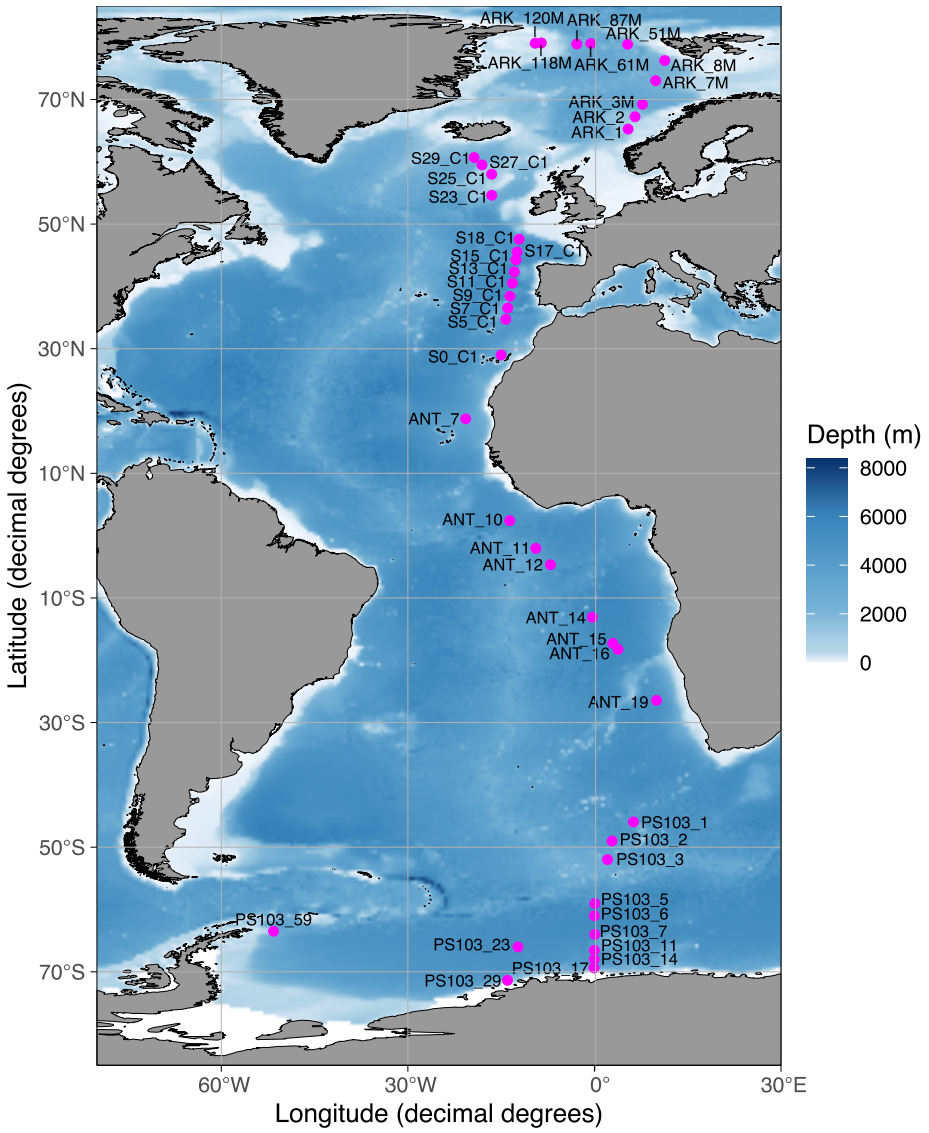
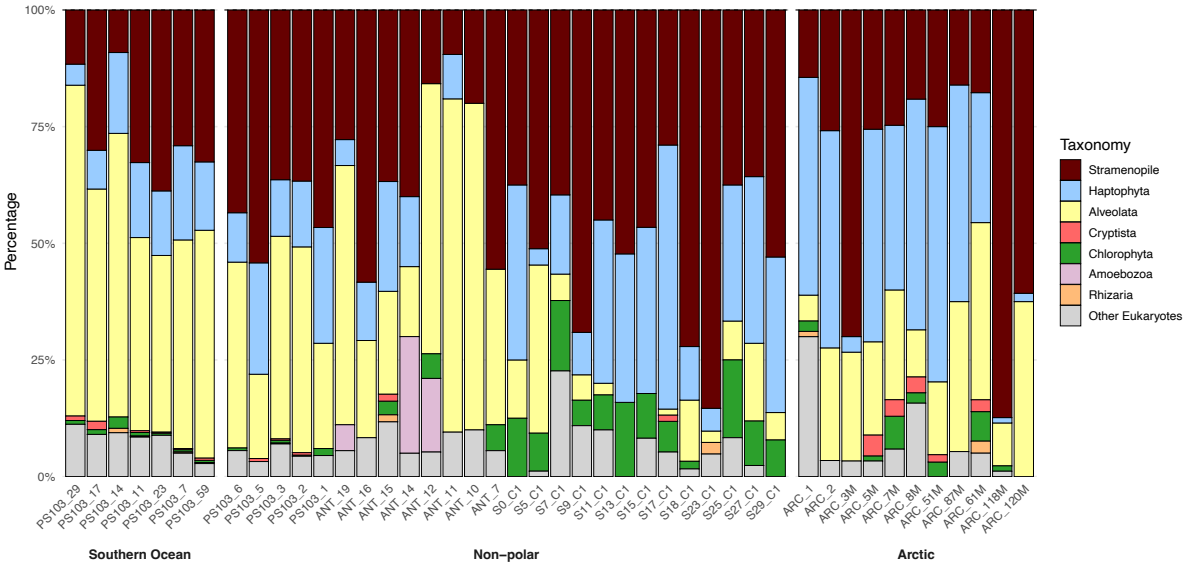
Supplementary Information

