

Methodology | [Open Access](#) | Published: 13 August 2018

Comparative performance of the BGISEQ-500 and Illumina HiSeq4000 sequencing platforms for transcriptome analysis in plants

Fu-Yuan Zhu, Mo-Xian Chen, Neng-Hui Ye, Wang-Min Qiao, Bei Gao, Wai-Ki Law, Yuan Tian, Dong Zhang, Di Zhang, Tie-Yuan Liu, Qi-Juan Hu, Yun-Ying Cao, Ze-Zhuo Su, Jianhua Zhang  & Ying-Gao Liu 

Plant Methods 14, Article number 14 (2018) | [6143](#) Accesses | [9](#) Citations

Abstract

Background

The next-generation sequencing (NGS) technologies have revolutionized transcriptomic studies, enabling genome-wide transcriptome analysis.

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Abstract

Background

Results

- The present case study provides a comprehensive reference dataset to validate the capability of BGISEQ-500 enabling it to be established as a competitive and reliable platform in plant transcriptome analysis.

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Gigascience. 2017 Aug 1;6(8):1-13. doi: 10.1093/gigascience/gix049.

Comparative performance of the BGISEQ-500 vs Illumina HiSeq2500 sequencing platforms for palaeogenomic sequencing.

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• *Although we acknowledge that our analyses were limited to animal material, our observations suggest that **the BGISEQ-500 holds the potential to represent a valid and potentially valuable alternative platform** for palaeogenomic data generation that is worthy of future exploration by those interested in the sequencing and analysis of degraded DNA.*

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Comparative performance of the BGI and Illumina sequencing technology for single-cell RNA-sequencing

Posted February 24, 2019.

Anne Senabouth, Stacey Andersen, Qianyu Shi, Lei Shi, Feng Jiang, Wenwei Zhang, Kris Maciej Daniszewski, Samuel W Lukowski, Sandy SC Hung, Quan Nguyen, Lynn Fink, Ant Alice Pébay, Alex W Hewitt, Joseph E Powell

doi: <https://doi.org/10.1101/552588>

This article is a preprint and has not been certified by peer review [what does this mean?].

Abstract Full Text Info/History Metrics 

Abstract

The libraries generated by high-throughput single cell RNA-sequencing platforms such as Chromium from 10x Genomics require considerable amounts of sequencing, typically at the large number of cells. The ability to use this data to address biological questions is impacted by the quality of the sequence data. Here we have compared the performance of Illumina NextSeq 500 and NovaSeq 6000 against the BGI MGISEQ-2000 platform using identical Single Cell 3' libraries consisting of over 70,000 cells. Our results demonstrate highly comparable performance between the NovaSeq 6000 and MGISEQ-2000 in sequencing quality, and cell, UMI, and gene detection. However, compared with the NextSeq 500, the MGISEQ-2000 platform performs consistently better, identifying more cells, genes, and equalised read depth. We were able to call an additional 1,065,659 SNPs from sequence data generated by the BGI platform, enabling an additional 14% of cells to be assigned to the correct donor from a multiplexed library. However, both the NextSeq 500 and MGISEQ-2000 detected similar frequencies of gRNAs from a pooled CRISPR single cell screen. Our study provides a benchmark for high capacity sequencing platforms applied to high-throughput single cell RNA-seq libraries.

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- Our results demonstrate a highly comparable performance between the NovaSeq 6000 and MGISEQ-2000 in sequencing quality, and cell, UMI, and gene detection. However, compared with the NextSeq 500, the **MGISEQ-2000 platform performs consistently better**, identifying more cells, genes, and UMIs at equalised read depth. We were able to call an additional 1,065,659 SNPs from sequence data generated by the BGI platform, enabling an additional 14% of cells to be assigned to the correct donor from a multiplexed library. However, both the NextSeq 500 and MGISEQ-2000 detected similar frequencies of gRNAs from a pooled CRISPR single cell screen. Our study provides a benchmark for high capacity sequencing platforms applied to high-throughput single cell RNA-seq libraries.

