METWARE BIO

'TM'
Widely-Targeted
Metabolomics

Technology introduction

"TM" Widely-Targeted Metabolomics combines high-resolution metabolite detection and QQQ metabolite quantification to achieve the perfect combination of high resolution, wide coverage, high sensitivity, and precise quantification. Metware's patented Widely-Targeted Metabolomics technology stands out with features such as:
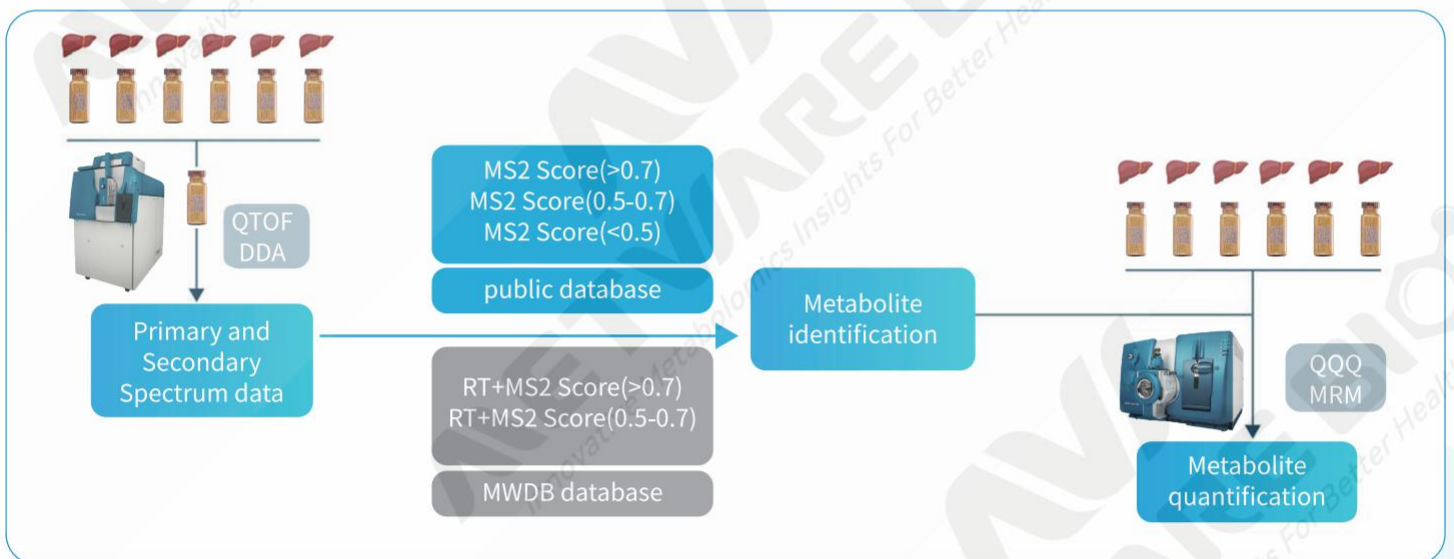
Using high-resolution mass spectrometers to allow unbiased collection of MS/MS spectrum data;

Highly curated metabolomics database providing accurate identification of over 1400 metabolites;

Using MRM analysis from QQQ to accurately quantify metabolites in each sample.

QTOF DDA

Primary and Secondary Spectrum data

MS2 Score(>0.7)
MS2 Score(0.5-0.7)
MS2 Score(<0.5)

public database

RT+MS2 Score(>0.7)
RT+MS2 Score(0.5-0.7)

MWDB database

Metabolite identification

QQQ MRM

Metabolite quantification

Technical Features

Large curated database

Collected ultra-high sensitivity data of over 280000 metabolites. Each sanmple can typically identify over 1400 metabolites.

Rigorous quality control

A mature quality control system monitoring all aspects of experimentation from sample preparetion to data collection.

Experienced

Stable and tested sample preparation protocol stemming from processing over 100000 samples a year.

Accurate identification

Combining AB SCIEX Q-TOF 6600 ultra-high resolution mass spectrum with our large curated database to achieve accurate metabolite identification.
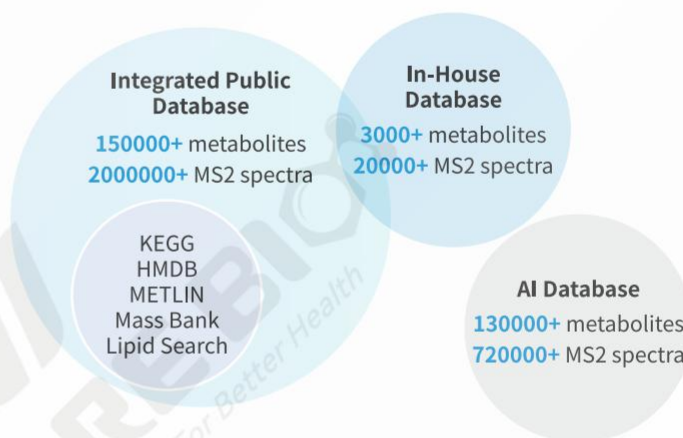
Accurate quantification

