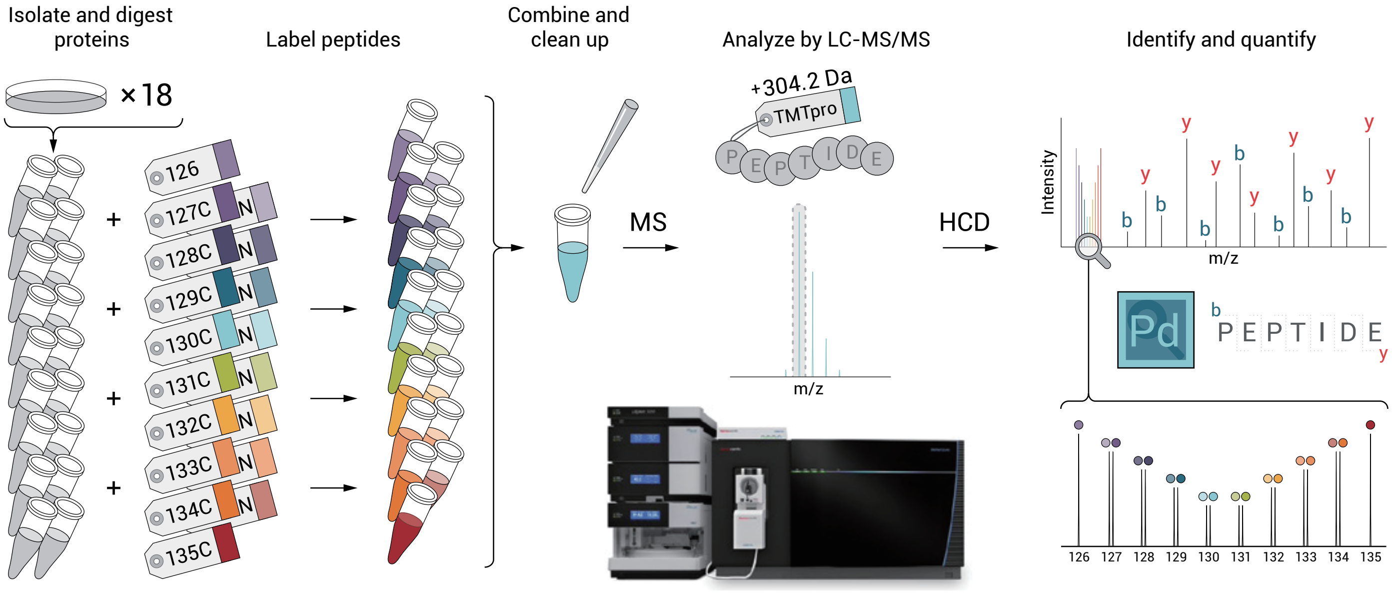
Isobaric Label Quantitative Proteomics Service Overview

Service Description

Quantitative proteomics refers to the identification and quantification analysis of proteins in two or more samples to obtain the differential expression and function information of relevant proteins. Quantitative proteomics is most often applied in research concerning the prevention, diagnosis, prognosis and efficacy monitoring of diseases, and in helping to develop therapeutic drugs.

BGI Genomics provides Isobaric Label Quantitative Proteomics services using TMT (Tandem Mass Tags for Quantitation) technologies.



TMTpro reagent workflow

Research Applications

- Disease biomarker research
- Drug efficacy evaluation
- Special behavior mechanisms and food/medicinal value research
- Plant growth and development research
- Plant disease resistance and insect resistance research
- Microbial stress and adversity physiology research

Isobaric Label Analysis Workflow

Protein extraction → Protein digestion → Isobaric labeling → HPLC fractionation → LC-MS/MS → Data analysis

BGI Genomics Service Advantages

High Throughput and Short Project Cycle

Simultaneous proteome quantification of less than 18 samples. More than 18 samples can be bridged by setting reference samples to realize the comparison of data, thus shortening project cycle

High Accuracy and Repeatability

Analysis of multiple labeled samples at the same time avoids poor repeatability issues connected to testing separately and with traditional gel samples

Wide Range of Biological Samples

Experience of wide range of species and various proteins including cytoplasmic protein, membrane protein, nuclear protein, extracellular protein. The protein abundance and molecular weight span are large

Cloud Platform Delivery

The Dr. Tom cloud platform was used for data delivery, which was convenient for data mining and autonomous association analysis with the transcriptome

Bioinformatics Analysis Workflow

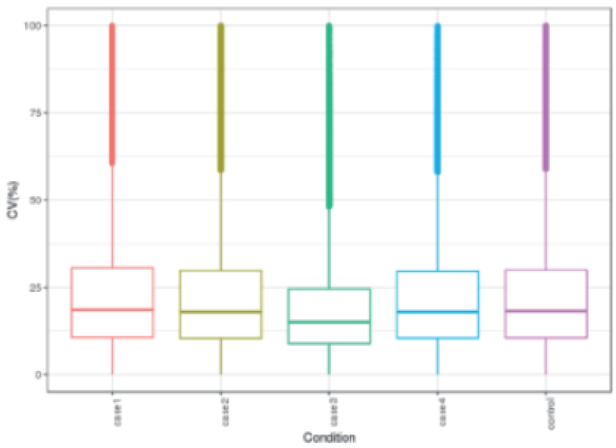
Standard:

