

Getting a paper to publication can be challenging at times and I'd like to thank the authors for making significant changes over a considerable time-frame. Overall these have improved the manuscript greatly.

My main comments for this version which need addressing:

Line 499: Bioinformatics method – in your results you have the numbers of reads and how many remained after QC. Please add to this section. A lot of reads didn't pass the QC. Mothur should tell you how many samples remain after each QC step and chimera removal please include if possible. Comment in the discussion about the high error rate and relate to the literature on the platform and other studies. I believe these primers (Caporaso) when used for salmon pick up a lot of host DNA and so have a high error rate so could you comment on the source of the read loss (ie chimeras, read length, host DNA contamination etc).

Recommended revision: Sentences in discussion discussing error rate where you already discuss low % of assigned species. More detail on QC.

I don't agree with having diversity measures to order level I think it is too high. In the previous version there was inconsistency between figures and text showing different levels so understandably choosing one level is easiest and is clearer, but for these analysis the standard is OTU-level or genus maybe family-level. For example in the results it is stated 'Alpha-diversity was similar among species and among types of samples' I'm highlighting this as I think that is likely you are just not looking deep enough and missing something interesting in your study. Unfortunately many of your reads did not assign at genus/family level. As you state only 16% of your reads were assigned taxonomically.

Recommended revision: Test alpha-diversity at OTU level.

The rarefaction results I would like to see at read-level to see the variation per group but also per sample. Especially given how many reads were removed through QC. From reading the manuscript there's no way of knowing if this is even per sample. The rarefaction at this level is crucial here. In fact you mention 'samples having 10 times the number of different orders found in other samples from the same type. Something similar was found for the samples from each species, meaning that there was high heterogeneity in samples used in this study (rarefaction curves for each species and sample type' Supplementary Figure 2)

Recommended revision: Rarefaction curve with reads after QC or OTU level per sample.

For the rest of the analysis it is fine to be at order level. The description of interesting genera in the discussion reads well.

Other comments:

Line 9: Remove 'is considered', remove sentence from partly (as you go on to say the same thing in the next sentence).

Line 334: change 'place where each individual was captured' to 'sampling location of each individual'.

Line 349: Ion torrent method – were samples pooled to equimolar concentrations? Perhaps add more brief but relevant details from the stated protocols.

Line 519: What R version?

Line 572: Keep sentence with how many OTUs found (is this 22,803?) and then how many taxonomically assigned remove the first part and put into methods as described above.

Figures:

Figure 1: I think Figure 1 and Figure 2b can go in supplements as one figure.

Recommended new figure 1a and b: A) Number of shared OTUs per sample type. I think this will be interesting as it tells us about the 84% of the community not tax assigned. Then Figure 2b) Number of shared orders per sample type.

Figure 5 should go to supplements as it is not needed. And the shark species cover parts of the plot the reader will want to see. See recommendation above for rarefaction curve.

Supplementary Figure 3: Labels on plot hard to read consider removing.

Image resolution quality may need to be improved for publication