Using MRM mode from AB SCIEX QQQ 6500 to achieve accurate relative quantification of metabolites.
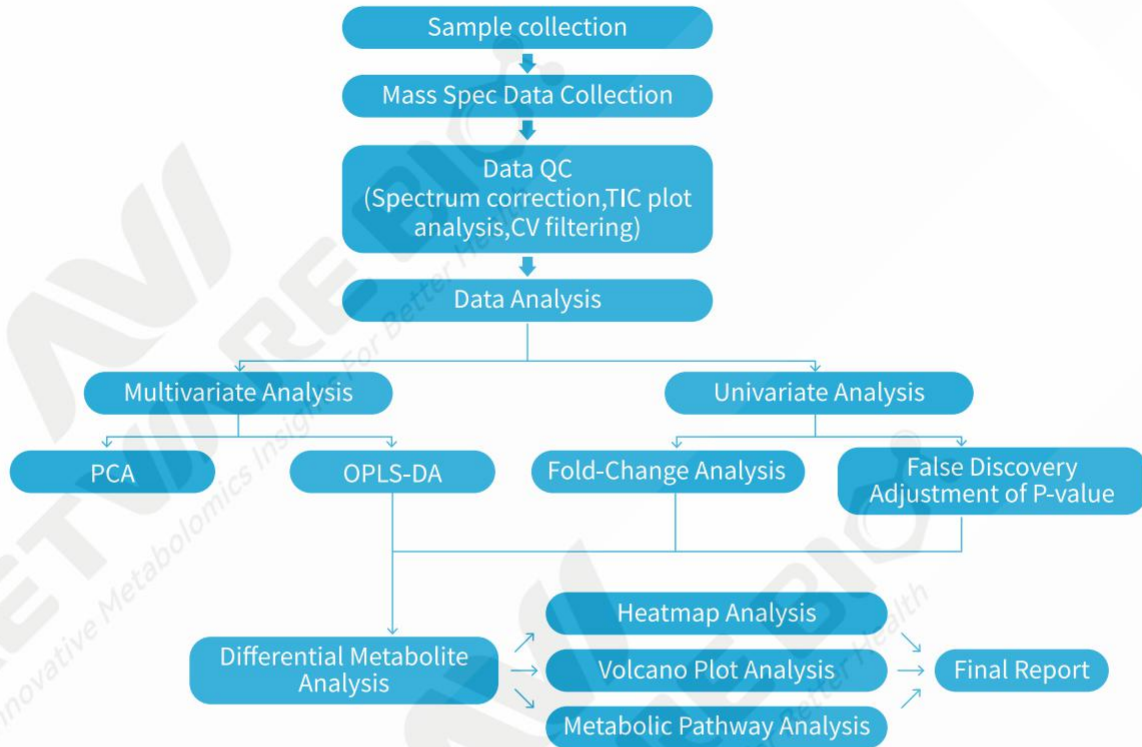
◆ List of metabolites

Our curated database contains over 280,000 metabolites, of which over 3,000 metabolites are from in-house standard database, over 150,000 metabolites from integrated public database, and over 130,000 metabolites from AI database. The integrated public database include KEGG, HMDB, Metlin, Mass Bank, Lipid Search and other common databases.

The in-house standard database contains 3000 metabolites with categories shown below:

Integrated Public Database
150000+ metabolites
2000000+ MS2 spectra

In-House Database
3000+ metabolites
20000+ MS2 spectra

KEGG
HMDB
METLIN
Mass Bank
Lipid Search

AI Database
130000+ metabolites
720000+ MS2 spectra

| Category	Quantity	Representative substance
Amino acids	600+	Glycine, L-threonine, L-arginine, N-acetyl-L-alanine
Organic acids	400+	3-hydroxybutyric acid, adipic acid, hippuric acid, kynurenine
Nucleotides	200+	Adenine, 5'-Adenine Nucleotide, Guanine, 2'-Deoxycytidine
Carbohydrates	100+	D-glucose, glucosamine, D-fructose 6-phosphate
Lipids	500+	O-acetylcarnitine, γ-linolenic acid, lysophosphatidylcholine 22:4
Benzenes	500+	Benzoic acid, 3,4-dimethoxyphenylacetic acid, 4-hydroxybenzoic acid
Coenzymes and vitamins	60+	Folic acid, pantothenic acid, vitamin D3
Alcohols, amines	150+	Dopamine, histamine, DL-1-amino-2-propanol
Aldehydes, ketones, esters	120+	Furfural, ethyl butyrate, α-pentyl cinnamaldehyde
Heterocyclic compound	200+	Pyridoxal, biopterin, indole-3-acetic acid
bile acid	40+	Glycocholic acid, deoxycholic acid, taurolithocholic acid
Hormones and hormone-related substances	100+	Juvenile hormone 3, epinephrine, 3,3'-diiodo-L-thyroxine
Tryptamine, choline, pigment	15+	Serotonin, bilirubin (E-E), urobilin
other	50+	Astaxanthin, hydroxyurea
total	3000+	3000+

