#### Supplementary information

# Zooming on dynamics of marine microbial communities in the phycosphere of *Akashiwo sanguinea* (Dinophyta) blooms

Running title: Microbial dynamics in Akashiwo sanguinea HABs

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21

22 Supplementary Figure 1. Sampling site located in Jangmok Bay Time-series Monitoring Site (JBTMS: 34° 59′

23 37'' N and 128° 40' 27'' E), a semi-closed bay on the southern coast of South Korea, a. b, sea water colour in

24 Akashiwo sanguinea bloom; c, light microscopic observation of Akashiwo sanguinea cells.





Supplementary Figure 2. Weekly and daily changes in the measured environmental factors and phytoplankton communities in Jangmok Bay Time-series Monitoring Site (JBTMS) from June 2016 to June 2017. a, water temperature and salinity; b, pH and dissolved oxygen; c, dissolved inorganic nitrogen (DIN), dissolved inorganic phosphorus (DIP), and dissolved silica (DSi); d, total bacterial abundance and dissolved organic carbon concentration.





Supplementary Figure 3. Daily changes in environmental factors under dominant presence of the pico-sized green alga, *Bathycoccus prasinos* in 2017. a, water temperature; b, salinity; c, pH; d, dissolved oxygen; e, dissolved inorganic nitrogen; f, dissolved silica; g, dissolved inorganic phosphorus; h, dissolved organic carbon; i, chlorophyll-*a*; j, total bacteria abundance. Coloured areas in the figure correspond to the common phytoplankton groups in 2017. r value in each figure (upper right) indicates Pearson correlation coefficient between changes in each environmental factor and *B. prasinos* abundance.



Supplementary Figure 4. Daily changes in relative abundance (%) of the microzooplankton (total Arthropoda)
communities and *Akashiwo sanguinea* feeding herbivores (*Calanus* spp. + *Oithona* spp. + *Dioithona* spp.)
obtained from metagenomic next-generation sequencing during *Akashiwo sanguinea* blooms in 2016, The
coloured areas in the figure correspond to the common phytoplankton groups in 2016.

### 43 Supplementary Tables

#### 44 Supplementary Table 1. Experimental information for PCR amplification of V3-V4 regions in 16s rDNA

Target region	Step	Primer		PCR reaction mixtures	PCR condition	Reference
	1	Forward	Reverse	(total 25-µL)		
6s DNA V3-V4 egion)	First PCR	Ilumina preadapter +Sequencing primer sequence+341F (5'- CCTACGGGN GGCWGCAG-3')	Ilumina preadapter +Sequencing primer sequence+800R (5'- TACCAGGGT ATCTAATCC-3')	200 $\mu$ mol L <sup>-1</sup> each dNTP, 1.5 mmol L <sup>-1</sup> MgCl <sub>2</sub> , 0.3 $\mu$ mol L <sup>-1</sup> each primer, 2.5 U Taq DNA polymerase (TaKaRa, EX Taq, Kyoto, Japan), and DNA template (20 ng $\mu$ L <sup>-1</sup> )	initial denaturation step at 95°C for 3 min, followed by 35 cycles of denaturation at 95°C for 10 s, annealing at 52°C for 45 s, and extension at 72°C for 1 min, and a final extension step of 72°C for 5 min.	
	Second PCR	Ilumina preadapter +Sequencing primer sequence+341F (5'- CCTACGGGN GGCWGCAG-3')	Ilumina preadapter +Sequencing primer sequence+800R (5'- TACCAGGGT ATCTAATCC-3')	200 $\mu$ mol L <sup>-1</sup> each dNTP, 1.5 mmol L <sup>-1</sup> MgCl <sub>2</sub> , 0.3 $\mu$ mol L <sup>-1</sup> each primer, 2.5 U Taq DNA polymerase (TaKaRa, EX Taq, Kyoto, Japan), and DNA template (800 ng), and Nextera XT index Kit (Illumina, CA, USA)	initial denaturation step at 95°C for 3 min, followed by 12 cycles of denaturation at 95°C for 10 s, annealing at 52°C for 45 s, and extension at 72°C for 1 min, and a final extension step of 72°C for 5 min.	1,2

Their DNA concentration was measured in a Bio-analyzer 2100 (Agilent Technologies, Palo Alto, CA, USA).

### 46 Supplementary Table 2. Experimental information for PCR amplification of V4-V5 regions in 18s rDNA

Target	Step	Prin	ner	PCR reaction mixtures (25-µL)	PCR condition	Reference
region		Forward	Reverse	- · · · · ·		
	First	Ilumina preadapter	Ilumina preadapter	200 $\mu$ mol L <sup>-1</sup> each dNTP, 1.5	initial denaturation step at $95^{\circ}$ C for 3 min, followed	
	ICK	sequence+	sequence+TAReuk	each primer, 2.5 U Taq DNA	annealing at $52^{\circ}$ C for 45 s, and extension at $72^{\circ}$ C for 1	
		TAReuk454FWD1	REV3 (5'-ACTTTC	polymerase (TaKaRa, EX Taq,	min, and a final extension step of 72°C for 5 min.	
		(5'-	GTTCTTGATYRA-	Kyoto, Japan), and DNA		
		CCAGCASCYGCG	3')	template (20 ng $\mu$ L <sup>-1</sup> )		
18s		GTAATTGG-3')				
IDNA	Second	Ilumina preadapter	Ilumina preadapter	200 $\mu$ mol L <sup>-1</sup> each dNTP, 1.5	initial denaturation step at 95°C for 3 min, followed	3.4
(V4-V5	PCR	+Sequencing primer	+Sequencing primer	mmol $L^{-1}$ MgCl <sub>2</sub> , 0.3 µmol $L^{-1}$	by 12 cycles of denaturation at 95°C for 10 s,	- )
• 、		sequence+	sequence+TAReuk	each primer, 2.5 U Taq DNA	annealing at 52°C for 45 s, and extension at 72°C for 1	
region)		TAReuk454FWD1	REV3 (5'-ACTTTC	polymerase (TaKaRa, EX Taq,	min, and a final extension step of 72°C for 5 min.	
		(5'-	GTTCTTGATYRA-	Kyoto, Japan), DNA template		
		CCAGCASCYGCG	3')	(600 ng), and Nextera XT		
		GTAATTGG-3')		index Kit (Illumina, CA, USA)		
	Dealine	Triplicate reaction pro	ducts (same amount) w	vere pooled and purified using a Q	iaquick PCR purification Kit (No. 28104, Qiagen Inc.).	
	Fooling	Their DNA concentrat	ion was measured in a E	Bio-analyzer 2100 (Agilent Techno	logies, Palo Alto, CA, USA).	

Supplementary Table 3. Summary of numbers of read counts and operational taxonomic units (OTUs) of bacterial community (16s rDNA V3-V4 regions) obtained from metagenomic next-generation sequencing analysis and the alpha-diversity indices of the Jangmok Bay Time-series Monitoring Site in 2016 (*Akashiwo sanguinea* bloom) and 2017 (No *A. sanguinea* bloom). Group I–IV in 2016 and Group I and II in 2017 were obtained from nMDS analysis presented in Figs. 2a and 2b.

Group	Date	Total sequence (mean)	Read Count (mean)	OTUs (mean)	Chao1 richness (mean)	Shannon diversity (mean)	Simpson evenness (mean)	Remark
Group I	Oct., 4 - 31, 2016	32,298,622- 62,271,417 (46,112,019)	73,321-140,807 (104,034)	261-406 (313)	407-677 (489)	2.804-3.680 (3.316)	0.564-0.773 (0.678)	Before <i>A. sanguinea</i> bloom
Group II	Nov., 7 – 28, 2016	7,696,433- 44,490,558 (23,987,481)	17,197-99,823 (53,723)	113-220 (162)	157-343 (242)	2.373-4.791 (3.791)	0.538-0.930 (0.821)	During A. sanguinea
Group III	Nov., 13 – 14, 2016	7,397,953- 13,327,844 (10,362,899)	16,499-29,667 (23,083)	104-119 (112)	178-199 (188)	2.988-3.107 (3.047)	0.798-0.807 (0.802)	- bloom
Group IV	Nov., 29 – Dec., 26, 2016	23,022,820- 82,174,372 (54,400,274)	51,437-183,273 (121,405)	179-296 (241)	245-433 (351)	4.380-4.837 (4.614)	0.893-0.939 (0.917)	After <i>A. sanguinea</i> bloom
Group I	Nov., 14 – Dec., 13, 2017	8,656,023- 69,720,710 (31,791,259)	19,470-156,620 (71,464)	135-310 (207)	176-434 (288)	3.539-4.295 (3.935)	0.759-0.889 (0.823)	Dominance of <i>B.</i> prasinos
Group II	Dec., 19 – 26, 2017	6,804,524- 7,552,004 (7,178,264)	15,400-17,180 (16,290)	105-109 (107)	167-169 (168)	2.971-3.025 (2.998)	0.662-0.768 (0.715)	After decrease of <i>B. prasinos</i>

Supplementary Table 4. Summary of numbers of read counts and operational taxonomic units (OTUs) of Nucleo Cytoplasmic Large DNA Viruses (NCLDVs) obtained
 from metagenomic next-generation sequencing analysis of the Jangmok Bay Time-series Monitoring Site in 2016 (*Akashiwo sanguinea* blooming period) and 2017 (No A.

*sanguinea* bloom period). Groups I–IV were obtained from nMDS analysis presented in Figs. 4a and 4b.

