

Marine eukaryote community responses to the climate and oceanographic changes in Storfjordrenna (southern Svalbard) over the past ~14.0 kyr BP: Insights from sedimentary ancient DNA analysis

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Supplementary figures

Figure S1: (a) Plot of alpha diversity indices, including richness ($q = 0$), Shannon diversity ($q = 1$), and Simpson diversity ($q = 2$), calculated using Hill number diversity (LH- Late Holocene, MH- Mid Holocene, EH- Early Holocene, YD- Younger Dryas, BA- Bølling-Allerød). (b) the Hill-Shannon between the main groups with the a Kruskal-Wails rank test, and the significance between them with a pairwise Wilcoxon rank sum test with adjusted p value (Benjamini-Hochberg).

Figure S2: plots of set ordination (FSO) based on Bray-Curtis dissimilarity matrix method for CSSlog1p normalization dataset between community composition and paleo proxies (p corrected (BH); **<0.01, *<0.05, .<0.1).

Figure S3: Relative abundance percentage of phytoplankton and mixoplankton communities in the study. Phytoplankton are categorized into four functional groups: diatoms, green algae, haptophyte algae, and autotrophic dinoflagellates. Mixoplankton are classified into mixotrophic dinoflagellates and silicoflagellates. The most dominant species within each group are displayed as line alongside their respective groups.

Figure S4: Relative abundance percentage of microzooplankton and mesozooplankton communities in the study. Microzooplankton are categorized into four main groups: Radiolarians, pelagic ciliophoran, and heterotrophic dinoflagellates and silicoflagellates. Mesozooplankton are classified into Arthropods (mostly copepods), and Larvaceans. The most dominant species within each group are displayed as line alongside their respective groups.

Figure S5: Relative abundance percentage of zoobenthos communities in the study, and categorized into five main groups: Annelids (mostly polychaetas), Ascidians, Cnidarians, Echinoderms, Molluscs (mostly bivalves). The most dominant species within each group are displayed as line alongside their respective groups.

Figure S6: Relative abundance percentage of parasites, and under other heterotrophs group MAST species in the study, parasites are categorized into three main groups: Apicomplexa, Oomycota, and dinoflagellate (parasites-Syndiniales). MAST species displayed under four sub group (MAST-1, MAST-3, MAST-9, and MAST-12). The most dominant species displayed alongside as line their respective groups.

Figure S7: Relative abundance percentage of cercozoan in the study, and categorized into three functional groups: parasitic cercozoan, predatory cercozoan, and bacterivorous cercozoan. (Cercozoan taxa that could not be classified at the class level in the taxonomic hierarchy are omitted)

Figure S7: Relative abundance percentage of cercozoan in the study, and categorized into three functional groups: parasitic cercozoan, predatory cercozoan, and bacterivorous cercozoan. (Cercozoan taxa that could not be classified at the class level in the taxonomic hierarchy are omitted)

Figure S8: Clustered image map (CIM) of the first two sPLS dimensions, displaying pairwise correlations between eukaryote ASVs of from the study associated with paleo environmental proxies. Correlations between ASVs and environmental parameters are depicted as a clustered heat map (only displayed ASVs with correlation ≥ 0.3) (detailed results in **Table S4**).

Figure S9: Heatmap of Spearman's rank correlations coefficients between eukaryote ASVs from the study and paleo environmental proxies. Correlations between ASVs and environmental parameters are depicted as a clustered heat map (only displayed ASVs with correlation ≥ 0.3 , and p values displayed as * $p < 0.1$, ** $p < 0.05$, *** $p < 0.01$). (detailed results in **Table S4**).

Figure S10: Potential warm water indicator species from the study (correlation >0.3 , $P < 0.05$, positive results from at least two method or more than one positive variable (displayed data as relative abundance %, and included the ASVs recorded in more than four samples)

Figure S11: Potential cold water indicator species from the study (correlation >0.3 , $P < 0.05$, positive results from at least two method or more than one positive variable (displayed data as relative abundance %, and included the ASVs recorded in more than four samples).

Figure S12: Heatmap of co-occurrence based on spearman rank coefficient analysis between eukaryote families represent in the study (illustrated only the positive correlation ≥ 0.4 , and P value adjusted (BH) < 0.05).

