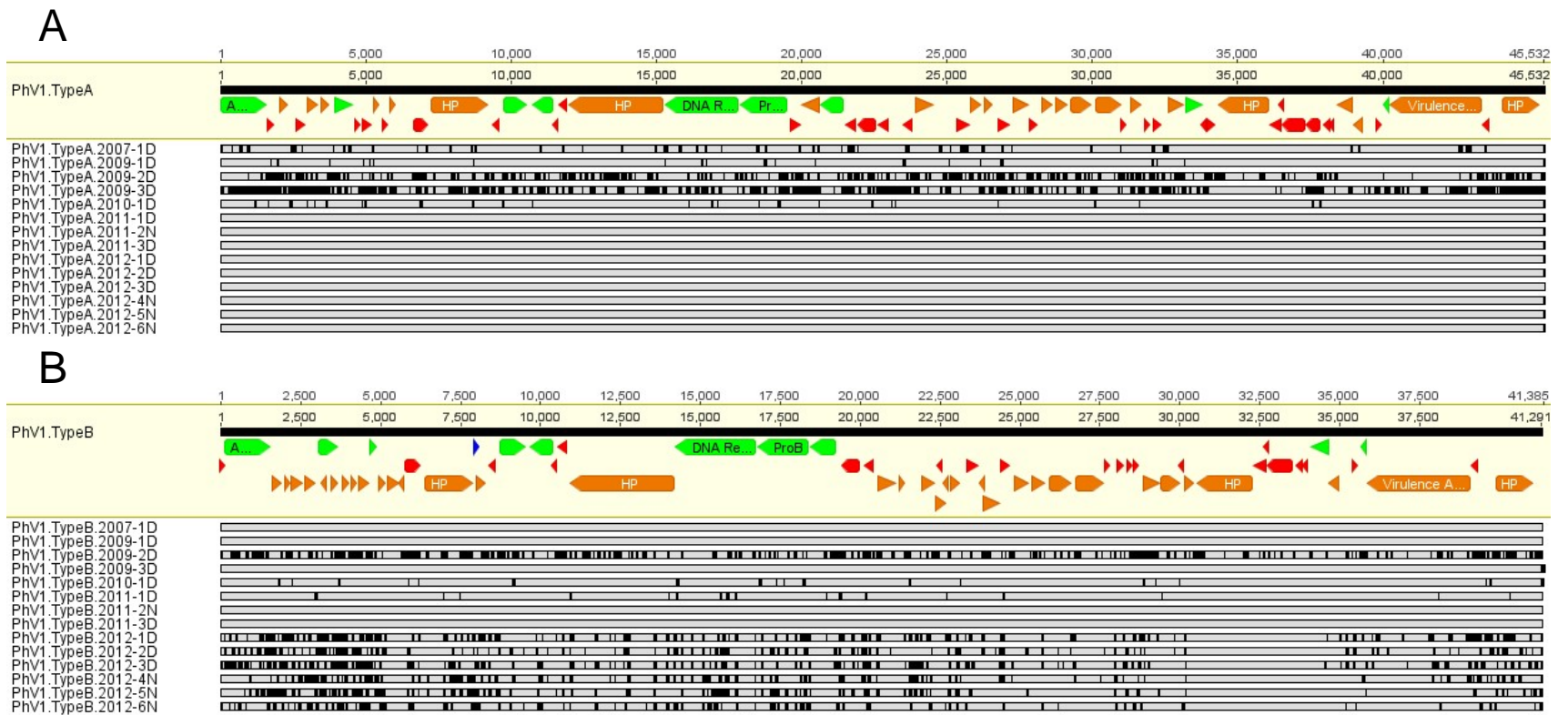
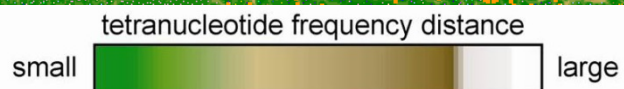
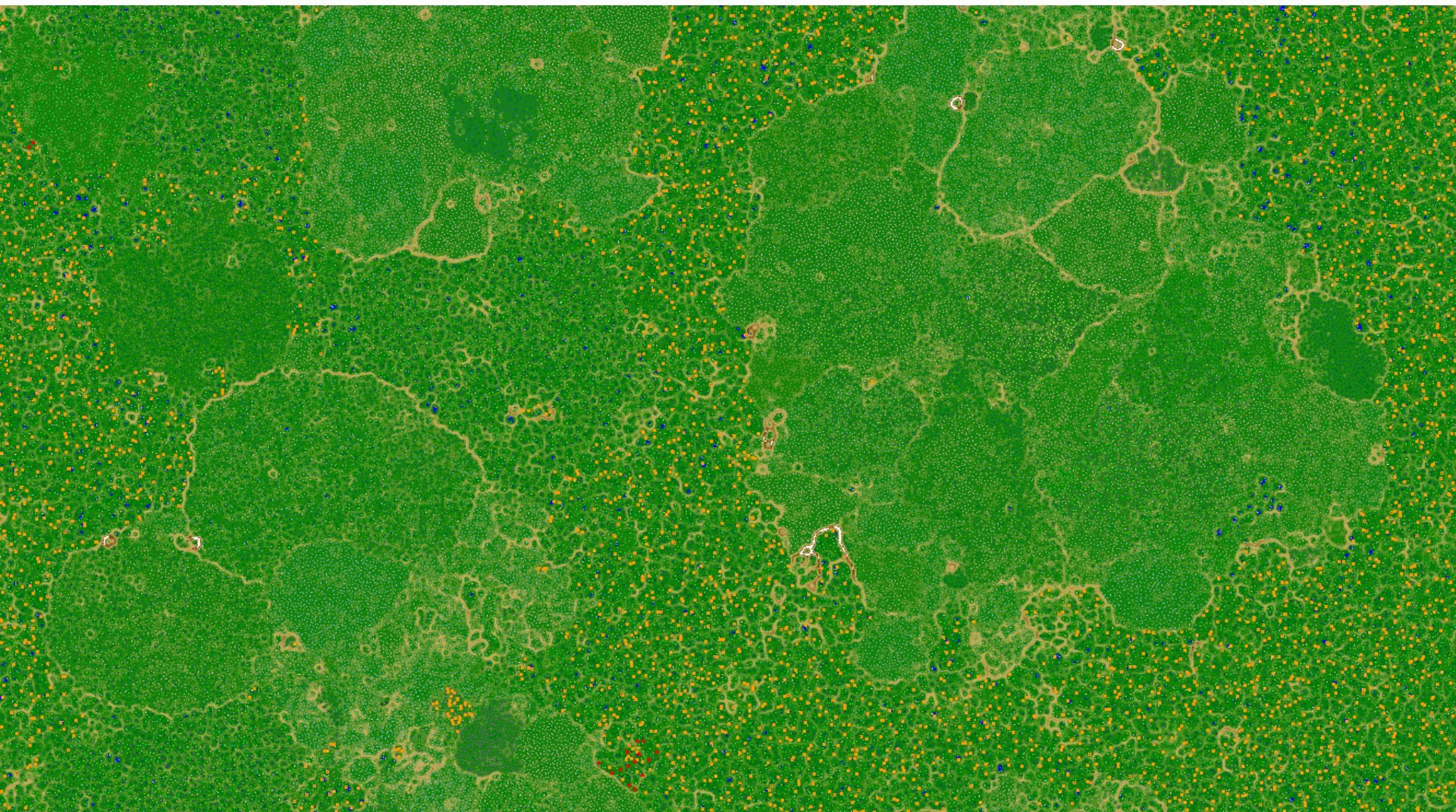


