

Supplementary material:

Table S1: Phytoplankton genera and species from different phyla that were tested for infection by the Arctic *Micromonas* virus isolates MpoV-44T, 45T, 46T and 47T. In none of the cultures occurred lysis. Cultures were maintained at 3 °C (except for *Ostreococcus* which was cultured at 15 °C) in MIX-TX medium at 16:8h light:dark and 70–90 $\mu\text{mol quanta m}^{-2} \text{s}^{-1}$ (see for details Materials & Methods). Species depicted with TX* are from the Netherlands Institute for Sea Research (NIOZ) TX culture collection and were isolated from Kongsfjorden at the same time as *Micromonas* TX-01. RUG** is from the culture collection of the University of Groningen (RuG), The Netherlands.

Phytoplankton species	Location of isolation
<i>Phaeocystis</i> sp. CCMP1374	Southern Ocean
<i>Phaeocystis antarctica</i> CCMP1871	Southern Ocean
<i>Phaeocystis Antarctica</i> TX17	Southern Ocean
<i>Imantonia</i> sp. TX*	Kongsfjorden
<i>Chrysochromulina</i> sp. CCMP1215	Bellingshausen Sea
<i>Chlamydomonas</i> sp. CCMP681	Bellingshausen Sea
<i>Pyramimonas</i> sp. RuG**	Southern Ocean
<i>Rhodomonas</i> sp. TX*	Kongsfjorden
<i>Proboscia alata</i> TX22	Southern Ocean
<i>Fragilariopsis kerguelensis</i> TX18	Southern Ocean
<i>Chaetoceros dichchaeta</i> TX19	Southern Ocean
<i>Chaetoceros debilis</i> TX20	Southern Ocean
<i>Chaetoceros brevis</i> TX21	Kongsfjorden
<i>Thalassiosira hispida</i> TX*	Kongsfjorden
<i>Porosira glacialis</i> CCMP650	Narragansett Bay
<i>Ostreococcus tauri</i> RCC745	Mediterranean Sea

Table S2: *P*-values of the burst size differences between groups, as tested by 1-way ANOVAs, to demonstrate inter- and intra-strain differences (e.g. for RCC2257 increasing temperature leads to significantly increased burst sizes of both viruses, but for RCC2258 this is only found for MpoV-45T). For each host strain, the effect of the used virus (44T x 45T) or temperature (3 °C x 8 °C) on burst size was tested within each separate treatment. Significant differences are depicted in bold.

	3 °C 44T x 45T	8 °C 44T x 45T	44T 3°C x 8°C	45T 3°C x 8°C
TX-01	0.493	-	-	-
RCC2257	0.130	0.855	0.044	0.045
RCC2258	0.008	<0.001	0.227	0.003

Table S3: Top 3 BLASTN hits of the isolates against KEGG environmental metagenomes with relevant information on sampling location and temperature. OSD: Ocean Sampling Day; TARA: TARA Oceans.

Isolate	Campaign	Region	Year	Temp (°C)	Identity	Sample
MpV46T	OSD	Greenland Sea	2014	-1.6	85%	OSD146_2014-06-21_5m_NPL022
	TARA	Southern Ocean	2001	-0.8	84%	85_DCM_0d2-3
	TARA	North Atlantic	2003	17.3	83%	151_SUR_0d2-3
MpV45T	OSD	Greenland Sea	2014	10.1	83%	OSD130_2014-06-21_1m_NPL022
	OSD	North Atlantic	2014	12.8	88%	OSD152_2014-06-20_1m_NPL022
	TARA	Southern Ocean	2012	7.3	81%	82_SRF_0d2-3
MpV47T	OSD	North Atlantic	2014	12.8	87%	OSD152_2014-06-20_1m_NPL022
	OSD	Greenland Sea	2014	10.1	82%	OSD130_2014-06-21_1m_NPL022
	TARA	South Atlantic	2012	7.3	80%	82_SRF_0d2-3
MpV44	TARA	Southern Ocean	2001	-0.8	80%	85_DCM_0d2-3
	TARA	South Atlantic	2009	12.8	80%	67_SUR_0d2-0d45
	TARA	North Pacific	2010	13.2	79%	133_DCM_0d2-3

