

Table S2. Fragment recruitment results for selected virus genomes used as references against sorted metagenomes G4000-40002. Highlighted values in gray represent results plotted in Figure 4. Avg., average.

Genome name	GenBank	Length (bp)	G4000		G4001		G4002	
			Avg. coverage	% coverage ^a	Avg. coverage	% coverage	Avg. coverage	% coverage
<i>Acanthamoeba polyphaga</i> mimivirus isolate M4	JN036606	981813	0.02	0.8	0.11	2.8	0.47	6.3
<i>Cafeteria roenbergensis</i> virus BV-PW1	GU244497	617453	0.03	1.1	0.15	3.7	0.81	11.0
<i>Phaeocystis globosa</i> virus 14T	HQ634144	452892	0.04	1.3	0.22	5.5	2.56	32.9
<i>Emiliana huxleyi</i> virus 208	JF974318	411003	0.03	0.8	0.12	2.8	0.46	4.9
<i>Emiliana huxleyi</i> virus 202	HQ634145	407516	0.03	0.6	0.11	2.7	0.47	4.8
Organic Lake phycodnavirus 1	HQ704802	344723*	0.03	1.4	0.23	5.7	2.52	30.7
<i>Paramecium bursaria</i> Chlorella virus 1 (PBCV-1)	JF411744	330611	0.07	2.2	0.39	7.7	0.55	9.0
Organic Lake phycodnavirus 2	HQ704803	282077*	0.05	1.8	0.31	7.7	2.98	35.3
Pelagibacter phage HTVC008M	KC465899	147284	1.56	35.8	3.19	50.4	0.41	13.4
Pelagibacter phage HTVC019P	KC465901	42084	1.27	16.4	2.18	12.8	0.43	9.0
Pelagibacter phage HTVC010P	KC465898	34892	1.01	14.6	0.31	7.5	0.31	9.2
Pelagibacter phage HTVC011P	KC465900	39921	0.29	9.0	0.20	9.7	0.10	3.5
<i>Prochlorococcus</i> phage P-SSM2	GU071092	252401	0.64	14.3	1.53	22.5	0.26	7.6
Puniceispirillum phage HMO-2011	GU557055	55282	10.30	28.6	0.59	16.5	0.32	7.9
<i>Ostreococcus lucimarinus</i> virus OIV4	JF974316	216925	0.16	3.3	2.24	45.6	0.97	12.7
<i>Micromonas pusilla</i> virus PL1	HQ633072	197060	0.16	3.3	2.72	57.1	1.25	16.7
<i>Ostreococcus tauri</i> virus 2	FN600414	184409	0.18	3.7	2.75	55.1	1.25	16.1
<i>Synechococcus</i> cyanophage syn9	DQ149023	177300	0.71	16.9	1.72	23.5	0.21	6.5
<i>Aeromonas</i> phage phiAS4	HM452125	163875	0.44	9.1	1.13	12.7	0.17	4.7
Cyanophage PSS2	GU071090	107530	0.10	2.4	0.09	2.1	0.07	1.6
<i>Prochlorococcus</i> phage P-SSP7	GU071093	45176	0.05	2.3	0.06	2.0	0.05	1.9

^aThe percentage of the genome covered at $\geq 1x$; *incomplete genome.