Reviewer Report

Title: "Genome sequence of pacific abalone (Haliotis discus hannai): the first draft genome in family Haliotidae."

Version: Original Submission **Date:** 1/15/2017

Reviewer name: Mathew Jenny

Reviewer Comments to Author:

The manuscript entitled "Genome sequence of Pacific abalone (Haliotis discus hannai): the first draft genome in family Haliotidae" by Nam et al, provides the initial results of the genome assembly for what is an ecologically and economically important molluscan species. The completion of this genome assembly and annotation will provide additional new resources that will be very valuable to the molluscan research community in general. While I believe the current state of the genome is sufficient for publication as a Data Note, I do have several suggestions for the authors to address prior to a final decision on publication,

Issues to address:

1) Citations for the references are not usually cited in the Abstract of a manuscript. I would recommend that the authors edit the Background section of the Abstract to be more general and save the specific details and citations for the main body of the manuscript.

2) On line 49, the authors state that the reads were pre-processed for bacterial sequences, duplicates and ambiguous nucleotides. I think it would be very helpful if the authors provided a little more detail on the specifics of the pre-processing, specifically with regards to the removal of likely DNA contamination since hemocyte cell isolates from hemolymph were used to generate the gDNA samples. The use of hemocytes over other tissues for the gDNA isolations could certainly contribute to significant contamination so it would be useful to know how this was specifically addressed.

3) The authors need to clarify the meaning of what they are trying to convey with the text on line 55 for a general audience. They also need to fix the typo on line 54 - an extra "f".

4) The authors misspell Crassostrea gigas both on line 69 and in Table 5.

5) The authors need to provide more details on the approach that they used to manually curate the consensus gene annotation discussed on line 81.

6) There are formatting and spacing issues for many of the tables in the pdf, although this may not be the fault of the authors and is simply a result of the pdf generator.

7) Some of the references need to be corrected. Reference #4 (Suleria et al) is listed as just accepted but it has a 2015 date. Reference #6 is not complete and contains a significant amount of

missing information. Reference #9 (Andrews) should include a link for the software program - "Reference Source, 2010" is not sufficient.

Level of Interest

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