

Transcriptome indices modified after Martínez and Reyes-Valdés (2008):

(1) Transcriptome diversity H_j : $H_j = \sum_{i=1}^g p_{ij} \log_2(p_{ij})$

p_{ij} = relative transcriptome frequency for the i th gene ($i = 1, 2, \dots, g$) in a functional category j th ($j = 1, 2, \dots, t$).

(2) Average gene frequency p_i : $p_i = \frac{1}{t} \sum_{j=1}^t p_{ij}$

(3) Gene specificity S_i : $S_i = \frac{1}{t} (\sum_{j=1}^t \frac{p_{ij}}{p_i} \log_2 \frac{p_{ij}}{p_i})$

(4) Functional specialization δ_j : $\delta_j = \sum_{i=1}^g p_{ij} S_i$

(5) Kullback–Leibler divergence D_j : $D_j = (-\sum_{i=1}^g p_{ij} \log_2(p_{ij})) - H_j$

Table S1: Taxonomic assignment of sequences (Seq.) and clustered operational taxonomic units (OTUs) in percentages.

	Microplankton						Nanoplankton					
	Station 21		Station 42		Station 61		Station 21		Station 42		Station 61	
	<i>Percentages</i>											
	Seq.	OTUs	Seq.	OTUs	Seq.	OTUs	Seq.	OTUs	Seq.	OTUs	Seq.	OTUs
Alveolata	68.3	45.5	64.0	56.9	44.8	21.8	83.5	41.4	97.4	62.2	26.7	21.9
<i>thereof Dinophyta</i>	99.0	92.4	99.8	91.4	99.0	93.6	97.5	92.0	97.3	90.2	99.5	93.5
Cryptophyta	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.7	0.6	0.7
Fungi	1.4	9.9	0.2	2.9	1.5	6.0	4.7	12.9	0.2	2.7	9.4	8.5
Haptophyceae	0.0	1.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0	1.9	4.6
Metazoa	14.5	10.4	0.3	6.9	1.8	1.9	0.1	3.3	0.0	0.7	0.2	2.1
Rhizaria	0.0	0.5	0.0	1.0	0.0	0.0	0.1	1.4	0.1	0.7	0.1	0.7
Rhodophyta	0.0	0.0	0.0	0.0	9.1	4.2	0.0	0.0	0.0	0.0	0.9	3.2
Stramenopiles (incl. Diatoms)	7.0	25.2	25.6	22.5	37.8	49.5	10.7	31.4	1.4	20.9	54.8	41
Viridiplantae	0.0	0.5	0.0	1.0	1.5	8.3	0.5	5.2	0.4	6.8	2.9	11
Unassigned	8.3	5.0	7.5	6.9	3.0	6.9	0.3	2.9	0.3	3.4	2.4	4.2
Undefined Eukaryota	0.4	2.0	2.3	2.0	0.6	0.9	0.0	1.0	0.1	2.0	0.3	1.8
Total (counts) (Sequences/OTUs)	5,777	202	8,477	102	8,341	216	9,361	210	9,969	148	11,103	283

Table S2: Most abundant transcripts across all samples per size fraction (highest average gene frequencies (p_i -values)).

