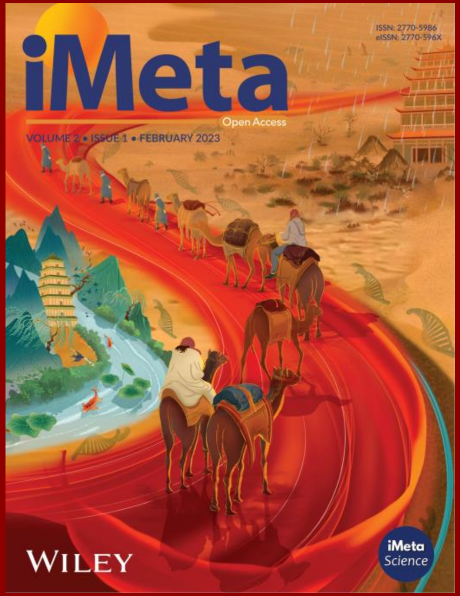
MetOrigin 2.0: 推进微生物代谢物的发现和溯源



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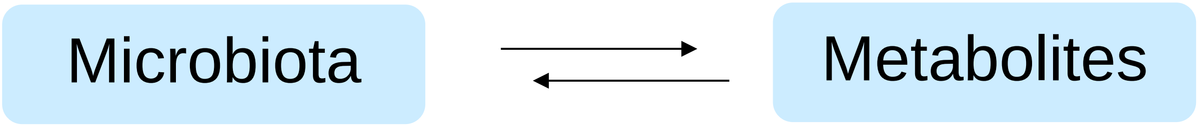
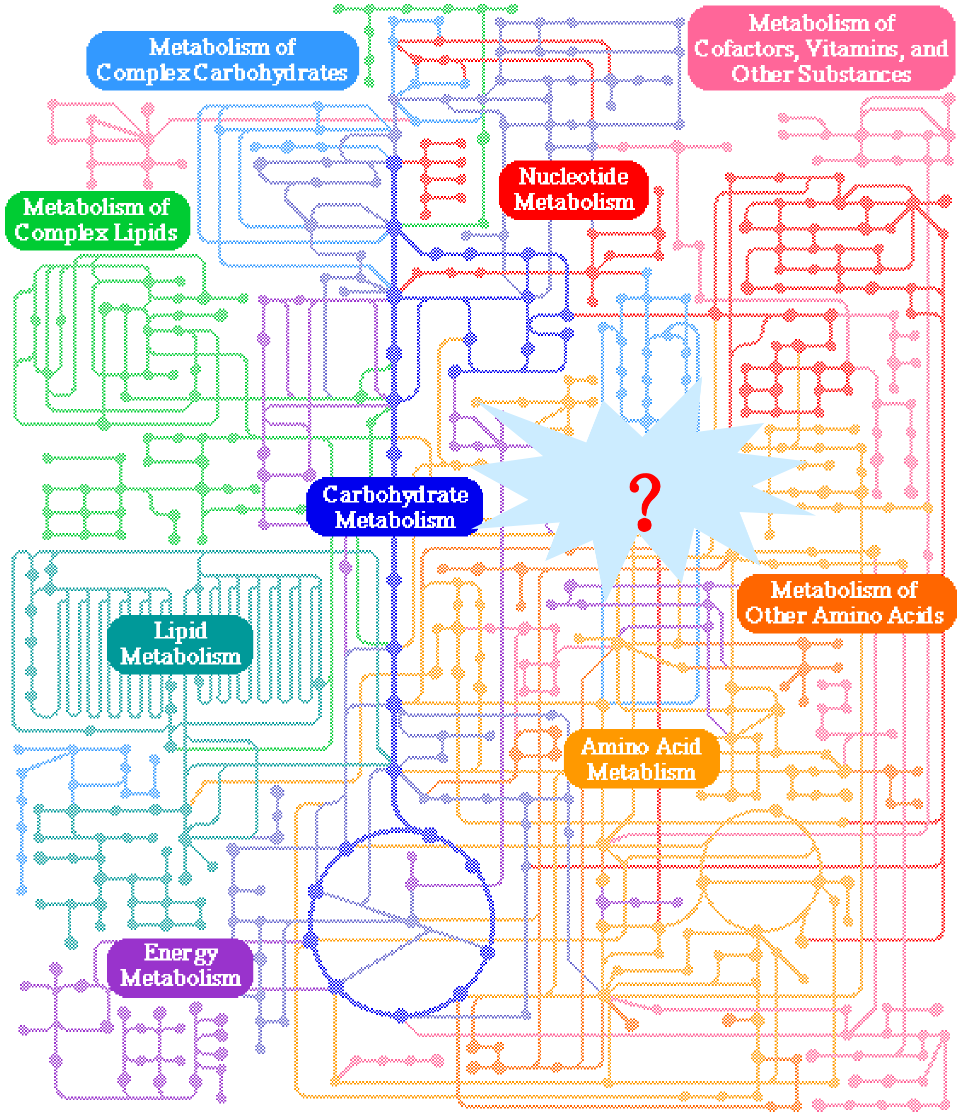
研究背景

