#### **Reviewer Report**

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

Version: Original Submission Date: 9/14/2016

**Reviewer name:** Frederic Brunet

#### **Reviewer Comments to Author:**

The paper presented here provides efficient combination of different programs used to characterise the genome of the Chinese clear head icefish.

I only can regret that the basic results provided here are way too succinct to get a full appreciation for the reviewers and the readers, lately. As an example, we are left with an final average value for the total number of transposable elements in this genome, but we are left with no idea about the proportions of each TE subdivisions. No evolutionary values are provided. Teleost fish are known to have a extra round of whole genome duplication, this result was not searched, nor discussed. Synteny hasn't been considered as well.

The authors put forward the methods they use and they provide minimalist details of the results. Why hasn't the homology annotation done using the tilapia and platyfish?

Having in hand such a genome could have been the opportunity for more results, to enhance the interest of this publication. As an example, some phylogenetical analyses of key genes.

Minor typos: 115 Missing blank space 142 no plural at cavefish (fishes only used when an exact number is provided) 1124 missing "p" in RepBase 1128 missing "o" in MaxPeriod 1151 we emplyed GLEAN (no need of article before GLEAN)

The bibliography has a strong record of missing names (e.g. ref 19 and 39, or layout problems, like in ref. 20, 21, 23)

## **Level of Interest**

Please indicate how interesting you found the manuscript: An article of limited interest

## **Quality of Written English**

Please indicate the quality of language in the manuscript: Acceptable

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