The authors have strengthened their analyses by introducing new filtering criteria and refining their methodological approach. Notable improvements include the application of transformation-centered log-ratio transformations and the Aitchison distance dissimilarity measure for ordination and PERMANOVA. Additionally, the study now integrates complementary analytical tools such as PICRUSt2 and ALDEx2, allowing for a more comprehensive inference of differentially abundant metabolic pathways within the foraminiferal microbiome in relation to the surrounding water column.

The results are clearly presented, and the methodology is well-documented. These refinements contribute to a more robust and informative study.

However, addressing the following points would further enhance the clarity, coherence, and reproducibility of the manuscript.

SPECIFIC COMMENTS:

On page 8, lines 165–168, the authors mention performing rarefaction and calculating alpha diversity metrics. However, corresponding rarefaction curves do not appear to be included in the supplementary material. Adding these curves is necessary as it would help assess whether the sampling effort was sufficient to capture the diversity of the prokaryotic community in both foraminifera and water samples.

In their response, the authors state:

> *"As reported under point 2 above, in our new analyses we have shown that "Station" drives 2.3% of the differences in ASV composition (rather than 49%), and is not significant (PERMANOVA, Adonis). However, the provenances "foraminifera" and "water column" are significantly different in both the FW and 101 datasets. Here then, we have been able to reject the null hypothesis that 4there were no differences in the ASV compositions between "Provenances" and accept the null hypothesis that there are no differences between "Station", indicating Provenance rather than Station (location) has more influence on the ASV composition"*

However, the multivariate analysis performed on the ‘Forams only’ subset indicates that 48.3% of the variation in foraminifera microbiome composition is attributed to station (lines 315-318, p. 16). In contrast, the same analysis on water samples (stations 101, 115, and 323) does not show a significant relationship with station (Fig. A1). Furthermore, when the ‘FW’ subset (including both water samples and foraminifera) is analyzed, station is no longer a significant factor. Based on these findings, the authors conclude that ‘provenance’ rather than location is the main factor shaping the foraminifera microbiome. However, these results appear to be somewhat contradictory. If station explains a substantial proportion of variation in the ‘Forams only’ subset but not in the water samples or the combined ‘FW’ subset, additional clarification/discussion is needed in the manuscript. To further investigate this discrepancy, I recommend adding another subset and repeating the analysis using only the foraminifera microbiome data from the same stations as the water samples (which likely corresponds to the ‘FW’ subset minus the water samples). This additional analysis could help determine whether the observed patterns in the ‘Forams only’ subset are driven by differences in water column composition, ultimately clarifying the influence of microbial community assembly processes in the surrounding water on the foraminifera microbiome. Given that the authors define the core microbiome using all foraminifera data, it is crucial to discuss the ecological and biological factors shaping its composition to ensure a comprehensive interpretation of the results.

The results support the previously hypothesized POM feeding mode and suggest that *N. pachyderma* also preys on living diatoms.

A recent study by Meilland et al. provides experimental evidence for this feeding behavior in cultured *N. pachyderma* from high latitudes (Type I). Citing this reference and incorporating its findings into the discussion would provide a more comprehensive context for interpreting the feeding ecology of *N. pachyderma*.

Meilland, J., Siccha, M., Morard, R., & Kucera, M. Continuous reproduction of planktonic foraminifera in laboratory culture. Journal of Eukaryotic Microbiology, e13022. https://doi.org/10.1111/jeu.13022

Throughout the manuscript, microbiome community structure in foraminifera and water samples is described using expressions such as "% of all ASVs" (e.g., line 329, p. 16) and "contained >50% chloroplast ASVs" (e.g., line 359, p. 18). These phrases describe the number of ASVs rather than their relative abundance (i.e., read proportions) but are referenced alongside figures that likely represent read proportions.

To avoid potential misinterpretation, I recommend explicitly clarifying that these values refer to read proportions and updating the y-axis labels in Figures 3 and 6 to specify "% reads."

The statement regarding raw sequence data (line 248, p. 12) should be moved to the "Data Availability" section. Additionally, to enhance reproducibility, I strongly encourage making the environmental contextual data, ASV table, and sequence files publicly accessible, as previously suggested.