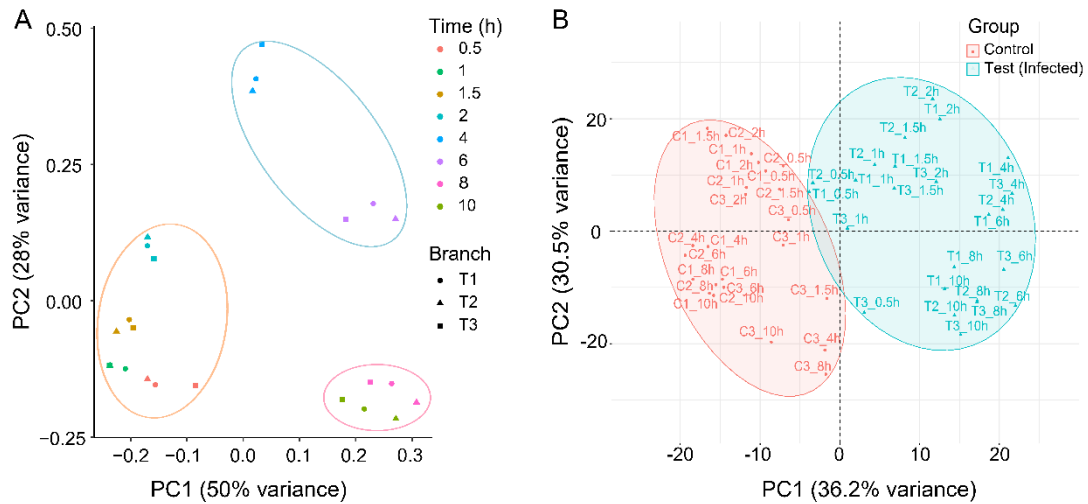


1 **Supplementary information**

2 **Supplementary figures and figure legends**

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5 **FIG S1** Principal component analysis (PCA) for clustering gene expression data, via

6 Hotelling's 95% confidence ellipses. (A) *Mic1* samples could be classified into three

7 groups corresponding to the early, middle and late phase in the lytic cycle. Colors

8 represent different infection time points, whereas shapes indicate three individual

9 infection experiments. (B) PCA on the top 500 genes of host *Microcystis* from control

10 (red) and infected (blue) cells, which shows a distinct clustering. Control: control cells;

11 Test: infected cells.

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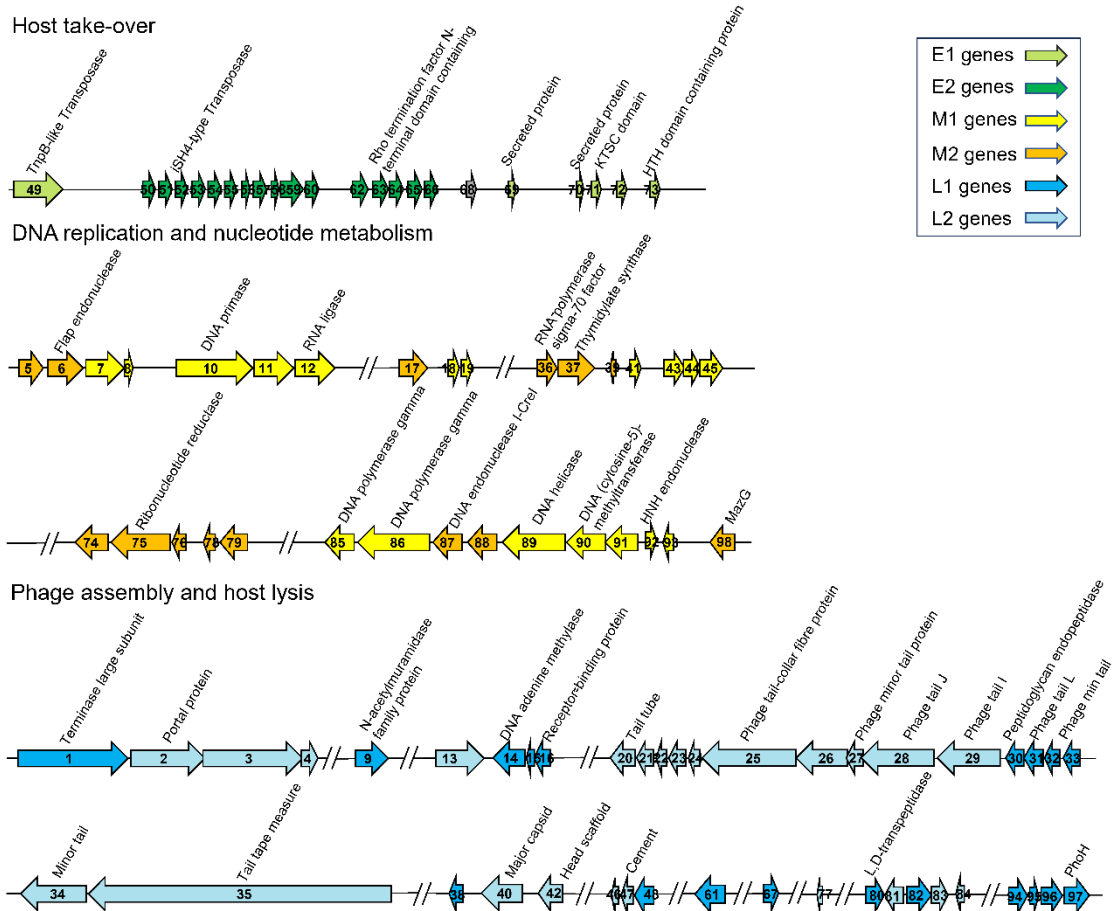
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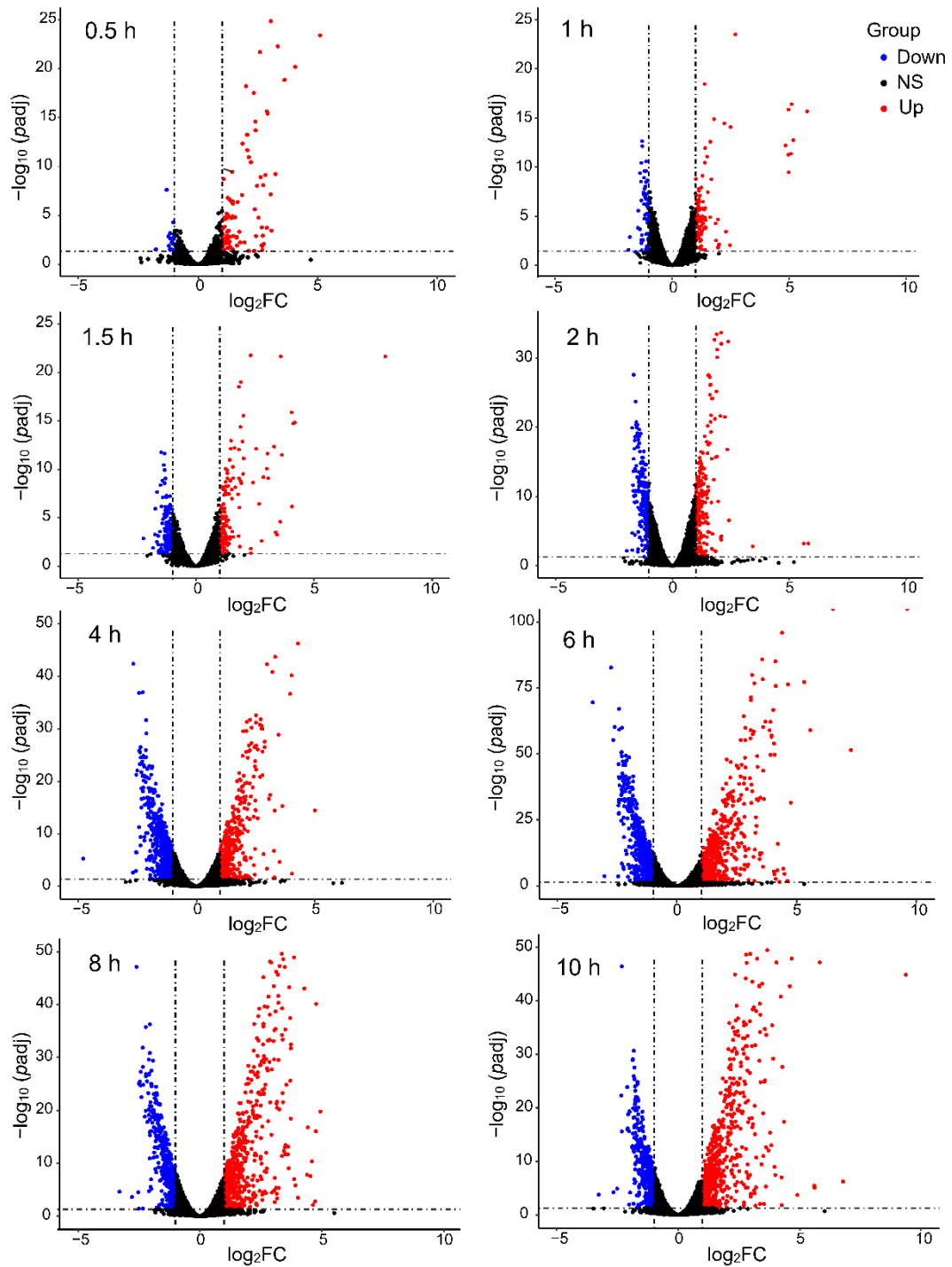
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22 **FIG S2** Presentation of 98 Mic1 genes according to the temporal expression patterns.

