(a) All bacteria

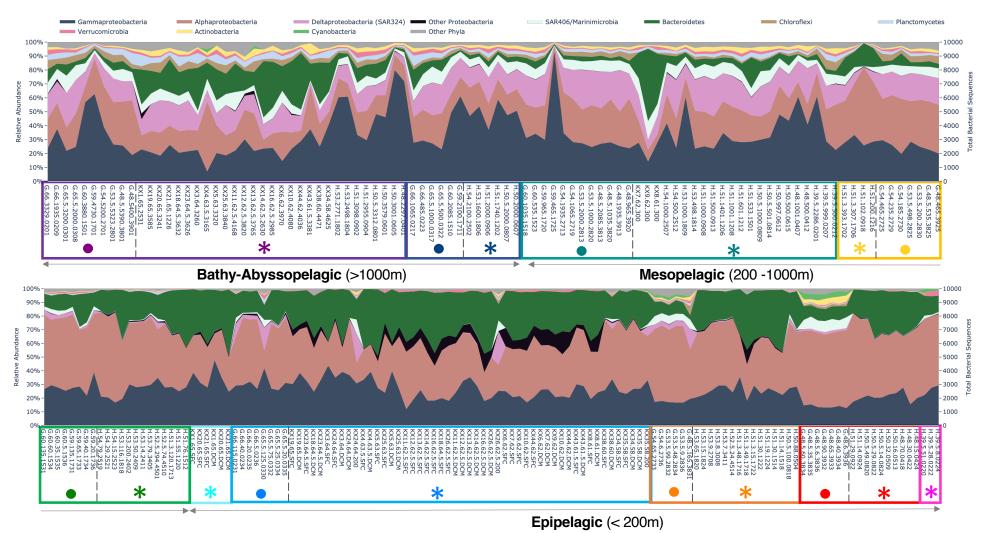
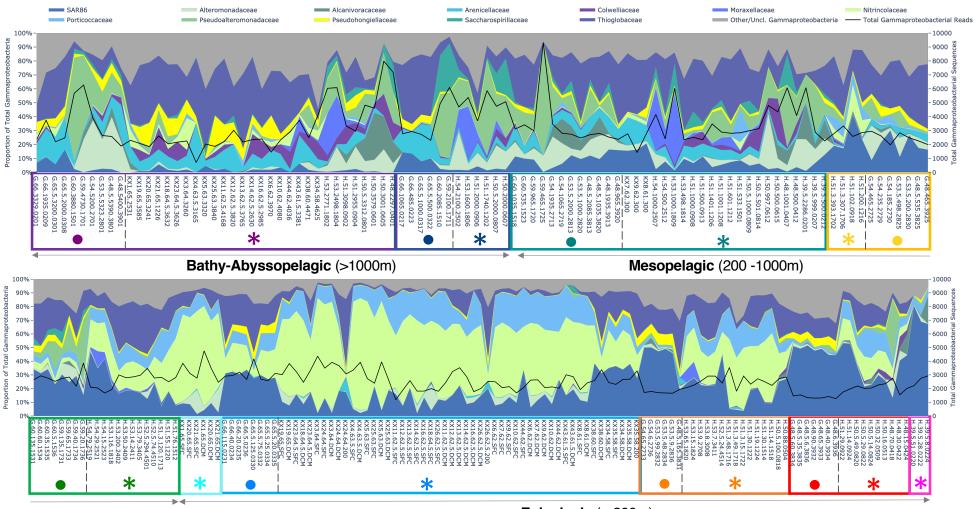
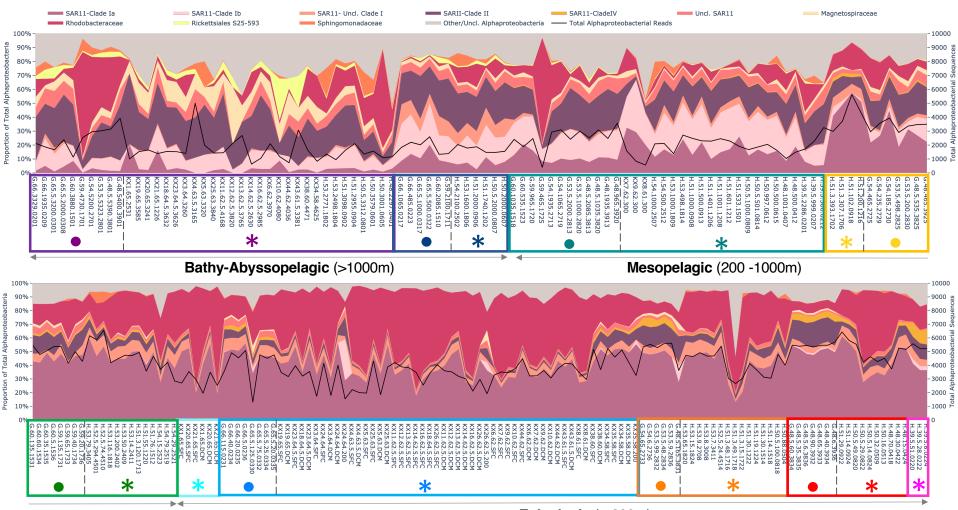


Fig. S6: (a) Full charts for relative abundance of major bacteria detected from the different water masses at phylum/class level, showing each of the 223 samples on the x-axis. Samples are arranged from high to low latitude in each water mass from the Pacific and Indian sector, as indicated by their respective sector/water mass symbols (see Fig. 1/Fig. 2 legends). Detailed charts of the main families within (b) Gammaproteobacteria, (c) Alphaproteobacteria and (d) Bacteroidetes is also shown. The full chart for archaeal relative abundance is shown in (e), and a detailed chart of the main *Nitrosopumilus* species/zOTUs is shown in (f).