Group	Date	Total sequence (mean)	Number of Virus contigs (mean)	Number of NCLDVs contigs (mean)	NCLDVs OTUs (mean)	Remark
Group I	Oct.24-31, Nov.15, 2016	1,688,012,192-2,358,455,848 (1,986,633,842)	1,557-1,643 (1,605)	1,080-1,241 (1,139)	92-95 (94)	Before <i>A. sanguinea</i> bloom
Group II	Nov. 7-11, 21, 2016	1,464,097,818-1,948,331,006 (1,770,470,006)	498-505 (463)	229-327 (282)	57-69 (64)	Early <i>A. sanguinea</i> bloom
Group III	Nov. 17, 2016	2,233,117,474	361	179	52	_
Group IV	Oct.10-17, Nov.13, 19, Nov.23-Dec.26, 2016	1,171,719,382-2,208,330,660 (1,793,789,254)	674-2,594 (1,407)	443-1,962 (1,072)	72-105 (87)	Before, Peak and decline <i>A. sanguinea</i> bloom
Group I	Nov., 15-Dec.19, 2017	1,541,147,082-2,348,387,360 (1,935,432,940)	3,272-5,260 (4,169)	2,789-4,161 (3388)	98-117 (108)	Dominance of <i>B.</i> prasinos
Group II	Dec.26, 2017	2,382,864,316	5,107	3,570	112	After decrease of <i>B</i> . <i>prasinos</i>

56 Supplementary Table 5. Summary of number of read counts and operational taxonomic units (OTUs) of eukaryotic plankton community (18s rDNA V4-V5 regions) at

57 size-fractions of  $>10 \ \mu m$  (focused on eukaryotic plankton and dinospores of *Amoebophrya* sp. in *A. sanguinea* cells) and 2–0.2  $\mu m$  (focused on free-living *Amoebophrya* sp. in *A. sanguinea* cells) and 2–0.2  $\mu m$  (focused on free-living *Amoebophrya* sp. in *A. sanguinea* cells) and 2–0.2  $\mu m$  (focused on free-living *Amoebophrya* sp. in *A. sanguinea* cells) and 2–0.2  $\mu m$  (focused on free-living *Amoebophrya* sp. in *A. sanguinea* cells) and 2–0.2  $\mu m$  (focused on free-living *Amoebophrya* sp. in *A. sanguinea* cells) and 2–0.2  $\mu m$  (focused on free-living *Amoebophrya* sp. in *A. sanguinea* cells) and 2–0.2  $\mu m$  (focused on free-living *Amoebophrya* sp. in *A. sanguinea* cells) and 2–0.2  $\mu m$  (focused on free-living *Amoebophrya* sp. in *A. sanguinea* cells) and 2–0.2  $\mu m$  (focused on free-living *Amoebophrya* sp. in *A. sanguinea* cells) and 2–0.2  $\mu m$  (focused on free-living *Amoebophrya* sp. in *A. sanguinea* cells) and 2–0.2  $\mu m$  (focused on free-living *Amoebophrya* sp. in *A. sanguinea* cells) and 2–0.2  $\mu m$  (focused on free-living *Amoebophrya* sp. in *A. sanguinea* cells) and 2–0.2  $\mu m$  (focused on free-living *Amoebophrya* sp. in *A. sanguinea* cells) and 2–0.2  $\mu m$  (focused on free-living *Amoebophrya* sp. in *A. sanguinea* cells) and 2–0.2  $\mu m$  (focused on free-living *Amoebophrya* sp. in *A. sanguinea* cells) and 2–0.2  $\mu m$  (focused on free-living *Amoebophrya* sp. in *A. sanguinea* cells) and 2–0.2  $\mu m$  (focused on free-living *Amoebophrya* sp. in *A. sanguinea* cells) and 2–0.2  $\mu m$  (focused on free-living *Amoebophrya* sp. in *A. sanguinea* cells) and 2–0.2  $\mu m$  (focused on free-living *Amoebophrya* sp. in *A. sanguinea* cells) and 2–0.2  $\mu m$  (focused on free-living *Amoebophrya* sp. in *A. sanguinea* cells) and 2–0.2  $\mu m$  (focused on free-living *Amoebophrya* sp. in *A. sanguinea* cells) and 2–0.2  $\mu m$  (focused on free-living *Amoebophrya* sp. in *A. sanguinea* cells) and 2–0.2  $\mu m$  (focused on free-living *Amoebophrya* sp. in *A. sanguinea* cells) and 2–0.2

58 spp. and nano-sized phytoplankton) obtained from metagenomic next-generation sequencing analysis, and alpha-diversity indices of the Jangmok Bay Time-series

59 Monitoring Site in 2016 (Akashiwo sanguinea blooming period). Groups I–III (>10 µm) and Groups I–III (2-0.2 µm) were obtained from nMDS analysis .

Filter size	Group	Sampling date	Total sequence (mean)	Read Count (mean)	OTUs (mean)	Chao1 richness (mean)	Shannon diversity (mean)	Simpson evenness (mean)	Remark
- > 10 um	Group I	Oct. 10-31, 2016	12,478,827- 47,051,009 (26,192,373)	30,295-113,485 (63,407)	208-289 (256)	273-353 (328)	3.373-4.983 (4.216)	0.715-0.919 (0.849)	Before <i>A. sanguinea</i> bloom
	Group II	Nov7-23, 2016	11,388,538- 69,954,522 (48,129,687)	27,244-167,974 (115,268)	59-160 (112)	101-243 (195)	0.108-0.805 (0.313)	0.018-0.275 (0.076)	During A. sanguinea bloom
	Group III	Nov.25-Dec.26	6,547,198- 107,637,393 (49,803,387)	15,642-257,281 (118,832)	114-307 (208)	193-403 (300)	0.758-2.437 (1.868)	0.191-0.693 (0.521)	After <i>A. sanguinea</i> bloom
	Group I	Nov. 11-21, 2016	20,334,734- 33,137,157 (27,951,474)	48,658-78,547 (66,663)	144-234 (185)	156-286 (240)	0.656-2.674 (1.842)	0.119-0.716 (0.455)	During A. sanguinea bloom
	Group II	Nov. 23-Dec.26, 2016	20,987,838- 49,915,365 (30,248,955)	50,178-118,849 (72,405)	216-329 (282)	229-389 (327)	2.084-5.916 (4.560)	0.464-0.964 (0.845)	After A. sanguinea
2-0.2 um	Group III	Dec. 13, 2016	9,663,458	23,109	201	214	5.940	0.960	010011
	Group I	Nov. 15 - Dec. 26, 2017	28,278,227- 61,578,514 (45,329,554)	68,221-147,961 (108,980)	176-392 (306)	257-454 (367)	2.065-5.285 (3.970)	0.517-0.942 (0.820)	No A. sanguinea bloom
	Group II	Nov. 17, 2017	17,867,369	42,759	207	224	5.698	0.951	

