Reviewer Report

Title: Chromosomal-level assembly of yellow catfish genome using third-generation DNA sequencing and Hi-C analysis

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Reviewer name: **Christiaan Henkel**

Reviewer Comments to Author:

This manuscript describes the assembly of the yellow catfish genome, using state-of-the-art methodology. I have a few questions/comments on the text, methodology and results, that I would ask the authors to address:

Page 2, line 12: ' genome character evaluation', I assume this refers to nucleotide identity (using Illumina sequence) as contrasted with structural assembly (using PacBio data)? Also, what were the lengths of the Illumina reads?
Page 3, line 2: I am not familiar with the Genome Puzzle Master method. Perhaps you could describe the methodology is some detail. For example, what are its assumptions when merging assemblies? Do these fit two long-read assemblies as input data? How does the method end up with a much larger (730 Mbp) assembly than either of the inputs (both around 690 Mbp)?
Page 3, line 5: plion -> Pilon
Page 3, HiC description: This section is much more detailed than the others, perhaps streamline this a bit. In the methods, I actually miss the crosslinking step?
Page 3, lines 40/55: please cite the ' previous study'/'previous reports'
Page 4, line 33: 'homologous SNP' -> homozygous SNP?
Figure 2: Please add a scale for the heatmap. Also, the assembly size used appears to be a 690 Mbp one instead of the final 730 Mbp assembly?
Figure 3: I a quite sure there are more than five teleost assemblies with contig N50s over 100 kbp. The scaffold N50 scale is, for the interesting assemblies, less of a measure of assembly quality than an illustration of chromosome length.

General comment: as a major biological interest for the use of this genome assembly is the study of sex determination, and you used a female (XY) specimen, I assume you could already identify the two sex chromosomes in the assembly (using either coverage or heteryzygosity)?

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