DNBSEQ™ SERVICE OVERVIEW
Single Cell Sequencing

Service Description

Single cell next generation sequencing enables researchers to examine the genomes or transcriptomes of individual cells, providing an in-depth view of cell-to-cell variation.

Single cell sequencing is particularly useful for the study of heterogeneous samples, rare cell types, cell lineage relationships, and disease evolution. By using deep sequencing of DNA and RNA from single cells, cellular functions of individual cells can be investigated and heterogeneity in time-dependent processes such as proliferation, and tumorigenesis can be explored.

BGI applies the superior method of Multiple Displacement Amplification (MDA) for single cell genomic DNA amplification (WGS/WES), and Switching Mechanism at 5′ End of RNA Template (Smart-seq II) for single cell RNA amplification (transcriptome/RNA quantification).

Sequencing Service Specification

BGI single cell DNA and RNA sequencing services are executed with the DNBSEQ™ technology platform.

Sample Preparation and Services

- Single cell amplification based on MDA or Smart-seq II
- PE100 sequencing options, depending on your application
- Raw data and bioinformatics analysis are available in standard file formats
- Custom bioinformatics data analysis is available
- Cloud-based data storage and delivery system

Sequencing Quality Standard

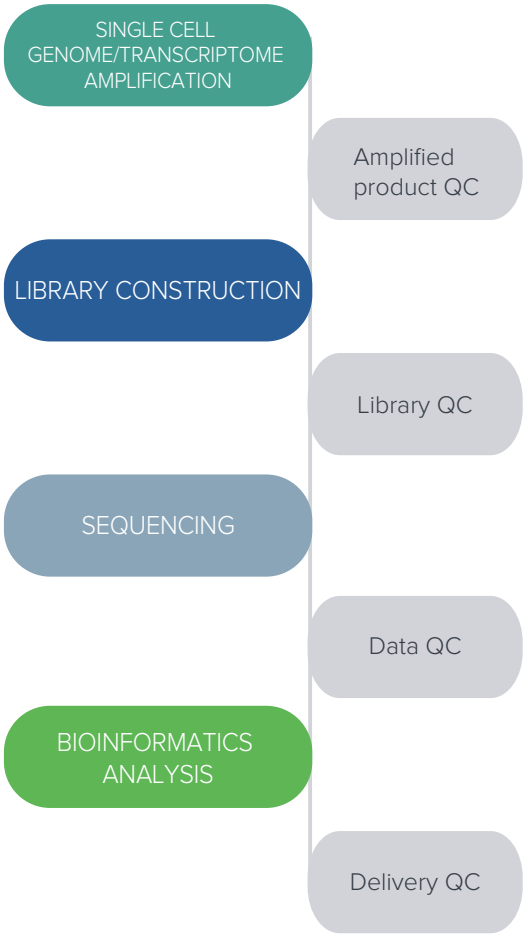
- Guaranteed ≥90% of bases with quality score of ≥Q20

Turnaround Time

- Typical 40 working days from sample acceptance to filtered raw data availability.
- Turnaround time will vary based on your specific application and sample. Please contact your local BGI representative for a personalized estimate.
- Expedited services are available, contact your local BGI specialist for details.

Project Workflow

We care for your samples from the start through to the result reporting. Highly experienced laboratory professionals follow strict quality procedures to ensure the integrity of your results.



Data Analysis

Besides clean data output, BGI offers a range of standard and customized bioinformatics pipelines for your single cell DNA or RNA sequencing project.
Reports and output data flies are delivered in industry standard file formats: FASTQ, BAM, VCF, .xls, .png

RNA SEQUENCING STANDARD ANALYSIS

- Data filtering
- Assessment of sequencing
- Gene expression and annotation
- Differential expressed genes analysis
- Expression pattern analysis of DEGs
- Gene ontology analysis of DEGs
- Pathway enrichment analysis of DEGs
- Refinement of gene structures
- Identification of alternative spliced transcripts

