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Interactive comment on "Vertical profiles of sediment methanogenic potential and communities in two plateau freshwater lakes" *by* Yuyin Yang et al.

Anonymous Referee #1

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Vertical profile of sediment methanogenic potential and communities in two plateau freshwater lakes

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The manuscript "Vertical profile of sediment methanogenic potential and communities in two plateau freshwater lakes" is comprehensive written. The aim of the study is clearly stated and well supported with data. The authors describe the methanogenic potential (MPP) of sediment incubations, quantify the archaeal and methanogenic community and analyses the community structure using NGS. They can show that the two lakes exhibit different patterns for almost all analyzed parameters and show some changes along a depth profile of 20cm. The MPP measurements would benefit from

a better time resolution and the additional measurement of the isotopic signal of the released methane. The quantification of the archaeal and methanogenic community supports in large previous findings for other lake systems. The NGS gives some new insights into the community structure. Especially NGS data for the mcrA gene are currently still scarce in the literature. In addition they contrast the sediment of two lakes and show a well resolved depth profile of the top 20cm of the respective sediment.

Specific comments: Introduction: Line 73: belonging to the archaeal... Line 74: Methanogens from seven archaeal orders

Methods: Line 110: Were the five replicate cores taken at the same location or at different spots around the lake? Line 112: What was the diameter of the columnar sediment sampler? Line 114: 14.8°C not 14.8 °C Line 130ff: Conrad et al. 2010 used a time series to estimate the methane production potential as maximal slope of the methane concentration over the time for several consecutive points. (Compare Liu et al 2016). Using endpoint values will largely underestimate the methanogenic potential since most incubations will have a lag phase in the beginning without any methane production (compare Liu et al. 2016 in your references). Likewise the time span of 28 days may be insufficient to establish the full potential of such samples at the low incubation temperatures (16°C). Line 134: a total of six sediment... Line 134: Why did you initially mix the five cores (line118) and now redistribute into six replicates? Line 145 the quality of the DNA was checked... Line 151 mcrA and archaeal 16S rRNA genes, respectively (change order!) Line 155: The range of the standards is rather small. The results for 16S rRNA are not covered! Line 168: how was the quality filtering done? Results Line 199: The hydrogenotrophic methanogenic potential is not equal to the methane production under CH_3F inhibition. CH3f partially inhibits the hydrogenotrophic methanogenesis as well; hence one has to use isotopic signals of the produced methane under both conditions together with dedicated fractionation factors to estimate the hydrogenotrophic contribution (Compare Conrad et al 201 as well as Liu et al 2016 in your referenences). Better use the term “inhibited samples” to

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describe the methanogenic potential of these samples. Line 206: between these two... (delete: in) Discussion General: You tend to discuss several depth related changes by comparing your results to previous studies. You should carefully check (and quote) the respective sampling depth. You are doing a relatively well resolved profile, while many others use deeper cores.

Line 331: rate could differ drastically between the two... Line 350: How did you calculate the contribution of hydrogenotrophic methanogenesis? See comments to line 199? I would describe this more carefully! If you e.g. use the concentration values given in Conrad et al. 2010 for lake batata in Fig 1. (2.3 vs. 0.5 kPA) you would estimate a contribution of roughly 20%; using the isotope values you reach 30-50% (Table 5). Line 357: How does the produced methane correlate with the organic carbon in your study? Line 374 Mthanogen? Line 447 Methanombacteriales (last letter is currently not italic)

References: Bastviken et al. 2009 and Conrad et al 2014: incomplete:missing pages!

Tables and Figures Fig 1: The unit is nmol/g dry weight/day. However it is unclear how you have quantified the dry weight and it is very unlikely that your estimates using only endpoint values will give a meaningful estimate of the potential. I would rather show the amount of methane produced. Fig 2b: check the x axis! It somehow has different scaling than Fig 2a. Fig 3: Fig 4: The tree has only very few reference strains incorporated. Where are the Methanocellales? (Close to OUT 10 OUT 11 I would guess??). Where is Methanobacterialles Fig 5: I am not good in statistics but you seem to feed in much more data in the 16S tree than sequences in the mcrA tree. How does that influence the tree structure? Fig4: OUT 7 and OUT 1 which have the most sequences originate from E4 and E6 respectively? Supplementary Figures: Check Order: Fig S1 is first mentioned in line 341; while Fig S2 (Line 261) and S3 (Line 293) are mentioned much earlier.

Fig S2: error bars missing. Fig S2: you find a relative high relative contribution of methanogens in the top sediment sample; in contrast the activity there is apparently

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low (Fig. 1). Likewise you find some sequences associated with Methanosarcinales; while in your NGS data (Fig S3) you do not find any Methanosarcinales? Fig S3: Give the clustername or related organisms in the figure legend (or legend) as well.

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