

## *Supplementary Material*

**Diatoms dominate the eukaryotic metatranscriptome during spring in coastal ‘dead zone’ sediments**

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Running title: Eukaryote metatranscriptome in hypoxic sediment

**Table S1** Sampling occasions in the coastal bay. Measurements were conducted in the bottom water overlying the sediment in the samples cores (WTV Multiline *in-situ* sensors, approximately 2-5 cm above the sediment surface); *n* denotes the amount of individual sediment cores sampled.

Year	WGS 84 coordinates	<i>n</i> <sup>1</sup>	<i>n</i> <sup>2</sup>	°C	O <sub>2</sub> mg/L	Sal ‰
2013 <sup>ref</sup>	57 53.545, 16 35.476	3 <sup>*</sup>	4	2.9	0.85	6.7
2016	57 53.531, 16 35.165	3	13	2.2	3.83	6.5
2017 <sup>**</sup>	57 53.587, 16 35.245	3	0	2.5	11.72	6.4

<sup>ref</sup> (Broman et al 2017)

<sup>1</sup> Top 1 cm sediment surface sliced in the field.

<sup>2</sup> Transferred back to the laboratory for incubation.

\* From these samples the top 1 cm sediment layer was sliced and 1 mL was collected to estimate dry and wet weight.

\*\* These samples were collected in the field to count diatom cells in the top 1 cm sediment surface.

## Reference

Broman E, Sjöstedt J, Pinhassi J, Dopson M (2017). Shifts in coastal sediment oxygenation cause pronounced changes in microbial community composition and associated metabolism. *Microbiome* **5**.

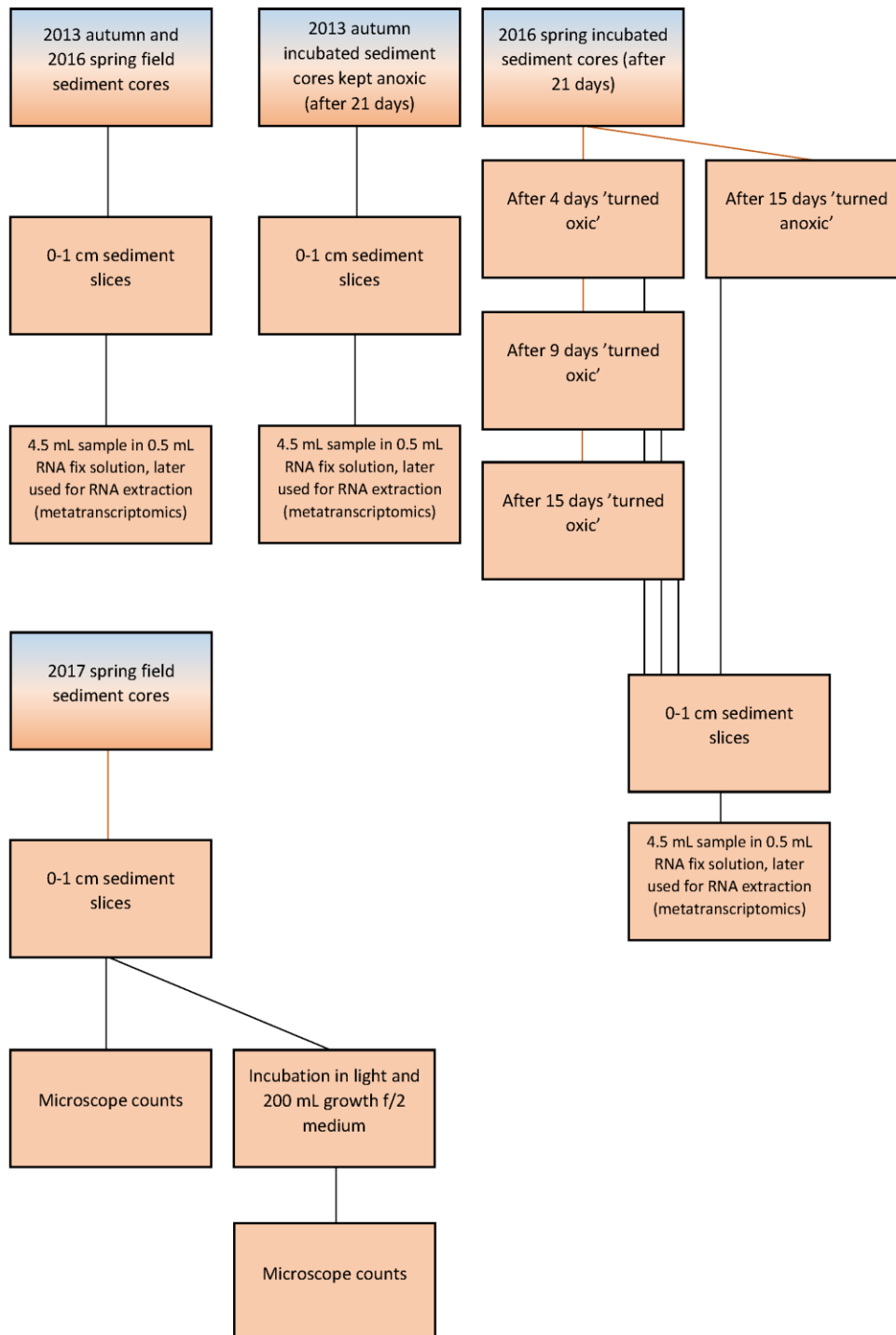
**Table S2.** The amount of sequences retrieved from the sequencing facility, reads left after quality trimming and the final average read length.

