**Supplemental Material 2**

**Library preparation, demultiplexion and follow-up bioinformatic analyses**

PCR products (n=190) were purified with AMPure® XP PCR Purification beads (Agencourt®, Brea, CA, USA) and quantified using a Qubit® Fluorometer (Life Technologies, Carlsbad, CA, USA). The two amplicons (16S rRNA and 18S rRNA) from each sample were pooled together at equimolar concentrations of 3 ng μL**−**1. One sample of 20 μL of RNA/DNA-free water (UltraPure™) was added as negative controls. Pooled amplicons were sent to the Genomics Facility of the University of Auckland (New Zealand) for library preparation. Sequencing adapters and sample-specific indices were added to each amplicon using the Nextera™Index kit. Amplicons were pooled into a single library and paired-end sequences (2 x 250) generated on a MiSeq instrument using the TruSeq™SBS kit (Illumina™). Sequence data were automatically demultiplexed using MiSeq Reporter (v2), and forward and reverse reads assigned to samples. Sequences have been deposited in the NCBI's Sequence Read Archive under BioProject ID PRJNA552692, Accession number SRR9644676 to SRR9644588.

Sequenced samples were demultiplexed by their 8-mer NexteraTM index, and then demultiplexed again by target gene using cutadapt (version 1.8; Martin 2011). Sample reads were denoised with the DADA2 program (Callahan et al. 2017) implemented in Qiime2 (version 2018.11; Bolyen et al. 2018) using the default parameters. Denovo chimera detection was performed using the consensus approach. Forward and reverse reads were truncated at 226 bp and 220 bp for 16S rRNA, and at 225 bp and 216 bp for 18S rRNA, respectively, and merged using a perfect minimum overlap of 20 bp. Taxonomic assignment was performed on each generated Amplicon Sequence Variant (ASV) with a naive bayes classifier (Pedregosa et al. 2011) implemented in Qiime2, trained with SILVA 16S rRNA or 18S rRNA database (release 132 clustered at 99 % similarity; Quast et al. 2012) trimmed with the primer pairs used in this study.