

High contribution of Rhizaria (Radiolaria) to vertical export in the California Current Ecosystem revealed by DNA metabarcoding

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Supplementary material

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Supplementary data

Deposited on Figshare at <https://figshare.com/s/a37291764f6ebb3cf9a1>

Supplementary Data S1. CCE Samples.xlsx. List of samples with metadata

Supplementary Data S2. CCE OTU 0.97.fasta. Fasta file with sequence of OTUs

Supplementary Data S3. CCE OTU table.xlsx. Read abundance table of OTUs (rows) vs Samples (Column). For each OTU the reference sequence and taxonomy are provided.

Supplementary Tables

Supplementary Table S1. List of samples included in the DNA metabarcoding analysis of 18S rRNA gene and associated metadata. Sample ID corresponds to that indicated in the OTU table deposited on Figshare (<https://doi.org/10.6084/m9.figshare.5944291>), date of sample collection or sediment trap recovery, size-fraction, (lat) latitude, (long) longitude, (T) temperature, (Sal) salinity. Samples 'A' and 'B' correspond to additional PCR replicates (see Materials and Methods and Supplementary Figure S1).

Sample ID	Sample name	Date	Depth (m)	Lat Long	Sample source	Size fraction	T (°C)	Sal
C1_Trp_fx_60m_08	Cycle1_fx_60m_08	14-Aug-14	60	34.2695 N 120.82 W	fixed trap	Total	nd	nd
C1_Trp_fx_60m_8.0	Cycle1_fx_60m_8.0	14-Aug-14	60	34.2695 N 120.82 W	fixed trap	>8- μ m	nd	nd
C2_10_08	Cycle2_10m_08	18-Aug-14	10	34.2248 N 120.816 W	water column	Total	33.4066	16.8686
C2_30_08	Cycle2_30m_08	18-Aug-14	30	34.2248 N 120.816 W	water column	Total	33.3903	14.956
C2_75_08	Cycle2_75m_08	18-Aug-14	75	34.2248 N 120.816 W	water column	Total	33.5308	10.8327
C2_Ct22_10m_8.0	Cycle2_10m_8.0	18-Aug-14	10	34.2248 N 120.816 W	water column	>8- μ m	33.4066	16.8686
C2_Ct22_30m_8.0	Cycle2_30m_8.0	18-Aug-14	30	34.2248 N 120.816 W	water column	>8- μ m	33.3903	14.956
C2_Ct22_75m_8.0	Cycle2_75m_8.0	18-Aug-14	75	34.2248 N 120.816 W	water column	>8- μ m	33.5308	10.8327
C2_free_60m_08	Cycle2_live_60m_08	20-Aug-14	60	34.0801 N 120.978 W	live trap	Total	nd	nd
C2_free_60m_8.0	Cycle2_live_60m_8.0	20-Aug-14	60	34.0801 N 120.978 W	live trap	>8- μ m	nd	nd
C2_free_100m_08	Cycle2_live_100m_08	20-Aug-14	100	34.0801 N 120.978 W	live trap	Total	nd	nd
C2_free_100m_08_A	Cycle2_live_100m_08_A	20-Aug-14	100	34.0801 N 120.978 W	live trap	Total	nd	nd
C2_free_100m_08_B	Cycle2_live_100m_08_B	20-Aug-14	100	34.0801 N 120.978 W	live trap	Total	nd	nd
C2_free_100m_8.0	Cycle2_live_100m_8.0	20-Aug-14	100	34.2248 N 120.816 W	live trap	>8- μ m	nd	nd
C2_free_150m_08	Cycle2_live_150m_08	20-Aug-14	150	34.0801 N 120.978 W	live trap	Total	nd	nd
C2_free_150m_8.0	Cycle2_live_150m_8.0	20-Aug-14	150	34.2248 N 120.816 W	live trap	>8- μ m	nd	nd
C2_fx_100m_08	Cycle2_fx_100m_08	20-Aug-14	100	34.0801 N 120.978 W	fixed trap	Total	nd	nd
C2_fx_100m_08_A	Cycle2_fx_100m_08_A	20-Aug-14	100	34.0801 N 120.978 W	fixed trap	Total	nd	nd
C2_fx_100m_08_B	Cycle2_fx_100m_08_B	20-Aug-14	100	34.0801 N 120.978 W	fixed trap	Total	nd	nd
C2_fx_100m_8.0	Cycle2_fx_100m_8.0	20-Aug-14	100	34.2248 N 120.816 W	fixed trap	>8- μ m	nd	nd
C3_Ct40_10m_08	Cycle3_10m_08	25-Aug-14	10	34.4158 N 121.046 W	water column	Total	33.3	18.7546
C3_Ct40_10m_08_A	Cycle3_10m_08_A	25-Aug-14	10	34.4158 N 121.046 W	water column	Total	33.3	18.7546
C3_Ct40_10m_08_B	Cycle3_10m_08_B	25-Aug-14	10	34.4158 N 121.046 W	water column	Total	33.3	18.7546