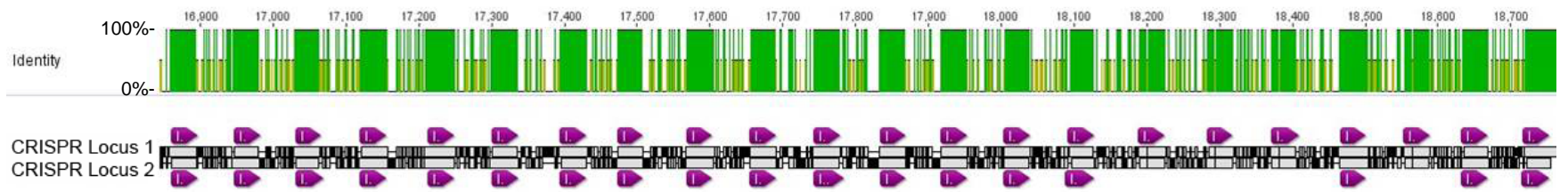
Supplemental Figure 1. Screen captures from Geneious showing reads mapped to PhV1.TypeA. Highlighted bases denote deviation from the template sequence; red arrow denotes low abundance genomic variant matching the template.



Supplemental Figure 2. Reads from each sample were mapped to consensus sequences of PhV1 genotypes to evaluate genome completeness in each sample. (A) reads mapped to PhV1 type A, (B) reads mapped to PhV1 type B. Green: genes which could be annotated, orange: hypothetical genes present in NR with no annotation, blue: region that matches a CRISPR III-B spacer, grey: regions with read coverage, black: regions lacking read coverage.



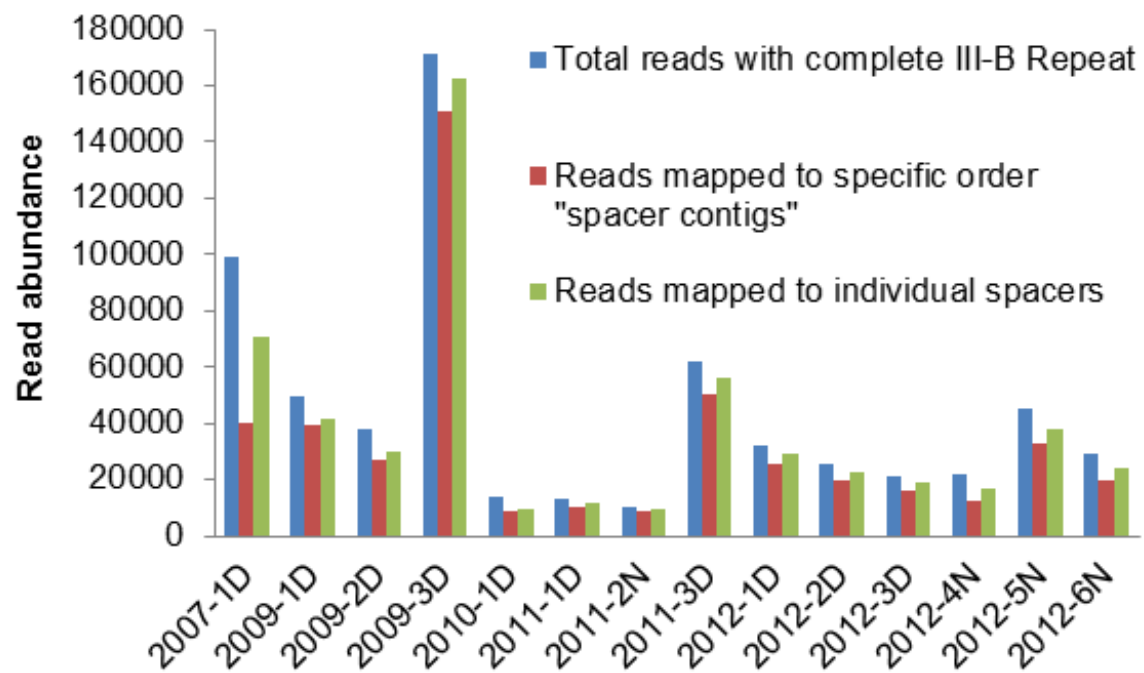
Supplemental Figure 4. Self organizing ESOM map of the MIS mat community. Each data point represents a 5-kb sequence fragment that has been spatially clustered according to tetranucleotide frequency. Sequences from Phormidium are shown in orange and those from PhV1 are shown in red. Data points from reference genomes included as internal standards and other metagenomic contigs are included but with minimized size because they are not relevant to the current study. To visualize genomic bins, the background color represents the euclidean tetranucleotide distance between data points as shown in the legend. Hence, bins appear as green areas and borders between bins appear as brown or white areas. Note the right and left edges, as well as the top and bottom edges, are contiguous