Origins of metabolites:

- Host
- **Microbiota**
- Food
- Drug
- Environment (air, water, living condition)

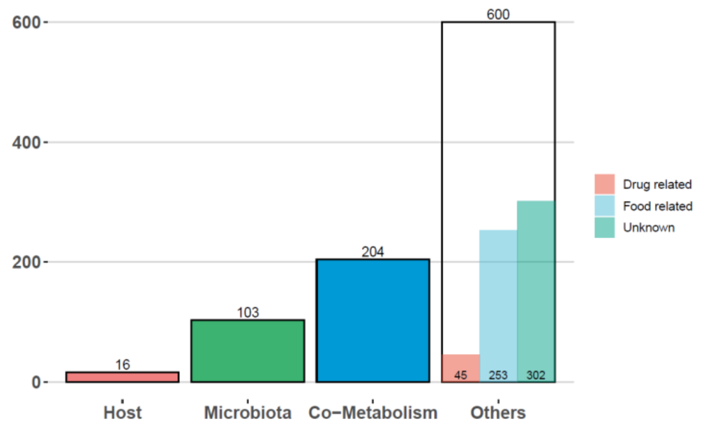


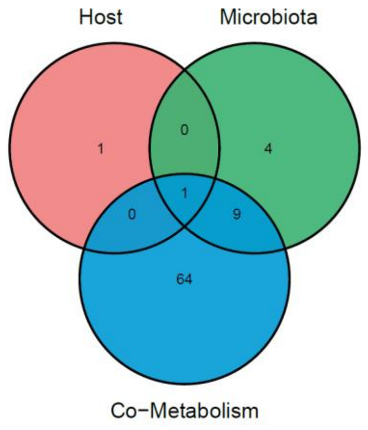
Metabolic pathway map



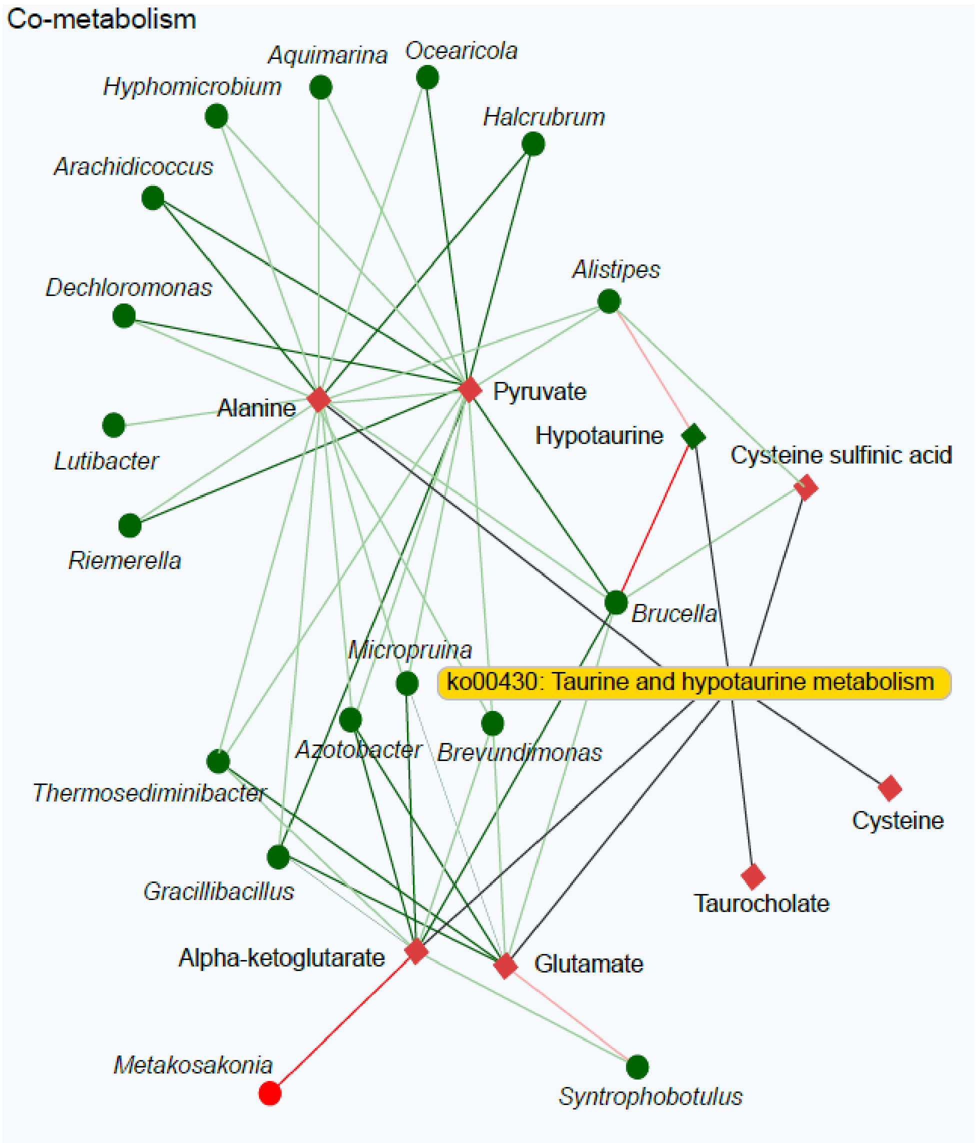
MetOrigin 1.0 核心功能

✓ Origin analysis and metabolic pathway enrichment analysis

