The authors investigated sections of a drill core from Lake Magadi (Hominin Sites and Paleolakes Drilling Project, HSPDP), a soda lake in Kenya, to reconstruct the microbial methane cycle of the lake system over the last 456 ka. The study is focused on molecular biomarker analysis, especially isoGDGTs, representing archaeal core lipids. Together with accompanying (organic-) geochemical data and published information, the authors interpret periodical shifts in microbial methane cycling (and consequently the archaeal community) to be associated with changes in the hydrothermal input at Lake Magadi. It is indicated that phases of low hydrothermal activity show increased microbial methane cycling as compared to phases of high hydrothermal activity.

Soda lakes are important habitats for life. Their investigation, including the microbial methane cycle over time, provides valuable information on these extreme environments and potential early Earth habitats. A detailed reconstruction of the microbial methane cycle of Lake Magadi over time does not exist so far. The findings of the study by Collins et al. are new, complement existing data, and improve our understanding of the Magadi system. The used core samples from the HSPDP are unique and represent excellent material to study archaeal communities/the microbial methane cycle of Lake Magadi over time. However, the manuscript needs to be substantially improved in some areas before publication:

1) The sampling strategy is not optimal (cf., l. 129–133). The authors focused on samples that were expected to have high total organic carbon contents (data not presented in the manuscript), which was only assessed by visual inspection (dark brown to black silty clay). The authors argue that those samples would yield the best results. This may have created a biased data set (also samples with low organic carbon contents may show a great molecular diversity). Additionally, the sampling scheme is not consistent. Between the defined intervals #1–6, several meters of core are not covered (3–15 m between single intervals), while within an interval the sampling steps are in parts as close as a few centimeters. It would be interesting to see, if microbial methane cycling was also active during the deposition of sediments with low organic carbon content.
    - **The reason that the strategy appears to not be optimal is in part a result of the relatively poor recovery of the core at ca. 55.4% (Line 126). As for the large spatial differences of 3-15 m between single intervals these are a result of areas with poorer core recovery where there was either no sample or the skipped intervals were too mineral rich or simply a brecciated material that could not be effectively sampled. We agree that a more ideal sampling strategy would be better, but it was not possible with the core that we have available.**
2) The study lacks bulk geochemical data of the samples, which would be important to contextualize the presented biomarker and isotope data (e.g., total organic and inorganic carbon contents, total sulfur content, bulk $^{13}C_{carb}$). Especially stable carbon isotope data of the carbonate phase ($\delta^{13}C_{carb}$) would improve the discussion of shifts in methane cycling (it seems that at least some samples contain carbonate, as the samples were acid-leached before $^{13}C_{org}$ analysis; l. 174–175).
    - **We agree with the reviewer, but the grant which was funding this research is no longer funded so we cannot go back and measure the total sulfur or the bulk $^{13}C_{carb}$. We have %TOC data as LOI_{500} and will include these data, but due to concerns of high temperatures (ca. 1000 C) potentially combusting the Na carbonates in the samples**

and creating lime in the furnace thus leading to potential fires, the %TIC values were not collected.

3) The presented bulk $\delta^{13}C_{org}$ data lack context. In lake systems primary production and/or terrestrial input usually govern the carbon cycle. The presented data do not allow the assessment of the role of microbial methane cycling in the lake's carbon cycle over time. It would help to present total abundances of compounds in relation to the total organic carbon content (amount per g TOC). In addition, the $^{13}C_{org}$ data should be discussed together with the leaf wax data to evaluate the influence of terrestrial input on the $^{13}C_{org}$ values. In the presented data set, only three values in interval #2 indicate methanotrophy (−48.1‰, −64.2‰, −89.4‰; Table 1), the rest of the $^{13}C_{org}$ values could also be explained by variations in primary production and/or terrestrial input.
    - **We will add a brief discussion of the major factors affecting d13org in lakes, noting that there is very little terrestrial input to Magadi through much of the record (as noted by n-alkane abundances), so that in lake processes likely dominate the overall C isotope systematics. Among in lake factors are included primary production, but also significant microbial primary and secondary production.**
4) The discussion of microbial sulfate reduction in the system (e.g., l. 366–379) is not based on a solid data set. In the current version, only $C_{17:0}$ FAME and the appearance of pyrite are used to track microbial sulfate reduction. The $C_{17:0}$ FAME, however, is not only produced by sulfate reducers and represents a weak biomarker. Furthermore, it seems that only few samples contain $C_{17:0}$ FAME, and it does not necessarily co-occur with pyrite (cf., Table 1). The authors also speculate on the sulfate availability without presenting any robust indication on sulfate levels. Without further data (e.g., sulfur content, stable sulfur isotope composition of the pyrites) this part of the discussion needs to be significantly reduced.
    - **We agree that this is overly speculative, so we plan to remove this part of the discussion from the paper. While there is a possible connection in the intervals where $C_{17:0}$ FAME and pyrite overlap, the lack of data outlined above (e.g., sulfur content, stable sulfur isotope composition of the pyrites) means that this connection to sulfate reduction is a speculative one.**
5) The interpretation of increased microbial methane cycling at times of low hydrothermal input (and vice versa) is mainly based on the correlation of MI with REE data and Ca/Na-ratio. These data sets, however, do not always match (cf., figure 4). The authors should discuss the discrepancies in more detail, and present some explanations for the major discrepancies (e.g., low Ca/Na at the end of interval #2, high Ca/Na together with low REE abundance in interval #5, high REE abundance together with low Ca/Na at the end of interval #6). The MI data set seems to be much more consistent.
    - **See answer to Reviewer #1's General Comment #3.**