### 60 Supplementary Table 6. Abbreviations and node sizes of significant factors (P<0.01 and Q<0.05) in the

61 Network analysis displayed in Fig. 7.

Factor         Abbreviation         Node size         Factor         Abbreviation         Classification           Competature         Temp.         0.47         Temperature         Temp.         0.47           Salinity         Sal.         0.63         Salinity         Sal.         0.67           Josebved inorganic         Dip         0.20         Disolved inorganic         DIN         0.37           Disolved inorganic         Dip         0.20         Disolved inorganic         DIN         0.37           Education of the second organic action         DO         0.23         Disolved organic         DIN         0.37           Disolved salina         O.14         0.22         Disolved organic         DIN         0.37           Disolved salina         D.1         0.31         Administra induces         Administra induces         DIN           Disolved salina         D.1         0.31         Administra induces         DIN         DIN           Disolved salina         D.1         Disolved salina         DIN         DIN         DIN         DIN           Disolved salina         DIN		2016			2017		
Tempentarie         Temp.         0.47         Tempentare         Temp.         0.47           pill         0.63         Saliairy         Sal.         0.63         Saliairy         Sal.         0.67           pill         0.84         pill         0.63         Saliairy         Sal.         0.67           pill         0.84         pill         0.63         Saliairy         Sal.         0.67           Disolved integration         DOC         0.23         Disolved integration         DOC         0.31           Disolved value         DSi         0.75         October and integration         0.64         0.28           Disolved value         J. Sant.         0.63         Identified Childs         0.61         0.28           Machine sangeninea         J. Sant.         0.63         Identified Childs         0.61         0.28           Usculued Stemmospile         U.Sr.         0.28         Identified Childs         0.61         0.28           Usculued Stemmospile         U.Sr.         0.28         Identified Childs         0.41         Disolved information of the	Factor	Abbreviation	Node size	Factor	Abbreviation	Node size	Classification
Saliniy         Sal.         0.63         Salinity         Sal.         0.7           Disolved inorganic Designers         DIP         0.20         Disolved inorganic Disolved inorganic         DIN         0.37         Environmental factor           Disolved inorganic Desioved syspen         DO         0.23         Disolved inorganic         DIN         0.34         factor           Disolved syspen         DO         0.25         Disolved syspen         DO         0.35           Disolved syspen         DO         0.63         Advention System         0.14         0.09           Matchine significat         A.san.         0.63         Advention System         0.30         Intercore remainment         A san.         0.31           Iterrecore remainment         Char core representation system         Tang.         0.43         Intercore remainment           A carria amorit         A anna.         0.13         Cyria tensity per core         0.30         Intercore remainment         Autotroph           A carria amorit         A anna.         0.13         Cyria tensity per core         0.43         Disolved system         0.30           Transmark         Core         Core         0.43         Disolved system         0.44           Acarria amorit	Temperature	Temp.	0.47	Temperature	Temp.	0.47	
pl1         pl1         0.47         Forwards         pl1         0.37         Forwards           Dissolved ioroganic         DIP         0.26         Dissolved ioroganic         DIN         0.37         Environmental factor           Dissolved ioroganic         DIN         0.37         Environmental factor         Dissolved ioroganic	Salinity	Sal.	0.63	Salinity	Sal.	0.67	
Description         DIP         0.26         Description         DIN         0.37         Environmental factor           Discription         Chio and DOC         0.23         Discription         DOC         0.34         Eator           Discription         Chio and DOC         0.25         Discription         Chi -         0.29           Discription         Dis         0.73         Eator         0.35           Discription         Dis         0.73         Eator         0.35           Machine sangutan         A.san.         0.61         defanotac elubors         A.san.         0.31           Heterocyner visualati         H.san.         0.33         Characeeros sp.         Characeeros sp.         0.34           Heterocyner visualati         H.san.         0.31         Cripti acor andrescens sp.         0.33           Heterocyner visualation acor         Transcenters sp.         Transcenters sp.         0.34           Acarria somerit         A.ama.         0.04         A.ama.         0.31           Transcenters sp.         Transcenters sp.         Transcenters sp.         1.35         Criptic heters sp.         0.34           Acarria somerit         A.ama.         0.09         Fonoresp.         0.31         Cripti cheo	pH	pH	0.48	pH	pH	0.39	
Displanta         Displanta <thdisplanta< th=""> <thdisplanta< th=""> <thd< td=""><td>Dissolved inorganic</td><td>DIP</td><td>0.26</td><td>Dissolved inorganic</td><td>DIN</td><td>0.37</td><td>Environmental</td></thd<></thdisplanta<></thdisplanta<>	Dissolved inorganic	DIP	0.26	Dissolved inorganic	DIN	0.37	Environmental
Chlorophylla         Chlas         0.29         Chlorophylla         Chlas         0.29           Disolved oxygen         DO         0.35         0.73         0.74         0.01           Alachno sanguinea         A.an.         0.63         Adenoide cludes         0.43         0.02           Heterocapar rotundata         II.rot.         0.23         Akashnov sanguinea         A.an.         0.43           Heterocapar rotundata         II.rot.         0.23         Akashnov sanguinea         A.an.         0.44           Linealunda Stranscopia         II.str.         0.23         Akashnov sanguinea         A.an.         0.44           Heterocapar rotundata         H.rot.         0.30         Heterocapar sonutality of the mark presents of the mark	Dissolved organic carbon	DOC	0.23	Dissolved organic carbon	DOC	0.34	factor
Dissolved singer         DO         0.35           Josabved singer         J.sam,         0.63         Advantov samguinee         A.sam,         0.21           Advantov samguinee         J.sam,         0.23         Advantov samguinee         A.sam,         0.21           Advantov samguinee         J.sam,         0.23         Advantov samguinee         A.sam,         0.21           Unealuard Stramenopile         U.Str.         0.23         Bardrycoccus pressions         Bardrycoccus pressions         0.23           Advantov Samguinee         H.sam,         0.21         Machinees and Samenopile         0.35           Macrinis stranger         Team,         0.14         Trelevalue any pressions         0.23           Acarria omorii         A.omo,         0.13         Crima hemisphereia         Laro,         0.35           Acarria steuerri         A.ste.         0.09         Drombiling caultizatisti an occurina         Naci.         0.21         Crima hemisphereia         Laro,         0.35           Acarria steuerri         A.ste.         0.09         Strombiling caultizatististi an occurina         Naci.         0.21         Crima hemisphereia         Laro,         0.13         Crima hemisphereia         Laro,         0.14         Amochyphynynyn         Naci.	Chlorophyll-a	Chl-a	0.29	Chlorophyll-a	Chl-a	0.29	
Dissolved silica         DSi         0.73           Machrio singuirea         A.am.         0.63         Adexindes eludors         A.am.         0.21           Hetercoguer rotundata         If. rot.         0.23         Machrios singuinea         A.am.         0.43           Hetercoguer rotundata         If. rot.         0.23         Machrios singuinea         A.am.         0.21           Unealtured Stranscoppic         U.Str.         0.28         Machrios singuinea         A.am.         0.44           Hetercoguer simulation         Grap.         0.44         0.30         Hetercoguer simulation         Comp.         0.44           Hetercoguer simulation         Transp.         0.41         Crist heurophereita         Transp.         0.41           Acartia sinters         Aste.         0.09         Fransp.         0.43         Fransp.         0.43           Caluma sinticus         Cain.         0.06         Norelinear scintillans         Nac.a.         0.01         Crist heurophereita         Scap.         0.10           Caluma sinticus         Cain.         0.06         Norelinear scintillans         Nac.a.         0.01         Machrios singuinea         Scap.         0.18           Advantia sisteeri         Aste.         0.04 <td>Dissolved oxygen</td> <td>DO</td> <td>0.25</td> <td>Dissolved oxygen</td> <td>DO</td> <td>0.35</td> <td></td>	Dissolved oxygen	DO	0.25	Dissolved oxygen	DO	0.35	
