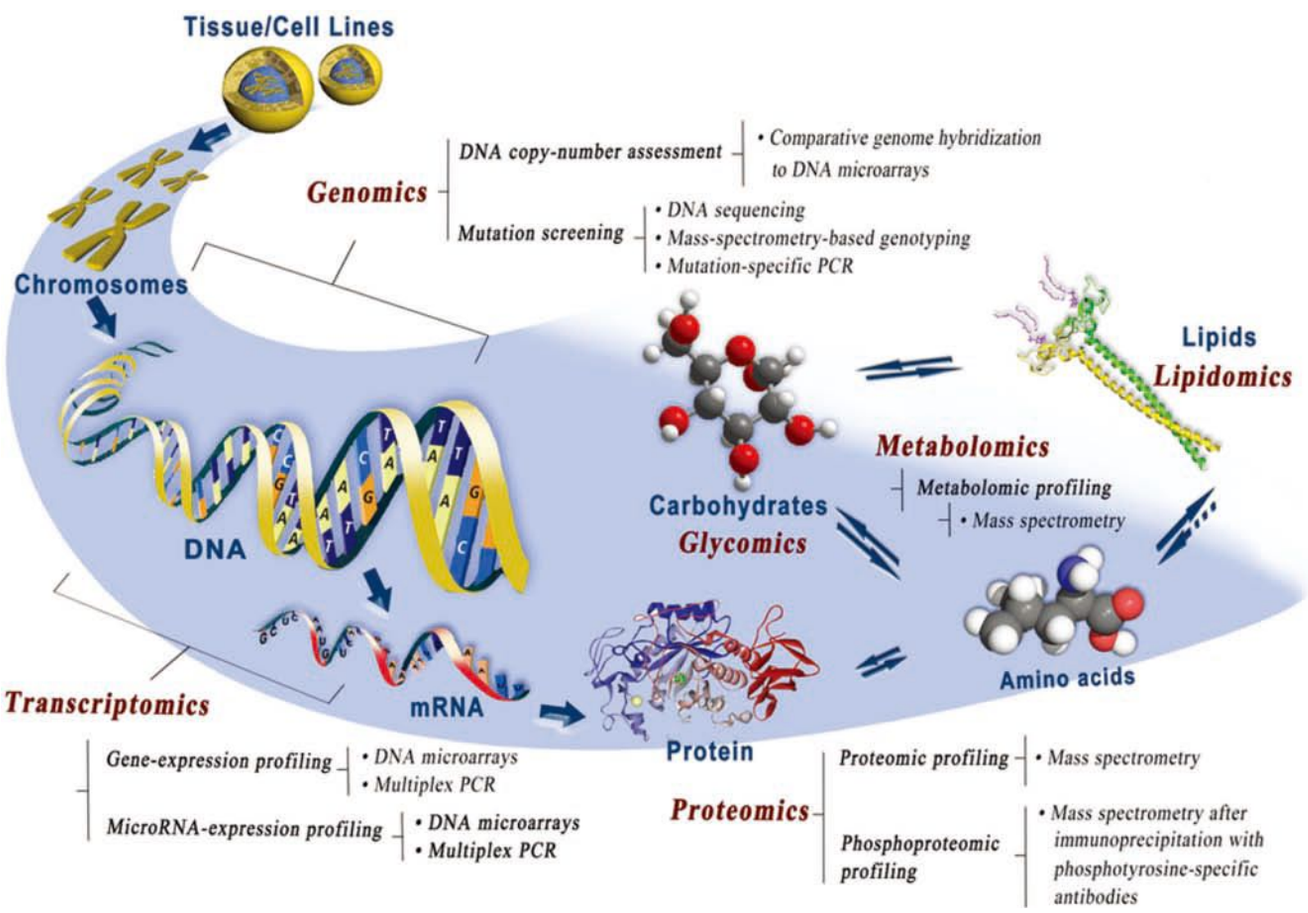
Multi-Omics Service Overview

Service Description

Multi-omics is the integrative biological analysis of different data sets from single omics areas for new insight. An integrated multi-omics approach to research enables a more comprehensive understanding of genotypic, phenotypic and environmental relationships and their association to disease and health of an organism.
We offer multi-omics services to look across genomics, transcriptomics, epigenomics, proteomics and metabolomics, with the flexibility to customize solutions that meet your specific needs. All projects are supported by a bioinformatics infrastructure.

