Reviewer Report

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

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Reviewer name: Jane Loveland

Reviewer Comments to Author:

The paper sets out to give a chromosome-scale assembly for the Masai giraffe, which is achieved. The results presented give a de novo assembly and chromosomal analyses.
I have a few general comments and specific queries.
1. It would have been great to draw out a few unique observations about the genes specifically referring to giraffe.
The abstract mentions "many missing fragments and fragmented genes" when introducing the previously published giraffe genome. Which were these fragmented genes and have they been improved?
No comparison with previous genome apart from BUSCO numbers. Which areas were improved the most? Is everything else the same?
Which genes were missing before? Are they in repeat regions? Are they any of the adaptation genes mentioned in the previous assembly paper?
2. I would have liked a summary figure of all of the chromosomes, as the data provided does not give this.
3. Data analyses: Why hg19 and not GRCh38?
Genome annotation: Ensembl 64 used. Very old, almost 10 years old. Ens 64 is no longer supported in the browser. For GRCh37 why not use Ens 75?
Which version of SwissProt was used of the analysis?
4. Figure 3: I'd like a better legend explaining this. It's not very clear.
5. Supp table 5: There are a few errors in this table.
Mean exon per gene. I am assuming this is an error as the numbers are in thousands of exons per gene?
CDS is in bp. Shouldn't that be in amino acids as it refers to protein?
"Final" row at end of table. Not clear why this number is or how it was derived.

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