Akachnov sanguinen A.san. 0.5 Adenodes eidens A.ehr. 0.08 Herrocquar ordnohidu Uncultured Stamenopile UStr. 0.23 Adenohov sanguinen A.san. 0.21 Uncultured Stamenopile UStr. 0.23 Machinov sanguinen A.san. 0.21 Herrocquar ordnohidu UStr. 0.23 Machinov sanguinen A.san. 0.35 Herrocquar ordnohidu Herrocquar	Dissolved silica	DSi	0.73				
<ul> <li>Heterocapar antandatia</li> <li>H. rol.</li> <li>Uscillured Stramenopile</li> <li>USr.</li> <li>Uscillured Stramenopile</li> <li>USr.</li> <li>USR.</li></ul>	Akashiwo sanguinea	A.san.	0.63	Adenoides eludens	A.elu.	0.08	
Calculated Municulpue     C.M.     0.8     Many texts priming     0.47       Calculated Municulpue     C.M.     0.8     Many texts priming     0.47       Calculated Municulpue     National Sciences intermissional     Charping and the second sciences of termissional     0.47       Many texts and the second sciences of termissional     Calculate and the second sciences of termissional     0.47       Acarita ambitacedia sep     Tatap     0.44       Televalues sp.     Televalues sp.     0.40       Ferrascents sp.     Televalues sp.     0.43       Pyraminonas australis     Paus.     0.33       Acarita amorti     A.amo,     0.13     Cylina henispherica     Chem.     0.07       Acarita statueri     Aste.     0.09     Fanistance calculation     Sciag.     0.18       Admoredphyray spl.     Amos spl.     0.17     Colina desispherica     Chem.       Annochery syngl.     Amos spl.     0.12     Endoperasition     Sciag.     0.14       Amoredphyray spl.     Amos spl.     0.21     Manochery spi.     Amos spl.     0.17       Amoredphyray spl.     Amos spl.     0.12     Endoparasitic dimensional acritica     Barc.     0.46       Ascidiacellubians     Adam.     0.25     Cribrihabitans marinas     Cmar.     0.31	Heterocapsa rotundata	H.rot.	0.23	Akashiwo sanguinea	A.san. B.m.a	0.21	
Checkeeres sp. chana Che sp. 0.30 Herrorcans roundar H rat 0.36 Minusocellas sp. Tet.sp. 0.13 Teleaulas amphiocia T.amp. 0.44 Teleaulas sp. Tet.sp. 0.13 Thelassistria occurica T.oce. 0.43 Paraminina startus p. 0.13 Totas variante frances for the sp. 0.14 Totas variante frances for the sp. 0.15 Totas variante frances for the sp. 0.14 Totas variante for t	Uncultured Stramenoplie	U.Str.	0.28	Chaetoceros teruissimus	в.pra. C tan	0.49	
Heerocapar Journalian     H. rot.     0.36     Autotoph       Heerocapar Journalian     H. rot.     0.31     Hetotoph       Helenaliaz amphinozian     T. Janp.     0.44       Helenaliaz amphinozian     T. Janp.     0.44       Helenaliaz amphinozian     T. Janp.     0.44       Herristin occurita     A. omo.     0.13     Col.       Actritia omorii     A. omo.     0.13     Col.     0.43       Actritia steueri     A.ste.     0.09     Laochammella     L.pro.     0.30       Columas sinicus     C.in.     0.06     Nocilicus scinitians     Noci.     0.30       Columas incus     C.in.     0.06     Nocilicus scinitians     Noci.     0.30       Columas incus     C.in.     0.07     Scin.     0.18       Aranto Aster.     0.09     Normholim sop.     Nos p.     0.11       Amochophryn sp.2.     Amos p.1.     0.11     Endoparastite       Amochophryn sp.2.     Amos p.2.     0.07     Other Synchinides     0.11       Amochophryn sp.2.     Amos p.2.     0.07     Other Synchinides     0.11       Amochophryn sp.2.     Amos p.2.     0.07     Other Synchinides     0.11       Amochophryn sp.2.     Anos     0.23     Ricinia arctica     B.				Chaetoceros sp.	Cha.sp.	0.28	
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$				Heterocapsa rotundata	H.rot.	0.36	A
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $				Minutocellus sp.	Min.sp.	0.13	Autotroph
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $				Teleaulax amphioxeia	T.amp.	0.44	
Accrita omorii     A.omo.     0.13     Decc.     0.43       Accrita severi     A.se.     0.09     Lackchannikla     Laro.     0.33       Calams sinicus     C.sin.     0.00     Nocilica scintillars     N.sci.     0.22       Calams sinicus     C.sin.     0.00     Nocilica scintillars     N.sci.     0.22       Calams sinicus     C.sin.     0.00     Nocilica scintillars     N.sci.     0.22       Calams sinicus     C.sin.     0.00     Noribus capitalins     N.sci.     0.22       Heterotroph     Other Syndinials     N.sci.     0.18     Modebophysis sp.2     0.17       Paracellesis     A.ses.     0.03     Noribubing sp.2     Mos.sp.2     0.17       Endepartsitic     Marespial Medebophysis sp.2     Mos.sp.2     0.11     Endopartsitic dinoftagellate       Alteresis     A.kie.     0.44     Anylibacter ulvae     A.ulv.     0.31       America kielensis     A.kie.     0.44     Anylibacter ulvae     A.ulv.     0.31       Angelacethabians     A.dan.     0.25     Cribritabians marinus     C.mar.     0.36       Angelacethabians     A.dan.     0.25     Cribritabians marinus     C.mar.     0.36       Angelacethabians     A.dan.     0.25     Cribritab				Teleaulax sp.	Tel.sp.	0.40	
Accrita conorti     A.omo.     0.13     Civita hemisphaerica     Chem.     0.07       Acarita steueri     A.ste.     0.09     prominional sustralis     Chem.     0.07       Calamus sinicus     C.sin.     0.00     prodinguta     Lpro.     0.33       Calamus sinicus     C.sin.     0.00     Nocilica seintillans     Nsci.     0.22     Heterotroph       Diliona davisae     Odav.     0.09     Strombiluim coupitatim     S.cap.     0.18       Ameebophryn spl.     Ano.spl.     0.21     Ameebophryn sp2.     0.17     Endoparasitic       Ameebophryn spl.     Ano.spl.     0.21     Ameebophryn sp2.     0.17     Endoparasitic       Ameebophryn spl.     Ano.spl.     0.23     Bizonia arctica     Barc.     0.46       Ascidaceibabians     Adon.     0.25     Cribritabitins marinus     Cmar.     0.36       Accidaceibabians     Adon.     0.25     Cribritabitins marinus     Cmar.     0.36       Bizonia arctica     Barc.     0.26     Cribritabitins marinus     Cmar.     0.36       Cycloclasticas sprillensus     Cant.     0.29     Euceya tangerina     Eun.     0.53       Floritabitins marinus     Cmar.     0.34     Fluritricola taffensis     F.af.     0.24				Tetraselmis sp.	Tet.sp.	0.13	
$ \begin{array}{c} Acurtia omorii & A.omo. \\ Acurtia steueri & A.ste. \\ Calama stricca & C.sin. \\ Other Synchigina & Lpro. \\ Other Synchigina & Lpro. \\ Other Synchigina & Lpro. \\ Other Synchigina \\ Acurtia steueri & A.ste. \\ Oddy \\ Definition \\ Acurtia steueri & A.ste. \\ Oddy \\ Definition \\ Acurtia steueri & A.ste. \\ Oddy \\ Arensia isteueri & A.ste. \\ A.ste. \\ Oddy \\ Arensia isteueri & A.ste. \\ Oddy \\ Arensia$				Pyramimonas australis	P aus	0.45	
Acartia stueriA.ste.0.09Lackmanniella prolonguiaLpro.0.30Calams sinicusC.sta.0.06Nocellikous scintillansN.sci.0.22HeterotrophParcadamus parvusP.par.0.22Strombidium captanusSco.p.0.18Acertia steveriA.ste.0.09Strombidium sp.Sco.p.0.18Amoelophyva spl.Amospl.0.21Amoebophyva sp.2Mos sp2.0.17Amoebophyva spl.Amospl.0.29Other Syndiniales0th.Syn.0.11EndoparasiticOther SyndinialesOth Syn.0.29Other Syndiniales0th.Syn.0.36ArcidiacethabbiansA.don.0.25Cribrihabitans marinusC.mar.0.36AccidiacethabbiansA.don.0.25Cribrihabitans marinusC.mar.0.36BarroticaB.arc.0.29Excebya tangerinaE.tan.0.53Cribrihabitans marinusC.mar.0.34Elivirional activaE.gra.0.54Cribrihabitans marinusC.mar.0.32Lacimitrig graclariaeLag.0.32Cribrihabitans marinusC.ant.0.19Laminiphila sylensisL.310.33Florita activa sprillensusC.ant.0.32Lacimitrig graclariaeL.32Cribrihabitans marinusC.ant.0.32Lacimitrig graclariaeL.320.33Florita activa sprillensusC.spi.0.32Lacimitrig graclariaeLag.0.32Cribrihabitans sprillensusC.spi.0.31<	Acartia omorii	A.omo.	0.13	Clvtia hemisphaerica	C.hem.	0.07	
According StellerA.Ste.0.09prolongataL.Pro.0.50Calamas situricasC.Stin.0.06Nocclica cintillansN.sci.0.22HeterotrophOthona davisaeO.dav.0.09Strombidium caulspineS.cau.0.10Amoetophyry spl.Amo.spl.0.21Amoetophyry sp.Amo.sp.0.18Amoetophyry spl.Amo.spl.0.21Amoetophyry sp.Amo.sp.0.11Amoetophyry spl.Amo.spl.0.21Amoetophyry spl.Amo.spl.0.11Amoetophyry spl.Amo.spl.0.21Amoetophyry spl.Amo.spl.0.31Amoetophyry spl.Amo.spl.0.22Other SyndinialesOth.Syn.0.11EndoparasticAmersia kielensisA.kie.0.44Anyilbacter ulvaeA.ulv.0.31EndoparasticAmoetophyry spl.A.kie.0.44Anyilbacter ulvaeA.ulv.0.31Amersia kielensisA.don.0.25Cribrihabitans marinusC.mar.0.36GonglaensisB.arc.0.29Eucebya tangerinaE.tan.0.33Barylloides leachtB.lea.0.06Flaviranulus ichthyoenteriF.ich.0.23Ichthyrou arritusC.mar.0.34Flaviranulus ichthyoenteriF.ich.0.23Flaviranulus ichthyoenteriF.ich.0.32Entibacter algarumLalg.0.32Flaviranulus ichthyoenteriF.ich.0.32Entibacter algarumLalg.0.34Flaviranulus ichthyoenteriF.ich.0.32 </td <td>4</td> <td>4</td> <td>0.00</td> <td>Laackmanniella</td> <td>I</td> <td>0.20</td> <td></td>	4	4	0.00	Laackmanniella	I	0.20	
