

Supplemental Figure 1. Large amount of foam generated in Maumee Bay, Lake Erie from the *Microcystis* dominated bloom on A, July 31; B, August 2; C, August 4, 2019. The photo from July 31 was taken from the Canadian Coast Guard Ship CCGC Limnos 11 km northeast of the Toledo Water Intake (credit: Robin Rozon, Fisheries and Oceans Canada)

A.



B.

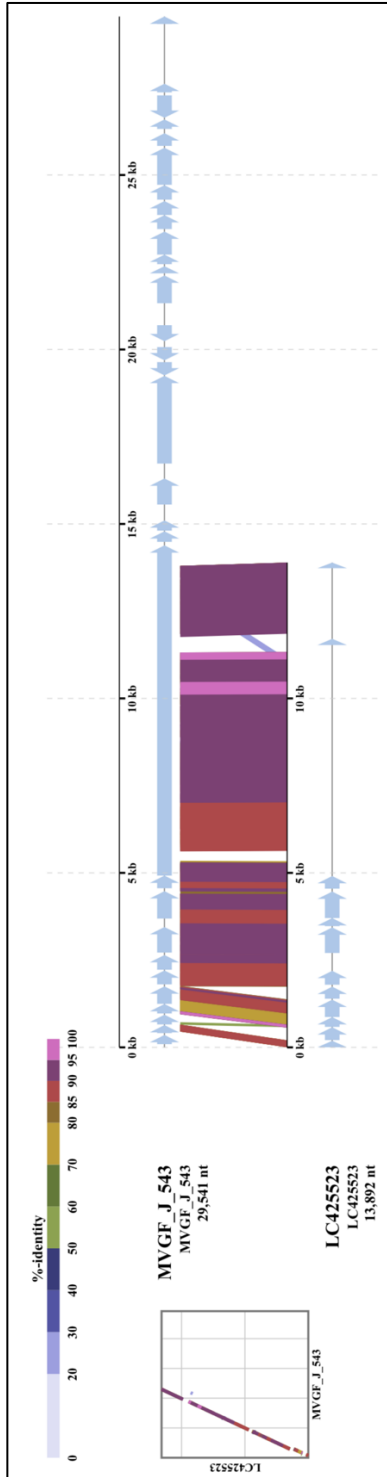


C.

