

## 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: Revision 1 Date:** 4/6/2018

**Reviewer name: Aleksey Zimin**

### Reviewer Comments to Author:

Thank you for the revisions. One further comment that is have is that since the Illumina-only assembly could not be obtained, you could assemble your Illumina Paired end reads yourself with MaSuRCA or SOAPdenovo2 and use big contigs from the assembly (>10000bp) to measure the consensus quality of your genome. Illumina-only assemblies are fast and relatively easy to produce.

### Level of Interest

Please indicate how interesting you found the manuscript: An article of importance in its field

### Quality of Written English

Please indicate the quality of language in the manuscript: Acceptable

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