

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

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Received and published: 2 October 2020

We thank the Referee 1 for the feedbacks and we appreciate the thoughtful discussion.

We changed the text, especially we used the words “gene copy numbers” instead of “cell concentrations”. We agree that using cell concentration for qPCR gene copy number is misleading as one cell (bacterial or fungal) does not harbor one ribosomal gene copy. We could have chosen to divide the qPCR results by four if we stated that it was the average copy number of 16S rRNA gene per bacterial genome (that we think remains erroneous), yet our conclusions would not have changed as we used gene copy numbers for relative comparisons (we did not consider absolute values). We think that taking the multi copy nature of ribosomal genes (in qPCR analysis) into account

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when considering overall microbial communities composed of thousands of bacterial and fungal species remains an important issue and we welcome all suggestions.

Interactive comment on Biogeosciences Discuss., <https://doi.org/10.5194/bg-2020-236>, 2020.

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