23 The arrows indicate the transcription direction. The annotations of genes that contribute
24 to the definite function of each temporal expression pattern are indicated.

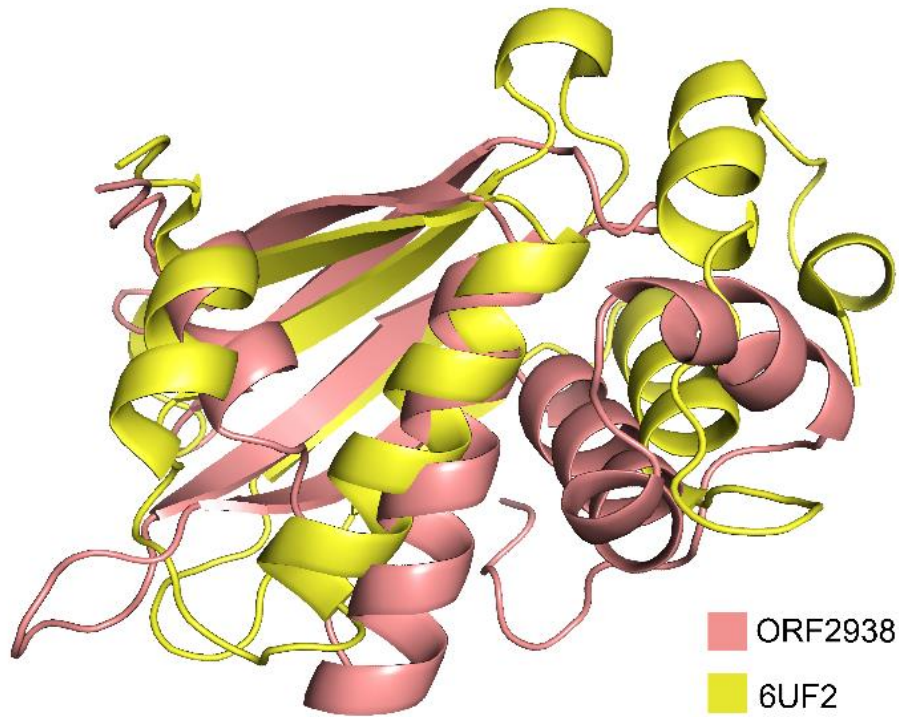
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36 **FIG S3** Volcano plots of the host DEGs at each time point. The \log_2 scale shows the
 37 fold change of genes, whereas the \log_{10} scale represents the significance. Down:
 38 downregulated host genes; NS: not significant changed genes; Up: upregulated host
 39 genes.