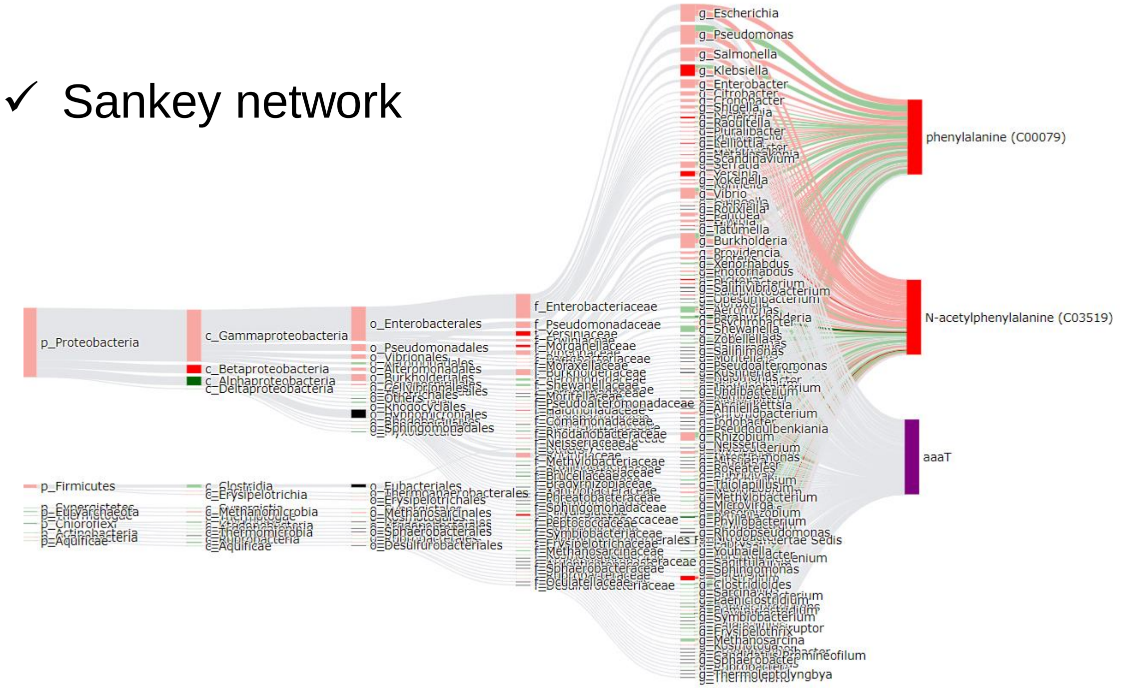




✓ Microbiome-metabolite co-network visualization



✓ Sankey network



MetOrigin 2.0 主要功能

Mode 1: Quick search

Required datasets: None

Functions:

- Metabolic reactions
- Sankey network

Aims:

- To search and provide metabolic reactions of a metabolite and their related bacteria.

