Reviewer Report

Title: Assessment of human diploid genome assembly with 10x Linked-Reads data

Version: Revision 1 **Date:** 10/17/2019

Reviewer name: Tobias Marschall

Reviewer Comments to Author:

The authors improved the manuscript substantially and implemented many of the suggested changes. I wonder, however, whether there was a mixup of document versions because not all changes described in the response are reflected in the manuscript (including trivial ones like fixing the "_Alignment", now in line 283; also Luo et al. is still not cited). Maybe the authors can double check that they indeed uploaded the latest version?
Beyond that, the only concern left for me is the poor concordance of small variant calls. For the Illumina and 10x calls, my guess is that they went into the evaluation completely unfiltered, where FreeBayes (and the LongRanger pipeline which is based on FreeBayes) usually attain an acceptable precision only when the calls are filtered (e.g. for QUAL>=10). Much more concerning is the observation that between a quarter and half of all calls are missed by the assembly strategy. How did the authors call variants from the assemblies? Given that the GIAB benchmark regions are (comparatively) easy genomic regions, I think that the authors should offer an explanation for the poor recall.

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