# Review of: "Compositional analysis of ruminal bacteria from ewes selected for somatic cell score and milk persistency"

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## General comments

- This study was to evaluate the associations of ruminal microbiota and its association with genetic lines selected by somatic cell score (SCS) or milk persistency (PERS), as well as milk performance. This research is interesting and meaningful. However, I am a little confused about the experimental design. Why not use the top extreme samples to do the discriminant analysis.

## The limitations and strengths.

1. Your objective and title is showing the associations between ruminal microbiota and somatic cell score (SCS) or milk persistency (PERS). However, you main finding is the correlation between ruminal microbiota and milk components. Please change the title and abstract or rearrange the experimental design.
2. You can use the 700 ruminal samples to analyzed the correlation between rumen microbiota and milk components traits. However, for the SCS and PERS, why not use the top 20 or 50 to firstly to do the discriminant analysis of SCS and PERS lines? In my opinion, the extreme grouping might help to find the representative ruminal bacteria to discriminate them.
3. Suggest use QIIME 2 to analyzed the 16S rRNA data and show the amplicon sequence variants (ASVs) not the OTU.
4. In the conclusion. You said "Although dilution of the ruminal samples by saliva could be expected, correction of the rumen microbiota for the number of sequences per sample could have reduced this effect." Did you do the correction? What is the correction data?