Mode 2: SMOA

Requried datasets:

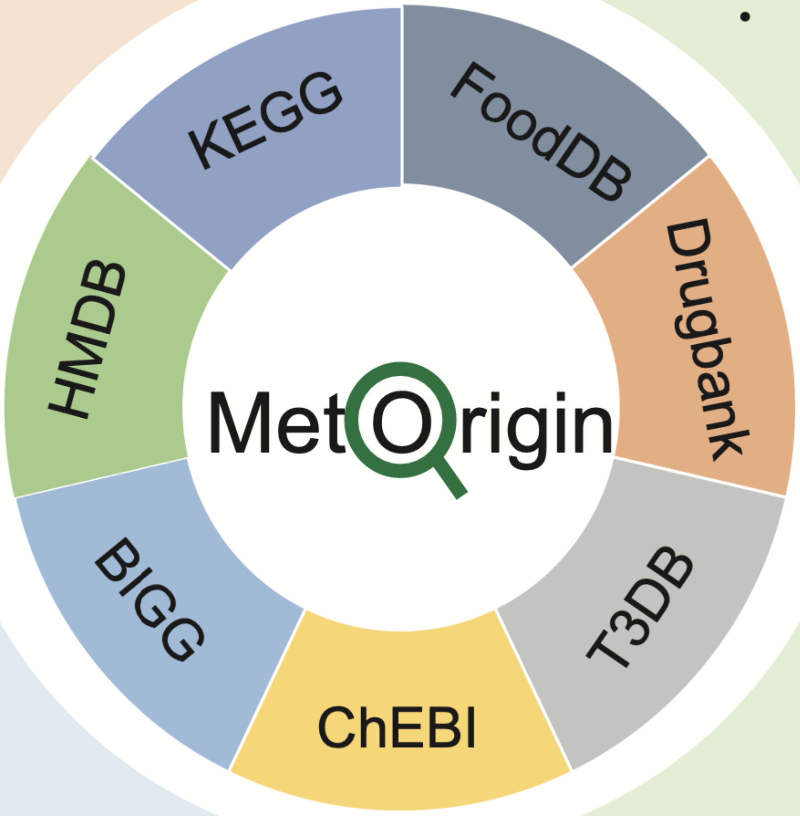
- Differential metabolite table

Functions:

- Origin analysis
- Pathway analysis
- Sankey network

Aims:

- To identify differential metabolic pathways, metabolic reactions, and their related bacteria.



