

## Reviewer Report

**Title: Cost-effective assembly of the African wild dog genome using linked reads.**

**Version: Original Submission**    **Date: 1/31/2018**

**Reviewer name: Andreas Chavez**

### Reviewer Comments to Author:

Manuscript Number: GIGA-D-17-00324

Title: Entering the era of conservation genomics: Cost-effective assembly of the African wild dog genome using linked reads.

Summary: The study reports a de novo genome assembly for the African Wild Dog and demonstrates a cost-effective approach for generating high-quality assemblies. Genome assemblies have been prohibitively expensive and labor-intensive for researchers focused on non-model organisms, particularly organisms with large genomes. This can be problematic for conservation geneticists that are trying to understand key genetic aspects of endangered taxa, such as their demographic history, inbreeding, and adaptive genetic variation, to name a few. This study demonstrated that high-quality reference genomes using 10X Genomics libraries and standard Illumina sequencing can be generated for around \$3,000 for an organism with a relatively large genomes (~2.5GB).

Major Essential Revision: I have not identified any major revisions that are needed for this manuscript.

Discretionary Revision: Perhaps it would be useful to run a PSMC-type analysis using multiple wild dog genomes to assess trends in historical population sizes in recent times for African wild dogs. This might produce useful results with conservation applications. There are several methods that have come out recently that can do a decent job with estimating population size in recent times.

Schiffels, S. and Durbin, R., 2014. Inferring human population size and separation history from multiple genome sequences. *Nature genetics*, 46(8), p.919.

Paul, J.S., Steinrücken, M. & Song, Y.S. An accurate sequentially Markov conditional sampling distribution for the coalescent with recombination. *Genetics* 187, 1115-1128 (2011).

Sheehan, S., Harris, K. & Song, Y.S. Estimating variable effective population sizes from multiple genomes: a sequentially Markov conditional sampling distribution approach. *Genetics*

194, 647-662 (2013).

Steinrücken, M., Paul, J.S. & Song, Y.S. A sequentially Markov conditional sampling distribution for structured populations with migration and recombination. *Theor. Popul. Biol.* 87, 51-61 (2013).

Edit: Line 444. The word "Heterozygosity" at the end of the paragraph seems out of place.

Recommendations: This study will be very valuable for researchers studying non-model organisms who are interested cost-effective approaches for genome assembly. The manuscript is also very well written and organized.

### **Methods**

Are the methods appropriate to the aims of the study, are they well described, and are necessary controls included? Yes

### **Conclusions**

Are the conclusions adequately supported by the data shown? Yes

### **Reporting Standards**

Does the manuscript adhere to the journal's guidelines on [minimum standards of reporting?](#) Yes

Choose an item.

### **Statistics**

Are you able to assess all statistics in the manuscript, including the appropriateness of statistical tests used? Yes, and I have assessed the statistics in my report.

### **Quality of Written English**

Please indicate the quality of language in the manuscript: Acceptable

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