Reviewer Report

Title: Chromosome-scale genome assembly of kiwifruit Actinidia eriantha with single-molecule sequencing and chromatin conformation capture

Version: Original Submission **Date:** 10/16/2018

Reviewer name: Jian-Feng Mao, Ph.D.

Reviewer Comments to Author:

This manuscript provides a high-quality chromosome-scale genome assembly and related resources for an important kiwifruit species. We saw significant improvement in the continuity of genome assembly reported over the previous ones. The genome assembly and related resources will be valuable for kiwifruit breeding and fruti science studies.
The manuscript is generally in good quality, and could be accepted after revision.
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Comments
1. A general process was reported for genome assembly, quality assessment, annotation and comparision, while details lost, such as settings, important parameters used for a specific software. More information is needed for the whole analytical process described. The availability of the full analytical pipeline is like a rule required by GigaScience, I think.
2. Genome estimatiion on K-mer size is lacking. Other than assembly, K-mer distribution provide another set of information, from which genome size, redundancy, heterozygosity, sequencing error rate could be derived independently to assembly. Please add this.
3. Details are lacking for Evolutionary and comparative analysis. How did you generate a phylogenetic tree? What (software, algorithm, data) you used to generated this tree? How many genes? How did you get those genes? How did you do molecular dating? Divergence time (> 200 mya) seems inconsistency to generally reported divergence time (around 120 mya) for monocots and dicots. It would be better to share the gene alignment used for phylogenetic reconstruction and the generated tree as supplementary files.
4. Citation to published papers or online databases and tools, is lacking for some instances, such as, citations to publised genomes are needed in Table 1. The NCBI nr protein database, TAIR, Swiss-Prot and TrEMBL, PANTHER, Pfam, SMART, and PROSITE databases, they all need citations in a proper way. Please also check supplementary tables, for citation and footnote. Full names are needed to be affiliated with abbreviates, such as SINEs, LINEs, LTRs et al., in the supplementary tables.
5. Page 9, lines 47-48. "In addition, variations between the two kiwifruit species could also contribute to this difference." "variation" may not be the good word. It is better to use "divergence" to describe the genetic difference among species. Please improve it. I am not native speaker, I am open for different tendency/ideas.
6. How did you generate mapping for genomic and RNA-seq data, when you did "Evaluation of the genome assembly"? "high mapping rates, ranging from 98.6% to 98.8%, and the properly paired read mapping rates were between 76.9% and 90.4%." these ranges are not exact enough for detailed

examination. The exact values could be presented in the supplementary tables, such as Table S1, and discussed specifically. Also, it would be interesting to present all the details on the inconsistence revealed by mapping of mate-paired reads to the assembly, in addition to simply the mapping rate values.
7. Personally, I would like to know whether the authors could set out to present the functional annotation of Vitamin C biosynthesis pathway or mineral processing pathway, given the pathways are important for kiwifruit community and fruit science. Comparsion among kiwifruit species on genetic composition of such pathways may also interest broader range of readers.
8. The absence of consecutive line numbers is making harder this review process. Please improved it in the revised version.

Level of Interest

Please indicate how interesting you found the manuscript: Choose an item.

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