KOG	KOG Name	Micro_St.21	Micro_St.42	Micro_St.61	p_i
Z	Ca ²⁺ -binding protein (centrin/caltractin), EF-Hand superfamily protein	808	1547	31596	4.23E-02
T	Calmodulin and related proteins (EF-Hand superfamily)	2725	18493	11372	4.09E-02
O	Ubiquitin-protein ligase	4219	3508	4862	1.78E-02
U	GTP-binding ADP-ribosylation factor Arf1	6769	1530	2026	1.67E-02
J	60S ribosomal protein L26	75	5522	7312	1.57E-02
O	Cyclophilin type peptidyl-prolyl cis-trans isomerase	3191	2188	4264	1.37E-02
J	40S ribosomal protein S27	726	2282	7158	1.29E-02
J	40S ribosomal protein S15/S22	2068	5866	719	1.16E-02
J	40S ribosomal protein S15	1740	2009	4612	1.12E-02
J	60S ribosomal protein L35	682	7291	487	1.05E-02
J	60S ribosomal protein L32	580	2581	4483	9.65E-03
O	Alkyl hydroperoxide reductase/peroxiredoxin	469	2434	4512	9.31E-03
O	Thioredoxin	613	1047	4699	8.16E-03
A	60S ribosomal protein 15.5kD/SNU13, NHP2/L7A family (includes ribonuclease P subunit p38), involved in splicing	707	67	4833	7.34E-03
J	60S ribosomal protein L31	864	3682	1057	7.23E-03
O	Predicted E3 ubiquitin ligase	1952	709	2220	7.14E-03
U	GTPase Rab2, small G protein superfamily	601	4809	279	7.12E-03
J	60S ribosomal protein L28	90	1201	4348	6.95E-03
O	Molecular chaperones HSP70/HSC70, HSP70 superfamily	3387	556	85	6.94E-03
O	FKBP-type peptidyl-prolyl cis-trans isomerase	256	2910	2321	6.77E-03
O	Peptidyl-prolyl cis-trans isomerase	428	4048	951	6.74E-03
C	Cytochrome b5	577	2525	1981	6.48E-03
D	Component of the U4/U6.U5 snRNP/mitosis protein DIM1	3015	355	384	6.39E-03
A	Component of the U4/U6.U5 snRNP/mitosis protein DIM1	3015	355	384	6.39E-03
U	Vesicle coat complex COPII, GTPase subunit SAR1	388	4347	424	6.37E-03
J	Translation initiation factor 5A (eIF-5A)	393	4171	500	6.26E-03
O	Molecular chaperone (DnaJ superfamily)	2195	909	881	6.16E-03
O	Glutathione S-transferase	874	1734	1854	5.93E-03
J	40S ribosomal protein S25	402	2716	1568	5.88E-03
J	60S ribosomal protein L19	545	3888	159	5.78E-03
T	GTPase Rab1/YPT1, small G protein superfamily, and related GTP-binding proteins	1469	2331	198	5.68E-03
B	Histone 2A	732	2506	1038	5.58E-03
J	40S ribosomal protein S11	645	2805	772	5.44E-03
J	60S ribosomal protein L30	2445	196	410	5.20E-03
J	40S ribosomal protein S14	741	2836	205	4.95E-03
J	60S ribosomal protein L22	267	3261	442	4.89E-03
A	H/ACA snoRNP complex, subunit NOP10	372	191	3106	4.74E-03
B	Histone H2B	479	1823	1290	4.62E-03
U	Clathrin adaptor complex, small subunit	1219	1426	567	4.61E-03
C	Vacuolar H ⁺ -ATPase V0 sector, subunits c/c'	1474	1051	527	4.58E-03
O	FOG: Predicted E3 ubiquitin ligase	854	520	1879	4.49E-03
J	40S ribosomal protein S16	523	2794	187	4.49E-03
J	40S ribosomal protein S21	746	2228	301	4.36E-03
J	60S ribosomal protein L21	172	2246	1122	4.35E-03
T	Serine/threonine protein phosphatase 2A, catalytic subunit	196	3340	22	4.33E-03
A	Small nuclear ribonucleoprotein (snRNP) Sm core protein	210	2808	469	4.28E-03
J	40S ribosomal protein S24	1368	1457	43	4.27E-03
J	60S ribosomal protein L2/L8	368	2186	603	4.00E-03
J	60S ribosomal protein L38	285	1442	1432	3.99E-03

