4.13)	Pyrimidine metabolism
PMM0502	93	530	–2.514 ↓	Single-stranded DNA-binding protein	Replication
PMM0243	124	570	–2.196 ↓	*thyX*, Thymidylate synthase thyX (EC 2.1.1.-)	Pyrimidine metabolism
PMM0330	100	456	–2.19 ↓	Possible LysM domain	Cell membrane
PMM0779	112	482	–2.11 ↓	*purS*, Phosphoribosylformylglycinamidine synthase (EC 6.3.5.3)	Purine metabolism
PMM0661	262	1109	–2.081 ↓	*nrdJ*, Ribonucleotide reductase class II (B12-dependent) (EC 1.17.4.1)	Purine and pyrimidine metabolism
PMM0576	131	549	–2.069 ↓	COG3339 conserved hypothetical protein	(unknown)
PMM0660	802	3322	–2.051 ↓	Possible RNA recognition motif (RRM)	Translational regulation
PMM0519	363	1410	–1.958 ↓	*talB*, Transaldolase (EC 2.2.1.2)	Pentose phosphate pathway
PMM0970	297	1109	–1.899 ↓	*urtA*, Urea ABC transporter, substrate binding protein UrtA	ABC transporters
N/A	147	544	–1.893 ↓	Protein family PM-1	(unknown)
PMM1611	164	599	–1.87 ↓	*thiC*, Thiamin biosynthesis protein ThiC	Thiamine metabolism
PMM1321	771	2759	–1.839 ↓	Bacterial histone-like DNA-binding protein	DNA-binding proteins
PMM1150	223	746	–1.741 ↓	Thioredoxin reductase (EC 1.8.1.9)	Pyrimidine metabolism
PMM0387	165	526	–1.676 ↓	*aroD*, 3-dehydroquinate dehydratase II (EC 4.2.1.10)	Phe, Tyr and Trp biosynthesis
PMM0920	197	624	–1.665 ↓	*glnA*, Glutamine synthetase type I (EC 6.3.1.2)	Alanine, aspartate and glutamate metabolism
PMM1657	391	1181	–1.596 ↓	*clpX*, ATP-dependent Clp protease ATP-binding subunit ClpX	Proteolysis
PMM1148	1281	3829	–1.579 ↓	Possible 7kD DNA-binding domain	DNA-binding proteins
PMM1697	367	1095	–1.579 ↓	Cyanobacteria-specific RpoD-like sigma factor, type-13	RNA polymerase
PMM0258	239	687	–1.52 ↓	*glyA*, Serine hydroxymethyltransferase (EC 2.1.2.1)	Glycine, serine and threonine metabolism
PMM1145	146	413	–1.502 ↓	*pntB*, NAD(P) transhydrogenase subunit beta (EC 1.6.1.2)	Nicotinate and nicotinamide metabolism
PMM1568	888	2513	–1.501 ↓	Hypothetical membrane protein	Membrane proteins

S4 Table (Part B)

Locus tag	Counts (RPKM)		Fold ch. (log$_2$)	Gene name and function	Pathway
	Dark	Light			
**** Infected: 0.5 h post-inoculation (phage) ****					
PMM0336	209	1465	–2.806 ↓	Plastoquinol terminal oxidase	Photosynthetic electron transport
PMM0817	110	657	–2.573 ↓	*hli17*, High light inducbile protein	Light stress response
PMM1135	300	1401	–2.226 ↓	*hli14*, High light inducbile protein	Light stress response
PMM1399	177	774	–2.127 ↓	*hli6*, High light inducbile protein	Light stress response
PMM0817	188	768	–2.028 ↓	*hli17*, High light inducbile protein	Light stress response
PMM0815	195	764	–1.972 ↓	*hli19*, High light inducbile protein	Light stress response
PMM1399	154	586	–1.926 ↓	*hli6*, High light inducbile protein	Light stress response
PMM1385	1246	4269	–1.777 ↓	*hli11*, High light inducbile protein	Light stress response
PMM1398	234	744	–1.668 ↓	*hli7*, High light inducbile protein	Light stress response
PMM1404	269	837	–1.639 ↓	*hli5*, High light inducbile protein	Light stress response
**** Infected: 1.5 h post-inoculation (phage) ****					
PMM0356	10006	1898	2.398 ↑	Proline iminopeptidase (EC 3.4.11.5)	Arginine and proline metabolism
**** Infected: 2.5 h post-inoculation (phage) ****					
PMM0356	14796	1292	3.518 ↑	Proline iminopeptidase (EC 3.4.11.5)	Arginine and proline metabolism
PMM1289	207	656	–1.666 ↓	Cyanobacteria-specific RpoD-like sigma factor, type-12	RNA polymerase
PMM1539	189	548	–1.533 ↓	*adk*, Adenylate kinase (EC 2.7.4.3)	Purine metabolism
**** Infected: 4.5 h post-inoculation (phage) ****					
PMM0356	17034	1229	3.793 ↑	Proline iminopeptidase (EC 3.4.11.5)	Arginine and proline metabolism
PMM1176	2236	451	2.311 ↑	Possible Helix-turn-helix protein, CopG family	Transcriptional regulation
PMM0348	2839	888	1.676 ↑	Possible Spectrin repeat	Cytoskeleton
PMM1289	89	707	–2.995 ↓	Cyanobacteria-specific RpoD-like sigma factor, type-12	RNA polymerase
PMM1711	251	1053	–2.07 ↓	*sps*, Sucrose phosphate synthase(EC:2.4.1.14)	Starch and sucrose metabolism
PMM0243	224	863	–1.946 ↓	*thyX*, Thymidylate synthase thyX (EC 2.1.1.-)	Pyrimidine metabolism
PMM0244	352	1286	–1.871 ↓	*dcd*, Deoxycytidine triphosphate deaminase (EC 3.5.4.13)	Pyrimidine metabolism
PMM1309	190	661	–1.801 ↓	*ftsZ*, Cell division protein FtsZ (EC 3.4.24.-)	Cell division
PMM0245	284	924	–1.701 ↓	cob(I)alamin adenosyltransferase	Porphyrin and chlorophyll metabolism
PMM0577	345	1038	–1.587 ↓	Cyanobacteria-specific RpoD-like sigma factor, type-14	Transcriptional regulation

