**Supplementary Material**

Supplementary data files

**Filename:** Danish\_Reefs\_Diver based observations.xlsx

**Explanation:** This is the file summarising all species observations collected by the divers.

**Filename:** Danish\_Reefs\_metadata.xlsx

**Explanation:** This file contains two sheets. Sheet 1 has station names, numbers, depth, Identifiers for sequence runs, sample dates, and information on replicates for all samples, including negative controls and mock communities. Sheet 2 shows the species lists for the two mock communities.

**Filename:** Danish\_Reefs\_eDNA\_gen.xlsx

**Explanation:** This is the combined output file from the bioinformatic analysis, including non-relevant species (H. sapiens, unicellular eukaryotes, etc), multiple ASV's per species, as well as raw sequence reads). This file can be used to trace all genetic observations to its source sample and documents how the species was identified.

**Filename:** Danish\_Reefs\_eDNA\_ecol.xlsx

**Explanation:** This is the processed data file derived from the combined output file “Danish \_Reefs\_eDNA\_gen.xlsx”. Here species observations are translated to presence/absence observations across all samples. We also took out typical contaminants (incl. fungi, unicellular eukaryotes, dog, huma, insects, spiders).

**Filename:** BioinformaticAnalysis.R

**Explanation:** This file contains the R script for the Dada2 workflow including cutadapt primer removal, cleaning, and denoising, taxonomic annotation of the cleaned ASVs, and some formatting to create the output files for further genetic and ecological analysis. The script refers to analysis of the 12S marker with regard to file names, primer sequences and reference libraries. Otherwise, it is similar to the other markers used in these analyses (18S, COI).