More specific comments:

- The title is misleading, as the manuscript is focusing on the reconstruction of the microbial methane cycle in Lake Magadi over time, driven by archaea, and not on the reconstruction of the entire microbial community and its change over time. Please replace "microbial" in the title by "archaeal".

- **This has been changed.**

- The errors for the $\delta^{13}C_{org}$ analyses should be presented (results section and Table 1).
  - **These values have been added**

- I suggest including more details on the statistical evaluation (Fig. 5; PCA and correlation matrix) into the methods section.
  - **A new section has been added in "Materials and Methods" (2.4) to address these deficiencies.**

- Why do the authors think the fatty acids $<C_{16:0}$ are degraded in the samples? I do not see any indication why this should be the case. The compounds were likely never present or below detection limit.
  - **We agree with the reviewer and have changed the manuscript to reflect this change as there is no way for us to determine whether the FAMEs were degraded, ever produced, or simply below instrument detection limits. Additionally, *n*-alkanes and FAMEs have been removed from the manuscript. See reasoning in answers to Reviewer #1.**

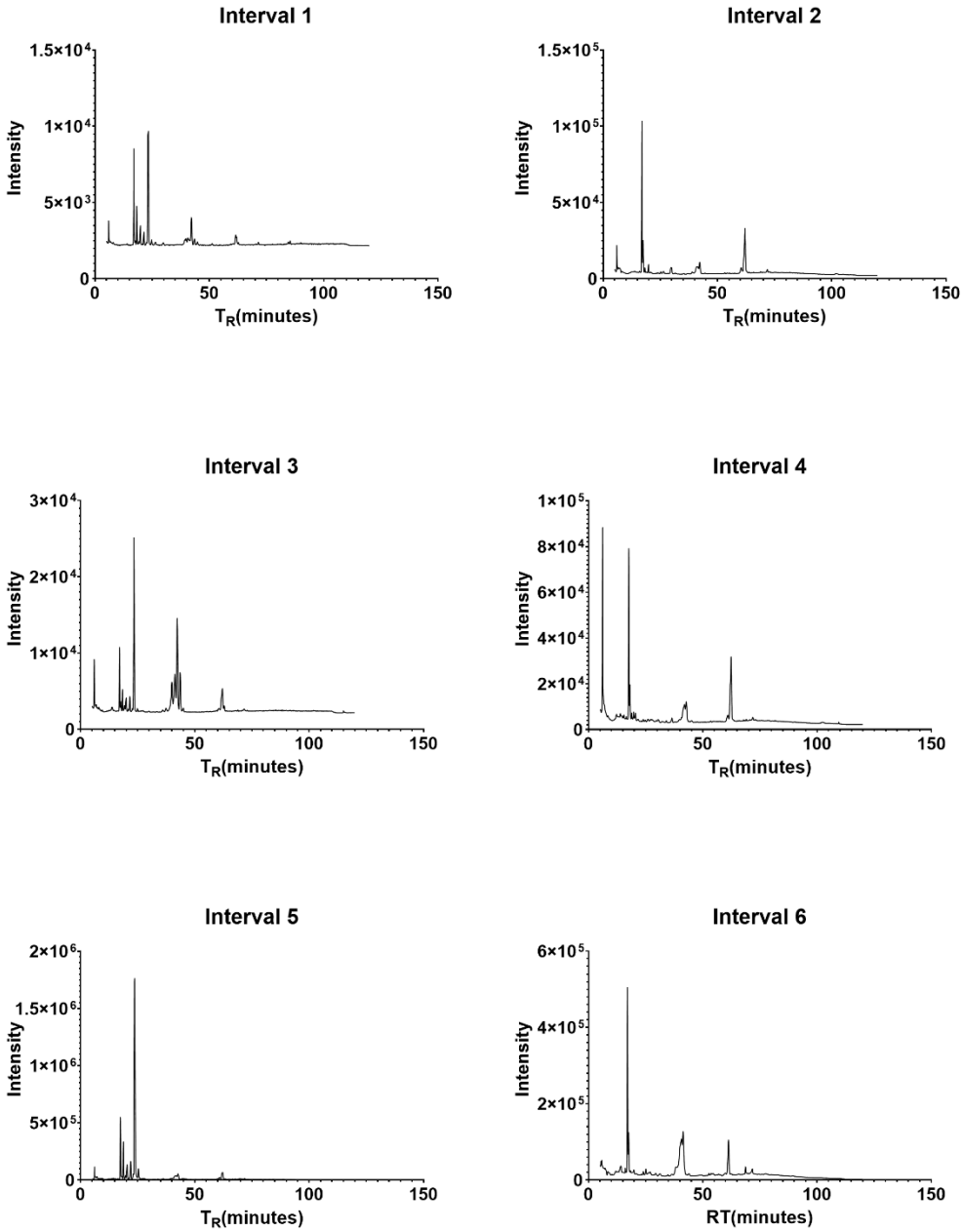
- In section 4.1.1 the authors discuss missing pyrite in some intervals and explain this by too small pyrite aggregates that could not be seen by the naked eye and/or sulfur incorporation into kerogen (l. 406–408). This is pure speculation. The authors could have easily checked the samples for small pyrite aggregates by using thin section microscopy and could have measured the total sulfur content.
  - **We agree, however, when the core was initially being described there were other items that were prioritized and now we do not have the funds to reevaluate core sections with thin section microscopy**

