S3 Table (Part A)

Locus tag	Counts (RPKM)		Fold ch.	Gene name and function	Pathway
	Inf.	Uninf.	($\log_2$)		
**** Light: 0.5 h post-inoculation (phage or spent medium) ****					
PMM1385	4269	1356	1.654 ↑	*hli11*, High light inducible protein	Light stress response
PMM1404	837	292	1.521 ↑	*hli5*, High light inducible protein	Light stress response
PMM1135	1401	500	1.487 ↑	*hli14*, High light inducible protein	Light stress response
PMM0336	1465	587	1.320 ↑	Plastoquinol terminal oxidase (PTOX)	Photosynthetic electron transport
PMM1399	774	347	1.156 ↑	*hli6*, High light inducible protein	Light stress response
PMM1398	744	379	0.972 ↑	*hli7*, High light inducible protein	Light stress response
PMM1629	1791	1124	0.672 ↑	Cyanobacteria-specific RpoD-like sigma factor, type-6	Transcription
PMM1663	588	910	–0.631 ↓	Photosystem I assembly related protein Ycf37	Photosynthesis: PSI
**** Light: 1.5 h post-inoculation (phage or spent medium) ****					
PMM0814	1820	1086	0.744 ↑	Cytochrome *c* oxidase subunit VIb-like	Photosynthetic electron transport
RNA_15	272	551	–1.021 ↓	tRNA-Arg2, tRNA-Arg-CCG	Protein translation
PMM0510	1266	2068	–0.708 ↓	Possible reverse transcriptase, RNA-dependent	Reverse transcription
PMM0573	4844	7419	–0.615 ↓	AbrB family transcriptional regulator	Transcriptional regulation
PMM0290	218	320	–0.558 ↓	Possible ABC transporter, ATP-binding component	Transport
PMM1309	533	771	–0.533 ↓	*ftsZ*, Cell division protein FtsZ (EC 3.4.24.-)	Cell division
**** Light: 2.5 h post-inoculation (phage or spent medium) ****					
PMM0223	25985	18992	0.452 ↑	*psbA*, Photosystem II protein D1 (PsbA)	Photosynthesis: PSII
PMM1167	297	510	–0.778 ↓	Macrophage migration inhibitory factor family	(unknown)
PMM1568	1580	2424	–0.617 ↓	Hypothetical membrane protein	Membrane proteins
**** Light: 4.5 h post-inoculation (phage or spent medium) ****					
PMM0272	6299	3626	0.797 ↑	*psbK*, Photosystem II protein PsbK	Photosynthesis: PSII
PMM0573	3204	4931	–0.622 ↓	AbrB family transcriptional regulator (part 2)	Transcriptional regulation
PMM1148	2821	3981	–0.497 ↓	Possible 7kD DNA-binding domain	DNA-binding domains
**** Light: 8.5 h post-inoculation (phage or spent medium) ****					
PMM0272	6608	3754	0.816 ↑	*psbK*, Photosystem II protein PsbK	Photosynthesis: PSII
RNA_17	1806	1051	0.781 ↑	tRNA-Val2, tRNA-Val-TAC	Protein translation
PMM0223	27918	19335	0.530 ↑	*psbA*, Photosystem II protein D1 (PsbA)	Photosynthesis: PSII
PMM1402	203	452	–1.152 ↓	Ferredoxin-NADP(+) reductase (EC 1.18.1.2) (FNR)	Photosynthetic electron transport
PMM0987	1481	3102	–1.067 ↓	*rpsU*, SSU ribosomal protein S21p	Ribosome
PMM1007	218	415	–0.928 ↓	Cell division protein FtsK	Cell division
PMM1183	2051	3476	–0.761 ↓	*rpmH*, LSU ribosomal protein L34p	Ribosome
PMM0870	3918	6476	–0.725 ↓	*rpmG*, LSU ribosomal protein L33p	Ribosome
PMM0732	657	1048	–0.674 ↓	Possible major surface glycoprotein	Cell surface glycoproteins
RNA_8	1792	2774	–0.630 ↓	tRNA-Lys1, tRNA-Lys-TTT	Protein translation
PMM0870	4417	6814	–0.625 ↓	*rpmG*, SSU ribosomal protein S18p	Ribosome
PMM0500	602	920	–0.611 ↓	Cyanobacterial protein slr0575	(unknown)
PMM1171	766	1160	–0.598 ↓	*isiB*, Flavodoxin 1	Photosynthetic electron transport
PMM1655	428	648	–0.598 ↓	*tig*, Cell division trigger factor (EC 5.2.1.8)	Cell division
PMM1344	1691	2522	–0.577 ↓	*rplU*, LSU ribosomal protein L21p	Ribosome
PMM0943	2555	3798	–0.572 ↓	*rpsO*, SSU ribosomal protein S15p (S13e)	Ribosome

S3 Table (Part B)

