

Wang et al. - Review no. 2

After revision, the manuscript of Wang et al. increased a lot in readability, most of my suggestions and the ones from reviewer 1 were included into the revised manuscript. Most formal corrections and requests have been addressed.

Still, there are details that have to be addressed, such as the sequencing statistics. This is something that is visible from the raw sequencing files and can hardly be unseen. It is not credible that the authors do not have access to these data, while stating that they did the analysis on their own. I would thus like to see the sequence quality files as part of the fastq files or the sequence raw data. In addition, I have to insist on the information of the sequencing chemistry and protocol, as there are contradicting information even on the type of sequencer between what is given in the methods part and in the NCBI sequence read archive.

Further, I still do not believe the quantification of microbes based on traces of DNA, the quantitative aspect of the metagenomics dataset is not credible based on a not representative amount of DNA, which has likely been subject to different degradation processes. How much DNA has been isolated in total?

Specific comments (track change version):

I. 102 remove second 'anhydrites', there are several repeated words down to line 128, please remove

I. 239 Rephrase: Using the `classify.seqs` command as part of the Mothur software package. Add a reference instead of a link

I. 247 replace 'in' by 'from'

I. 393 I don't see genes indicating nitrogen fixation, here

I. 455 'propose'

I. 810 ff 'A. borkumensis',... genome was deposited at the NCBI database, Bioproject...