(b) Gammaproteobacteria



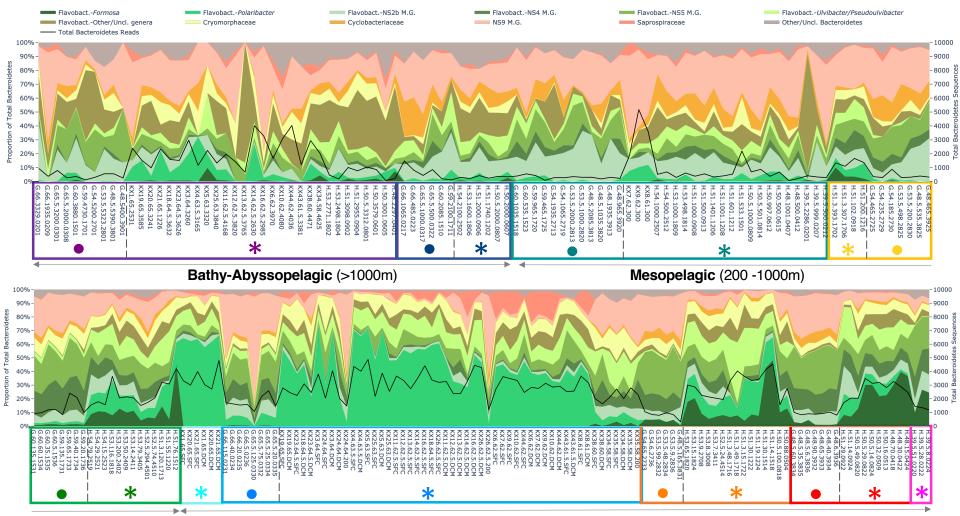
Epipelagic (< 200m)



(c) Alphaproteobacteria

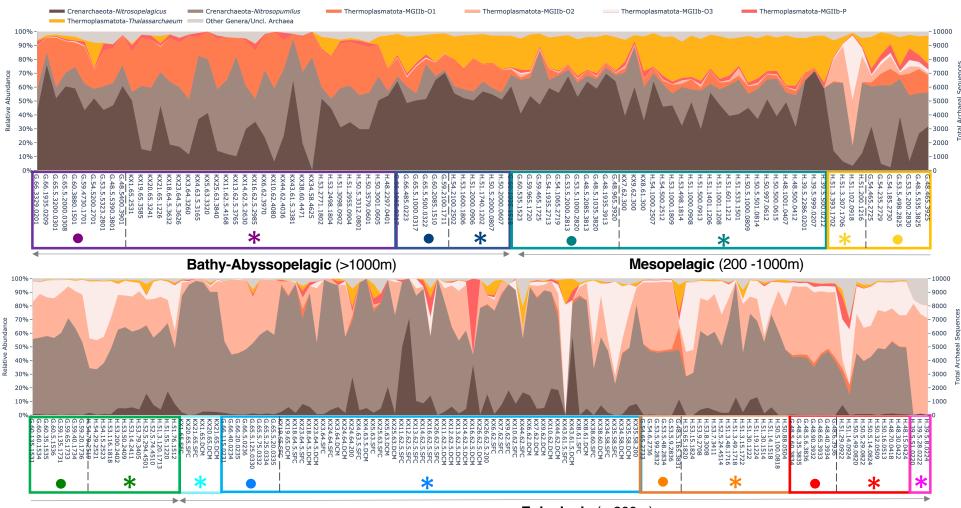
Epipelagic (< 200m)





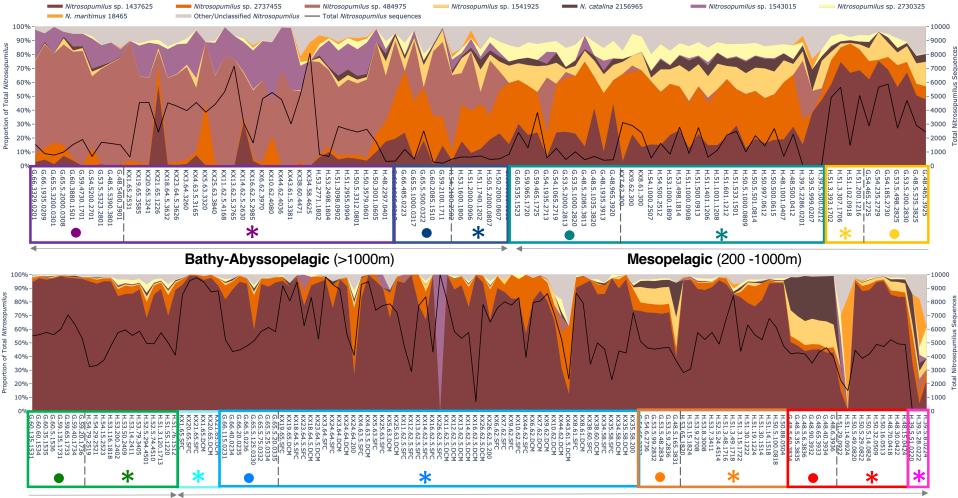
Epipelagic (< 200m)

(e) All archaea



Epipelagic (< 200m)

(f) Nitrosopumilus



Epipelagic (< 200m)