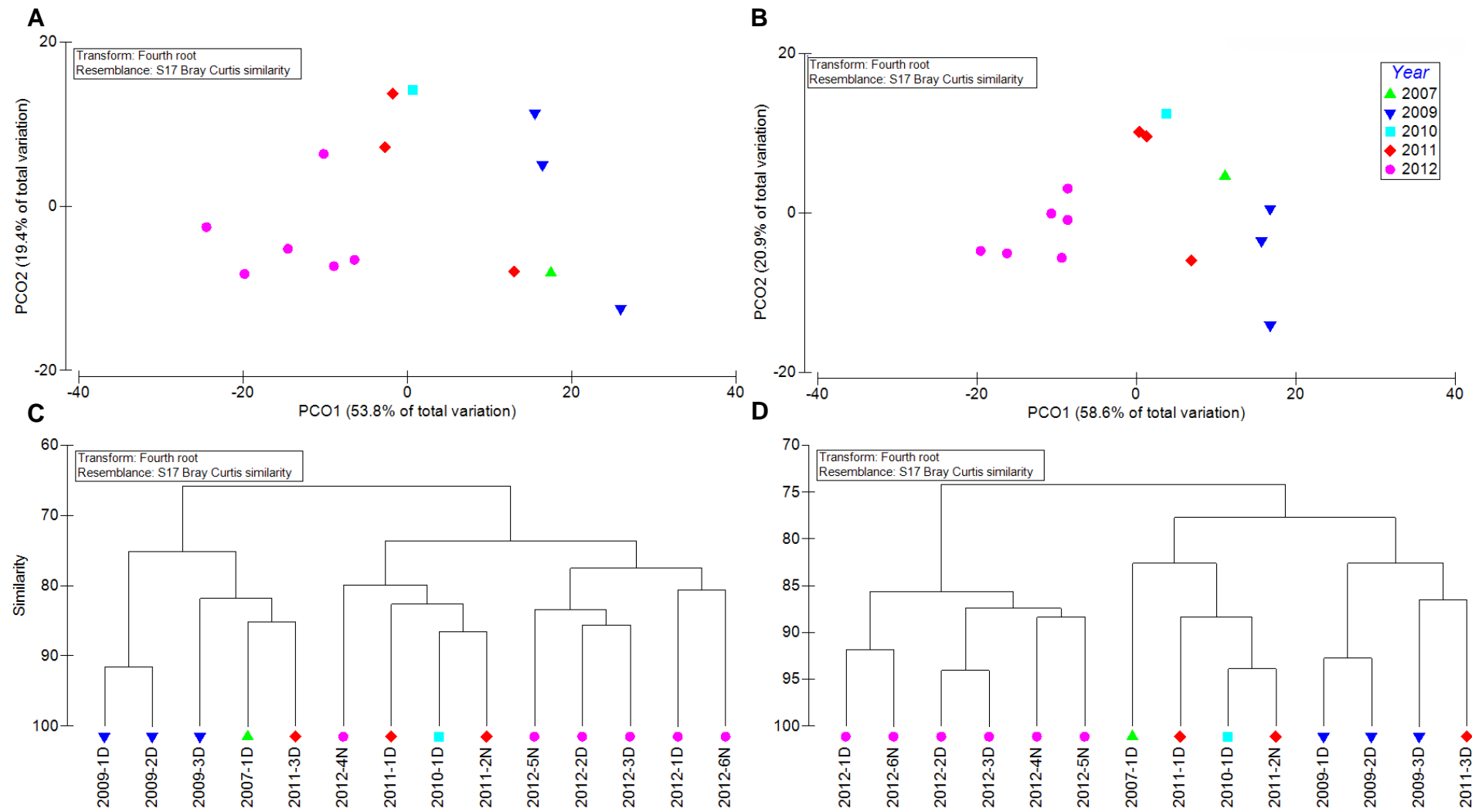
Supplemental Figure 5. Nucleotide alignment of the *Phormidium* Type III-B CRISPR region from Locus 1 and Locus 2. Purple: CRISPR repeats with spacers located between repeats, grey: areas of nucleotide agreement, black: nucleotide disagreement.



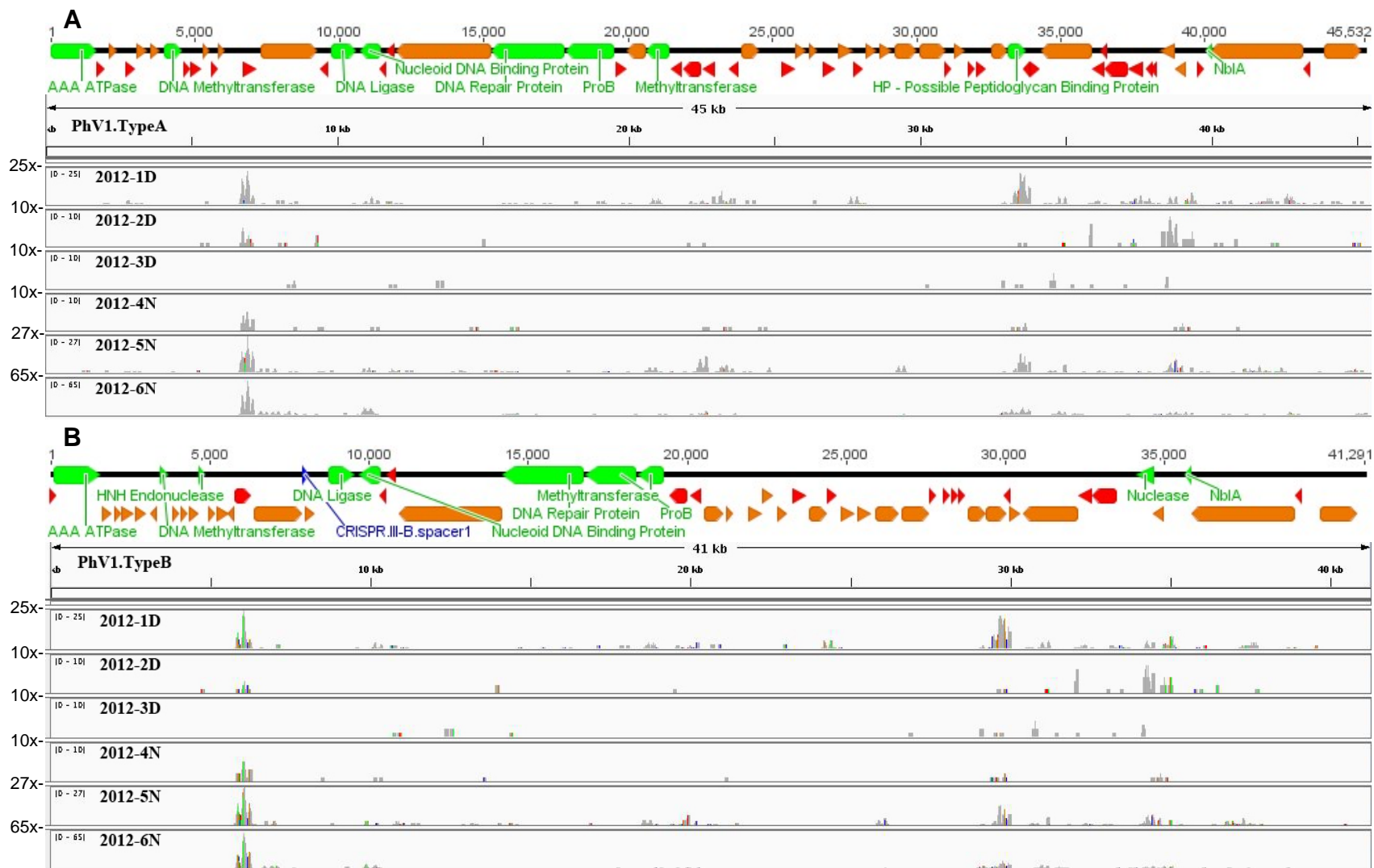
Supplemental Figure 6. Nucleotide alignment of Phormidium CRISPR subtype III-B Locus1 showing sequence conservation in each of the 14 samples. Green: genes which could be annotated, orange: hypothetical genes present in NR with no annotation, purple: CRISPR repeats with spacers located between repeats, grey: regions of nucleotide agreement.