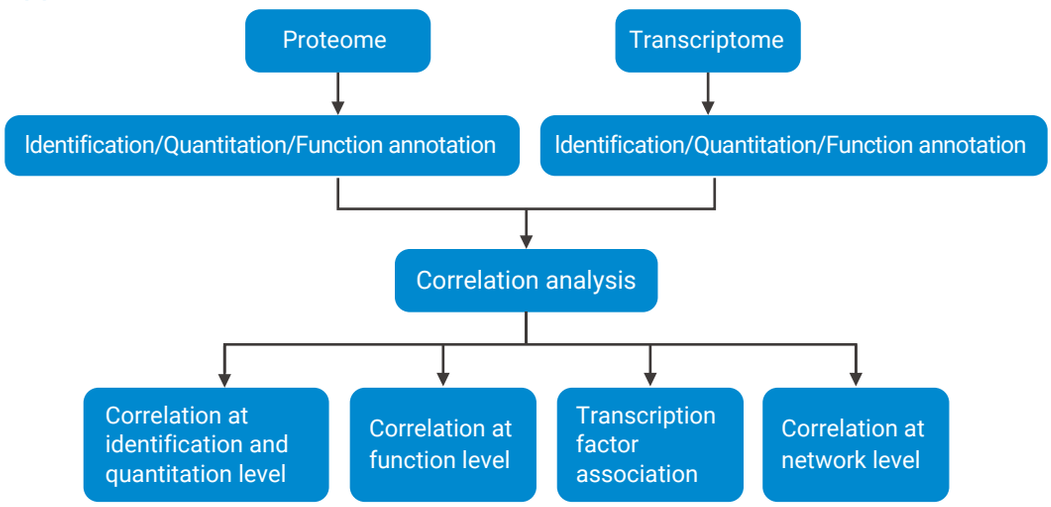


Schema of omics technologies, their corresponding analysis targets, and assessment methods. DNA (genomics) is first transcribed to mRNA (transcriptomics) and translated into protein (proteomics) which can catalyze reactions that act on and give rise to metabolites (metabolomics), glycoproteins and carbohydrates (glycomics), and various lipids (lipidomics). The assessment methods for genomics include DNA copy-number assessment with comparative genome hybridization to DNA microarrays, together with mutation screening with DNA sequencing, mass-spectrometry-based genotyping, and mutation-specific PCR. The assessment methods for transcriptomics include gene-expression profiling with DNA microarrays and multiplex PCR, together with microRNA-expression profiling with DNA microarrays and multiplex PCR. The assessment methods for proteomics include proteomic profiling with mass spectrometry, together with phosphoproteomic profiling with mass spectrometry after immunoprecipitation with phosphotyrosine-specific antibodies. The assessment method for metabolomics includes metabolomic profiling with mass spectrometry (based on Sawyers, 2008).

Proteome + Transcriptome Correlation Analysis

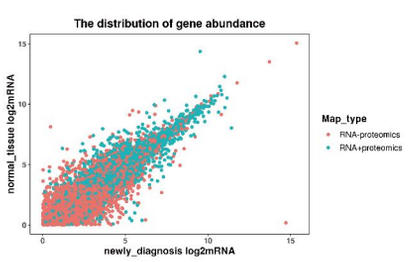
Using a multi-omics approach to correlate transcriptomics with proteomics data provides a more comprehensive overview of expression patterns and enables researchers to interpret deeper biological implications.

Research Approaches

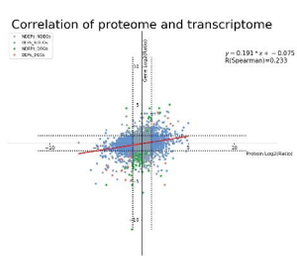


Note: Sample selection for Transcriptome and Proteome should be as consistent as possible.

