

Supplementary Figures and Data

Supplementary Figure 1. A. Proportion of reads assigned host sponge and naturally sampled DNA (nsDNA) across the four sponges used in this study. B. Proportion of reads assigned to each prokaryotic and eukaryotic phylum across the four sponges used in this study. Note that the reads assigned to each host sponge species are still included here. C. Proportion of reads assigned to each metazoan phylum across the four sponges used in this study. Note that the reads assigned to each host sponge species are still included here. D. Proportion of reads assigned to each metazoan phylum across the four sponges used in this study, but in this case the reads assigned to each host sponge species were removed.

Supplementary Figure 2. Arthropods detected using sponge nsDNA across biogeographic regions. A. Bubble plot depicting arthropods detected at species level. Circle size indicates read proportions of detected species in a sponge sample. Colours represent the host species. Samples are listed at the bottom (ID details in Supplementary Data 1).

Supplementary Figure 3. Rarefaction curves for the samples used in the study. The samples are named as in Supplementary Data 1, column "Label".

Supplementary Figure 4. Indicator species by A. biogeographic region and B. depth range.

Supplementary Data 1. Metadata for the 97 sponge samples used in this study with full details on latitude, longitude, depth, biogeographic region, and date of collection per sample.

Supplementary Data 2. Summary table of the total number of reads obtained for each sponge species and their proportion of reads in the sequencing run.

