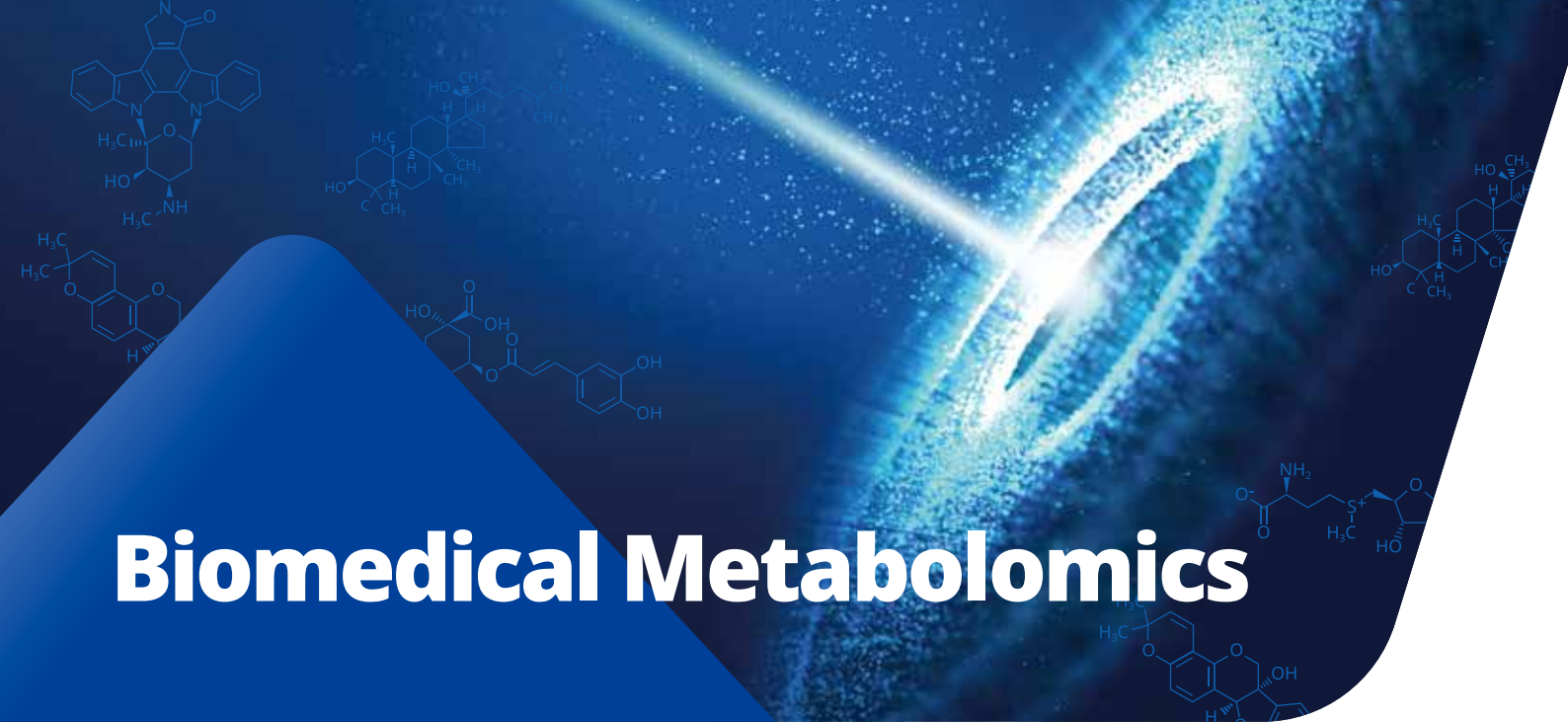


Biomedical Metabolomics

METWARE BIO

Innovative Multi-Omics Insights for Better Health

Genes will tell you what may happen,
Metabolites tell you what is happening or has happened.

Artemisinin
-
Taxol
-
Ginsenoside

Dopamine
-
Serotonin
-
Neurotransmitter

Epinephrine

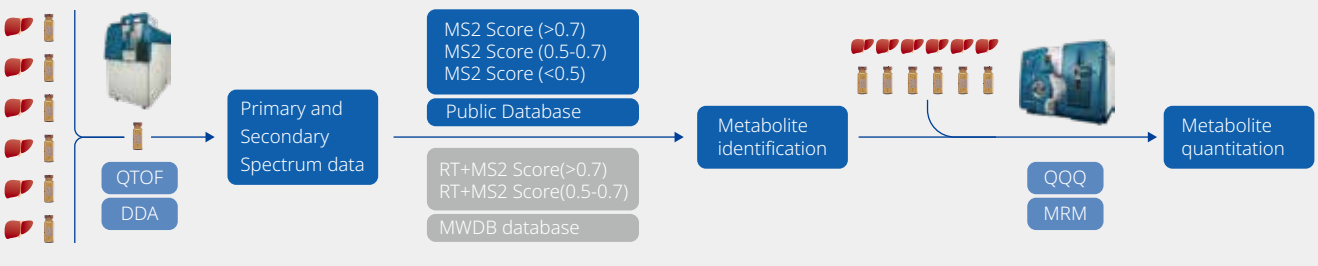
Vitamin
-
Polyphenol
-
Fatty Acid

Uric Acid
-
Blood Sugar
-
Blood Fat

The Power of Widely-Targeted Metabolomics Technology

Widely-Targeted Metabolomics

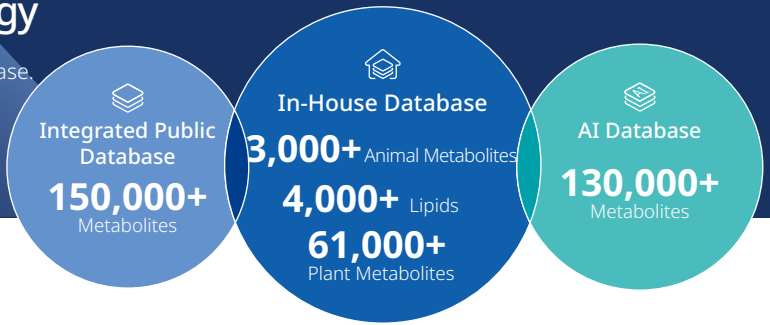
- Large-Curated Database
- Wide Coverage of Metabolites
- High-throughput
- Accurate Identification and Precise Quantitation



Global Metabolite Profiling	Targeted Metabolomics	Lipidomics	Our Expertise
61,000+ plant metabolites	1,000+ metabolites	4,000+ lipids	100+ patents
3,000+ animal metabolites			1,000+ publications
			20,000+ projects

Comprehensive Identification Strategy

Accurate Identification based on our large-curated in-house database.



In-house Biomedical Database

Category	Quantity	Representative substance
Amino acids and their derivatives	600+	glycine, L-threonine, L-arginine, N-acetyl-L-alanine
Organic acids and their derivatives	400+	3-hydroxybutyric acid, adipic acid, hippuric acid, kynurenine
Nucleotides and their derivatives	200+	adenine, 5'-adenine nucleotide, guanine, 2'-deoxycytidine
Carbohydrates and their derivatives	100+	D-glucose, glucosamine, D-fructose 6-phosphate
Lipids	500+	O-acetylcarnitine, γ-linolenic acid, lysophosphatidylcholine 22:4
Benzene and its derivatives	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 compounds	200+	pyridoxal, biopterin, indole-3-acetic acid
Bile acids	40+	glycocholic acid, deoxycholic acid, taurolithocholic acid
Hormones and hormone-related substances	100+	juvenile hormone 3, epinephrine, 3,3'-diiodo-L-thyroxine
Tryptamines, Cholines, Pigments	15+	serotonin, bilirubin (E-E), urobilin
Others	50+	astaxanthin, hydroxyurea
Total		**3,000+**

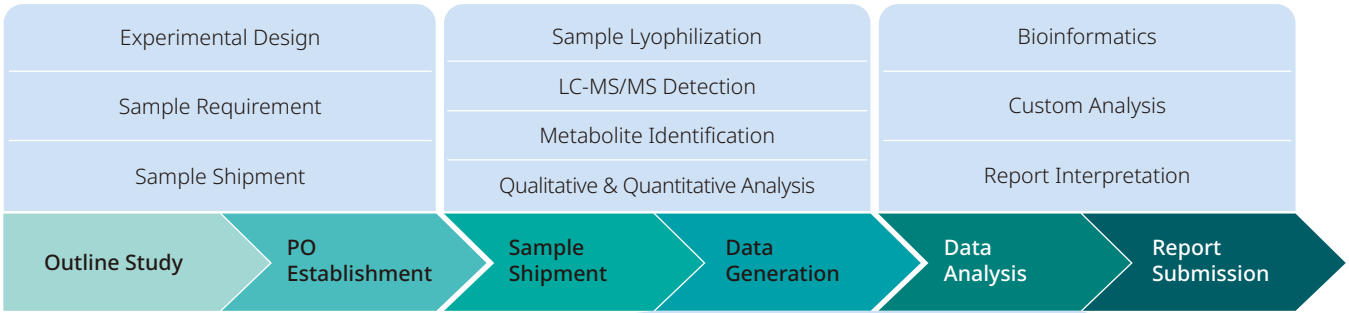
Precise Quantitation

- **Gold Standard for Quantitation**

  Using MRM mode from AB SCIEX Triple Quad 6500+

- **Rigorous Quality Control**

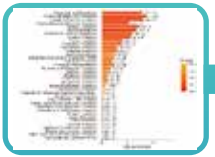
  Monitoring all aspects of experimentation from sample preparetion to data analysis.