C3_Ct40_35m_08	Cycle3_35m_08	25-Aug-14	35	34.4158 N 121.046 W	water column	Total	32.9983	13.807
C3_Ct40_60m_08	Cycle3_60m_08	25-Aug-14	60	34.4158 N 121.046 W	water column	Total	33.2172	11.4226
C3_Ct40_10m_8.0	Cycle3_10m_8.0	25-Aug-14	10	34.4158 N 121.046 W	water column	>8-µm	33.3	18.7546
C3_Ct40_10m_8.0_A	Cycle3_10m_8.0_A	25-Aug-14	10	34.4158 N 121.046 W	water column	>8-µm	33.3	18.7546
C3_Ct40_10m_8.0_B	Cycle3_10m_8.0_B	25-Aug-14	10	34.4158 N 121.046 W	water column	>8-µm	33.3	18.7546
C3_Ct40_35m_8.0	Cycle3_35m_8.0	25-Aug-14	35	34.4158 N 121.046 W	water column	>8-µm	32.9983	13.807
C3_Ct40_60m_8.0	Cycle3_60m_8.0	25-Aug-14	60	34.4158 N 121.046 W	water column	>8-µm	33.2172	11.4226
C3_free_60m_08	Cycle3_live_60m_08	25-Aug-14	60	34.4171 N 121.027 W	live trap	Total	nd	nd
C3_free_60m_8.0	Cycle3_live_60m_8.0	25-Aug-14	60	34.4171 N 121.027 W	live trap	>8-µm	nd	nd
C3_free_100m_8.0	Cycle3_live_100m_8.0	25-Aug-14	100	34.4171 N 121.027 W	live trap	>8-µm	nd	nd
C3_free_150m_08	Cycle3_live_150m_08	25-Aug-14	150	34.4171 N 121.027 W	live trap	Total	nd	nd
C3_free_150m_8.0	Cycle3_live_150m_8.0	25-Aug-14	150	34.4171 N 121.027 W	live trap	>8-µm	nd	nd
C3_fx_100m_08	Cycle3_fx_100m_08	25-Aug-14	100	34.4171 N 121.027 W	fixed trap	Total	nd	nd
C3_fx_100m_8.0	Cycle3_fx_100m_8.0	25-Aug-14	100	34.4171 N 121.027 W	fixed trap	>8-µm	nd	nd
C4_Ct50_10m_08	Cycle4_10m_08	29-Aug-14	10	33.6121 N 122.433 W	water column	Total	33.0255	19.3298
C4_Ct50_70m_08	Cycle4_70m_08	29-Aug-14	70	33.6121 N 122.433 W	water column	Total	33.0614	14.0467
C4_90_08	Cycle4_90m_08	29-Aug-14	90	33.6121 N 122.433 W	water column	Total	33.0531	11.4751
C4_Ct50_10m_8.0	Cycle4_10m_8.0	29-Aug-14	10	33.6445 N 122.399 W	water column	>8-µm	33.0255	19.3298
C4_Ct50_70m_8.0	Cycle4_70m_8.0	29-Aug-14	70	33.6445 N 122.399 W	water column	>8-µm	33.0614	14.0467
C4_free_60m_08	Cycle4_live_60m_08	29-Aug-14	60	33.6445 N 122.399 W	live trap	Total	nd	nd
C4_free_60m_8.0	Cycle4_live_60m_8.0	29-Aug-14	60	33.6445 N 122.399 W	live trap	>8-µm	nd	nd
C4_free_100m_08	Cycle4_live_100m_08	29-Aug-14	100	33.6445 N 122.399 W	live trap	Total	nd	nd
C4_free_100m_8.0	Cycle4_live_100m_8.0	29-Aug-14	100	33.6445 N 122.399 W	live trap	>8-µm	nd	nd
C4_free_100m_8.0_A	Cycle4_live_100m_8.0_A	29-Aug-14	100	34.0801 N 120.978 W	live trap	>8-µm	nd	nd
C4_free_100m_8.0_B	Cycle4_live_100m_8.0_B	29-Aug-14	100	34.0801 N 120.978 W	live trap	>8-µm	nd	nd
C4_free_150m_08	Cycle4_live_150m_08	29-Aug-14	150	33.6445 N 122.399 W	live trap	Total	nd	nd
C4_free_150m_8.0	Cycle4_live_150m_8.0	29-Aug-14	150	33.6445 N 122.399 W	live trap	>8-µm	nd	nd
C4_fx_100m_08	Cycle4_fx_100m_08	29-Aug-14	100	33.6445 N 122.399 W	fixed trap	Total	nd	nd
C4_fx_100m_8.0	Cycle4_fx_100m_8.0	29-Aug-14	100	33.6445 N 122.399 W	fixed trap	>8-µm	nd	nd
C4_fx_100m_8.0_A	Cycle4_fx_100m_8.0_A	29-Aug-14	100	34.0801 N 120.978 W	fixed trap	>8-µm	nd	nd
C4_fx_100m_8.0_B	Cycle4_fx_100m_8.0_B	29-Aug-14	100	34.0801 N 120.978 W	fixed trap	>8-µm	nd	nd