(continued on next page)

S4 Table (Part B) (continued)

Locus tag	Counts (RPKM)		Fold ch.	Gene name and function	Pathway
	Dark	Light	($\log_2$)		
				**** Infected: 8.5 h post-inoculation (phage) ****	
PMM0356	15827	1379	3.521 ↑	Proline iminopeptidase (EC 3.4.11.5)	Arginine and proline metabolism
PMM1176	2772	517	2.424 ↑	Possible Helix-turn-helix protein, CopG family	Transcriptional regulation
PMM0348	4088	1155	1.824 ↑	Possible Spectrin repeat	Cytoskeleton
PMM1400	3120	1043	1.581 ↑	Possible hemagglutinin-neuraminidase	Viral proteins
PMM1289	72	731	–3.35 ↓	Cyanobacteria-specific RpoD-like sigma factor, type-12	RNA polymerase
PMM1309	67	597	–3.145 ↓	*ftsZ*, Cell division protein FtsZ (EC 3.4.24.-)	Cell division
PMM0577	140	1113	–2.994 ↓	Cyanobacteria-specific RpoD-like sigma factor, type-14	Transcriptional regulation
PMM0245	115	895	–2.957 ↓	cob(I)alamin adenosyltransferase	Porphyrin and chlorophyll metabolism
PMM0244	165	1232	–2.9 ↓	*dcd*, Deoxycytidine triphosphate deaminase (EC 3.5.4.13)	Pyrimidine metabolism
PMM1711	168	1251	–2.896 ↓	*sps*, Sucrose phosphate synthase(EC:2.4.1.14)	Starch and sucrose metabolism
PMM0243	136	725	–2.412 ↓	*thyX*, Thymidylate synthase thyX (EC 2.1.1.-)	Pyrimidine metabolism
PMM0502	99	523	–2.403 ↓	Single-stranded DNA-binding protein	Replication
PMM1321	663	2902	–2.131 ↓	Bacterial histone-like DNA-binding protein	DNA-binding proteins
PMM1145	112	445	–1.99 ↓	*pntB*, NAD(P) transhydrogenase subunit beta (EC 1.6.1.2)	Nicotinate and nicotinamide metabolism
PMM0661	260	1014	–1.96 ↓	*nrdJ*, Ribonucleotide reductase class II (B12-dependent) (EC 1.17.4.1)	Purine and pyrimidine metabolism
RNA_15	107	409	–1.938 ↓	tRNA-Arg2, tRNA-Arg-CCG	Protein translation
PMM0576	124	474	–1.936 ↓	COG3339 conserved hypothetical protein	(unknown)
PMM0779	123	469	–1.929 ↓	*purS*, Phosphoribosylformylglycinamidine synthase (EC 6.3.5.3)	Purine metabolism
PMM1697	308	1134	–1.879 ↓	Cyanobacteria-specific RpoD-like sigma factor, type-13	RNA polymerase
PMM1146	212	746	–1.815 ↓	PntA-2, NAD(P) transhydrogenase alpha subunit (EC 1.6.1.2)	Nicotinate and nicotinamide metabolism
PMM1380	184	624	–1.761 ↓	HAD-superfamily hydrolase, subfamily IA, variant 3	Hydrolase (unknown)
PMM1150	211	694	–1.719 ↓	Thioredoxin reductase (EC 1.8.1.9)	Pyrimidine metabolism
PMM0258	214	690	–1.692 ↓	*glyA*, Serine hydroxymethyltransferase (EC 2.1.2.1)	Glycine, serine and threonine metabolism
PMM0660	810	2438	–1.59 ↓	Possible RNA recognition motif (RRM)	Translational regulation
N/A	267	804	–1.589 ↓	tRNA-Leu3, tRNA-Leu-CAA	Protein translation
PMM1611	189	549	–1.536 ↓	*thiC*, Thiamin biosynthesis protein ThiC	Thiamine metabolism
PMM0740	362	1041	–1.524 ↓	*petN*, Cytochrome b6f complex subunit VIII	Photosynthesis
PMM0117	404	1158	–1.52 ↓	TPR-repeat protein, specific for cyanobacteria	(unknown)
PMM0128	356	1018	–1.515 ↓	*rpaA*, Two-component system response regulator	Two-component system
PMM0970	353	1010	–1.515 ↓	*urtA*, Urea ABC transporter, substrate binding protein UrtA	ABC transporters
PMM0444	186	531	–1.514 ↓	*ctaE*, Cytochrome c oxidase polypeptide III (EC 1.9.3.1)	Oxidative phosphorylation