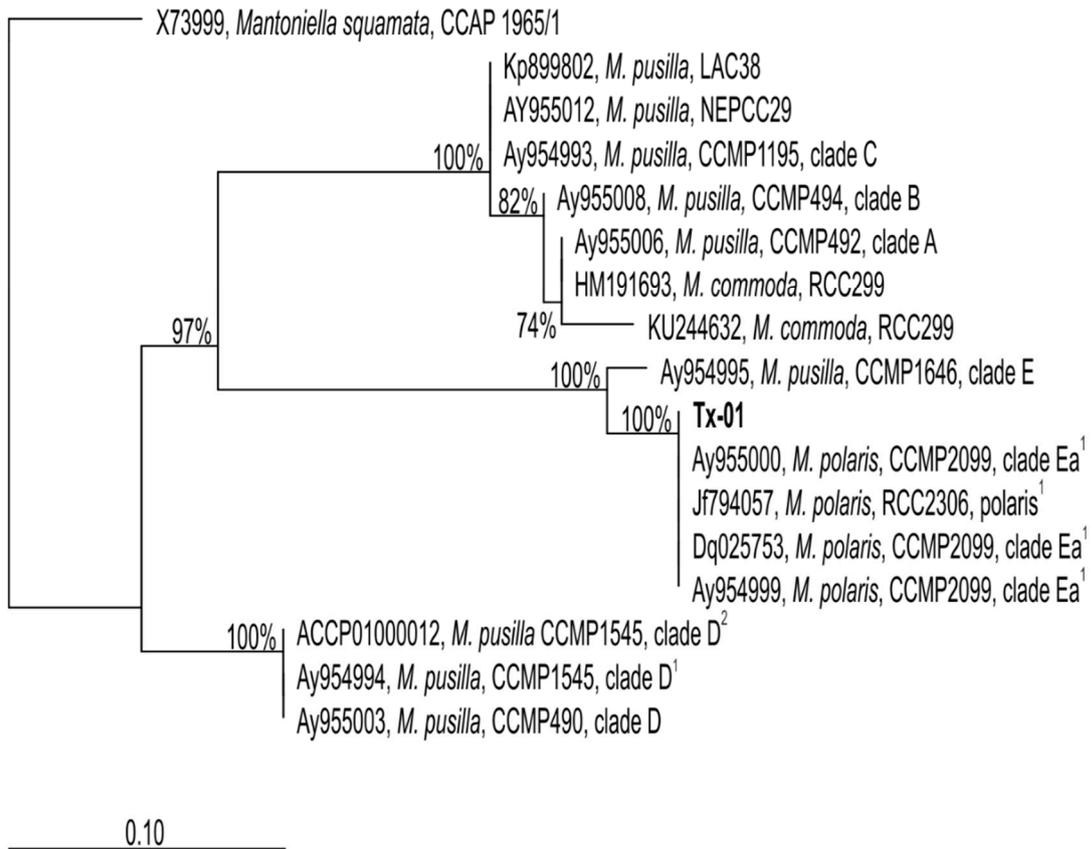


Figure S1: Position of strain TX-01 in a Maximum-Likelyhood dendrogram of 18S rRNA sequences (1574 valid columns) of *Micromonas* strains with clade designations A-E from Slapeta et al. [43] and Ea from Lovejoy et al. [16]. The letter M. stands for the genus *Micromonas*. ¹Simon et al. [48]; ²Van Baren et al. [47].

