Reviewer Report

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

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Reviewer name: Marcela Uliano da Silva, Ph.D

Reviewer Comments to Author:

I thank the authors for the work presented on the manuscript "A chromosomal-level genome assembly for the giant African snail Achatina fulica". It is a great contribution for future studies of mollusk genomics and for the study of the molecular basis of invasiveness. I just have a few recommendations and comments.
1-) I would like to see the kmer distribution plot presented on the manuscript. It helps future researchers to understand the composition of this mollusk genome, and to plan future projects.
2-) On lines 133-137: Canu and Falcon are both good assemblers generating high quality data. After deciding to move forward with the Falcon assembly, I would like to know why the authors have decided not to run FALCON-Unzip on the assembly? The phasing of haplotypes has been shown to help avoid assembly errors in genomic areas of complex structural variation between haplotypes. Even though the further analysis (mapping quality, etc) show the assembled genome to be in good shape, it would be a good standard practice to run Falcon-Unzip before HiC scaffolding.
3-) After Lanchesis, around 1000 contigs were not placed into chromosomes. Have you investigated the composition of such contigs? Can you present also the size distribution of them?
4-) The sequencing of the transcriptome with IsoSeq technology was only briefly mentioned. Could you describe the evaluation of such transcripts in a few lines? For example, was it possible to find full-length transcripts sequenced?
5-) Finally, just a last read to review the English would be advised. Two examples of misspelling: The tittle on line 409. And 'fro' on line 223.

Level of Interest

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