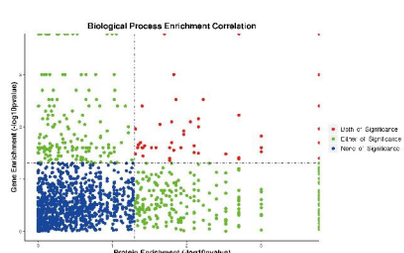
Analysis Options



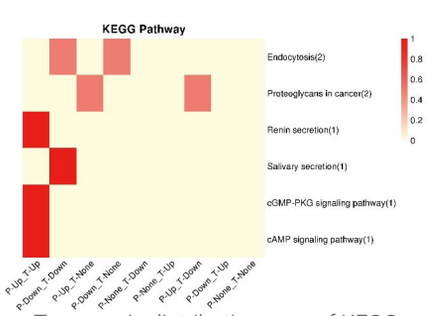
Scatter plots of correlated and uncorrelated gene expression levels



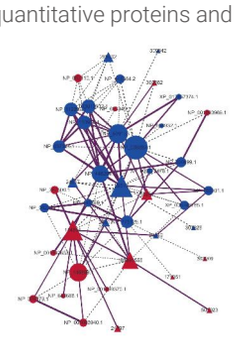
Expression correlation diagram of all quantitative proteins and genes



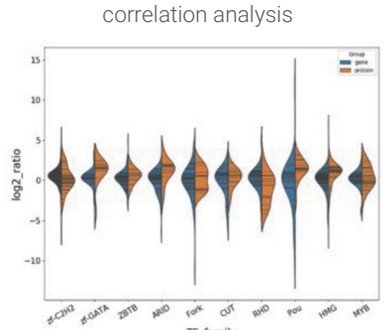
Distribution diagram of GO enrichment correlation analysis



Taxonomic distribution map of KEGG enrichment correlation analysis



Network interaction diagram of differential proteins and genes



The identification number and expression distribution of transcription factors in each transcription factor family

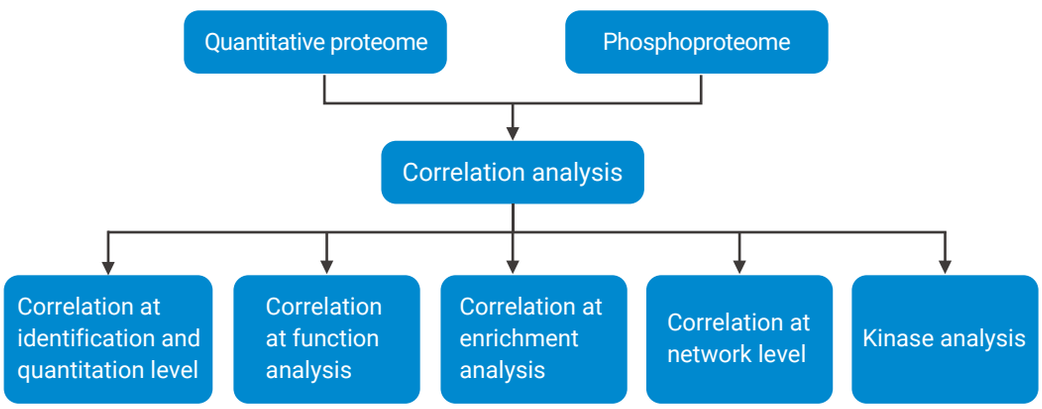
Application Cases

1. Pan-cancer proteomic map of 949 human cell lines. Cancer Cell. 2022 Aug 8;40(8):835-849.e8.
2. Integrated transcriptome and proteome analysis of developing embryo reveals the mechanisms underlying the high levels of oil accumulation in Carya cathayensis Sarg. Tree Physiol. 2022 Mar 9;42(3):684-702. (BGI Participation)
3. The combination of RNA-seq transcriptomics and data-independent acquisition proteomics reveals the mechanisms underlying enhanced salt tolerance by the ZmPDI gene in Zoysia matrella [L.] Merr. Front Plant Sci. 2022 Aug 8;13:970651.
4. Transcriptomics coupled to proteomics reveals novel targets for the protective role of spermine in diabetic cardiomyopathy . Oxid Med Cell Longev. 2022 Apr 9;2022:5909378.
5. Discovery of missing proteins from an aneuploidy cell line using a proteogenomic approach.J Proteome Res. 2021 Dec 3;20(12):5329-5339. (BGI Publication)
6. A novel protein AXIN1-295aa encoded by circAXIN1 activates the Wnt/β-catenin signaling pathway to promote gastric cancer progression. Mol Cancer. 2021 Dec 4;20(1):158. (BGI Participation)