- The headline of section 4.2 should be changed to something like "The influence of hydrothermal activity on the microbial methane cycle".
  - **We agree and have made a change to reflect this suggestion.**

- The REE data should be discussed in more detail in section 4.2.
  - **We have expanded on the REEs in the text to better contextualize the hydrothermal inputs and how these REEs relate to those inputs.**

- Figures 3 and 4 should be turned 90° and stretched (differences e.g. in interval #1 are barely visible in the current version), with age/depth on the y-axis. It would also be important to include the stratigraphic units and different lithologies.
  - **We appreciate that the reviewers have preferences for figure orientation, but we find that the information is well-conveyed as the figures are currently. If editors insist, we can make the suggested change, but feel it is not necessary to the paper.**

- Please carefully check the color coding of the symbols in figure 6. Shouldn't the cross at ca. 67% crenarchaeol be green or is the cross incorrect? What about the triangle at ca. 6% GDGT-2 (maybe blue or incorrect symbol)?
    - **We have reviewed the values to make sure there were no errors in how we reported the data and there is one anomalous value in Interval 3 as discussed on Line 269. Otherwise, all of the data appear to be correct on the ternary plot.**
- Please add some representative GC chromatograms for each interval to the supplement.
    - **Since we have removed the *n*-alkanes and FAMEs, LC chromatograms of the GDGTs have been added; see below for representative chromatograms from each Interval outlined in the manuscript:**



Minor comments:

These will be addressed once editor approval has been granted for submitting the manuscript.

L. 30: Please list some studies that have investigated soda lake sediments/sedimentary rocks over geologic time scales here (some are already mentioned in the manuscript, incl. those from Lake Magadi).

L. 30/31: Delete space before full stop.

L. 87: Delete bracket in front of [2].

L. 92: Replace “microbial” by “archaeal” (please also do so in other relevant areas of the manuscript not mentioned here).

L. 95: The “n” of *n*-alkanes should be written in italics.

L. 117: Insert space in front of “Although”; delete comma behind “it”.

L. 188–190: Please check for correct phrasing (verb missing?).

L. 282: Please also calculate a mean value without the three outliers.

L. 324–326: Please check for correct phrasing (verb missing?).

L. 336: Replace “microbial” by “archaeal”.

L. 349: Change “biomarkers” to “a potential biomarker”.

L. 350: Change “(FAMEs) were identified” to “($C_{17:0}$ FAME) was identified”.

L. 456: What do the authors mean by the “green checkered pattern”?

L. 606: Replace “predominantly microbial inputs” by “archaeal communities”.

L. 607: Delete “archaeal”.

Figure caption of figure 6: High MI is shown in green, not yellow.

Table 1: It would be great, if the color for “MI on” periods in the table would match the color used in the figures (green).

Citation: https://doi.org/10.5194/egusphere-2024-3006-RC2