Reviewer Report

Title: A chromosomal-level genome assembly for the giant African snail Achatina fulica

Version: Revision 1 **Date:** 6/3/2019

Reviewer name: Reuben William Nowell, Ph.D.

Reviewer Comments to Author:

Thanks to the authors for their responses to my comments. They have addressed the majority of my concerns, and I have only a few minor suggestions that might improve the ms before publication.

1. Contamination. It's good that the authors checked their raw data for contamination from non-target organisms prior to assembly. I think they should just briefly mention this fact in the main text of the manuscript, as it will increase confidence from colleagues that their data is of high quality.
2. Kmer spectra / heterozygosity. I think the authors may have tried to supply a supplementary figure here that was not attached to the revised PDF. In any case, I am content that their final assembly does not overly contain coassembled heterozygous regions. I have only a final minor comment: I would say that the kmer spectrum presented does in fact show some evidence for bimodality - look at the 'shoulder' around ~160X, at approximately 2 times the value of the main coverage peak. This is unlikely to be due to heterozygosity, as those regions would manifest as a peak around half the value of the main coverage peak - but it does suggest that there might be an excess of regions present as 2x duplications in the A. fulica genome. Something the authors may wish to investigate in the future!

Minor edits:

- Line 86: "chromosome-level genome"
- Line 86, 88, 91: typos with the name: A. chatina?
- Line 149: via kmer analysis, the genome is 2.12 Gb, but the final assembly size is considerably smaller (~1.85 Gb) - can the authors include a brief explanation for this difference?
- Line 168: in my own experience, the major error mode with pacbio data is small (usually 1-bp) deletions at both homopolymers and heterozygous sites. If these deletions hit CDS, they can result in fragmented gene models and low-quality gene annotations. They may also influence SNP calling between samples. Since heterozygosity is low, this seems unlikely to be an issue in this case, and anyway should have been corrected by the Pilon polishing with the Illumina data (which do not suffer from such errors), but I encourage the authors to check the results of Pilon to check that indeed such errors are being corrected here.

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