Reviewer Report

Title: **Binning Enables Efficient Host Genome Reconstruction in Cnidarian Holobionts**

Version: **Original Submission**  Date: **4/19/2018**

Reviewer name: **Beate Slaby**

Reviewer Comments to Author:

In their manuscript „Binning Enables Efficient Host Genome Reconstruction in Cnidarian Holobionts,” Celis and colleagues describe and validate their attempt to bin the genome of the coral Porites rus from hologenomic data. To my knowledge, this is the first attempt to bin a eukaryotic genome from hologenomic data, a logical step and great advancement to this bioinformatics-focused approach to genome sequencing. Overall, the manuscript is well written and sound regarding the methodology. I only have minor comments/suggestions:

- I know that you did not aim at comparing different assembly methods. Yet, looking at the low contiguity of the assembly: did you test other assemblers? A small comparison would have been nice. But at this point, I don't think it is necessary to go back and do this, but rather include a clear statement that the results could vary/improve depending on the algorithms that perform best with the data at hand.
- Line 167: "Blastx” is in italics, "r2cat" is not.
- Table 1: Why not include the values for the other genomes (Table S2) here? It would be good to have this comparison directly in the paper and not only in the supplements.
- Figures: there is a mix-up in the attached figures. "Fig. 4" is actually again "Fig. 3b", "Fig. 5" should be "Fig. 4" and so on.

**Methods**

Are the methods appropriate to the aims of the study, are they well described, and are necessary controls included? Choose an item.

**Conclusions**

Are the conclusions adequately supported by the data shown? Choose an item.

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**Statistics**

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