The following supplement accompanies the article

Vertical export of marine pelagic protists in an ice-free high-Arctic fjord (Adventfjorden, West Spitsbergen) throughout 2011–2012

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Supplementary material:

The samples collected in this study were part of a larger study at the Isfjorden-Adventfjorden (IsA) time-series station (Marquardt et al. 2016; Kubizyn et al., 2016; Stübner et al., 2016; Wiedmann et al., 2016; Brandner et al., 2017). In the following we present two more tables and three more figures supporting this present study. Material and methods are described in the manuscript. To make available the detailed description of the IsA hydrography is not just important for the present study but also for the prolongation of the IsA time-series station.

Table S1: Pyrosequencing raw data, filtering and OTU statistics from DNA libraries. The three 454 plates used in this study also contained samples from other projects (*Marquardt et al. 2016 and unpublished data). 80 out of 113 samples sequenced were used in this present study. Percentages are given relative to the reads available from the preceding step.

Processing step	**All samples (3 projects, 113 samples)***
Pre-filtering:	
Total Reads	1259321
Mean Length	442 bp
Post-filtering:	
Reads retained after quality control	871769 (69 %)
Mean Length	414 bp
Chimeras removed	844556 (97 %)
Of those reads retained for Seditrap project (80 samples)	739034 (88 %)
Global singletons removed	734264 (99%)
No hit	871 (0.1 %)
OTU clustering (97 % level)	
Seditrap project	7036
Min OTUs per sample	52
Max OTUs per sample	1077
Mean OTUs per sample	549

Figure S1: Density anomaly relative to surface pressure (σ_{t0} = ρ -1000 kg/m^3) profiles from the Isfjorden-Adventfjorden sampling site (IsA) obtained in the time periods indicated in the legend box. The profiles are low-pass filtered with a 5-dbar window. The magenta coloured profile that shows approximately a one-layered system is obtained in September 2012 during the upwelling event.

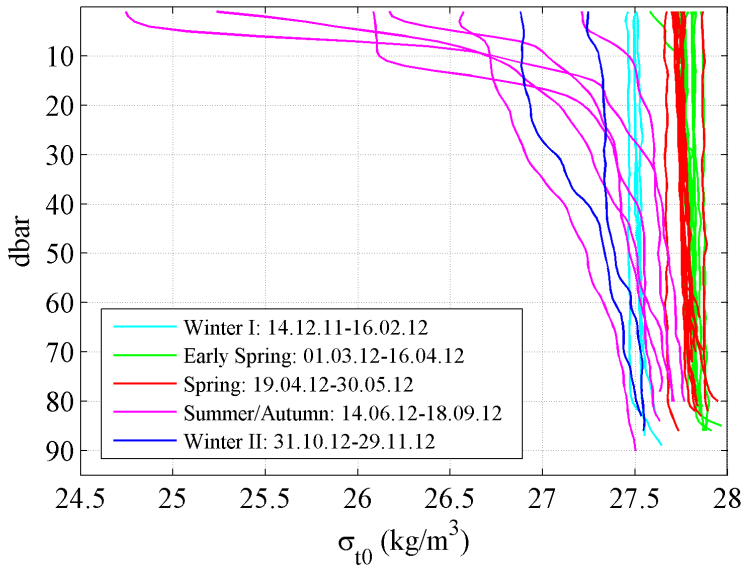


Figure S2: Cluster dendogram based on Bray Curtis similarity, illustrating similarities and clustering of all samples (input: weighted raw data). Bootstrapping n=1000. Season (W= Winter, S= Spring and A= Autumn). Depth_Suspended/Trap (S= small suspended fraction, L= large suspended fraction, T= total exported sample)

