

Reviewer Report

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

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Reviewer name: Robert VanBuren

Reviewer Comments to Author:

Suo et al report a chromosome scale assembly of *D. oleifera*, a diploid relative of hexaploid persimmon. They used a combination of Illumina, 10x, PacBio, and HiC to generate the chromosome scale assembly *D. oleifera*. The inclusion of high coverage Illumina data and scaffolding with 10x likely ensured that most of the residual indels from the PacBio only assembly were corrected. The HiC contact map in Figure 2 has no obvious inversions or misplacements, suggesting the genome is well assembled. This resource will be useful for the comparative genomics and persimmon research communities. I have a few minor concerns that should be addressed before this manuscript is published.

1. The estimated heterozygosity of *D. oleifera* is quite high (1.1%) and this would have likely resulted in assembly issues related to haplotype specific contigs. How many primary and alternate contigs were assembled by FALCON?

2. Akagi et al. (<https://www.biorxiv.org/content/early/2019/05/05/628537.full.pdf>) report a chromosome scale assembly of diploid persimmon (*D. lotus*). The authors could cite this preprint in their manuscript and if the genome is publicly available, survey macrosynteny.

3. The identification of homologs of sex determination genes from kiwi and *D. lotus* is not informative, as the kiwi sex determination system is likely completely different from *D. oleifera* and sex chromosomes may have an independent origin in *D. lotus* and *D. oleifera*. It is fine to leave this in the paper, but the statement that candidate sex determination genes were identified should be removed from the abstract

4. The identification of a WGD event in *D. oleifera* is interesting, and figure S2 could probably be moved to the main text. Based on this figure, it looks like there could have been two WGD events in *D. oleifera*.

Minor

Page 6, line 152. homologous should not be use here

Versions are provided or most but not all bioinformatics software. Where appropriate, versions should be added.

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