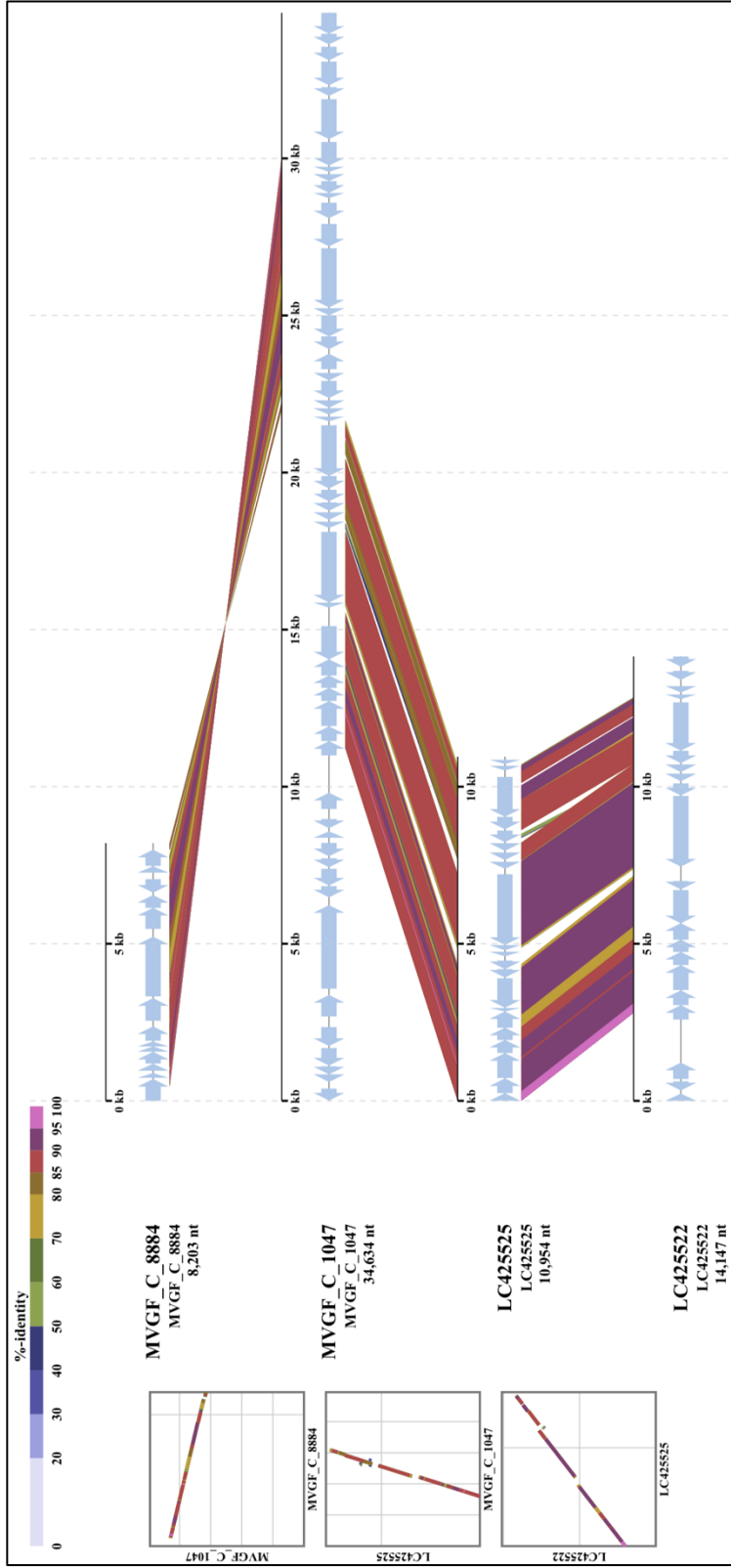


Supplemental Figure 2. Proteomic relatedness between each of the non-dominant *Microcystis* Viral Gene Fragments (MVGFs) and its closest related MVGF as described in Morimoto et al. [1].

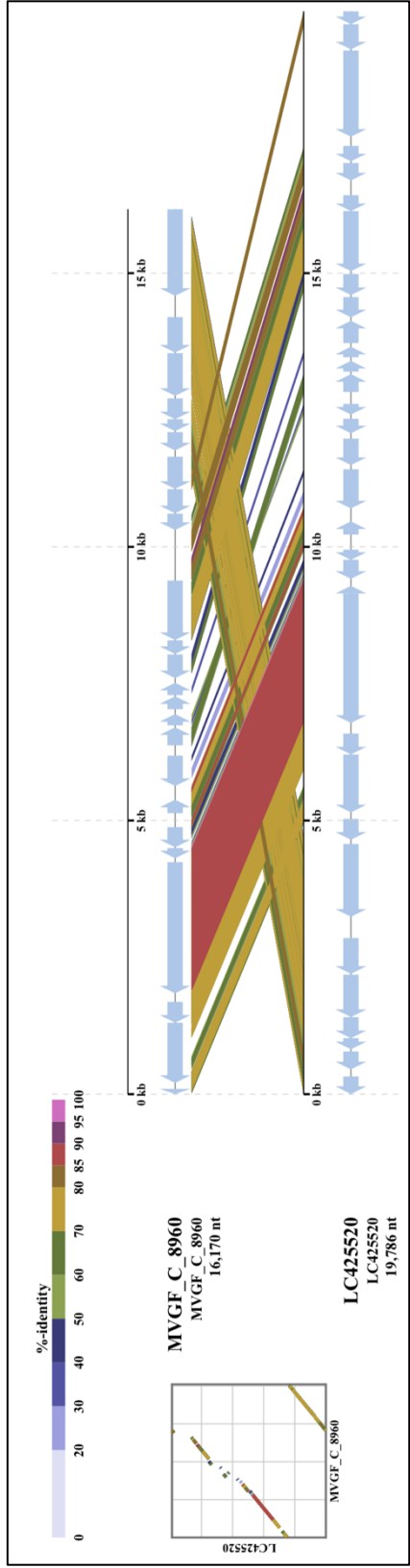
A.



