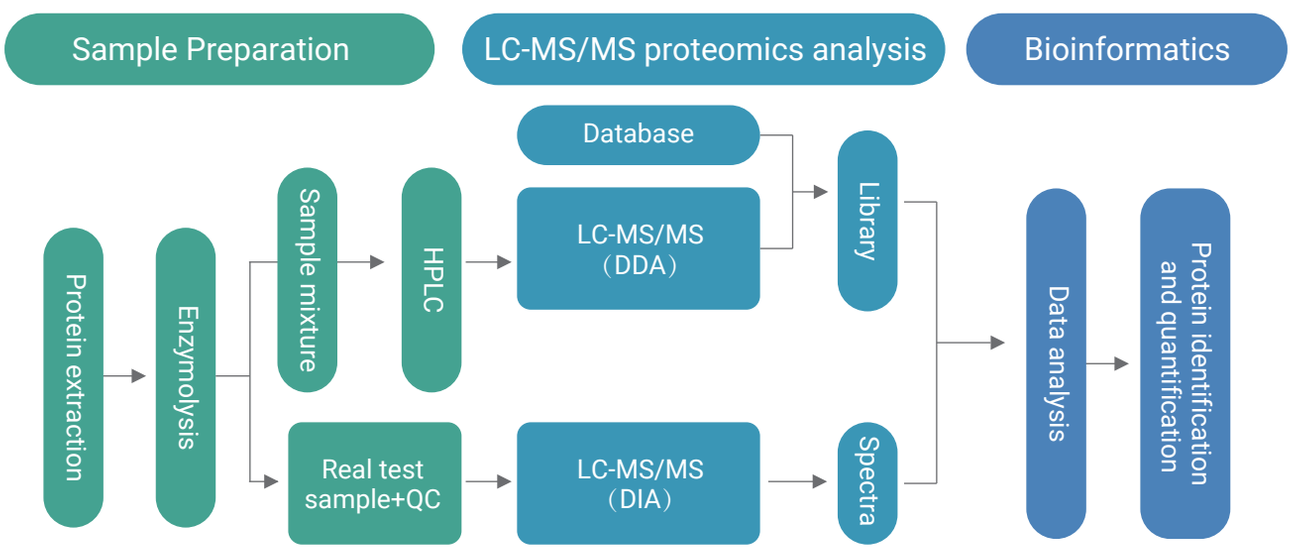
Overview of the Label-Free DIA Quantitative Proteomics Service

An Overview of The Service

Traditional data-dependent acquisition (DDA) can only identify a certain number of peptide molecules in MS1 (for example, the top 10 ions with the strongest signal intensity) when doing label-free protein quantification using MS. In contrast, data-independent acquisition (DIA) is a method that constantly establishes a variety of mass-to-charge ratio windows throughout time, guaranteeing that all peptide ions passing through the window are fragmented and detected in MS2. This makes DIA methodology excellent for the discovery proteomics and phenotypic comparison as it enables enhanced peptide identification with better precision, stability, and repeatability.

Process Workflow



Highlights

- Method of labeling that is free of the issue of a single-time comparison group number
- Allows increased identification of protein numbers with higher accuracy and reproducibility
- Participates in quantitative performance evaluation and standardization and harmonization of Multi-National DIA proteomics analyses in support of precision medicine research*
- For data delivery, the Dr.Tom cloud platform was utilized, which was suitable for data mining and autonomous association analysis with the transcriptome.

Bioinformatics Analysis

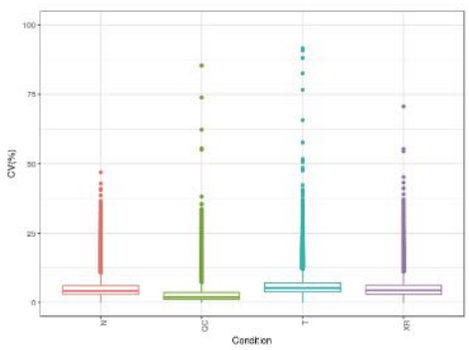
Standard:

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

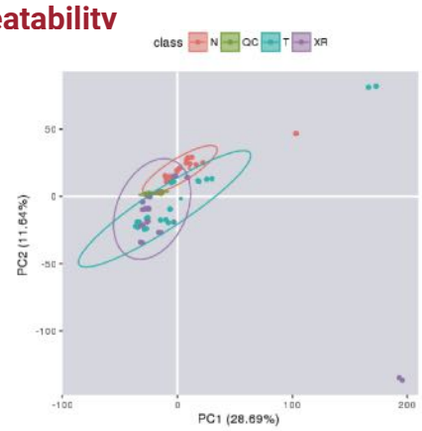
Customized:

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

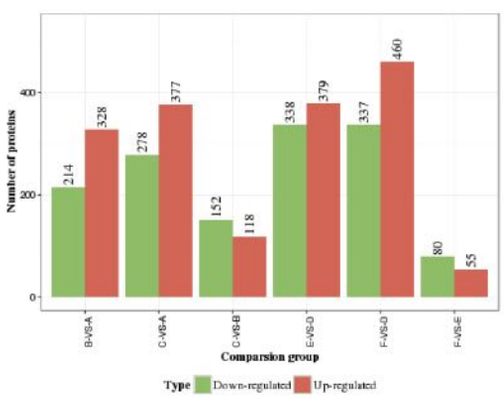


CV Distribution

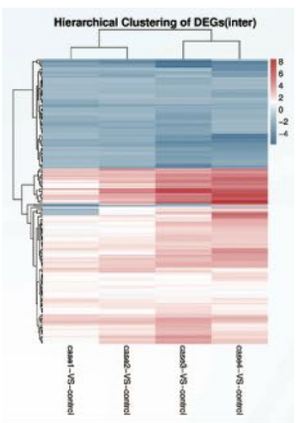


PCA Analysis

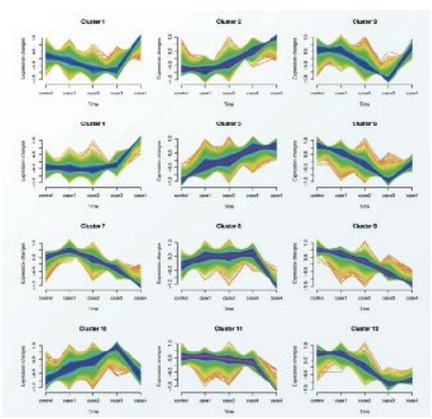
Examples of Protein Quantification Analysis



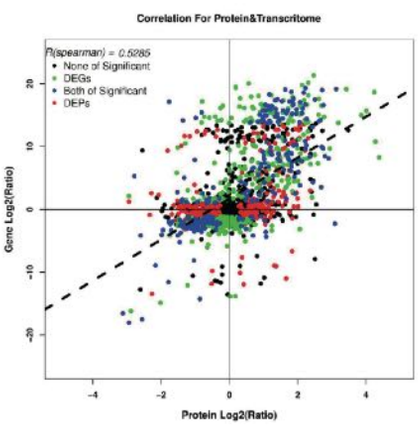
Quantification Statistics



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

The turnaround time for Label-Free DIA Quantitative Proteomics, from sample QC acceptance to data report delivery, is approximately 4-5 weeks.

*Multi-laboratory assessment of reproducibility, qualitative and quantitative performance of SWATH-mass spectrometry. Nature communications.
Standardization and harmonization of distributed multi-center proteotype analysis supporting precision medicine studies. Nature communications.

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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