Calams sinicusC.sin.0.06Noccilinea scintillamsN.sci.0.22HeterotrophParacaloms parvusP.par.0.22Sirombidium capitalium sp.Sca.0.18Accruit steveriAste.0.09Sirombidium sp.Sto sp.0.18Amochophrya spl.Amo spl.0.11Amochophrya sp.2Amo sp2.0.17Amochophrya spl.Amo sp1.0.21Amochophrya sp.2Amo sp2.0.11EndoparasiticAmochophrya spl.Amo sp1.0.29Oth Syn.0.31EndoparasiticAmochophrya sp.2Amo sp2.0.46AscidiaccibiolitansA.kie.0.44Anylibacter ubvaeA.ulv.0.31EndoparasiticAscidiaccibiolitansA.don.0.25Cribrihabitans marinusC.mar.0.36Bicionia arcticaB.arc.0.29Eucebaja tangerinaE.tan.0.53Borylloides leachiB.lea.0.06Flaviramulus ichthypoenteriF.ich.0.23Cribrihabitans marinusC.mar.0.34Lemitaccer algarum L.alg.0.33Lemitaccibactores anarcticusGant.0.19Lamitaphilus splensisL.go.Floviramulus ichthypoenteriF.ich.0.23Lacimaria casculation casculation ichthypoenteri0.33Lemitaccer algarumL.alg.0.36Marking.0.33Lemitaccer algarumL.alg.0.36Marking.0.32Cribrihabita spinlensisL.cas.0.17Lishihenia casculation casculation casculation casculation casculation cascul	Acartia steueri	A.ste.	0.09	prolongata	L.pro.	0.30	
	Calanus sinicus	C.sin.	0.06	Noctiluca scintillans	N.sci.	0.22	Heterotroph
Particularity parvis $P_par.$ $0.22$ Strombalum causiyond $S.cu.$ $0.18$ Advacta stever $Axte.$ $0.09$ Strombalum causiyond $S.cu.$ $0.18$ Anno-sp2. $0.07$ Other Syndiniales $016$ Syn. $0.11$ EndoparasiticAnno-sp2. $0.07$ Other Syndiniales $016$ Syn. $0.11$ EndoparasiticOther Syndiniales $016$ Syn. $0.29$ $0.29$ $0.11$ EndoparasiticAnveltacer ulvae $A.ulv.$ $0.32$ Bizionia arctica $B.arc.$ $0.46$ Asceidaceihabitans $A.ulv.$ $0.32$ $Bizionia arcticaB.arc.0.46AsceidaceihabitansA.don.0.22Cribrihabitans marinusC.mar.0.36Bizionia arcticaB.arc.0.29Excelya tangerinaE.tan.0.53Borrylloides leachiB.lea.0.06HaviramulusF.ch.0.23Cribrihabitans marinusC.mar.0.34Fluvicola taffensiaE.gra.0.54Flaviramulus ichthyoenteriF.ich.0.32Leinithacter algarumL.alg.0.35Leinibacter algarumL.alg.0.36MethylophilusM.met.0.40MethylophilusM.met.0.36MethylophilusM.met.0.40MethylophilusM.met.0.36MethylophilusM.met.0.40MethylophilusM.met.0.31Mether acastinitylicaL.cas.0.31MethylophilusM.met.<$	Oithona davisae	O.dav.	0.09	Strombidium capitatum	S.cap.	0.10	
Andra Sateri Manedophrya spl.       Ans. 10       0.21       Amoebophrya sp.2.       0.17       Endoparasitic dinoflagellate         Amoebophrya spl.       Amo. spl.       0.21       Amoebophrya sp.2.       0.17       Endoparasitic dinoflagellate         Ahrensia kielensis       A kie.       0.44       Amylibacter ulvae       A.ulv.       0.31         Amrensia kielensis       A kie.       0.44       Amylibacter ulvae       A.ulv.       0.31         Amrensia kielensis       A.don.       0.22       Cibrihabitans marinus       C.mar.       0.36         Gonglaensis       A.don.       0.25       Cribrihabitans marinus       C.mar.       0.36         Bizonia arctica       B.arc.       0.29       Euzebya tangerina       E.tan.       0.53         Borylloides leachi       E.lea.       0.06       Flaviranulus       F.ich.       0.24         Cycloclasticus spirillensus       C.spi.       0.32       Lacimuric gracitariae       L.gra.       0.54         Floviranulus is ichnyoenetri       F.ich.       0.32       Lacimur praceiram       Laig.       0.32         Floviranulus iconhyoenetri       F.ich.       0.32       Lacimurce acientifytica       L.cas.       0.25         Ciribrihabitana caseinlytica       L.cas.	Paracalanus parvus	P.par.	0.22	Strombidium caudispina	S.cau.	0.18	
Amozopol Ju - p.2       Amozop.       0.07       Other Syndiniales       01.1       Endoparasitic dinoflagellate         Other Syndiniales       Other Syndiniales       01.1       Endoparasitic dinoflagellate         Ahrensia kielensis       A.kie.       0.44       Anylibacter u/vae       A.u/v.       0.31         Amrensia kielensis       A.kie.       0.44       Anylibacter u/vae       A.u/v.       0.36         Adrensia kielensis       A.don.       0.25       Cribrihabitans marinus       C.mar.       0.36         Baronia arctica       B.arc.       0.29       Euzebya tangerina       E.tan.       0.53         Barylibactes u/vae       C.mar.       0.34       Fluvirola taffensis       F.taf.       0.24         Cycloclasticus spirillensus       C.mar.       0.34       Fluvirola taffensis       E.tan.       0.53         Fluvironarula tigenum       L.alg.       0.32       Lembacter algarum       L.alg.       0.32         Cribrihabitans marinus       C.mar.       0.34       Fluvirola taffensis       E.taf.       0.54         Fluvironarula tigenum       L.alg.       0.35       Entipoter algarum       L.alg.       0.35         Lemibacter algarum       L.alg.       0.36       Mesonia algae       M.al	Amoebophrya spl	Ano spl	0.09	Amoebonhvra sp 2	Amo sp?	0.18	
Other Syndimales         Oth. Syn.         0.29         Constraints         dmollagellate           Ahrensia kielensis         A.kie.         0.44         Amylibacter ulvae         A.ulv.         0.31           Anylibacter ulvae         A.ulv.         0.32         Bizionia arctica         B.arc.         0.46           Ascidiaceihabitans         Adon.         0.25         Cribrihabitans marinus         C.mar.         0.36           Bizionia arctica         B.arc.         0.29         Euceby tangerina         E.tan.         0.53           Flaviramulus         Flaviramulus         F.tan.         0.53         Flaviramulus         0.24           Cribrihabitans marinus         Cmar.         0.34         Fluvicola taffensis         F.taf.         0.24           Eventioclastics spirillensus         C.spi.         0.32         Lacimutric graculariae         L.gar.         0.54           Fluviramulus ichthyconetri         F.taf.         0.32         Lacimutriphilus syliensis         L.syl.         0.38           Cribrihabitans marinus         C.mar.         0.17         Lishichenia caseini/ptica         L.cas.         0.25           Cribrihabitans         Martio         0.31         Mediage accessinthytica         Loss.         0.36 <t< td=""><td>Amoebophrya sp1.</td><td>Amo.sp2.</td><td>0.07</td><td>Other Syndiniales</td><td>Oth.Svn.</td><td>0.11</td><td>Endoparasitic</td></t<>	Amoebophrya sp1.	Amo.sp2.	0.07	Other Syndiniales	Oth.Svn.	0.11	Endoparasitic
Ahrensia kielensis       A.kie.       0.44       Amylibacter ulvae       A.ulv.       0.31         Amylibacter ulvae       A.ulv.       0.32       Bizionia arctica       B.arc.       0.46         Ascidiaceithabitans       A.don.       0.25       Cribrihabitans marinus       C.mar.       0.36         Bizionia arctica       B.arc.       0.29       Euzebya tangerina       E.tan.       0.53         Botrylloides leachi       B.lea.       0.06       Fichriramulus       C.mar.       0.24         Cycloclasticus spirillensus       C.mar.       0.34       Fluvicola taffensis       F.taf.       0.24         Cycloclasticus spirillensus       C.mar.       0.34       Enviscola taffensis       F.taf.       0.24         Cycloclasticus spirillensus       C.mar.       0.31       Eanibacter algarum       Lalg.       0.33         Fluvicola taffensis       F.taf.       0.12       Linihichnia case.       0.25       Gramulosicoccus antarcticus       G.ant.       0.19       Linihichnia case.       0.35         Lentihacter algarum       Lalg.       0.36       Meesonia algae       M.alg.       0.36         Laistichenia casenilytica       L.cas.       0.31       Meesonia algae       N.ait.       0.46         <	Other Syndiniales	Oth.Syn.	0.29	<u>.</u>	,		dinoflagellate
Anylibacter ulvae Ascidaccihabitans donghaensisA.don.0.32Bizionia arcticaB.arc.0.46Ascidaccihabitans donghaensisA.don.0.25Cribrihabitans marinusC.mar.0.36Bizionia arcticaB.arc.0.29Eucepya tangerinaE.tan.0.53Borylioides leachiB.lea.0.06FlaviramulusF.ich.0.23Cribrihabitans marinusC.mar.0.34FlaviranulusF.ich.0.24Cycloclasticus spiriflensusC.spi.0.23Leniutrix graciclariaeL.gra.0.55Flaviramulus ichthyoenteriF.ich.0.32Leniutrix graciclariaeL.gra.0.54Flaviramulus ichthyoenteriF.ich.0.32Leniutrix graciclariaeL.gra.0.53Granulosicoccus antarcticusG.ant.0.19Luminiphilus syltensisL.syl.0.38Lentibacter algarumL.alg.0.36Mesonia algaeM.alg.0.33Lentibacter algarumL.alg.0.36Mesonia algaeM.alg.0.31Mesonia algaeM.alg.0.36Novesphingobium accidphilumN.acci.0.31Mesonia algaeN.nit.0.38Planktomarina temperataP.tem.0.24Novasphingobium acturphilusN.acci.0.33Reinekea aestaariiR.aes.0.31Mesonia algaeN.nit.0.38Planktomarina temperataP.tem.0.24Novasphingobium acturphilusN.acci.0.33Reinekea aestaariiR.aes.0.31Owen	Ahrensia kielensis	A.kie.	0.44	Amylibacter ulvae	A.ulv.	0.31	