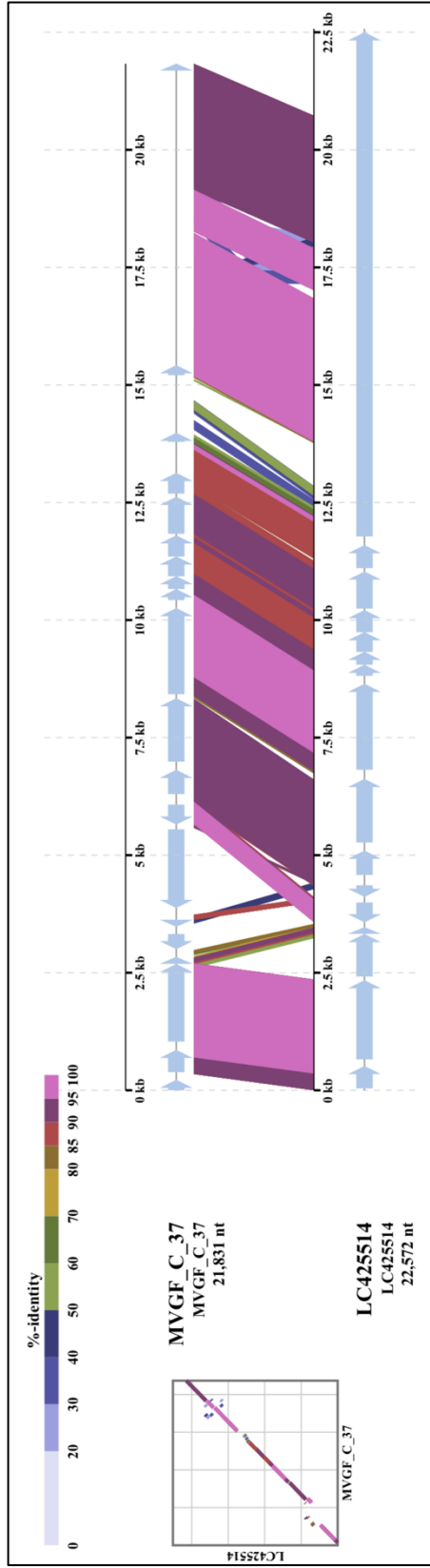
B.



C.



D.



Supplemental Table 1. Metagenomic reads associated with target genes for *Microcystis aeruginosa* NIES-834 for comparative analysis of qPCR assay.

Site	Gene	Primer Start	Primer Stop	Total Raw Reads	Ratio between 16S	Ratio to total 16S
Surge Well	16S_1	1885973	1886202	2555.30	0.4236	NA
Surge Well	16S_2	3598365	3598594	3476.45	0.5764	NA
Surge Well	mcyB	3495004	3495107	611.88	NA	0.1014
Surge Well	mcyD	3517110	3517230	574.38	NA	0.0952
Intake	16S_1	1885973	1886202	2217.78	0.3637	NA
Intake	16S_2	3598365	3598594	3880.10	0.6363	NA
Intake	mcyB	3495004	3495107	212.13	NA	0.0348
Intake	mcyD	3517110	3517230	213.50	NA	0.0350

Supplemental Table 2. G-block sequences used for standard curve of qPCR assay.