Quality Control

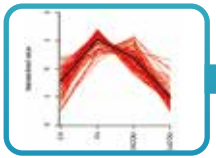
Instrument Monitoring	Data Generation	Data Analysis
Solvent QC	Internal Standards	QC-PCA
Mixed-Standards	Mixed Sample	QC-RSD
Plasma QC	Blank Sample	
Repeated Injection of QC	Random Sampling	

Comprehensive Bioinformatics Analysis



MSEA Enrichment

HMDB Enrichment

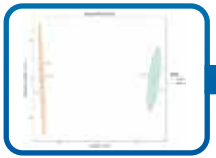


K-means Cluster

Z-value Map

Chord Diagram

Radar Map



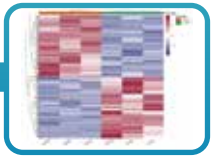
OPLS-DA Analysis

KEGG Regulation Network

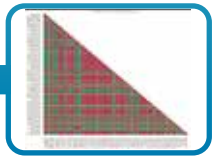
KEGG Pathway

Correlational Network

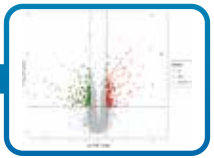
Cluster Heatmap



Correlation Analysis



Volcano Plot



PCA Analysis

Solutions for All Industries

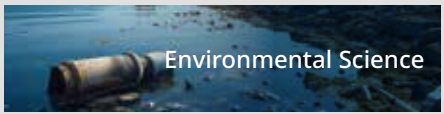
- Clinical Marker Discovery
- Disease Mechanisms

- Plant Stress Resistance Analysis
- Crop Quality Improvement
- Growth and Development Regulation

- Mechanism of Treatment
- Toxic Side Effect Evaluation

- Genetic Breeding
- Feed Nutrition
- Animal Diseases

- Efficacy Evaluation
- Drug Toxicity Assessment



- Environmental Toxicology Research

Comprehensive analytical portfolio

Global Metabolite Profilling	Targeted Metabolomics	Multi-Omics
Widely-Targeted Metabolomics	Energy Metabolism, Bile Acid	Transcriptome+Metabolomics
Untargeted Metabolomics	Oxylipin, Amino Acid, SCFA	Microbiome+Metabolome
Spatial Metabolomics	Steroid Hormone, Tryptophan Metabolism	Proteomics+Metabolomics
Lipidomics: Quantitative Lipidomics	Neurotransmitter, Phytohormone	Transcriptomics + Proteomics + Metabolomics
	Carotenoid, Anthocyanin	
	Customized Targeted Assay	

For other multi-omics services, contact us please!

Untargeted Metabolomics Plus

The untargeted metabolomics is used for unbiased detection of metabolites in samples by LC-MS/MS and to obtain their qualitative and quantitative information. The main research idea is to compare the case group with the control group to find the differential metabolites and metabolic pathways between the groups, which can provide clues and directions for the research of disease biomarker development, pathogenesis and drug treatment mechanism. In our novel untargeted metabolomics approach, employing a HILIC column in addition to the C18 column substantially enhances the detection of highly polar metabolites, such as amino acids and their derivatives, nucleotides, and other metabolites crucial to energy metabolism.

Large Curated Database
Over **280,000** metabolites

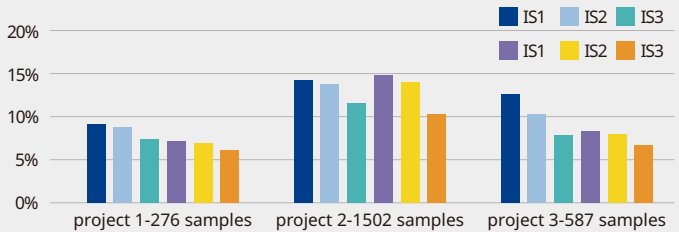
Comprehensive Identification Strategy
① In-house standard database
② Integrated public database
③ AI database
④ metDNA algorithm

Comprehensive Metabolic Detection
Covering metabolites with strong polar and non-polar compounds using C18 and HILLIC column

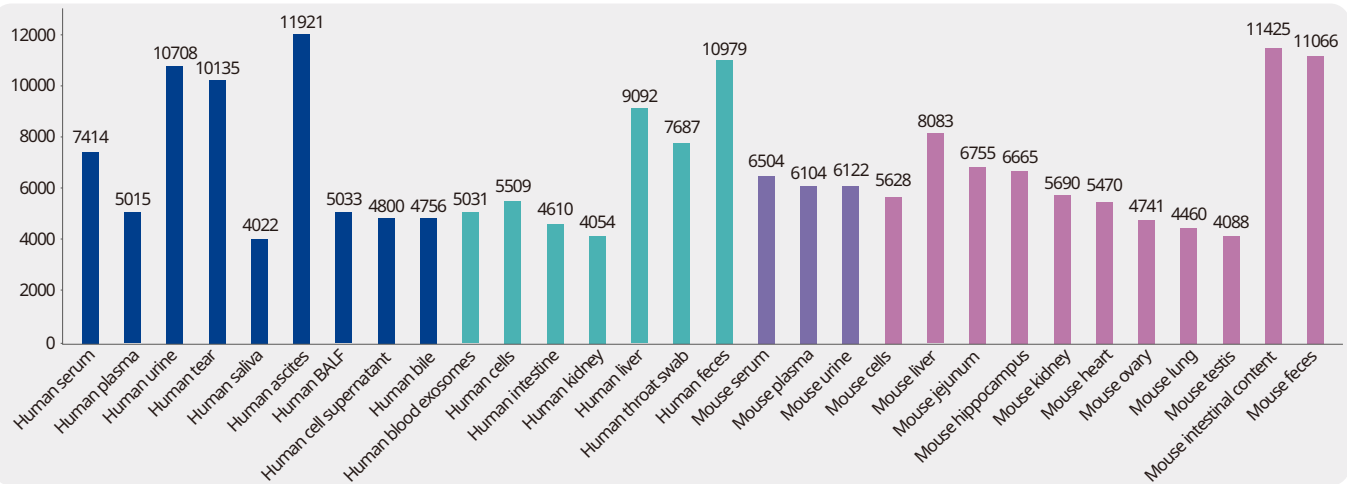
Rigorous Quality Control
Monitoring all aspects of experimentation from sample preparation to data collection.

Stability

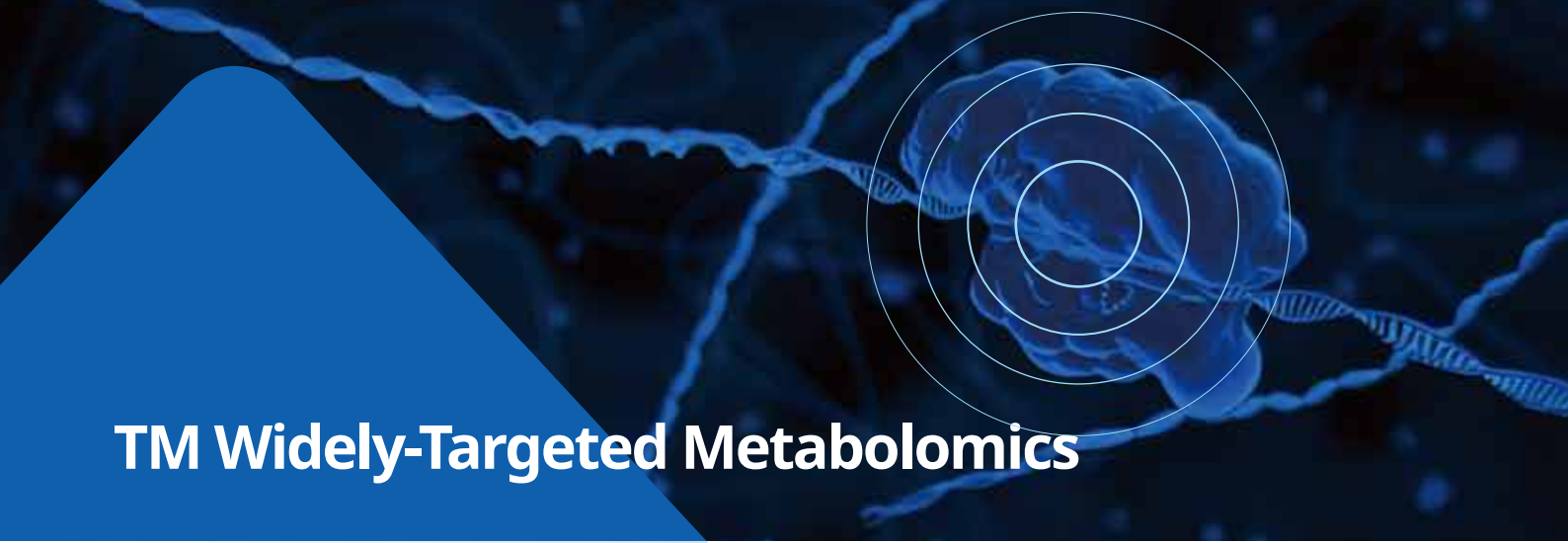
Highly stable detection for untargeted metabolomics analysis. Coefficient of variation (CV) of six internal standards are less than 15% in large cohort samples from 3 projects.



Project Experience



Number of metabolites identified from various sample types using MetwareBio's untargeted metabolomics approach.



TM Widely-Targeted Metabolomics

The TM Widely-Targeted Metabolomics assay combines an untargeted approach using QTOF in DDA mode with a targeted approach using QQQ in MRM mode, achieving accurate relative quantification while maintaining broad metabolite coverage. This integrated strategy typically enables the identification and annotation of over 1,400 metabolites with high quantitative precision across a wide range of sample types.