Ascidiaceihabitans donghaensisA.don.0.25Cribrihabitans marinusC.mar.0.36donghaensisB.arc.0.29Euzebya tangerinaE.tan.0.53Borrylloides leachiB.lea.0.06Flaviramulus ichthyoenteriF.ich.0.23Cribrihabitans marinusC.mar.0.34Fluviramulus ichthyoenteriF.ich.0.23Cycloclasticus spirillensusC.spi.0.23Lacimutrix gracilariae Legra.L.gg.0.32Fluviramulus ichthyoenteriF.ich.0.32Lacimutrix gracilariae Legra.L.agg.0.32Fluviranulus ichthyoenteriF.itf.0.17Lishithenia caseinlytica MethylophusL.agg.0.33Lentibacter algarumL.alg.0.36Mesonia algae methylotrophusM.alg.0.35Lishithenia caseinlyticaL.cas.0.15methylotrophus methylotrophusM.met.0.46Mesonia algaeM.alg.0.36Coverweeksia hongkongensis0.31BacteriaMethylophilus methylotrophusN.nit.0.38Planktomarina temperata Naci.0.40Novosphingobium accidphilumN.aci.0.33Reinekea aestuarii R.aes.0.31Methylophilus methylotrophusN.nit.0.35Reinekea aestuarii R.aes.0.31Methylophilus methylotrophusN.aci.0.33Reinekea aestuarii R.aes.0.31Polarophus Mingobium AccidphilumN.aci.0.33Reinekea aestuarii R.aes.0.31Polarophilos maris	Amylibacter ulvae	A.ulv.	0.32	Bizionia arctica	B.arc.	0.46	
adorgations Bizionia arcticaB arc.0.29Euzebya tangerinaE.tan.0.53Borrylloides leachiB.lea.0.6Flaviramulus ichthyoenteriF.ich.0.23Cribrihabitans marinusC.mar.0.34Fluvitcola taffensisF.taf.0.24Cycloclasticus spirillensusC.spi.0.23Lacinutrix gracilariaeL.gra.0.54Fluvitcola taffensisF.taf.0.32Lenitbacter algarumLalg.0.32Fluvitcola taffensisF.taf.0.17Lishizhenia caseinilyticaL.cas.0.25Granulosicoccus antarcticusGant.0.19Luminiphilus syltensisL.syl.0.38Lenitbacter algarumLalg.0.36MethylophilusM.met.0.46Luminiphilus syltensisL.syl.0.26Nisaea mitritreducensN.nit.0.40Mesonia algaeM.alg.0.36Novosphingobium acidiphilumN.aci.0.31Methylophilus methylotrophusM.met.0.38Plankomarina temperataP.tem.0.24Novosphingobium acatidphilumN.aci.0.33Reinekea aestuarii R.aes.0.31Overweeksia hongkongensisO.hon.0.37Salmicrepens0.31Plankomarina temperate P.tem.P.tem.0.24Plankomarina temperateP.tem.0.24Plankomarina temperate P.tem.P.tem.0.21Plankomarina temperateT.aip.0.21Plankomarina temperate P.tem.P.tem.0.22Sedimenticola thiotaurini S.tud.	Ascidiaceihabitans	A.don.	0.25	Cribrihabitans marinus	C.mar.	0.36	
Borylloides leachiB.lea.0.06Flaviramulus ichthyoenteriF.ich.0.23Cribrihabitans marinusC.mar.0.34Fluviicola taffensisF.taf.0.24Cycloclasticus spirillensusC.spi.0.23Lacinutr's gracilinaticaL.gra.0.54Fluviranulus ichthyoenteriF.ich.0.32Lacinutr's gracilinaticaL.ag.0.32Fluviscola taffensisF.taf.0.17Lishizhenia caseinilyticaL.cas.0.25Granulosicoccus antarcticusG.ant.0.19Luminiphilus syltensisL.syl.0.38Lentibacter algarumLadg.0.36Mesonia algaeM.alg.0.35Lishizhenia caseinilyticaL.cas.0.15Methylophilus methylorophusM.met.0.46Luminiphilus syltensisL.syl.0.26Nisaea nitritireducensN.nit.0.40Mesonia algaeM.alg.0.36Novosphingobium acidiphilumN.aci.0.31Methylophilus methylotrophusM.met.0.31Overweeksia hongkongensis0.hon.0.37Nisaea nitritireducensN.nit.0.38Plankomarina temperataP.tem.0.24Novosphingobium acidiphilumN.aci.0.35Reinekea aestuariiRaes.0.31Overweeksia hongkongensisO.hon.0.37Salinirepens amainensisS.ama.0.25Phaecoystidibacter huanghezhanensisP.mar.0.45Sedimenticola thiotauriniS.thi.0.24Planktomarina temperate P.pen.O.hon.0.3	Bizionia arctica	B.arc.	0.29	Euzebya tangerina	E.tan.	0.53	
Cribrihabitans marinusC.mar.0.34Filmicical taffensisF.taf.0.24Cycloclasticus spirillensusC.spi.0.23Lacinutrix graculariaeL.gra.0.54Flaviramulus ichthyoenteriF.taf.0.17Lishizhenia caseinilyticaL.cas.0.25Granulosicoccus antarcticusG.ant.0.19Luminiphilus syltensisL.syl.0.38Lentibacter algarumLalg.0.36Mesonia algaeM.alg.0.35Lishizhenia caseinilyticaL.cas.0.15MethylophilusM.met.0.46Luminiphilus syltensisL.syl.0.26Nisaea nitritireducensN.nit.0.40Mesonia algaeM.alg.0.36Mesonia algaeN.aci.0.31BacteriaMethylophilusM.met.0.31OwenweeksiaO.hon.0.37MethylophilusMethylophilusM.met.0.31OwenweeksiaO.hon.0.37MethylophilusNisaea nitritireducensN.nit.0.38Planktomarina temperataP.tem.0.24Nisaea nitritireducensN.nit.0.37Salinirepens amamiensisS.ama.0.25PhaeocystidibacterP.mar.0.45Sedimenticola thiotauriniS.thi.0.24Planktomarina temperateP.tem.0.22Sedimenticola thiotauriniS.thi.0.21Planktomarina temperateP.tem.0.22Sedimenticola thiotauriniS.thi.0.21Planktomarina temperateP.tem.0.22Sedimenticola thiotauriniS.thi.0.21 <td>Botrylloides leachi</td> <td>B.lea.</td> <td>0.06</td> <td>Flaviramulus ichthyoenteri</td> <td>F.ich.</td> <td>0.23</td> <td></td>	Botrylloides leachi	B.lea.	0.06	Flaviramulus ichthyoenteri	F.ich.	0.23	
Cycloclasticus spirillensusC.spi.0.23Lacitmutrix gracilariaeL.gr.0.54Flaviroanulus ichthyoenteriF.ich.0.32Lentibacter algarumL.alg.0.32Flaviroanulus ichthyoenteriF.ich.0.32Lentibacter algarumL.alg.0.32Granulosicoccus antarcticusG.ant.0.19Luminiphilus syltensisL.syl.0.38Lentibacter algarumL.alg.0.36Mesonia algaeM.alg.0.35Lishizhenia caseinifyticaL.cas.0.15MethylophilusM.met.0.46Luminiphilus syltensisL.syl.0.26Nisaea nitritireducensN.nit.0.40Mesonia algaeM.alg.0.36NovosphingobiumN.acci.0.31BacteriaMethylophilusM.met.0.31Owenweeksia hongkongensisO.hon.0.37BacteriaNisaea nitritreducensN.nit.0.38Planktomarina temperataP.tem.0.24Novosphingobium acidiphilumN.acci.0.35Reinekea aestuariiR.aes.0.31Owenweeksia hongkongensis oplotrophusO.hon.0.37Salinirepens amaniensisS.ama.0.25Phaeocystilibacter PhaeocystilibacterP.mar.0.45Sedimenticola thiotauriniS.thi.0.24Planktomarina temperate Peudohongiella spirulinae P.hua.0.17Tenacibaculum aiptasiaeT.aip.0.21Planktomarina temperateri P.hua.0.13Tenacibaculum aiptasiaeT.aip.0.21Planktomarina temperateri P.hua.	Cribrihabitans marinus	C mar	0.34	Fluviicola taffensis	F taf	0.24	
Flaviramulus ichthyoenteriF.ich.0.32Lentibacter algarumL.alg.0.32Flaviricola taffensisF.icf.0.17Lishizhenia caseinilyticaL.cas.0.25Granulosicoccus antarcticusG.ant.0.19Luminiphilus syltensisL.syl.0.38Lentibacter algarumL.alg.0.36Mesonia algaeM.alg.0.35Lishizhenia caseinilyticaL.cas.0.15methylopriphusM.met.0.46Luminiphilus syltensisL.syl.0.26Nisaea nitritireducensN.nit.0.40Mesonia algaeM.alg.0.36acidiphilumN.aci.0.31BacteriaMethylophilus methylotorophusM.met.0.31Owenweeksia hongkongensisO.hon.0.37Nisaea nitritireducensN.nit.0.38Planktomarina lemperataP.tem.0.24Novosphingobium acidiphilumN.aci.0.35Reinekea aestuariiR.aes.0.31Owenweeksia hongkongensisO.hon.0.37Salinirepens amamiensisS.ama.0.25Phaecoystidibacter 	Cycloclasticus spirillensus	C.spi.	0.23	Lacinutrix gracilariae	L.gra.	0.54	
Fluvicola taffensis       F.taf.       0.17       Lishizhenia caseinilytica       L.cas.       0.25         Granulosicoccus antarcticus       G.ant.       0.19       Luminiphilus syltensis       L.syl.       0.38         Lentibacter algarum       L.alg.       0.36       Mesonia algae       M.alg.       0.35         Lishizhenia caseinilytica       L.cas.       0.15       Methylophilus       M.met.       0.46         Luminiphilus syltensis       L.syl.       0.26       Nisaea nitriitreducens       N.nit.       0.40         Mesonia algae       M.alg.       0.36       Novosphingobium acidiphilum       N.aci.       0.31       Bacteria         Methylophilus       M.met.       0.31       Overweeksia       O.hon.       0.37         Nisaea nitriitreducens       N.nit.       0.38       Planktomarina temperata       P.tem.       0.24         Novosphingobium       N.aci.       0.35       Reinekea aestuarii       R.aes.       0.31         Owenweeksia hongkongensis       O.hon.       0.37       Salinirepens amainensis       Sama.       0.25         Phaeocystidibacter       P.mar.       0.45       Sedimenticola thiotaurini       S.thi.       0.21         Planktomarina temperate       P.tem.       0.22 </td <td>Flaviramulus ichthyoenteri</td> <td>F.ich.</td> <td>0.32</td> <td>Lentibacter algarum</td> <td>L.alg.</td> <td>0.32</td> <td></td>	Flaviramulus ichthyoenteri	F.ich.	0.32	Lentibacter algarum	L.alg.	0.32	
Granulosicoccus antarcticusG.ant.0.19Luminipilius syltensisL.syl.0.38Lentibacter algarumL.alg.0.36Mesonia algaeM.alg.0.35Lishizhenia caseinilyticaL.cas.0.15MethylophilusM.met.0.46Luminiphilus syltensisL.syl.0.26Nisaea nitritireducensN.nit.0.40Mesonia algaeM.alg.0.36acidiphilumN.aci.0.31BacteriaMethylophilusM.met.0.31OversweeksiaO.hon.0.37BacteriaMethylophilusM.met.0.31OversweeksiaO.hon.0.37Distaea nitritireducensN.nit.0.24NovosphingobiumN.aci.0.35Reinekea aestuariiR.aes.0.31O.24NovosphingobiumN.aci.0.35Reinekea aestuariiR.aes.0.31Owenweeksia hongkongensisO.hon.0.37Salinirepens amamiensisS.ama.0.25PhaecystidibacterP.mar.0.45Sedimenticola thiotauriniS.thi.0.24Planktomarina temperateP.tem.0.22Sedimentialea todarodisS.tod.0.33PolaribacterP.hua.0.17Tenacibaculum aiptasiaeT.aip.0.21Pseudohongiella spirulinaeP.spi.0.18Salinirepens amamiensisS.ama.0.27Sedimenticola thiotauriniS.thi.0.32Syle alicataS.pli.0.17Uncultured Alpha-0.17Unp#20.18Unp#20.18	Fluviicola taffensis	F.taf.	0.17	Lishizhenia caseinilytica	L.cas.	0.25	
Lenitbacter algarumL.alg.0.36Messnia algaeM.alg.0.35Lishizhenia caseinilyticaL.cas.0.15Methylophilus methylotrophusM.met.0.46Luminiphilus syltensisL.syl.0.26Nisaea nitritireducensN.nit.0.40Mesonia algaeM.alg.0.36acidiphilum horgkongensisN.aci.0.31Methylophilus methylotrophusM.met.0.31Owenweeksia 	Granulosicoccus antarcticus	G.ant.	0.19	Luminiphilus syltensis	L.syl.	0.38	
