The following supplement accompanies the article

Metagenomic assessment of viral diversity in Lake Matoaka, a temperate, eutrophic freshwater lake in southeastern Virginia, USA

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Supplementary Materials

Table S1. Environmental metadata

	Temp (°C)	**pH**	**Bact ml^{-1} (10^5)**	**Virus ml^{-1} (10^7)**	**VBR**	**BP (µg C L^{-1} h^{-1})**	**Cond (µS cm-^{1})**	**O_2 (mg L^{-1})**	**TP (µM)**	**NO_2 + NO_3 (µM)**	**NH_4 (µM)**	**Chl-a (µg L^{-1})**	**TSS (mg L^{-1})**	**DOC (mg L^{-1})**
PM	8.8	7.35	3.71 (1.54)	0.904 (0.25)	24.4	0.237 (0.014)	213.1	10.3	0.023	2.53	1.022	13.6	1.67	2.36
CDM	8.4	7.64	5.06 (0.40)	1.14 (0.39)	22.6	0.0219 (0.0030)	207.5	10.8	0.093	1.31	1.702	14.1	1.75	2.83
MO	8.5	7.35	4.17 (0.65)	1.02 (0.22)	24.5	0.146 (0.0033)	208.0	10.5	0.291	3.84	0.576	18.5	3.92	2.65

CDM, Crim Dell Mouth; PM, Pogonia Mouth; MO, Matoaka Open. Values given in parentheses represent standard deviations of 3 replicate measurements; Temp, temperature; VBR, virus-to-bacterium ratio as calculated from average values; BP, bacterial production; Cond, conductivity; TP, total phospohorus; Chl-a, chlorophyll-a; TSS, total suspended solids; DOC, dissolved organic carbon.

Table S2. Classification of Reads Hitting Bacterial Sequences

Phylum	**CDM** (%)	**PM** %)	**MO** (%)
Acidobacteria	0.38	0.50	0.47
Actinobacteria	3.69	3.07	3.97
Aquificae	0.12	0.13	0.14
Bacteroidetes	7.57	7.48	5.99
Chlamydiae	0.12	0.05	0.10
Chlorobi	1.09	1.05	1.02
Chloroflexi	1.65	2.21	2.39
Chrysiogenetes	0.00	0.02	0.00
Cyanobacteria	1.38	1.62	1.38
Deferribacteres	0.01	0.03	0.03
Deinococcus-Thermus	0.22	0.31	0.29
Dictyoglomi	0.03	0.02	0.01
Elusimicrobia	0.06	0.04	0.06
Fibrobacteres	0.01	0.01	0.00
Firmicutes	10.84	11.08	9.59
Fusobacteria	0.64	0.40	0.35
Gemmatimonadetes	0.03	0.08	0.07
Lentisphaerae	0.08	0.07	0.08
Nitrospirae	0.03	0.07	0.05
Poribacteria	0.00	0.01	0.02
Proteobacteria	**40.36**	**38.65**	**43.22**
Spirochaetes	0.33	0.45	0.42
Synergistetes	0.10	0.06	0.08
Tenericutes	0.18	0.22	0.09
Thermotogae	0.06	0.07	0.05
Verrucomicrobia	0.63	0.62	0.91
unclassified (derived from Bacteria)	0.26	0.01	0.28

CDM, Crim Dell Mouth; PM, Pogonia Mouth; MO, Matoaka Open. Assignments made according to best BLASTx hit (E-value cutoff 10^{-5}) using MG-RAST. Bolded values indicate majority representation within a metagenome.

Table S3. Contig Assembly Statistics

Metagenome	**CDM**	**PM**	**MO**
Total Contigs	454	801	731
Avg. contig size, bp	1291	1251	1306
Largest contig, bp	34,868	29,873	34,762
Reads assembled (%)	7604 (25.6)	13,645 (29.3)	13,386 (28.4)
Singletons (%)	18,336 (61.7)	26,726 (57.4)	28,067 (59.5)

CDM, Crim Dell Mouth; PM, Pogonia Mouth; MO, Matoaka Open.

