Reviewer Report

Title: An integrated chromosome-scale genome assembly of the Masai Giraffe (Giraffa camelopardalis tippelskirchi)

Version: Original Submission **Date:** 4/1/2019

Reviewer name: Derek Bickhart

Reviewer Comments to Author:

Summary: In this manuscript, Farre et al. detail the generation of a new reference for the Masai Giraffe using a combination of short read sequence data, Dovetail Hi-C and reference-guided scaffold correction. The assembly statistics, as presented, show higher degrees of scaffold continuity and BUSCO completeness than the previous Giraffe reference. It's highly likely that this assembly will be of use to the community and that Giraffe represents an interesting leaf in the Artiodactyla clade. Still, I found several areas where the manuscript did not provide enough context or details on the analysis.
Pg 5 Line 23: The details of the PCR chimera check need further fleshing out. Did the authors use genomic DNA as the template or sequencing libraries? Since not all SF joint boundaries were tested via PCR amplification, it would be helpful to supply a supplementary table showing which boundaries were tested. Finally, how was the 158X physical coverage threshold determined?
Pg 7 Line 32: The fragmentary X chromosome assembly is only mentioned in the abstract but it represents a major limitation of this assembly version. A reason why this chromosome was not successfully scaffolded should be listed here or in the previous sections.
Table1: The listed assembly lengths vary considerably. It would be helpful to list the percentages of gap sequence in each assembly iteration.
Figure3: If one were to believe the BUSCO scores, the original assembly scaffolds (SOAPdenovo) were the "most complete" version of the assembly and subsequent scaffolding actually removed single copy genes from the assembly. This is a known issue with BUSCO evaluation, but it deserves mentioning in the results and discussion. Confirming that BUSCO single copy genes were deleted by RACA or Chicago edits would be important to report.
References: Citations to the manuscripts that accompanied the release of the cattle and goat reference genomes are missing.

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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