

# Referee report 1

I think the authors have done a good job improving the manuscript and it is now suitable for publication in Biogeosciences. Even though the data is based on single cores collected at various water depths I think the overall conclusions, based on all samples from all stations, holds and makes ecological sense. With both the isotope and microbiology data indicating a low contribution of methane-derived-carbon to the biomass of the studied macrofauna.

I just have a few technical minor comments that can be fixed with a quick resubmission or potentially during the proofing stage.

**Answer: We thank the anonymous referee for the positive feedback and helpful comments.**

## MINOR COMMENTS

Page 5, line 2: Clarify that DNA was pooled after library preparation.

**Answer: Thank you we have added this.**

Page 5, line 2: It would be useful to mention the sequencing setup used with the MiSeq to know the fragment length sequenced. If it is the same as Han et al (2020) it should say: paired-end 2 x 300 bp.

**Answer: Thank you we have added this missing information.**

Page 5, line 5: It would be great if it would be possible to write a few sentences summarizing the workflow of the bioinformatics done. I know this is mentioned in Han et al (2020) but considering the subheading says "Bioinformatics analyses" at least something is expected. For example at the end of line 5 there could be two new sentences: Briefly, raw sequence data was initially quality trimmed using seqtk (ref), paired-end reads merged using FLASH (ref). This was followed by a final quality filtering using prinseq (ref), and the sequences were then used to generate ZOTUs with USEARCH unoise3 using a 97% clustering identity (ref).

**Answer: Thank you for the suggestions. We have added a few more sentences as suggested.**

page 8, line 40: Why is this text Bold? It also ends with a parenthesis.

**Answer: Thank you for noticing. We had a technical issue and have fixed this now.**

page 9, line 35: "for" misspelled

**Answer: Thank you for spotting this. We corrected this.**

page 9, line 38: Why is this text Bold? It also ends with a semicolon.

page 0, line 14: Why is this text Bold? It also ends with a parenthesis.

**Answer: Thank you for spotting this. We have again fixed this.**

Table 1: The O<sub>2</sub> data is shown as a range without an explanation in the table legend. Is this duplicate samples? Or perhaps a range of values from seasonal sampling?

**Answer: Thank you for noticing. We have clarified this in the table caption. These are indeed oxygen (O<sub>2</sub>) concentrations over the time course of one year.**

Table 2: This table shows +/- values with no explanation in the table legend if this is standard deviation or standard error, also the number of replicates are not mentioned.

**Answer: Thank you for noticing. We have made the table caption more clear. These are average  $\pm$  standard deviation values for all macrofauna samples that could be matched with corresponding TOC values from the same sediment depth ( $\pm$  2cm).**

Table 3: Here it could be useful to clarify which of the tested factors were higher for each test, e.g. in the first cell it could say: \*\*\*, Oligochaetes higher, (p=0.000002).

**Answer: Thank you for pointing this out. We have changed this as suggested.**