Quantitative proteome + Phosphoproteome Correlation Analysis

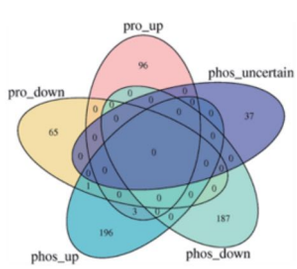
Single phosphoproteomics can only explain the scientific problem of protein phosphorylation level. With the publication of a large number of high-level (CNS) research articles on correlation analysis between phosphoproteomics and quantitative proteomics, this "golden partners" has been widely used in many research fields. Correlation analysis between quantitative proteome and phosphoproteome can more accurately locate the dominant regulatory role and clarify the importance of protein expression difference or phosphorylation modification level changed in the body. Multi-omics analysis of biological reaction mechanism, combined with kinase analysis, is more conducive to the deep excavation of regulation and molecular mechanism.

Research Approaches

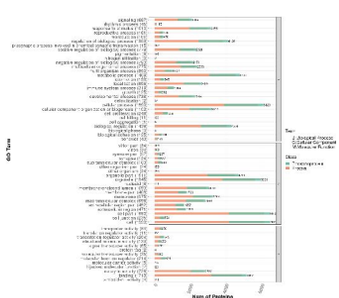


Note: Sample selection for Quantitative proteome and Phosphoproteome should be as consistent as possible.

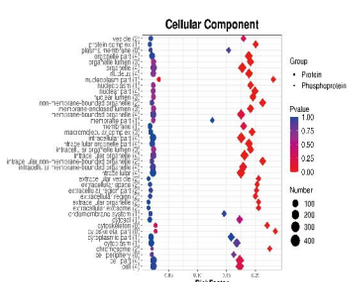
Analysis Options



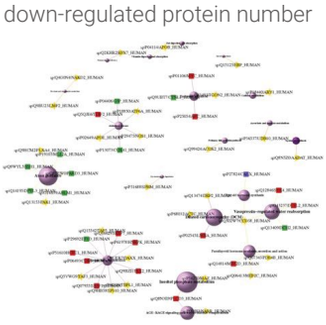
Venn diagram of up and down-regulated protein number



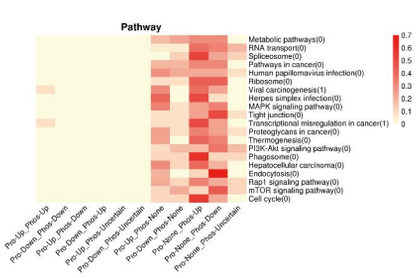
Statistical chart of GO functional correlation analysis



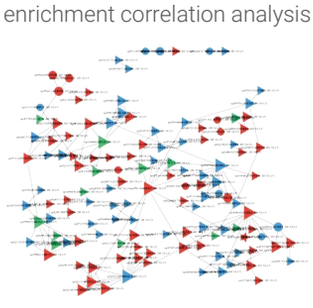
Bubble diagram of GO enrichment correlation analysis



Clustering heat map of GO enrichment correlation analysis



Taxonomic distribution map of KEGG enrichment correlation analysis



Network interaction diagram of differential proteins and phosphoproteins

Application Cases

1. Quantitative phosphoproteomics reveals diverse stimuli activate distinct signaling pathways during neutrophil activation. Cell Tissue Res. 2022 Aug; 389(2): 241-257.

2. Quantitative proteomics and phosphoproteomics elucidate the molecular mechanism of nanostructured TiO_2-stimulated biofilm formation. J Hazard Mater. 2022 Jun 15; 432: 128709.

3. Quantitative phosphoproteomics uncovers dysregulated kinase networks in Alzheimer's disease. Nat Aging. 2021 June; 1: 550–565.