Figure S1

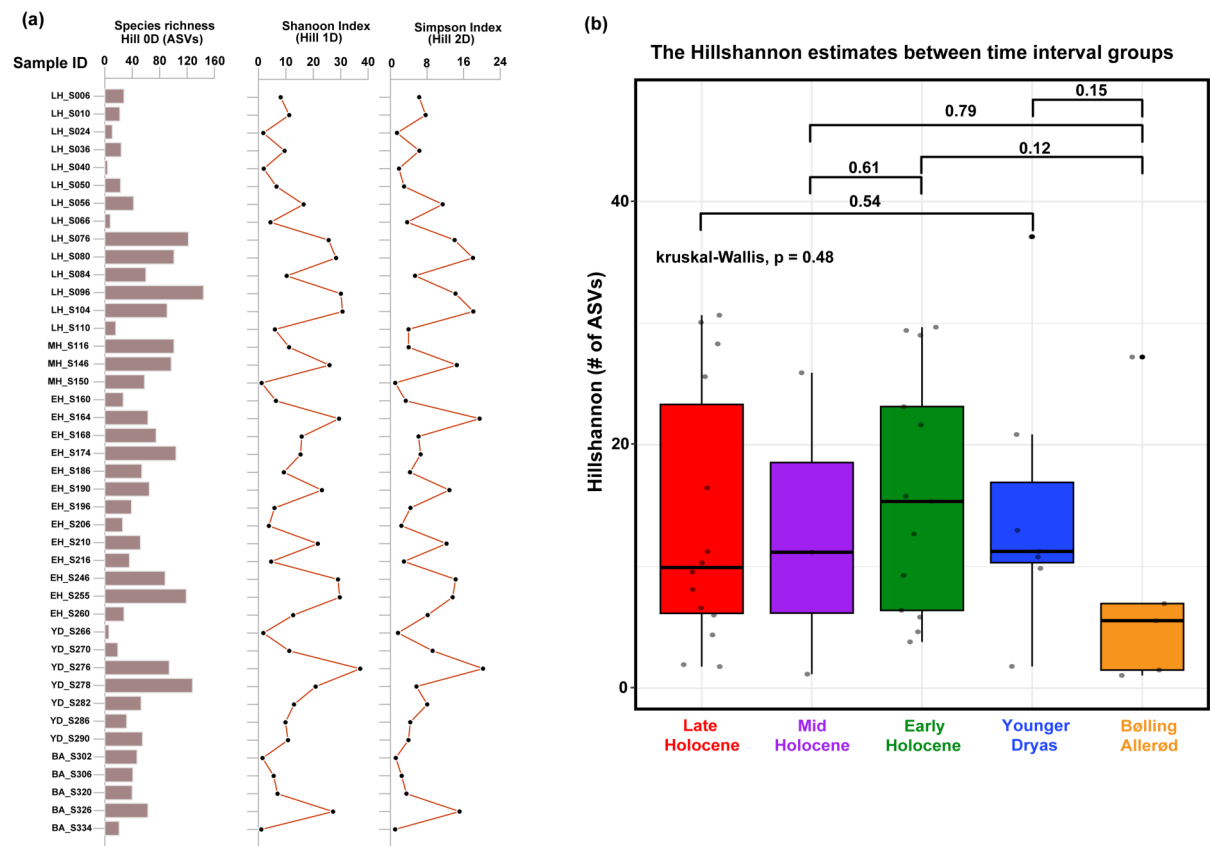


Figure S2

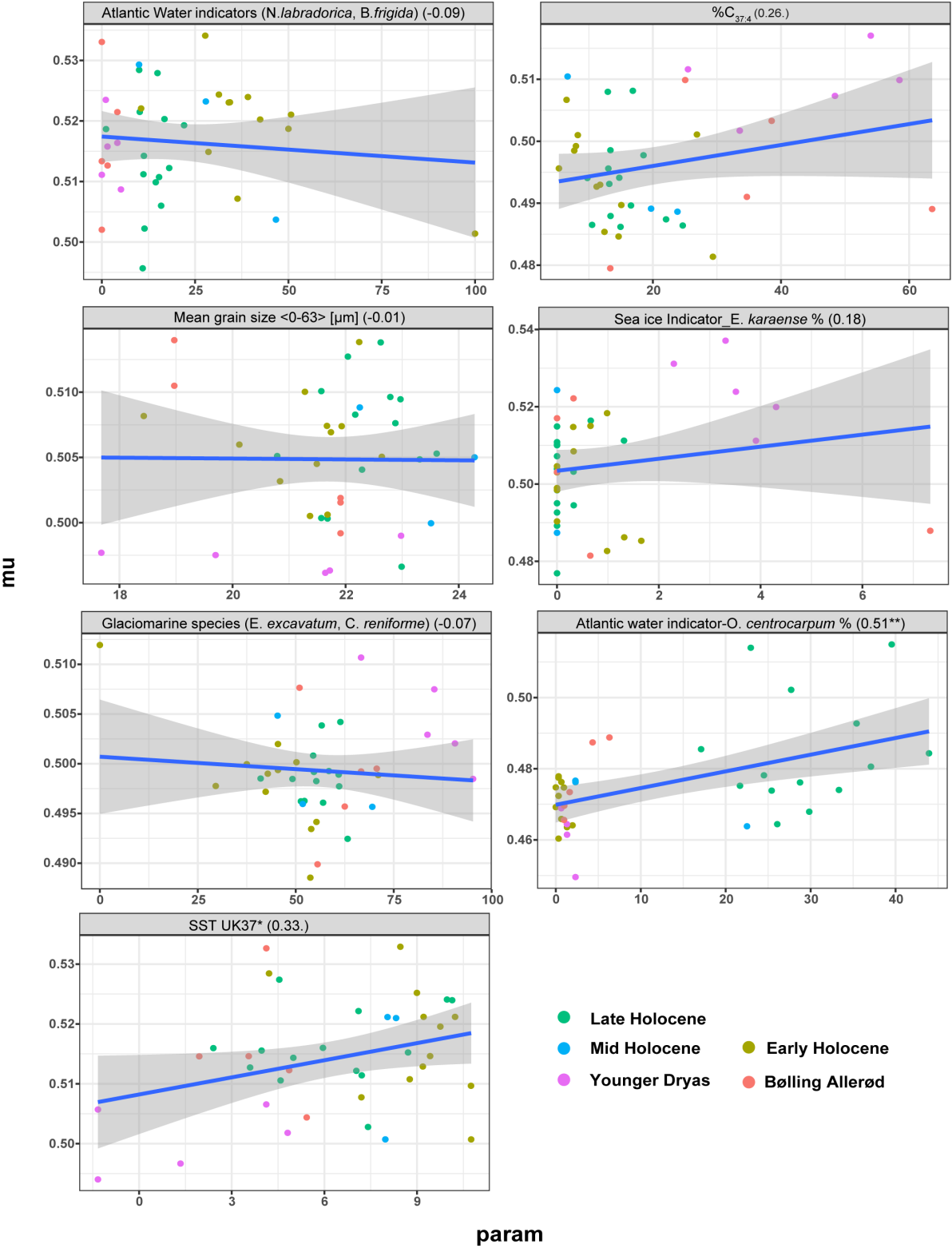


