

Supplement 2

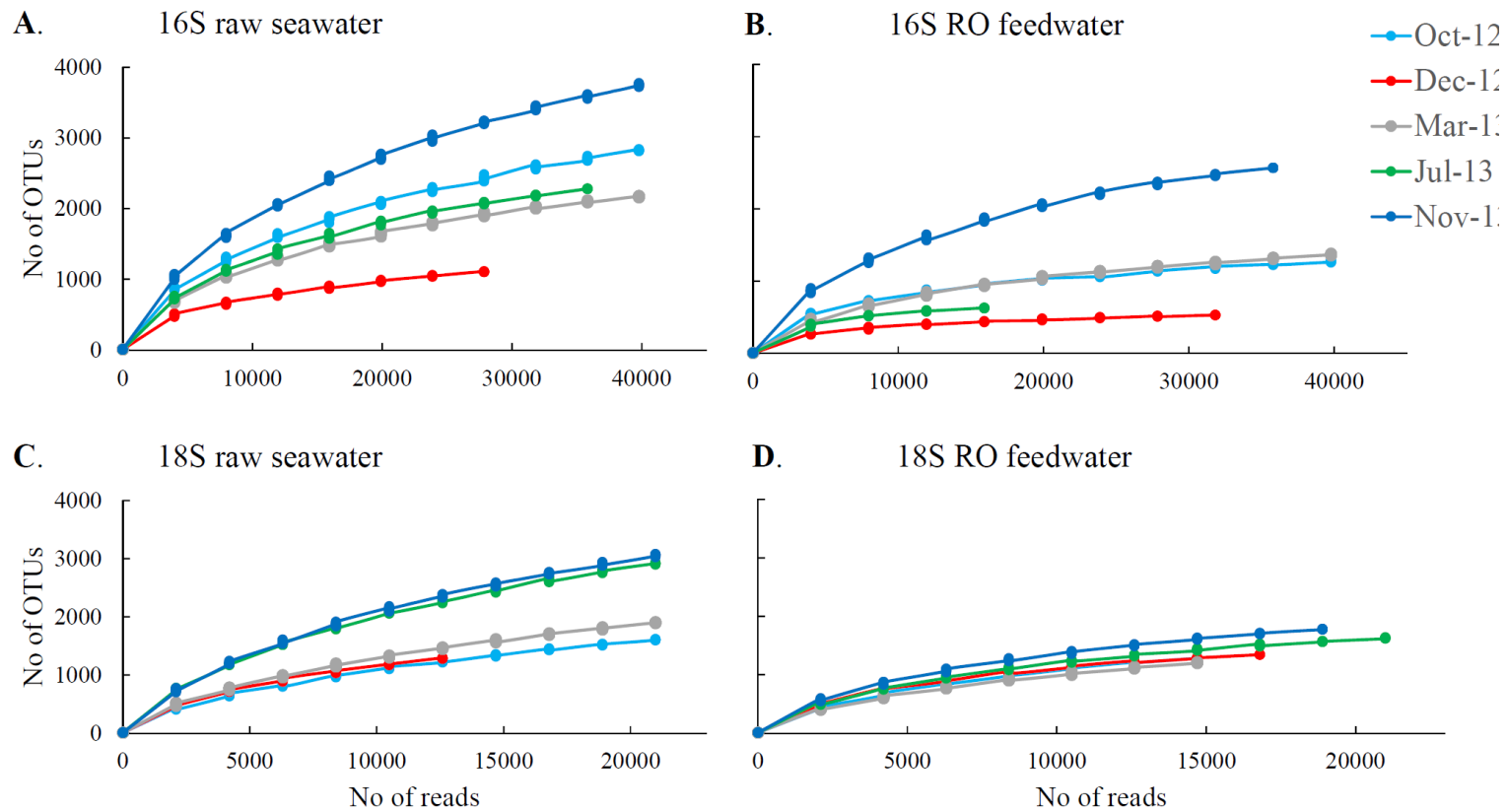


Fig. S1. Accumulation curves, representing the OTU richness in each sample, as function of the number of reads sequenced for (A-B) the 16S and (C-D) the 18S rRNA gene libraries in (A, C) raw seawater and (B, D) RO feedwater.