Large Curated Database

Over 3,000 metabolites are from in-house purified chemical standards

Rigorous Quality Control

10 QC Indicators

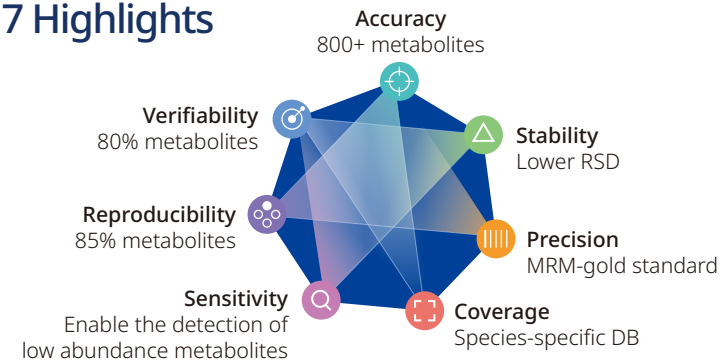
Accurate Identification

AB SCIEX QTOF 6600+

Precise Quantitation

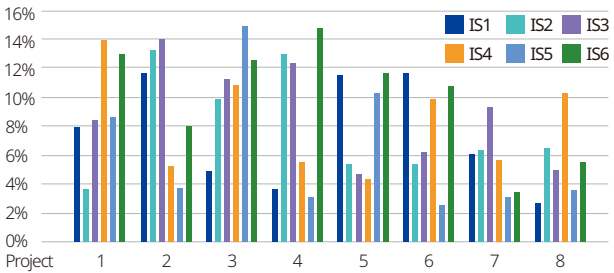
AB SCIEX Triple Quad 6500+

7 Highlights

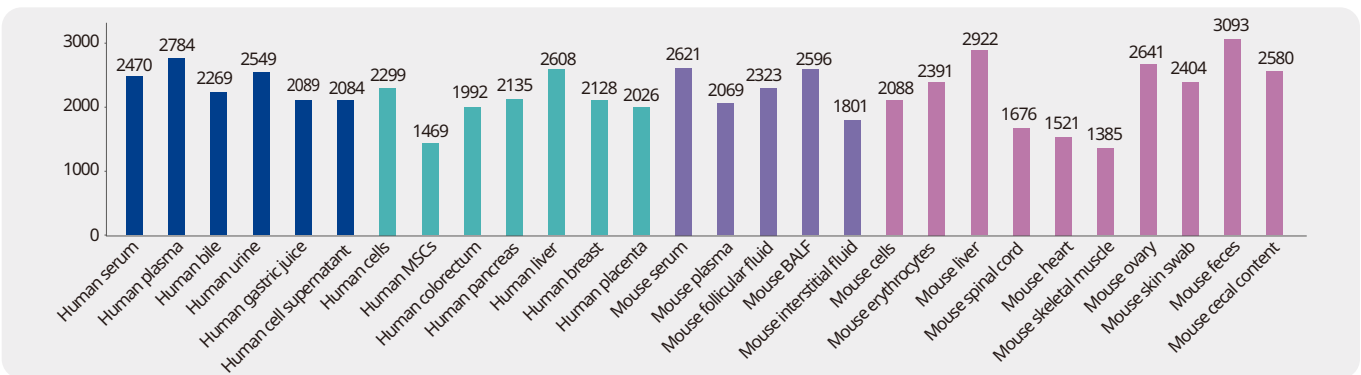


High Stability

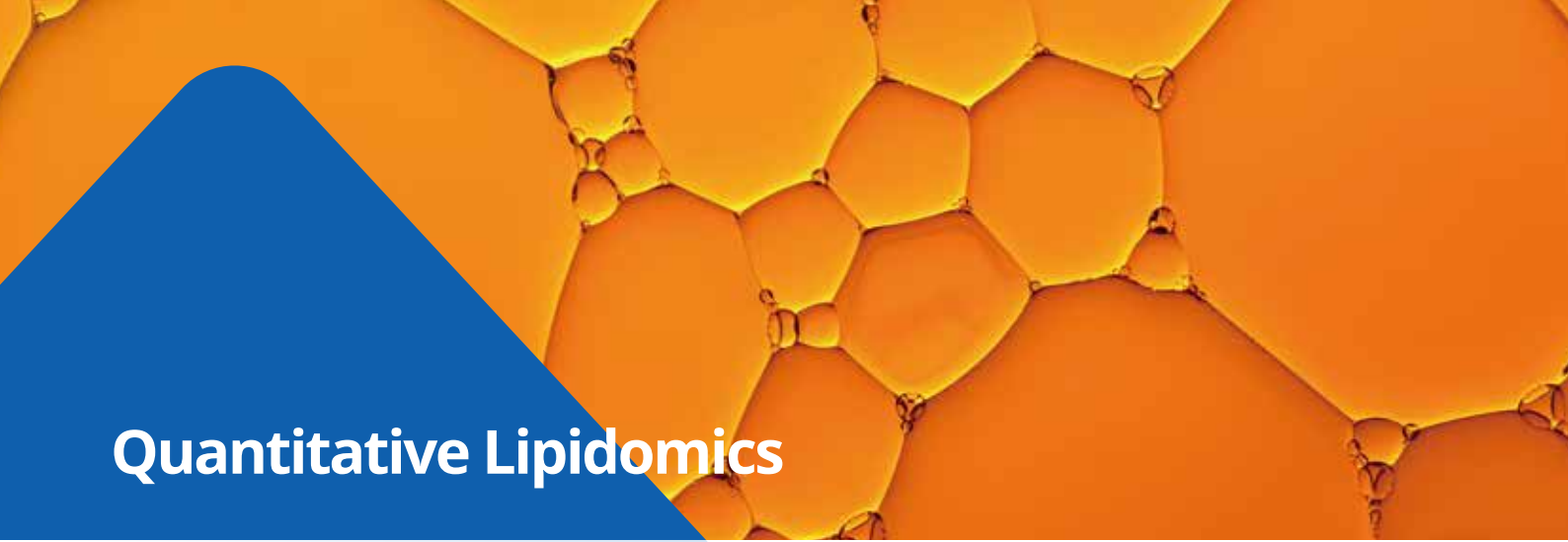
CV of six internal standards over 8 projects.



Project Experience



Number of metabolites identified from various sample types using MetwareBio's TM widely-targeted metabolomics approach.



Quantitative Lipidomics

Quantitative Lipidomics is a high-throughput targeted approach to enable the simultaneous identification and absolute quantitation of thousands of lipids in a single experiment.

High-Throughput
4,000+ lipids

High Accuracy
200+ chemical standards
54 internal standards
absolute quantitation

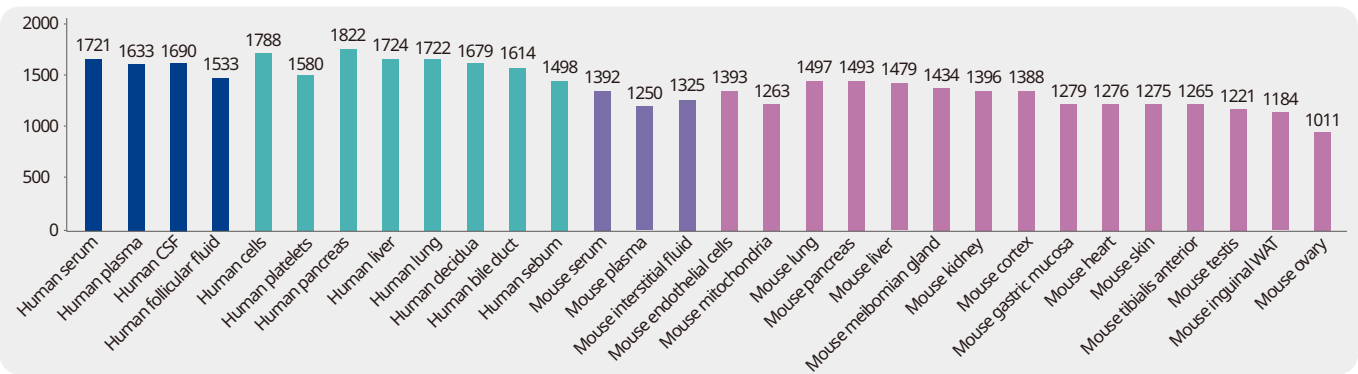
High Sensitivity
pg level

High Reproducibility
data correction

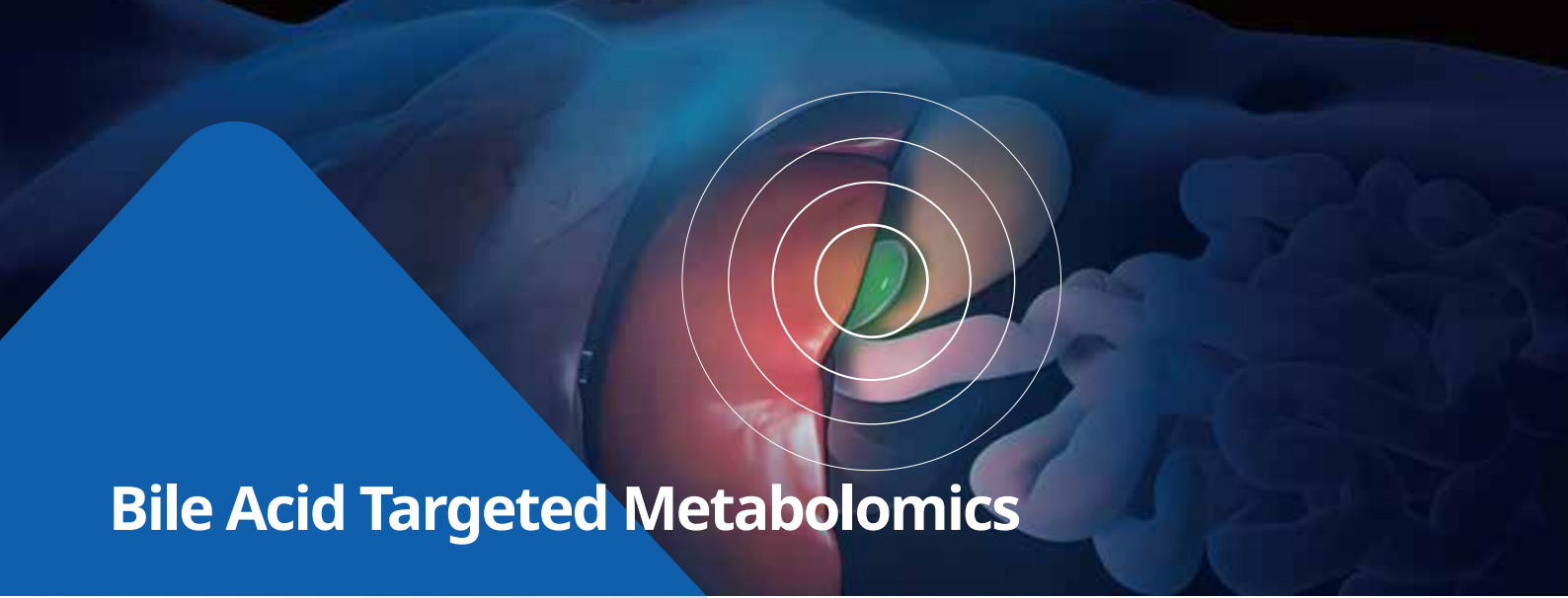
List of Lipids

Number of Lipids		
Class I	**Class II**	**Number**
Fatty Acyls (FA)	CAR, FFA, Eicosanoid, FAHFA	270
Glycerolipids (GL)	DG,DG-O,MG, TG,TG-O,MGDG,DGDG	1,015
Glycerophospholipids (GP)	LPC,LPC-O,LPE,LPE-P,LPG,LPS,PC,PC-O,PE,PE-P,PE- O,PG,PS,LPI,PI,LPA,PA,PMeOH,BMP,HMBP,LNAPE	1,800
Sphingolipids (SL)	SPH, CerP, HexCer, SM, Cer, Cert	828
Sterol Lipids (ST)	Cho, CE, BA, CASE	122
Prenol Lipids (PR)	CoQ	3
Total	**4,000+**	

Project Experience



Number of lipids identified from various sample types using MetwareBio's quantitative lipidomics approach.



