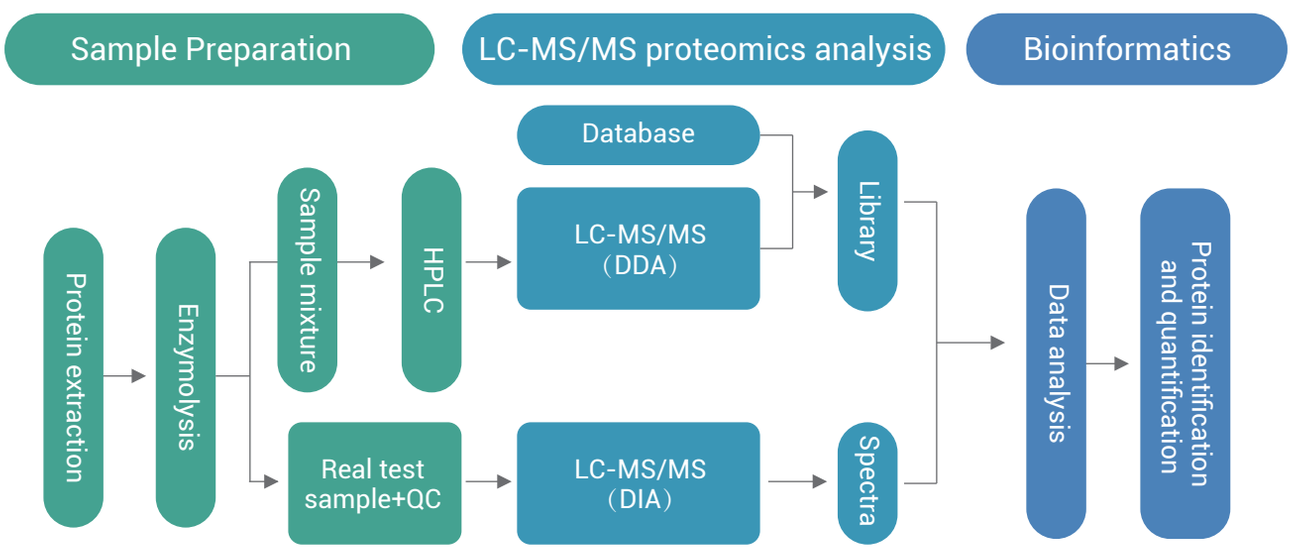
Service Overview

Label-Free Data Independent Acquisition (DIA) Quantitative Proteomics

Service Description

In MS-based label-free protein quantification, traditional data-dependent acquisition (DDA) can only detect a specific number of peptide molecules in MS1 (such as the top 10 ions with the strongest signal intensity). By comparison, DIA is a data-independent acquisition method that continuously sets a range of mass-to-charge ratio windows over time, ensuring that all the peptide ions passing through the window are fragmented and detected in MS2. Consequently, DIA methodology allows increased identification of the number of peptides, with higher accuracy, stability and repeatability, which is ideal for discovery proteomics and phenotype comparison.

Technical Workflow



Highlights

- Free from the issue of one-time comparison group number of labeling method
- Allows increased identification of protein numbers with higher accuracy and reproducibility
- Participates in quantitative performance assessment as well as standardization and harmonization of Multi-National DIA proteomics analysis supporting precision medicine studies*
- 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

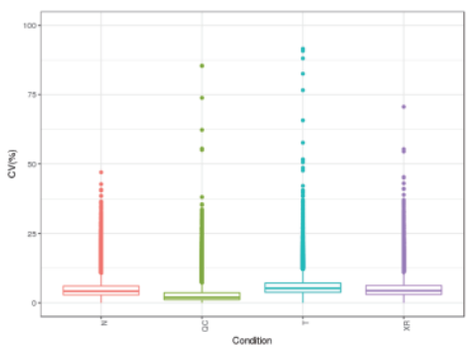
Standard:

01 Project overview	02 Data quality control	03 DDA library identification result
04 Protein identification and quantification list	05 Differential proteins data statistics and volcano plot	06 Principal component analysis (PCA)
07 Expression pattern cluster analysis	08 Time series analysis	09 Protein GO/COG/KOG/ Pathway annotation
10 GO/COG/KOG enrichment analysis of differential proteins	11 Protein-protein interaction analysis	12 Protein subcellular localization analysis

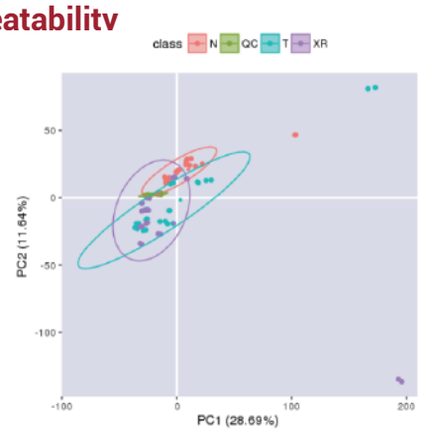
Customized:

