Paleoceanography and Paleoclimatology

Supporting Information for

Sedimentary ancient DNA from Kronotsky Peninsula: how sea ice, salinity and insolation dynamics have shaped diatom composition and richness over the past 20,000 years

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Additional Supporting Information (Files uploaded separately)
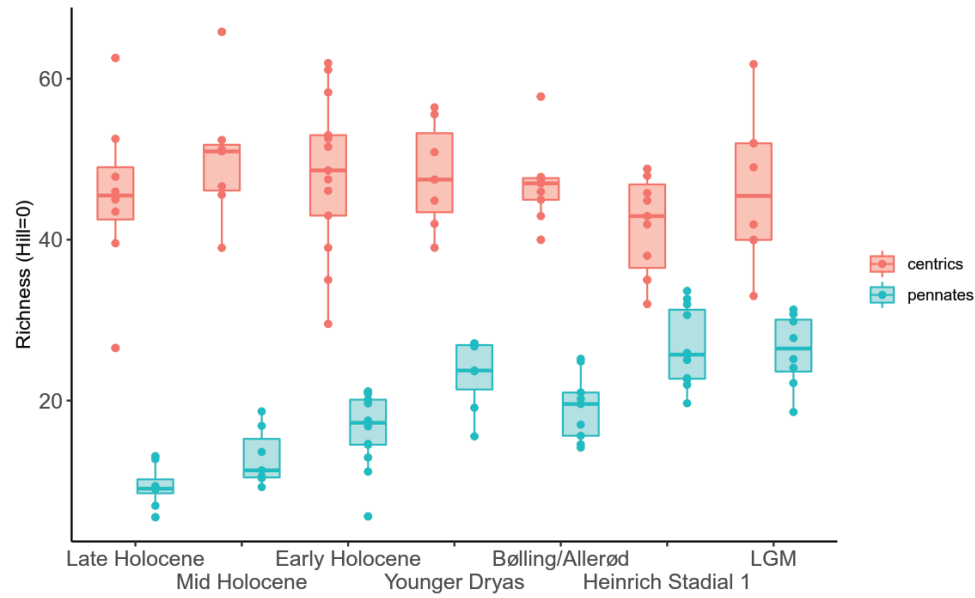
Figure S1. Boxplot of rarefied richness (Hill number 0) of amplicon sequence variants (ASVs) assigned to centric (red) and pennate (blue) diatoms according to climatic phases of the past ~19.9 cal kyr BP. The points represent the distribution of rarefied richness for each sample in the corresponding phases. The first and third quartiles are represented by the lower and upper limits of the box, the horizontal line inside the box represents the median and the whiskers

represent the maximum and minimum of 1.5 times the interquartile range, respectively. Points beyond whiskers are outliers.
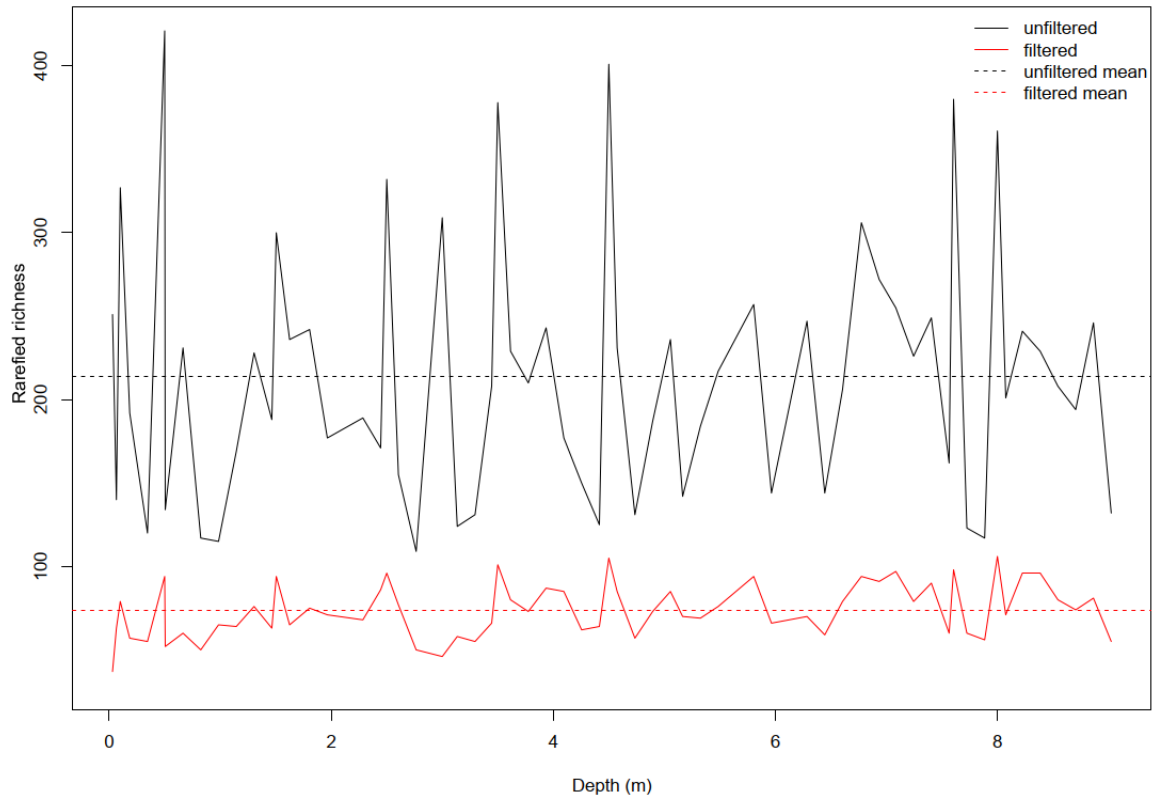

