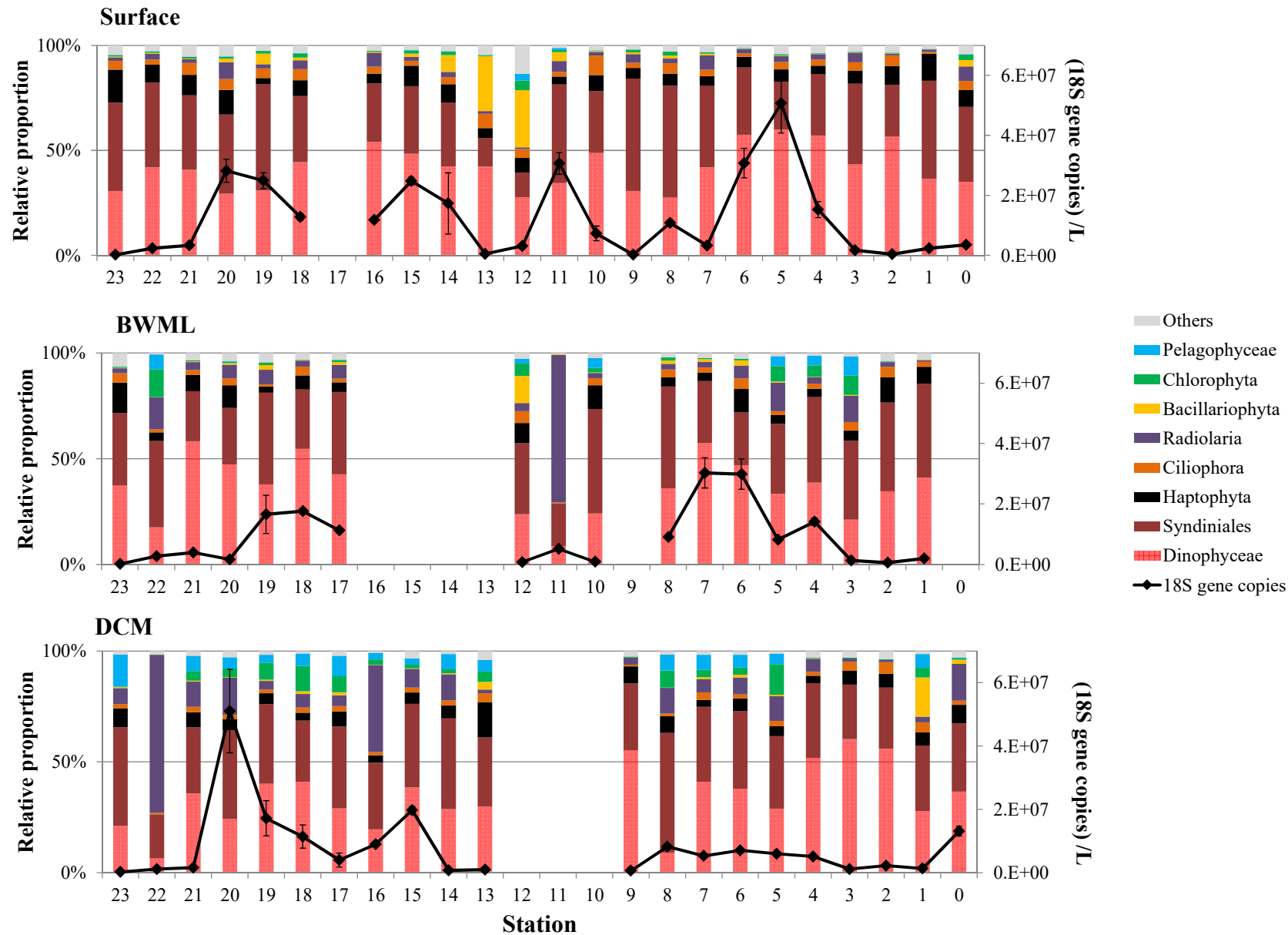


**Fig. S1.** Accumulation curves of the operational taxonomy units (OTUs) representing sequences clustered at 95 % identity. The curves are shown for (A) samples pooled by their depths features or for (B) individual samples.



**Fig. S2.** Relative abundance (left axis) of the different protistan taxa and number of the 18S rRNA gene copies (right axis) in the SPM collected during the HCC cruise. Relative abundance data were inferred by high throughput sequencing of the conserved V4 region of the 18S rRNA gene, whereas the number of 18S rRNA gene copies was inferred by quantitative PCR.