Mode 3: DMOA

Requried datasets:

- Sample Information
- Metabolome table
- Microbiome table
- Phenotype table
- KEGG orthology table

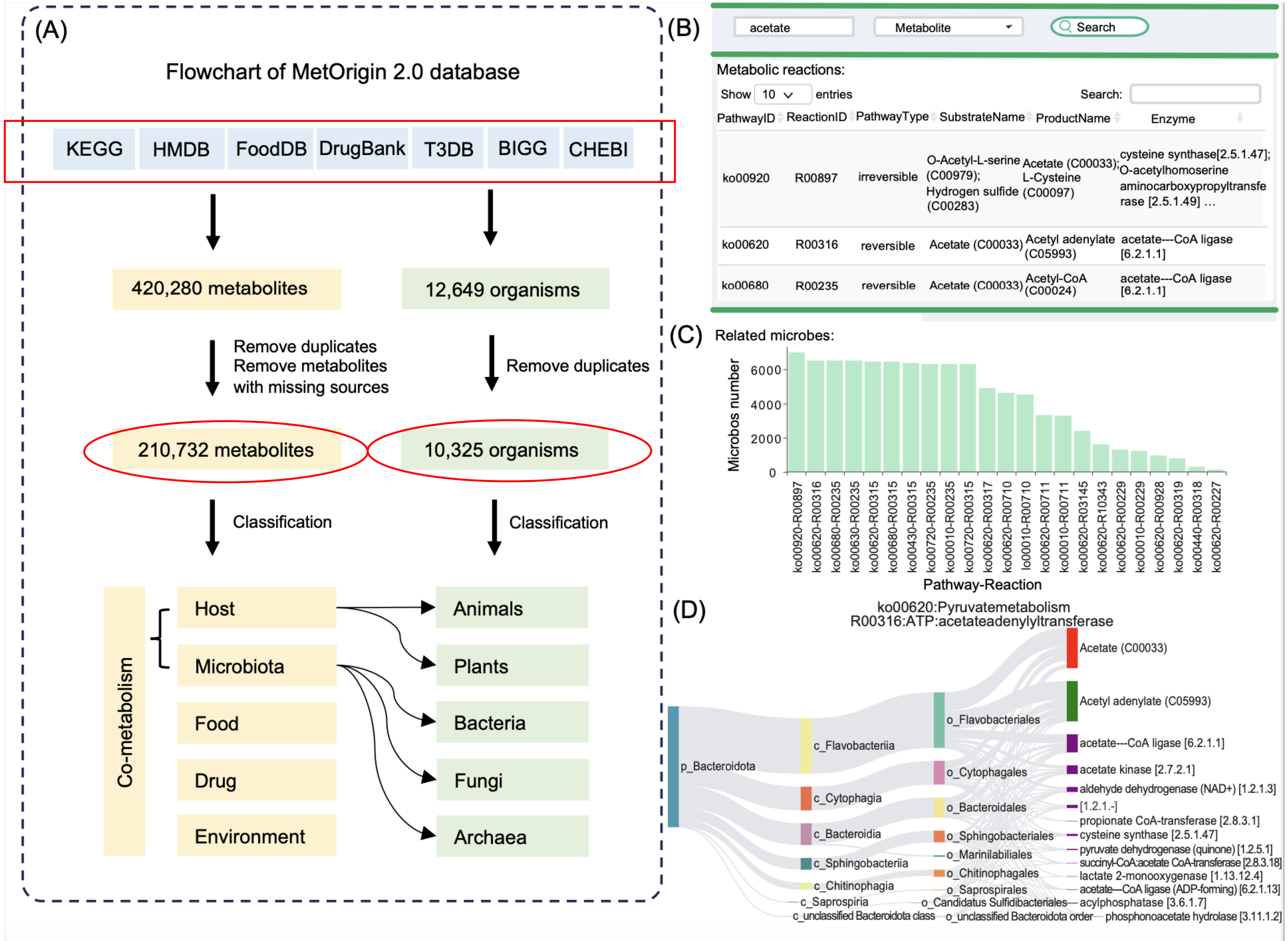
Functions:

- Origin analysis
- Pathway analysis
- Correlation analysis
- Sankey network
- Orthology analysis
- Mediation analysis
- Network analysis

Aims:

- To explore the correlations between microbiome and metabolome step by step, from statistical, biological, to casual relationship.

