

## Reviewer Report

**Title:** "Whole genome sequencing of Chinese clearhead icefish, *Protosalanx hyalocranius*"

**Version:** Revision 1      **Date:** 10/19/2016

**Reviewer name:** Christiaan Henkel

### Reviewer Comments to Author:

I thank the authors for responding to the minor issues I raised, and for their inclusion of additional evolutionary analyses. I am satisfied with their responses, however I still have a few minor suggestions:

- Regarding the genome size calculation, thank you for the clarification. As I read the formula, it is now clear that this calculation is based on a subset of the data. This is of course fine (and wise), but to avoid confusion I would suggest explicitly stating this in line 88 or 95.
- Regarding the assembly size, I think the total gap length could be included in table 1.

As for the evolutionary analyses, these are interesting and appropriate, however in both cases I suggest rephrasing the final lines summarizing the results, as these are now slightly ambiguous.

- Line 185/186: 'the close relationship between clearhead icefish and zebrafish & medaka'. Zebrafish and medaka are themselves not closely related fish species at all. Perhaps it is better to simply state that the data demonstrate the phylogenetic position of the clearhead icefish.

-Line 206: 'clearhead icefish also experienced the WGD, and it appeared more recently than medaka'. This could be read as a more recent WGD than in the case of medaka, when it is of course the same WGD (at exactly the same time).

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