

Reviewer Report

Title: Draft Genome of the Protandrous Chinese Black Porgy, *Acanthopagrus schlegelii*

Version: Revision 2 **Date:** 08 Dec 2017

Reviewer name: Ingo Braasch

Reviewer Comments to Author:

The manuscript has further improved but some issues remain:

1. It is not explicitly mentioned in the text that the actinopterygian BUSCO set was used, so please revise:

I. 120: The final BUSCO score reached 89.1%, (C:89.1% [S:86.2%, D:2.9%], F:2.5%, M:8.4%, Actinopterygii gene set, n:4584).

I. 148: ... and the final BUSCO score was up to 85.5% (C:85.5% [S:82.3%, D:3.2%], F:2.8%, M:11.7%, Actinopterygii gene set, n:4584).

It would also be helpful for the readers to define C, S, D, F, and M in the main text.

2. Table 3 unfortunately remains unrevised with regard to gene orthologies. Now that the authors have performed PhyML analyses and submitted results to GigaDB in support of the genes' actual orthologies (see response to reviewers; but a reference to the GigaDB data should also be put in the main text), they finally would need to revise the table and provide individual rows for known vertebrate and teleost paralogs based on these phylogenetic trees, such as (but not limited to): *wnt4a*, *wnt4b*; *sox9a*, *sox9b*, etc. Such change of table 3 in my opinion is necessary for publication, as it will also enable the authors to confirm whether or not some of the extra copies found in the black porgy genome are derived from the teleost fish genome duplication (as currently speculated in I. 222-223).

Btw. I don't think that *oct4/pou5f1* does exist in teleosts, see publication PMID 23659605. The sequence reported is likely a different *pou5f* gene.

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