数据库更新 & 快速搜索功能



①

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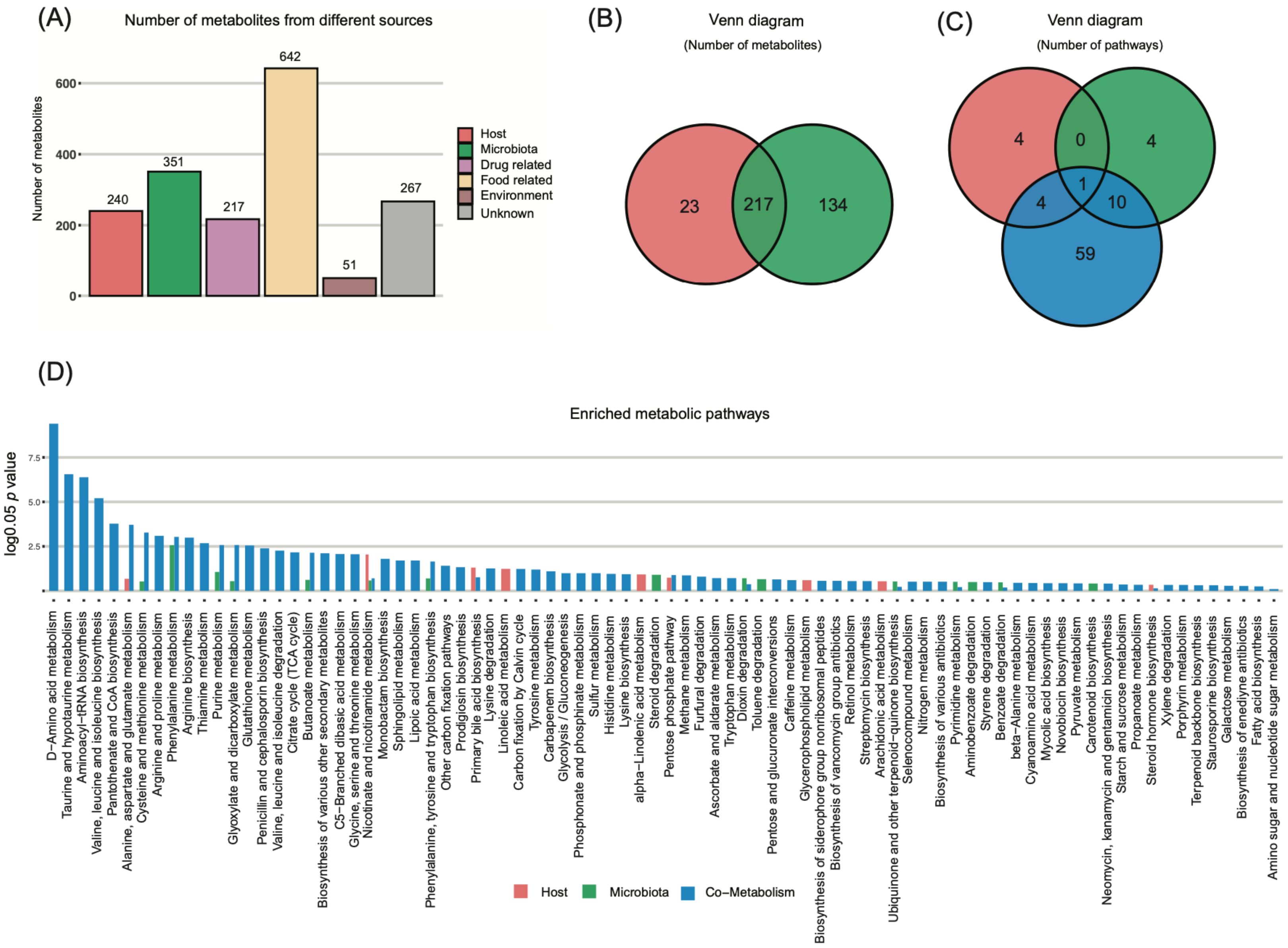
溯源分析 & 代谢通路富集分析



