

Interactive comment on “Microbial functional signature in the atmospheric boundary layer” by Romie Tignat-Perrier et al.

Anonymous Referee #1

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I thank the authors for their replies and would like to comment again on the qPCR issue. The authors now explain the use of gene copy numbers as cell concentrations with unproductive corrections of metagenomic data sets. For metagenomic data, this appears true, but these data are from qPCR. A more solid estimation of cell concentration could be obtained when estimates of ribosomal copy numbers for fungi and bacteria are taken into account. By using the gene copy numbers directly as cell concentrations, the authors count one gene copy as one cell. But due to the multi copy nature of ribosomal genes, these gene copy number derived cell concentrations represent false high cell concentrations. Thus, it would be better and less miss-leading to the readers to use the words "gene copy numbers" instead of "cell concentrations" in the text, if the authors cannot find estimates of gene copy numbers for ribosomal genes of fungi and

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bacteria in the literature to calculate more solid values for cell concentrations.

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