We thank the reviewer for their helpful comments and constructive suggestions which have resulted in a much-improved manuscript overall. Below you can find our full response to each point raised.

Response to Anonymous Referee #1
Review of the Biogeosciences Discuss. Paper "Predominance of methanogens over methanotrophs contributes to high methane emissions in rewetted fens by Wen et al. The authors present high throughput sequencing and qPCR data of microbial communities of two rewetted fens in northern Germany. Next to the microbial analyses the pore water chemistry, dissolved methane and the isotopic signal of the methane C was analyzed. The paper is well written but hampers in the experimental design and some missing analyses. First of all there are no datasets or samples available which connect the rewetting treatment to a control or a pre-disturbance measurement. With pre-disturbance we can argue the existence of the drained fen performance or even the performance of the fen before drainage. So to what can the results be compared? I thought that the lateral scanning of the fens by different sampling points could explain this but actually the data is not discussed in this sense. At least at Huettelmoor the gradient goes away from the dam.

**We agree, it would indeed be nice, to have pre-rewetting data. However, there were no pre-rewetting peat samples available to compare our microbial data to. For this reason, we performed an extensive literature search comparing the published geochemical and microbial characteristics of drained versus rewetted fens to the fens in this study, and we are confident that is a valid approach for discussing post-rewetting conditions. Having pre-rewetting data to compare to is, unfortunately, very rare for temperate, restored fens; thus, we rather discuss the post-rewetting conditions of the two fens and highlight differences among drained versus rewetted fens using information that is published and available.**

The data is also not discussed to the methane fluxes of the different sampling points. For Huettelmoor they exist because there have been chamber measurements which should match quite close to the H1-4 cores if they are not exactly at the same spot. I also wonder why no potential activity measurement was performed to assess the activity of methane production and oxidation. Can this still be performed because it would give much information which is not told by the community analyses of gene copy numbers.

**You are correct our approach does not allow a detailed consideration of different sampling plots. However, our aim was not to present plot-scale interpretations but rather discuss the ongoing high methane fluxes on a larger scale. The location of available chamber measurements do not match the locations for the analysis presented here, thus we consider emissions on an ecosystem- rather than plot-level scale.**
**For this study we did not perform incubations to determine rates of production or oxidation. Methane production is indeed high for both fens and this can also be inferred from the persistently high dissolved methane concentrations we present in this study and from unpublished earlier anaerobic incubations. In more detail, incubations were performed with Zarnekow peat and these data have been added to the manuscript as supplemental information. We have added an additional author (Paul Bodelier) as he has provided us with the incubation data. The data show that besides methane production the**

**potential for efficient methane oxidation also exists. Incubations provide ideal conditions for the organisms, and thus overestimate actual *in situ* methane oxidation. Specifically, in methane oxidation incubations excess of oxygen is available for methanotrophs which opposes *in situ* conditions in both fens where methane oxidation is overprinted by other processes. Unfortunately, no methane oxidation incubation data are available for the Hütelmoor because earlier attempts to measure methane oxidation in this site have failed.**

Next I miss in the qPCR approach the measurement for Archaea. Why has this not been measured.

**In our study we were seeking for microbial controls for ongoing high emissions of methane in the two studied fens and consequently sought the ratio between methanotrophs and methanogens using qPCR. We further wanted to assess the relative contribution of both groups with regard to total bacteria and archaea and therefore performed deep sequencing using the Illumina platform. With this we could already answer our initial question. Seeking a final proof for our qPCR analysis we also quantified total bacteria with qPCR. The ratio of methanotrophs to total bacteria based on qPCR is very much in line with the sequencing results supporting the robustness of our qPCR assays. The quantification of total archaea using qPCR was thus not necessary for answering our initial questions. Finally, as the reviewer may be aware of, primer- or probe-based quantifications of total archaea targeting their 16S rRNA gene is often hampered through co-amplification of bacteria given the large sequence similarities. In summary, we refrained from qPCR data for the archaeal community since it does not add to the presentation of our major finding(s).**

In the MM section the authors should tell which depths have been sampled at each site. I can see the depths in the Figs BUT they need to be told in the MM.

