Reviewer Report

Title: Genome sequence of the barred knifejaw Oplegnathus fasciatus (Temminck & Schlegel, 1844): the first chromosome-level draft genome in the family Oplegnathidae

Version: Revision 1 **Date:** 1/7/2019

Reviewer name: Christiaan Henkel

Reviewer Comments to Author:

The authors have restructured and considerably improved the manuscript, accommodating most of my suggestions. I have some final comments, which are mostly cosmetic:
My previous comments 3/4, on the k-mer distribution - now at lines 112: this is still not very clear. I understand that the repeat content is based on fitting a model to the distribution. I do not fully agree that the peak labeled as repeated k-mers should be identified with generic repeat content, I think these are very clearly duplications (which are, of course, technically repeat content).
I would suggest to clarify the genome size calculation itself, which is now incorrect (line 112): 8.09 x10^10 / 100 = 777.5 Mb.
Line 132, 'complexity ... such as heterozygosity': This does not fit the very low heterozygosity levels just identified from the k-mer profile. Possibly structural variants instead of SNPs? I don't think the high duplication levels can explain this?
Line 162: 'filter all base sequences than 500 bp': more than 500 bp? Less than 500 bp?
There is a lot of redundancy between tables 1 & 3, I would suggest either merging these or moving the finer details of the assembly to table 3 (and keep table 1 as an overview of the final results, just N50/genome size/coverage).
Table 2 would be more appropriate in the supplementary information.

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