Reviewer Report

Title: An improved ovine reference genome assembly to facilitate in depth functional annotation of the sheep genome

Version: Original Submission **Date:** 8/30/2021

Reviewer name: Aaron Shafer

Reviewer Comments to Author:

My comments are minimal as the paper is succint. The authors present an improved genome, largely in the form of contiguity, and provide a number of statistics to support their argument. There are literally dozens upon dozens of different wayts to assemble and polish a genome and I see no value in suggesting changes in this regard as the approach more-or-less reflects the state-of-the-art. I also might question the description of "substantial improvement" as this really reflects the improvement in contiguity and less so the BUSCO, annotation. Also, scaffold L50 of the two available genomes is quite good, but not reported in Table 1, which I would suggest. The other Oar reference genomes were published 4 and 6 years ago, with this study offering the addition of nanopore sequence.
Minor
L55 - long read vs long sequence? Do you mean contigs or scaffolds?
L233- does freebayes do polishing? This is what is suggested by the current wording

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