DNBseq™ SERVICE OVERVIEW
Single Cell 3’ RNA Sequencing

Service Description

We provide high-throughput single cell gene expression profiling service using 10x Genomics Chromium Single Cell Platform to enable 3’ end counting of mRNA transcripts. Our turn-key solution (cell/tissue-to-report) and premade library service (library-to-data) for Single cell RNA-Seq provide flexible tool set for you depending on your preference, equipment accessibility and schedule. Sequencing of the single cell libraries can be conducted on our proprietary DNBSEQ™ platform to ensure the downstream service quality, or the Illumina® platform (HiSeq and NovaSeq) by customer’s preference.

Applications

- Differentiation of different cell types and subtypes within a tissue
- Analysis of cellular heterogeneity
- Analysis of individual cellular signaling pathways
- Study of cellular ecosystems of tumors
- Analysis of individual cell differentiation

Service Specification

BGI Single Cell sequencing services are executed with the DNBseq sequencing technology, featuring cPAS and DNA Nanoballs (DNB™) technology for superior data quality.

Sample preparation and services

- 1X10^6 fresh frozen cells/100 mg fresh frozen tissue per sample submission
- PE 100 sequencing is offered
- 20K read pairs/cell recommended
- Raw data and bioinformatics analysis are available in standard file formats
- Standard single cell 3’ RNA seq data analysis
- Advanced and custom bioinformatics data analysis
- Cloud-based data storage and delivery system

Sequencing Quality Standard

- Guaranteed ≥80% of bases with quality score of ≥Q30

Turn Around Time

Single Cell 3’ RNA Sequencing Solution (tissue/cell-to-report)

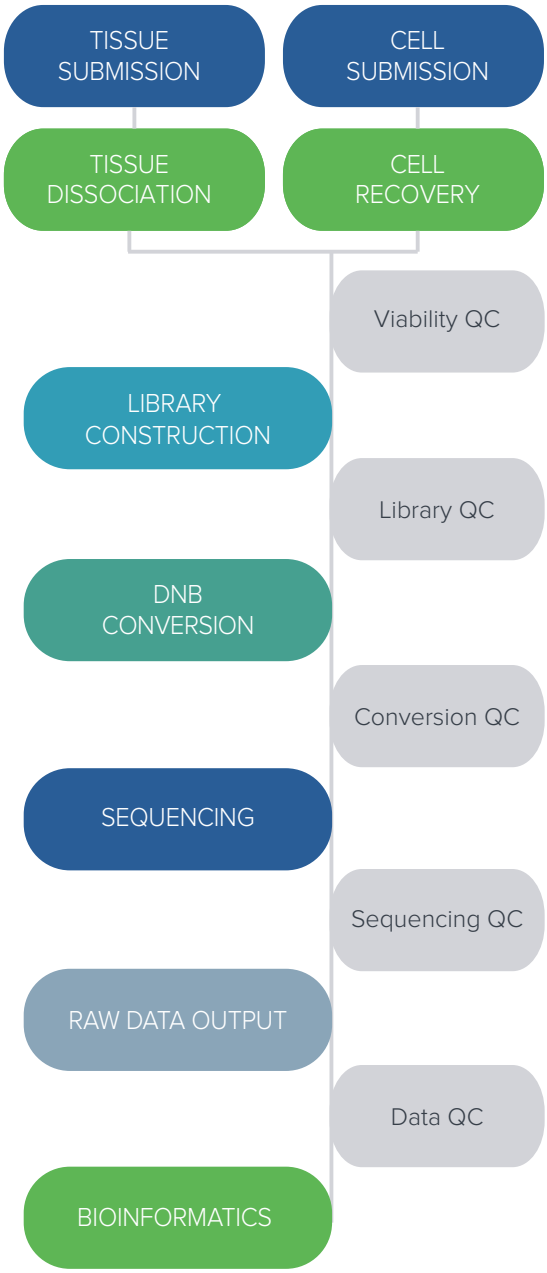
- Guaranteed 6 weeks from tissue/cell QC acceptance to filtered RAW data availability.

Single Cell 3’ RNA self-prepared libraries sequencing (library-to-data)

- Guaranteed 4 weeks from library QC acceptance to filtered RAW data availability. Faster turnaround time is available with qualified sample volume. Contact your local BGI specialist for details.

Project Workflow

We employ rigorous QC steps following each phase of the service workflow as described by the flow chart below. The qualified sequencing data will be offered for download and bioinformatics service is available upon request.



Sample Requirements

Cell line and tissue submission

BGI recommends placing 1x10^6 cells in 1 ml of freezing media per cryotube.

Tissue submission

BGI recommends minimum 100 mg gradient cryopreserved fresh tissue for each sample.

Premade library submission

BGI also provides sequencing services for customer self-prepared libraries using 10x Genomics® Chromium™ system Single Cell 3′ Library Construction Kit v3 and Next GEM Single Cell 3' Library Construction Kit v3.1, that meet the following requirements:

Library parameter	Requirement	Preferred QC method
Fragment size	400bp±100bp	Agilent 2100
Concentration	≥2ng/ul	Qubit
Total amount	≥30 ng	Qubit

Once the sample is ready, please contact your local BGI specialist for dry ice shipping arrangement.Please visit our website for detailed sample preparation and submission guidelines.

Data Analysis

In addition to raw data output, BGI offers a range of standard and customized bioinformatics pipelines for your single cell sequencing project.

STANDARD BIOINFORMATICS

- Sequencing data QC
- Data mapping
- Quantitative analysis
- Cell cluster analysis
- Differentially expressed genes identification
- Marker genetic identification
- Ontology analysis of Differentially Expressed Genes (DEGs)
- Pathway analysis of DEGs
- Transcription factor (TF) coding ability prediction of DEGs
- Protein interaction analysis of DEGs
- Genetic correlation network analysis

References

1. Reliable Multiplex Sequencing with Rare Index Mis-Assignment on DNB-Based NGS Platform https://bmcgenomics.biomedcentral.com/articles/10.1186/s12864-019-5569-5
2. Single-cell Transcriptomic Landscape of Nucleated Cells in Umbilical Cord Blood. bioRxiv 346106 (2018). doi:10.1101/346106 https://doi.org/10.1101/346106
3. Comparative analysis of sequencing technologies for single-cell transcriptomics. Genome Biology, volume 20, Article number: 70 (2019) https://genomebiology.biomedcentral.com/articles/10.1186/s13059-019-1676-5
4. Comparative performance of the BGI and Illumina sequencing technology for single-cell RNA sequencing. bioRxiv 552588 (2019). doi:10.1101/552588 https://www.biorxiv.org/content/10.1101/552588v2
5. Effects of Index Misassignment on Multiplexing and Downstream Analysis (Illumina white paper, 2017).

Request Information or Quotation

Contact your BGI account representative for the most affordable rates in the industry, 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

Contact Us

BGI Americas
One Broadway, 14th 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-Pacific
16 Dai Fu Street,
Tai Po Industrial Estate,
New Territories, Hong Kong
Tel:+852 36103510

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We Sequence, You Discover