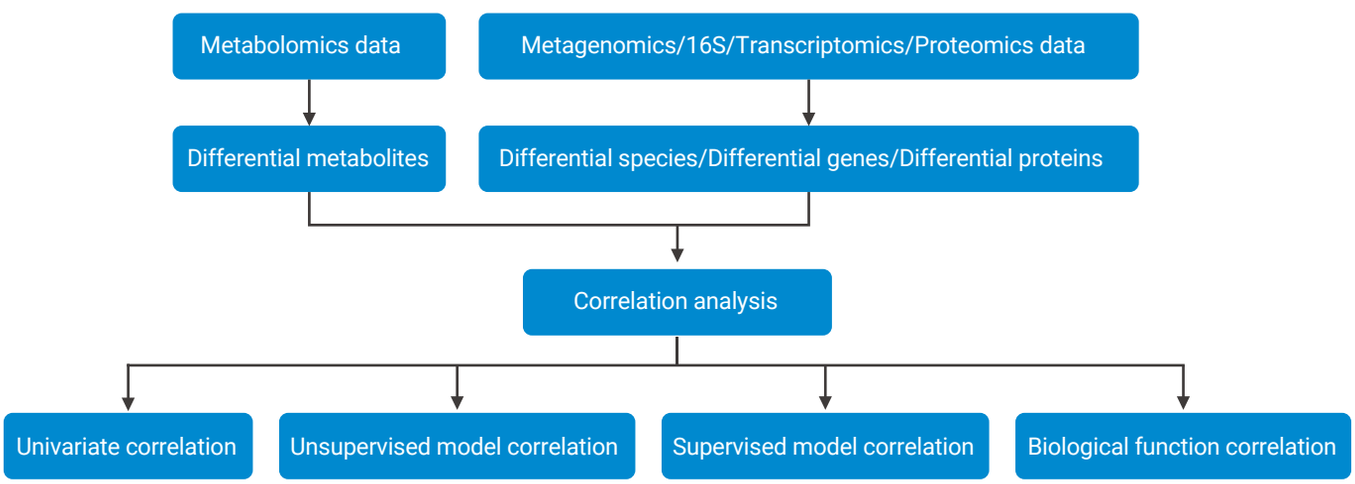
Metabolome + Metagenome / 16S Correlation Analysis

In recent years, research on gut related diseases has developed rapidly and it is now thought that nearly 90% of diseases may be related to gut microbiota health. Metagenome/16S + metabolome correlation analysis enables researchers to establish a correlation model between host metabolism and gut microbiota and explore the causal relationships between microbes and disease.

Metabolome + Transcriptome / Proteome Correlation Analysis

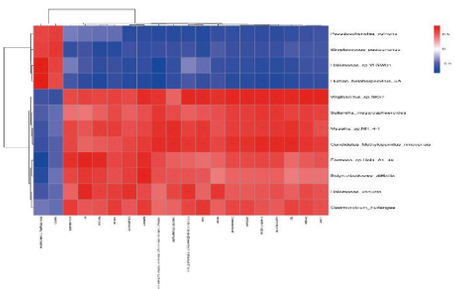
Correlation analysis of metabolome and transcriptome / proteome can simultaneously explore biological problems from the two levels of "cause" and "effect", mutually verified, and screen out key genes, proteins, metabolites and metabolic pathways, which enables researchers to in-depth follow-up research and applications to fully understand the regulatory mechanism of biological systems. Correlation analysis of metabolome and transcriptome / proteome has been widely used in research of disease pathogenesis, disease diagnosis and typing, animal and plant growth and development, plant stress resistance regulation and other fields.

Research Approaches

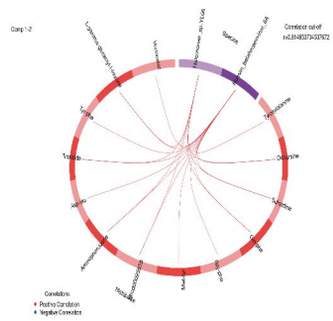


Note:
Stools and intestinal contents samples are recommended for Metagenome/16S services; blood samples (serum, plasma) are recommended for Metabolome services.
No “Biological function correlation” for differential metabolites and differential species.
Sample selection for correlation analysis should be as consistent as possible.

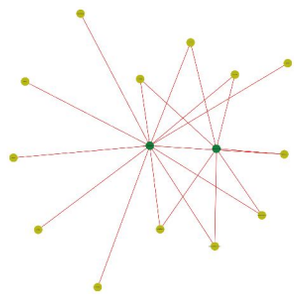
Analysis Options



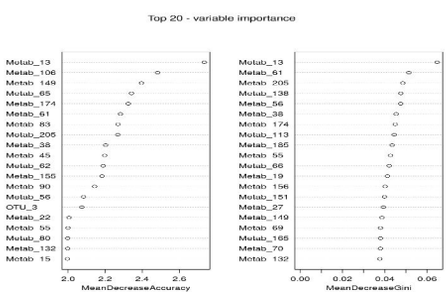
Spearman correlation heatmap



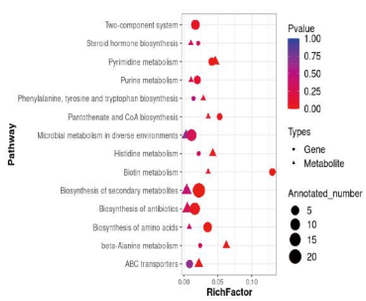
Chord plots of CCA correlations



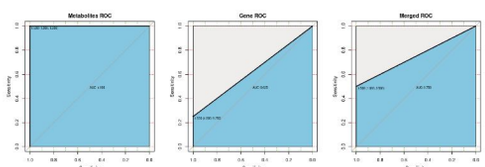
Interaction map of CCA correlation network