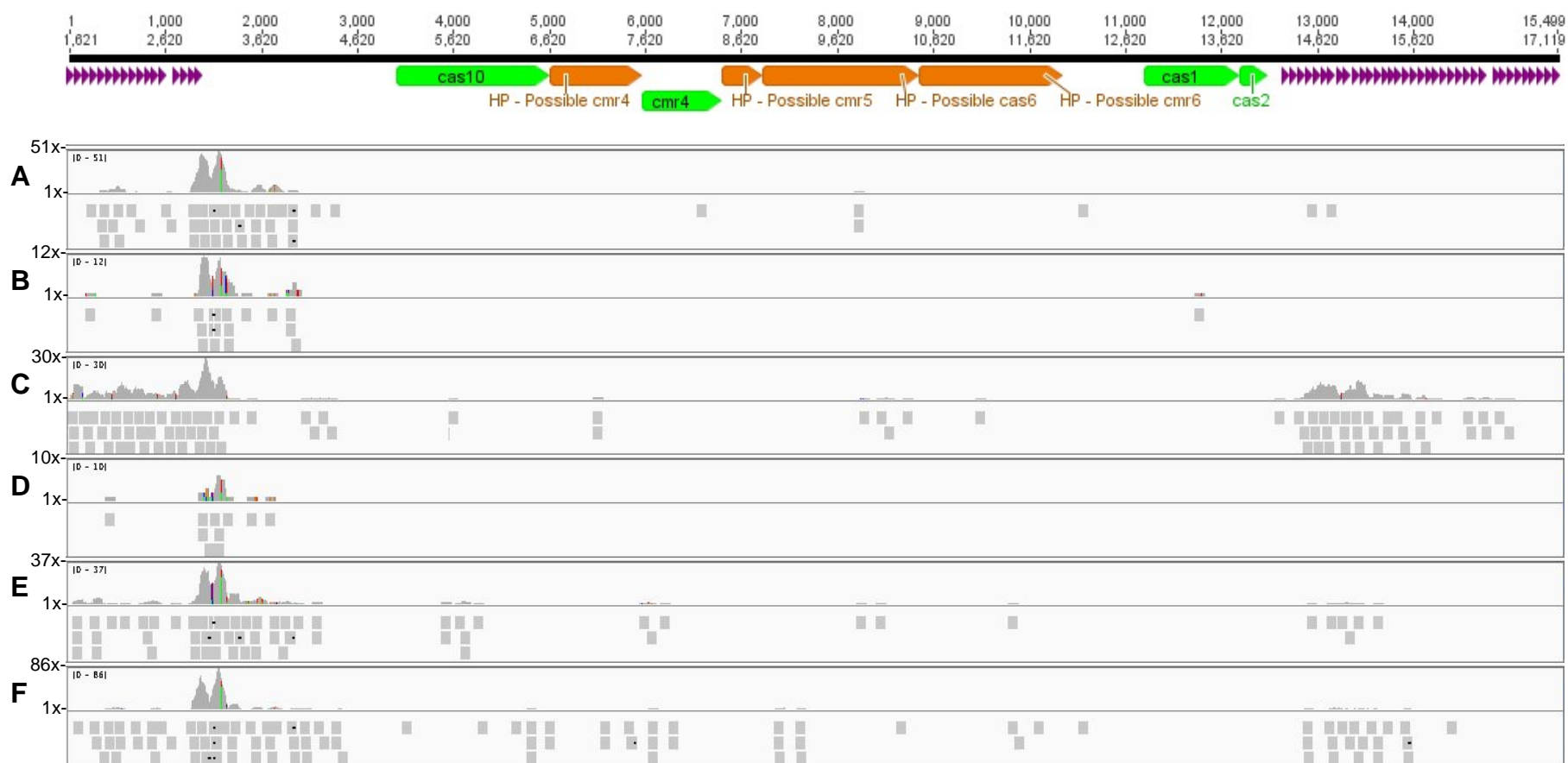
Supplemental Figure 7. CRISPR subtype III-B individual spacer and conserved order "spacer contigs" normalized average read abundance.



