

## Reviewer Report

**Title: Improved de novo genome assembly and analysis of the Chinese cucurbit *Siraitia grosvenorii*, also known as monk fruit or luo-han-guo**

**Version: Original Submission**    **Date: 1/9/2018**

**Reviewer name: Aleksey Zimin**

### Reviewer Comments to Author:

This is a nicely written data note about an important genome. MAJOR COMMENTS I would like these comments addressed before the paper is accepted for publication. 1. The English must be improved, especially singular/plural verbs such as in this sentence on line 112: "...the alignment files WAS manipulated...". I suggest that the authors ask a native English speaker to proof-read the paper. 2. I have a few concerns about the experimental design and methods. First, quality of the assembled consensus was evaluated by mapping Illumina RNAseq reads to the consensus. Naturally only reads containing few differences would map, yielding a biased consensus quality measurement. The real consensus quality is likely lower than the authors estimated. Instead I suggest estimating the consensus quality of the assembly by mapping the assembly to the contigs from the previous Illumina-only based assembly and evaluating the fidelity of long (10Kb+) mutual best matches. 3. I would like also to see how BUSCO results improved compared to initial Illumina-only assembly. MINOR COMMENTS/SUGGESTIONS Authors do not have to satisfy these comments for publication -- these are merely suggestions. One other reason I am concerned about the consensus quality is that the genome is not inbred, and 73x total PacBio coverage (which works out to about 37x per haplotype) may not be enough to generate high enough consensus quality in regions of high heterozygosity from PacBio -only data. I would recommend getting some 60-100x whole genome Illumina data for the same sample and polishing the assembly with Pilon. Also for the same reason using only 25x of the corrected reads may not be optimal -- I suspect assembly contiguity could be better if 35 or 40x of the longest corrected reads are used.

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Please indicate the quality of language in the manuscript: Needs some language corrections before being published

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