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41 **FIG S4** Structural superposition of *Microcystis* ORF2938 (salmon, predicted by
42 Alphafold2) against the biofilm-related protein Se0862 from *Synechococcus elongatus*
43 PCC 7942 (yellow, PDB: 6UF2).
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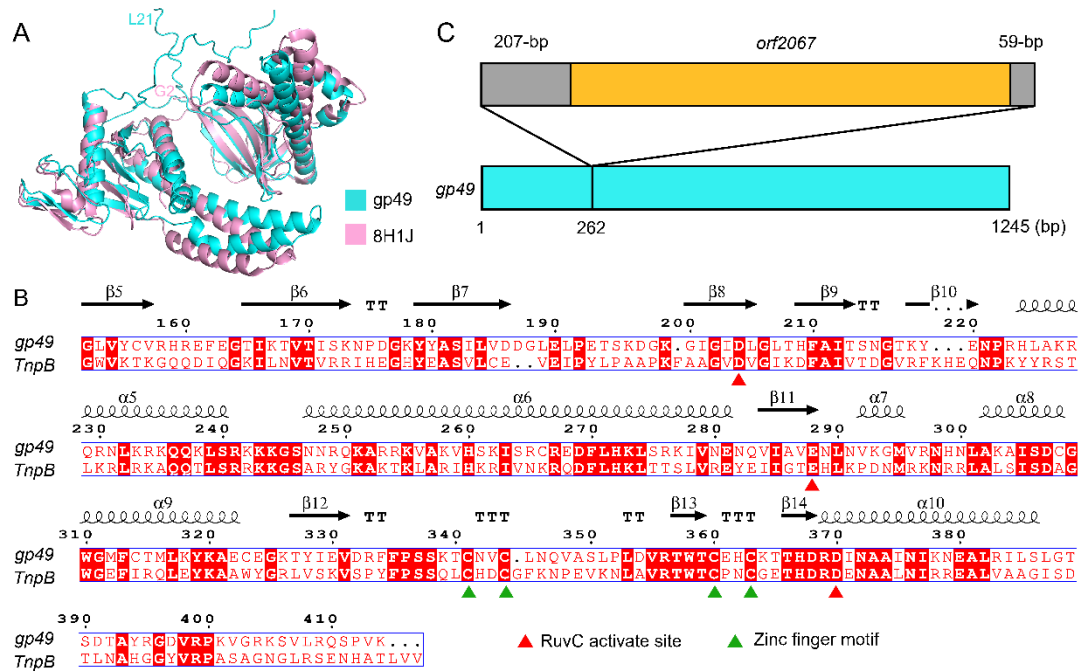
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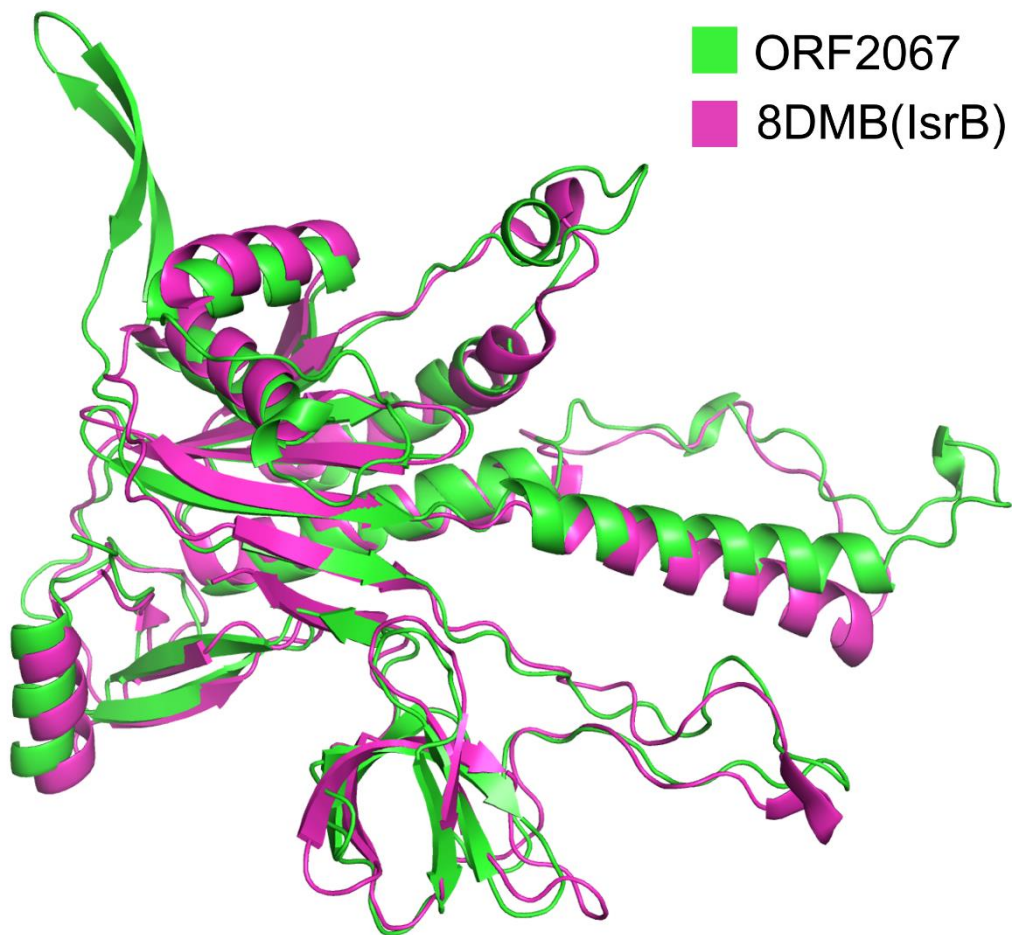
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58 **FIG S5** Analyses of Mic1 E1 gene *gp49*. (A) Structural superposition of the Mic1 *gp49*
 59 (cyan, predicted by AlphaFold2) against the RNA-guided DNA endonuclease TnpB
 60 from *Deinococcus radiodurans* R1 (pink, PDB: 8H1J). (B) Primary sequence alignment
 61 of the *gp49* against TnpB. The key residues of zinc finger motif and RuvC activate site
 62 are indicated with green and red triangles, respectively. (C) A diagram of Mic1 *gp49*
 63 inserted with the host gene *orf2067*. Cyan: Mic1 *gp49*; yellow: *Microcystis orf2067*;
 64 gray: the upstream and downstream region of *orf2067*.
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76 **FIG S6** Structural comparison of *Microcystis* ORF2067 (magenta, predicted by
77 Alphafold2) against *Desulfovibrio thermocuniculi* IsrB (green, PDB: 8DMB).

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88 **Supplementary tables**

89 **TABLE S2** Summary of the host response gene number after infection.

Time (h)	0.5	1	1.5	2	4	6	8	10
Up-regulated genes	109	113	163	241	410	560	588	583
Down-regulated genes	17	71	164	220	476	513	446	384

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106 **TABLE S3** Transcriptional level of a polyketide synthase pathway in the *Microcystis* genome after Mic1 infection.