Figure S3

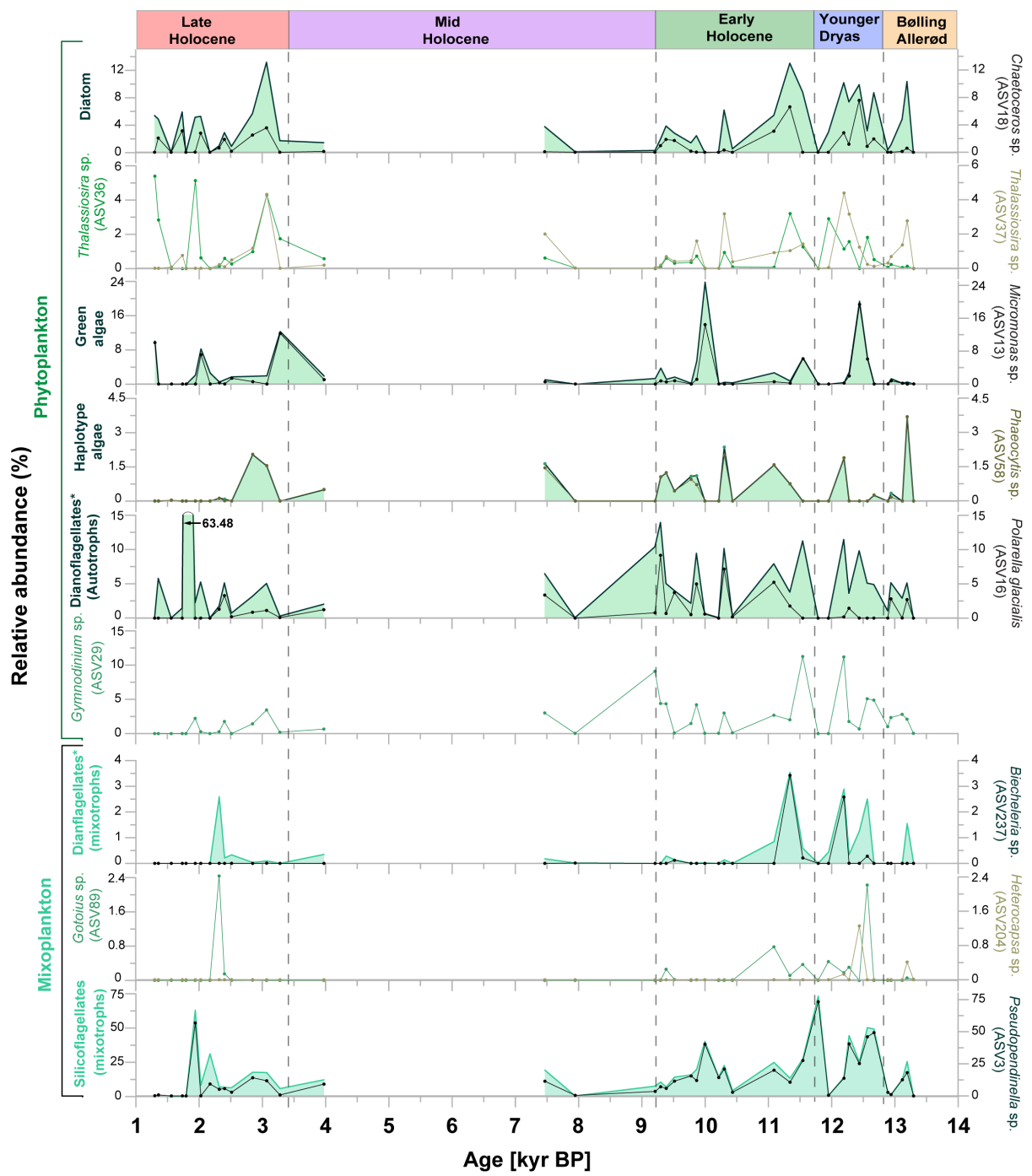


Figure S4