The importance score plot of random forest analysis



Bubble plot of pathway enrichment analysis



The ROC curves of random forest analysis

Application Cases

1. Liu X, Tong X. et al. Mendelian randomization analyses support causal relationships between blood metabolites and the gut microbiome. Nature Genetics. 2022 Jan; 54(1): 52-61.

2. Li TP, Zhou CY. et al. Endosymbionts reduce microbiome diversity and modify host metabolism and fecundity in the planthopper *Sogatella furcifera*. mSystems. 2022 Apr 26; 7(2): e0151621.

3. Li TP, Zha SS. et al. Two newly introduced *Wolbachia* endosymbionts induce cell host differences in competitiveness and metabolic responses. Applied and Environmental Microbiology. 2021 Oct 28; 87(22): e0147921.

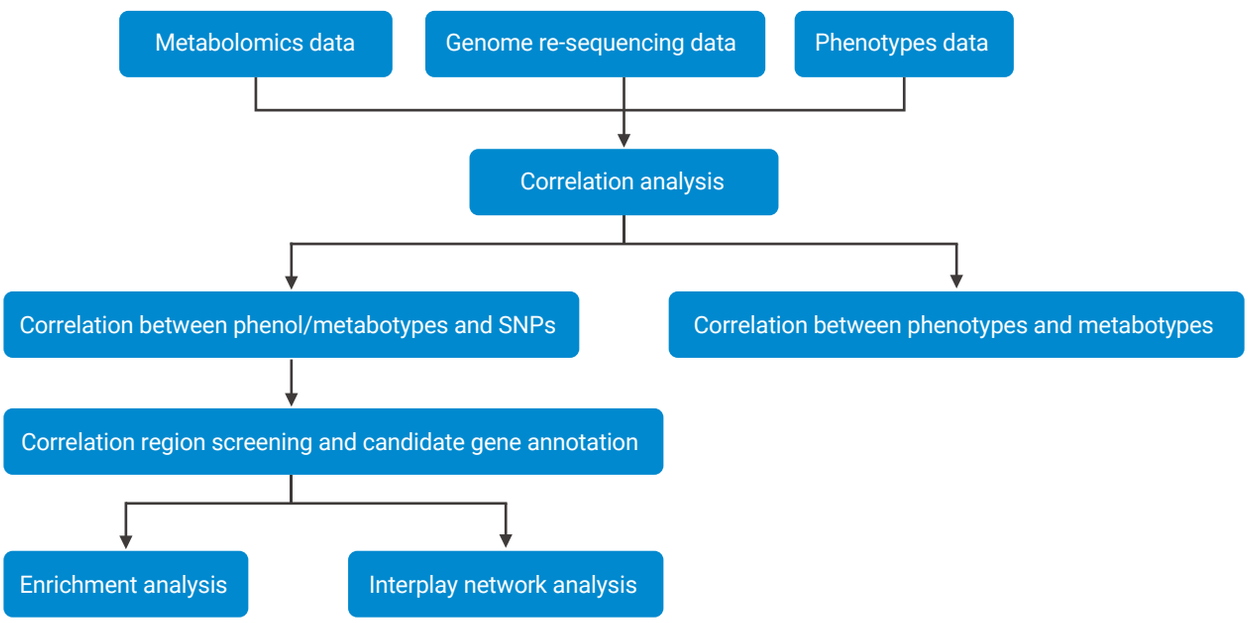
4. Li Y, Hou G. et al. Multi-platform omics analysis reveals molecular signiature for COVID-19 pathogenesis, prognosis, and drugtarget discovery. Signal Transcluction and Targeted Thevapy. 2021 Apr 15; 6(1): 155.

