

Untargeted Medical Metabolomics Service Overview

Service Description

The metabolome refers to the collection of all small molecule metabolites (< 1500 Da) in cells, tissues, organs or biological organisms, metabolites produced by microorganisms, and all exogenous substances from heterologous organisms.

Metabolomics is a research method comprising qualitative and quantitative analysis of all metabolites in an organism. It involves the comparison of the metabolome between control and test groups (for example, a specific gene mutation or environmental change), screening of differential metabolites by statistical analysis, and metabolic pathway analysis of differential metabolites, to identify differences between metabolites and physiological/pathological changes.

Untargeted Metabolomics is an important branch of metabolomics and is designed to obtain a metabolite profile and screen for differentially-expressed molecules in the sample. In turn, untargeted medical metabolomics is an important branch of untargeted metabolomics. As many metabolites from different cell samples, microbial samples, animal samples or clinical samples as possible are measured and compared between control and test groups without bias.

We have experience in the field of untargeted medical metabolomics with well-developed reliable workflows using innovative technologies and a bioinformatics infrastructure.

Research Applications



- Disease biomarkers research
- Pathogenesis and prognosis study on diseases
- Drug compound identification, toxicity assessment and drug efficacy evaluation
- Regulation mechanism of tissue development
- Microbial infection and its pathogenesis
- Animal special behavior mechanism and food/medicinal value research

Technology Platforms



QE-HFX



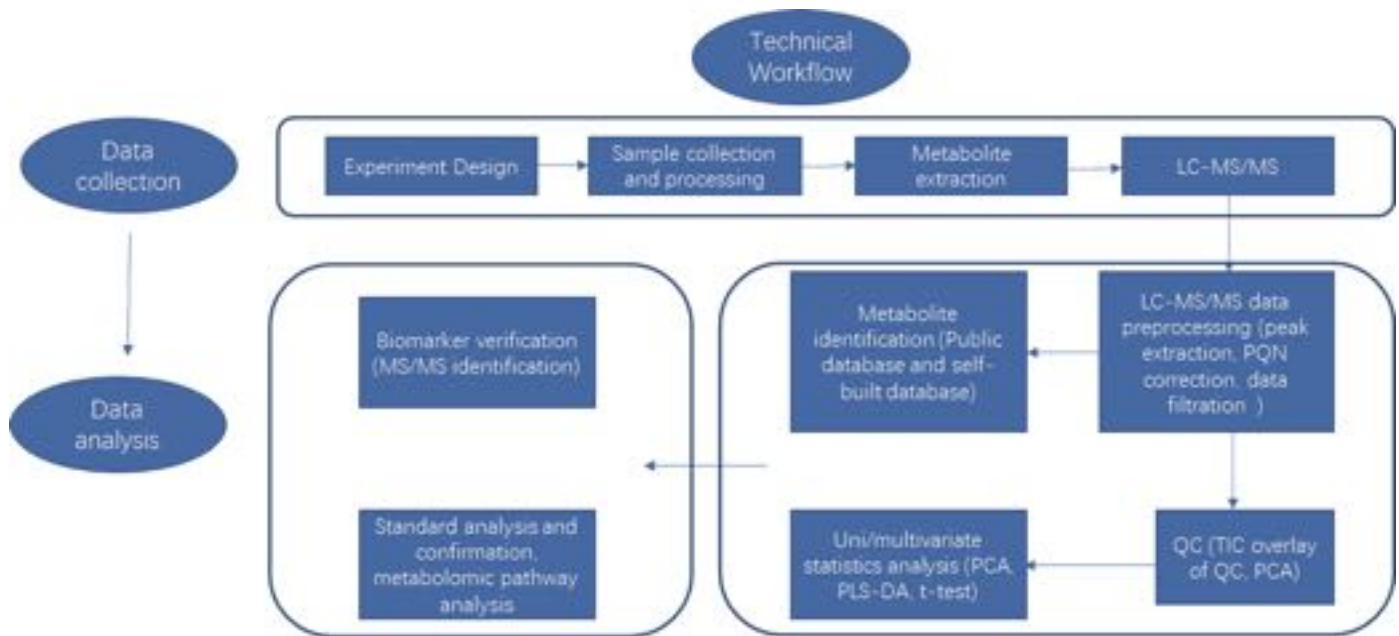
Vanquish UHPLC

- Column: BEH C18 & BEH Amide

Service Advantages

State-of-the-art LC-MS/MS systems	Rich large sample experience	High-precision identification results	Strict quality control system
<ul style="list-style-type: none">• Thermo Q Exactive™ HF-X• Resolution up to 24,000, ensuring high spectral quality and accurate results	<ul style="list-style-type: none">• High throughput automated sample preparation• Real-time monitoring instrument detection process	<ul style="list-style-type: none">• Self-built standard library + Thermo mzcloud (4000+)• 100% identification is achieved through the standards• Identification credibility rating	<ul style="list-style-type: none">• Strict protocols governing the whole workflow• Double quality control procoess of isotopic internal standard and QC samples