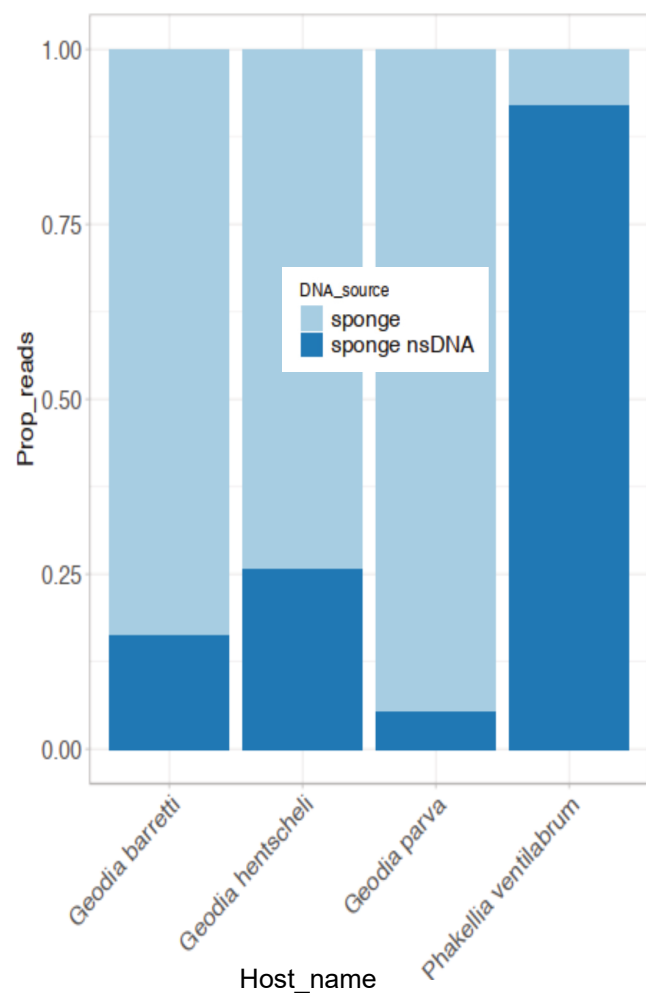
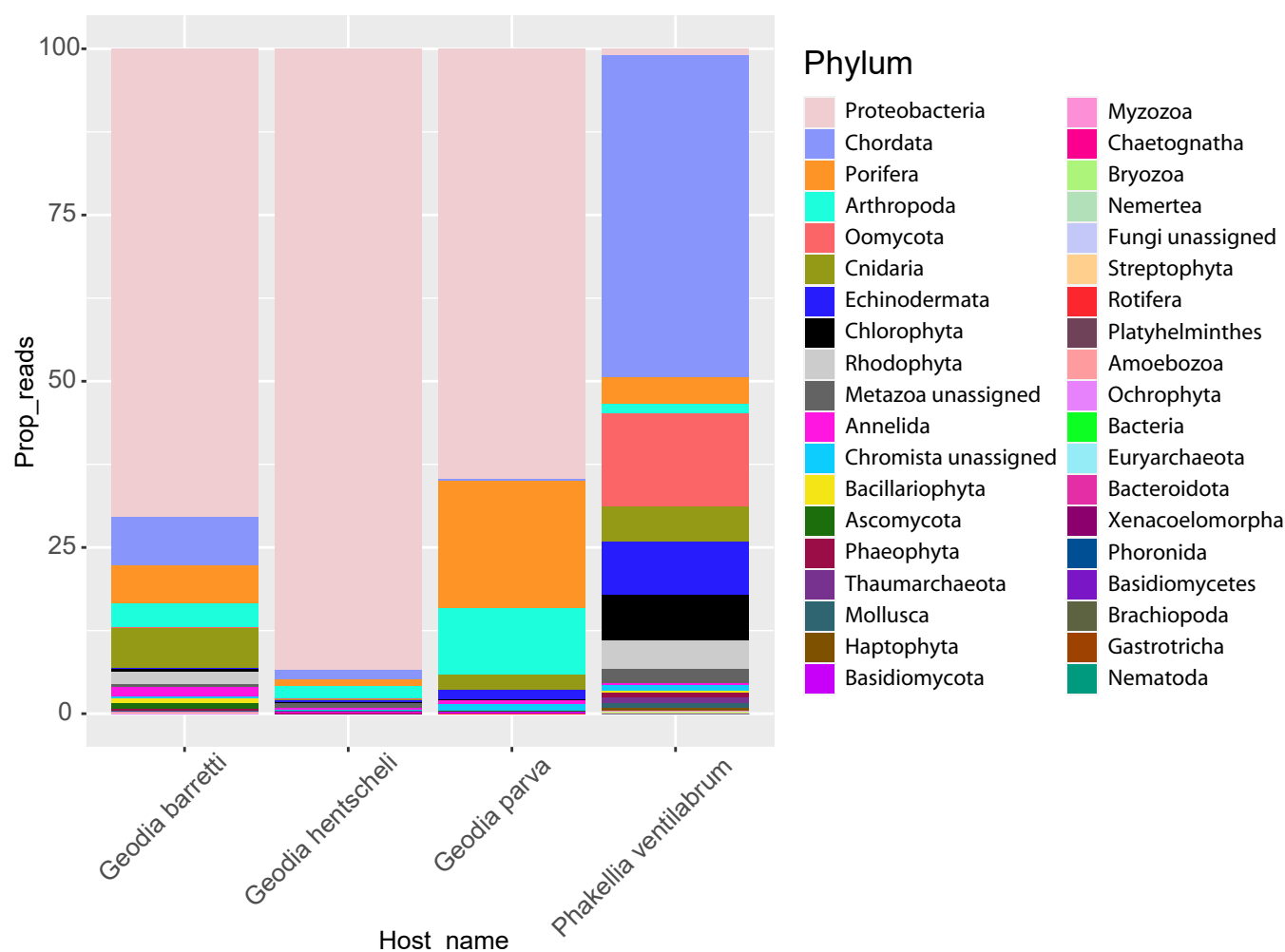
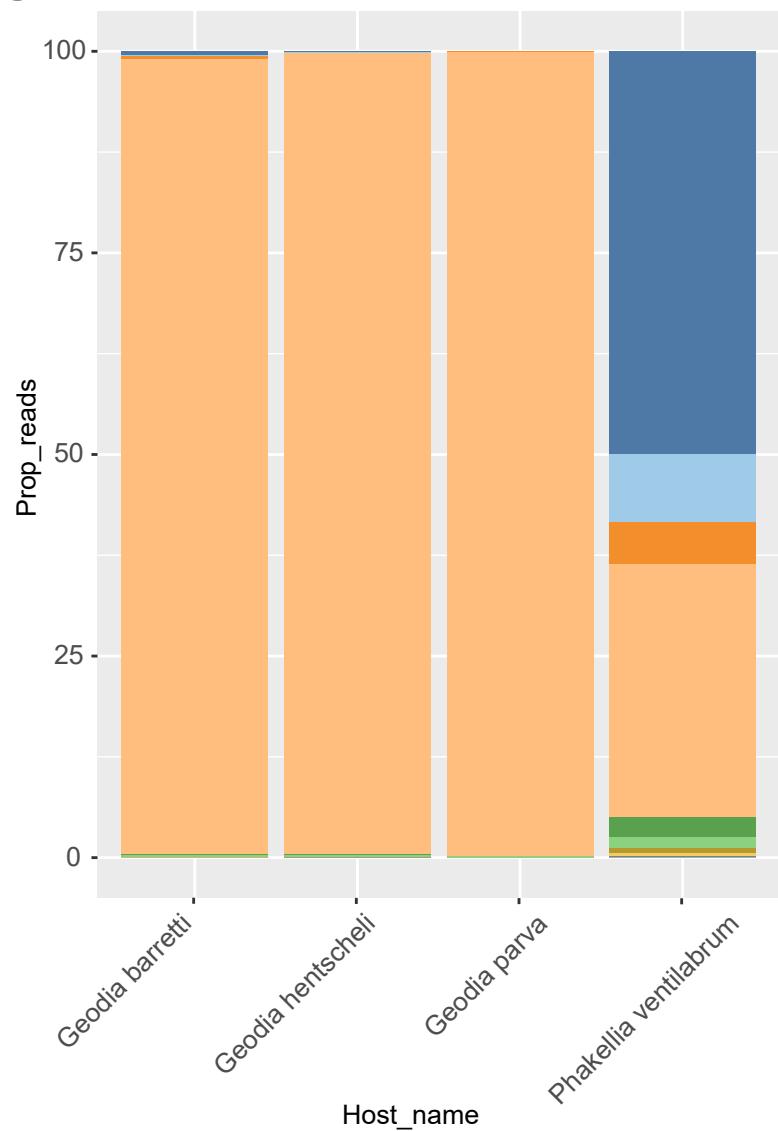