Bile Acid Targeted Metabolomics

Bile acid products can be divided into free and conjugated bile acids, or primary and secondary bile acids. With our own bile acid database, MetwareBio offers absolute quantitation of **82** bile acids in a single run.

r>0.99

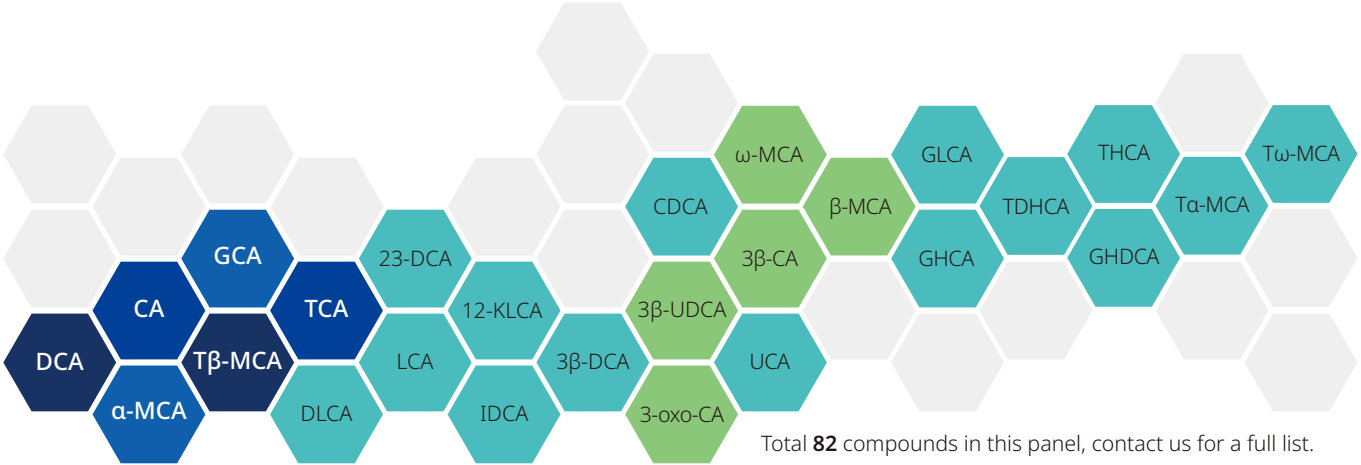
Absolute Quantitation
82 standard curves, r > 0.99,
15 isotope internal standards

ng/ml

High Sensitivity
ng/ml level

82

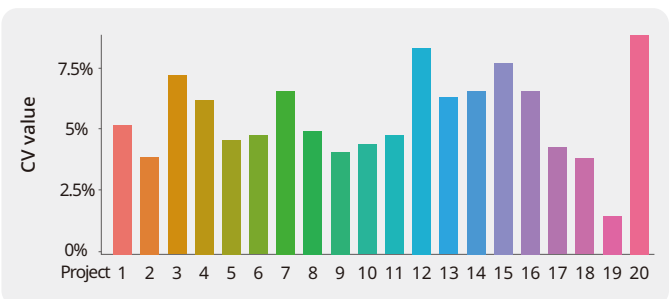
Wide Coverage
Covering large number of essential bile acids



Total **82** compounds in this panel, contact us for a full list.

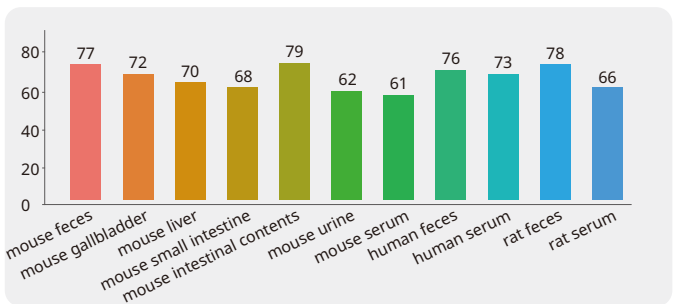
High Stability

Highly stable detection for bile acid analysis. Coefficient of variation (CV) of detected metabolites are less than 8% in mixed QC samples.



Project Experience

A total of 82 metaolites could be detacted from various tissue samples, with an average detection of 71 metabolites.



Acceptable Samples: liquid (plasma, serum, hemolymph, bile), tissue (animal tissue, placenta, thrombus), feces and intestinal contents.

Energy Metabolism

Energy metabolism is the process of generating energy (ATP) from nutrients such as glucose and fatty acids through pathways such as the amino acid pathway, glycolysis pathway, tricarboxylic acid cycle (TCA cycle), and pentose phosphate pathway (PPP). MetwareBio's Energy Metabolism Targeted Metabolomics obtains absolute quantitative results on 80 energy related metabolites from various fluid and tissue samples.

r>0.99

Absolute Quantitation

80 standard curves, r>0.99,
38 isotope internal standards

ng/ml

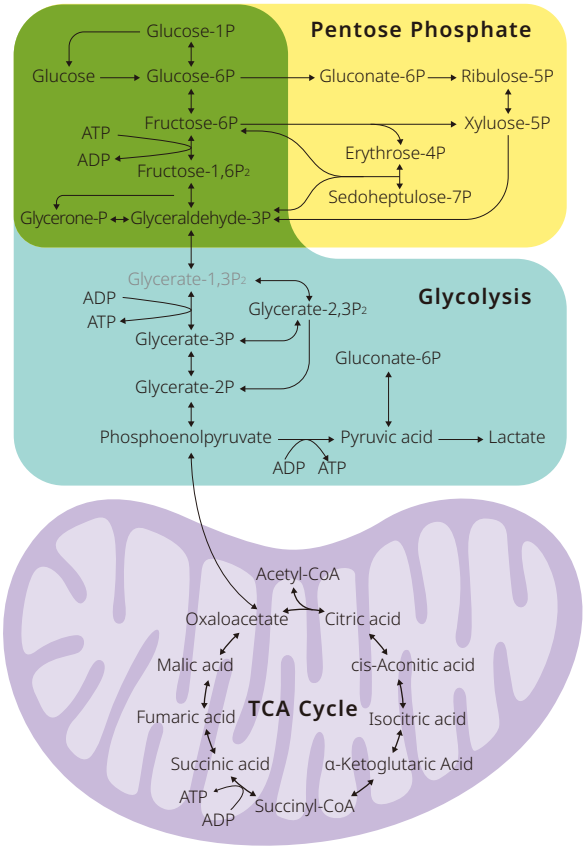
High Sensitivity

ng/ml concentration can be detected

80 compounds

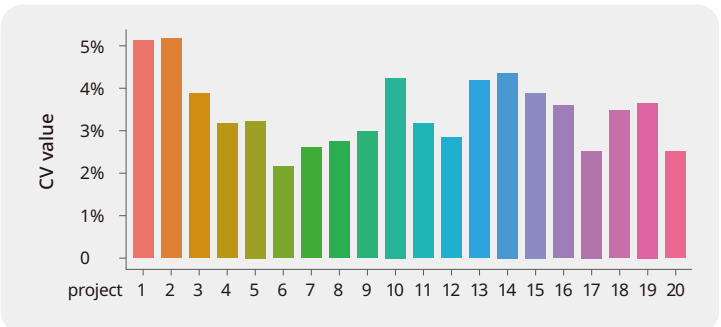
Wide Coverage

the panel covers 80 compounds in the three major pathways



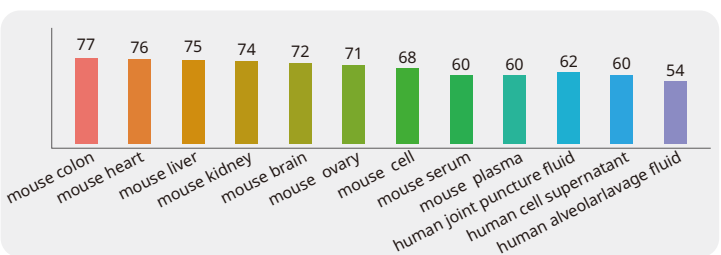
High Stability

The detected metabolites showed a coefficient of variation (CV) of less than 6% in mixed QC samples.



Project Experience

A total of 80 metabolites could be detected from various tissue samples, with an average detection of 68 metabolites.