Untargeted Medical Metabolomics Workflow



Bioinformatics Analysis Workflow

Standard:

1.1 Data Processing

01

Peak extraction

02

Peak alignment

03

Metabolite identification

04

Missing value filling

05

Normalization

06

Low quality data filtering

1.2 Data Quality Control

01

BPC overlapping diagram of QC samples

02

PCA analysis of QC samples and real samples

03

CV distribution of metabolites in QC samples

1.3 Annotation of Metabolites

01

Classification and annotation of metabolites

02

Pathway annotation of metabolites

1.4 Statistical Analysis and Screening of Differential Metabolites

01

Univariate analysis (fold change and T test)

02

Multivariate analysis (PCA,PLS-DA)

03

Screening of differential metabolites

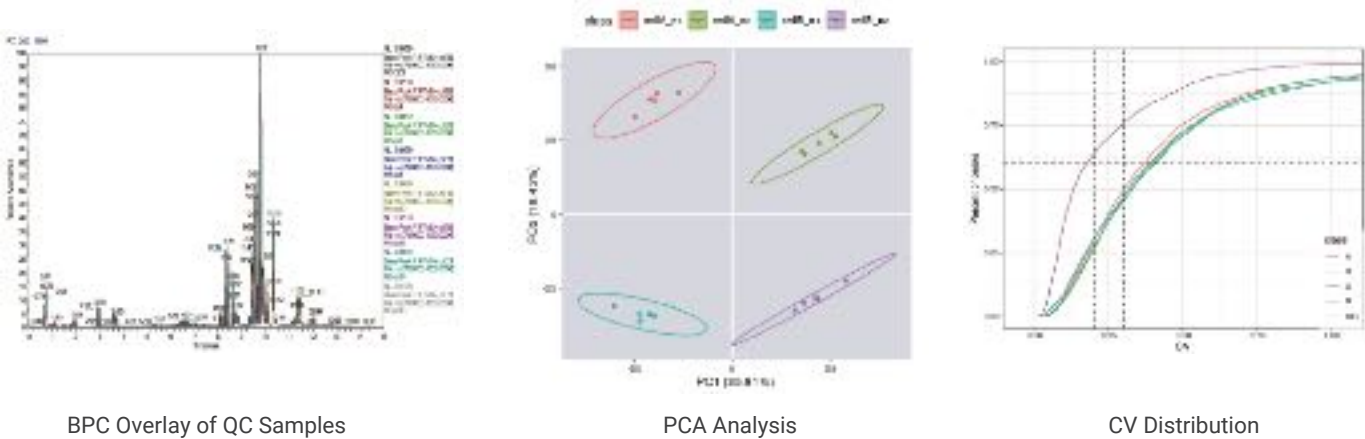
1.5 Cluster Analysis and Correlation Analysis of Differential Metabolites

1.6 Enrichment Analysis of Metabolic Pathways of Differential Metabolites

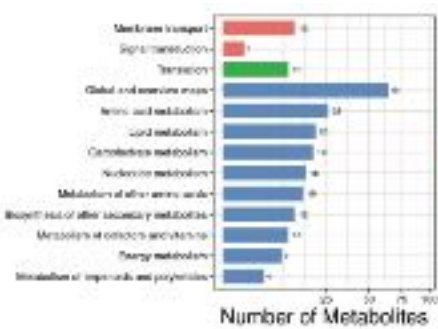
Customized:

- 16S/Metagenome + metabolome correlation analysis
- Transcriptome + metabolome correlation analysis
- Proteome + metabolome correlation analysis

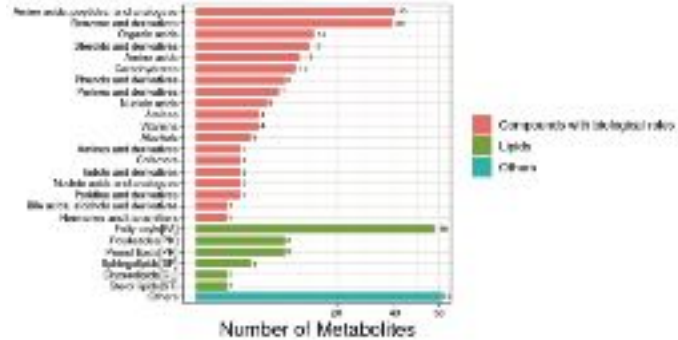
Examples of Data QC Analysis - Stability and Repeatability