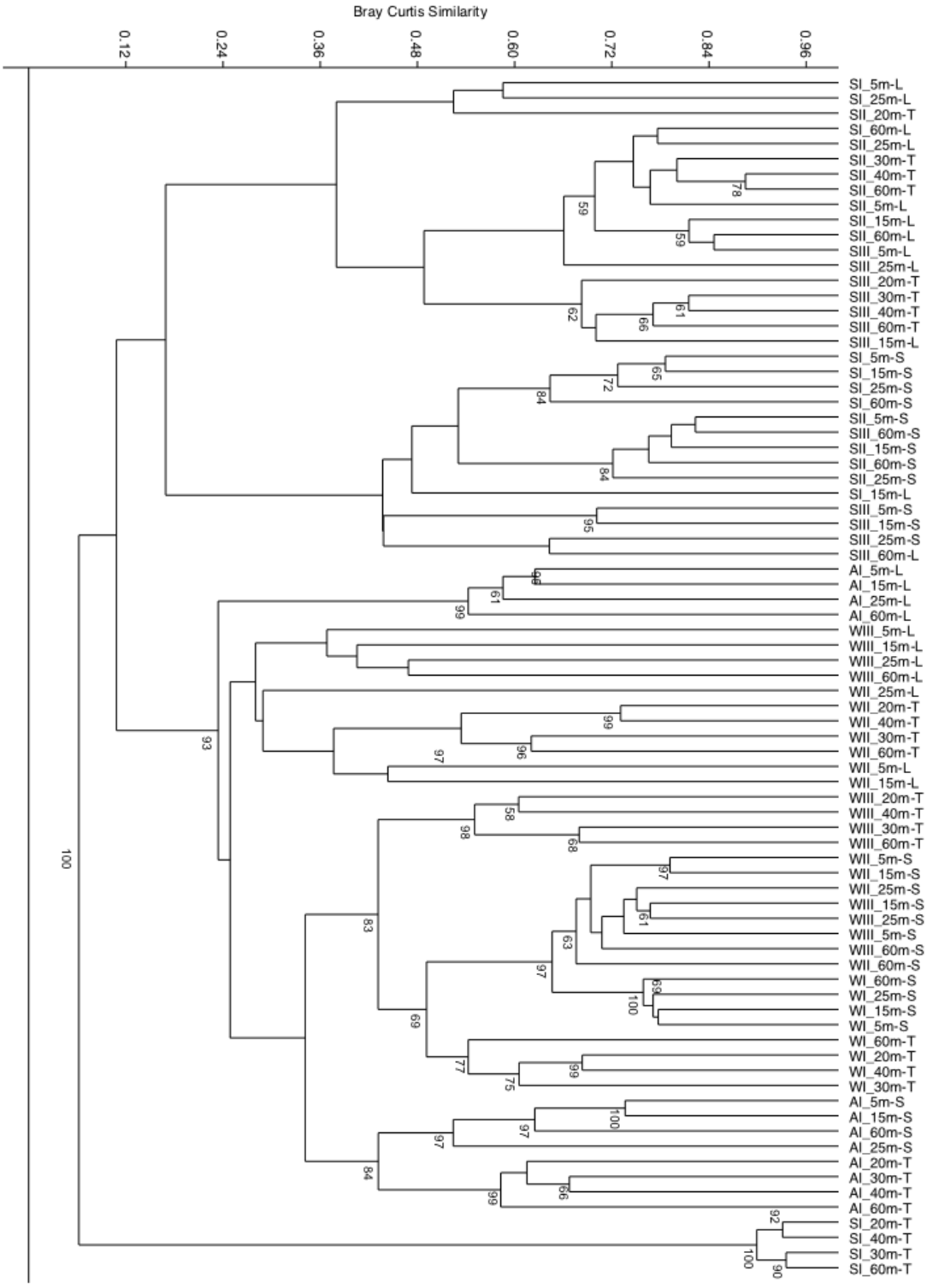


Table S2: Overview of the 10 most abundant (i.e. highest total DNA reads) OTUs (0.45-10 µm) per sampling date at 25 m, re-analysed data from Marquardt et al. (2016). The presence of a certain OTU at a certain date/depth is indicated by colors: Dinophyceae – green, MALVs – wine red, Ciliophora – orange, MASTs – yellow, Bacillariophyceae – turquoise, Eukaryote others – olive green, Rhizaria – light green, Picozoa – blue, Haptophyta – purple, Choanoflagellida – grey, Chlorophyta – red. On top: indication of present watermass LW1: Local Water first period (December 14th to February 16th, and March 8th; TAW: Transformed Atlantic Water (March 1th to April 16th); LW2: Local Water second period (April 19th to 30th).