O	Ubiquitin-like proteins	858	410	1553	3.97E-03
Z	Microtubule-associated anchor protein	122	2232	890	3.96E-03
KOG	KOG Name	Nano_St.21	Nano_St.42	Nano_St_61	pi
G	Aquaporin (major intrinsic protein family)	7019	15	34	1.63E-01
O	Ubiquitin-specific protease	8	0	430	1.55E-02
J	60S ribosomal protein L22	116	114	175	1.45E-02
O	Ubiquitin and ubiquitin-like proteins	101	177	85	1.40E-02
J	Ribosomal protein S18	0	155	106	1.13E-02
J	40S ribosomal protein S2	70	145	58	1.07E-02
J	Predicted RNA-binding protein containing PIN domain and involved in translation or RNA processing	93	73	137	1.06E-02
J	40S ribosomal protein S4	57	93	118	1.00E-02
O	Cyclophilin type peptidyl-prolyl cis-trans isomerase	65	134	51	9.83E-03
O	Multifunctional chaperone (14-3-3 family)	68	124	54	9.51E-03
J	40S ribosomal protein S14	105	95	42	8.54E-03
Z	Alpha tubulin	9	158	15	8.44E-03
J	60s ribosomal protein L19	68	102	54	8.44E-03
J	60S ribosomal protein L3 and related proteins	39	121	45	8.39E-03
J	40S ribosomal protein S6	22	70	113	7.93E-03
J	40S ribosomal protein S7	53	98	43	7.54E-03
O	Molecular chaperone (DnaJ superfamily)	99	53	66	7.19E-03
J	60S ribosomal protein L37	50	102	30	7.17E-03
J	60s ribosomal protein L2/L8	31	102	42	7.15E-03
J	40S ribosomal protein S12	110	13	108	7.00E-03
J	60s ribosomal protein L6	71	84	36	6.97E-03
J	60s ribosomal protein L34	31	122	5	6.86E-03
J	60S ribosomal protein L13a	8	66	97	6.86E-03
J	40S ribosomal protein SA (P40)/Laminin receptor 1	31	82	59	6.84E-03
J	60S ribosomal protein L35A/L37	62	106	4	6.75E-03
J	40S ribosomal protein S19	96	37	72	6.55E-03
H	S-adenosylhomocysteine hydrolase	3	66	91	6.54E-03
J	Ribosomal protein S7	33	42	103	6.49E-03
J	60S ribosomal protein L11	53	74	47	6.49E-03
J	60S ribosomal protein L10A	25	32	121	6.44E-03
J	60s ribosomal protein L10	26	81	53	6.44E-03
J	40s ribosomal protein s10	31	103	12	6.15E-03
O	Molecular chaperones HSP70/HSC70, HSP70 superfamily	19	55	85	6.14E-03
U	Signal recognition particle, subunit Srp9	259	0	0	5.93E-03
J	60S ribosomal protein L27	17	70	60	5.92E-03
O	Cysteine proteinase Cathepsin L	79	33	69	5.90E-03
J	60S ribosomal protein L14	54	22	99	5.85E-03
T	Calmodulin and related proteins (EF-Hand superfamily)	53	25	96	5.84E-03
J	60S ribosomal protein L7	8	58	77	5.76E-03
J	Translation initiation factor 5A (eIF-5A)	37	64	49	5.73E-03
T	G protein beta subunit-like protein	20	54	74	5.71E-03
J	40s ribosomal protein S26	6	33	109	5.66E-03
O	Ubiquitin-protein ligase	45	60	44	5.49E-03
J	60S ribosomal protein L28	40	35	79	5.45E-03
O	Thioredoxin/protein disulfide isomerase	25	42	79	5.43E-03
J	60S acidic ribosomal protein P0	34	69	36	5.39E-03
J	60S ribosomal protein L26	3	61	60	5.18E-03
J	Ubiquitin/40S ribosomal protein S27a fusion	67	68	6	5.03E-03
J	Ribosomal protein S4	51	3	97	4.81E-03
C	Fumarate reductase, flavoprotein subunit	68	25	56	4.79E-03

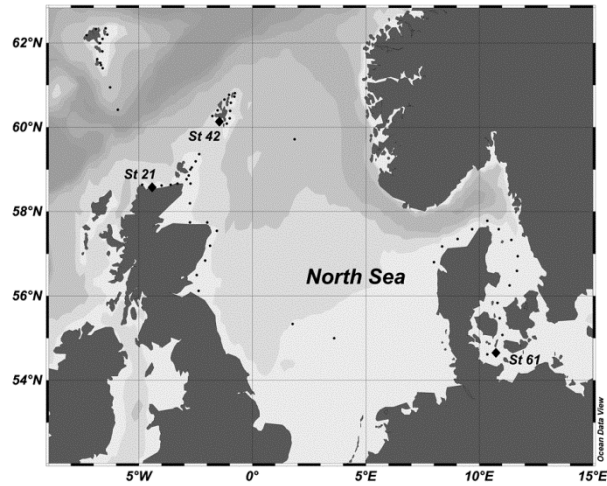


Figure S1: Station map of research cruise HE358 with *R/V Heincke* with respective sampling locations Station 21 (St 21, UTC 30.05.2011 / 15:44:00 / 58° 34,54' N / 4° 24,73' W; chlorophyll maximum at ~ 12 m depth), Station 42 (St 42, UTC 05.06.2011 / 05:46:00 / 60° 07,94' N / 1° 27,13' W; chlorophyll maximum at ~ 5 m depth), and Station 61 (St 61, UTC 09.06.2011 / 14:07:00 / 54° 38,99' N / 10° 44,13' E; chlorophyll maximum at ~ 10 m depth).