Locus tag	Counts (RPKM)		Fold ch.	Gene name and function	Pathway
	Inf.	Uninf.	(log$_2$)		
**** Dark: 0.5 h post-inoculation (phage or spent medium) ****					
No differentially expressed genes detected above thresholds					
**** Dark: 1.5 h post-inoculation (phage or spent medium) ****					
No differentially expressed genes detected above thresholds					
**** Dark: 2.5 h post-inoculation (phage or spent medium) ****					
PMM0263	33247	21973	0.597 ↑	*amt1*, Ammonium transporter family	Transport
RNA_15	178	483	–1.435 ↓	tRNA-Arg2, tRNA-Arg-CCG	Protein translation
PMM0689	283	634	–1.164 ↓	*hli22*, High light inducbile protein	Light stress response
RNA_20	198	426	–1.106 ↓	tRNA-Ser1, tRNA-Ser-GCT	Protein translation
PMM0740	401	839	–1.065 ↓	*petN*, Cytochrome b_6f complex subunit VIII	Photosynthetic electron transport
PMM0686	295	601	–1.029 ↓	*clpS*, ATP-dependent Clp protease adaptor protein ClpS	Proteolysis
PMM0814	832	1686	–1.019 ↓	Cytochrome *c* oxidase subunit VIb-like	Photosynthetic electron transport
PMM1503	250	495	–0.986 ↓	Possible NDP-sugar pyrophosphorylase, LPS biosynthesis	Lipopolysaccharide biosynthesis
PMM1588	269	527	–0.971 ↓	Possible conserved carboxylase domain	(unknown)
**** Dark: 4.5 h post-inoculation (phage or spent medium) ****					
PMM0806	1559	933	0.740 ↑	Bacterial regulatory proteins, Crp family	Transcriptional regulation
PMM0941	3461	2090	0.727 ↑	Possible cAMP phosphodiesterases class-II precursor	Signal transduction
RNA_3	19142	12513	0.613 ↑	tRNA-Ile1, tRNA-Ile-GAT	Protein translation
RNA_4	10701	7789	0.458 ↑	tRNA-Ala1, tRNA-Ala-TGC	Protein translation
PMM0263	29002	21119	0.458 ↑	*amt1*, Ammonium transporter family	Transport
PMM0689	151	371	–1.294 ↓	*hli22*, High light inducbile protein	Light stress response
PMM1400	1763	3777	–1.099 ↓	Possible hemagglutinin-neuraminidase	Viral proteins
PMM1122	599	1237	–1.046 ↓	*apt*, Adenine phosphoribosyltransferase (EC 2.4.2.7)	Purine metabolism
PMM0814	1071	1970	–0.879 ↓	Cytochrome *c* oxidase subunit VIb-like	Photosynthetic electron transport
RNA_16	214	389	–0.864 ↓	tRNA-Cys1, tRNA-Cys-GCA	Protein translation
PMM1663	924	1645	–0.832 ↓	Photosystem I assembly related protein Ycf37	Photosynthesis: PSI
PMM0691	209	370	–0.824 ↓	Tryptophan-rich protein DUF2389, Ssr2843 homolog	(unknown)
PMM0747	205	360	–0.812 ↓	*pcyA*, Phycocyanobilin:ferredoxin oxidoreductase (EC 1.3.7.5)	Porphyrin and chlorophyll metabolism
PMM1437	4805	8345	–0.796 ↓	*groES*, Heat shock protein 60 family co-chaperone GroES	Molecular chaperones
PMM0949	195	338	–0.795 ↓	COG1939: Ribonuclease III family protein	Nucleases
PMM2011	271	466	–0.781 ↓	Possible chorismate binding enzyme	(unknown)
PMM1181	209	358	–0.775 ↓	*tyrA*, Chorismate mutase II (EC 5.4.99.5)	Phe, Tyr and Trp biosynthesis
PMM1459	258	441	–0.771 ↓	*ccdA*, Cytochrome *c*-type biogenesis protein CcdA	Photosynthetic electron transport
PMM0686	460	777	–0.756 ↓	ATP-dependent Clp protease adaptor protein ClpS	Proteolysis
**** Dark: 8.5 h post-inoculation (phage or spent medium) ****					
PMM0806	1652	1046	0.659 ↑	Bacterial regulatory proteins, Crp family	Transcriptional regulation
RNA_4	12439	8693	0.517 ↑	tRNA-Ala1, tRNA-Ala-TGC	Protein translation
PMM1119	4183	2991	0.484 ↑	*som*, Possible porin	Transport
PMM1121	8685	6262	0.472 ↑	*som*, Possible porin	Transport
PMM0263	17076	12368	0.465 ↑	*amt1*, Ammonium transporter family	Transport
RNA_41	4234	3140	0.431 ↑	5S RNA	Protein translation
PMM1402	393	681	–0.794 ↓	Ferredoxin-NADP(+) reductase (EC 1.18.1.2) (FNR)	Photosynthetic electron transport
PMM1629	739	1246	–0.753 ↓	Cyanobacteria-specific RpoD-like sigma factor, type-6	Transcription