C5_Ct60_10m_08	Cycle5_10m_08	1-Sep-14	10	32.8112 N 123.862 W	water column	Total	33.0911	19.809
C5_Ct60_10m_80	Cycle5_10m_8.0	1-Sep-14	10	32.8112 N 123.862 W	water column	>8- μ m	33.0911	19.809
C5_Ct60_25m_8.0	Cycle5_25m_8.0	1-Sep-14	25	32.8112 N 123.862 W	water column	>8- μ m	33.0911	19.8709
C5_Ct60_50m_8.0	Cycle5_50m_8.0	1-Sep-14	50	32.8112 N 123.862 W	water column	>8- μ m	33.1451	16.6913
C5_Ct60_70m_8.0	Cycle5_70m_8.0	1-Sep-14	70	32.8112 N 123.862 W	water column	>8- μ m	33.1275	14.9474
C5_free_100m_08	Cycle5_live_100m_08	2-Sep-14	100	32.7883 N 123.8 W	live trap	Total	nd	nd
C5_free_100m_8.0	Cycle5_live_100m_8.0	2-Sep-14	100	32.7883 N 123.8 W	live trap	>8- μ m	nd	nd
C5_free_150m_02	Cycle5_live_150m_02	2-Sep-14	150	32.7883 N 123.8 W	live trap	Total	nd	nd
C5_free_150m_8.0	Cycle5_live_150m_8.0	2-Sep-14	150	32.7883 N 123.8 W	live trap	>8- μ m	nd	nd
C5_fx_100m_08	Cycle5_fx_100m_08	2-Sep-14	100	32.7883 N 123.8 W	fixed trap	Total	nd	nd
C5_fx_100_08	Cycle5_fx_100m_08	2-Sep-14	100	32.7883 N 123.8 W	fixed trap	Total	nd	nd
C5_fx_100m_8.0	Cycle5_fx_100m_8.0	2-Sep-14	100	32.8112 N 123.862 W	fixed trap	>8- μ m	nd	nd

Supplementary Table S2. Summary of Illumina results and filtering steps.

Step	All	Unique
Number of read pairs	18 019 134	
Number of contigs after selecting reads with length > 200 and for which Q >20 for 75% of the reads	9 676 884	
After removing ambiguities	3 846 053	
Afer pcr.seq - pdiffs=2	3 788 366	1 001 090
After removing short sequences < 200 and singletons	2 937 528	150 252
After preclustering pdiffs = 2	2 937 528	31 215
After removing chimeras	2 890 723	30 709
After removing negative controls	2 888 947	30 683
After removing sequence with less than 10 representatives	2 802 466	6 296
OTUs at 0.03 level (97% similarity)		2 662

Supplementary Table S3. Most abundant eukaryotic OTUs recovered from water column, fixed 43 and live trap samples. Read abundance (# Reads), mean percentage read abundance across samples (% Reads), read percentage across methods (% Method), taxonomic affiliation (Division, Genus) and description of the best BLAST identified hit and pairwise percent identity (% identity). Protistan OTUs are shown in bold.