Amino Acid Targeted Assay

Delivering absolute quantitation of a wide-coverage of **94 amino acid compounds** (inculding 8 essential amino-acid) from wide varieties of species and tissue types.

r>0.99

Absolute Quantitation

94 standard curves,**r>0.99**, isotope internal standards

ng/ml

High Sensitivity

Detection at **ng/mL** level

94 compounds

Broad Coverage

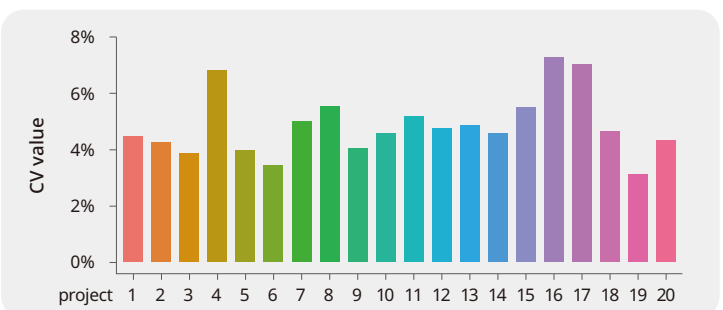
Up to **94** amino acid compounds

94 Amino Acid Compounds

2-Aminoethanesulfonic Acid	L-Proline	N6-Acetyl-L-Lysine	Homo-L-arginine
L-Cystine	L-Serine	Phosphorylethanolamine	L-Tryptophyl-L-glutamic acid
1,3-Dimethyluric Acid	L-Tryptophan	Anserine	Nicotinuric Acid
N-Propionylglycine	L-Phenylalanine	Trans-4-Hydroxy-L-Proline	N-Acetylneuraminic Acid
N-Isovaleroylglycine	Sarcosine	D-Homocysteine	N,N-Dimethylglycine
Succinic Acid	L-Pipecolic Acid	α-Aminoadipic acid	4-Acetamidobutyric Acid
5-Hydroxy-tryptophan	L-Theanine	L-Ornithine	L-Carnosine
3,7-Dimethyluric Acid	Ethanolamine	L-tyrosine methyl ester	3-Chloro-L-Tyrosine
Glycine	3-N-Methyl-L-Histidine	γ-Glutamate-Cysteine	S-(5-Adenosy)-L-Homocysteine
L-Alanine	Homoserine	Nα-Acetyl-L-glutamine	N'-Formylkynurenine
L-Valine	Creatine	N-Acetyl-L-Tyrosine	···
L-Leucine	Kinurenine	γ-Aminobutyric Acid	
L-Methionine	L-Cystathionine	D-Alanyl-D-Alanine	**Contact for a full list.**

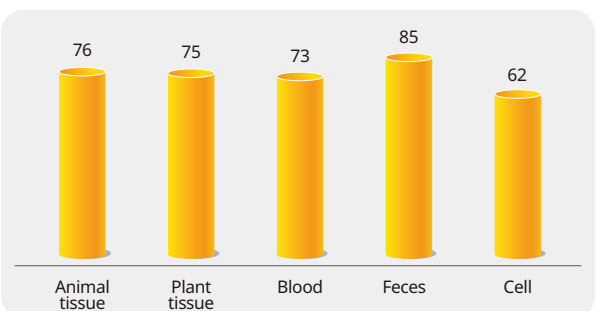
High Stability

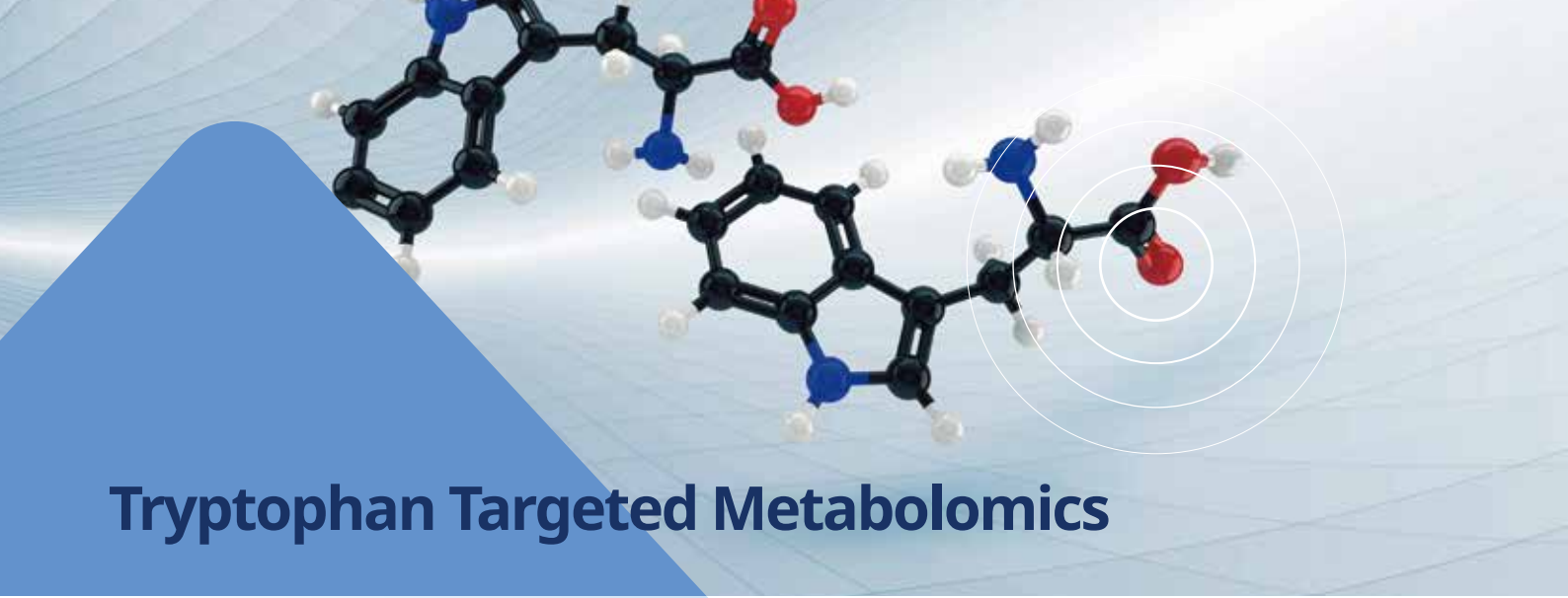
Highly stable detection for amino acid analysis. Coefficient of variation (CV) of detected metabolites are less than 8% in mixed QC samples.



Project Experience

Average detected metabolites in different tissue and sample types.





Tryptophan Targeted Metabolomics

Tryptophan acts as a precursor to serotonin, melatonin, and vitamin B3, and a crucial member of in the kynurenine pathway and AhR Pathway. Metwarebio's tryptophan-targeted metabolomics assay enables simultaneous absolute quantification of 38 metabolites associated with tryptophan.

r>0.99

Absolute Quantitation

38 standard curves, r>0.99, 24 isotope internal standards

ng/ml

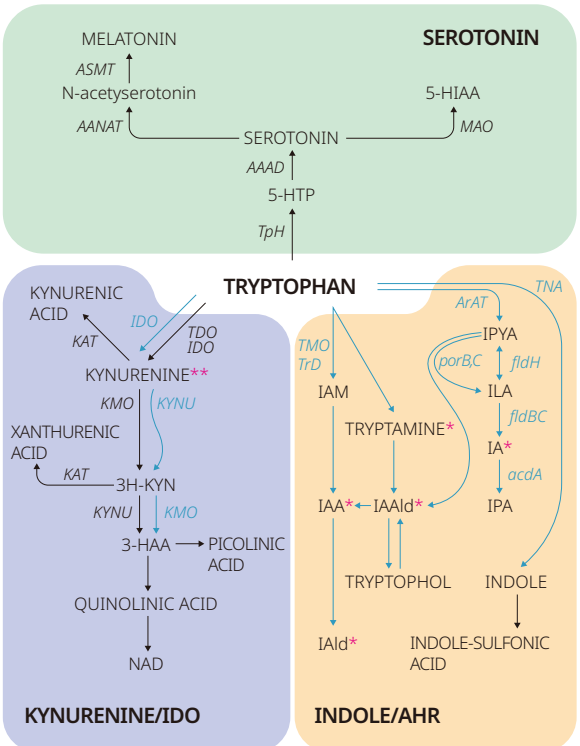
High Sensitivity

ng/ml concentration can be detected

38

Wide Coverage

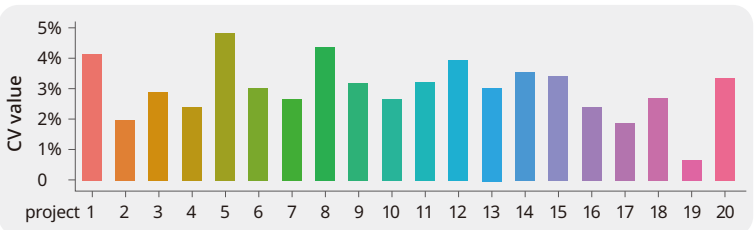
Covering 38 compounds in three pathways



* AhR ligands
** Potential AhR ligand but in supraphysiological concentrations
→ Host pathway
→ Microbial pathway

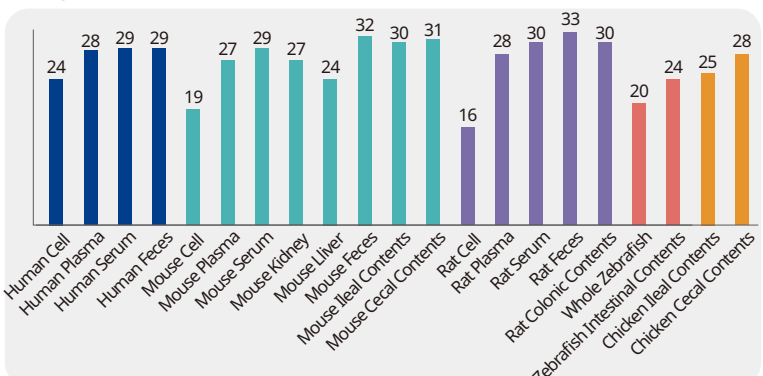
High Stability

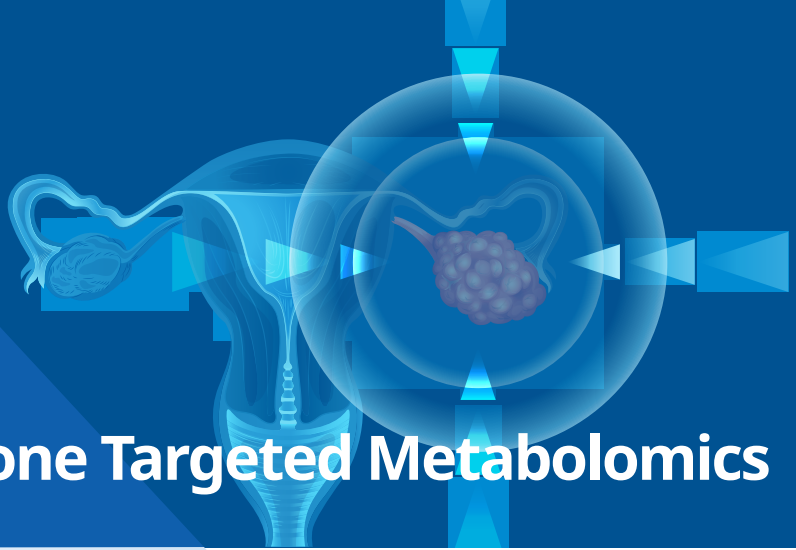
The detected metabolites showed a coefficient of variation (CV) of less than 6% in mixed QC samples.