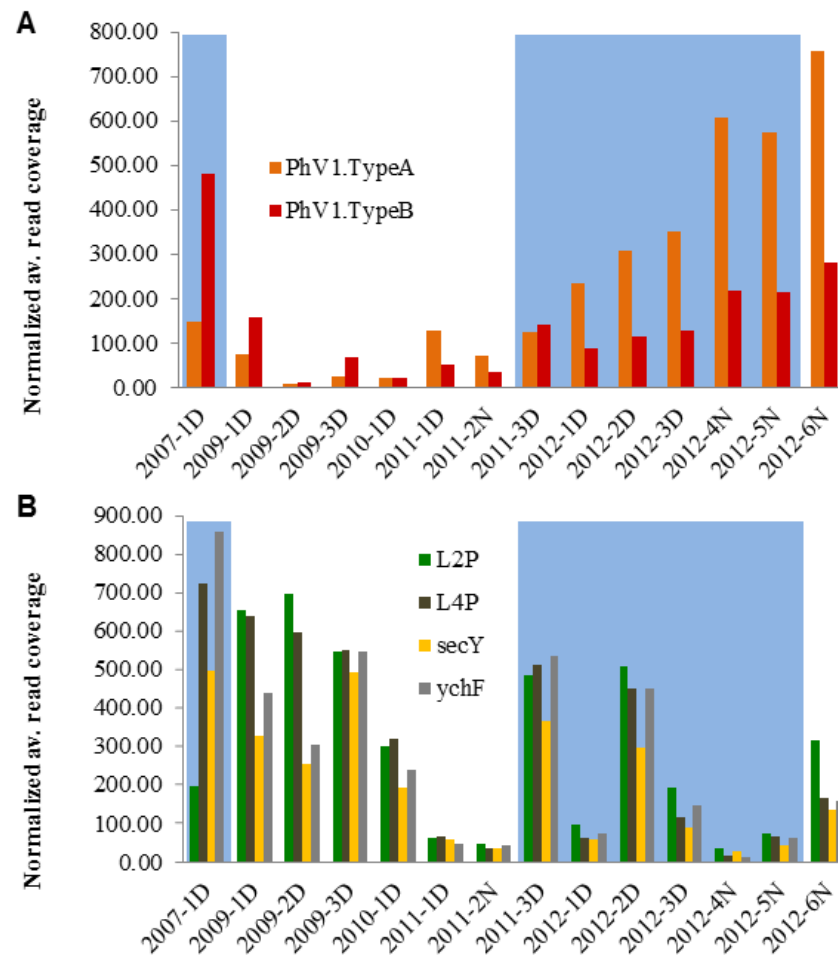
Supplemental Figure 8. Multivariate analysis of CRISPR spacer contigs and individual spacers. (A) Principal coordinate analyses of CRISPR spacer contigs by year, (B) principal coordinate analyses of individual CRISPR spacers by year, (C) group average analysis of CRISPR spacer contigs by year, (D) group average analysis of individual CRISPR spacers by year.



Supplemental Figure 9. cDNA from 2012 samples mapped to PhV1. Note that peaks range from 1x-65x coverage. (A) PhV1 type A; (B) PhV1 type B. Green: genes which could be annotated, orange: genes with no known function, red: novel genes, blue: region that matches a CRISPR III-B spacer.



Supplemental Figure 10. cDNA from 2012 samples mapped to CRISPR Locus1 . (A) Sample 2012-1D, (B) sample 2012-2D, (C) sample 2012-3D, (D) sample 2012-4N, (E) sample 2012-5N; (F) sample 2012-6N, Green: genes which could be annotated, orange: hypothetical genes, purple: CRISPR repeats, with spacers located between repeats. Grey boxes under peaks: individual reads with window cut off at 3x read depth.



Supplemental Figure 11. Normalized gDNA read abundance of *Phormidium* and viruses PhV1 typeA and B in each sample. (A) abundance of virus PhV1 type A and B based on reads mapped to each genome, (B) abundance of *Phormidium* based on reads mapped to four different single copy housekeeping genes. Blue background shows samples that contain CRISPR.III-B.spacer1 that matches PhV1.TypeB. Samples collected during the day are indicated by D and samples collected at night are indicated by N.

Supplemental Table 1. PHV1.TypeA Annotations

Start	Stop	Length	Annotation	Direction
1	1,575	1,575	AAA ATPase	forward
1,580	1,873	294	Novel 1	forward
2,017	2,319	303	HP	forward
2,600	2,932	333	Novel 2	forward
2,952	3,350	399	HP	forward
3,429	3,764	336	HP	forward
3,927	4,571	645	DNA Methyltransferase	forward
4,652	4,816	165	Novel 3	forward
4,860	5,210	351	Novel 4	forward
5,250	5,483	234	HP	forward
5,568	5,774	207	Novel 5	forward
5,823	6,041	219	HP	forward
6,643	7,149	507	Novel 6	forward
7,256	9,217	1,962	HP	forward
9,329	9,601	273	Novel 7	reverse
9,728	10,558	831	DNA Ligase	forward
10,713	11,459	747	Nucleoid DNA Binding Protein	reverse
11,456	11,614	159	Novel 8	reverse
11,614	11,919	306	Novel 9	reverse
11,989	15,270	3,282	HP	reverse
15,274	17,829	2,556	DNA Repair Protein	reverse
17,865	19,526	1,662	ProB	reverse
19,596	19,967	372	Novel 10	forward
19,978	20,634	657	HP	reverse
20,638	21,453	816	Methyltransferase	reverse
21,516	21,878	363	Novel 11	reverse
21,946	22,566	621	Novel 12	reverse
22,623	23,015	393	Novel 13	reverse
23,497	23,823	327	Novel 14	reverse
23,925	24,545	621	HP	forward
25,327	25,809	483	Novel 15	forward
25,806	26,171	366	HP	forward
26,267	26,581	315	HP	forward
26,768	27,172	405	Novel 16	forward
27,287	27,838	552	HP	forward
27,841	28,140	300	Novel 17	forward
28,256	28,645	390	HP	forward
28,723	29,172	450	HP	forward
29,266	30,003	738	HP	forward
30,110	31,009	900	Hypothetical Phage Gene	forward
31,006	31,209	204	Novel 18	forward
31,302	31,688	387	HP	forward
31,806	32,021	216	Novel 19	forward
32,098	32,403	306	Novel 20	forward
32,629	33,183	555	HP	forward
33,193	33,801	609	HP - Possible Peptidoglycan Binding Protein	forward
33,796	33,906	111	Novel 21	reverse
33,939	34,262	324	Novel 22	forward
34,351	36,096	1,746	HP	reverse
36,093	36,515	423	Novel 23	reverse
36,472	36,579	108	Novel 24	reverse
36,524	37,327	804	Novel 25	reverse
37,358	37,855	498	Novel 26	reverse
37,946	38,191	246	Novel 27	reverse
38,192	38,311	120	Novel 28	reverse
38,431	38,994	564	HP	reverse
38,975	39,334	360	HP	reverse
39,740	39,979	240	Novel 29	forward
40,058	40,219	162	NbIA	reverse
40,230	43,418	3,189	Virulence Associated E Protein	reverse
43,415	43,666	252	Novel 30	reverse
44,133	45,413	1,281	HP	forward