Locus tag	Strand	Annotation	Log ₂ FoldChange							
			0.5 h	1 h	1.5 h	2 h	4 h	6 h	8 h	10 h
<i>orf2639</i>	+	Transcriptional regulator	2.4612084	/	/	/	-1.63345	-1.04477	/	1.473188
<i>orf2640</i>	-	Hypothetical protein VL20_5146	6.4102847	5.760095	4.118665	2.086657	-2.36636	-1.2546	/	2.363854
<i>orf2641</i>	+	Polyketide synthase PksJ	5.5519478	4.958536	2.315594	/	-2.53106	-1.60033	/	2.872712
<i>orf2642</i>	+	Hypothetical protein	5.8659139	4.976635	2.669211	/	-2.19939	-1.68823	-1.72036	2.718858
<i>orf2643</i>	+	Phthiocerol/phenolphthiocerol synthase type I PpsB	6.1315641	5.076128	2.774814	/	-1.93521	-1.42861	-1.40167	2.546412
<i>orf2644</i>	+	Phenolphthiocerol synthesis polyketide synthase type I Pks15/1	4.2143615	4.194029	1.583222	/	-1.6985	-1.36727	-1.10605	2.13411
<i>orf2645</i>	+	Peptide synthetase	4.9906953	4.96781	3.370554	/	-1.32123	/	/	2.237928
<i>orf2646</i>	-	Multidrug resistance protein MdtC	4.4218152	4.516152	3.026797	/	/	1.207171	/	2.281126
<i>orf2647</i>	-	Solvent efflux pump periplasmic linker SrpA	2.5826113	2.702131	1.53083	/	/	/	/	1.953742
<i>orf2648</i>	-	VPDSG-CTERM motif (stress sensor)	5.8360923	5.209478	4.066525	1.042213	-1.83363	-1.59634	-1.65425	1.78915
<i>orf2649</i>	-	PEP-CTERM sorting domain-containing protein	5.3130824	5.166991	4.184787	2.426615	/	-1.07259	/	1.910546
<i>orf2650</i>	-	VPDSG-CTERM motif	5.0948386	4.977906	4.05174	1.836686	-1.93539	-1.46646	/	1.515961
<i>orf2651</i>	-	Dehydrogenase	4.0568476	4.604382	3.307606	/	-1.7753	-1.26227	-1.23494	2.398548
<i>orf2652</i>	-	Putative MFS-type transporter YcaD	2.8082371	3.475419	2.418648	/	-1.10678	-1.01994	/	2.195439
<i>orf2653</i>	-	Polyketide biosynthesis protein PksE 3-hydroxyacyl-[acyl-carrier-protein] dehydratase	3.7209192	4.277037	2.997778	/	-1.07291	/	/	2.102777
<i>orf2654</i>	-	FabA	4.9043982	4.83869	3.571569	1.689592	-1.87002	-1.4065	-1.07553	2.139205
<i>orf2655</i>	-	Polyketide synthase PksN	5.2274829	5.09874	3.641738	/	-1.46475	-1.20346	-1.13286	2.445249
<i>orf2656</i>	-	Polyketide synthase modules and related proteins Phenolphthiocerol synthesis polyketide synthase	4.4503857	4.411876	3.054075	/	-1.77759	/	-1.16285	2.398233
<i>orf2657</i>	-	type I Pks15/1	4.2318081	4.171043	2.852323	/	-1.28183	/	/	2.402555

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109 **TABLE S4** Transcriptional level of a type III-B CRISPR pathway in the *Microcystis* genome after Mic1 infection.

Locus tag	Strand	Annotation	Log ₂ FoldChange							
			0.5 h	1 h	1.5 h	2 h	4 h	6 h	8 h	10 h
<i>orf1109</i>	-	Cas_Csm6	/	/	/	1.30323	/	3.301023	4.283178	4.280763
<i>orf1110</i>	-	Type III-B CRISPR module RAMP protein Cmr6	/	/	/	/	1.372048	3.541163	4.530266	4.295065
<i>orf1111</i>	-	CRISPR-associated protein Cmr5	/	1.197197	/	1.474082	1.336261	3.615945	4.767138	4.59428
<i>orf1112</i>	-	Uma2 family endonuclease	/	/	1.114649	1.111276	1.416458	4.009954	5.256806	5.262678
<i>orf1113</i>	-	Type III-B CRISPR module RAMP protein Cmr4	/	/	/	1.290125	1.248191	4.106955	5.095018	5.106959
note=CRISPR with 2 repeat units										
<i>orf1114</i>	-	CRISPR-associated protein Cmr3	/	/	/	1.260325	/	2.896936	3.923709	3.66849
<i>orf1115</i>	-	Type III-B CRISPR-associated protein Cas10/Cmr2	1.00252	/	/	/	/	/	/	/
<i>orf1116</i>	-	WYL domain-containing protein	/	/	/	/	/	/	/	1.120162
note=CRISPR with 7 repeat units										

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118 **TABLE S5** KEGG enrichment analysis of the *Microcystis* downregulated protein-coding genes after Mic1 infection.

Locus tag	Gene name	Annotation	Log ₂ FoldChange								
			0.5 h	1 h	1.5 h	2 h	4 h	6 h	8 h	10 h	
Photosynthesis pathway											
<i>orf141</i>	<i>psbJ</i>	Photosystem II reaction center protein J	/	/	/	/	/		-1.201243	-2.087642	/
<i>orf143</i>	<i>psbF</i>	Cytochrome b559 subunit beta	/	/	/	/		-1.250366	-1.569605	-1.40205	-1.138037
<i>orf144</i>	<i>psbE</i>	Cytochrome b559 subunit alpha	/	/	/	/		-1.315481	-1.519895	-1.573858	-1.053689
<i>orf330</i>	<i>psaB</i>	Phosphorylase	/	/	/	/		-1.925144	-1.81953	-1.882642	-1.388888
<i>orf331</i>	<i>psaA</i>	Photosystem I core protein PsaA	/	/	/	-1.304793	-2.34749	-2.317547	-2.209604	-1.733649	
<i>orf345</i>	<i>psaJ</i>	Photosystem I subunit IX	/	/	/	-1.178315	-2.190563	-2.218158	-2.258534	-1.844846	
<i>orf346</i>	<i>psaF</i>	Photosystem I reaction center subunit III	/	/	/	-1.051194	-2.072846	-2.189871	-2.094665	-1.886535	
<i>orf377</i>	<i>psbO</i>	Photosystem II manganese-stabilizing polypeptide	/	/	/	/		-1.455193	-1.420518	-1.051832	/
<i>orf475</i>	<i>psaK</i>	Photosystem I reaction center subunit PsaK	/	/	-1.285305	-1.524465	-2.133878	-2.427376	-2.219605	-1.869541	
<i>orf489</i>	<i>cpcC</i>	Photosystem I reaction center subunit XII	/	/	-1.095086	-1.523684	-2.399969	-2.410539	-2.342115	-2.008888	
<i>orf490</i>	<i>cpcC</i>	Photosystem I reaction center subunit XII	/	/	-1.053396	-1.510809	-2.284716	-2.450062	-2.345996	-2.000975	
<i>orf491</i>	<i>cpcA</i>	Phycocyanin subunit alpha	/	/	-1.181315	-1.607822	-2.502661	-2.42828	-2.498428	-2.078517	
<i>orf492</i>	<i>cpcB</i>	Phycocyanin subunit beta	/	/	-1.211637	-1.646318	-2.542182	-2.339128	-2.432239	-2.101509	
<i>orf555</i>	<i>psbZ</i>	Photosystem II reaction center protein Z	/	/	-1.281835	-1.658332	-2.050432	-1.978609	-1.783488	-1.69584	
<i>orf569</i>	<i>psaK</i>	Photosystem I reaction center subunit PsaK	/	/	/	/		-1.237088	-1.185189	-1.425413	-1.107851
<i>orf594</i>	<i>psaE</i>	Photosystem I reaction center subunit IV	/	/	-1.100902	-1.172105	-2.274811	-2.161566	-1.658397	-1.866168	
<i>orf661</i>	<i>psaI</i>	Photosystem I reaction center subunit VIII	/	/	/	-1.468384	-2.554494	-2.317852	-2.001605	-1.204219	
<i>orf662</i>	<i>psaL</i>	Photosystem I reaction center protein subunit XI	/	/	/	-1.027162	-2.382945	-2.292118	-2.039346	-1.633021	
<i>orf760</i>	<i>pethH</i>	Ferredoxin--NADP(+) reductase	/	/	/	/		-1.69618	-1.849362	-1.650852	-1.194849
<i>orf1273</i>	<i>apcE</i>	Photosystem I reaction center subunit X	/	/	/	-1.306494	-2.126029	-2.266192	-2.000028	-1.760948	
<i>orf1322</i>	<i>apcD</i>	Allophycocyanin subunit alpha	/	/	/	-1.133682	-1.9737	-1.902514	-1.816066	-1.760642	
<i>orf1402</i>	<i>ATPF1B, atpD</i>	ATP synthase subunit beta	/	/	/	-1.259526	-1.859781	-2.045115	-2.025824	-1.671682	
<i>orf1403</i>	<i>ATPF1E, atpC</i>	ATP synthase epsilon chain	/	/	-1.019071	-1.265868	-1.879405	-1.999593	-1.650046	-1.492712	
<i>orf1433</i>	<i>cpcG</i>	Phycobilisome rod-core linker polypeptide CpcG	/	/	-1.148142	-1.613261	-2.421204	-2.210494	-2.122146	-1.828206	

