

TABLE S3. UniProtKB-Prokka annotation and metadata for 10 circular viral assembled genomes (VAGs).

NOTE: Data for only non-hypothetical proteins presented here; bold indicates VAGs that were presented in Figure 5 of the main text

VAG#	vOTU ID	WGCA module	Water-column distribution	Genome size (bp)	Total ORFs	Contig hit	EC number	UniProtKB code	UniProtKB gene ID	UniProtKB viral ID	UniProtKB viral lineage
6	VIRSorter_NODE_47_length_54735_cov_16_1727	none	abundant at 5m, present at 15m	54,735	91	KNFAEGHP_00023 KNFAEGHP_00051 KNFAEGHP_00082	NA 2.7.7.- NA	Q05235 P21442 Q9Z29	Minor tail protein Gp28 Integrase Probable transcriptional regulator Whi8TM4	<i>Mycobacterium phage L5 (Mycobacteriophage L5)</i> <i>Haemophilus phage HP1 (strain HP1c1) (Bacteriophage HP1)</i> <i>Mycobacterium phage TM4 (Mycobacteriophage TM4)</i>	Viruses > Caudovirales > Siphoviridae > Fromanvirus Viruses > Caudovirales > Myoviridae > Peduovirinae > Hpunavirus > Haemophilus phage HP1 Viruses > Caudovirales > Siphoviridae > Timquatrovirus > Mycobacterium virus TM4
7	VIRSorter_NODE_11_length_101329_cov_28_0366	none	only present at 5m, largest genome (>100kb), 150-160 ORFs	101,329	159	GCLMJFHJ_00029 GCLMJFHJ_00058 GCLMJFHJ_00059	NA 1.17.4.1 1.17.4.1	P25480 O64174 Q76RD8	Probable portal protein Ribonucleoside-diphosphate reductase subunit beta Ribonucleoside-diphosphate reductase large subunit	<i>Escherichia phage P2 (Bacteriophage P2)</i> <i>Bacillus phage SPbeta (Bacillus phage SPbc2) (Bacteriophage SP-beta)</i> <i>Vaccinia virus (strain Ankara) (VACV)</i>	Viruses > Caudovirales > Myoviridae > Peduovirinae > Peduovirus Viruses > Caudovirales > Siphoviridae > Spbetavirus Viruses > Poxviridae > Chordopoxvirinae > Orthopoxvirus > Vaccinia virus
5	VIRSorter_NODE_30_length_42405_cov_14_8062	J (metalimnion)	present everywhere but 5m, very abundant at 15m	42,350	63	none					
8	VIRSorter_NODE_4_length_87432_cov_13_5877	N	present only in metalimnion, especially at 15m	87,432	155	LOFIEDBH_00018 LOFIEDBH_00019	3.4.-. 3.4.21.-	P85500 Q6QGD7	Capsid polyprotein Prohead protease	<i>Pseudomonas phage PAJU2</i> <i>Escherichia phage T5 (Enterobacteria phage T5)</i>	Viruses > Caudovirales > Siphoviridae > Detrevirus > unclassified Detrevirus Viruses > Caudovirales > Siphoviridae > Tequintavirus
9	VIRSorter_NODE_13_length_64037_cov_26_883	T (bacterio-chlorophyll-e-likes pigments)	unique to 28m, pretty abundant	64,037	91	KBGDBGMK_00072 KBGDBGMK_00078 KBGDBGMK_00088 KBGDBGMK_00089	NA NA 2.7.7.7 NA	P68928 P06153 P19822 P04526	Terminase small subunit Immunity repressor protein DNA polymerase Sliding-clamp-loader gp44 subunit	<i>Bacillus phage SF6 (Bacteriophage SF6)</i> <i>Bacillus phage phi105 (Bacteriophage phi-105)</i> <i>Escherichia phage T5 (Enterobacteria phage T5)</i> <i>Enterobacteria phage T4 (Bacteriophage T4)</i>	Viruses > Caudovirales > Siphoviridae > unclassified Siphoviridae Viruses > Caudovirales > Siphoviridae > unclassified Siphoviridae Viruses > Caudovirales > Siphoviridae > Tequintavirus Viruses > Caudovirales > Myoviridae > Tevenvirinae > Tequatrovirus