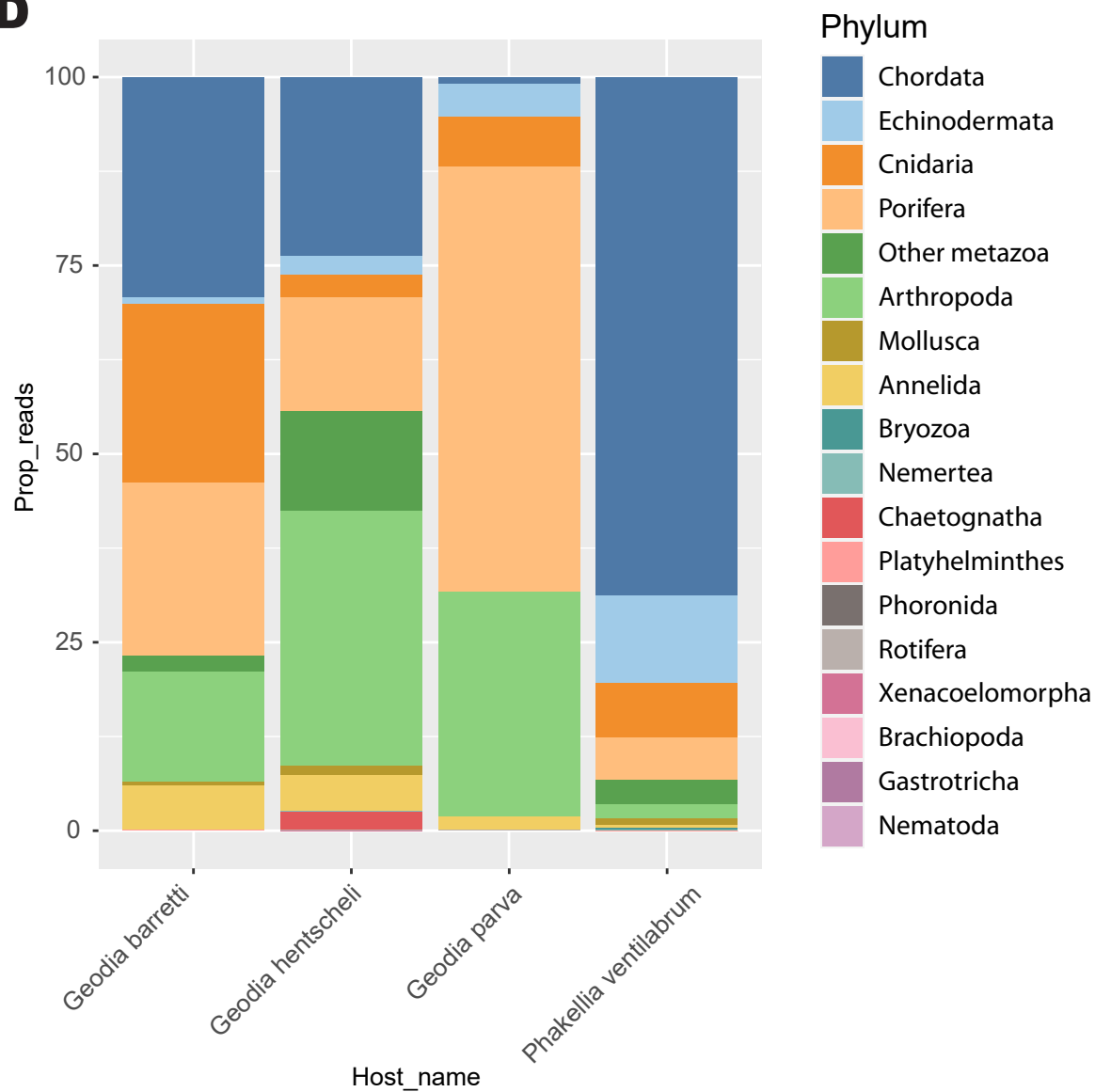
Supplementary Data 3. Summary table of abundance of OTUs, species and sequencing depth across the four sponge species (the number of samples per sponge species indicated in parentheses) assigned to each kingdom and then to each metazoan phyla.

