

We would like to thank the editor and reviewers for their time and comments that have ultimately improved our manuscript.

Next, we list a point-by-point response to the concerns raised by Reviewer 2

#### 1. Introduction:

1) The introduction provides a good overview of the Atacama Desert and its unique environmental conditions. However, it could benefit from a more detailed discussion of previous studies on microbial communities in similar desert lakes, highlighting the gaps that this study aims to fill.

We are thankful for the reviewer's suggestion. We have included references for studies carried out in other desert lakes, including a review that reflects previous investigations done in different locations worldwide. However, there is an important gap in knowledge regarding the unique Atacama Desert lakes, given their local geochemistry and the intense mining industry maintained in the area; the few studies from the Atacama Desert lakes were already included in the previous version of this manuscript. Furthermore, we agree with the reviewer that a detailed discussion would enrich this study, and more perspective has been added, for example, highlighting the methanogens role that is in accordance with our results. See lines 87-92 and some discussion sections in the revised manuscript.

2) The introduction could also include a clearer hypothesis or research question, guiding the reader through the study's objectives.

We have now added lines 101-102 to emphasize that our research question aimed to describe geo-microbial dynamics and establish a baseline study in this underexplored lake under constant anthropological pressures.

#### 2. Methods:

1) The methods section is detailed and well-structured, providing clear descriptions of the sampling, DNA extraction, and sequencing procedures. However, the section could include more information on the quality control measures used during sequencing and data analysis to ensure reliability.

We have included more details of quality control in lines 157-158, also the section: "Sediment sample processing and DNA extraction" details precautions and measures taken to ensure the samples were not cross-contaminated. Also, during the sequencing data processing, strict quality controls were carried out on the raw data (line 167) and the resulting analysis to avoid overestimations and misinterpretations (170-171). We also used validated methods, pipelines and packages to ensure reliability and replicability of our results.

#### 3. Results:

1) The results are presented clearly with detailed figures and tables. The identification

of three distinct microbial zones is a significant finding, but the study could benefit from more detailed statistical analyses to support these observations.

We acknowledge the reviewer's comments. From the physical-chemical properties point of view, our group statistically determined these zones in a previously published paper (Pérez-Portilla et al., 2024) using a data integration model (which we refer to in figure 6). In this work, the taxonomic composition analysis reflected the zone differentiation (which is supported by Wilcoxon statistical tests to compare means between the identified zones for all tested Alpha diversity indices). Additionally, beta diversity analysis using Hellinger transformed Bray Curtis distances shows a clear segregation of the samples into well-defined groups, confirming also all previous findings. On the other hand, the significance of the selected geochemical variables was also tested statistically with ANOVA. This is detailed in lines 177-185 and can be observed in Figure 3.

2) The correlation between microbial diversity and geochemical properties is compelling, but the study could explore potential mechanisms underlying these correlations, such as specific metabolic pathways or ecological interactions.

We initially did not explore these underlying mechanisms further since the microbial community's functional potential is out of the scope of this study. Our results focus on taxonomic composition and abundance; additionally, most of the microorganisms found along the sampled core are unknown or yet to be classified; this novelty prevents partial conclusions based on lower taxonomic groups. However, in the results and discussion sections, we have included more details based on previous investigations and our metabolic estimation based on the taxonomic composition. See lines 231-237, 240-241

#### 4. Discussion:

1) The discussion effectively links the findings to broader ecological and environmental contexts. However, it could delve deeper into the implications of the study for understanding microbial adaptations to extreme environments and potential applications in bioremediation or astrobiology.

We have included statements that suggest ecological interactions among the microbial communities and their importance in the study of the origin of life, life in other planets, and potential biotechnological importance of these microorganisms that are very under-characterized. See lines 334-339

2) The discussion could also address potential limitations of the study, such as the reliance on a single sediment core and the assumptions made in functional predictions. We have also highlighted the limitations of this study in the revised manuscript. See lines 371-376.