Project workflow

```
Sample collection
      ↓
Mass Spec Data Collection
      ↓
Data QC
(Spectrum correction, TIC plot
analysis, CV filtering)
      ↓
Data Analysis
```

- Multivariate Analysis
  - PCA
  - OPLS-DA
- Univariate Analysis
  - Fold-Change Analysis
  - False Discovery Adjustment of P-value

- Differential Metabolite Analysis
  - Heatmap Analysis
  - Volcano Plot Analysis
  - Metabolic Pathway Analysis
- Final Report

Analysis content display

Sample Correlation Analysis

Intuitively see the correlation of metabolite contents between samples and sample groups.

In this plot, the labels along the left and the diagonal represent sample names. The color boxes represent Pearson correlation coefficients. The darker the red, the stronger the correlation and the darker the blue, the weaker the correlation.
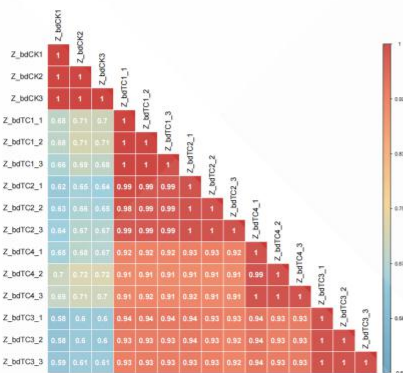
Principal Component Analysis (PCA)

Quickly determine the variance between samples and sample groups.

In PCA plot, each dot represents a sample and samples in the same group are shown with the same color. PC1 and PC2 represent the first and second principal component, respectively. Percentage value describe how well a principal component can explain the sample variance.
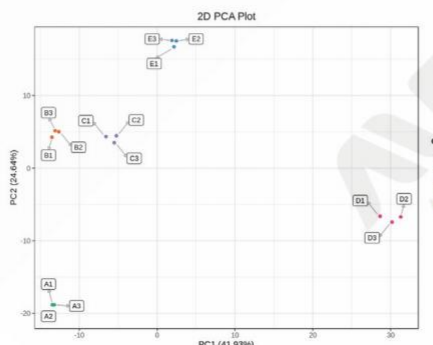
Orthogonal Projections to Latent Structures Discriminant Analysis (OPLS-DA)

OPLS-DA is a statistical model to find which variables are driving the difference between two groups. In this plot, the X-axis represents the predicted principal component and measures the difference between groups. The Y-axis represents the orthogonal principal component and measures the difference within a group. Percentage value indicates the degree to which the component explains the data set. Each dot in the figure represents a sample, samples in the same group are shown with the same color.
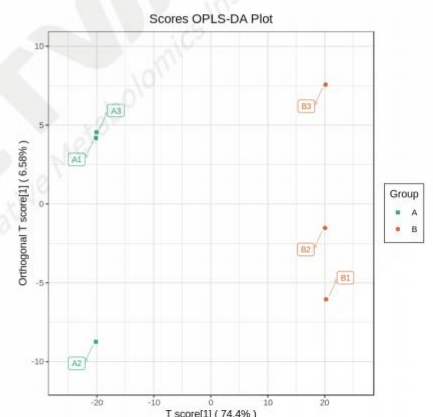
Volcano plot

A visual representation of relative differences and the statistical significance of metabolites between two samples or groups. Each point in the volcano plot represents a metabolite with green points represent significantly down-regulated metabolites, red points represent significantly up-regulated metabolites, and gray points represent detected metabolites with no significant differences. The X-axis represents the log2(fold-change) value of metabolites between two groups. The Y-axis represents the level of significance (-log10(p-value)). The size of each dot represents the Variable Importance in Projection (VIP) value.
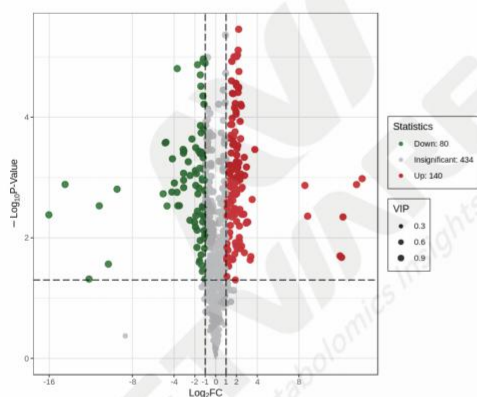
Chord Plot