OTU	# Reads	% Reads	% Method	Genus	Division	% Ident
WATER COLUMN						
Otu0002	107813	9.9	76.5	Dinophyta	Ptychodiscus	100%
Otu0010	49579	7.9	94.6	Metazoa	Paracalanus	100%
Otu0012	41459	4.1	85.2	Dinophyta	Dino-Group-I-Clade-1_X	100%
Otu0005	37329	2.9	34.5	Metazoa	Oithona	100%
Otu0014	29931	6.5	80.2	Metazoa	Calanus	100%
Otu0015	28828	3.4	80.2	Metazoa	Clausocalanus	100%
Otu0025	26381	2.5	99.8	Radiolaria	Collodaria_unclassified	75%
Otu0027	25667	1.5	97.6	Dinophyta	Dino-Group-I-Clade-1_X	100%
Otu0033	19011	1.4	98.0	Dinophyta	Dino-Group-II-Clade-10-and-11_X	99%
Otu0009	18616	1.5	29.8	Dinophyta	Dinophyceae_XXX	100%
Otu0021	18292	1.6	63.0	Dinophyta	Warnowia	98%
Otu0034	17434	2.3	90.8	Chlorophyta	Prasino-Clade-VII-B-1	100%
Otu0029	17369	1.9	66.8	Dinophyta	Dino-Group-I-Clade-1_X	100%

Otu0018	16626	1.4	54.9	Metazoa	Oithona	98%	ribosomal RNA gene, partial sequence Oithona sp. 1 New Caledonia-RJH-2001 18S ribosomal RNA gene, partial sequence
Otu0008	14092	1.3	21.3	Metazoa	Abylopsis	100%	Abylopsis eschscholtzii voucher NHMUK MCF 185546846 18S ribosomal RNA gene, partial sequence
Otu0041	13071	1.5	94.4	Metazoa	Liriope	100%	Liriope tetraphylla small subunit ribosomal RNA gene, partial sequence
Otu0006	11603	0.5	13.4	Metazoa	Eucalanus	99%	Eucalanus inermis 18S ribosomal RNA gene, partial sequence
Otu0036	11564	0.8	64.0	Metazoa	Conchoecia	100%	Conchoecia sp. OC-2001 18S ribosomal RNA gene, partial sequence
Otu0043	10363	1.4	92.1	Dinophyta	Blastodinium	100%	Blastodinium contortum clone BOUM50 small subunit ribosomal RNA gene, partial sequence
Otu0046	10112	1.0	92.5	Dinophyta	Dino-Group-II-Clade-10-and-11	100%	Uncultured marine Syndiniales clone RA071004T.057 18S ribosomal RNA gene, partial sequence
Otu0049	9611	0.3	99.9	Radiolaria		86%	Uncultured Polycystinea partial 18S rRNA gene, clone BIO3_C6
Otu0031	9053	1.7	38.2	Metazoa	Neocalanus	98%	Undinula vulgaris 18S ribosomal RNA gene, partial sequence
Otu0051	8747	0.4	94.1	Radiolaria	Collodaria	90%	Collophidium ovatum isolate Sat4 18S ribosomal RNA gene, partial sequence
Otu0042	8191	0.3	65.3	Metazoa	Corycaeus	97%	Corycaeus speciosus 18S ribosomal RNA gene, partial sequence
Otu0050	7861	0.8	83.2	Dinophyta	Neoceratium	100%	Neoceratium kofoidii isolate FG77 small subunit ribosomal RNA gene, partial sequence
Otu0048	7269	0.4	74.4	Dinophyta	Dino-Group-I-Clade-4	100%	Uncultured dinoflagellate gene for 18S rRNA, partial sequence, clone: PM58
Otu0001	7218	1.7	2.6	Metazoa	Metridia	100%	Metridia gerlachei 18S ribosomal RNA gene, partial sequence
Otu0054	7174	1.4	84.6	Metazoa	Subeucalanus	100%	Subeucalanus pileatus voucher Co355.2.2 18S small subunit ribosomal RNA gene, partial sequence
Otu0030	6794	0.4	27.7	Metazoa	Acoelomorpha	94%	Convolutidae sp. Favts2M-4 18S ribosomal RNA gene, partial sequence
Otu0056	6706	0.5	85.2	Dinophyta	Blastodinium	100%	Blastodinium mangini clone BOUM19 small subunit ribosomal RNA gene, partial sequence
FIXED TRAPS							
Otu0004	120222	2.2	99.8	Radiolaria	Gigartacon	100%	Acantharia sp. JD-2012 isolate Vil162 18S ribosomal RNA gene, partial sequence