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[https://www.researchgate.net/publication/331163782 Comparative performance of the BGI and Illumina sequencing technology for single-cell RNA-sequencing](https://www.researchgate.net/publication/331163782_Comparative_performance_of_the_BGI_and_Illumina_sequencing_technology_for_single-cell_RNA-sequencing)

Short Report | [Open Access](#) | Published: 09 April 2019

Comparative analysis of sequencing technologies for single-cell transcriptomics

[Kedar Nath Natarajan](#) , [Zhichao Miao](#), [Miaomiao Jiang](#), [Xiaoyun Huang](#), [Hongpo Zhou](#), [Jiarui Xie](#), [Chunqing Wang](#), [Shishang Qin](#), [Zhikun Zhao](#), [Liang Wu](#), [Naibo Yang](#), [Bo Li](#), [Yong Hou](#), [Shiping Liu](#)  & [Sarah A. Teichmann](#) 

Genome Biology 20, Article number: 70 (2019) | [Cite this article](#)

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Abstract

Single-cell RNA-seq technologies require library preparation prior to sequencing. Here, we present the first report to compare the cheaper BGISEQ-500 platform with the Illumina HiSeq platform.

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Abstract

Background

Results

- **New Study shows BGI's DNBseq™ Technology Platform has Comparable Sensitivity and Accuracy to Illumina HiSeq platform, at a Lower Cost.**

Source (click for full paper): <https://genomebiology.biomedcentral.com/articles/10.1186/s13059-019-1676-5>

Advantages and disadvantages between microarray and RNA-seq

Microarray	RNA-seq
<p>Advantages</p> <ul style="list-style-type: none">• Well-defined protocols for hybridization• Well-defined analysis pipelines• Standardised approaches for data submission• Relatively low cost <p>Disadvantages</p> <ul style="list-style-type: none">• Analysis only for pre-defined sequences• Dynamic range limited by scanner• Relies on hybridisation• Hybridisation potentially non-specific• Might not give paralogue information• High variance for low expressed genes• Will generally not identify splice variants	<p>Advantages</p> <ul style="list-style-type: none">• Not reliant on previous sequence information• High dynamic range (no saturation)• Direct sequence alignment, no hybridization• Alternative splicing detected if aligned to genome• Paralogous genes can be defined• Can be used for SNP identification <p>Disadvantages</p> <ul style="list-style-type: none">• Protocols still not fully optimised• High cost (but continually reducing)• Requires high power computing facilities• High set-up costs if carried out in house• Complex analysis of splice variants• Analysis can be complex if paralogues present

• All disadvantages will be fixed by outsourcing the project to BGI.

• They gave reliable service with good price!!



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RESEARCH ARTICLE

Comparison of RNA-Seq and Microarray in Transcriptome Profiling of Activated T Cells

Shanrong Zhao, Wai-Ping Fung-Leung, Anton Bittner, Karen Ngo, Xuejun Liu

Published: January 16, 2014 • <https://doi.org/10.1371/journal.pone.0078644>

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Introduction

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To demonstrate the benefits of RNA-Seq over microarray in transcriptome profiling, both RNA-Seq and microarray analyses were performed on RNA samples from a human T cell activation

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RNA-Seq is **more sensitive** in detecting genes with very low expression and **more accurate** in detecting expression of extremely abundant genes. RNA-Seq also has **a wider dynamic range** than microarray.

This is likely because RNA-Seq sequencing technology is new to most researchers, more expensive than microarray, data storage is more challenging and analysis is more complex. We expect that once these barriers are overcome, the RNA-Seq platform will become the predominant tool for transcriptome analysis.

Research article | [Open Access](#) | Published: 03 September 2015

Comparison of stranded and non-stranded RNA-seq transcriptome profiling and investigation of gene overlap

[Shanrong Zhao](#) , [Ying Zhang](#), [William Gordon](#), [Jie Quan](#), [Hualin Xi](#), [Sarah Du](#), [David von Schack](#)  & [Baohong Zhang](#) 

BMC Genomics **16**, Article number: 675 (2015) | [Cite this article](#)

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Abstract

Background

While RNA-sequencing (RNA-seq) is becoming a powerful technology in transcriptome profiling, one significant shortcoming of the first-generation RNA-seq protocol is that it does not retain the strand specificity of origin for each transcript. Without strand

Source (click for full paper):

<https://bmcgenomics.biomedcentral.com/articles/10.1186/s12864-015-1876-7>

- Stranded RNA-seq provides a more accurate estimate of transcript expression compared with non-stranded RNA-seq, and is therefore the recommended RNA-seq approach for future mRNA-seq studies.