Supplementary Data 4. Final OTUs table for the taxa found in the study (prokaryotes and the eukaryotes) including details for number of reads, proportion by sample, and all metadata associated as in Supplementary Data 1.

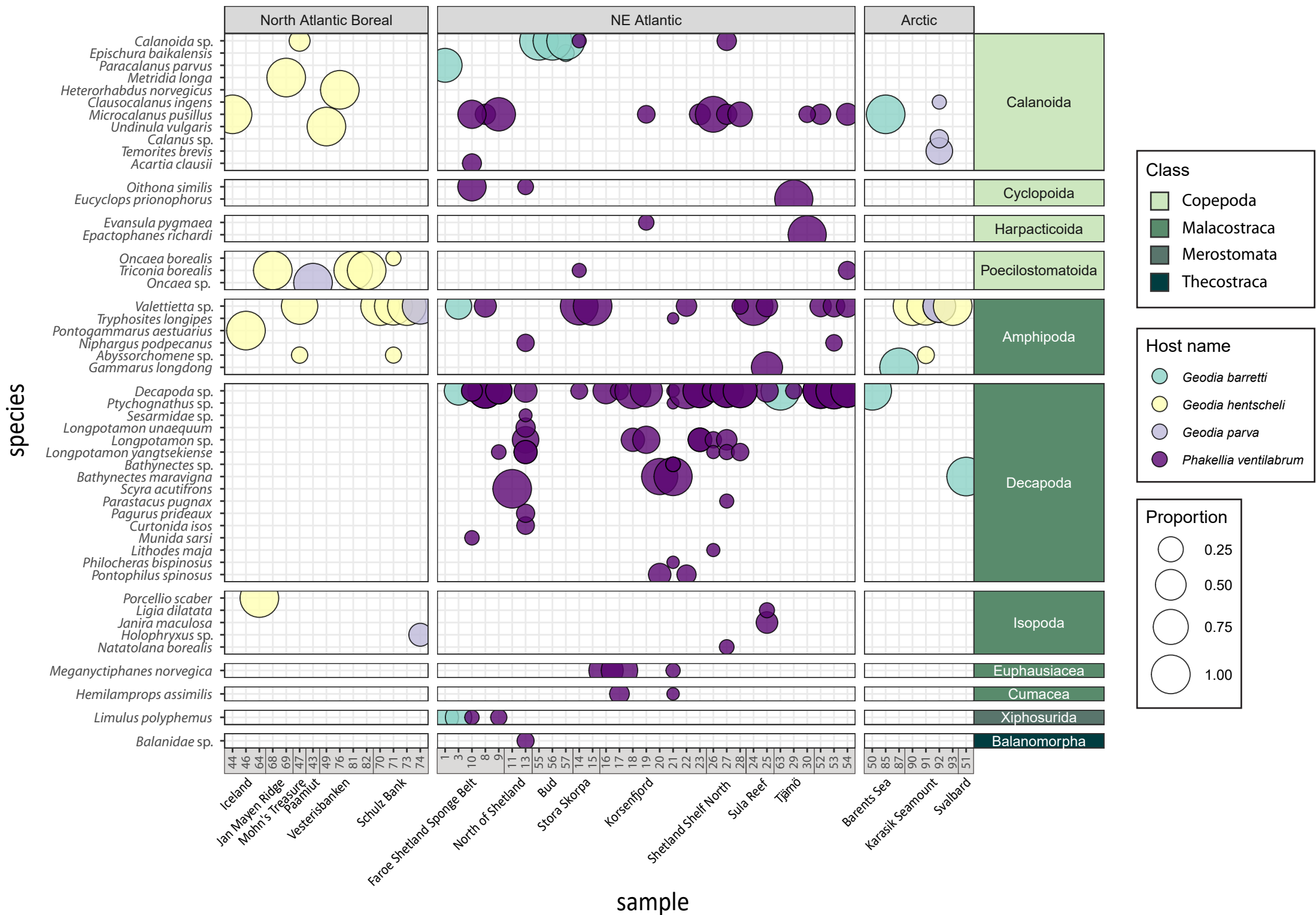
Supplementary Data 5. ANOVA tests for differences on alpha diversity of each biogeography, depth and site (A.1-A.3), and PERMANOVA results using Bray-Curtis distances for B.1 all sponge species by biogeographic region and depth. B.2. Only reads obtained from *Geodia barretti* tested