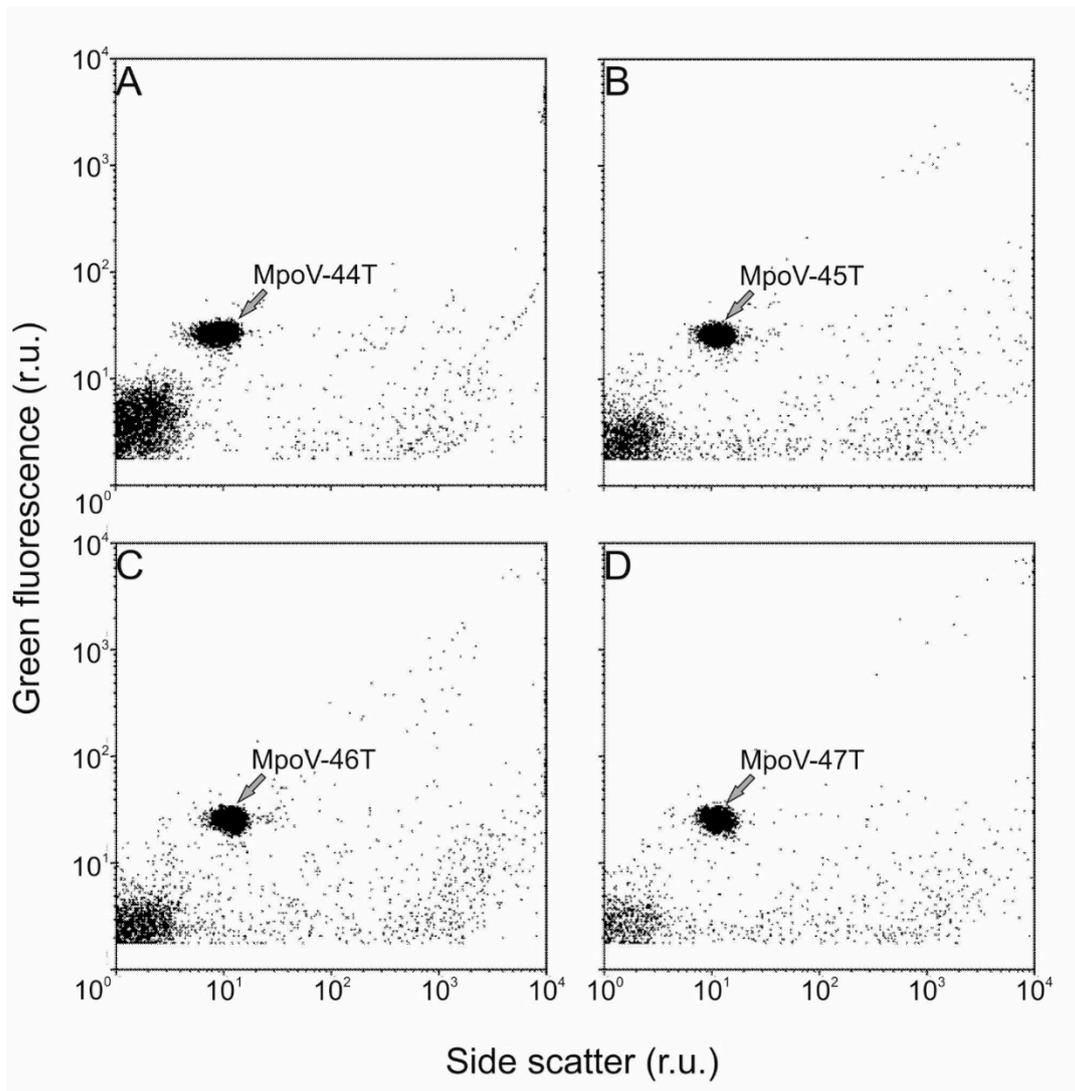


Figure S2: Flow cytograms of the four *Micromonas* virus strains MpoV-44T, 45T, 46T and 47T (A, B, C, D) with green fluorescence on the Y-axis and side scatter on the X-axis. The grey arrow, which is on the same location in each plot, indicates the MpV cluster.