Supplemental Table 2. PhV1.TypeB Annotations

Start	Stop	Length	Name	Direction
1	161	161	Novel 31	forward
106	1,575	1,470	AAA ATPase	forward
1,597	1,923	327	HP	forward
1,999	2,196	198	HP - Possible Hydrolase	forward
2,207	2,599	393	HP	forward
2,628	2,989	362	HP	forward
3,058	3,696	639	DNA Methyltransferase	forward
3,161	3,340	180	HP	reverse
3,430	3,696	267	HP	forward
3,804	4,037	234	HP	forward
4,086	4,286	201	HP	forward
4,322	4,645	324	HP	forward
4,642	4,878	237	HNH Endonuclease	forward
4,936	5,170	235	HP	forward
5,217	5,588	372	HP	forward
5,592	5,750	159	HP	reverse
5,768	6,274	507	Novel 6	forward
6,381	7,910	1,530	HP	forward
7,994	8,281	288	HP - Possible Membrane Protein or Specificity Protein	forward
8,376	8,627	252	Novel 7	reverse
8,730	9,560	831	DNA Ligase	forward
9,679	10,398	720	Nucleoid DNA Binding Protein	reverse
10,395	10,550	156	Novel 8	reverse
10,550	10,855	306	Novel 9	reverse
10,925	14,206	3,282	HP	reverse
14,210	16,768	2,559	DNA Repair Protein	reverse
16,804	18,396	1,593	ProB	reverse
18,460	19,275	816	Methyltransferase	reverse
19,437	20,015	579	Novel 12	reverse
20,107	20,433	327	Novel 14	reverse
20,537	21,157	621	HP	forward
21,284	21,391	108	HP	forward
21,925	22,354	430	HP - Phage Protein 7.7 Like	forward
22,351	22,716	366	HP	forward
22,413	22,577	165	Novel 32	reverse
22,574	22,771	198	HP	reverse
22,832	23,146	315	HP	forward
23,334	23,738	405	Novel 16	forward
23,735	23,911	177	HP	reverse
23,852	24,403	552	HP	forward
24,406	24,705	300	Novel 17	forward
24,821	25,282	462	HP	forward
25,360	25,809	450	HP	forward
25,903	26,640	738	HP	forward
26,733	27,632	900	HP - Possible gp37/gp68 Phage Gene	forward
27,629	27,832	204	Novel 18	forward
28,039	28,254	216	Novel 19	forward
28,344	28,532	189	Novel 20	forward
28,594	28,701	108	CDS	forward
28,852	29,406	555	HP - Possible Endonuclease	forward
29,416	30,024	609	HP - Possible Peptidoglycan Binding Protein	forward
30,019	30,114	96	Novel 21	reverse
30,147	30,470	324	HP	forward
30,559	32,304	1,746	HP	reverse
32,301	32,723	423	Novel 23	reverse
32,680	32,787	108	Novel 24	reverse
32,732	33,535	804	Novel 25	reverse
33,626	33,862	237	Novel 27	reverse
33,863	33,982	120	Novel 28	reverse
34,111	34,674	564	Nuclease	reverse
34,655	35,014	360	HP	reverse
35,419	35,547	129	Novel 29	forward
35,684	35,845	162	NbIA	reverse
35,856	39,104	3,249	Virulence Associated E Protein	reverse
39,101	39,352	252	Novel 30	reverse
39,908	41,080	1,173	HP	forward

Supplementary Table 3. Occurrence of NblA proteins in finished cyanobacterial genomes

<u>IMG Gene ID</u>	<u>IMG Locus Tag</u>	<u>Genome</u>
2504130049	Anacy_0427	Anabaena cylindrica PCC 7122
2504133118	Anacy_3451	Anabaena cylindrica PCC 7122
2562228843	ANA_C11286	Anabaena sp. 90
646568884	Ava_3383	Anabaena variabilis ATCC 29413
2504093934	Cal6303_0950	Calothrix sp. PCC 6303
2504093985	Cal6303_1001	Calothrix sp. PCC 6303
2504094115	Cal6303_1131	Calothrix sp. PCC 6303
2505800739	Cal7507_2470	Calothrix sp. PCC 7507
2505803407	Cal7507_5089	Calothrix sp. PCC 7507
2510438685	Cha6605_2686	Chamaesiphon minutus PCC 6605
2510438724	Cha6605_2725	Chamaesiphon minutus PCC 6605
2510439667	Cha6605_3668	Chamaesiphon minutus PCC 6605
2503610247	Chro_0004	Chroococciopsis thermalis PCC 7203
2503612764	Chro_2501	Chroococciopsis thermalis PCC 7203
2503612774	Chro_2511	Chroococciopsis thermalis PCC 7203
2504684288	Cri9333_1853	Crinalium epipsammum PCC 9333
2503745738	Cyan10605_1477	Cyanobacterium aponinum PCC 10605
2503746430	Cyan10605_2159	Cyanobacterium aponinum PCC 10605
2503366269	Cyast_0866	Cyanobacterium stanieri PCC 7202
2503367732	Cyast_2308	Cyanobacterium stanieri PCC 7202
643479281	PCC7424_1012	Cyanothece sp. PCC 7424
643481400	PCC7424_3154	Cyanothece sp. PCC 7424
643583228	Cyan7425_0220	Cyanothece sp. PCC 7425
643585814	Cyan7425_2827	Cyanothece sp. PCC 7425
648185141	Cyan7822_0149	Cyanothece sp. PCC 7822
643474262	PCC8801_1176	Cyanothece sp. PCC 8801
643474263	PCC8801_1177	Cyanothece sp. PCC 8801
644979216	Cyan8802_1203	Cyanothece sp. PCC 8802
644979217	Cyan8802_1204	Cyanothece sp. PCC 8802
2509768698	CylstDRAFT_2658	Cylindrospermum stagnale PCC 7417
2509769273	CylstDRAFT_3233	Cylindrospermum stagnale PCC 7417
2509553335	Dacsa_0949	Dactylococcopsis salina PCC 8305
2503609352	GEI7407_3338	Geitlerinema sp. PCC 7407
2503609353	GEI7407_3339	Geitlerinema sp. PCC 7407
2503792581	Glo7428_0036	Gloeocapsa sp. PCC 7428
2503795029	Glo7428_2459	Gloeocapsa sp. PCC 7428
2503635059	PCC7418_0351	Halothece sp. PCC 7418
2022828762	CYJSC1_DRAFT_04660	Leptolyngbya sp. JSC-1
2022832707	CYJSC1_DRAFT_60860	Leptolyngbya sp. JSC-1
2022832938	CYJSC1_DRAFT_59660	Leptolyngbya sp. JSC-1
2022833971	CYJSC1_DRAFT_66220	Leptolyngbya sp. JSC-1

