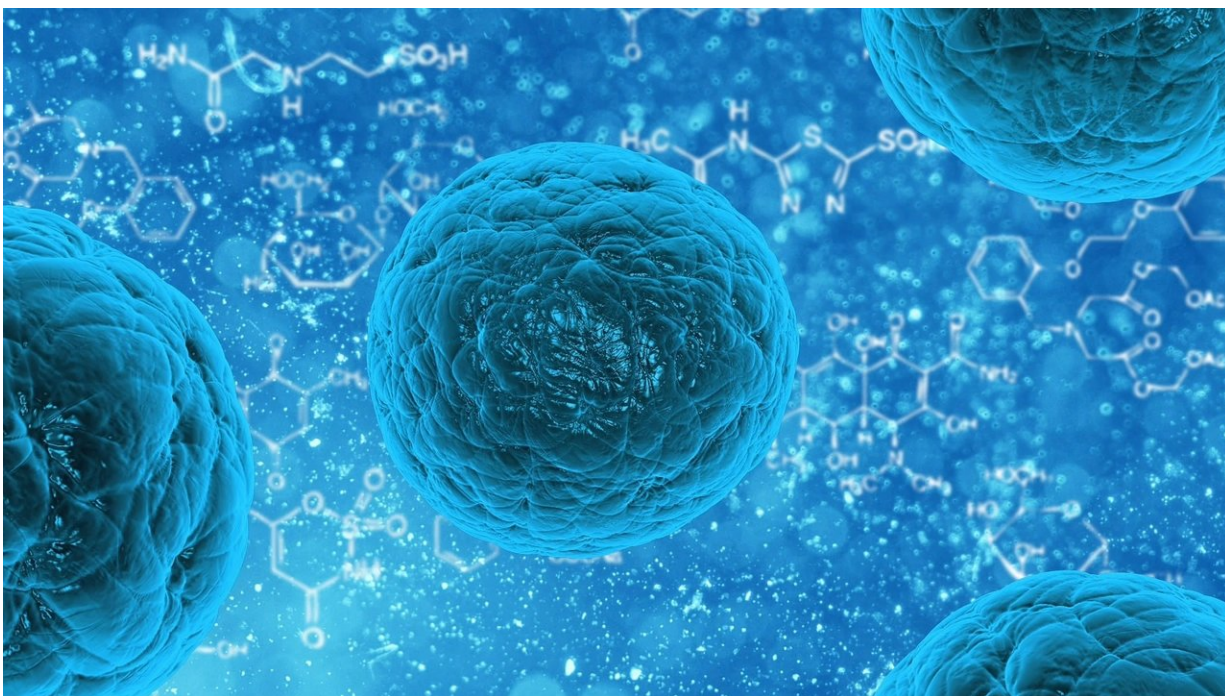


Single cell transcriptomics: A new sequencing approach

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Researchers from University of Southern Denmark, Wellcome Sanger Institute and BGI have published a study in the journal *Genome Biology* comparing the library preparation and sequencing platforms for single-cell RNA-sequencing (scRNA-seq).

Single cell transcriptomics (i.e. scRNA-seq) is a next-generation

sequencing approach that simultaneously measures the messenger RNA concentrations of thousands of genes in [individual cells](#). This enables researchers to gain a high-resolution view of cells to unravel heterogeneous cell populations and better understand individual cell functions in the body. Although several single-cell protocols exist, the sequencing has traditionally been performed using Illumina technology and sequencing platforms.

The authors performed the first comparison of traditional Illumina platforms to an alternative BGISEQ-500 short-read sequencing platform for single-cell transcriptomics. The authors profiled 468 individual cells by scRNA-seq using two different protocols (SMARTer and Smart-seq2), generating 1297 single-cell libraries for sequencing across both Illumina HiSeq and BGISEQ-500 platforms. By using two different cell types (Human immortalized leukemia cells "K562" and mouse embryonic stem [cells](#) 'mESCs') and spiking synthetic RNA control [sequences](#), the authors benchmarked the performance between sequencing platforms. The study found that BGISEQ-500 was highly comparable in sensitivity, accuracy and reproducibility of detected RNA molecules to the Illumina platform

Although sequencing reagents and personnel costs are subject to geographical constraints, BGISEQ-500 typically has higher data throughput at slightly lower costs. "The combination of higher throughput with marginally increased cost per lane makes the BGISEQ-500 an attractive alternative for scRNA-seq projects, where significant multiplexing is required alongside considerable read depth per cell," notes Dr. Miaomiao Jiang, BGI's co-lead author on the paper.

"This is the first study to compare Illumina HiSeq with BGISEQ-500 sequencing [platform](#) for single-cell RNA-sequencing, offering researchers with an alternative sequencing option. Our study finds very similar performance in the compared metrics between the platforms.

This would be extremely useful for large scale single-cell sequencing initiatives, generating reference maps of all human cell types and enhancing our understanding of human health."

Dr. Kedar Natarajan is the lead and co-corresponding author on the paper. Dr. Natarajan heads his single-cell group at Department of Biochemistry and Molecular Biology at SDU.

More information: Kedar Nath Natarajan et al. Comparative analysis of sequencing technologies for single-cell transcriptomics, *Genome Biology* (2019). [DOI: 10.1186/s13059-019-1676-5](https://doi.org/10.1186/s13059-019-1676-5)

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