DNA SEQUENCING STANDARD ANALYSIS

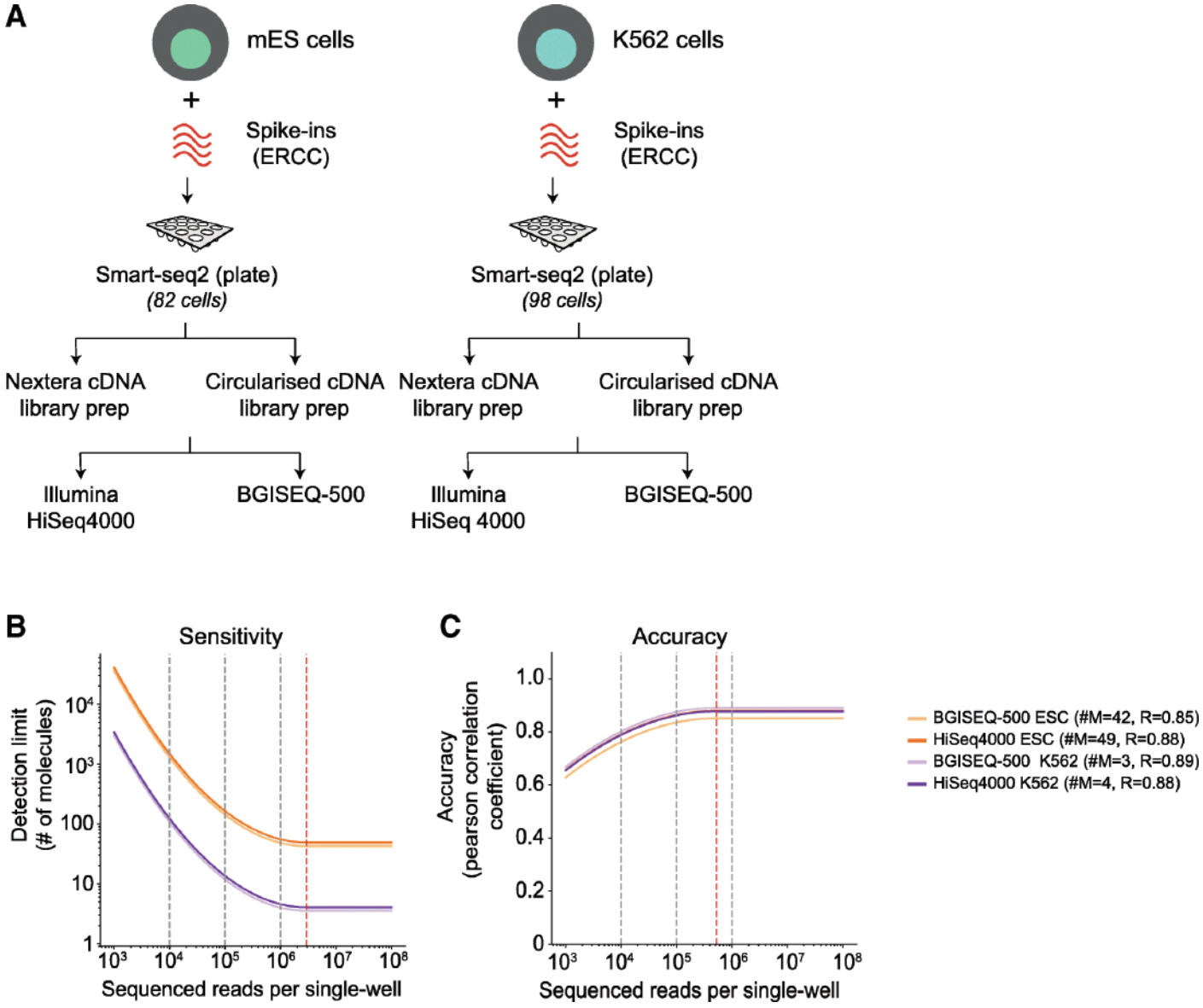
- Data filtering
- Alignment, summary of data production
- SNP calling annotation and statistics
- InDel calling annotation and statistics
- CNV calling annotation and statistics (only for WGS)
- SV calling annotation and statistics (only for WGS)

CUSTOMIZED ANALYSIS

Further customization of Bioinformatics analysis to suit your unique project is available:
Please contact your BGI technical representative

Single Cell Data Comparison between DNBSEQ and Illumina Platforms.

Matched single-cell cDNA from mESCs and K562s were used to generate 600 BGISEQ-500 sequencing libraries in both single- and paired-end configurations and 121 HiSeq 4000 paired-end sequencing libraries.



B: The sensitivity of mESCs and K562s cells between the sequencing platforms is highly similar.

C: The accuracy of mESCs and K562s have similar accuracies, across both sequencing platform.

Ref: Natarajan K.N, Miao Z, Jiang M, Liu S & Teichmann S.A. *et al.* 2019. Comparative analysis of sequencing technologies for single-cell transcriptomics. *Genome Biol* 20:70

Sample Requirements

SAMPLE TYPE	FOR DNA-SEQUENCING	FOR RNA-SEQUENCING
Single cell	1-2 cells in 4 µl PBS buffer	1-2 cells in 4 µl lysis buffer
Few cells	2-1000 cells in 4 µl PBS buffer	2-1000 cells in 4 µl lysis buffer
Amplified single cell gDNA/cDNA	Concentration >20 ng/µl, Quantity >3 µg	Concentration >0.2 ng/µl, Quantity >1 ng
Total RNA for low input library construction	N/A	Concentration >50pg/µl, Quantity > 2 ng; RNA 28S/18S ≥ 1, RIN ≥ 7

BGI Single Cell Publications

[1] Liu L, Liu C, Quintero A, Wu L, Yuan Y, Wang M, Cheng *et al.* 2019. Deconvolution of single-cell multi-omics layers reveals regulatory heterogeneity. *Nat Com*. 10:470

[2] Xu X, Hou Y, Yin X, Bao L, Tang A, Song L, Li Fu *et al.* 2012. Single-Cell Exome Sequencing Reveals Single-Nucleotide Mutation Characteristics of a Kidney Tumor . *Cell*. 148, 886–895.

[3] Hou Y, Song L, Zhu P, Zhang B, Tao Y, Xu X, Li F *et al.* 2012. Single-Cell Exome Sequencing and Monoclonal Evolution of a JAK2-Negative Myeloproliferative Neoplasm. *Cell*. 148, 873–885.

Request for Information or Quotation

Contact your BGI account representative for the most affordable rates in the industry and to discuss how we can meet your specific project requirements or for expert advice on experiment design, from sample to bioinformatics.

info@bgi.com
www.bgi.com

International Head Offices

BGI Americas
One Broadway, 3rd Floor
Cambridge, MA 02142, USA
Tel: +1 617 500-2741

BGI Europe
Ole Maaløes Vej 3,
DK-2200 Copenhagen N,
Denmark
Tel: +45 7026 0806

BGI Asia
16 Dai Fu Street,
Tai Po Industrial Estate,
New Territories, Hong Kong
Tel: +852 36103510

BGI Australia
L6, CBCRC, 300 Herston
Road, Herston, Brisbane,
Queensland 4006, Australia
Tel: +61 (07) 3362 0475

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