This plot captures the correlation of a metabolite with other metabolites. In this figure, the outermost layer shows the differential metabolites. The second layer shows log2FC value as circles and the circle size proportional to FC values. The color for the first and second layer represent different metabolite classification. The chords in the inner most layer reflect the Pearson correlation between the connected metabolites. Red chords represent positive correlation and the blue chords represent neg.
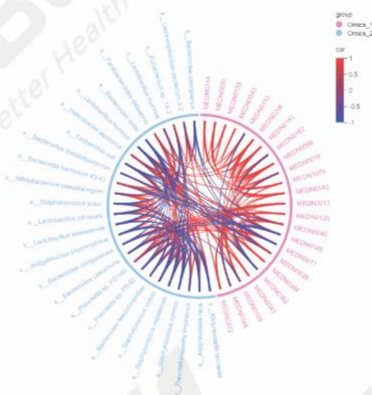
Venn diagram

It is a powerful way to depict differential metabolites that are unique or shared between comparisons. Each enclosure represents a comparison group. The number in overlapped parts represent the number of common differential metabolites between comparison groups, and the number in non-overlapped parts represents the number of unique differential metabolites.
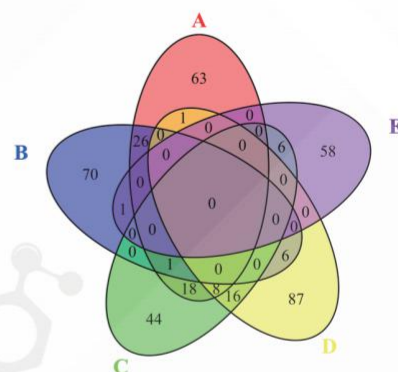
◆ Sample requirements

Sample type	Sample	Recommended sample	Minimum sample	Biological duplication
liquid	Plasma, serum, hemolymph, milk, egg white	100 μL	20μL	samples＞6 clinical samples＞30
	Cerebrospinal fluid, tear fluid, interstitial fluid, uterine fluid, pancreatic fluid and bile, pleural effusion, follicular fluid, corpse fluid	100 μL	20μL	samples＞6 clinical samples＞30
	Seminal plasma, amniotic fluid, prostate fluid, rumen fluid, respiratory condensate, gastric lavage fluid, alveolar lavage fluid, urine, sweat, saliva, sputum	500 μL	100 μL	samples＞6 clinical samples＞30
tissue	Animal tissue, placenta, thrombus, fish skin, mycelium, nematode	100 mg	20 mg	samples＞6 clinical samples＞30
	Whole body, aircraft (wings), pupae	500 mg	20 mg	samples＞6 clinical samples＞30
	Zebrafish organs, insect organs	20	10	samples＞6 clinical samples＞30
cell	Adherent cells	1*10^6	5*10^5	samples＞6
	Escherichia coli and other microorganisms	1*10^10	5*10^8	samples＞6
stool	Feces, intestinal contents	200 mg (Wet weight)	50 mg (Wet weight)	samples＞6 clinical samples＞30

Applications

"TM" widely-targeted metabolomics is perfect for:

Clinical marker discovery and development

Understanding mechanisms behind disease progression

Studying drug efficacy and toxicity

Environmental toxicology research

Selected publications

Year	Journal	Title
2022	Food Research International	Transcriptomic and metabolomic analysis reveals the potential mechanisms underlying the improvement of β-carotene and torulene production in Rhodosporidiobolus colostri under low temperature treatment
2021	Signal Transduction and Targeted Therapy	SARS-CoV-2 infection causes immunodeficiency in recovered patients by downregulating CD19 expression in B cells via enhancing B-cell metabolism
2021	Theranostics	Multi-omic profiling of plasma reveals molecular alterations in children with COVID-19
2021	Clinical and Translational Medicine	Genome-wide association study of metabolites in patients with coronary artery disease identified novel metabolite quantitative trait loci
2021	Clinical infectious disease	Plasma metabolomic profiling of patients recovered from COVID-19 with pulmonary sequelae 3 months after discharge
2021	Brain Behavior and Immunity	Metformin restores hippocampal neurogenesis and learning and memory via regulating gut microbiota in the obese mouse model
2020	Signal Transduction and Targeted Therapy	Omics study abnormal alterations of breastmilk proteins and metabolites in puerperant women with COVID-19
2020	National Science Review	Plasma Metabolomic and Lipidomic Alterations Assocaitaed with COVID-19
2020	Science of the Total Environment	Transcriptomic and metabolomic landscape of the molecular effects of glyphosate commercial formulation on Apis mellifera ligustica and Apis cerana cerana