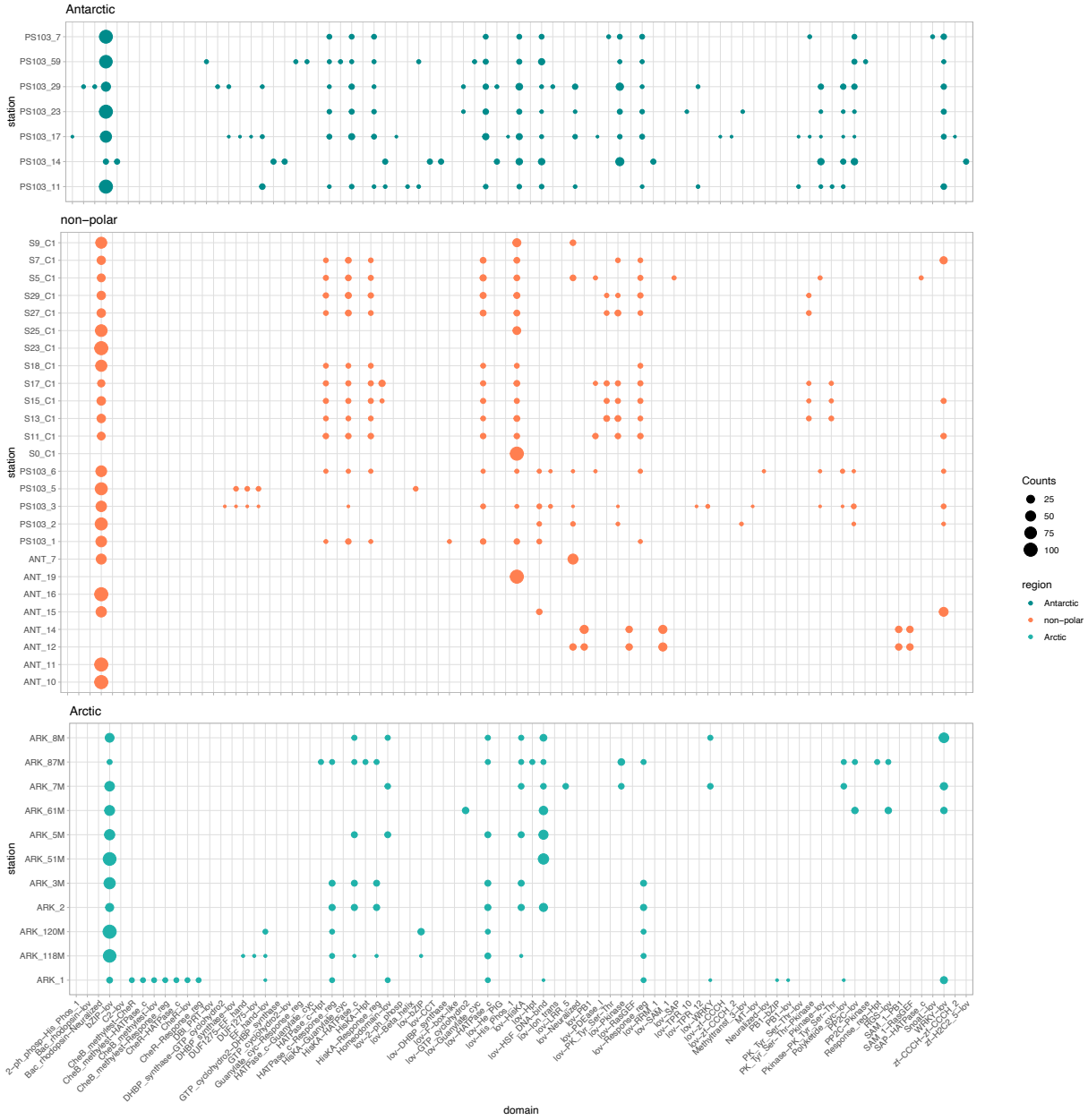
Pole-to-pole LOV-domain receptor diversity points to an early stramenopile origin and global dominance of Aureochromes