- 01 Project overview
- 02 Data quality control
- 03 Protein identification and quantification list
- 04 Differential proteins data statistics and volcano plot
- 05 Principal component analysis (PCA)
- 06 Expression pattern cluster analysis
- 07 Protein GO/COG/KOG/ Pathway annotation
- 08 GO/COG/KOG enrichment analysis of differential proteins
- 09 Repeatability analysis
- 10 Protein-protein interaction analysis
- 11 Protein subcellular localization analysis

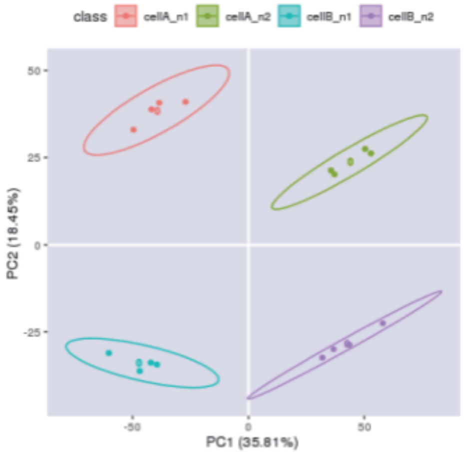
Customized Solutions:

- 01 Proteome and transcriptome/ RNA-seq correlation analysis
- 02 Proteome and metabolome correlation analysis
- 03 Quantitative proteomics and phosphoproteomics correlation analysis

Examples of Data QC Analysis - Stability and Repeatability

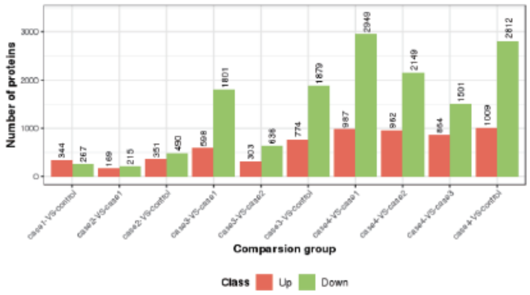


CV Distribution

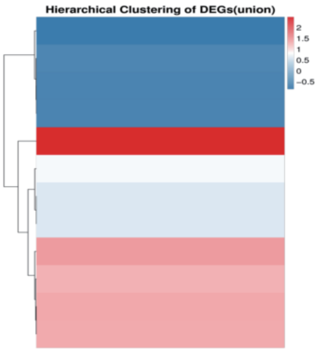


PCA Analysis

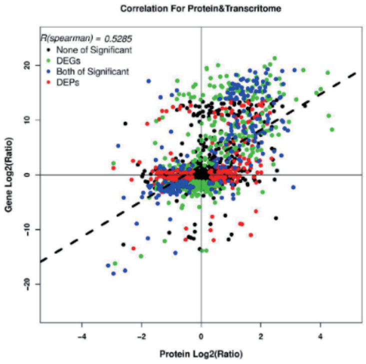
Examples of Protein Quantification Analysis



Quantification Statistics



Cluster Analysis



Proteome-Transcriptome Correlation Analysis

General Sample Requirements

SAMPLE TYPE		AMOUNT	
		RECOMMEND	MINIMUM
Animal	Common animal tissues: animal internal organs (heart, liver, spleen, lung, kidney), skin, muscle, brain, etc	≥ 10 mg	≥ 1 mg
	Mollusks (Toxoplasma, Schistosomiasis, Drosophila, Acarid, Plutella xylostella, Laodelphax, Cestode, Cicada, Hematodinium, etc.)	≥ 10 mg	≥ 2 mg
Cell	Suspended cells, adherent cells	$\geq 1\times10^7$	$\geq 1\times10^6$
	Cell culture supernatant	≥ 10 mL	
Exosome	Exosome isolated by customer	≥ 50 μg, ≥ 0.5 μg/μL	
Fluid	Plasma, serum (remove highly-abundant protein)	≥ 200 μL	≥ 200 μL
	Plasma, serum (with highly-abundant protein)	≥ 10 μL	≥ 3 μL
	Amniotic fluid, cerebrospinal fluid, semen, etc. (remove highly-abundant protein)	≥ 1 mL	≥ 500 μL
	Amniotic fluid, cerebrospinal fluid, semen, etc. (with highly-abundant protein)	≥ 200 μL	≥ 100 μL
	Saliva, milk	≥ 200 μL	≥ 100 μL
	Urine	≥ 30 mL	≥ 15 mL
	Tear	≥ 15 μL	≥ 10 μL
Plant	Twigs of plants (leaf buds, tender leaves), algae	≥ 300 mg	≥ 200 mg
	Old leaves, roots, stems, bark of plants	≥ 1 g	≥ 500 mg
	Plant buds, pollen	≥ 100 mg	≥ 50 mg
	Plant seeds (rice/wheat seeds, etc.), fruits (apples, peaches, pears)	≥ 1 g	≥ 500 mg
Microorganism	Prokaryotic bacteria (E. coli, Staphylococcus aureus, etc.), fungi (yeast, etc.)	Thallus ≥ 50 mg cells $\geq 5\times10^6$	
Protein solution	Complex protein solution, protein powder	≥ 100 μg, ≥ 0.5 μg/μL	≥ 50 μg, ≥ 0.5 μg/μL

Turn Around Time

Sample size: 1 batch, 4-5weeks

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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