Project Experience

A total of 38 metabolites could be detected from various samples, with an average detection of 26 metabolites.





Steroid Hormone Targeted Metabolomics

Steroid hormones, derived from cholesterol and produced by the gonads and adrenal glands, include androgens, estrogens, progestogens, glucocorticoids, and mineralocorticoids, regulating processes like reproduction, stress response, and fluid balance. MetwareBio's steroid hormone targeted metabolomics service offers simultaneous absolute quantification of 43 steroid hormones.

r>0.99

Absolute Quantitation

43 standard curves, **r>0.99**

ng/ml

High Sensitivity

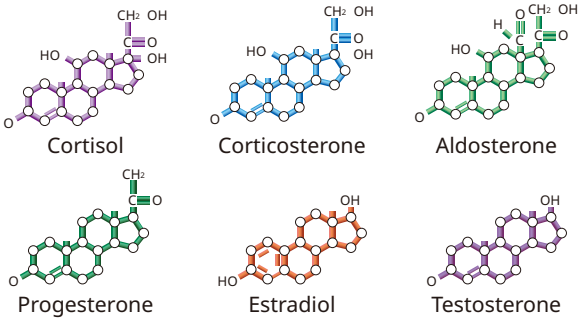
ng/ml concentration can be detected

43

Wide Coverage

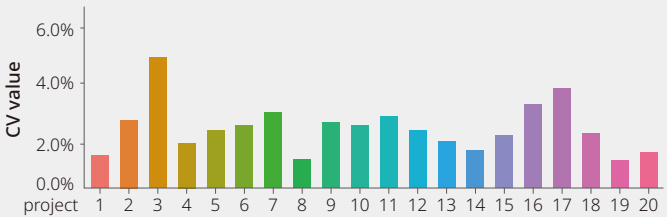
Covering **43** steroid hormones

Six Steroid Hormone Classes



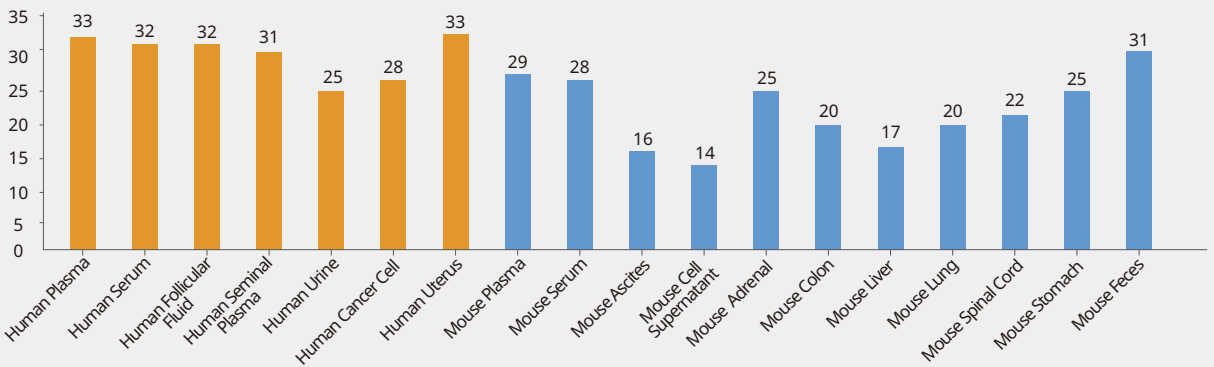
High Stability

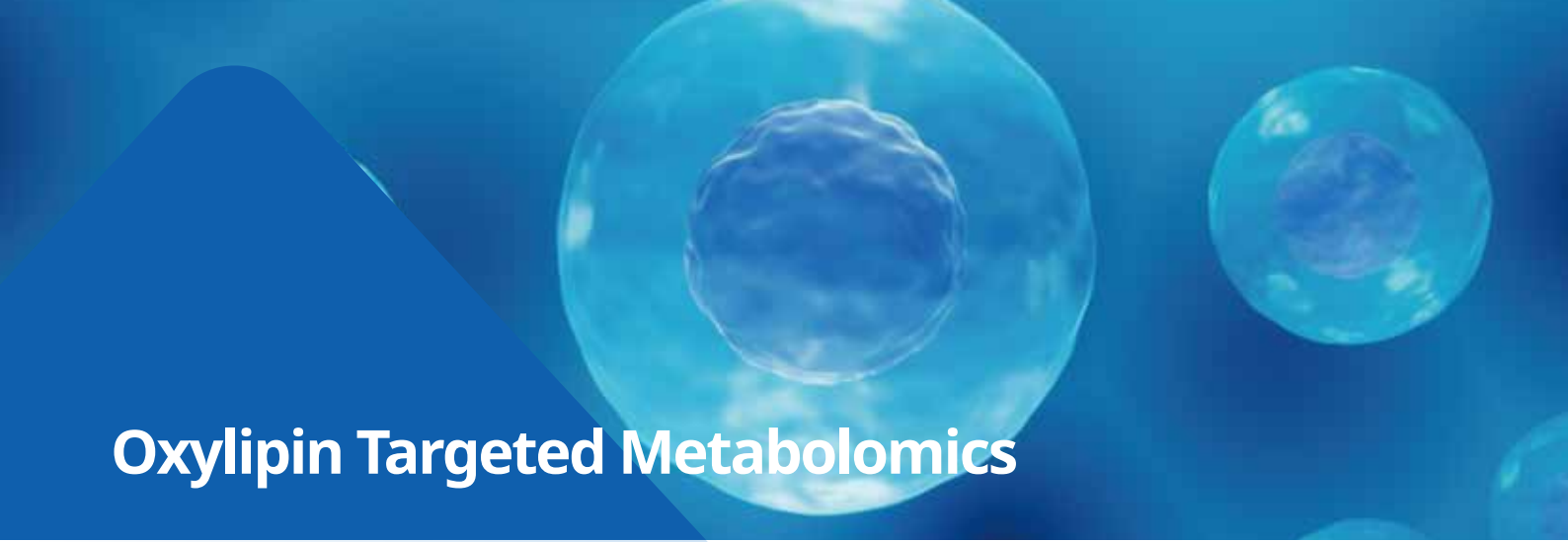
The detected metabolites showed a coefficient of variation (CV) of less than 5% in mixed QC samples.



Project Experience

A total of 43 metabolites could be detected from various samples, with an average detection of 25 metabolites





Oxylipin Targeted Metabolomics

Oxylipins, bioactive lipids derived from the oxidation of omega-3 and omega-6 PUFAs via COX, LOX, and CYP enzymes, regulate key processes like inflammation, immunity, blood flow, and cellular signaling. MetwareBio's oxylipin targeted metabolomics assay enables simultaneous absolute quantification of 141 oxylipins.

r>0.99

Absolute Quantitation

141 standard curves
r>0.99, 25 isotope internal standards

ng/ml

High Sensitivity

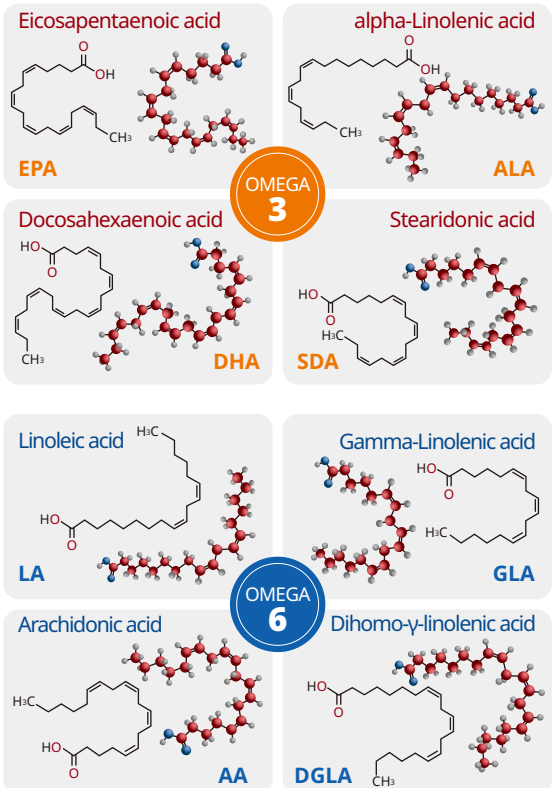
ng/ml concentration can be detected

141

Wide Coverage

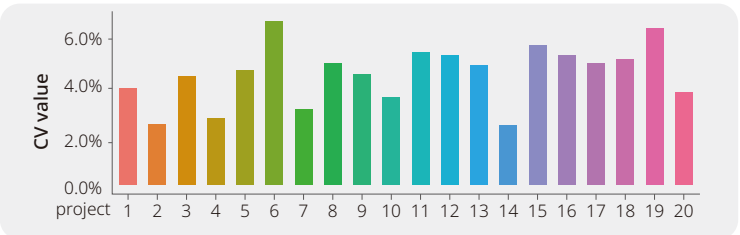
Covering **141** oxylipins

Key precursor fatty acids



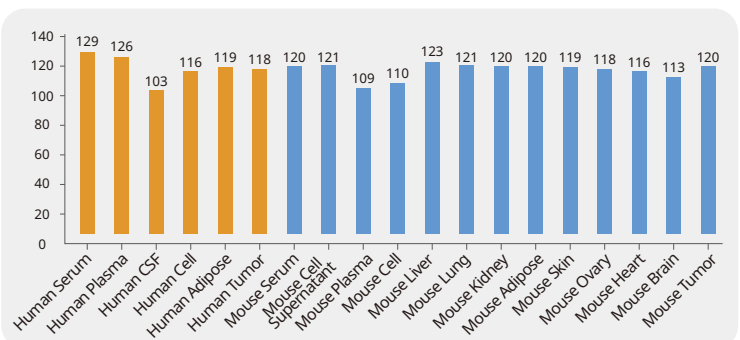
High Stability

The detected metabolites showed a coefficient of variation (CV) of less than 7% in mixed QC samples.



