

Supplementary Table 1. List of primers used in this study.

Primer	Target group	Sequence (5' → 3')	Reference
TAREuk454FWD1 ^{FWD}	All eukaryotes	CCA GCA SCY GCG GTA ATT CC	Stoeck et al. (2010)
TAREukREV3 ^{REV}	All eukaryotes	ACT TTC GTT CTT GAT YRA	Stoeck et al. (2010)
HaptoR1 ^{REV}	Haptophyta	CGA AAC CAA CAA AAT AGC AC	Egge et al. (2013)
341F ^{FWD}	Bacteria	CCT ACG GGA GGC AGC AG	Muyzer et al. (1993)
907R ^{REV}	Bacteria	CCG TCA ATT CMT TTG AGT TT	Lane et al. (1985)
27F ^{FWD}	Bacteria	AGR GTT YGA TYM TGG CTC AG	Alm et. al (1996)
Uni522R ^{REV}	Bacteria	GWA TTA CCG CGG CKG CTG	Alm et. al (1996)

^{FWD} – forward primer, ^{REV} – reverse primer

References

- Alm, E. W., Oerther, D. B., Larsen, N., Stahl, D. A., Raskin, L. (1996). The oligonucleotide probe database. *Appl Environ Microbiol* 62: 3557-3559.
- Egge, E., Bittner, L., Andersen, T., Audic, S., de Vargas, C., and Edvardsen, B. (2013) 454 Pyrosequencing to Describe Microbial Eukaryotic Community Composition, Diversity and
- Lane, D.J., Pace, B., Olsen, G.J., Stahl, D.A., Sogin, M.L., and Pace, N.R. (1985) Rapid determination of 16S ribosomal RNA sequences for phylogenetic analyses. *Proceedings of the National Academy of Sciences of the United States of America* **82**: 6955-6959.
- Muyzer, G., Dewaal, E.C., and Uitterlinden, A.G. (1993) Profiling of complex microbial populations by denaturing gradient gel-electrophoresis analysis of polymerase chain reaction-amplified genes-coding for 16S ribosomal-rRNA. *Applied and Environmental Microbiology* **59**: 695-700.
- Stoeck, T., Bass, D., Nebel, M., Christen, R., Jones, M.D.M., Breiner, H.-W., and Richards, T.A. (2010) Multiple marker parallel tag environmental DNA sequencing reveals a highly complex eukaryotic community in marine anoxic water. *Molecular Ecology* **19**: 21-31.