Otu0003	118405	11.3	97.8	Radiolaria	Arachnosphaera	100%	Arachnosphaera myriacantha gene for 18S ribosomal RNA, partial sequence
Otu0005	56011	2.4	51.7	Metazoa	Oithona	100%	Oithona similis voucher LEGO-CYC036 18S ribosomal RNA gene, partial sequence
Otu0011	49579	5.4	99.9	Radiolaria	Spumellarida_unclassified	92%	Spongotrochus glacialis gene for 18S rRNA, partial sequence, isolate: OS0727
Otu0013	48062	15.0	99.1	Radiolaria	Spumellarida_XX	100%	Uncultured Rhizaria clone HL5aSCM10.64 18S ribosomal RNA gene, partial sequence
Otu0009	37046	1.9	59.4	Dinophyta	Dinophyceae_XXX	100%	Uncultured dinoflagellate gene for 18S rRNA, partial sequence, clone: HP09D-4
Otu0019	30123	3.3	99.9	Radiolaria	Spumellarida_XX	92%	Spongotrochus glacialis gene for 18S rRNA, partial sequence, isolate: OS0727
Otu0020	29412	2.5	98.2	Radiolaria	Spumellarida-Group-I_X	99%	Uncultured marine Polycystinea clone OLI011-75m.32 18S ribosomal RNA gene, partial sequence
Otu0026	26284	3.4	99.9	Radiolaria	Collozoum	100%	Collozoum inerme isolate Pan14 18S ribosomal RNA gene, partial sequence
Otu0002	24367	1.3	17.3	Dinophyta	Ptychodiscus	100%	Ptychodiscus noctiluca small subunit ribosomal RNA gene, partial sequence
Otu0017	24100	3.0	79.3	Radiolaria	Spumellarida-Group-I_X	99%	Uncultured Polycystinea partial 18S rRNA gene, clone BIO10_G12
Otu0028	24075	5.9	92.2	Radiolaria	Chaunacanthida_XX	100%	Chaunacanthida sp. Adult_20 18S ribosomal RNA gene, partial sequence
Otu0032	19192	4.9	97.7	Radiolaria	Acantharea-Group-VI_XX	100%	Uncultured marine Acantharea clone Ma121_1A29 18S ribosomal RNA gene, partial sequence
Otu0035	19092	2.1	99.9	Radiolaria	Spumellarida_unclassified	92%	Spongotrochus glacialis gene for 18S rRNA, partial sequence, isolate: OS0727
Otu0040	14022	2.9	99.6	Radiolaria	Spumellarida_XX	96%	Uncultured rhizarian clone BCB5F14RM4A03 18S ribosomal RNA gene, partial sequence
Otu0044	11085	0.2	100.0	Radiolaria	Dictyocoryne	98%	Dictyocoryne truncatum gene for 18S rRNA, partial sequence
Otu0037	10357	0.2	64.6	Metazoa	Oikopleura	100%	Oikopleura dioica gene for 18S rRNA, partial sequence
Otu0021	9633	0.4	33.2	Dinophyta	Warnowia	98%	Warnowia sp. BSL-2009a isolate Florida 18S ribosomal RNA gene, partial sequence
Otu0047	9351	0.2	89.7	Radiolaria	RAD-A	95%	Uncultured marine Polycystinea clone OLI011-75m.82 18S ribosomal RNA gene, partial sequence
Otu0053	8975	0.3	99.6	Radiolaria	Trizona	100%	Trizona brandti isolate Ros6 18S ribosomal RNA gene, partial sequence

