

Reviewer Report

Title: Accurate assembly of the olive baboon (*Papio anubis*) genome using long-read and Hi-C data

Version: Original Submission **Date:** 3/15/2020

Reviewer name: Xiao-Guang Qi

Reviewer Comments to Author:

This manuscript reports a new whole genome assembly for a significantly useful nonhuman primate species, *Papio anubis*. Overall, the manuscript is clear to follow. Some questions may be helpful to improve the manuscript.

Reference style is not identical, examinations are needed.

Both package versions and parameter settings of the software used should be given.

In my view, during the assembly process, the Nanopore long-reads should be polished by Illumina paired-end reads firstly.

The figure legend of the Hi-C heatmap need to be improved, some details are missing.

I can not understand the meaning of the Fig.3. What is the reader supposed to conclude from the figure?

The genome completeness assesment shows that the completeness of Panu_3.0 is better than that of Panubis1.0 (93.4% Vs 93%), please explaine this.

It would be good for the authors to explain how they have addressed the main problem with the HiC for the accurate orientation of the inversions within the scaffolds.

Level of Interest

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

Quality of Written English

Please indicate the quality of language in the manuscript: Choose an item.

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