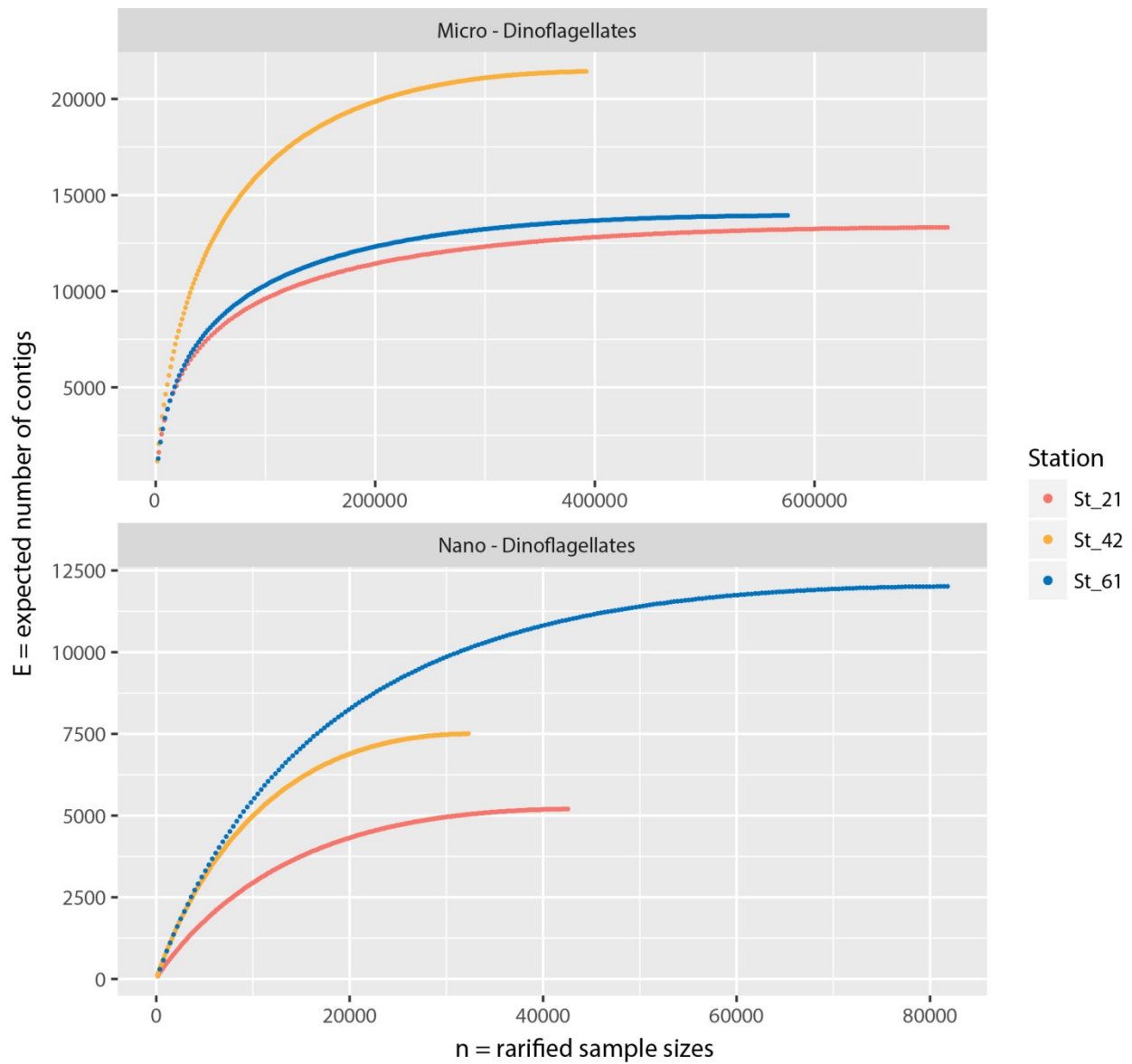


Figure S2: Rarefaction curves of the cDNA libraries for both size fractions. ; Rarefaction curves were calculated with the program 'aRarefactWin' (<https://www.uga.edu/strata/software/>).