Otu0001	8890	0.2	3.2	Metazoa	Metridia	100%	Metridia gerlachei 18S ribosomal RNA gene, partial sequence
Otu0057	7825	0.1	100.0	Radiolaria	Chaunacanthida	96%	Chaunacanthida sp. Adult_20 18S ribosomal RNA gene, partial sequence
Otu0061	7019	0.9	97.9	Radiolaria	Collozoum	100%	Collozoum inerme isolate Vil338 18S ribosomal RNA gene, partial sequence
Otu0064	6975	0.7	99.9	Radiolaria	Spumellarida	91%	Spongotrochus glacialis gene for 18S rRNA, partial sequence, isolate: OS0727
Otu0062	6892	0.3	96.6	Ciliophora	Scuticociliatia-1	97%	Uncultured Scuticociliatia partial 18S rRNA gene, clone BIO7_E8
Otu0065	6828	0.1	99.9	Radiolaria	Dictyocoryne	99%	Dictyocoryne truncatum gene for 18S rRNA, partial sequence
Otu0006	6417	0.1	7.4	Metazoa	Eucalanus	99%	Eucalanus inermis 18S ribosomal RNA gene, partial sequence
Otu0068	6412	0.1	99.8	Dinophyta	Dinophyceae	88%	Gyrodinium cf. spirale AR-2015 isolate AR308 small subunit ribosomal RNA gene, partial sequence
Otu0067	5768	0.1	84.6	Metazoa	Calocalanus	98%	Calocalanus sp. 1 AC-2013 18S ribosomal RNA gene, partial sequence
Otu0063	5744	0.7	80.9	Radiolaria	Spumellarida-Group-I	99%	Uncultured Polycystinea partial 18S rRNA gene, clone BIO3_A1
LIVE TRAPS							
Otu0001	255362	25.1	93.3	Metazoa	Metridia	100%	Metridia gerlachei 18S ribosomal RNA gene, partial sequence
Otu0007	72464	3.9	96.8	Metazoa	Caenogastropoda_unclassified	98%	Austrolittorina antipodum partial 18S rRNA gene, specimen voucher NANT.NZS.1
Otu0006	68309	4.8	79.1	Metazoa	Eucalanus	99%	Eucalanus inermis 18S ribosomal RNA gene, partial sequence
Otu0008	32870	6.9	49.6	Metazoa	Abylopsis	100%	Abylopsis eschscholtzii voucher NHMUK MCF 185546846 18S ribosomal RNA gene, partial sequence
Otu0016	30450	5.3	92.2	Metazoa	Aetideus	100%	Aetideus armatus voucher Co183.3.2 18S small subunit ribosomal RNA gene, partial sequence
Otu0024	27083	1.3	99.4	Metazoa	Heterobranchia_unclassified	100%	Hyalocylis striata 18S ribosomal RNA gene, complete sequence
Otu0023	26695	3.0	96.3	Stramenopiles	Caecitellus	100%	Caecitellus parvulus 18S ribosomal RNA gene, partial sequence
Otu0022	20840	3.9	75.0	Metazoa	Pleuromamma	100%	Pleuromamma scutullata gene for 18S ribosomal RNA, partial sequence
Otu0030	16955	1.4	69.0	Metazoa	Acoelomorpha_unclassified	94%	Convolutidae sp. Favts2M-4 18S ribosomal RNA gene, partial sequence
Otu0005	14886	3.2	13.7	Metazoa	Oithona	100%	Oithona similis voucher LEGO-CYC036 18S ribosomal RNA

