Reviewer Report

Title: Chromosome-scale assembly comparison of the Korean Reference Genome KOREF from PromethION and PacBio with Hi-C mapping information

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Reviewer name: Brock Peters, Ph.D.

Reviewer Comments to Author:

Kim et al. generated multiple de novo assemblies of the Korean Reference Genome KOREF using nanopore and PacBio sequence data. These assemblies were polished with available short read data and further scaffolded with HiC data. These should be useful assemblies for the scientific community. All the data appears proper. I have a few issues that I think need to be resolved below:

1. Page 9, 7-16 talks about scaffold N50s, those same N50 lengths are referred to as contigs in the abstract. Which is it scaffolds or contigs? These two things are not the same.
2. Table 2 and Figure 1. Scaffolds and contigs are mixed here again. Why? This is confusing. These two things should be separated, they aren't the same. Perhaps with nanopore/Pacbio data only there's no difference between contig and scaffold length. However, the addition of HiC data would be expected to increase scaffold length but have little effect on contig length.

Minor/interesting analyses:

Perhaps you are already doing this for another manuscript, but I think it would be interesting to compare between the different assemblies to see what regions are present/missing in nanopore versus PacBio.

Was diploid assembly possible?

If you try to call variants off of this assembly how well does it perform, perhaps since it's not diploid this won't work well.

Level of Interest

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Quality of Written English

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