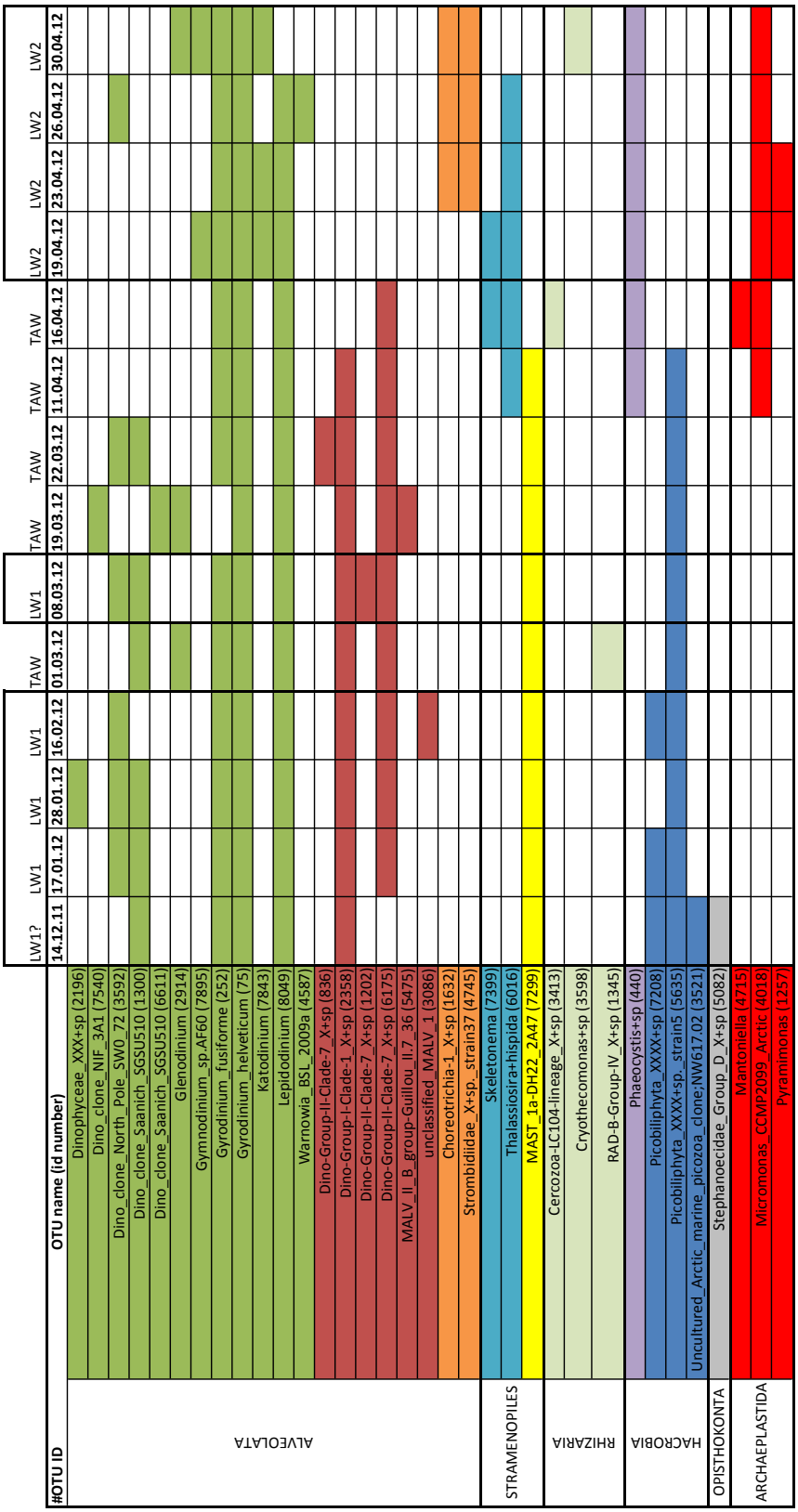
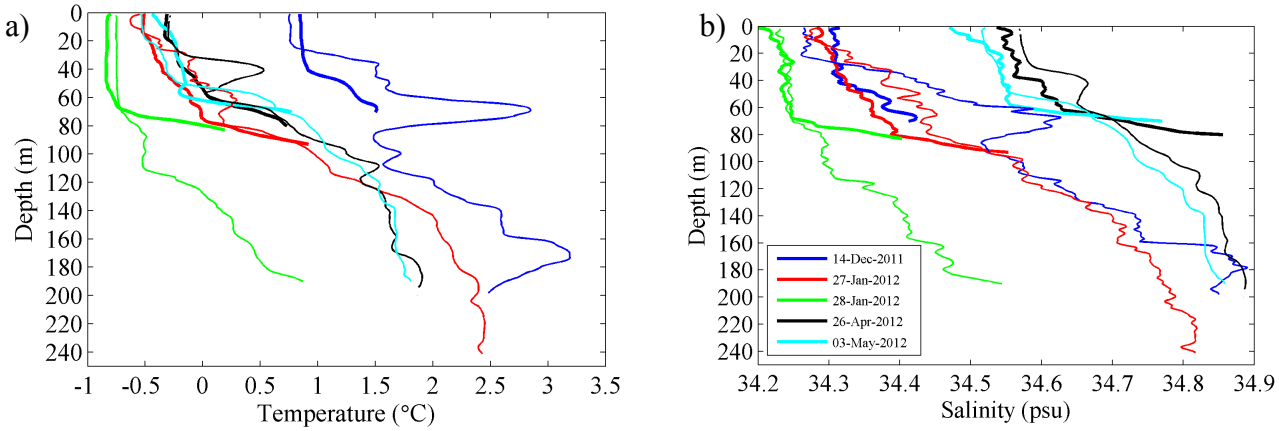


Figure S3: (a) Temperature profiles and (b) salinity profiles from the Isfjorden-Adventfjorden sampling site (IsA, thick line) and Isfjorden proper (Isf, thin line) obtained the same day within ~0-9 hrs on the dates indicated in the legend box in (b).



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