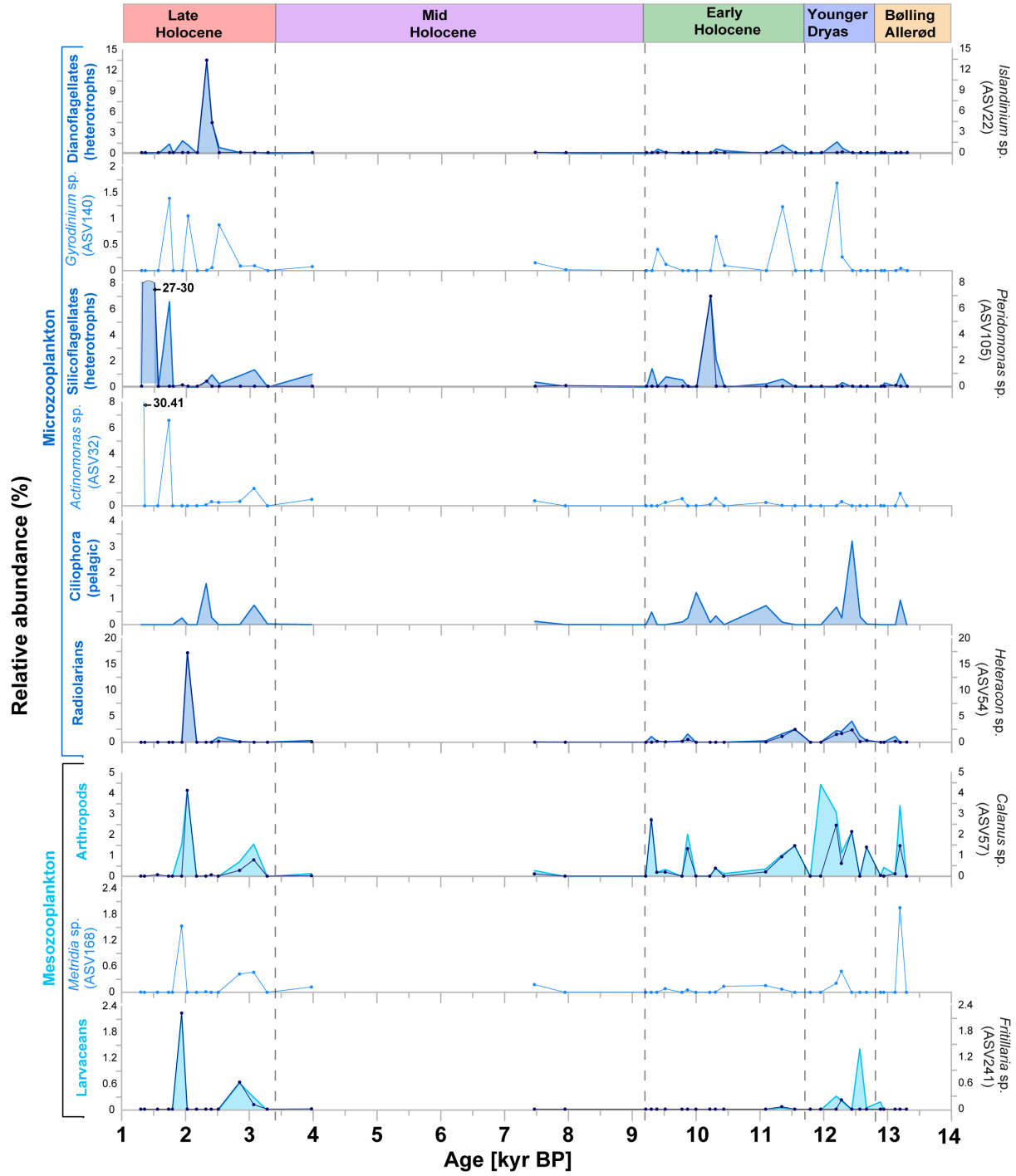


Figure S5

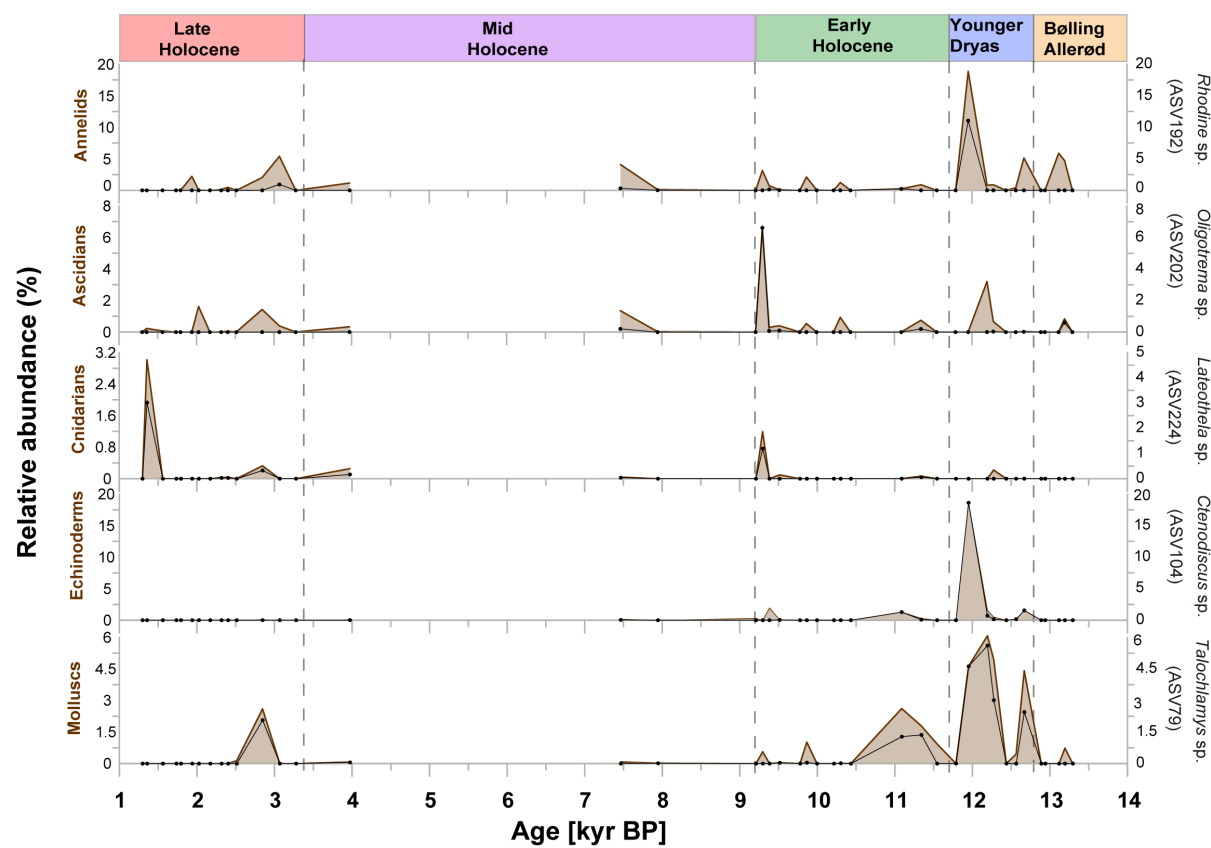


