Reviewer Report

Title: Chromosomal-level assembly of the blood clam, Scapharca (Anadara) broughtonii, using long sequence reads and Hi-C

Version: Original Submission **Date:** 3/16/2019

Reviewer name: Kevin Kocot

Reviewer Comments to Author:

This data note describes the chromosome-level assembly of the bivalve mollusc Scapharca broughtonii. This is an economically important species and this genome will represent the first from the clade Arcidae. The genome assembly appears to be very high quality and this should be useful resource. Howeer, there are a number of revisions that I feel need to be made before this manuscript is ready for publication.

The English of the manuscript is poor. In most places where there are issues, it is just awkward but in some places the meaning is not clear.

Major points:

Was the DNA / material used all from the same individual?

How were the reads filtered (line 91)?

How many cycles of Pilon were used?

What were the BUSCO results of the merged assembly before removal of redundancy with Numer?

Were other tools such as Redundans explored for redundancy reduction?

Methods used for Hi-C library preparation are inadequate.

The procedure described on lines 124-125 is not well explained. Why was this performed?

Line 157: "the results of the three approaches" - unclear which three steps are referred to.

Lines 160-161: The procedure to detect pseudogenes is not adequately described.

Availability of Data and Materials - what about the predicted transcripts and protein sequences?

Minor points:

Line 38: To my knowledge, "ark shell" is a common name used for the entire family Arcidae, not just this species.

Line 40: Correct "lived" to "lives"

Line 43: Correct "mollusk" to "molluscs"

Line 61: Correct "libraries" to "library"

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