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Interactive comment on “Plankton-derived environmental DNA extracted from abyssal sediments preserves patterns of plankton macroecology” *by* Raphael Morard et al.

Anonymous Referee #1

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The manuscript entitled ”Plankton-derived environmental DNA extracted from abyssal sediments preserves patterns of plankton macroecology” address relevant scientific question within the scope of BG. The manuscript focuses on the identification of planktonic foraminifera from marine surface sedimentary DNA using a metabarcoding approach. The manuscript uses already available data and focuses on a data subset from data in which the entire foraminifera diversity(including benthic taxa) was analysed. The authors are specifically interested in the planktonic taxa, because this offer the opportunity to investigate imprints of the ocean surface biota and its processes of transport and deposition of planktonic eDNA to the oceans bottom.

I like the idea of the manuscript, because there are especially in the marine realm only

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Discussion paper

a few papers that focus on sedimentary DNA. Especially in deep ocean sediments it is a valid question to ask how much eDNA from planktonic organisms reaches the bottom and which is then also usable as an archive for planktonic taxa diversity changes.

As the author have specific knowledge about the planktonic taxa and a well-documented reference database, the detection of specific and rare taxa seems to be possible and valid. However, I have the feeling that the small subset of the entire data might be problematic in terms of the complete diversity of planktonic taxa. I have the feeling that the dominance of benthic taxa in their re-analysed data set is caused by the effect that DNA from benthic organisms is less degraded and is therefore preferentially amplified by PCR. By this the reads are dominated by benthic taxa, which reduces the number of planktonic sequences. I would be interested to see next to the relative proportion also the absolute number of sequence reads of benthic compare to planktonic reads. If you have strong variations between the total read numbers of the samples, this might be the reason that in some cases you detected only a very small fraction of planktonic reads, which is then not representative for the sample in terms of abundance and diversity. I think this makes it difficult to see global trends in planktonic foraminifera taxa in this dataset. Further I would suggest that the author show that the genetic marker used is equally specific to benthic as well as planktonic taxa.

Please see more comments in the pdf attached.

Please also note the supplement to this comment:
http://www.biogeosciences-discuss.net/bg-2016-486/bg-2016-486-RC1-supplement.pdf

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