by biogeographic region. Abbreviations refer to: NAB: North Atlantic Boreal; NEA: Northeastern Atlantic.

Supplementary Data 6. Indcspecies results for biogeographic region and depth range.

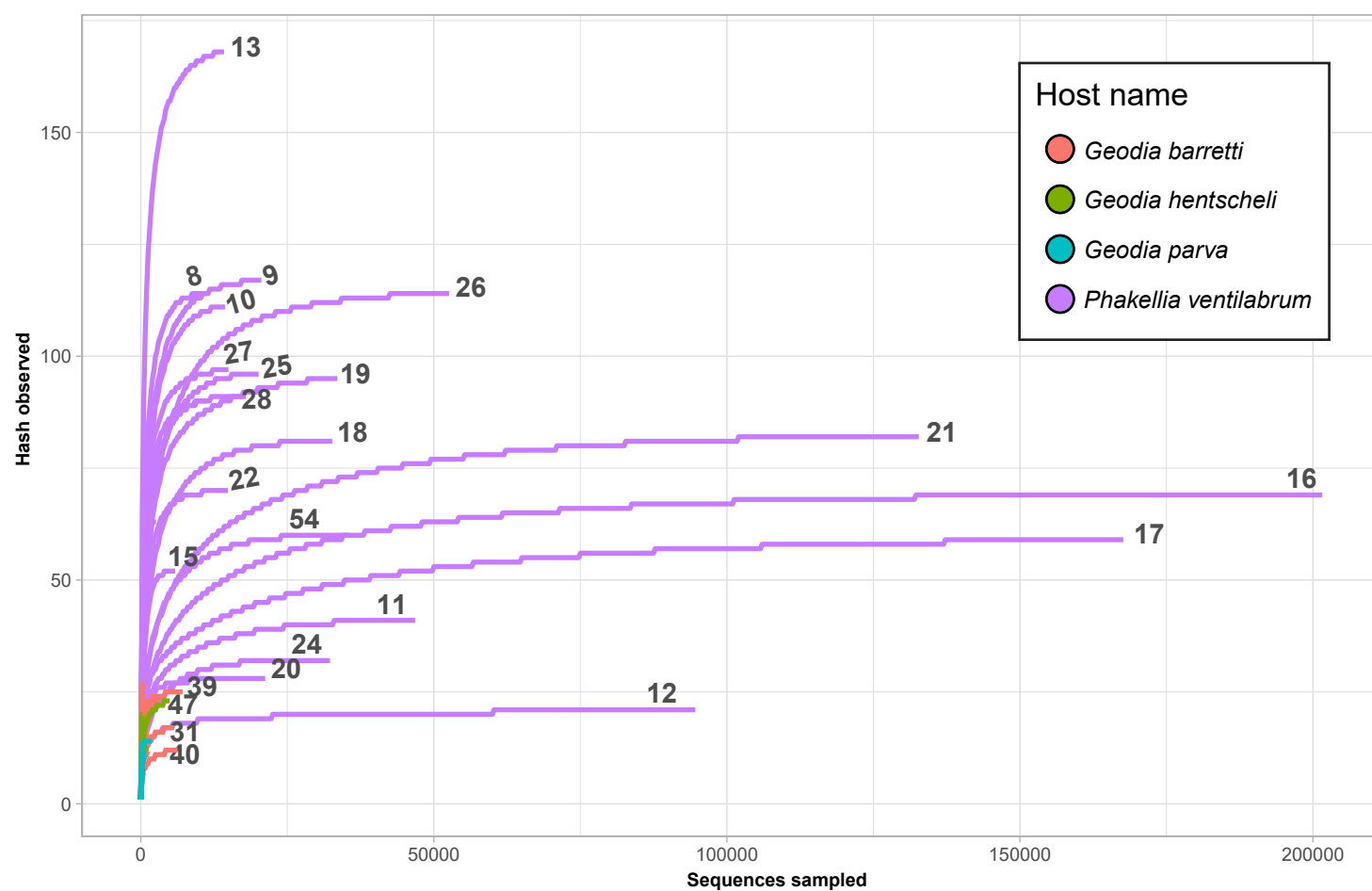
A Supplementary Figure 1**B****C****D**

Supplementary Figure 2

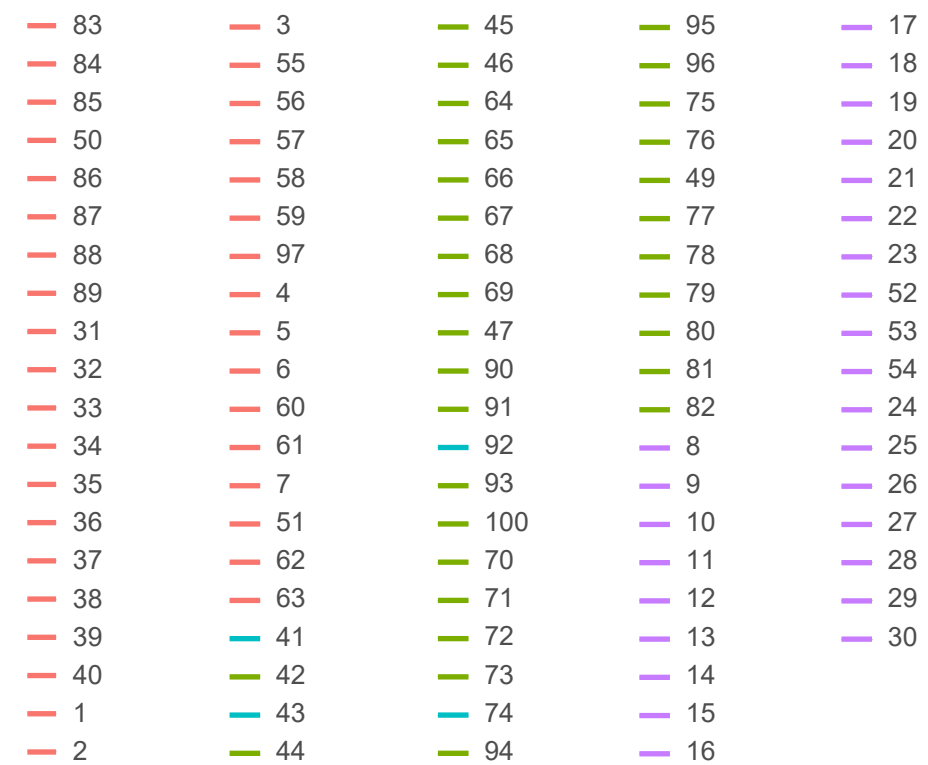


A