<i>orf1599</i>	<i>psbV</i>	Cytochrome c-550	/	/	/	-1.175374	-2.19253	-2.008311	-1.762699	-1.446373
<i>orf1863</i>	<i>cpcE</i>		/	-1.139688	/	/	/	/	-1.106831	/
<i>orf2052</i>	<i>atpI</i>	ATP synthase protein I	/	/	/	/	-1.533646	-1.74822	-1.58791	-1.195098
<i>orf2053</i>	<i>ATPF0A, atpB</i>	AtpB	/	/	/	/	-1.496058	-1.67446	-1.660346	-1.270855
<i>orf2054</i>	<i>ATPF0C, atpE</i>	ATP synthase F0 subunit C	/	/	/	-1.03497	-1.413663	-1.793516	-2.041615	-1.421271
<i>orf2055</i>	<i>ATPF0B, atpF</i>	F0F1 ATP synthase subunit B'	/	/	-1.269863	-1.508116	-1.720013	-1.840708	-1.617089	-1.458756
<i>orf2056</i>	<i>ATPF0B, atpF</i>	ATP synthase subunit B	/	/	-1.051844	-1.370558	-1.783724	-1.76669	-1.577814	-1.391811
<i>orf2057</i>	<i>ATPF1D, atpH</i>	F0F1 ATP synthase subunit delta	/	/	/	-1.269876	-1.615655	-1.667103	-1.594624	-1.302267
<i>orf2058</i>	<i>ATPF1A, atpA</i>	ATP synthase subunit alpha	/	/	/	-1.088211	-1.50464	-1.575348	-1.511965	-1.139905
<i>orf2059</i>	<i>ATPF1G, atpG</i>	F0F1 ATP synthase subunit gamma	/	/	/	-1.12453	-1.616107	-1.632777	-1.367676	-1.26374
<i>orf2091</i>	<i>petF</i>	Ferredoxin	/	/	/	/	/	-1.019241	-1.253178	/
<i>orf2121</i>	<i>petA</i>	Apocytochrome f	/	/	/	/	-1.275579	-1.564538	-1.404608	/
<i>orf2122</i>	<i>petC</i>	Cytochrome b6-f complex iron-sulfur subunit	/	/	/	/	-1.462803	-1.577591	-1.370307	/
<i>orf2306</i>	<i>psaD</i>	Photosystem I reaction center subunit II	/	/	-1.255751	-1.586505	-2.30004	-2.302488	-2.049052	-1.709965
<i>orf2316</i>	<i>psb27</i>	Photosystem II protein Psb27	/	/	/	-1.072767	-1.663375	-1.951865	-1.773887	-1.405001
<i>orf2448</i>	<i>psb28-2</i>	Photosystem II reaction center protein Psb28	/	/	/	-1.024929	-1.577191	-1.296547	/	-1.296862
<i>orf2456</i>	<i>apcC</i>	Phycobilisome core linker protein	/	/	/	/	/	-1.380081	-1.352839	-1.021501
<i>orf2457</i>	<i>apcB</i>	Allophycocyanin subunit beta	/	-1.024325	-1.208384	-1.675588	-2.316682	-2.434112	-2.461914	-2.025557
<i>orf2458</i>	<i>apcA</i>	Allophycocyanin subunit alpha	/	/	-1.207004	-1.684449	-2.3219	-2.454783	-2.396376	-2.061688
<i>orf2517</i>	<i>psbH</i>	Photosystem II reaction center protein H	/	/	/	/	-1.180627	-1.141909	/	/
<i>orf2537</i>	<i>psb28</i>	Photosystem II reaction center protein Psb28	/	/	/	/	-1.111062	-1.03049	/	/
<i>orf2689</i>	<i>apcF</i>	Phycobiliprotein beta chain	/	/	/	-1.070592	-1.957198	-2.001398	-1.943838	-1.732666
<i>orf2950</i>	<i>petF</i>	Ferredoxin	/	/	/	/	-1.116738	/	/	/
<i>orf3286</i>	<i>psbU</i>	Photosystem II extrinsic protein	/	/	/	/	-1.487493	-1.471319	-1.328205	-1.047037
<i>orf3379</i>	<i>psaC</i>	Photosystem I subunit VII	/	/	/	-1.006419	-2.123557	-1.898789	-2.059773	-1.751667
<i>orf3634</i>	<i>psbX</i>	Photosystem II PsbX protein	/	/	/	/	-1.442145	-1.276505	-1.001694	-1.217276
Porphyrin and chlorophyll Metabolism										
<i>orf221</i>	<i>chlH, bchH</i>	Magnesium chelatase subunit H	/	/	/	-1.160131	-1.911091	-2.130854	-1.795053	-1.619046
<i>orf304</i>	<i>hemE, UROD</i>	Uroporphyrinogen decarboxylase	/	/	/	/	-1.947086	-1.936584	-1.427503	-1.431571