Sequencing facility ID	Sample name	Sampling year	Million read pairs (HiSeq 2x126)	Read pairs after quality trimming	Average read length after quality trimming
P2263_105	Anoxic to oxic	2013	39.80	35,440,383	125
P2263_106	Anoxic to oxic	2013	44.74	35,140,253	125
P2263_110	Anoxic control	2013	44.92	36,401,296	125
P2263_111	Anoxic control	2013	45.98	37,968,678	125
P6252_101	Field 1	2016	15.72	10,109,315	123
P6252_102	Field 2	2016	12.42	11,218,544	123
P6252_103	Field 3	2016	14.38	8,641,720	122
P6252_104	turned oxic day 5	2016	16.73	16,275,191	124
P6252_105	turned oxic day 5	2016	17.65	16,897,319	124
P6252_106	turned oxic day 5	2016	19.97	18,750,661	124
P6252_107	turned oxic day 9	2016	16.24	15,227,368	124
P6252_108	turned oxic day 9	2016	22.70	21,537,838	125
P6252_109	turned oxic day 9	2016	19.83	18,493,288	124
P6252_110	turned oxic day 15	2016	16.67	15,380,129	124
P6252_111	turned oxic day 15	2016	18.60	15,893,954	124
P6252_112	turned oxic day 15	2016	17.89	15,700,766	124
P6252_113	turned oxic day 15	2016	20.02	19,653,029	125
P6252_114	turned anoxic day 15	2016	22.39	22,260,472	125
P6252_115	turned anoxic day 15	2016	19.35	16,885,623	125
P6252_116	turned anoxic day 15	2016	19.81	19,182,448	125

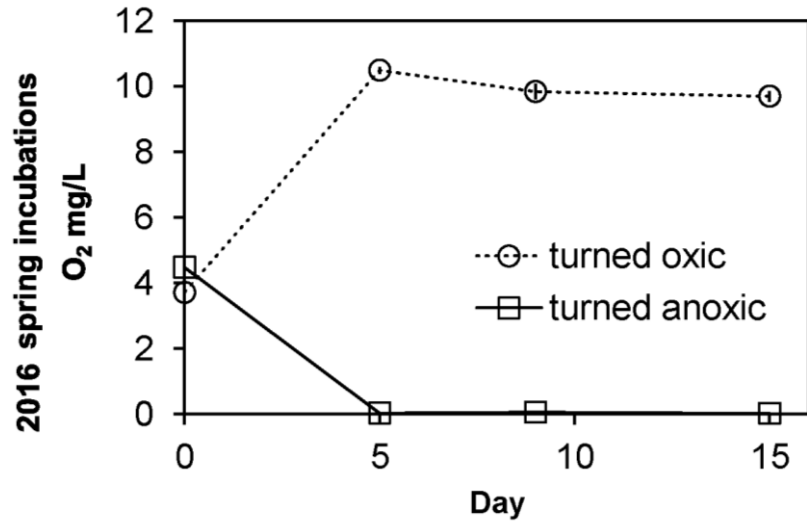
**Table S3.** Eukaryotic taxonomical annotations based on the RNA-seq data extracted from MEGAN 6. Values are shown as raw read counts. A separate .xls file has been uploaded.

**Table S4.** Eukaryotic Gene Ontology categories and InterPro annotations based on the RNA-seq data extracted from MEGAN 6. Values are shown as raw read counts. A separate .xls file has been uploaded.

**Table S5.** The table shows hits affiliated with diatoms in the InterPro database. Values are shown as CPM (counts per million). Differential expression analysis was conducted with edgeR and statistically significant proteins are denoted either as blue (higher than 2016 ‘turned anoxic’ day 15,  $p < 0.05$ ) or red (lower than 2016 ‘turned anoxic day 15’,  $p < 0.05$ ). CPM values are shown in white text for statistically significant proteins from the edgeR analysis. A separate .pdf file has been uploaded.



**Figure S1.** The scheme shows how 2013 autumn and 2016 spring sediment cores were incubated and handled for RNA extraction plus microscope counts of the 2017 spring samples.



**Figure S2.** Oxygen concentrations in the water phase of the 2016 spring sediment cores at the start, throughout, and at the end of the incubation experiment, SD = 1. Sediment cores were sacrificed throughout the incubation. Replicates were as follows: ‘turned oxic’ day 0 and 5,  $n = 10$  individual cores; day 9,  $n = 7$ ; and day 15,  $n = 15$ . The ‘turned anoxic’ cores were sacrificed at the end of the experiment and therefore remained  $n = 3$  until the end.