Figure S6

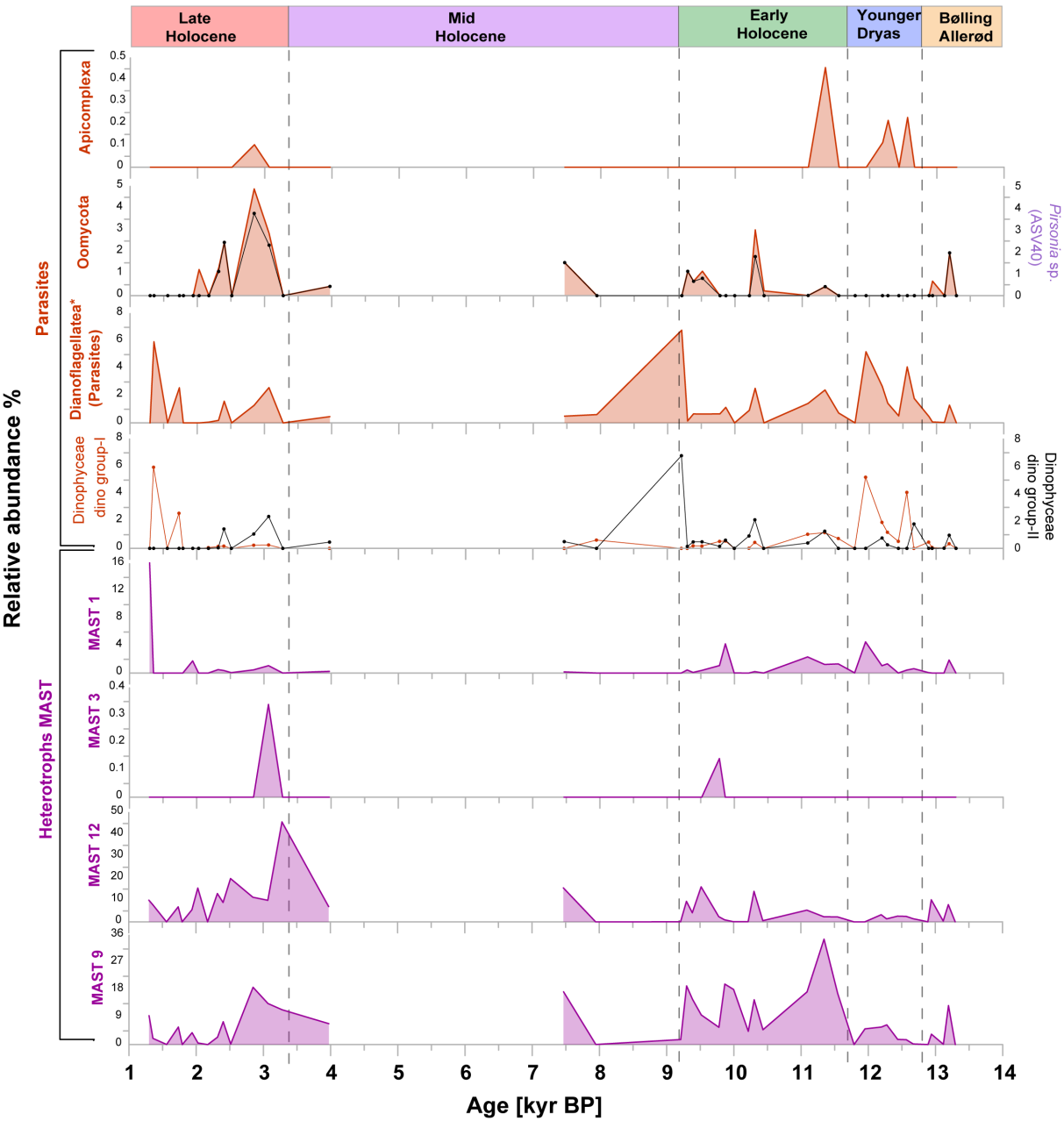


Figure S7