Metabolome + Genome re-sequencing Correlation Analysis（mGWAS）

Early correlation studies only focused on individual and highly heritable macrophenotypes, with the aim to identify a few common major gene variants. Fast advances in high-throughput sequencing technologies, have allowed scientists to expand their targets to rare variants on a genome-wide scale and focus on elucidating the genetic basis of complex human diseases, or quantitative traits in animals and plants.

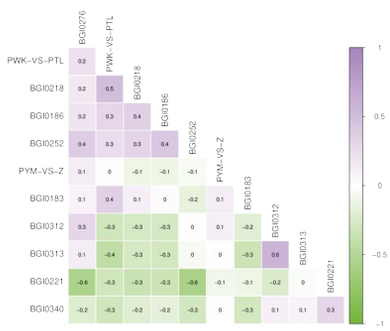
Metabolomics, based on high-throughput mass spectrometry, can decompose a small number of macroscopic phenotypes into metabolic molecular phenotypes, and find significantly associated metabolic indicators and gene variants through mGWAS, which can more directly reveal the molecular mechanism behind macroscopic phenotypes such as diseases. As a research hotspot in recent years, mGWAS has been widely used in animal and plant variety breeding, human disease research and other fields.

Research Approaches

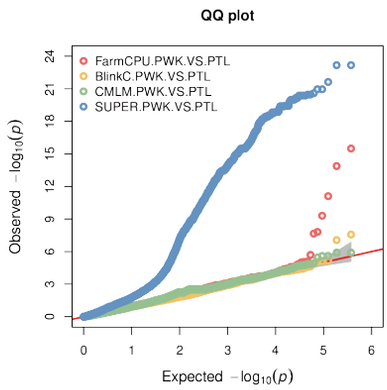


Note:
Sample selection for Metabolome and Genome re-sequencing should be as consistent as possible.
Phenotypes data is optional.

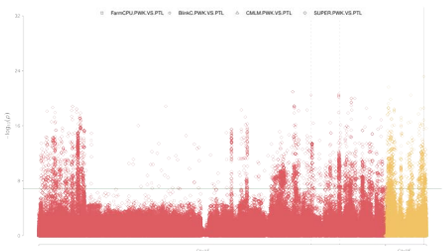
Analysis Options



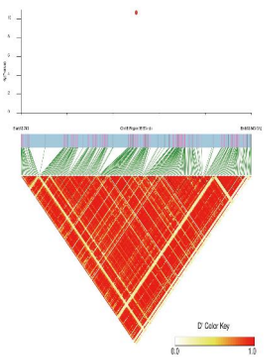
Heatmap for top-correlated metabotype



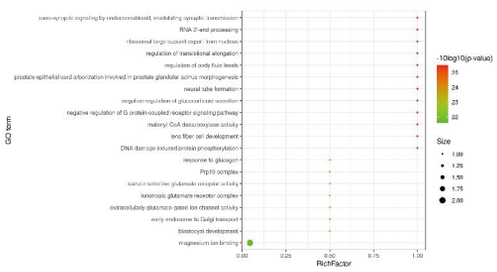
Q-Q plot



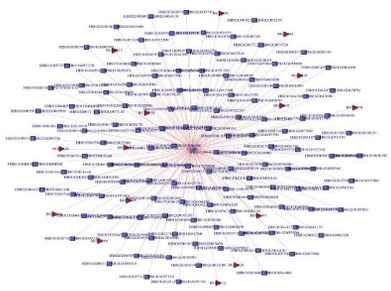
Manhattan plot



Regional association plot for linkage disequilibrium block



Pathway enrichment analysis



Network for top-associated metabolites, genes and pathway maps

Application Cases

1. Zhou Y, Zhang Z. et al. Graph pangenome captures missing heritability and empowers tomato breeding. Nature. 2022 Jun; 606(7914): 527-534.
2. Cheng Y, Schlosser P. et al. Rare genetic variants affecting urine metabolite levels link population variation to inborn errors of metabolism. Nature Communications. 2021 Feb 11; 12(1): 964.
3. Wang X, Kadarmideen HN. Metabolite genome-wide association study (mGWAS) and gene-metabolite interaction network analysis reveal potential biomarkers for feed efficiency in pigs. Metabolites. 2020 May 15; 10(5): 201.
4. Zhu G, Wang S. et al. Rewiring of the fruit metabolome in tomato breeding. Cell. 2018 Jan 11; 172(1-2): 249-261.

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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