Response to the final editorial comments:

Dear Denise,

Thank you very much for accepting the manuscript and for your final suggestions and edits. We will go through line by line and reply and your suggestions singly.

l. 27: Thank you for the suggestion. However, we would like to keep the reference for Fig. 1, since it is hard to find good chances to point at this very broad summarizing figure. In addition, Referee #2 suggested to include more references for Fig. 1.

l. 33 and others: Thank you for this hint. We decided to change all "cDNA" to "RNA" except in the lines: 266, 267, 277 and within Fig. 4. Furthermore, we would slightly adapt the caption of Fig. 1 to:

"Figure 4: Bubble plots showing the microbial community composition and relative abundances from all sampling locations along the surface water salinity gradient (a) and the sampling location HC2 (b and c). On the y-axes the taxonomical groups on order (methanogens, methanotrophs), class (sulfate reducing bacteria (SRB)) and genus level (anaerobic methanotrophic archaea (ANME)) are displayed. The x-axes show a) the locations HC1-4 and sampling depths, where codes correspond to the following depths: 1 = 0-5, 2 = 5-20, 3 = 20-40, 4 = 40-50 cm and b) and c) the depth in cm. Coloring reflects the different microorganism groups. Circle sizes represent relative abundances (sqrt transformed) of different taxonomic groups from a, b) DNA- and c) **RNA-based** sequencing **(cDNA data derived from RNA extraction)**. Note, that groups are not adding up globally, but sum up to 100% within each group (methanogens, methanotrophs, SRB, ANME). Please, also note that preservation methods differed slightly between the studies."

l. 72 and others: Thank you for the suggestions. However, we would like to keep the domain names as lowercase.

l. 111: Thanks for paying attention to the introduction of abbreviations. Actually, SRB were introduced in line 69, so line 83 should be remain as it is. But we will remove the sulfate reducing bacteria and only leave the SRB in l. 111.

l. 154: We will delete the comma, thanks for the hint.

l. 221: Thanks, we will close the parenthesis.

l. 233: Ok, we will define ICP-OES as "inductively coupled plasma optical emission spectrometry" and insert ICP-OES into the parenthesis.

l. 255: Thank you very much for this correction. We will change the sentences to: "DNA concentrations were quantified using a Qubit 2.0 Fluorometer (ThermoFisher Scientific, Darmstadt, Germany), following the protocol of the DNA **High Sensitivity** and Broad Range Assay Kit (**dsDNA HS and BR Assay**, ThermoFisher, Berlin, Germany)."

l. 258: We will also adapt this sentence slightly to "RNA concentrations were also quantified with the Qubit 2.0 Fluorometer and the RNA **High Sensitivity** Assay Kit (**RNA HS Assay**, ThermoFisher, Berlin, Germany)."

l. 270: Thank you for the careful read. We will add the missing part and change to: 1 µl 0.1M DTT.

l. 275: Ok, yes, we will include references and add them to the reference list, as well as to the sentence: "Amplification via polymerase chain reaction (PCR) of 16S rRNA genes of DNA and cDNA samples was performed using the universal primer combination Uni515-F/ Uni806-R **(Caporaso et al., 2011)**, for both, bacteria and archaea, and primer combination S-D-Arch-0349-a-S-17/ S-D-Arch-0786-a-A-20 **(Takai and Horikoshi, 2000)** for more precise archaea detection."

l. 279: We agree that the term "backup" was misleading since it suggests redundancy of data. We had intended to say that the sequencing reads obtained with the universal primer provides support for the absolute quantification since the universal primer targets both bacteria and archaea. Therefore, the relative abundance of methanogens based on read counts can be put in context with the mcrA gene copy numbers retrieved through qPCR. We will change the wording in the manuscript to " We decided for the universal primer, because it has equal resolution for bacteria, but covers both, bacteria and archaea providing **some support for the qPCR data**."

l. 296-298: Yes, we will change the sentences accordingly to: "Whereas primers for 16S rRNA **genes** (Eub341-F/Eub534-R) target general prokaryotic microorganisms, primers used to amplify mcrA, pmoA, and drsB are specific **to genes encoding enzymes used by** methanogenic archaea (mcrA, mlas-F/mcrA-R), aerobic methanotrophic bacteria (pmoA, pmoA189-F/pmoA661-R) and **SRB** (dsrB, DsrB2060-F/DsrB4-R)."

l. 303: We will insert "gene" behind 16S rRNA.

l. 304: We will add "gene copy numbers" and delete "of concentrations".

l. 305: Would "genes" not belong behind 16S rRNA to be consisted with the other text? We will insert it as you suggested so long.

l. 306: We will insert "gene" behind 16S rRNA.

l. 307: We will use the abbreviation SRB.

l. 318: Yes, you are right, pre-processing was done on our data only. Therefore, we would like to include the sentence almost at the very end of the paragraph: "The Illumina paired-end (PE) sequences were preprocessed by the method described in Krauze et al. (2021) and Yang et al. (2021). Briefly, demultiplexing was implemented by combining mothur (version 1.39.0) (Schloss et al., 2009), BBTools (Bushnell, 2014) and a custom python script. The PE reads were processed with the 'make.contigs' function of mothur and the resultant report and groups files were parsed with a custom python script to get sequence identifiers of the good quality contigs (minimum overlap length > 25, mismatch bases <5 and without ambiguous base) for each sample. Next, PE sequences were extracted for each sample with the 'filterbyname.sh' function of BBTools. After these steps, orientation of PE sequences was corrected by 'extract_barcodes.py' function of QIIME (version 1.8) (Caporaso et al., 2010). After removing primers with awk command, the PE sequences were fed to DADA2 (Callahan et al., 2016) for filtering, dereplication, chimera check, sequence merge, and amplicon sequence variants (ASV) calling. **All sequencing reads, including those from Wen et al. (2018) and Unger et al. (2021) were merged into a common ASV file which provided the basis for all following analyses.** Taxonomic assignment was referred to SILVA138 (Quast et al., 2013) in platform QIIME2 (Bolyen et al., 2019)."

l. 330: Thank you for the hint. However, we would like to keep the heading in its original state. Also, because in addition to microbial data, pore water data and their analysis are described here (see l. 349).

p.11, below: Thank you for this valuable hint for the future. We shared this among the co-authors and will consider this method in further studies.

l. 424: We will delete "afterwards".

l. 529: We would like to change the sentence to: "Sulfate was however **not a significant variable among** the bacterial nor the archaeal communities."