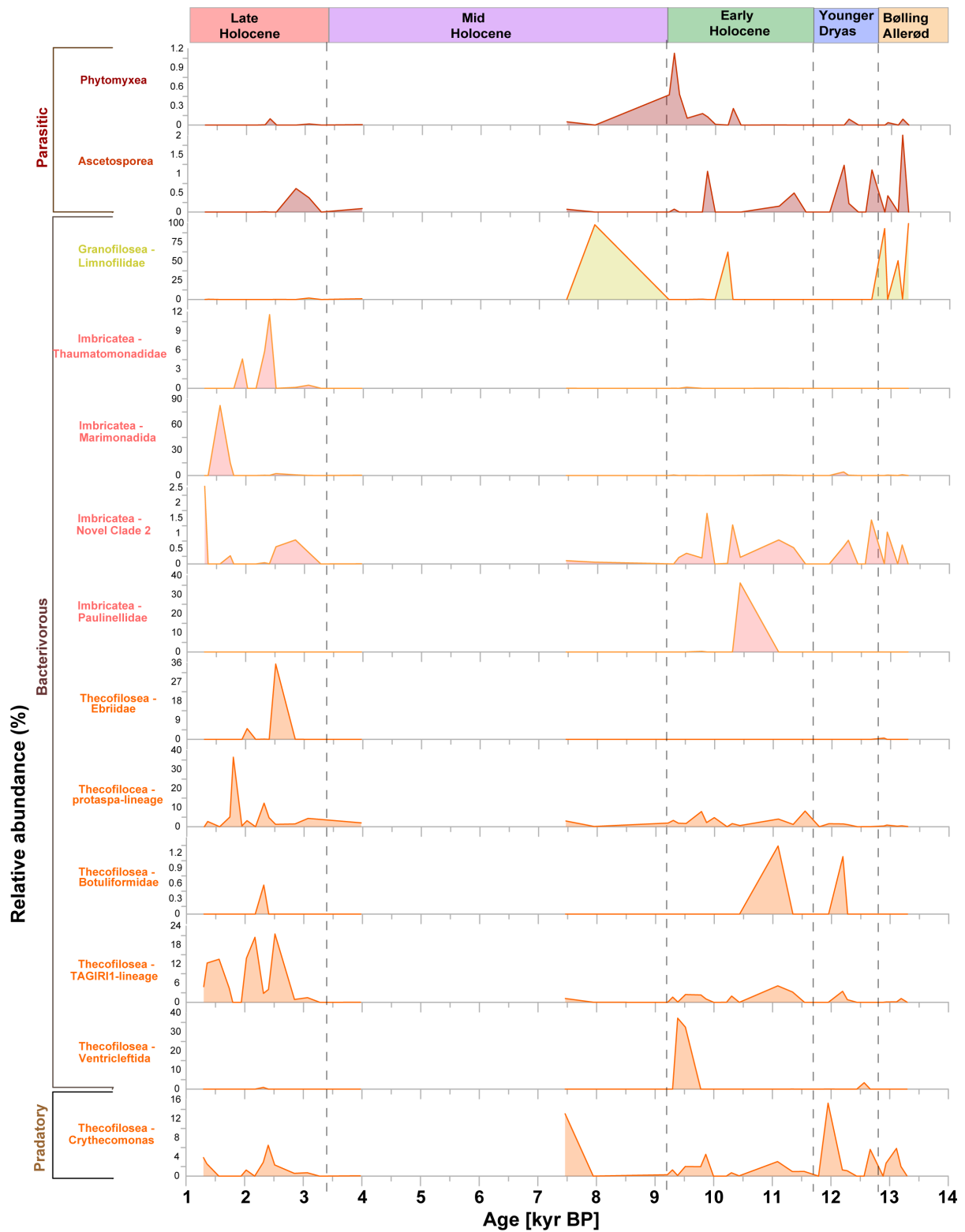


Figure S8

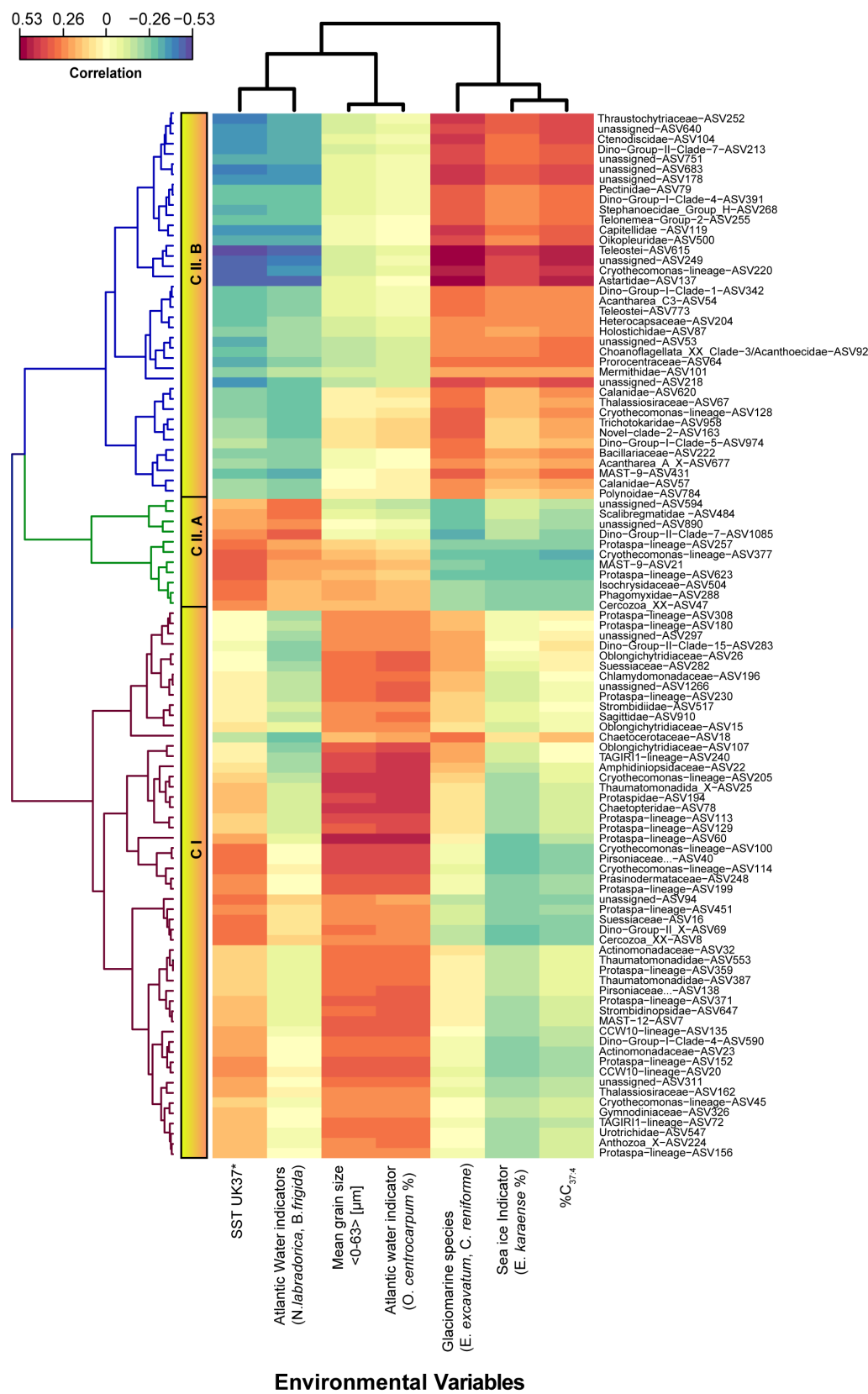