Figure S2. Rarefied richness (number of sequence variants) of the unfiltered diatom sedaDNA dataset in comparison to the filtered dataset used in our study.
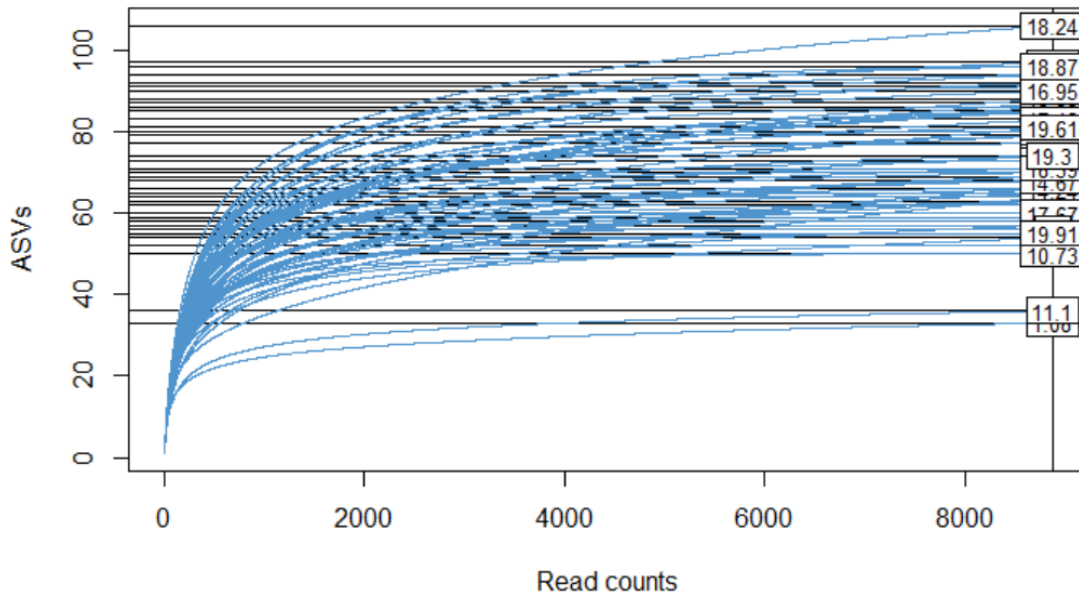
Figure S3. Rarefaction curves (blue lines) of the diatom *sed*aDNA data. The vertical line marks the number of read counts, which was used as the basis for resampling (n = 8,882), while the horizontal black lines mark the rarefied richness estimates per for each sample.

Table S1. Amplicon sequence variants (ASVs) that were assigned a taxonomic name based on 90-100% similarity to an entry in the EMBL nucleotide reference database (release 138) using OBITools (separate Excel file).

Table S2. Amplicon sequence variants (ASVs) that were assigned to negative controls.

Table S3. Pearson correlation coefficients and corresponding p-values of pennate and centric diatom richness with environmental variables.

	pennate		centric	
	R	**p-value**	**R**	**p-value**
June insolation	-0.49	0.0024	0.07	0.4304
IP_{25}	0.48	0.0031	-0.01	0.9354
salinity	0.05	0.7910	-0.07	0.6764
NGRIP $\delta^{18}O$	-0.68	5.2e-06	0.14	0.6990