2558008581	Oscopy1DRAFT_01646	Leptolyngbya sp. JSC-1
2558012300	Oscopy1DRAFT_05371	Leptolyngbya sp. JSC-1
2558012513	Oscopy1DRAFT_05584	Leptolyngbya sp. JSC-1
2558013490	Oscopy1DRAFT_06562	Leptolyngbya sp. JSC-1
2503886033	Lepto7376_0438	Leptolyngbya sp. PCC 7376
2503888145	Lepto7376_2529	Leptolyngbya sp. PCC 7376
2503889028	Lepto7376_3398	Leptolyngbya sp. PCC 7376
2509435054	Mic7113_3219	Microcoleus sp. PCC 7113
2509436586	Mic7113_4751	Microcoleus sp. PCC 7113
2563163497	NSP_44910	Nodularia spumigena CCY9414
648051302	Aazo_3770	Nostoc azollae 0708
648051456	Aazo_3966	Nostoc azollae 0708
642601385	Npun_F2237	Nostoc punctiforme PCC 73102
642602108	Npun_F3014	Nostoc punctiforme PCC 73102
642602782	Npun_R3808	Nostoc punctiforme PCC 73102
2503741444	Nos7107_2795	Nostoc sp. PCC 7107
2509812345	Nos7524_4777	Nostoc sp. PCC 7524
2509420338	Oscil6304_1131	Oscillatoria acuminata PCC 6304
2509425186	Oscil6304_5979	Oscillatoria acuminata PCC 6304
2504089000	Osc7112_2468	Oscillatoria nigro-viridis PCC 7112
2504089688	Osc7112_3155	Oscillatoria nigro-viridis PCC 7112
2509574340	Ple7327_2457	Pleurocapsa sp. PCC 7327
2509574488	Ple7327_2605	Pleurocapsa sp. PCC 7327
2509574998	Ple7327_3115	Pleurocapsa sp. PCC 7327
2509575233	Ple7327_3350	Pleurocapsa sp. PCC 7327
2509576537	Ple7327_4655	Pleurocapsa sp. PCC 7327
2510090234	Riv7116_5088	Rivularia sp. PCC 7116
2510090676	Riv7116_5530	Rivularia sp. PCC 7116
2503798897	Sta7437_0830	Stanieria cyanosphaera PCC 7437
2503800960	Sta7437_2865	Stanieria cyanosphaera PCC 7437
2503802052	Sta7437_3947	Stanieria cyanosphaera PCC 7437
2503802363	Sta7437_4257	Stanieria cyanosphaera PCC 7437
637617653	syc1965_c	Synechococcus elongatus PCC 6301
637800572	Synpcc7942_2127	Synechococcus elongatus PCC 7942
637877162	CYB_2772	Synechococcus sp. JA-2-3B'a(2-13)
2509429187	Syn6312_1146	Synechococcus sp. PCC 6312
2509430470	Syn6312_2429	Synechococcus sp. PCC 6312
641611943	SYNPCC7002_A1933	Synechococcus sp. PCC 7002
651079119	SYNGTS_1378	Synechocystis sp. GT-S, PCC 6803
651079120	SYNGTS_1379	Synechocystis sp. GT-S, PCC 6803
637010821	ssl0453	Synechocystis sp. PCC 6803
637010822	ssl0452	Synechocystis sp. PCC 6803
2562386647	MYO_113900	Synechocystis sp. PCC 6803

2562386648	MYO_113910	Synechocystis sp. PCC 6803
2515003719	S6july2012_01456	Synechocystis sp. PCC 6803 (updateJune2012)
2515003720	S6july2012_01457	Synechocystis sp. PCC 6803 (updateJune2012)
2514153713	SYNPCCN_1377	Synechocystis sp. PCC 6803, GT-I
2514153714	SYNPCCN_1378	Synechocystis sp. PCC 6803, GT-I
2514150496	SYNPCCP_1377	Synechocystis sp. PCC 6803, PCC-N
2514150497	SYNPCCP_1378	Synechocystis sp. PCC 6803, PCC-N
2524499062	SYNPCCP_1377	Synechocystis sp. PCC 6803, PCC-P
2524499063	SYNPCCP_1378	Synechocystis sp. PCC 6803, PCC-P

Supplemental Table 4. III-B CRISPR repeats

	<u>Repeat Sequence</u>
III-B.Repeat .A	CTCCCCACTCGTTGGGGAAACTAATTGAATGGAAAC
III-B.Repeat .B	CTCCCCACTCGCTGGGGAAACTAATTGAATGGAAAC
III-B.Repeat .C	GTCGCTTCTATTCGTAGAAAGTGAATTAATGGAAAC
III-B.Repeat .D	GTCCCCACTCGCTGGGGAAACTAATTGAATGGAAAC
III-B.Repeat .E	CCCTACCGATGGGTTTAAATCGGATTAGTTGGAAAC

