Meta-analysis of the Cetacea gut microbiome: diversity, co-evolution, and interaction with the anthropogenic pathobiome

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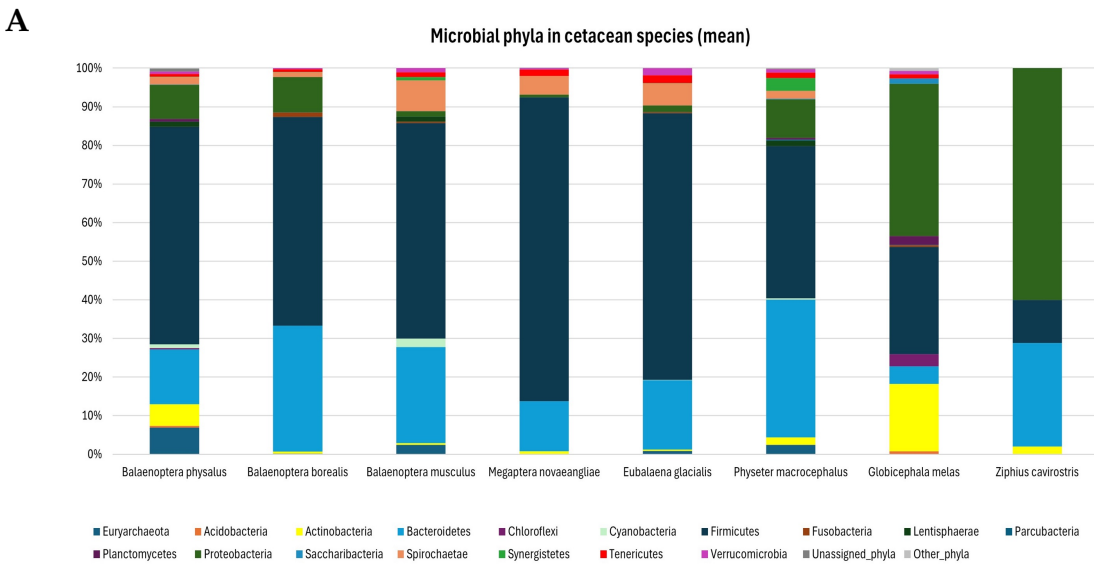
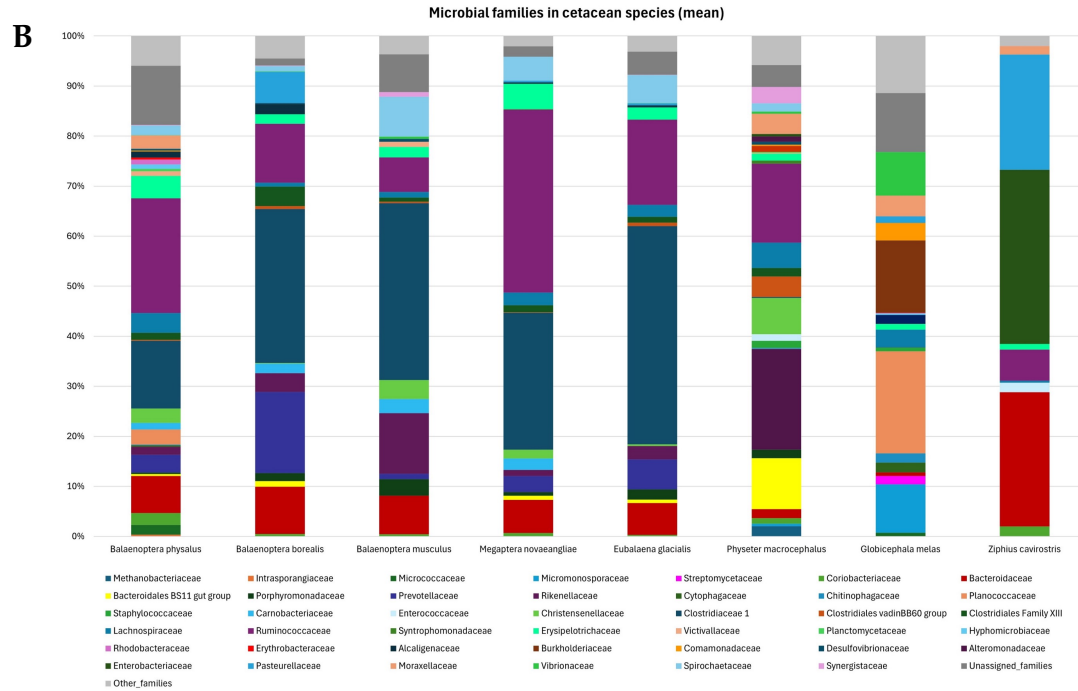
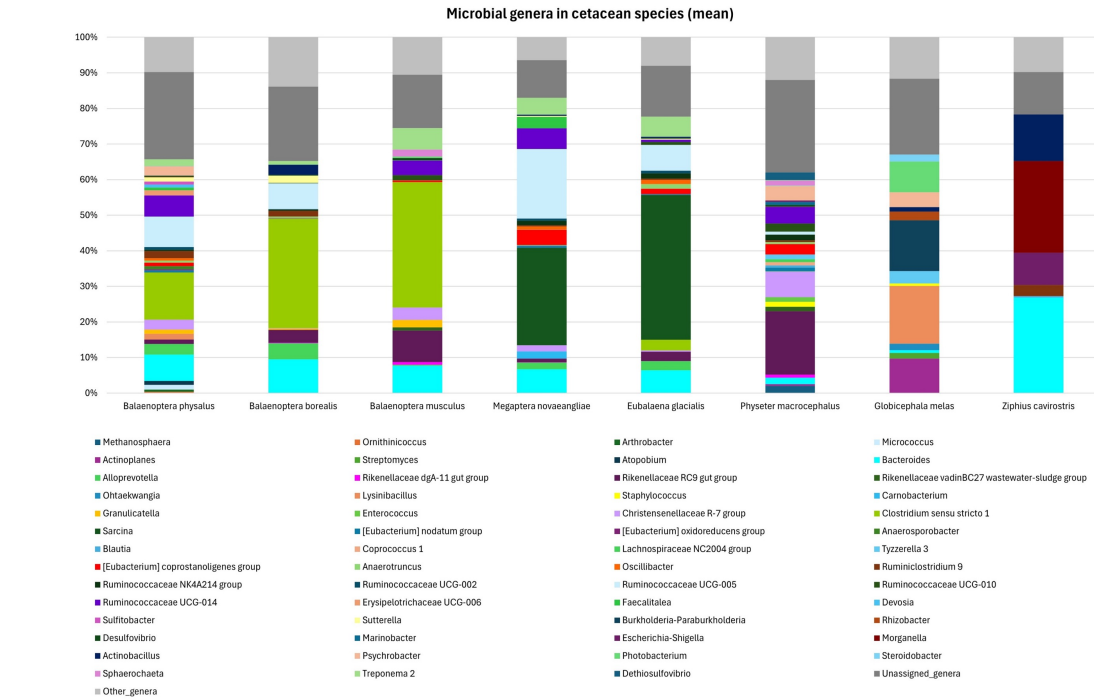
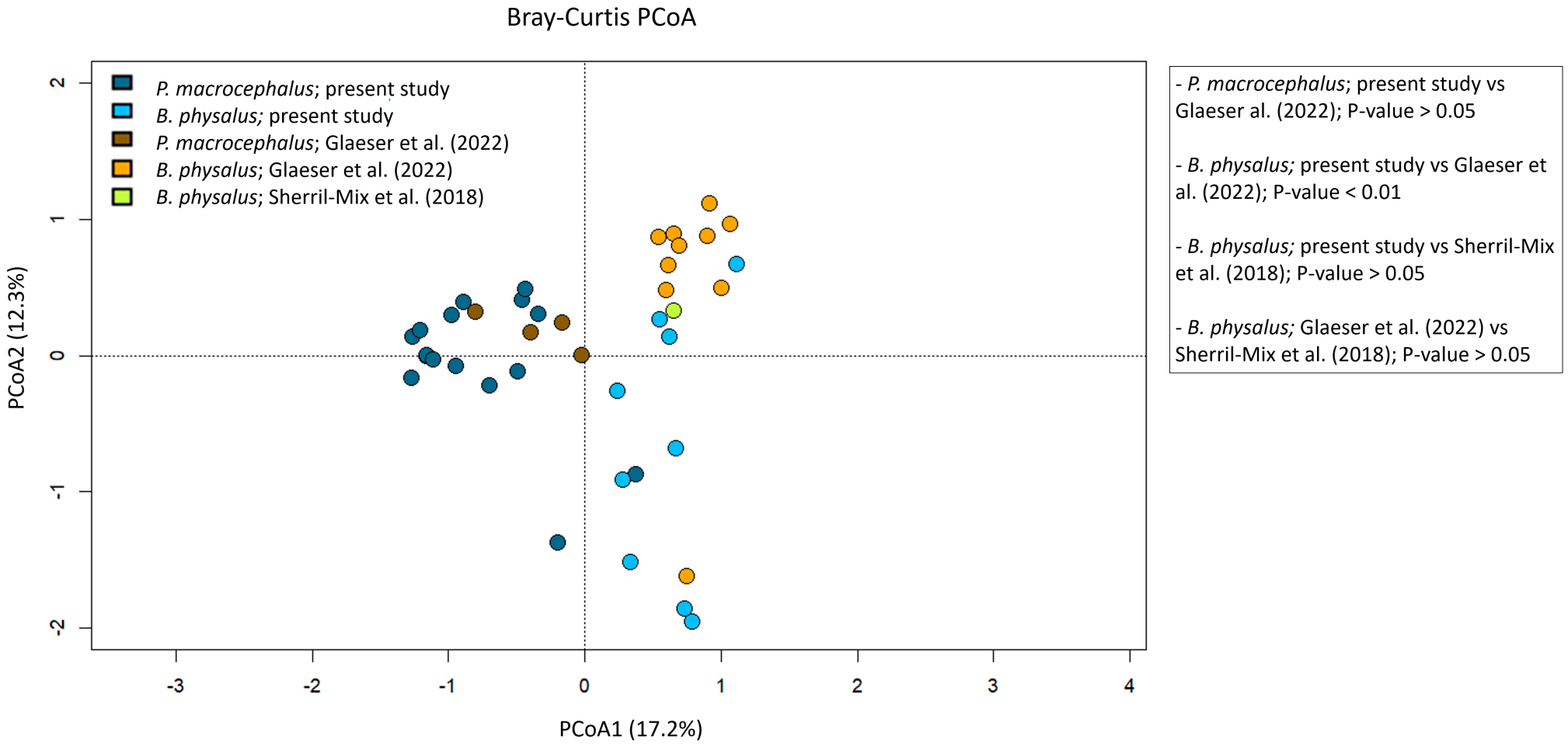


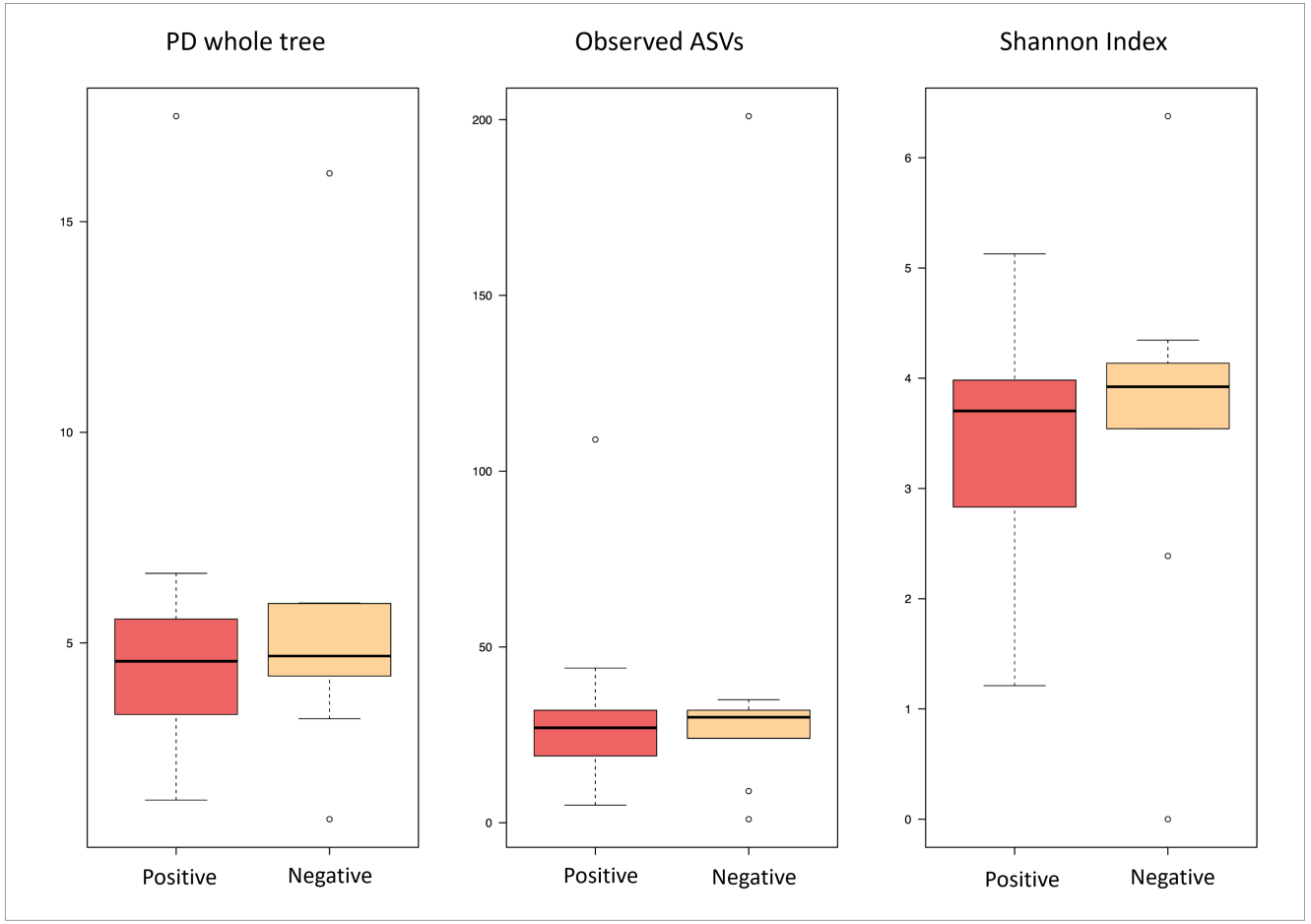




Supplementary Figure 1 – Taxonomic composition of the cetacean gut microbiome. Barplots summarizing the phylum **(A)**, family **(B)** and