

Reviewer Report

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

Version: Revision 1 **Date:** 8/15/2020

Reviewer name: Xiao-Guang Qi

Reviewer Comments to Author:

The description of the repeats is still very simple. Despite that total length of repeats by RepeatMasker are present in supplementary figure, this is not enough. Much details are missing, do they perform this based on homology or de novo? maybe both. From their results, the repeats for Panubis1.0 is not higher even lower than Panu_3.0. This is strange, please make some new efforts to provide more evidences. I do not know if the de novo method will work but the authors should try it.

The authors used the Euarchontoglires gene set instead of the broader Mammalia gene set provided by BUSCO. However, the result is not very good. At least, no new evidence to show the high quality of their genome. I do not know if this are related with their assembly strategy. I am wondering if the 15x ONT coverage could be used for assembly directly, it is hard to estimate from the sequence coverage. But the authors should think about this carefully and some more work needed to be done to fix this problem.

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