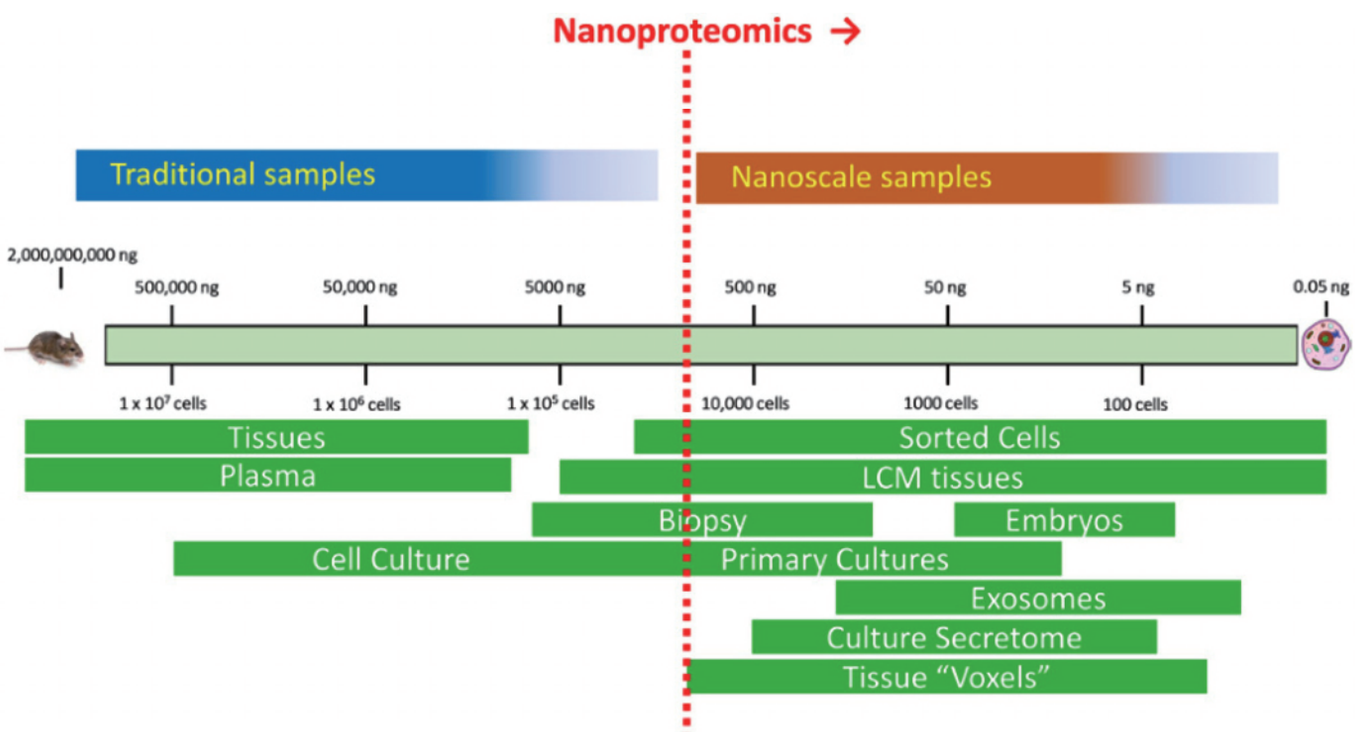
Nanoproteomics Service Overview

Service Description

To date, most proteomics studies have been based on proteins obtained from the homogenization of large volumes of cells or tissues. However, with the advancement of medical research, there is a growing need for the analysis of highly specialized specimens within specific applications and research areas such as trace specimens identified by forensic experts, or intra-tumor heterogeneity research.

Nanoproteomics refers to quantitative proteomics analysis of small cell populations (typically < 5,000 cells) by the combination of in-situ cleavage and label free technology, and offers possibilities for analysis unavailable with conventional protein extraction and mass spectrometry.

BGI Genomics has extensive experience in the field of nanoproteomics spanning cellular heterogeneity research across rare cell populations, hard-to-obtain clinical specimens, and pathological tissues.