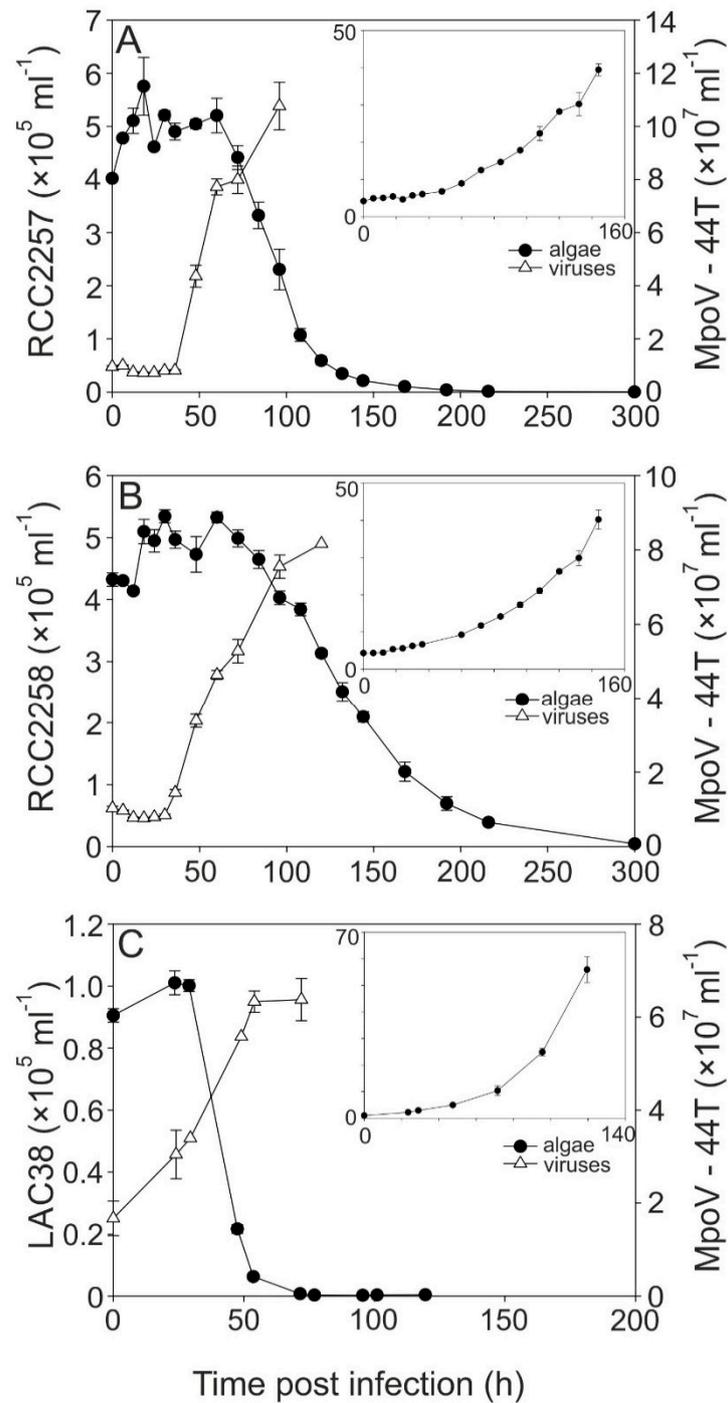


Figure S3: Growth curves of the infection cycle of MpoV-44T infecting *M. polaris* RCC2257 (A), *M. polaris* RCC2258 (B) and *M. commoda* LAC38 (C) as illustration of MpoV-44T - host combinations that do not show the growth extent of the infected TX-01 infected with this virus. Algal cell abundances (mean \pm s.d.; n=3) are depicted as filled circles, of which the temporal dynamics of the infected cultures are shown in the main panel and those of the of the non-infected controls in the inlay panel. Viral abundances (mean \pm s.d.; n=3) over time are depicted as open triangles. Invisible error bars fall within the symbol.

