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

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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 num-ber is misleading as one cell (bacterial or fungal) does not harbor one ribosomal genecopy. We could have chosen to divide the qPCR results by four if we stated that it wasthe average copy number of 16S rRNA gene per bacterial genome (that we think re-mains erroneous), yet our conclusions would not have changed as we used gene copynumbers for relative comparisons (we did not consider absolute values). We thinkthat taking the multi copy nature of ribosomal genes (in qPCR analysis)

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Discussion paper

into accountC1 BGDInteractivecommentPrinter-friendly versionDiscussion paperwhen considering overall microbial communities composed of thousands of bacterialand fungal species remains an important issue and we welcome all suggestions.

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