An illustration of traditional and nanoproteomics domains
L. Yi, et al., Advances in microscale separations towards nanoproteomics applications, *J. Chromatogr. A* (2017)

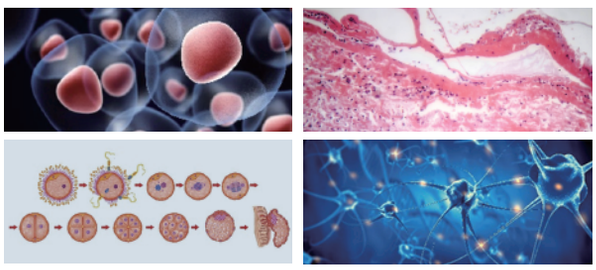
Common Challenges with Nanoproteomics Studies

Low starting sample amounts and sample loss during processing.

Inherent sensitivity issues with MS instrumentation.

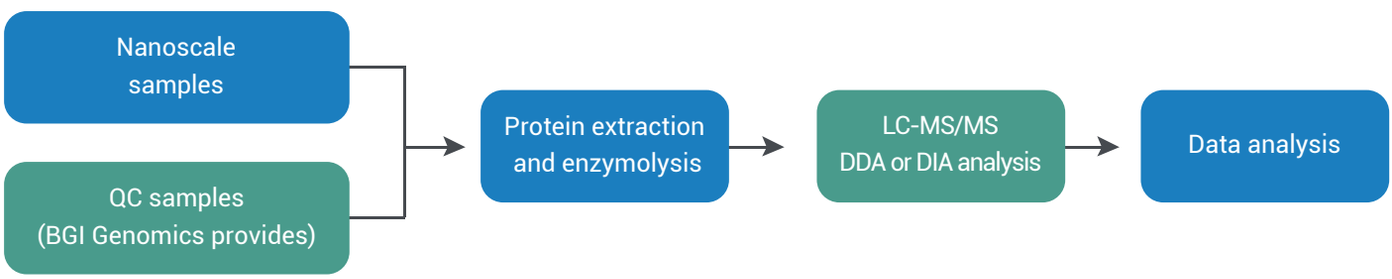
The computational complexity involved in identifying individual cell types.

Research Applications



- Cell heterogeneity studies
- Tissue substructure research
- Embryonic development research
- Precious samples research
- Nervous system research
- Immune cells research
- Stem cell differentiation research

Workflow



Our Service Advantages

We can process projects with low initial cell amounts from 100 cells for general projects or single egg cells.

We have extensive experience across a huge range of sample types with high project success rates.

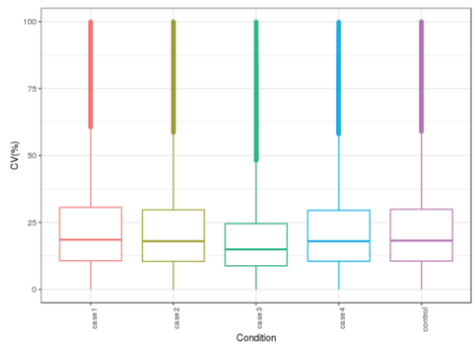
Our data quality metrics including protein identification number and technical stability consistently meet or exceed common industry standards.

We provide a simple one-stop service including single-cell transcriptome sequencing, flow cytometry sorting and single-cell proteome services providing customers with comprehensive multi-omics correlation analysis at the single-cell level.

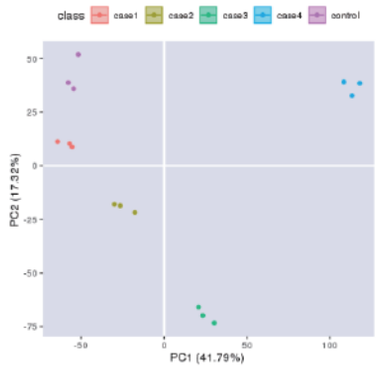
Bioinformatics Analysis Standard Workflow

01 Data output statistics	02 Protein identification and quantification list	03 Protein GO/COG/KOG/ pathway analysis
04 Differential proteins GO enrichment analysis	05 Differential proteins pathway enrichment analysis	06 Reproducibility analysis
07 Clustering analysis of expression patterns across multiple samples	08 Differential proteins subcellular localization	09 Differential proteins interaction analysis