<i>orf962</i>	<i>HO, hmuO</i>	<i>pbsA1</i>	Heme oxygenase (biliverdin-producing)	/	/	/	-1.308417	-2.2459	-2.324744	-2.089241	-2.103153
<i>orf1136</i>	<i>acsF, chlE</i>		Magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase	/	/	/	/	-1.730521	-1.624501	-1.293144	-2.320904
<i>orf1528</i>	<i>chlL</i>		Ferredoxin:protochlorophyllide reductase (ATP-dependent) iron-sulfur ATP-binding protein	/	/	-1.021894	-1.326652	-2.117079	-2.412089	-1.90514	-1.802095
<i>orf1530</i>	<i>chlN</i>		Ferredoxin:protochlorophyllide reductase (ATP-dependent) subunit N	/	/	/	/	-1.875984	-2.310835	-1.525526	-1.542646
<i>orf1769</i>	<i>hemA</i>		Glutamyl-tRNA reductase	/	/	/	-1.167893	-1.889357	-1.628732	-1.535361	-1.157239
<i>orf1801</i>	<i>cobH-cbiC</i>		Precorrin-8X methylmutase	-1.102074	/	/	/	/	/	/	/
<i>orf1802</i>	<i>cobI-cbiL</i>		Precorrin-2 C(20)-methyltransferase	-1.243997	/	/	/	/	/	/	/
<i>orf1998</i>	<i>acsF, chlE</i>		Magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase 1	/	/	/	-1.312134	-2.425128	-2.42925	-1.916258	-1.662659
<i>orf2087</i>	<i>hemC, HMBS</i>		Hydroxymethylbilane synthase	/	/	/	/	-1.020639	-1.3712	-1.245735	-1.083423
<i>orf2157</i>	<i>chlP, bchP</i>		Geranylgeranyl reductase	/	/	/	/	-2.19933	-2.420374	-2.076469	-1.749383
<i>orf2339</i>	<i>COX10, cyoE</i>	<i>ctaB</i>	Protoheme IX farnesyltransferase	/	/	/	/	/	/	/	-1.123575
<i>orf2340</i>	<i>COX15, ctaA</i>		Heme A synthase	/	/	/	/	-1.163557	/	-1.003792	-1.367286
<i>orf2571</i>	<i>chlB</i>		Ferredoxin:protochlorophyllide reductase (ATP-dependent) subunit B	/	/	/	/	-2.143678	-2.441956	-1.973517	-1.794203
<i>orf2593</i>	<i>cobB-cbiA</i>		Cobyrinic acid a,c-diamide synthase	/	/	/	/	-1.159765	/	/	/
<i>orf2613</i>	<i>bciB</i>		Hypothetical protein	/	/	/	/	-1.68647	-1.68953	-1.269966	-1.154242
<i>orf3679</i>	<i>BLVRA, bvdR</i>		Gfo/Idh/MocA family oxidoreductase	/	/	/	/	/	-1.07051	-1.173084	-1.254367
<i>orf3768</i>	<i>pcyA</i>		Phycocyanobilin:ferredoxin oxidoreductase	/	/	/	/	/	-1.041524	-1.030239	/
<i>orf3782</i>	<i>CPOX, hemF</i>		Coproporphyrinogen III oxidase	/	/	/	-1.176253	-1.753001	-1.967197	-1.883035	-1.767562
<i>orf3918</i>	<i>hemB, ALAD</i>		Delta-aminolevulinic acid dehydratase	/	/	/	/	-1.494445	-1.450056	-1.408465	-1.520044
<i>orf4253</i>	<i>EARS, gltX</i>		Glutamate--tRNA ligase	/	/	/	/	-1.292691	-1.709524	-1.284351	-1.200924
Carbohydrate Metabolism											
<i>orf023</i>	<i>ISA, treX</i>		Glycogen debranching enzyme	/	/	/	/	/	/	-1.201634	-1.072206
<i>orf149</i>	<i>GAPDH, gapA</i>		Type I glyceraldehyde-3-phosphate dehydrogenase	/	/	/	-1.060369	-1.124256	/	/	/
<i>orf291</i>	<i>PRK, prkB</i>		Phosphoribulokinase	/	/	/	/	/	-1.098592	/	/
<i>orf664</i>	<i>PGK, pgk</i>		Phosphoglycerate kinase	/	/	/	-1.1844	-1.753299	-1.988866	-1.984338	-1.611036