Project Experience

A total of 141 metabolites could be detected from various samples, with an average detection of 117 metabolites



Neurotransmitter Targeted Metabolomics

Neurotransmitters are chemical messengers enabling communication between neurons and other cells, crucial for mood, cognition, motor control, and physiological functions. MetwareBio's neurotransmitter targeted metabolomics service offers simultaneous absolute quantification of 57 neurotransmitters.

r>0.99

Absolute Quantitation

57 external & **45** internal standards, **r>0.99**

ng/ml

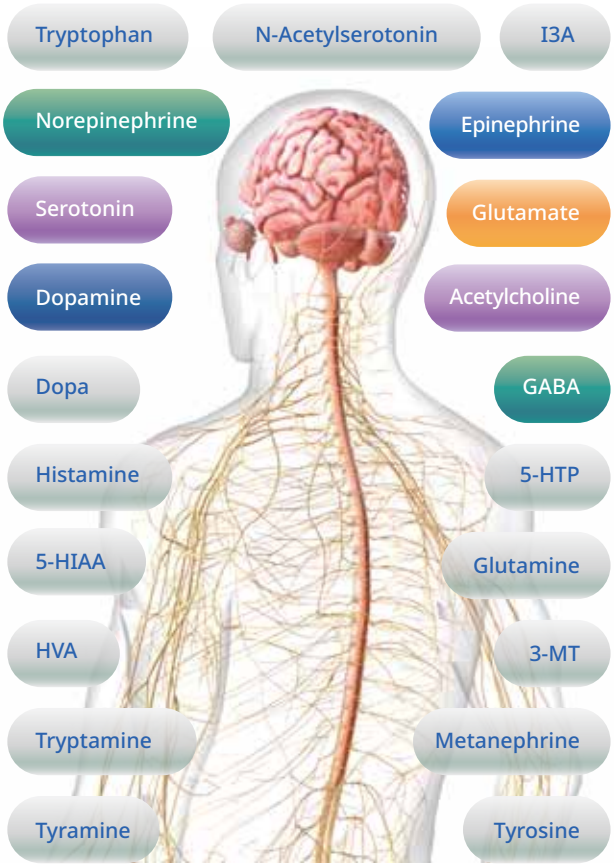
High Sensitivity

ng/ml concentration can be detected

57

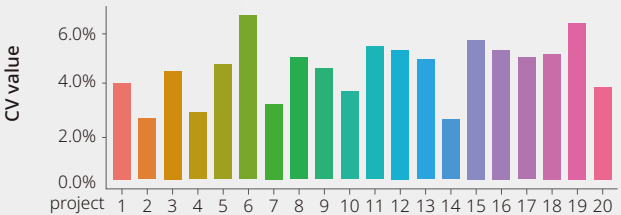
Wide Coverage

Covering **57** neurotransmitters



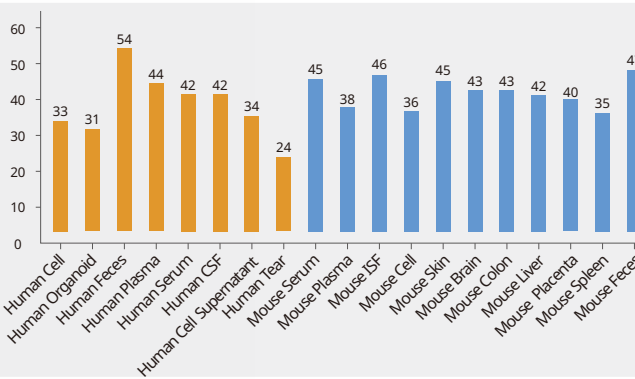
High Stability

The detected metabolites showed a coefficient of variation (CV) of less than 7% in mixed QC samples.



Project Experience

A total of 57 metabolites could be detected from various samples, with an average detection of 40 metabolites



Short-chain Fatty Acids

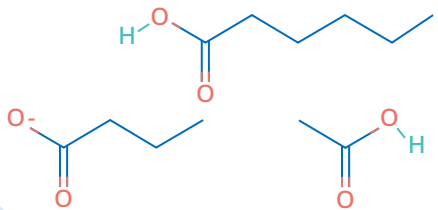
Short-chain fatty acids (SCFAs), also referred to as volatile fatty acids, are organic fatty acids characterized by carbon chains that vary in length from 1 to 6 carbon atoms. They primarily encompass acetic acid, propionic acid, isobutyric acid, butyric acid, isovaleric acid, valeric acid, and hexanoic acid, among others. MetwareBio offers absolute quantitation of **11 molecules** in a single run.

Absolute Quantitation

11 Short-chain Fatty Acids

High Sensitivity

Detection at **ng/mL** level



List of SCFAs

- 2-methylbutyrate
- Acetate
- Butyrate
- Crotonate
- Hexanoate
- Isobutyrate
- Isohexanoate
- Isovalerate
- Octanoate
- Propionate
- Valerate

Functions

- Providing energy
- Protecting the intestinal mucosal barrier
- Regulating the immune system
- Inhibiting tumor growth

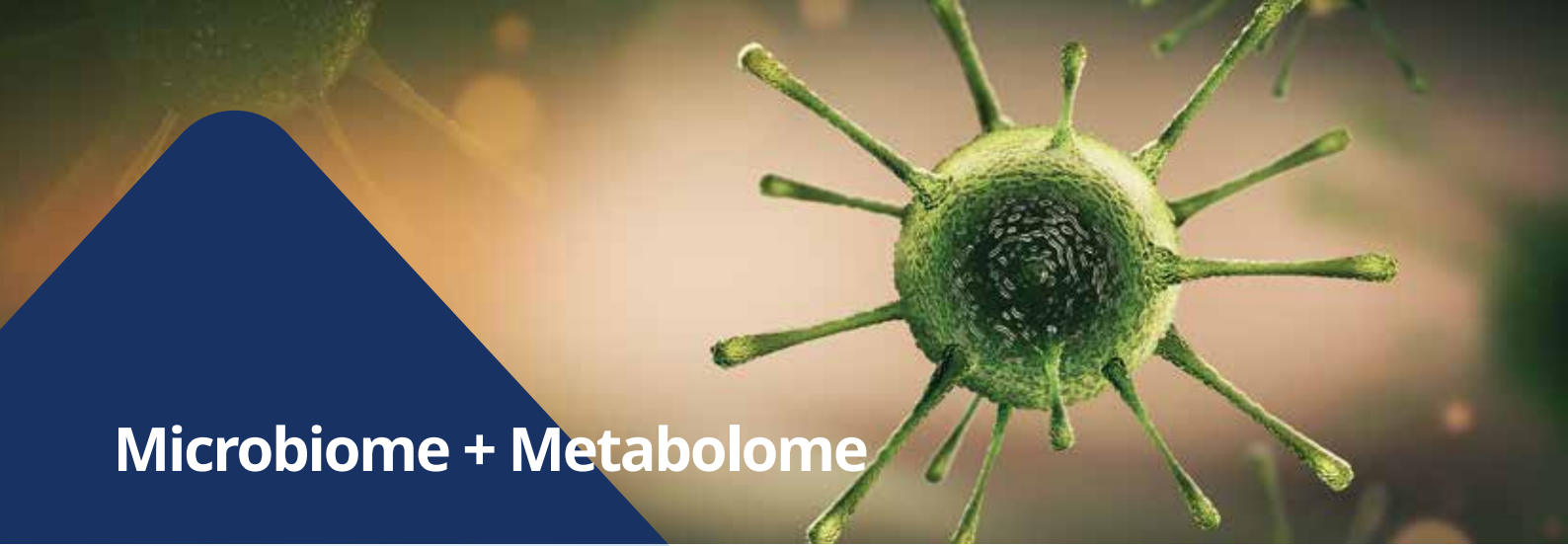
Applications

Research on diseases
Inflammatory diseases of the gastrointestinal tract, colon cancer, cardiovascular and kidney diseases, etc.

Mechanisms to the gut microbiota
Mechanisms of SCFAs in metabolic regulation and the brain-gut axis.

Food and nutrition
Research on poultry feed breeding and the development of nutritional products.

Medicines and supplements
Targeting drugs related to gastrointestinal inflammation and the development of dietary supplements.



Microbiome + Metabolome

Microbial metabolomics focuses on the study of all small-molecule metabolites produced by a microbial community, uncovering key metabolites associated with microbial changes during host pathology. The correlation analysis between the microbiome and metabolome provides clues for understanding the mechanisms of microbial-host interactions.