Lishizhenia caseinilyticaL.cas.0.15InterfujorinasM.met.0.46Luminiphilus syltensisL.syl.0.26Nisaea nitritireducensN.nit.0.40Mesonia algaeM.alg.0.36Novosphingobium acidiphilumN.aci.0.31Methylophilus methylotrophusM.met.0.31Overweeksia hongkongensis0.hon.0.37Nisaea nitritireducensN.nit.0.38Planktomarina temperataP.tem.0.24Novosphingobium acidiphilumN.aci.0.35Reinekea aestuariiR.aes.0.31Owenweeksia hongkongensisO.hon.0.37Salinirepens amainensisS.ama.0.25Phaeocystidibacter marisrubriP.mar.0.45Sedimenticola thiotauriniS.thi.0.24Planktomarina temperateP.tem.0.22Sedimenticola thiotauriniS.thi.0.24Planktomarina temperate P.hua.P.tem.0.22Sedimenticola thiotauriniS.thi.0.24Planktomarina temperate P.hua.P.tem.0.22Sedimenticola thiotauriniS.thi.0.24Pinachobacter Thiohalobacter Thiohalobacter Thiohalobacter0.16Tenacibaculum aiptasiaeT.aip.0.21Sedimenticola thiotaurini S.thi.0.18S.ama.0.27Sedimenticola thiotauriniS.thi.0.21Sedimenticola thiotaurini S.thi.0.17Uncultured Alpha P.ten.0.17Tenacibaculum aiptasiaeT.aip.0.21Polacibacter thiotauriniS.thi.0.32S.am	Lentibacter algarum	L.alg.	0.36	Mesonia algae Methylophilus	M.alg.	0.35	
Luminiphilus syltensisL.syl.0.26Nisaea nitritireducensN.nit.0.40Mesonia algaeM.alg.0.36acidiphilumN.aci.0.31Methylophilus methylotrophusM.met.0.31Owenweeksia hongkongensisO.hon.0.37Nisaea nitritireducensN.nit.0.38Planktomarina temperataP.tem.0.24Novosphingobium acidiphilumN.aci.0.35Reinekea aestuariiR.aes.0.31Owenweeksia hongkongensis 	Lishizhenia caseinilytica	L.cas.	0.15	methylopnius	M.met.	0.46	
Mesonia algaM.alg.0.36Novosphingobium acidiphilumN.aci.0.31BacteriaMethylophilusM.met.0.31Owenweeksia hongkongensisO.hon.0.37Nisaea nitritireducensN.nit.0.38Planktomarina temperataP.tem.0.24Novosphingobium acidiphilumN.aci.0.35Reinekea aestuariiR.aes.0.31Owenweeksia hongkongensisO.hon.0.37Salinirepens amaniensisS.ama.0.25Phaeocystidibacter marisrubriP.mar.0.45Sedimenticola thiotauriniS.thi.0.24Planktomarina temperateP.tem.0.22Sedimenticola thiotauriniS.thi.0.24Planktomarina temperateP.tem.0.22Sedimenticola thiotauriniS.thi.0.24Planktomarina temperateP.tem.0.22Sedimenticola thiotauriniS.thi.0.24Planktomarina temperateP.tem.0.22Sedimentitalea todarodisS.tod.0.33Polaribacter huanghezhanensisP.hua.0.17Tenacibaculum aiptasiaeT.aip.0.21Pseudohongiella spirulinaeP.spi.0.16Salinirepens amaniensisS.ama.0.27Sedimenticola thiotauriniS.thi.0.32Style plicataS.pli.0.17Uncultured Alpha- meterbacterium (OTU #2)UAp#20.180.18	Luminiphilus syltensis	L.syl.	0.26	Nisaea nitritireducens	N.nit.	0.40	
Methylophilus methylotrophusM.met.0.31Owenweeksia hongkongensisO.hon.0.37Nisaea nitritireducensN.nit.0.38Planktomarina temperataP.tem.0.24Novosphingobium acidiphilumN.aci.0.35Reinekea aestuariiR.aes.0.31Owenweeksia hongkongensisO.hon.0.37Salinirepens amaniensisS.ama.0.25Phaecoystidibacter marisrubriP.mar.0.45Sedimenticola thiotauriniS.thi.0.24Planktomarina temperateP.tem.0.22Sedimenticola thiotauriniS.thi.0.24Planktomarina temperateP.tem.0.22Sedimenticola thiotauriniS.thi.0.24Planktomarina temperateP.tem.0.22Sedimenticola thiotauriniS.thi.0.24Planktomarina temperateP.hua.0.17Tenacibaculum aiptasiaeT.aip.0.21Pseudohongiella spirulinaeP.spi.0.16Thiohalobacter thiocyanaticusT.thi.0.18Salinirepens amaniensisS.ama.0.27Sedimenticola thiotauriniS.thi.0.32Style plicataS.pli.0.17 </td <td>Mesonia algae</td> <td>M.alg.</td> <td>0.36</td> <td>Novosphingobium</td> <td>N.aci.</td> <td>0.31</td> <td></td>	Mesonia algae	M.alg.	0.36	Novosphingobium	N.aci.	0.31	
methylotrophusInitial0.01hongkongensis0.010.001Nisaea nitritireducensN.nit.0.38Planktomarina temperataP.tem.0.24NovosphingobiumN.aci.0.35Reinekea aestuariiR.aes.0.31Owenweeksia hongkongensisO.hon.0.37Salinirepens amaniensisS.ama.0.25PhaeocystidibacterP.mar.0.45Sedimenticola thiotauriniS.thi.0.24Planktomarina temperateP.tem.0.22Sedimenticola thiotauriniS.thi.0.24Planktomarina temperateP.tem.0.22Sedimenticola thiotauriniS.thi.0.24PolaribacterP.hua.0.17Tenacibaculum aiptasiaeT.aip.0.21Pseudohongiella spirulinaeP.spi.0.16111111ThiohalobacterT.thi.0.18Salinirepens amaniensisS.ama.0.27Sedimenticola thiotauriniS.thi.0.32Style a plicataS.pli.0.17Uncultured Alpha- meroteobacterium (OTUL#2)UAp#20.1818	Methylophilus	M met	0.31	Owenweeksia	0 hon	0.37	Bacteria
Novosphingobium acidiphilumN.aci.0.35Reinekea aestuariiR.aes.0.31Owenweeksia hongkongensis Phaeocystidibacter marisrubriO.hon.0.37Salinirepens amaniensisS.ama.0.25Phaeocystidibacter marisrubriP.mar.0.45Sedimenticola thiotauriniS.thi.0.24Planktomarina temperate huanghezhanensisP.tem.0.22Sedimentitalea todarodisS.tod.0.33Polaribacter huanghezhanensisP.hua.0.17Tenacibaculum aiptasiaeT.aip.0.21Pseudohongiella spirulinae thiocyanaticusP.spi.0.160.1311Thiohalobacter thiocyanaticusT.thi.0.183211Salinirepens amaniensis S ama.S.ama.0.27111Sedimenticola thiotaurini thiocyanaticusS.thi.0.3211Sultirepens amaniensis S ama.S.pli.0.1711Uncultured Alpha- rectorbacterium (CTU #2)UAp#20.1811	methylotrophus Nisaea nitritireducens	N nit	0.38	hongkongensis Planktomarina temperata	P tem	0.24	
actiophilum0.37Salinirepens amaniensisS.ama.0.25Owenweeksia hongkongensisO.hon.0.37Salinirepens amaniensisS.ama.0.24Phaeocystidibacter marisrubriP.mar.0.45Sedimenticola thiotauriniS.thi.0.24Planktomarina temperateP.tem.0.22Sedimentitalea todarodisS.tod.0.33Polaribacter huanghezhanensisP.hua.0.17Tenacibaculum aiptasiaeT.aip.0.21Pseudohongiella spirulinaeP.spi.0.16Thiohalobacter thiocyanaticusT.thi.0.18Salinirepens amaniensisS.ama.0.27Sedimenticola thiotauriniS.thi.0.32Stylea plicataS.pli.0.17UAp#20.18	Novosphingobium	N.aci.	0.35	Reinekea aestuarii	R.aes.	0.31	
Phaeocystidibacter marisrubriP.mar.0.45Sedimenticola thiotauriniS.thi.0.24Planktomarina temperate PolaribacterP.tem.0.22Sedimentitalea todarodisS.tod.0.33Polaribacter huanghezhanensisP.hua.0.17Tenacibaculum aiptasiaeT.aip.0.21Pseudohongiella spirulinae Tenacibaculum aiptasiaeT.aip.0.130.130.13Thiohalobacter thiocyanaticusT.thi.0.1850.13Salinirepens amamiensis Styela plicataS.pli.0.170.170.12Uncultured Alpha- revotobacterium (OTUL#2)UAp#20.180.18	aciaiphilum Owenweeksia hongkongensis	O.hon.	0.37	Salinirepens amamiensis	S.ama.	0.25	
Intervention0.21Sedimentitalea todarodisS.tod.0.33Polaribacter huanghezhanensisP.hua.0.17Tenacibaculum aiptasiaeT.aip.0.21Pseudohongiella spirulinaeP.spi.0.16111Pseudohongiella spirulinaeP.spi.0.16111Thiohalobacter thiocyanaticusT.thi.0.18111Salinirepens amamiensisS.ama.0.271111Sytela plicataS.pli.0.170.18111Uncultured Alpha- rectorobacterium (OTU #2)UAp#20.180.1811	Phaeocystidibacter marisrybri	P.mar.	0.45	Sedimenticola thiotaurini	S.thi.	0.24	
Polaribacter       P.hua.       0.17       Tenacibaculum aiptasiae       T.aip.       0.21         Pseudohongiella spirulinae       P.spi.       0.16       0.13       0.13       0.13         Thiohalobacter       T.thi.       0.18       0.18       0.21         Salinirepens amaniensis       S.ama.       0.27       0.23         Styela plicata       S.pli.       0.17       0.17         Uncultured Alpha-       UAp#2       0.18	Planktomarina temperate	P.tem.	0.22	Sedimentitalea todarodis	S.tod.	0.33	
Pseudohongiella spirulinae       P.spi.       0.16         Tenacibaculum aiptasiae       T.aip.       0.13         Thiohalobacter       T.thi.       0.18         Salinirepens amamiensis       S.ama.       0.27         Sedimenticola thiotaurini       S.thi.       0.32         Styela plicata       S.pli.       0.17         Uncultured Alpha- merateobacterium (OTU #2)       UAp#2       0.18	Polaribacter huanghezhanensis	P.hua.	0.17	Tenacibaculum aiptasiae	T.aip.	0.21	
Tenacibaculum aiptasiaeT.aip.0.13ThiohalobacterT.thi.0.18thiocyanaticusS.ama.0.27Salinirepens amaniensisS.ama.0.32Styla plicataS.pli.0.17Uncultured Alpha- restorbacterium (CTU #2)UAp#20.18	Pseudohongiella spirulinae	P.spi.	0.16				
Thiohalobacter thiocyanaticusT.thi.0.18Salinirepens amamiensisS.ama.0.27Sedimenticola thiotauriniS.thi.0.32Stylela plicataS.pli.0.17Uncultured Alpha- presterbacterium (OTU #2)UAp#20.18	Tenacibaculum aiptasiae	T.aip.	0.13				
Salini repens amamiensis       S. ama.       0.27         Sedimenticola thiotaurini       S. thi.       0.32         Styela plicata       S. pli.       0.17         Uncultured Alpha- restoebacterium (OTU #2)       UAp#2       0.18	Thiohalobacter thiocyanaticus	T.thi.	0.18				
Sedimenticola thiotaurini     S. thi.     0.32       Styela plicata     S.pli.     0.17       Uncultured Alpha- restorebacterium (OTU #2)     UAp#2     0.18	Salinirepens amamiensis	S.ama.	0.27				
Styela plicataS.pli.0.17Uncultured Alpha- protecheterium (OTU #2)UAp#20.18	Sedimenticola thiotaurini	S.thi.	0.32				
Uncultured Alpha- protechecterium (OTU #2) UAp#2 0.18	Styela plicata	S.pli.	0.17				
	Uncultured Alpha- proteobacterium (OTU #2)	UAp#2	0.18				