<i>orf959</i>	<i>tktA, tktB</i>	Transketolase	/	/	/	/	-1.39782	-1.126337	/	/
<i>orf1011</i>	<i>gmd, GMDS</i>	GDP-mannose 4,6-dehydratase	/	/	-1.072568	-1.145948	-1.006162	/	/	/
<i>orf1085</i>	<i>gap2</i>	Glyceraldehyde-3-phosphate dehydrogenase 2	/	/	-1.170231	-1.431752	-2.190859	-2.241147	-2.038929	-1.776055
<i>orf1156</i>	<i>nanE</i>	N-acetylmannosamine-6-phosphate 2-epimerase	/	-1.284792	-1.297003	-1.54504	-1.389105	-1.462729	-1.028215	/
<i>orf1212</i>	<i>PDHB, pdhB</i>	Alpha-ketoacid dehydrogenase subunit beta	/	/	/	-1.00962	-1.590848	-1.448146	-1.110622	/
<i>orf1326</i>	<i>glgA</i>	Starch synthase	/	/	-1.172735	-1.257534	-1.780259	-2.161627	-2.058277	-1.499022
<i>orf1421</i>	<i>DLD, lpd, pdhD</i>	Dihydrolipoyl dehydrogenase	/	/	/	/	/	/	-1.042142	/
<i>orf1443</i>	<i>treZ, glgZ</i>	Malto-oligosyltrehalose trehalohydrolase	/	/	/	/	-1.541588	-1.445924	-1.05268	-1.063685
<i>orf1485</i>	<i>K16149</i>	Glycoside hydrolase	/	/	/	/	-1.286263	-1.651033	-1.702122	-1.269093
<i>orf1770</i>	<i>glpX-SEBP</i>	Fructose-bisphosphatase class II	/	/	-1.254271	-1.578668	-2.147261	-2.208697	-2.169432	-1.730002
<i>orf1864</i>	<i>PK, pyk</i>	Pyruvate kinase	/	-1.089382	/	/	-1.056363	/	/	/
<i>orf1870</i>	<i>glgC</i>	Glucose-1-phosphate adenylyltransferase	/	/	-1.24163	-1.436757	-2.004339	-2.141168	-1.834495	-1.662528
<i>orf2128</i>	<i>UXS1, uxs</i>	NAD-dependent epimerase/dehydratase family protein	/	/	-1.044495	-1.050978	-1.351149	-1.68754	-1.511221	-1.149849
<i>orf2319</i>	<i>pgm</i>	Alpha-D-glucose phosphate-specific phosphoglucomutase	/	/	/	/	/	/	-1.078875	/
<i>orf2329</i>	<i>glgA</i>	Starch synthase	/	/	/	/	-1.068973	-1.228965	-1.238921	/
<i>orf2519</i>	<i>GBE1, glgB</i>	1,4-alpha-glucan branching enzyme	/	/	/	/	/	-1.091795	-1.198979	/
<i>orf2595</i>	<i>pckA</i>	Phosphoenolpyruvate carboxykinase (ATP)	/	/	/	/	-1.690188	-1.694098	-1.327352	-1.473663
<i>orf3143</i>	<i>rpe, RPE</i>	Ribulose-phosphate 3-epimerase	/	/	/	-1.070903	-1.664308	-1.837612	-1.81189	-1.481863
<i>orf4218</i>	<i>rfbE</i>	CDP-paratose 2-epimerase	/	/	-1.178217	-1.037836	-1.344658	/	/	/
<i>orf4219</i>	<i>rfbS</i>	NAD(P)-dependent oxidoreductase	/	/	-1.24379	/	-1.895303	/	/	/
<i>orf4439</i>	<i>FBA, fbaA</i>	Fructose-1,6-bisphosphate aldolase	/	/	/	/	/	-1.049788	-1.148942	/
Amino acid Metabolism										
<i>orf2583</i>	<i>psp</i>	Histidine phosphatase family protein	/	-1.334204	-1.297605	-1.574947	-1.842474	-1.889604	-1.713603	-1.439689
<i>orf2776</i>	<i>serA, PHGDH</i>	Phosphoglycerate dehydrogenase	/	-1.376746	-1.314191	-1.519293	-1.410412	/	/	/
<i>orf4389</i>	<i>trpA</i>	Tryptophan synthase subunit alpha	/	-1.044023	-1.127266	-1.464781	-1.401029	-1.376036	/	/
Lipid Metabolism										
<i>orf260</i>	<i>accC</i>	Acetyl-CoA carboxylase biotin carboxylase subunit	/	-1.053166	-1.170331	-1.472398	-1.435671	-1.186436	/	/
<i>orf960</i>	<i>fabI</i>	3-oxoacyl-[acyl-carrier-protein] synthase 2	/	/	/	/	/	-1.244559	-1.270107	/

<i>orf961</i>	<i>acpP</i>	Acyl carrier protein	/	/	/	/	-1.134346	-1.445378	-1.120403	-1.00068
<i>orf1757</i>	<i>E1.14.19.3</i>	Acyl-CoA desaturase	/		-1.000802	-1.032509	-1.412987	/	/	/
<i>orf2241</i>	<i>accB, bccP</i>	Acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	/		-1.22623	-1.160208	-1.553536	-1.402846	-1.462059	-1.445981
<i>orf2654</i>	<i>fabA</i>	3-hydroxyacyl-[acyl-carrier protein] dehydratase / trans-2-decenoyl-[acyl-carrier protein] isomerase	/	/	/	/	-1.870018	-1.406499	-1.075531	/
<i>orf2657</i>	<i>fabD</i>	Polyketide synthase	/	/	/	/	-1.281834	/	/	/
<i>orf2735</i>	<i>fabI</i>	Enoyl-[acyl-carrier protein] reductase I	/	/	/	/	-1.299971	-1.286843	-1.219711	/
<i>orf2818</i>	<i>fabZ</i>	Beta-hydroxyacyl-ACP dehydratase	/		-1.011676	-1.223857	-1.290788	-1.21654	-1.243417	-1.023701
<i>orf3348</i>	<i>fadD</i>	Long-chain acyl-CoA synthetase	/	/	/	/	/	-1.02831	-1.247851	-1.116828
<i>orf3378</i>	<i>ACSS, acs</i>	Acetyl-coenzyme A synthetase	/		-1.027548	-1.166988	-1.178968	-1.388212	-1.396544	-1.451172
Carbon fixation										
<i>orf3712</i>	<i>ccmK</i>	Microcompartments protein	/	/		-1.084617	-1.544011	-2.013013	-2.332908	-1.993407
<i>orf3713</i>	<i>ccmK</i>	Carbon dioxide-concentrating mechanism protein CcmK	/	/	/	/		-1.531553	-1.598937	-1.74274
<i>orf3714</i>	<i>ccmL</i>	Carbon dioxide concentrating mechanism protein CcmL	/	/		-1.321839	-1.722478	-2.074549	-2.318592	-1.875113
<i>orf3715</i>	<i>ccmM</i>	Carbon dioxide concentrating mechanism protein CcmM	/	/		-1.146145	-1.547201	-2.015334	-2.072119	-1.934726
<i>orf3716</i>	<i>ccmN</i>	Carbon dioxide concentrating mechanism protein	/		-1.014512	-1.299227	-1.659696	-2.017927	-2.022599	-1.706354
<i>orf3717</i>	<i>rbcL</i>	Ribulose-bisphosphate carboxylase large subunit	/	/		-1.072348	-1.386194	-2.227396	-2.262108	-1.991006
<i>orf3719</i>	<i>rbcS</i>	Ribulose bisphosphate carboxylase small subunit	/	/		-1.274913	-1.460708	-2.125579	-2.269645	-1.779566
Oxidative phosphorylation										
<i>orf945</i>	<i>ndhD</i>	NAD(P)H-quinone oxidoreductase subunit D4	/	/	/	/		-1.573704	-1.778697	-1.564252
<i>orf947</i>	<i>ndhF</i>	NAD(P)H-quinone oxidoreductase subunit F	/	/	/	/		-1.349375	-1.416703	-1.564401
<i>orf1155</i>	<i>ppa</i>	Inorganic pyrophosphatase	/	/	/	/	-1.40926	-1.678185	-1.708454	-1.733365
<i>orf1234</i>	<i>ndhA</i>	NADH-quinone oxidoreductase subunit H	/	/	/	/		-1.073315	-1.133462	-1.296859
<i>orf1235</i>	<i>ndhI</i>	NAD(P)H-quinone oxidoreductase subunit I	/	/	/	/		-1.199853	-1.0175	/
<i>orf1236</i>	<i>ndhG</i>	NADH:ubiquinone oxidoreductase subunit J	/	/	/	/		-1.08541	/	/
<i>orf1402</i>	<i>ATPF1B, atpD</i>	ATP synthase subunit beta	/	/	/	/		-1.259526	-1.859781	-2.045115
<i>orf1403</i>	<i>ATPF1E, atpC</i>	ATP synthase epsilon chain	/	/		-1.019071	-1.265868	-1.879405	-1.999593	-1.650046