2	VIRSorter_NODE_8_length_62171_cov_111_284	none	unique to metalimnion, especially at 15m	62,116	106	CGDLDOEA_00094	NA	Q05233	Minor tail protein Gp26	<i>Mycobacterium phage L5 (Mycobacteriophage L5)</i>	Viruses > Caudovirales > Siphoviridae > Fromanvirus
10	VIRSorter_NODE_10_length_54657_cov_20_8832	none	unique to metalimnion	54,657	72	NKNDGJMO_00050 NKNDGJMO_00065 NKNDGJMO_00069 NKNDGJMO_00071	3.2.1.17 2.7.7.7 3.1.11.1 3.1.22.-	P11187 P19822 P04536 P03015	Endolysin DNA polymerase Exodeoxyribonuclease Serine recombinase gin	<i>Bacillus phage phi29 (Bacteriophage phi-29)</i> <i>Escherichia phage T5 (Enterobacteria phage T5)</i> <i>Enterobacteria phage T4 (Bacteriophage T4)</i> <i>Escherichia phage Mu (Bacteriophage Mu)</i>	Viruses > Caudovirales > Podoviridae > Picovirinae > Salasvirus Viruses > Caudovirales > Siphoviridae > Tequintavirus Viruses > Caudovirales > Myoviridae > Tevenvirinae > Tequatrovirus Viruses > Caudovirales > Myoviridae > Muvirus
4	VIRSorter_NODE_29_length_49320_cov_59_3851	U (monimolimnion)	abundant at 28 and 40m	49,265	76	ICIEGKNE_00023 ICIEGKNE_00055	2.7.7.- 2.7.7.7	P03692 P19822	DNA primase/helicase DNA polymerase	<i>Enterobacteria phage T7 (Bacteriophage T7)</i> <i>Escherichia phage T5 (Enterobacteria phage T5)</i>	Viruses > Caudovirales > Podoviridae > Autographivirinae > Teseptimavirus > Escherichia virus T7 Viruses > Caudovirales > Siphoviridae > Tequintavirus
1	VIRSorter_NODE_36_length_44859_cov_34_6262	T (bacterio-chlorophyll-e-likes pigments)	only present at 28m	44,805	50	DHLCPJL_00019 DHLCPJL_00021 DHLCPJL_00025 DHLCPJL_00028 DHLCPJL_00035 DHLCPJL_00036 DHLCPJL_00041	3.6.4.- 2.7.7.6 NA NA NA NA 3.1.-.-	P11107 P00573 P03728 P19727 P03746 P03747 P03694	Probable helicase D10 T7 RNA polymerase Portal protein Minor capsid protein Tail tubular protein gp11 Tail tubular protein gp12 Terminase, large subunit gp19	<i>Escherichia phage T5 (Enterobacteria phage T5)</i> <i>Enterobacteria phage T7 (Bacteriophage T7)</i> <i>Enterobacteria phage T7 (Bacteriophage T7)</i> <i>Enterobacteria phage T7 (Bacteriophage T7)</i> <i>Enterobacteria phage T7 (Bacteriophage T7)</i> <i>Enterobacteria phage T7 (Bacteriophage T7)</i> <i>Enterobacteria phage T7 (Bacteriophage T7)</i>	Viruses > Caudovirales > Siphoviridae > Tequintavirus Viruses > Caudovirales > Podoviridae > Autographivirinae > Teseptimavirus > Escherichia virus T7 Viruses > Caudovirales > Podoviridae > Autographivirinae > Teseptimavirus > Escherichia virus T7 Viruses > Caudovirales > Podoviridae > Autographivirinae > Teseptimavirus > Escherichia virus T7 Viruses > Caudovirales > Podoviridae > Autographivirinae > Teseptimavirus > Escherichia virus T7 Viruses > Caudovirales > Podoviridae > Autographivirinae > Teseptimavirus > Escherichia virus T7 Viruses > Caudovirales > Podoviridae > Autographivirinae > Teseptimavirus > Escherichia virus T7 Viruses > Caudovirales > Podoviridae > Autographivirinae > Teseptimavirus > Escherichia virus T7
3	VIRSorter_NODE_144_length_30467_cov_60_9971	B (mixolimnion & oxygen)	very abundant at 5m, present at 15m	30,412	33	FIEOHON_00024	NA	B4YNG0	Putative capsid protein V20	<i>Sputnik virophage</i>	Viruses > Lavidaviridae > Sputnikvirus > Mimivirus-dependent virus Sputnik