Figure S9

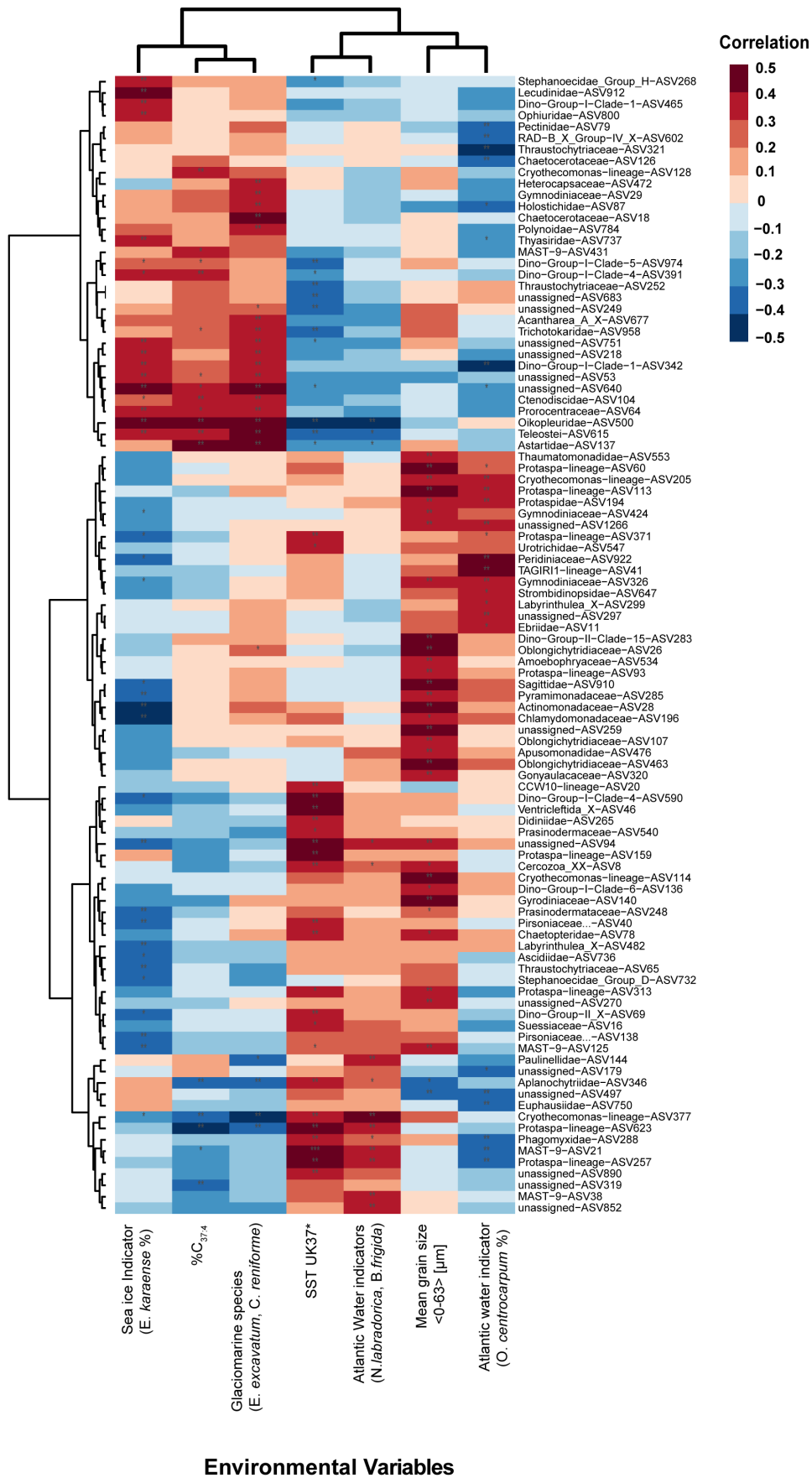


Figure S10

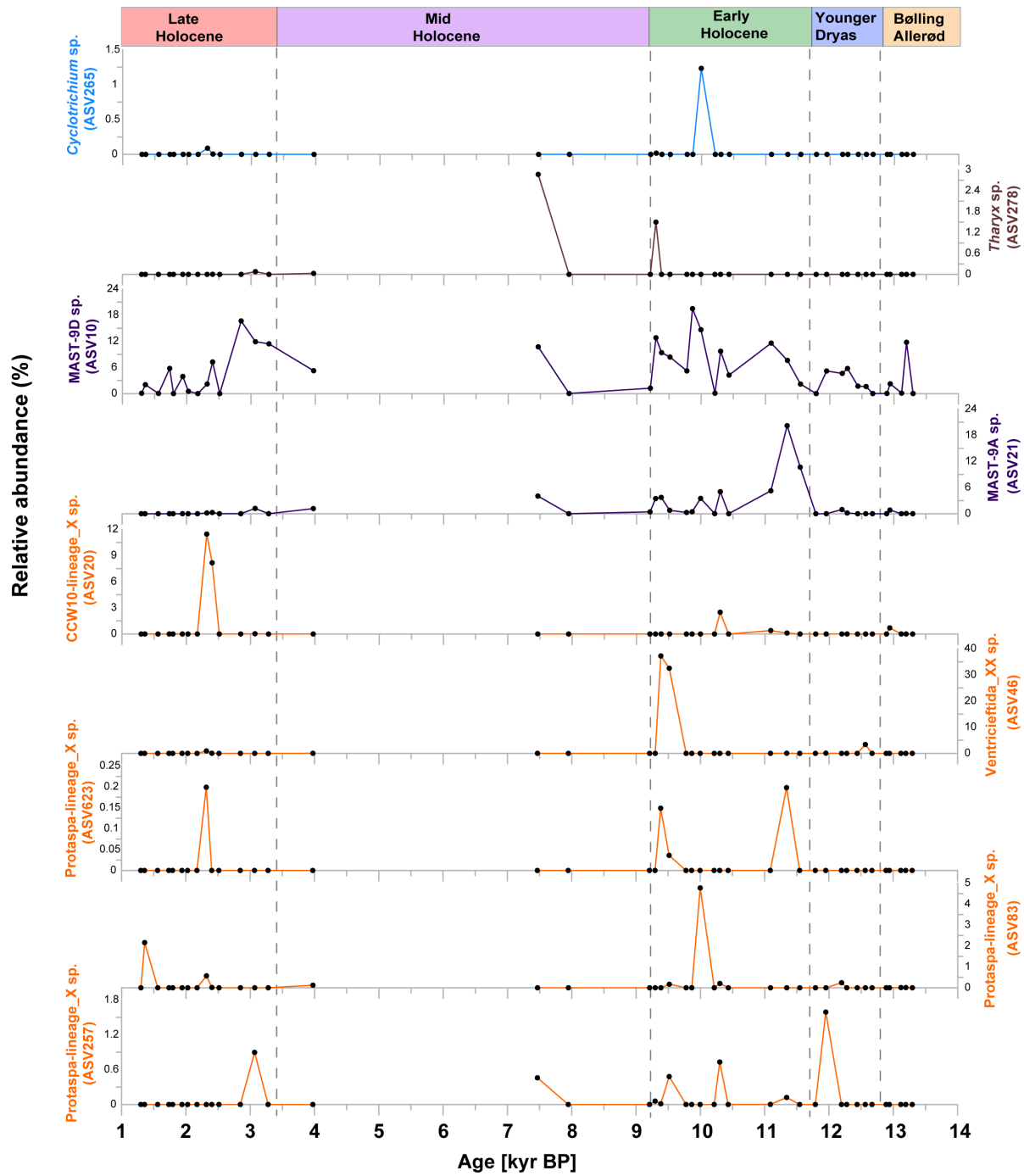


