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.

Innomics 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

Innomics 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

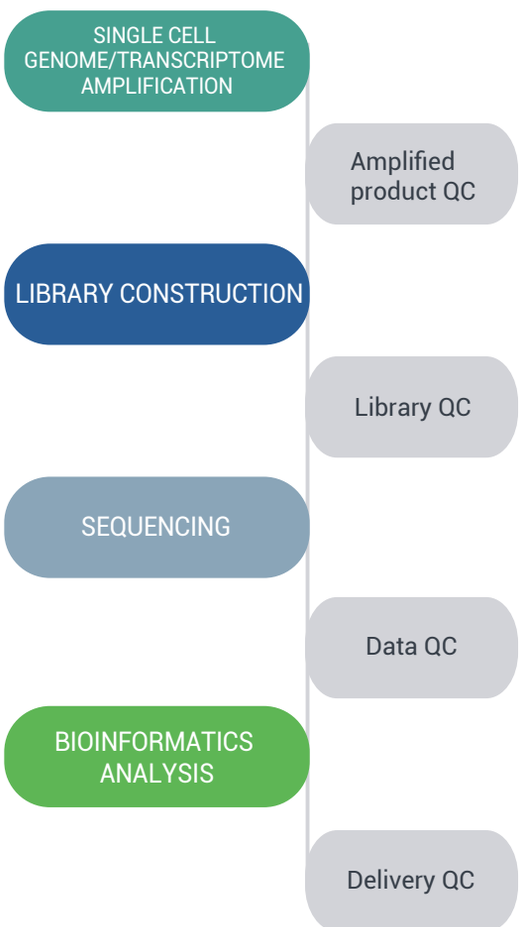
Turnaround Time

- 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 Innomics representative for a personalized estimate.
- Expedited services are available, contact your local Innomics specialist for details.

Quality Data | Fast TAT | Cost Effective

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, Innomics 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 Innomics technical representative

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

To Learn more

If you have any questions or would like to discuss how our services can help you with your research, please don't hesitate to contact us at P_contact@innomics.com. We look forward to hearing from you!

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