<i>orf1818</i>	<i>ndhM</i>	NAD(P)H-quinone oxidoreductase subunit M	/	/	-1.136791	-1.122891	-1.956112	-1.416938	/	-1.185531
<i>orf2053</i>	<i>ATPFOA, atpB</i>	AtpB	/	/	/	/	-1.496058	-1.67446	-1.660346	-1.270855
<i>orf2054</i>	<i>ATPFOC, atpE</i>	ATP synthase F0 subunit C	/	/	/	-1.03497	-1.413663	-1.793516	-2.041615	-1.421271
<i>orf2055</i>	<i>ATPFOB, atpF</i>	F0F1 ATP synthase subunit B'	/	/	-1.269863	-1.508116	-1.720013	-1.840708	-1.617089	-1.458756
<i>orf2056</i>	<i>ATPFOB, atpF</i>	ATP synthase subunit B	/	/	-1.051844	-1.370558	-1.783724	-1.76669	-1.577814	-1.391811
<i>orf2057</i>	<i>ATPF1D, atpH</i>	F0F1 ATP synthase subunit delta	/	/	/	-1.269876	-1.615655	-1.667103	-1.594624	-1.302267
<i>orf2058</i>	<i>ATPF1A, atpA</i>	ATP synthase subunit alpha	/	/	/	-1.088211	-1.50464	-1.575348	-1.511965	-1.139905
<i>orf2059</i>	<i>ATPF1G, atpG</i>	F0F1 ATP synthase subunit gamma	/	/	/	-1.12453	-1.616107	-1.632777	-1.367676	-1.26374
<i>orf2249</i>	<i>ndhF</i>	NAD(P)H-quinone oxidoreductase subunit F	/	/	/	/	/	-1.401208	-1.301029	-1.320056
<i>orf2339</i>	<i>COX10, ctaB, cyoE</i>	Protoheme IX farnesyltransferase	/	/	/	/	/	/	/	-1.123575
<i>orf2340</i>	<i>COX15, ctaA</i>	Heme A synthase	/	/	/	/	-1.163557	/	-1.003792	-1.367286
<i>orf2341</i>	<i>coxB, ctaC</i>	Cytochrome C oxidase subunit II	/	/	/	/	-1.485754	-1.686257	-1.465255	-1.202403
<i>orf2342</i>	<i>coxA, ctaD</i>	Cytochrome c oxidase subunit I	/	/	/	/	-1.49678	-1.698612	-1.479239	-1.185729
<i>orf2343</i>	<i>coxC, ctaE</i>	Heme-copper oxidase subunit III	/	/	/	/	-1.399835	-1.50053	-1.269476	-1.03879
<i>orf2351</i>	<i>sdhC, frdC</i>	Putative succinate dehydrogenase cytochrome b subunit	/	/	/	/	-1.020112	-1.152493	-1.202111	-1.055951
<i>orf3477</i>	<i>ndhD</i>	NAD(P)H-quinone oxidoreductase subunit D4	/	/	/	-1.156445	-2.079242	-2.204658	-2.075789	-1.788747
<i>orf4060</i>	<i>ndhB</i>	NAD(P)H-quinone oxidoreductase subunit 2	/	/	/	/	-1.06573	-1.440463	-1.560607	-1.24706
<i>orf4254</i>	<i>ndhN</i>	NAD(P)H-quinone oxidoreductase subunit N	/	/	/	/	-1.468605	-1.621216	-1.78127	-1.155769

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124 **TABLE S6** Transcriptional levels of copy number variation genes in the *Microcystis* genome after Mic1 infection.

Locus tag	Length (bp)	Overlap (bp)	Strand	Annotation	Log ₂ FoldChange							
					0.5 h	1 h	1.5 h	2 h	4 h	6 h	8 h	10 h
<i>orf3029</i>	482	46	-	Hypothetical protein	/	-1.318264	-1.332001	-1.500621	-1.50249	-1.42433	-1.11091	-1.244936
<i>orf3030</i>	1286	1287	-	DEDD_Tnp_IS110; Transposase	/	/	/	/	/	3.502497	3.619751	3.833235
<i>orf3031</i>	380	279	-	Hypothetical protein	/	/	/	1.303704	/	/	/	/
<i>orf3032</i>	260	261	-	Hypothetical protein	/	/	/	/	/	/	/	/
<i>orf3033</i>	314	315	-	Hypothetical protein	/	/	/	1.498289	/	/	/	/
<i>orf3034</i>	1052	1053	-	Lambda repressor-like; SpoIIID	/	/	/	/	/	/	/	/
<i>orf3035</i>	248	249	+	Lambda repressor-like; HTH_3_3	/	/	/	/	/	1.288747	1.200416	/
<i>orf3036</i>	932	933	+	Lipid binding protein	/	/	/	/	1.022143	/	/	/
<i>orf3037</i>	236	237	+	Hypothetical protein	/	/	/	/	/	/	/	/
<i>orf3038</i>	569	570	-	Phage integrase	/	/	/	/	/	/	/	/
<i>orf3039</i>	1193	1194	+	Enolase	/	/	/	/	/	/	/	/
<i>orf3040</i>	2003	2004	+	Hypothetical protein	/	/	/	/	/	/	/	/
<i>orf3041</i>	812	813	+	Hypothetical protein	/	/	/	/	/	4.186136	4.419668	4.359621
<i>orf3042</i>	371	372	+	Hypothetical protein	/	/	/	/	/	/	/	/
<i>orf3043</i>	386	387	+	Hypothetical protein	/	/	/	/	/	4.409537	3.645612	3.962079
<i>orf3044</i>	401	402	+	Hypothetical protein	/	/	/	/	/	4.465152	4.391242	4.253675
<i>orf3045</i>	467	468	+	Hypothetical protein	/	/	/	/	/	4.172835	4.591515	5.614151
<i>orf3046</i>	617	618	+	N-terminal Ig-like domain in baseplate protein	/	/	/	/	/	4.101424	3.172164	5.606252
<i>orf3047</i>	434	435	+	Hypothetical protein	/	/	/	/	/	3.212233	/	2.037753
<i>orf3048</i>	800	801	+	LamG-like jellyroll fold domain-containing protein	/	/	/	/	/	2.975675	3.864765	3.607104
<i>orf3049</i>	230	231	+	Hypothetical protein	/	/	/	/	/	/	3.068401	3.182221
<i>orf3050</i>	440	441	+	D-Ala-D-Ala carboxypeptidase family metallohydrolase	/	/	/	/	1.074036	1.042993	/	1.327406
<i>orf3051</i>	248	57	-	Acetyltransferase (GNAT) domain	/	/	/	/	/	/	/	/

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