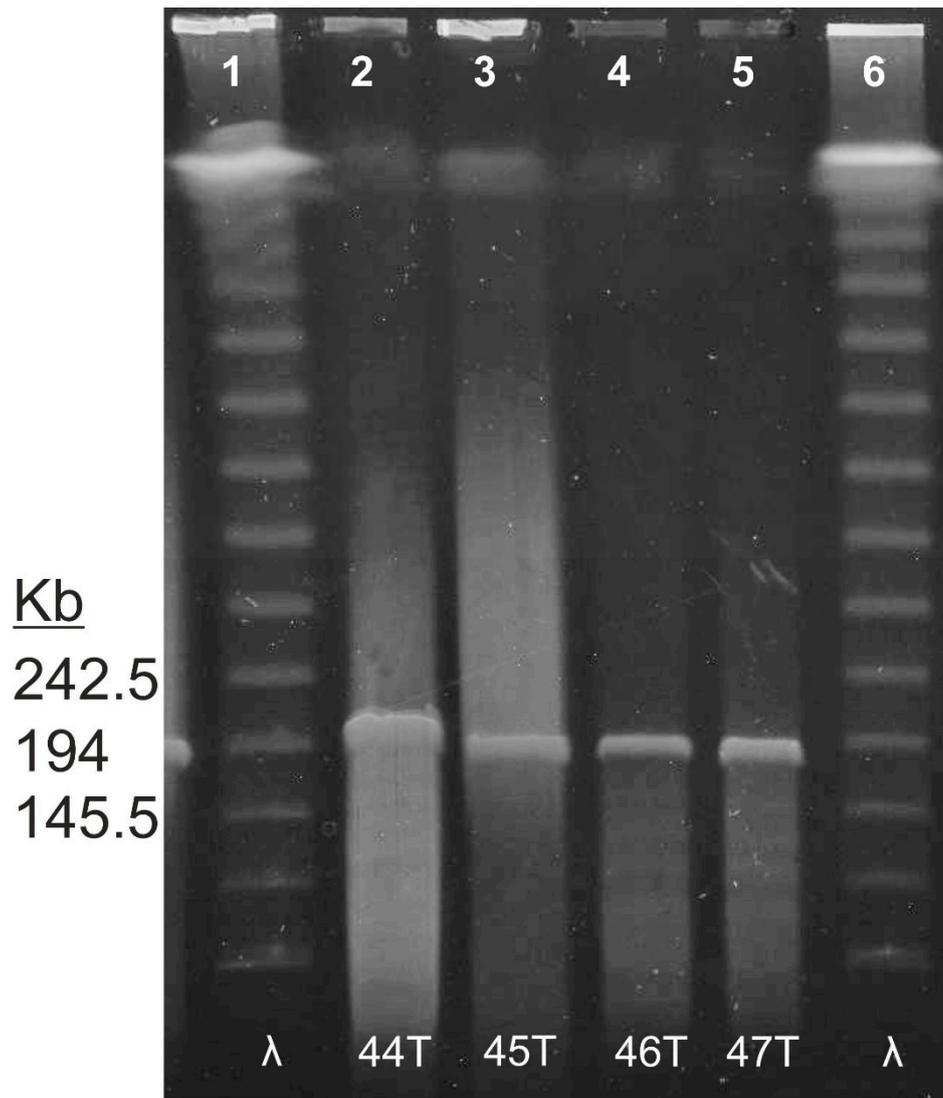


Figure S4: Photograph of a Pulse Field Gel Electrophoresis (PFGE) gel for viral genome size estimation. The virus isolates MpoV-44T to 47T are depicted below lanes 2 to 5. The DNA Lambda ladder is shown in lane 1 and 6 (indicated λ symbol), with the relevant band sizes in Kb on the left.