**As suggested the sampling depths were added to the text in the materials and methods section in lines 161-165.**

You have also to discuss in the Ms why the depth sampling was so different between fens and within the Huettelmoor fen. Probably the fens were never mentioned to be published together otherwise the sampling would be convergent.

**As suggested, we have altered the text in lines 165-167 and 177-179 to explain why the sampling and depth resolution was different between the fens. We'd like to emphasize that the data were indeed collected with comparison of the two fens in mind. The reason for the difference in sampling depth is that previous studies from Zarnekow show that the peat stratigraphy is much less variable than the stratigraphy at the Hütelmoor. Difference in porewater sampling methods was due to accessibility and sampling difficulty: the permanent porewater dialysis samplers could not be installed at the sampling locations in the Hütelmoor.**

In the MM section I miss the sample n AND I want to point out that you have not replicated your study design. In my opinion this is a harsh critique. Taking two within replicates for DNA extraction is not the same you should have two to three adjacent lines.

**You are correct, sample n should be given. We have added the sample n to our revised manuscript in the materials and methods section in lines 159-160. With this study, our aim was not to argue for differences between the sampling points within the fens, but to seek differences and similarities among both fens. In this regard, we have four (n=4) and five replicates (n=5), respectively.**

In the Intro and Discussion it is stressed that elevated methane emissions after rewetting is dangerous. I doubt that. First the dried peatland lost a lot of CO2 due to peat degradation and the onset of methane emission after restoration is a hint that peat formation starts to accelerate again and this process fixes more C than it loses. There is scientific literature around this and you may bring this into your discussion.

**We did not intend to state that methane emissions after rewetting are "dangerous" but in the flooded peatlands we know they are elevated and also for a quite substantial duration. It was generally assumed in rewetting projects that peat methane production returns to near neutral levels within several years but flooded hypertrophic fens might behave differently. This question puzzled us for quite some time, now but the data we present here may solve a part of that puzzle in that one reason could be the disproportionately low abundance of methanotrophs compared to other microbes. We have adjusted the text in the introduction so it does not imply that methane emissions are solely a negative phenomenon but may only be temporary.**

In the MM I do not see if the rewetted Huettelmoor water table is 0.6 m above or below peat surface (line 126).

**As suggested, the text was adjusted in line 136 to indicate that water level was 0.6 m above the peat surface.**

In the Results of the MM statistical chapter I miss information of have many sequences were retrieved. How many OTUs were obtained and the bubble data is generated on and how many observations.

**For archaea, a total of 6844177 valid sequences were obtained, ranging from 60496 to 398660 in individual samples. These sequences were classified into 402 OTUs. Then the OTU table was collapsed at higher taxonomic level to generate the bubble plot. For bacteria, a total of 2586148 valid sequences were obtained, ranging from 22826 to 164916 in individual samples. These sequences were classified into 843 OTUs. Then the OTU table was collapsed at higher taxonomic level to generate the bubble plot. This information was added to the materials and methods section in lines 243-248.**

In lines 201-202 is something I do not understand. Three PCR products of the same sample were combined. OK but why. But the next sentence says PCR products of different samples were pooled...???

**The samples were pooled to reduce amplification bias. We adjusted the text in lines 220-221 so that it is clear why the samples were pooled.**

On lines 273-276 give the percentage of Methanotrophs out of the total. You tell them in the discussion. This so, because you present for Methanogens this data on line 280.

**As suggested, in our revised manuscript we added the specific methanotroph abundances to the results section in lines 296-298.**

Looking at the Figs you have no real depth separation in your measured variables at Zarnekow. WHY?

**As detailed above, we have provided an explanation for the different sampling depths and lower depth resolution in Zarnekow in the methods section. (lines 165-167 and 177-179)**

For the end; line 78-80 states wrong: there are more publications to the theme Reumer et al. 2018. Impact of peat mining, and restoration on methane turnover potentials and methane-cycling microorganisms in a northern bog. Applied and Environmental Microbiology 84, 3 e02218-17. https://doi.org/10.1128/AEM.02218-17. Putkinen et al. 2018. Recovery of methane turnover and the associated microbial communities in restored cut-away peatlands is strongly linked with increasing Sphagnum abundance. Soil Biology & Biochemistry 116: 110-119.

**Thank you for suggested citations. We have adjusted the text accordingly and added the reference to line 84.**