#### 63 Supplementary Table 6. Continued

201	6		2017			
Factor	Abbreviation	Node size	Factor	Abbreviation	Node size	Classification
Acanthocystis turfacea chlorella virus 1	AtcV1	0.30	Acanthamoeba polyphaga moumouvirus	ApmoV	0.76	
<i>Bathycoccus</i> sp. RCC1105 virus BpV1	BpV1	0.57	Aureococcus anophagefferens virus	AaV	0.67	
Cafeteria roenbergensis virus BV-PW1	CrVBV-PW1	0.65	Bathycoccus sp. RCC1105 virus BpV1	BpV1	0.37	
Cedratvirus A11	CV-A11	0.23	Cafeteria roenbergensis virus BV-PW1	CrVBV-PW1	0.56	
Chrysochromulina ericina virus	CeV	0.50	Chrysochromulina ericina virus	CeV	0.52	
Diachasmimorpha longicaudata entomopoxvirus	DleV	0.07	Dishui lake phycodnavirus 1	DlpV1	0.50	
<i>Diadromus pulchellus</i> ascovirus 4a	DpaV4a	0.10	Emiliania huxleyi virus 86	EhV86	0.55	
Dishui lake phycodnavirus 1 Ectocarpus siliculosus virus 1	DlpV1 EsV1	0.10 0.20	Heterosigma akashiwo virus 01 Megavirus chiliensis	HaV01 McV	0.63 0.73	
Emiliania huxleyi virus 86	EhV86	0.36	Micromonas sp. RCC1109 virus MpV1	MpV1	0.40	
Eptesipox virus	EpV	0.63	Micromonas pusilla virus SP1	MpV-SP1	0.43	
European catfish virus	EcV	0.11	Mimivirus terra2	MVt2	0.70	
Heterosigma akashiwo virus 01	HaV01	0.22	Mollivirus sibericum	MsV	0.21	
Invertebrate iridovirus 22	IiV22	0.17	Only Syngen Nebraska virus 5	OSNV5	0.68	
Invertebrate iridescent virus 6	liV6	0.16	Ostreococcus lucimarinus virus 1	OIV1	0.23	
Lymphocystis disease virus - isolate China	LdV	0.63	Ostreococcus lucimarinus virus OIV5	OIV5	0.35	
Lymphocystis disease virus Sa Megavirus chiliensis	LdVSa McV	0.08 0.24	Ostreococcus tauri virus 2 Pandoravirus dulcis	OtV2 PdV	0.30 0.37	
Micromonas sp. RCC1109 virus MpV1	MpV1	0.36	Pandoravirus inopinatum	PiV	0.46	NCLDVs
Micromonas pusilla virus 12T	MpV12T	0.65	Pandoravirus macleodensis	PmV	0.17	
<i>Micromonas pusilla</i> virus SP1 <i>Mimivirus terra</i> 2	MpV-SP1 MVt2	0.36 0.63	Pandoravirus neocaledonia Pandoravirus quercus	PnV PqV	0.48 0.49	
Ostreococcus lucimarinus virus OIV5	OIV5	0.36	Pandoravirus salinus	PsV	0.51	
Ostreococcus mediterraneus virus 1	OmV1	0.25	Phaeocystis globosa virus	PgV	0.62	
Only Syngen Nebraska virus 5	OSNV5	0.58	Yellowstone lake mimivirus	YlmV	0.36	
Ostreococcus tauri virus OtV5	OtV5	0.13				
Paramecium bursaria chlorella virus 1	PbcV1	0.36				
Paramecium bursaria chlorella virus CVA-1	PbcV-CVA1	0.28				
Paramecium bursaria chlorella virus FR483	PbcV-FR483	0.26				
Paramecium bursaria chlorella virus NY2A	PbcV-NY2A	0.54				
Paramecium bursaria chlorella virus NYs1	PbcV-NYs1	0.39				
Phaeocystis globosa virus	PgV	0.63				
Pandoravirus dulcis	PdV	0.13				
Pandoravirus macleodensis	PmV	0.30				
Pandoravirus quercus	PqV	0.44				
Pandoravirus salinus	PsV	0.32				
Ranavirus maximus	RmV	0.30				
Trichoplusia ascovirus 2c	TaV2c	0.32				
Taterapox virus	TpV	0.13				
Trichoplusia ni ascovirus 2c	TnaV2c	0.32				
Yellowstone lake mimivirus	YlmV	0.23				
Yellowstone lake phycodnavirus 1	YlpV1	0.36				
Yellowstone lake phycodnavirus 3	YlpV3	0.45				
Yokapox virus	YpV	0.47				

Х	Y	LS	Xs	Ys	Length	Delay time (d)	SPCC	P <sub>SPCC</sub>
Chl-a		0.727	2	1	16	4	0.706	0.002
DIP	1	0.694	1	1	16	0	0.739	0.001
Sal.	A.san.	-0.582	1	1	16	0	-0.866	0.000
Temp.		0.622	1	1	16	0	0.769	0.000
	PpV	-0.898	1	1	16	0	-0.834	0.000
	H.rot.	-0.684	1	1	16	0	-0.587	0.035
	A.ste.	-0.581	1	1	16	0	-0.510	0.075
	U.Str.	-0.857	1	1	17	0	-0.793	0.000
	A.omo	-0.610	1	1	17	0	-0.650	0.005
	Amo.sp1.	0.722	1	2	16	-2	0.594	0.015
	Oth.Syn.	-0.660	1	1	17	0	-0.823	0.000
	N.aci.	-0.660	1	1	17	0	-0.738	0.001
1	UAp #2	0.665	1	1	16	0	0.679	0.003
A.sun.	A.ulv.	-0.746	1	1	15	0	-0.753	0.001
	P.mar.	0.686	1	2	13	-2	0.575	0.020
	M.alg.	-0.684	1	3	15	-4	-0.812	0.000
	F.taf.	0.665	1	3	15	-2	0.595	0.025
	S.ama.	-0.706	1	1	16	0	-0.790	0.000
	L.syl.	-0.689	1	2	16	-2	-0.737	0.004
	C.spi.	-0.707	1	2	16	-2	-0.851	0.000
	T.thi.	-0.556	1	2	16	-2	-0.855	0.000
	EsV1	0.638	1	3	15	-4	0.502	0.067

66 Supplementary Table 7. Description of LS correlations displayed of network analysis in Figure 7a.

 $\begin{array}{cccc} \textbf{67} & \mbox{Abbreviations: LS, local similarity; SPCC and P_{SPCC} are the Spearman's Correlation Coefficient and the associated P-value, respectively for the OTUs listed. Delay indicates time-lag day. Xs and Ys note the day in \\ \end{array}$ 

69 which the LS correlation begins, and 'Length,' indicates the length of the LS correlation in day.

X	Y	LS	Xs	Ys	Length	Delay time (d)	SPCC	P <sub>SPCC</sub>
pН	B.pra.	-0.712	1	1	15	0	0.717	0.019
	S.tod.	0.564	2	1	14	2	0.857	0.000
	L.alg.	-0.547	5	1	11	8	-0.895	0.000
	T.aip.	-0.501	1	1	15	0	-0.663	0.007
B.pra.	B.arc.	0.544	1	2	14	-2	0.739	0.003
	E.tan.	0.545	1	1	15	0	0.709	0.003
	OlV5	-0.541	1	1	15	0	-0.823	0.001
	OlV2	-0.555	5	4	11	2	-0.743	0.002

71 Supplementary Table 8. Description of LS correlations displayed of network analysis in Figure 7b.

Abbreviations: LS, local similarity; SCC and P<sub>SCC</sub> are the Spearman's Correlation Coefficient and the associated 72 73

P-value, respectively for the OTUs listed. Delay indicates time-lag day. Xs and Ys note the day in which the LS

74 correlation begins, and 'Length,' indicates the length of the LS correlation in day.

Strain name	Genus	Phylum	Target phytoplankton	Killing Type	Reference
ACEM 21	Cellulophaga		Raphidophyceae, Dinoflagellate, Diatoms	Indirect	5
A5Y	Cytophaga		Raphidophyceae, Diatoms.	Direct	6
41-DBG2	Cytophaga		Dinoflagellate	Indirect	7
N/D	Cytophaga		Raphidophyceae,	Direct	8
MC8	Cytophaga		Raphidophyceae.	Direct	9
J18/M01	Cytophaga		Raphidophyceae, Diatoms	Direct	10
LR2	Cytophaga		Dinoflagellate	Unknown	11
AA8-2	Cytophaga	Bacteriodetes	Dinoflagellate	Direct	12
AMA-01	Cytophaga	Durining	Dinoflagellate	Indirect	13
5N-3	Elavobactarium		Dinoflagellate	Indirect	14
C/10	Flavobacterium		Panhidonhyceae	Unknown	15
5598-5	Saprospira		Distoms	Direct	16
SS K1	Saprospira		Diatoms	Direct	17
ACEM 20	Zahallia		Diatoinis Damhi damhu agas Dimoflagallata	Indinast	5
ACEM 20	Zobellia		Distoma	Unknown	19
V12			Diatoms	Indinast	10
SP 14	Alteromonas		Diatoms	Indirect	19
SK-14	Alteromonas			Indirect	20
ANS W 2-2	Alteromonas		Dinollagenate Daubidauburan Dinafla allata	Indirect	21
E401	Alteromonas		Raphidophyceae, Dinoflagellate	Indirect	21
MC2/	Alteromonas		Raphidophyceae	Indirect	22
GY21	Alteromonas		Raphidophyceae	Indirect	22
GY9501	Alteromonas		Rap., Dinoflagellate	Indirect	23
S	Alteromonas		Raphidophyceae, Dinoflagellate, Diaotms.	Indirect	24
K	Alteromonas		Raphidophyceae, Dinoflagellate, Diaotms.	Indirect	24
D	Alteromonas		Raphidophyceae, Dinoflagellate, Diaotms.	Indirect	24
A25	Pseudoalteromonas		Diatoms	Indirect	25
A28	Pseudoalteromonas		Raphidophyceae, Diatoms	Indirect	26
Y	Pseudoalteromonas		Raphidophyceae, Dinoflagellate	Indirect	27
ACEM 4	Pseudoalteromonas	Gamma-proteobacteria	Raphidophyceae, Dinoflagellate	Indirect	5
R	Pseudoalteromonas	Gamma-proteobaeteria	Raphidophyceae, Dinoflagellate, Diatoms	Indirect	24
AMA-02	Pseudoalteromonas		Dinoflagellate	Indirect	13
T827/2B	Pseudomonas		Diatoms	Indirect	28
LG-2	Pseudomonas		Dinoflagellate	Indirect	29
EHK-1	Pseudomonas		Dinoflagellate	Indirect	30
G42	Pseudomonas		Raphidophyceae	Unknown	15
O-2-2	Pseudomonas		Raphidophyceae, Dinoflagellate	Indirect	31
T27	Vibrio		Raphidophyceae, Dinoflagellate	Unknown	32
A47	Vibrio		Raphidophyceae	Unknown	15
B42	Vibrio		Diatoms	Unknown	15
C4	Vibrio		Raphidophyceae, Diatoms	Unknown	15
G62	Vibrio		Raphidophyceae, Dinoflagellate	Unknown	15
AMA-03	Ruegeria		Dinoflagellate	Indirect	13
IRI-60	Shewanella		Dinoflagellate	Direct	33
ACEM 32	Bacillus		Raphidophyceae. Dinoflagellate	Indirect	5
SY-1	Bacillus	Firmicutes	Dinoflagellate	Indirect	34
ACEM 22	Planomicrohium	1	Ranhidonhyceae Dinoflagellate	Indirect	5
LG-1	Micrococcus		Dinoflagellate	Indirect	35
LG-5	Micrococcus	Actinobacteria	Dinoflagellate	Indirect	36
SV-13	Micrococcus	1 ionnoouotoria	Dinoflagellate	Indirect	30
OT-1	Kordia		Diatoms	direct	37
H51985_4	Unknown		Ranhidonhyceae Dinoflagellate Distore	indirect	30
H60585 15	Unknown	Unknown	Raphidophyceae, Dinoflagellate, Distores	indirect	30
LIG0585-15	Unknown		Raphidophyceae, Dinoflagellate, Didtollis	indirect	20
поозво-22	Unknown		Raphidophyceae, Dinollagenate, Diatoms	manect	39

## 76 Supplementary Table 9. The list of the previous studies of algicidal bacteria.

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