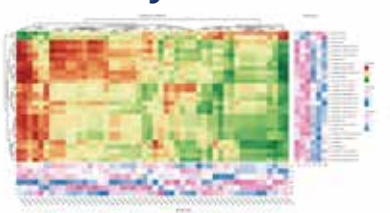
Holistic View of Biological Systems

Comprehensive Reports

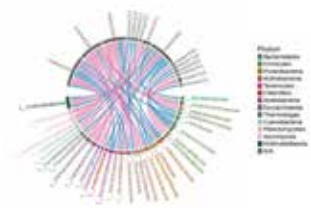
Personalized Analysis

SCFA: propionic acid, butyric acid, caproic acid, etc.	Firmicutes Clostridium	Pathogens inhibition; Cholesterol synthesis; Insulin resistance.
Bile acid: cholate, deoxycholate, ursodeoxycholate, etc.	Lactobacillus, Bifidobacterium, Enterobacter, Bacteroidetes.	Dietary absorption; Triglycerides, cholesterol, glucose, and energy homeostasis.
Cholines: methylamine, trimethylamine oxide, betaine, etc.	Prevotella, Bifidobacterium.	Lipid metabolism and glucose homeostasis. NAFLD, diet-induced obesity, and cardiovascular disease.
Indole derivatives: N-acetyl tryptophan, indole acetyl glycine (IAG), melatonin, etc.	Clostridium sporogenes, Escherichia coli.	Gastrointestinal tract protection; Gastrointestinal pathology and neurological disorders.
Vitamins: vitamin K, vitamin B12, thiamine, etc.	Bifidobacteria.	Supplementary source of endogenous vitamins; Immune function; Cell proliferation regulation.
Polyamines: putrescine, spermidine, spermine, etc.	Campylobacter jejuni, Clostridium glycolytica.	Produce genotoxic effects, anti-inflammatory and anti -tumor effects on the host.
Lipids: fatty acids, GP, sphingomyelin, etc.	Bifidobacterium, Roseburia, Lactobacillus, Klebsiella.	Gut-brain-liver axis to regulate glucose homeostasis; Chronic systemic inflammation.

Joint Analysis

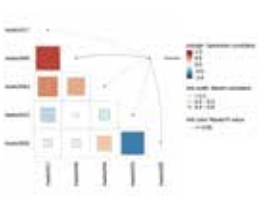


Correlation Clustering Heatmap

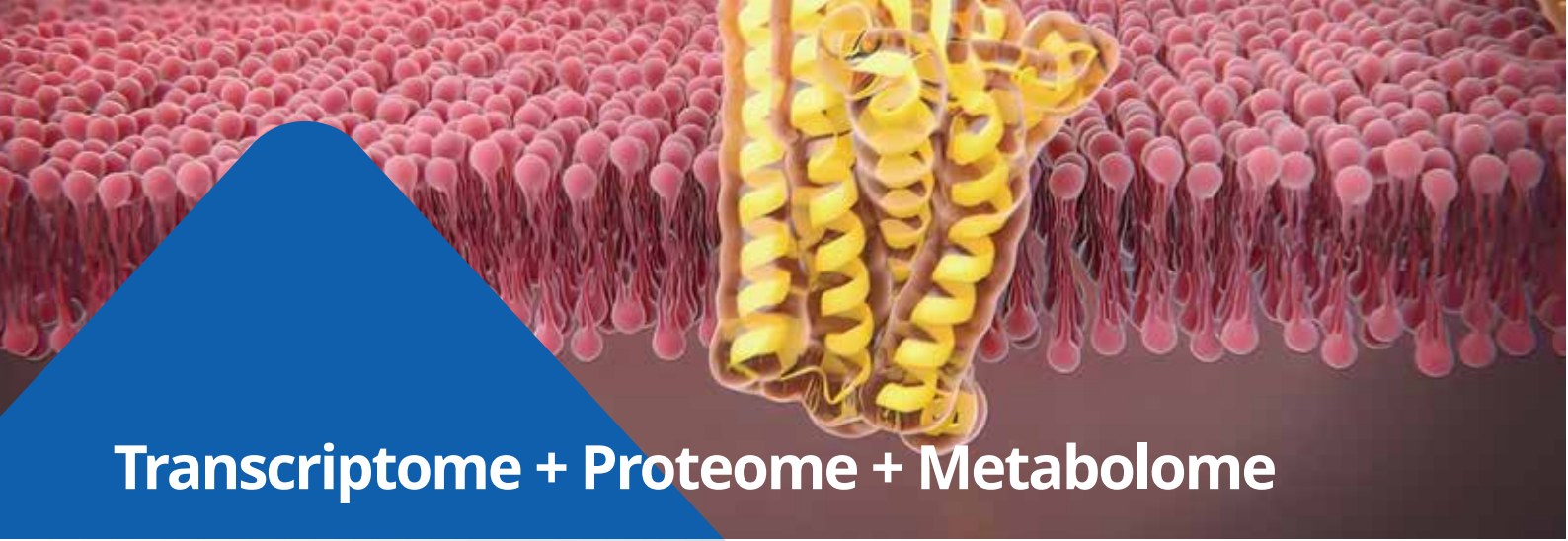


Correlation Chord Diagram

KEGG Map



Mantel Test Analysis



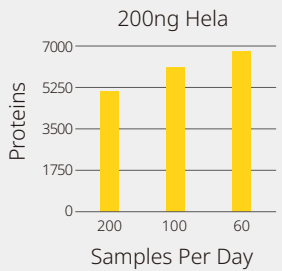
Transcriptome + Proteome + Metabolome

In systems biology research, biological processes and gene regulatory networks are complex and dynamic. It is often insufficient to use a single dataset to study systems biology. Correlating transcriptomic data that has a large number of differentially expressed genes together with differential proteins detected by proteomics, and metabolites detected by metabolomics, can pinpoint key genes, proteins, metabolites, and metabolic pathways that are closely associated with internal changes in the system, and thereby explain biological problems in a more holistic approach.

- Coexpressed transcriptome, proteome and metabolome
- Converged metabolic pathway
- Major regulation networks construction
- Holistic view of biological systems

The Power of Our Proteomics Technology

High Throughput

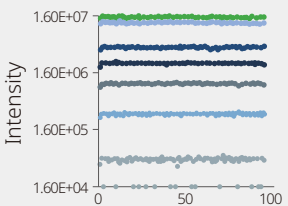


High Sensitivity

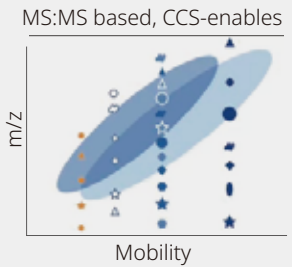
	Unique peptide sequence	Proteins
TIMS-PASEF	39,000	5,200
TIMS-PASEF OFF	20,000	3,200

TIMS-PASEF Advantage

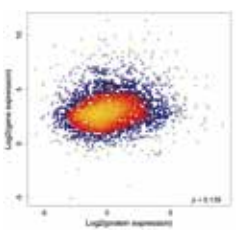
High Stability



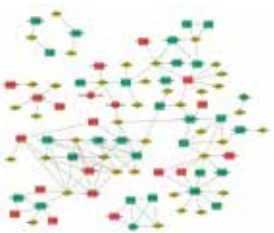
Accurate Identification



Joint Analysis

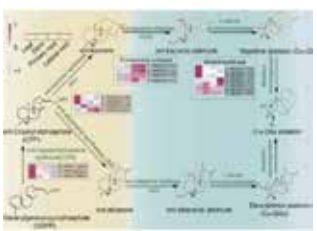


Gene Enrichment Circle Map



Correlation Network

KEGG Map



Converging Metabolic Pathway

Analyze Metabolomics Data With Ease

Cloud Tools

- Data Processing
- Difference Analysis
- Functional Enrichment Analysis

50+
Cloud tools

- Multi-omics Association Analysis
- Gene Sequence Analysis
- File Format Conversion

Cloud Process

Customize analysis parameters.

Get started for FREE!

https://cloud.metwarebio.com/

Sample Requirements

Categories	Sample	Recommended Sample	Minimum Sample size
Liquid Samples	Plasma, Serum, Hemolymph, Whole Blood, Milk, Cerebrospinal Fluid (CSF), Interstitial Fluid (TIF), Pancreatic Juice, Bile, Pleural Effusion, Follicular Fluid, Culture Medium (liquid), Culture Supernatant, Tears, Bone Marrow (liquid)	100 μL	20 μl (Steroid Hormones, SCFAs 50 μl)
	Seminal Plasma, Amniotic Fluid, Respiratory Condensate, Gastric Lavage Fluid, Bronchoalveolar Lavage Fluid (BALF), Urine, Sweat, Saliva, Sputum	500 μl	100 μl
Tissue Samples	Small Animal Tissues, Placenta, Blood Clot, Mycelium, Nematode, Zebrafish (whole fish), Bone Marrow (solid), Nail	100 mg	20 mg
	Large Animal Tissues, Whole Insect Body, Wings (of insects), Pupa, Eggs, Large Fungi (mushroom types), Large Algae (red algae), Cartilage, Bone (solid)	500 mg	20 mg (SCFAs 50 mg)
	Zebrafish Organs, Insect Organs, Whole Microinsect Body (e.g., Drosophila)	20 units	10 units
Solid Samples	Feces, Intestinal Contents, Microbial Fermentation Product (solid), Culture Medium (solid), Earwax, Lyophilized Tissue Powder, Lyophilized Plant Powder	200 mg	20 mg
Cell Samples	Adherent Cells, Animal Cell Lines	1×10^7 cells	1×10^6 cells
	E. Coli, Yeast	1×10^10 cells	5×10^8 cells
	Unicellular Algae (Cyanobacteria), Large Quantities of Bacterial Hyphae (sediment), Mucilaginous Protoplasmic Clusters (hyphae)	100 mg	20 mg
Subcellular Samples	Lysosomes, Mitochondria, Endoplasmic Reticulum	4×10^7 cells	1×10^7 cells
	Exosomes, Extracellular Vesicles	2×10^9 particles	1×10^9 particles

Replicates: A minimum of 3 replicates is required; 3-6 replicates for animal samples; 6-10 for clinical samples.

Innovative Multi-Omics Insights for Better Health

Metware Biotechnology Inc. (MetwareBio) is focused on developing and applying innovative multi-omics technologies to life science and health research. By leveraging state-of-the-art mass spectrometry technologies, unique detection workflow, and large curated in-house database, MetwareBio offers one-stop multi-omics solutions to academic research, clinical studies, and biotech/pharmaceutical developments.

MetwareBio's technical achievements have been presented and published in over 1,000 publications, including Cell, Nature, Nature Metabolism, Circulation, Signal Transduction and Targeted Therapy, Nature Genetics, PNAS, Nature Communications, National Science Review, and many other international peer-reviewed journals. Working with MetwareBio means you have all the metabolomics expertise supporting your research and development.

10
Data QC Indicators

3000+
Verified Biomedical Metabolites Database

61,000+
Purified Plant Metabolites Database

METWARE BIO

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