Supplementary Figure 1: Sample sites used for metatranscriptomic analysis across the globe based on the 'Sea of Change' dataset. Magenta colored dots show the geographical position of each station while the label defines the station code.

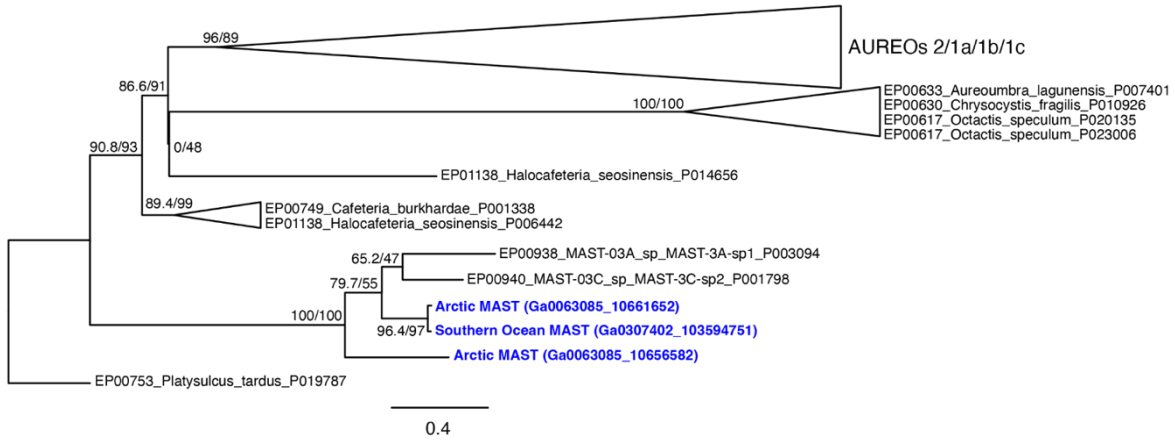


Supplementary Figure 2: Relative taxonomic composition of eukaryotic transcripts per station inferred from the ‘Sea of Change’ metatranscriptome dataset, sorted by latitude. Taxa without reliable classification were grouped as *Other Eukaryotes* and bacterial sequences were removed prior to analysis. Colors indicate major taxonomic categories.



Supplementary Figure 3: Relative abundance of different eukaryotic LOV-domain proteins in combination with other domains across the different stations and areas across the globe, inferred from transcripts of the 'Sea of Change' metatranscriptomic dataset. Stations are ordered by latitude and grouped into three regions: Antarctic (cyan), non-polar (orange), and Arctic (light blue). Each dot represents the proportional contribution (%) of a specific domain to the total domain count of a station. Dot size corresponds to the relative percentage within each station.

Supplementary Figure 4: Schematic visualization of unique eukaryotic domain combinations identified in the 'Sea of Change' metatranscriptome dataset. Each row represents a unique domain architecture. Domains were categorized into functional groups as shown in the legend.



Supplemental Figure 5: Phylogenetic placement of AUREO sequences from heterotrophic MAST species identified within the Sea of Change metatranscriptome dataset.