Figure S11

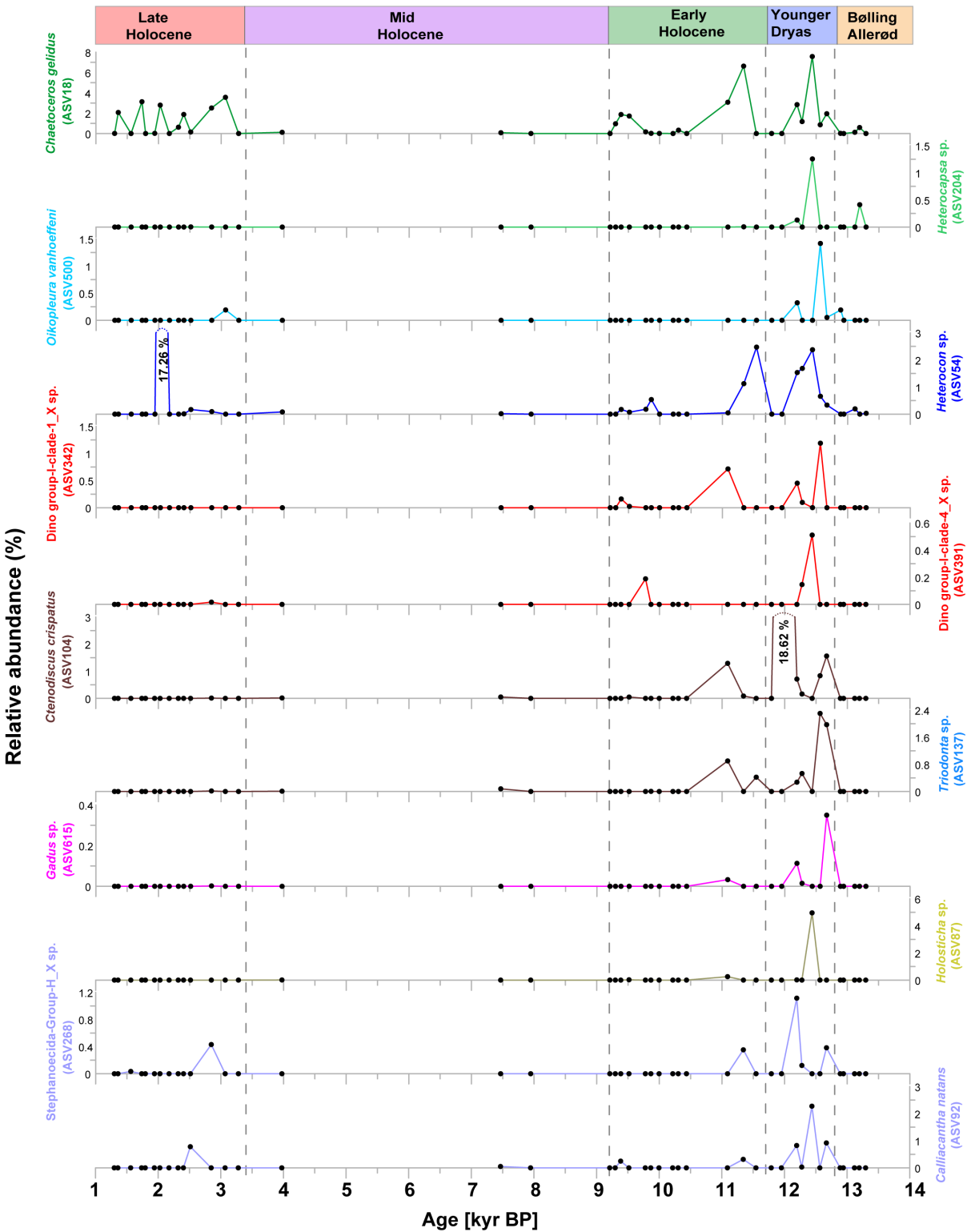


Figure S12