Table S4. ORF statistics

	CDM	**PM**	**MO**
Total Predicted ORFs	1245	2442	2513
ORFs with function (%)	15.14	14.78	15.04
ORFans (%)	84.86	85.22	84.96

CDM, Crim Dell Mouth; PM, Pogonia Mouth; MO, Matoaka Open.

Table S5. Mapping of reads to fully sequenced reference genomes

Metagenome	**CDM**	**PM**	**MO**
Most abundant reference genome	*Puniceispirillum phage HMO-2011*	*Puniceispirillum phage HMO-2011*	*Puniceispirillum phage HMO-2011*
Genome type	dsDNA, circular	dsDNA, circular	dsDNA, circular
Genome size (bp)	55282	55282	55282
Coverage (%)	51.55	55.17	55.89

CDM, Crim Dell Mouth; PM, Pogonia Mouth; MO, Matoaka Open.

Figure S1. Rank-abundance curves obtained using the PHACCS analysis system on each metagenome; PM, Pogonia mouth; CDM, Crim Dell mouth; MO, Matoaka open.

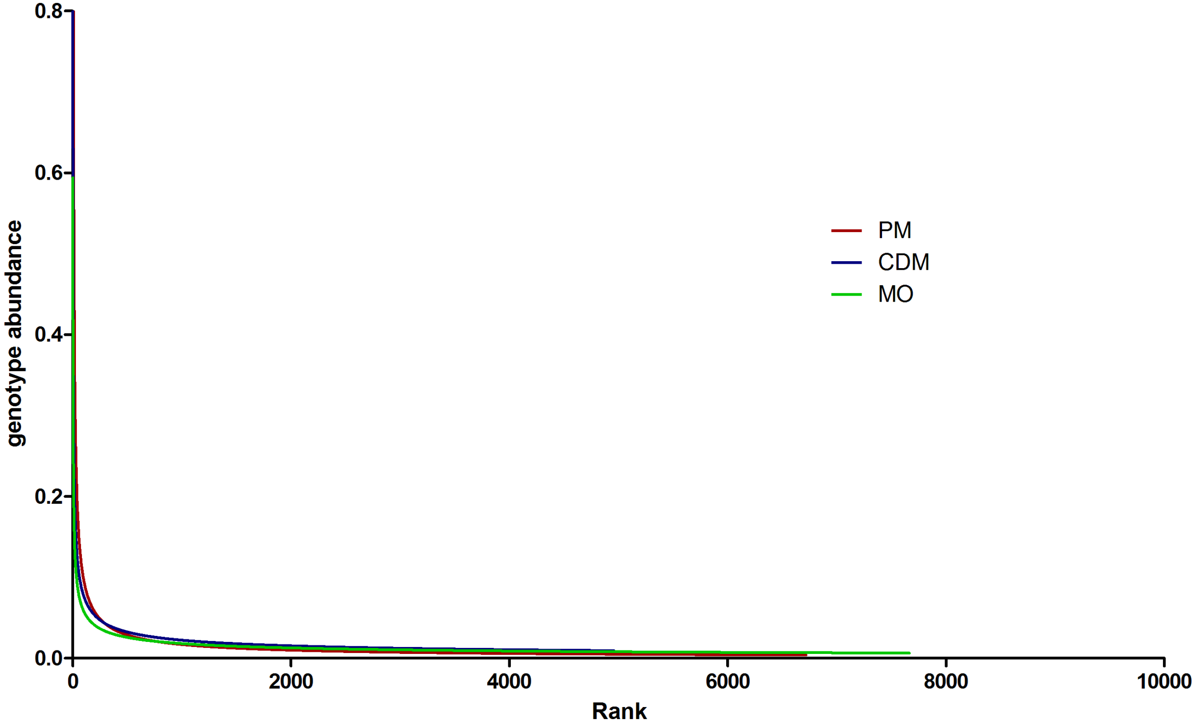

Figure S2. Principal coordinates analysis of aquatic viromes run in MG-RAST to compare patterns in variation across sample types. Colors indicated different sample types: blue, marine; purple, wastewater treatment plant; pink, Saharan gueltas; orange, French lakes; green, Lake Matoaka (present study); red, Chesapeake Bay; brown, Tilapia aquaculture ponds.