

Reviewer Report

Title: "A reference human genome dataset of the BGISEQ-500 sequencer"

Version: Original Submission **Date:** 10/11/2016

Reviewer name: Justin Zook

Reviewer Comments to Author:

The authors present a useful public dataset from a new sequencing instrument. As far as I know, this is the first public dataset from the BGISEQ-500, so it's very useful to make this available. I recommend publication if more details about the methods are given, such as those below:

1. Please give version of all tools and exact parameters used in analysis pipeline. Was GATK unifiedgenotyper or haplotypcaller used?
2. What version of high-confidence calls from GIAB was used? The authors may want to use the most recent version available at ftp://ftp-trace.ncbi.nlm.nih.gov/giab/ftp/release/NA12878_HG001/latest/
3. Would it be possible to stratify the false positives and negatives by genome context to better understand the strengths and weaknesses? For example, the authors could use bed files at <https://github.com/ga4gh/benchmarking-tools/tree/master/resources/stratification-bed-files>
4. Could the authors label the Venn diagrams in the figure with the originating callsets to make it easier to interpret?

Level of Interest

Please indicate how interesting you found the manuscript: An article of importance in its field

Quality of Written English

Please indicate the quality of language in the manuscript: Acceptable

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