Proteome and transcriptome/RNA-seq correlation analysis
Quantitative proteomics and phosphoproteomics correlation analysis
Proteome + metabolome correlation analysis

Examples of Data QC Analysis - Stability and Repeatabilitv

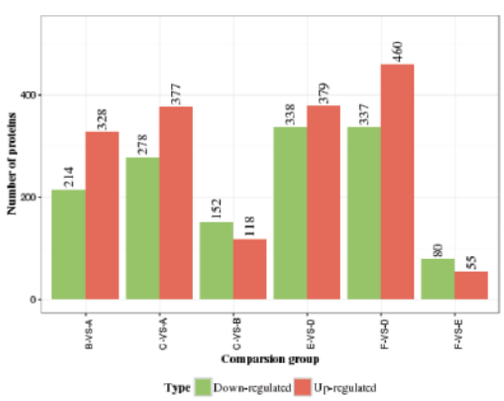


CV Distribution

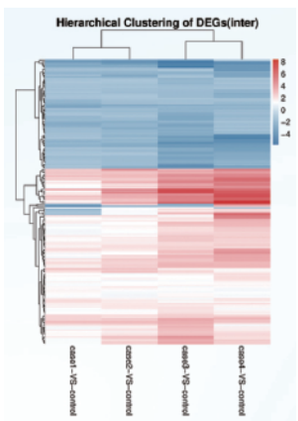


PCA Analysis

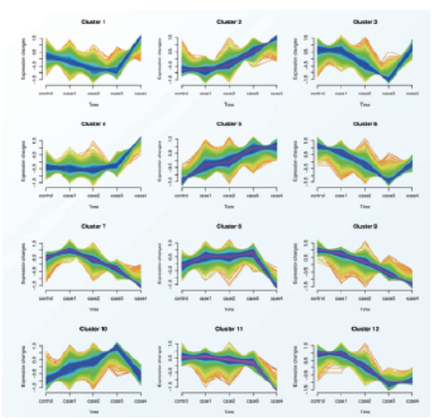
Examples of Protein Quantification Analysis



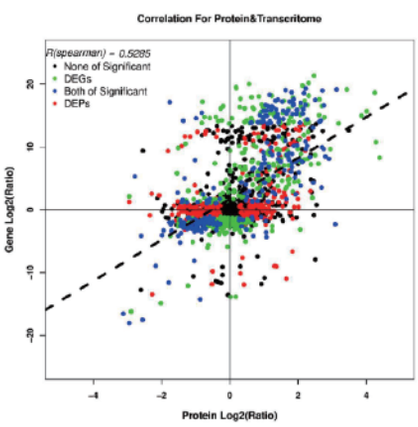
Quantification Statistics



Cluster Analysis



Time Series Analysis



Proteome-Transcriptome Correlation Analysis

Sample Requirements

Sample type		Amount	
		Recommend	Minimum
Animal	Common animal tissues: animal internal organs (heart, liver, spleen, lung, kidney), skin, muscle, brain, etc	≥ 5 mg	≥ 1 mg
	Mollusks (Toxoplasma, Schistosomiasis, Drosophila, Acarid, Plutella xylostella, Laodelphax, Cestode, Cicada, Hematodinium, etc.)	≥ 5 mg	≥ 2 mg
Cell	Suspended cells, adherent cells	≥ 1×10^7	≥ 1×10^6
	Cell culture supernatant	≥ 5 mL	
Exosome	Exosome isolated by customer	≥ 20 μg, ≥ 0.5 μg/μL	
Fluid	Plasma, serum (remove highly-abundant protein)	≥ 200 μL	≥ 50 μL
	Plasma, serum (with highly-abundant protein)	/	/
	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 ≥ 5×10^6	
Protein solution	Complex protein solution, protein powder	≥ 40 μg, ≥ 0.5 μg/μL	≥ 20 μg, ≥ 0.5 μg/μL

Turn Around Time

Typical 4-5 weeks from sample QC acceptance to data report delivery for Label-Free DIA Quantitative Proteomics

*Multi-laboratory assessment of reproducibility, qualitative and quantitative performance of SWATH-mass spectrometry. *Nature communications*. 2017 (BGI Genomics contribution No.10)

Standardization and harmonization of distributed multi-center proteotype analysis supporting precision medicine studies. *Nature communications*. 2020 (BGI Genomics contribution No.7)

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.

info@bgi.com
www.bgi.com

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