Reviewer Report

Title: Comparative analysis of seven short-read sequencing platforms using the Korean Reference Genome: MGI and Illumina sequencing benchmark for whole-genome sequencing

Version: Original Submission **Date:** 6/4/2020

Reviewer name: Inge Seim

Reviewer Comments to Author:

The authors compare various short-insert, short-read whole-genome sequencing platforms used by academic researchers and clinical scientists.
My minor comments and suggestions are:
â— As stated by the authors, Illumina platforms are indeed now considered 'historical.' However, many Illumina sequencers are still heavily used - in particular in pathology labs. This manuscript may prove very useful when arguing for an instrument upgrade in such a setting.
â— You may like to comment on single tube long fragment read (stLFR), which enables the sequencing of long transcripts by sequencing bar-coded reads on the BGISEQ-500 platform [and, thus, probably also MGISEQ-T7) (10.1101/gr.245126.118). This technology is relatively cheap and is likely to decrease in cost - another argument for the adaption of MGI platforms in the laboratory.
â— You may want to comment on Illumina library kits. It is possible that revisions [in the five-six years since the data in your study were generated] to these kits could improve the sequencing results (e.g., see 10.1371/journal.pone.0113501). I realize the effect may be minor, but it may nevertheless be useful to remind the reader about the potential for *slightly* better raw read statistics.

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