

## Reviewer Report

**Title:** A high-quality chromosomal genome assembly of *Diospyros oleifera*

**Version:** Revision 1      **Date:** 9/26/2019

**Reviewer name:** Manuel Spannagl

### Reviewer Comments to Author:

The authors complemented their study with a number of comparative genome analyses which indeed provide some, but limited novel biological insights.

Some points from the first review round should be addressed or at least there should be some explanation why these issues are not relevant:

- 1.) transcriptome data: I appreciate the addition of the paragraph on extraction, library construction and sequencing but I still wonder why these data are not used in the analysis, eg. to establish transcription levels for gene or gene families of interest. It seems that the data may be of good quality, multiple tissues etc but there is no statistics or data description anywhere. Will/is the transcriptome data deposited in some public archive?
- 2.) Phylogeny: how about the bias possibly introduced by just picking the single copy orthologs for the construction of the phylogenetic tree? This set is just a very small subset of the full gene content. To me lines 260/261, and thus construction of the phylogeny, are largely unclear.
- 3.) Gene families: I'm not sure whether there is any biological conclusion on the genes and enrichments that were identified as *D.oleifera* specific? Can the terms be related to any biological features?
- 4.) Expansion/Contraction: what parameters were used for CAF $\tilde{\%}$ ? CHS expansion results should be outlined in the text. What does "different degrees of expansion" mean? An obvious additional and worthwhile analysis would be check expanded/contracted gene families for their expression patterns. What is the conclusion of LAC gene family contraction?
- 5.) Positively selected genes: I'm really not sure about the significance of this analysis. Are the terms identified somewhat related to any biological features?
- 6.) Please check the formats and structure of your files provided. Testing the GFF files with Gff3Validator results in an error for example: "gt gff3validator Dol.gff3" gt gff3validator: error: child on line 44626 in file Dol.gff3" has "different sequence id than its parent on line 44625 ('Chr4' vs. "fragScaff\_scaffold\_95:::fragment\_2:::debris")
- 7.) Especially the newly added text needs significant improvement in language and grammar.

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### Quality of Written English

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