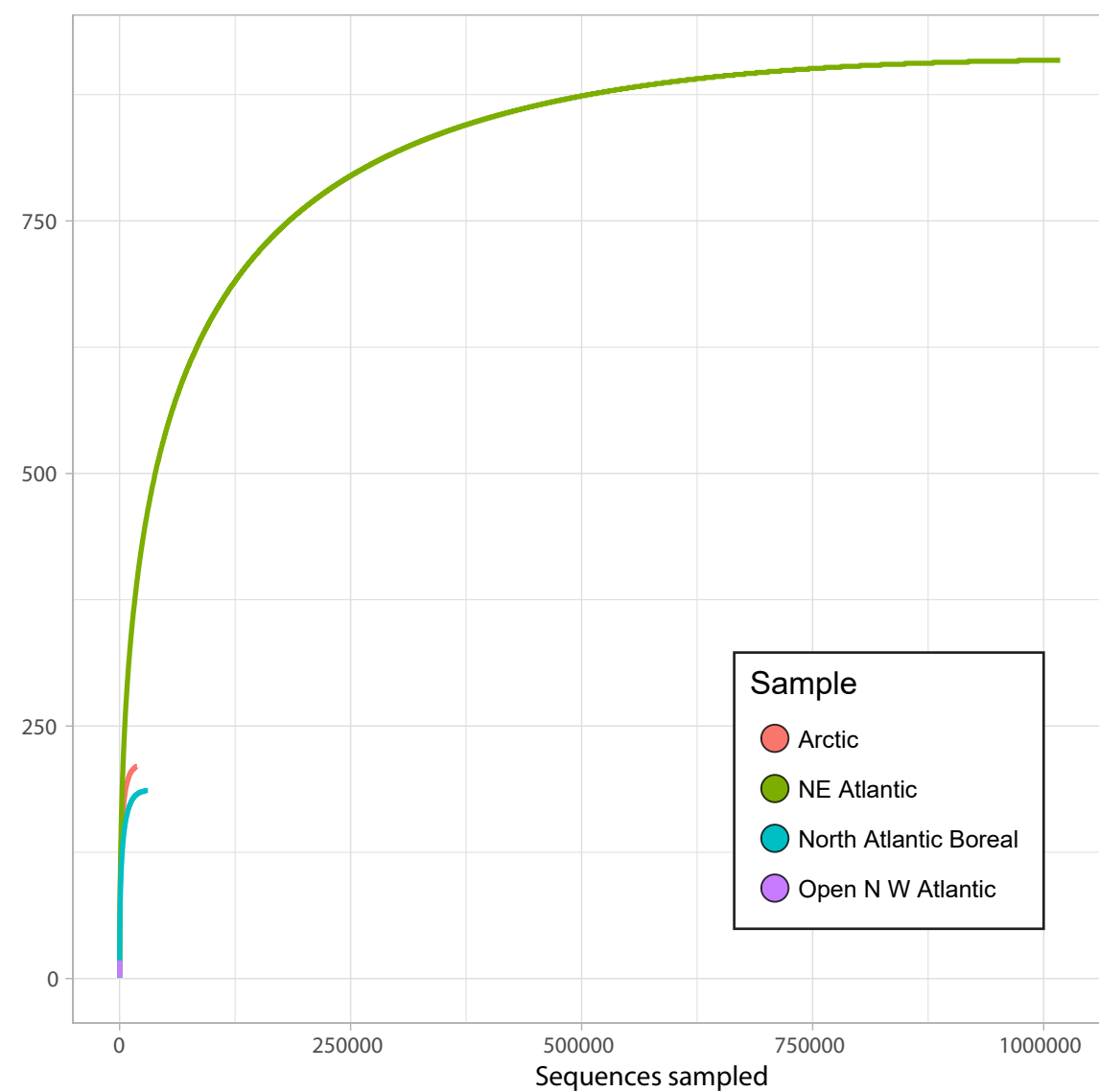
Supplementary Figure 3



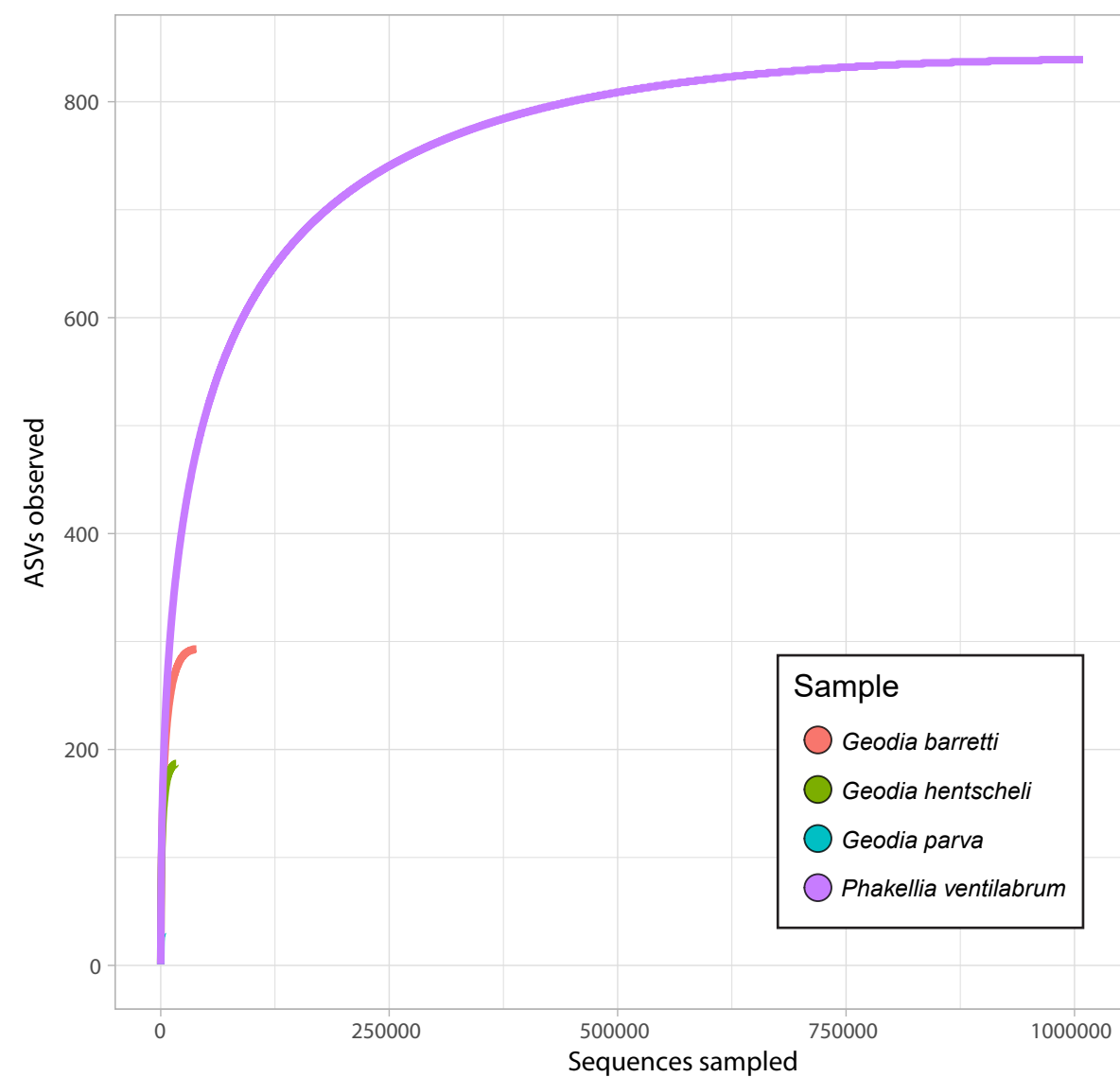
Sample



B

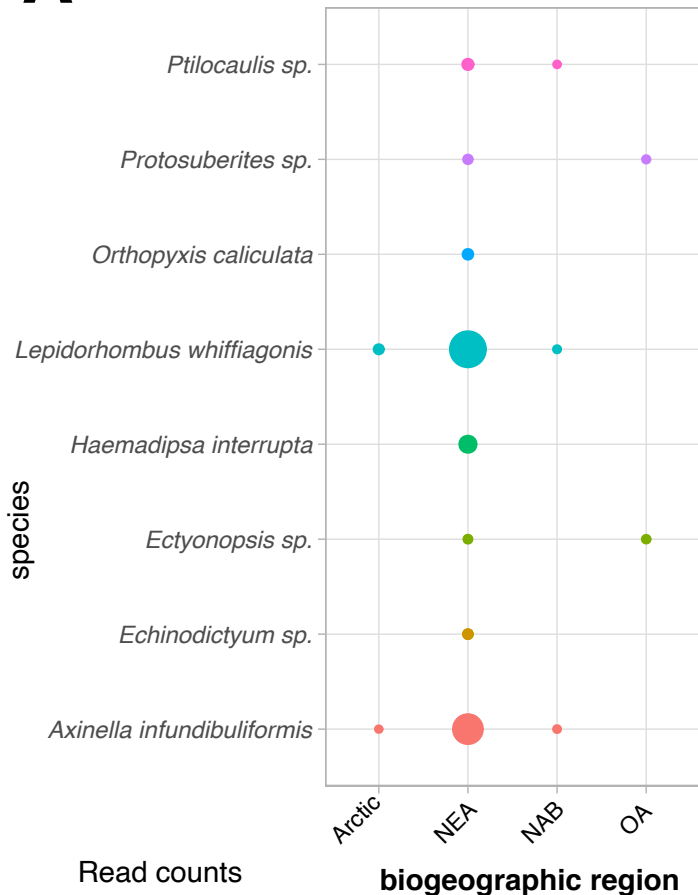


C



A

Supplementary Figure 4



B

