

## General comments

The revised version of the manuscript, although clearer in some aspects, does not address some of the concerns. Even if the authors are convinced that the extremely different sequencing depth among samples (48 to 124,355 reads per library) does not affect their analyses and conclusions they should have made the exercise of testing such potential bias and adequately discuss the problem. This is particularly relevant considering that they are including clearly un-saturated samples (Caribbean samples). I think that the authors have to justify convincingly the inclusion of samples with such an extremely low library size (<100 reads) and clearly define which size they consider defective. I could agree that sub-sampling all the libraries to the lowest library size (once excluding those defective samples with extremely low number of reads) would imply a considerable loss of data. However, there are alternative methodologies to account for widely varying library sizes. Sequence counts can be also normalized, for example, with the *r* package *deseq2* (Love et al. 2014). This method accounts for differential sample depth and is appropriate for normalizing high-variance data sets from high-throughput sequencing.

On the other hand, the authors must discuss in more detail why the transfer of organic matter to the deep ocean and the preservation of planktonic DNA in oceanic sediments “should apply” to other taxa, as affirmed by the authors. There are some literature to this respect that they could include. For example, Capo et al (2015) showed that Cryptophyta and Haptophyta are not well preserved in lake sediments; and Boere et al (2011) discussed the possible causes behind the variation in the level of DNA preservation among diatoms and dinoflagellates in oceanic sediments. In addition, I do not believe that “there are no have no reason to believe that the transfer of organic matter from the top to the bottom of the ocean acts differently depending on taxonomic group” as stated by the authors.

## Specific comments

Figure 4. I do not see that “the Caribbean and Japan areas (red and purple) are perfectly disjoint” at the taxonomic level of morphospecies. The authors can conduct some statistical analysis to test that (e.g. PERMANOVA and ANOSIM). In addition, the separation observed based on absolute number or on Dice index mostly derives from the very different level of taxonomic saturation between Japan and Caribbean samples (figure 3), as the authors mention in the manuscript.

## References

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Love M, Anders S, Huber W (2014) Differential analysis of count data—the DESeq2 package.