

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: 5/29/2020**

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Reviewer Comments to Author:

The submitted study has characterized sequencing quality, uniformity of coverage, %GC coverage, and variant accuracy of seven sequencing platforms. They found that MGI platforms showed a higher concordance rate of SNP genotyping than HiSeq series. The study is of interest to genomics and sequencing technologies areas. Two concerns must be addressed prior to acceptance.

- 1)The author defined low-quality reads as those that had more than 30% of bases with a sequencing quality score lower than 20. I am wondering whether the results is stable once the definition changed ?
- 2)It looks the author ignored a highest duplicate ratio was found in MGISEQ-T7. More discussion and analysis should be preformed to make this clear. The author claimed that duplicates and adapter contamination may be more affected by the process of sample preparation than by the sequencing instrument. However, again, no evidence was provided.

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