						gene, partial sequence
Otu0038	14477	2.8	90.8	Stramenopiles	Caecitellus	100% Caecitellus paraparvulus strain HFCC71 18S ribosomal RNA gene, partial sequence
Otu0031	12576	4.2	53.1	Metazoa	Neocalanus	98% Undinula vulgaris 18S ribosomal RNA gene, partial sequence
Otu0018	8782	1.3	29.0	Metazoa	Oithona	98% Oithona sp. 1 New Caledonia-RJH-2001 18S ribosomal RNA gene, partial sequence
Otu0002	8488	1.3	6.0	Dinophyta	Ptychodiscus	100% Ptychodiscus noctiluca small subunit ribosomal RNA gene, partial sequence
Otu0029	7667	1.3	29.5	Dinophyta	Dino-Group-I-Clade-1	100% Uncultured syndiniales clone PROSOPE.EM-110m.238 18S ribosomal RNA gene, partial sequence
Otu0009	6704	1.0	10.7	Dinophyta	Dinophyceae	100% Uncultured dinoflagellate gene for 18S rRNA, partial sequence, clone: HP09D-4
Otu0036	6469	0.4	35.8	Metazoa	Conchoecia	100% Conchoecia sp. OC-2001 18S ribosomal RNA gene, partial sequence
Otu0012	6332	1.0	13.0	Dinophyta	Dino-Group-I-Clade-1	100% Uncultured dinoflagellate clone RM13 18S ribosomal RNA gene, partial sequence
Otu0039	5427	0.7	34.5	Metazoa	Lopadorrhynchus	98% Lopadorrhynchus sp. THS-2009 18S ribosomal RNA gene, partial sequence
Otu0052	5029	0.7	55.0	Dinophyta	Warnowia	98% Warnowia sp. FG20 18S ribosomal RNA gene, partial sequence
Otu0015	5028	0.8	14.0	Metazoa	Clausocalanus	100% Clausocalanus arcuicornis voucher CA51SA4 18S small subunit ribosomal RNA gene, partial sequence
Otu0017	4862	0.1	16.0	Radiolaria	Spumellarida-Group-I	99% Uncultured Polycystinea partial 18S rRNA gene, clone BIO10_G12
Otu0058	4116	0.5	54.2	Metazoa	Maxillopoda	99% Uncultured metazoan partial 18S rRNA gene, isolate AhypMOTU15, clone Ahyp4322c01
Otu0091	4029	0.5	99.9	Radiolaria		86% Spongocore puella gene for 18S rRNA, partial sequence, isolate: OS1201
Otu0042	3907	0.4	31.1	Metazoa	Corycaeus	97% Corycaeus speciosus 18S ribosomal RNA gene, partial sequence
Otu0066	3866	0.7	56.6	Metazoa	Maxillopoda	97% Uncultured metazoan partial 18S rRNA gene, isolate AhypMOTU31, clone Ahyp4323c14
Otu0059	3571	0.8	49.6	Metazoa	Maxillopoda	100% Uncultured eukaryote clone SCM28C39 18S ribosomal RNA gene, partial sequence
Otu0090	3446	0.7	83.7	Cercozoa		89% Aulacantha scolymantha gene for 18S rRNA, partial sequence, isolate: Au6

Otu0077	3157	0.4	61.5	Metazoa	Maxillopoda	95%	Uncultured metazoan partial 18S rRNA gene, isolate AhypMOTU31, clone Ahyp4323c14
Otu0109	2961	0.3	96.5	Metazoa	Dolabrifera	98%	Dolabrifera dolabrifera 18S ribosomal RNA gene, complete sequence

SUPPLEMENTARY FIGURES

Supplementary Figure S1. (a) Non-parametric multidimensional scaling ordination plot in 2-dimension configuration ($K=2$) based on Bray-curtis dissimilarity between protist OTU community composition in samples for which three PCR replicates were sequenced independently, and (b) the relative sequence abundance of major eukaryotic taxonomic groups.

Supplementary Figure S2. Water-column physico-chemical and biological properties during each cycle. (a) Temperature, salinity, nitrate, and fluorescence mean (\pm SD) profiles ($n=7$). (b) Hierarchical dendrogram based on variables in Table 1 (Euclidean distance of $\log + 1$ transformed values and Ward algorithm). (c) Surface Chl a size fraction distribution ($< 1 \mu\text{m}$ (0.2 - 1.0 μm), $< 3 \mu\text{m}$ (1.0 - 3.0 μm), $< 8 \mu\text{m}$ (3.0 - 8.0 μm), $< 20 \mu\text{m}$ (8.0 - 20 μm), $< 200 \mu\text{m}$ (20 - 200 μm)).

Supplementary Figure S3. Rarefaction curves with estimated number of (a) protistan and (b) metazoan OTUs for different cycles and individual samples (inlet).

Supplementary Figure S4. nMDS ordination based on protistan community composition dissimilarities for samples from the (a) water column, (b) fixed and (c) live traps. The length of the vectors is proportional to the correlation between ordination and environmental variable, while the direction points towards the space of the ordination with stronger gradient for the environmental variable. (T) Temperature, ($Z_{\text{Nitracline}}$) Nitracline depth.

Supplementary Figure S5. Mean percentage of reads for each eukaryotic group in samples from the (a) water column, (b) fixed, and (c) live traps. Total ($>0.8 \mu\text{m}$) and large ($>8 \mu\text{m}$) size-fractions are presented in the left and right bottom of each sampling type, respectively.

Supplementary Figure S6. Mean relative contribution of the 30 most abundant (a) protistan and (b) all eukaryotes (including metazoans) OTUs ranked in water-column, fixed- and live-trap samples. OTUs with $> 1.5 \%$ contribution include taxonomic affiliation in addition to OTU number.