G-block name	Sequence	Length
Phage portal protein (MVGF_J_348)	CGTAAACTTCGCCTTTTGATAAAAATCGCCGGTTC AATTCA TAATCACCAATTTTTAAAGTCCCCGACAAAACCGCCAAA TCTAACCATTTTTTTGTAAATTCTTTTGTGCAATCGCCGGA TTAACCACGACTGAATCACCCGATAGTTATCCCTCTCATC CATCAAGGATGTTTCGCGCCGAGGAGTAACTGGTATTAGA GAAATCCCGCGATAAAGCCTCATAGGATAGCCCAATCCC CGCCGCCACCCCCCGCAGCATCATCTGATAAAAAGCATC AAACCCCTGATTGGGACGAGTGGGGGCAAATCCCTCGAA AGACTCTCCTGGATTCAAACCTCGATCGCCCCGGCTCC AAACTGGTCACGCGCTGGCCTGCCATTTCTTCCGGAGCAT AAACATCCGGGTGCGGCGTAGTAATAAACCCCATCACCG CCGCCTGCGCCCGGGCTGCAACCAACTCAGCCTCTGTGT AACCCCC	480
Phage tail collar (MVGF_J_19)	AATCGCGCCAATCATACGGGAACACAGGCAGCCAATACT ATATACGATCTATCTGACACAGTGCGGGCGTTTGCATTTA TTGCCGACATGCTGGCTGATATAACCATTCTAGAGAATG AACTAGAGGAATTACGCGACGACCTATTCGGTGATGGTG AGTTACAGCAGATCATTAAATAACATACAGCAGTTAGTCA ATGATCTAATTGATAACCTAGCTGCTGCCGTAGGTGAGTT AACTATAATTCAGAACCTACAGACATGCTGCGATACTAA CACAACCTGCTATCAGTGGTTTACAGACTCAATTTACTACA CTGAGTAACCAAATAACTGCTCAGATAGCCACCATCAAT TCCACAATCAGTGATATAAACAACAGACTCAACCTAGAA ATACCTAAGATAGTAGCATTACAGAAT	420
<i>Microcystis</i> mcyD	AAAAAAAAAAGGTTTCGCCTGGTCAAAGTAATTATGCCGC AGCTAATGCTTTCATGGATGCTCTAATGCAGCAACGGCA AAGTTTAGGATTACCTGGTATTAGTATTAATTGGGGAGCT TGGGAGACGGGCAACCAAATTGATCAACAACGTTTCGCT AATTGGGGTTTGCAGATGATGCCCTCTGAGCAAGCGTTTC AATATCTCAGTCAGGTAATTTTAGGTGATATTACTCAAGG GATAGTTCTCGATATTGATTGGTCGATTTTTTAATCAAAC TTCAACATTAGTCAACCCTTTAGCGAGG	308
<i>Microcystis</i> mcyB	GATTATCCTACCGAGCGCTTGGGGGATATCCTCTCAGATT CGGGGGTTTCTTTGGTGTTAACTCAGGAATCTTTAGGGGA TTTTCTTCCC	90
<i>Microcystis</i> 16S	GCCGCGAGGTGAAACCTAATTGGCCTGAAGAAGAGCTTG CGTCTGATTAGCTAGTTGGTGGGGTAAAAGCCTACCAAG GCGACGATCAGTAGCTGGTCTGAGAGGATGAGCAGCCAC ACTGGGACTGAGACACGGCCAGACTCCTACGGGAGGCA GCAGTGGGGAATTTCCGCAATGGGCGAAAGCCTGACGG AGCAACGCCGCGTGAGGGAGGAAGGTCTTTGGATT	230

Supplemental Table 3. Standard curve characteristics for qPCR methods for cyanobacteria and cyanophages. Dynamic range and limit of detection are reported in copies per reaction. The dynamic range is the lowest to highest standard analyzed in copies per qPCR reaction. The limit of detection is the lowest value that can reasonably be detected with some certainty. The detection limit is 1 copy per reaction unless there are detections in blanks.

DNA assay	Dynamic range	Standard curve efficiency	R ² value	Limit of detection
Phage portal protein (MVGJ J_348)	95 - 9.5E+07	1.05	0.9874	1
Phage tail collar (MVGJ J_19)	108.5 - 1.085E+08	1.25	0.9905	1
<i>Microcystis</i> mcyD	19.9 – 1.99E+07	1.10	0.9973	1
<i>Microcystis</i> mcyB	19.2 – 1.92E+07	1.03	0.9989	1
<i>Microcystis</i> 16S	39.7 - 3.97E+07	1.01	0.9978	1

References:

- [1] Morimoto D, Tominaga K, Nishimura Y, Yoshida N, Kimura S, Sako Y, Yoshida T. 2019. Cooccurrence of broad- and narrow-host-range viruses infection the bloom-forming toxic cyanobacterium *Microcystis aeruginosa*. *Appl Environ Microbiol* 85:1–17.