Examples of Annotation of Metabolites

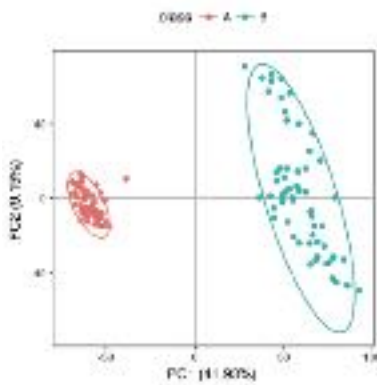


Metabolite Classification Bar Chart

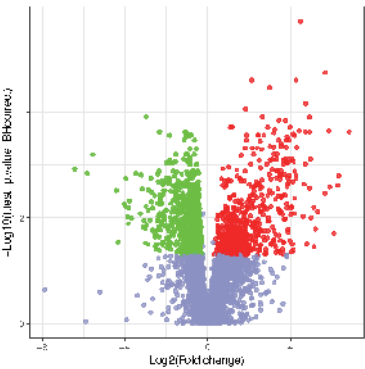


KEGG Function Comment Bar Chart

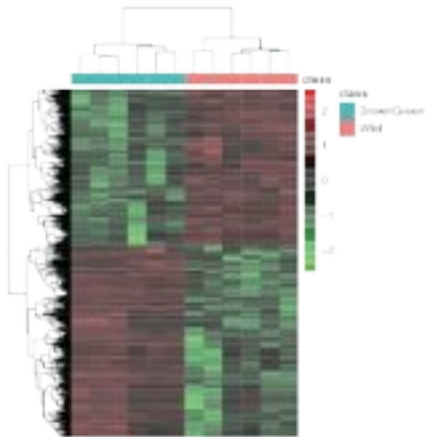
Examples of Statistical Analysis of Differential Metabolites



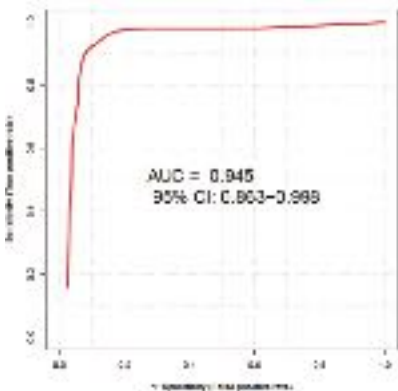
Score Graph of PLS-DA



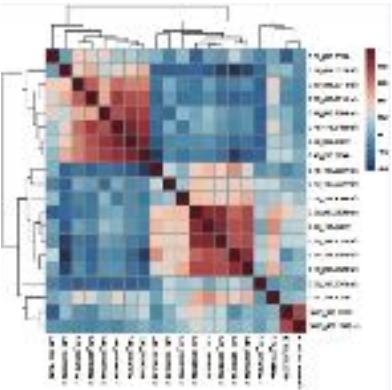
Volcano Plot



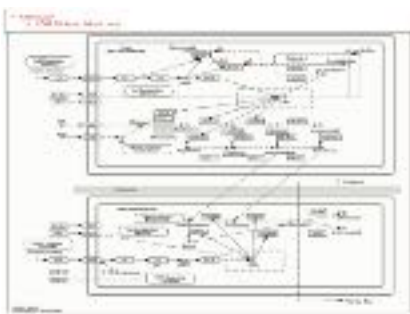
Cluster Analysis



ROC Curve



Metabolite Correlation Analysis



KEGG Metabolic Pathway

General Sample Requirements

SAMPLE TYPE	RECOMMENDED SAMPLE AMOUNT	MINIMUM SAMPLE AMOUNT
Serum, plasma,urine	≥ 300 μL	≥ 100 μL
Animal and clinical tissues	≥ 200 mg	≥ 25 mg
Feces and intestinal contents	≥ 200 mg	≥ 25 mg
Cell	≥ 1×10 ⁷	≥ 5×10 ⁶
Microorganism	≥ 1×10 ⁷ or ≥ 100 mg	≥ 5×10 ⁶ or ≥25 mg
Culture medium, fermentation medium	≥ 1 mL	≥ 100 μL
Plant tissue	≥ 1 g	≥ 100 mg
Milk	≥ 1 mL	≥ 100 uL
Other body fluids (amniotic fluid, saliva, hemolymph, cerebrospinal fluid, etc.)	≥ 300 μL	≥ 100 μL

Turn Around Time

Sample size: 1-50, 3-5 weeks



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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