Supplemental Table 5. Parameters used for bioinformatics software

Program Name: Geneious v6.1.5		<u>Cost</u>	<u>Gap Open</u>	<u>Gap extend</u>	<u>Type</u>	<u>Iterations</u>	
<u>Function</u>	<u>Algyorythem</u>	<u>Matrix</u>					
Multiple Alignment	Geneious Alignment	93%	12	3	Global alignment with free end gaps	3	
				<u>Max Gap</u>			
<u>Function</u>	<u>Sensitivity</u>	<u>Trim</u>	<u>Max Gap</u>	<u>Size</u>	<u>Min Overlap</u>	<u>Overlap ID</u>	<u>Max Mismatches</u>
Map to Reference	Custom	None	10%	10bp	60	100%	2%
				<u>Max Gap</u>			
<u>Function</u>	<u>Sensitivity</u>	<u>Trim</u>	<u>Max Gap</u>	<u>Size</u>	<u>Min Overlap</u>	<u>Overlap ID</u>	<u>Max Mismatches</u>
De Novo Assemble	Custom	None	10%	10bp	60	100%	2%

Program Name: Velvet v1.2.08		<u>kmer values</u>	<u>Read Type</u>
<u>Function</u>			
Assembly	91, 75, 61	Paired	

Program Name: MetaVelvet v1.2.02		<u>Paramaters</u>
<u>Function</u>		
Correct Assembly		Default

Program Name: BWA v0.7.4		<u>Paramaters</u>
<u>Function</u>		
sampe		Default

Program Name: Samtools v0.1.19		<u>OVERLAP</u>	<u>MINID</u>
<u>Function</u>			
minimus2		200bp	98%

Program Name: BLAST v2.2.27		<u>Min ID</u>	<u>Min Bitscore</u>	<u>e value</u>	<u>Target</u>
<u>Function</u>	<u>Output format</u>				
blastp	6	60%	50	1.00E-05	Function
			<u>Min Bitscore</u>		
<u>Function</u>	<u>Output format</u>	<u>Min ID</u>		<u>e value</u>	<u>Target</u>
blastp	6	30%	50	1.00E-05	Homology

Supplemental Table 6. Sample read accession information

Sample Alias	Sample Title	BioProject ID	BioSample ID	Accession #
MISgDNA_2007-1D	Finger 2007-1D gDNA	PRJNA72255	SAMN02228699	SRS455884
MISgDNA_2009-1D	Prostrate Mat 2009-1D gDNA	PRJNA72255	SAMN02228700	SRS455885
MISgDNA_2009-2D	Finger 2009-2D gDNA	PRJNA72255	SAMN02228701	SRS455886
MISgDNA_2009-3D	Finger 2009-3D gDNA	PRJNA72255	SAMN02230180	SRS455906
MISgDNA_2010-1D	Finger 2010-1D gDNA	PRJNA72255	SAMN02228702	SRS455888
MISgDNA_2011-1D	Prostrate Mat 2011-1D gDNA	PRJNA72255	SAMN02228703	SRS455889
MISgDNA_2011-2N	Prostrate Mat 2011-2N gDNA	PRJNA72255	SAMN02228704	SRS455890
MISgDNA_2011-3D	Finger 2011-3D gDNA	PRJNA72255	SAMN02228705	SRS455891
MISgDNA_2012-1D	Finger 2012-1D gDNA	PRJNA72255	SAMN02228706	SRS455892
MISgDNA_2012-2D	Finger 2012-2D gDNA	PRJNA72255	SAMN02228707	SRS455893
MISgDNA_2012-3D	Finger 2012-3D gDNA	PRJNA72255	SAMN02228708	SRS455894
MISgDNA_2012-4N	Finger 2012-4N gDNA	PRJNA72255	SAMN02228709	SRS455895
MISgDNA_2012-5N	Finger 2012-5N gDNA	PRJNA72255	SAMN02228710	SRS455896
MISgDNA_2012-6N	Finger 2012-6N gDNA	PRJNA72255	SAMN02228711	SRS455898
MIScDNA_2012-1D	Finger 2012-1D cDNA	PRJNA72255	SAMN02230071	SRS455900
MIScDNA_2012-2D	Finger 2012-2D cDNA	PRJNA72255	SAMN02230072	SRS455901
MIScDNA_2012-3D	Finger 2012-3D cDNA	PRJNA72255	SAMN02230073	SRS455902
MIScDNA_2012-4N	Finger 2012-4N cDNA	PRJNA72255	SAMN02230074	SRS455903
MIScDNA_2012-5N	Finger 2012-5N cDNA	PRJNA72255	SAMN02230075	SRS455904
MIScDNA_2012-6N	Finger 2012-6N cDNA	PRJNA72255	SAMN02230076	SRS455905

Supplemental Table 7. Sequence accession information

<u>Sequence Title</u>	<u>BioProject ID</u>	<u>Accession #</u>
Phormidium Phage MIS-PhV1.TypeA	PRJNA72255	KF437907
Phormidium Phage MIS-PhV1.TypeB	PRJNA72255	KF437908
Spacer Contigs 1-33	PRJNA72255	KF487036 - KF487068
CRISPR III-B Type1	PRJNA72255	KF487069
CRISPR III-B Type1 v2	PRJNA72255	KF487070
CRISPR III-B Type2	PRJNA72255	KF487071
L2P	PRJNA72255	KF487072
L4P	PRJNA72255	KF487073
ychF	PRJNA72255	KF487074
secY	PRJNA72255	KF487075
nblA	PRJNA72255	KF487076 - KF487081

Supplemental Table 8. Accession numbers for NblA tree

<u>nblA source</u>	<u>NCBI accession number</u>
Bacillus subtilis BEST7613	BAM51709.1
Microcystis aeruginosa PCC 7806	CAO88905.1
Arthrospira sp. PCC 8005	CCE19972.1
Synechocystis sp. PCC 6803	BAA17955.1
Synechococcus elongatus PCC 7942	AAA89103.1
Microcystis aeruginosa DIANCHI905	ELS45963.1
Microcystis aeruginosa TAIHU98	ELP52921.1
Microcystis aeruginosa PCC 9701	CCI36768.1
Microcystis sp. T1-4	CCI31263.1
Planktothrix phage PaV-LD	ADZ31529.1
Microcystis phage Ma-LMM01	YP_851019
Phormidium Phage PhV1.TypeA	KF437907
Phormidium Phage PhV1.TypeB	KF437908
MIS Phormidium 1	KF487076
MIS Phormidium 2	KF487077
MIS Phormidium 3	KF487078
MIS Phormidium 4	KF487079
MIS Oscillatoria 1	KF487080
MIS Oscillatoria 2	KF487081