genus-level **(C)** bacterial composition of both the present study and the publicly available cetacean species. Microbial families and genera with relative abundance < 5% and microbial phyla with relative abundance < 2% were filtered as "others".



Supplementary Figure 2 – Microbiome community structure of *Physeter macrocephalus* and *Balaenoptera physalus* according to the study of origin. Representation of *P. macrocephalus* and *B. physalus* samples (present study and publicly available, except for Sanders et al., 2015) by Principal Coordinates Analysis (PCoA) based on Bray-Curtis distances where different colors match the study of origin: dark and light blue for the present study, dark and light orange for Glaeser et al. (2022), green for Sherril-Mix et al. (2018) (permutation test with pseudo-F ratio, see pairwise p-values for the same cetacean species compared in different studies on the right panel); the first and second principal components (PCoA1 and PCoA2) are plotted and the percentage of variance in the dataset explained by each axis is shown.



Supplementary Figure 3 – Alpha diversity of infected and non-infected cetaceans from the present study. Boxplots showing the alpha diversity of the gut microbiome of the present study cetacean species (n=30), considering both positive (parasites detected) and negative (parasites not detected) individuals, based on the Faith's Phylogenetic Diversity (PD whole tree), the number of observed ASVs and the Shannon index. No significant differences were found for any of the metrics (Wilcoxon rank-sum test, $p > 0.05$).