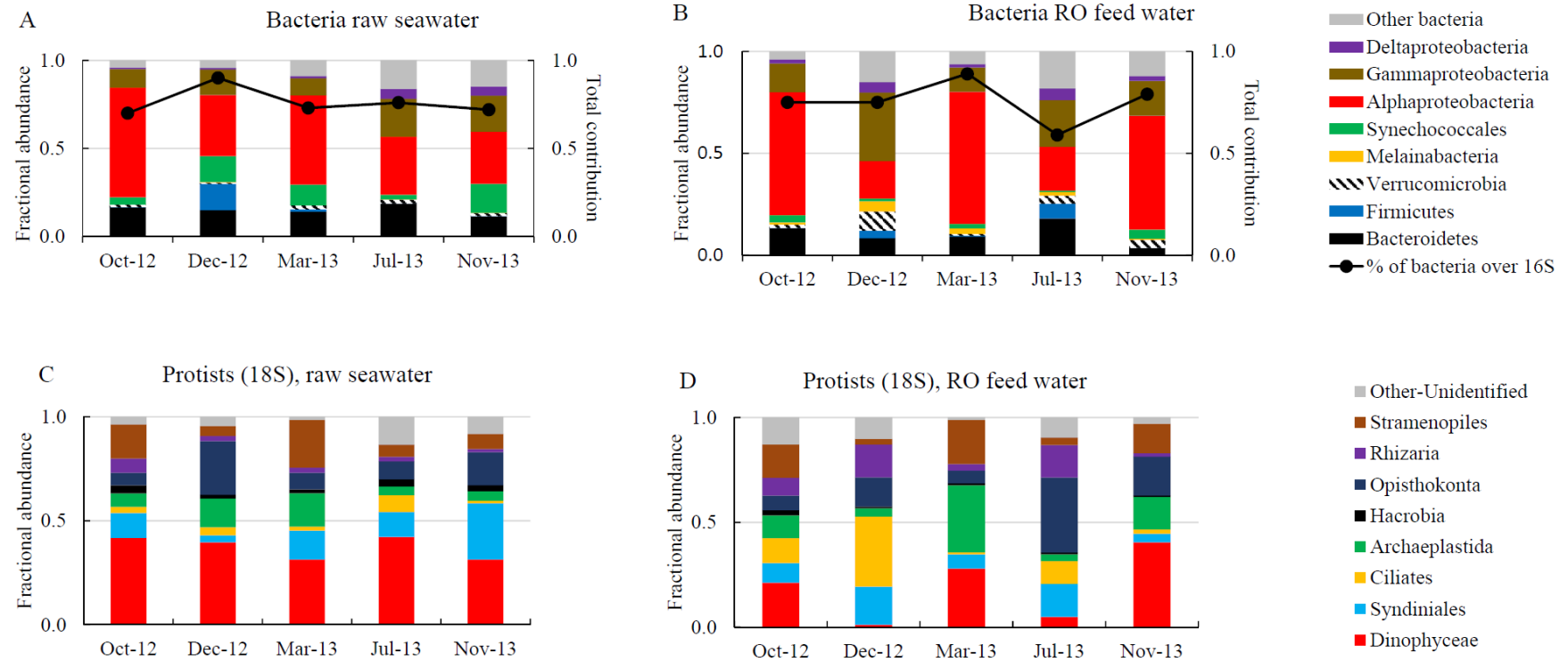


Fig. S2. Taxonomic composition of bacterial and protistan communities sequenced from the seawater pre-treatment system Penneshaw SWRO plant. Samples were collected October 27th (Oct-12) and December 19th (Dec-12) 2012, as well as March 27th (Mar-13), July 3rd (Jul-13) and November 25th (Nov-13) 2013. Distribution of (A-B) bacteria and (C-D) protists inferred from the 16S rRNA and 18S rRNA gene libraries, respectively. Samples were collected from (A, C) raw seawater and (B, D) RO feed water of Penneshaw SWRO plant during the period of study.

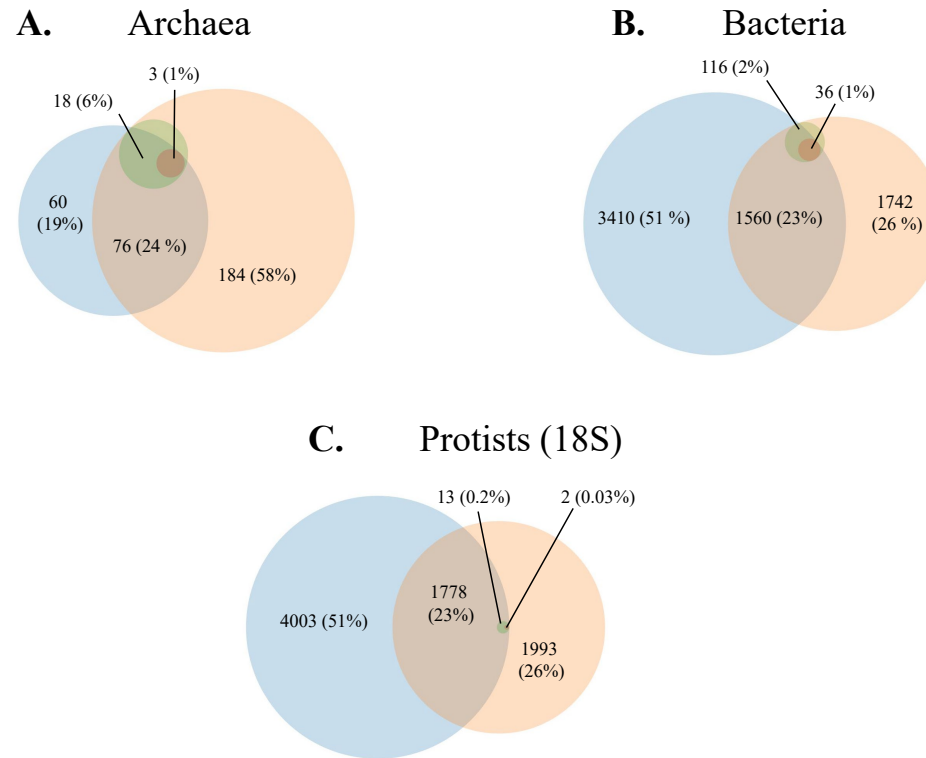


Fig. S3. Venn diagrams representing similarities and differences between the microbial communities of (A) Archaea, (B) bacteria, (C) protists, identified in raw seawater (light blue circles) and RO feed water (pink circles) of the Penneshaw SWRO plant. Values indicate the number of OTUs followed by their percentage contribution to total reads. The two small circles within each pink circle represent the OTUs found to be persistent (occurring at each time point) in RO feed water as well as in all samples (both raw seawater and RO feedwater), respectively.