Examples of Data QC Analysis - Stability and Repeatability

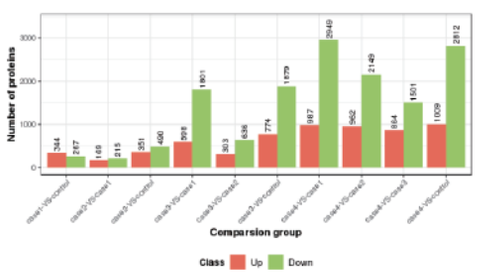


CV Distribution

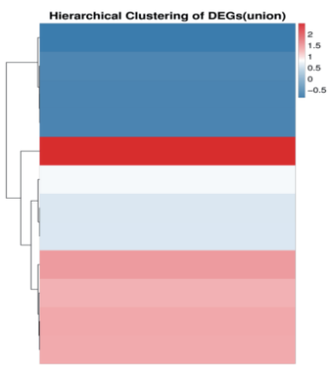


PCA Analysis

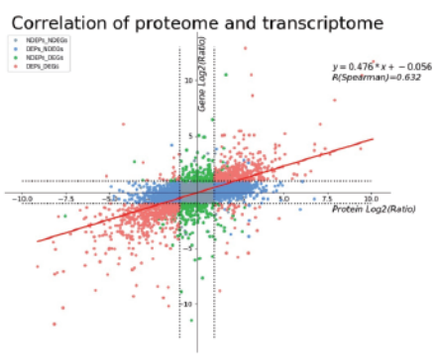
Examples of Protein Quantification Analysis



Quantification Statistics



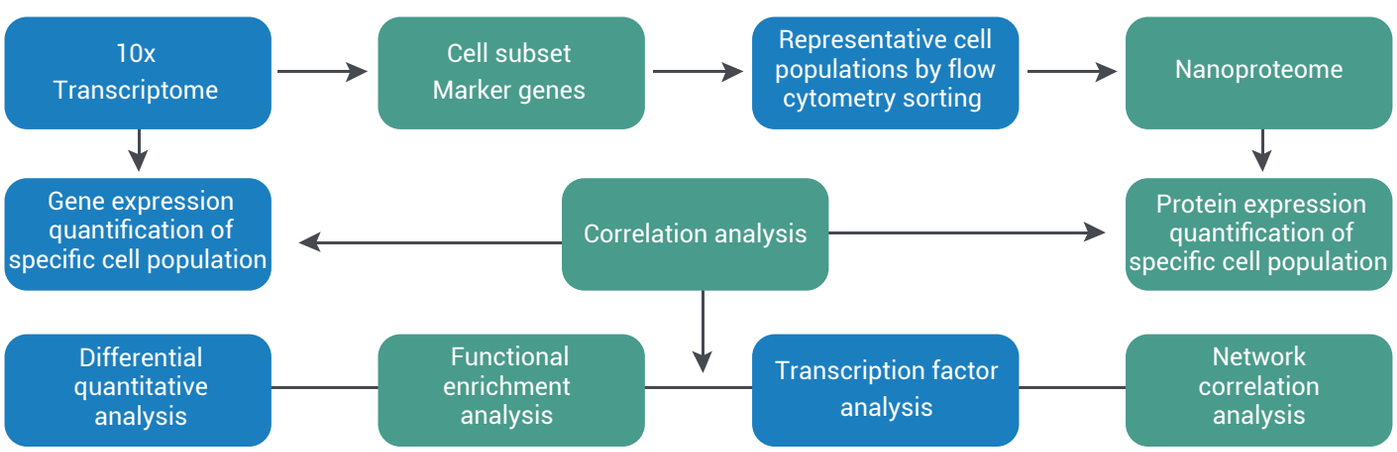
Cluster Analysis



Proteome-Transcriptome Correlation Analysis

Transcriptome + Nanoproteome Correlation Analysis Option

Using a multi-omics approach to correlate transcriptomics with nanoproteomics data provides a more comprehensive overview of expression patterns and enables researchers to interpret deeper biological implications.



General Sample Requirements

SAMPLE TYPE		AMOUNT	NOTE*
Nanoscale samples	Mammalian cells	> 100	Collected cells with 200 μL low adsorption PCR tube and stored in 2-5 μL PBS solution
	Egg cell or early embryo cell	>1, and 3-5 is better	

Turn Around Time

Sample size: 1-25, 5-6 weeks

Request for Information or Quotation

Contact a BGI Genomics representative to discuss how we can meet your specific needs or for expert advice on experiment design, from sample to bioinformatics.

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