同源分析

1 Pathway analysis

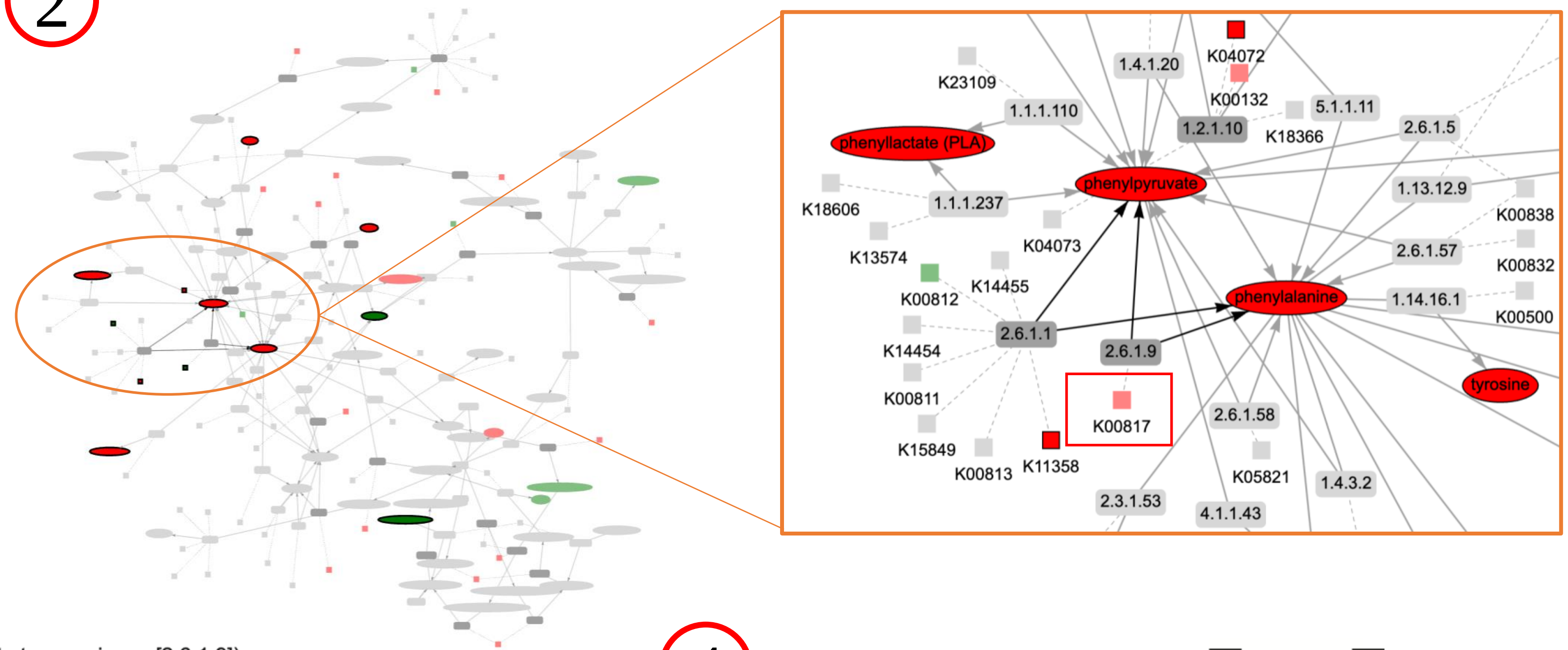
Microbiota

Show 10 entries Search:

No.	ID	Name	Pvalue	Sig. Metabolite ID	Sig. Metabolites
1	ko00360	Phenylalanine metabolism	5.05e-03	C03519; C05607	N-acetylphenylalanine; phenyllactate (PLA)
2	ko00984	Steroid degradation	0.047	C00599	4-cholesten-3-one
3	ko00621	Dioxin degradation	0.084	C00180	benzoate

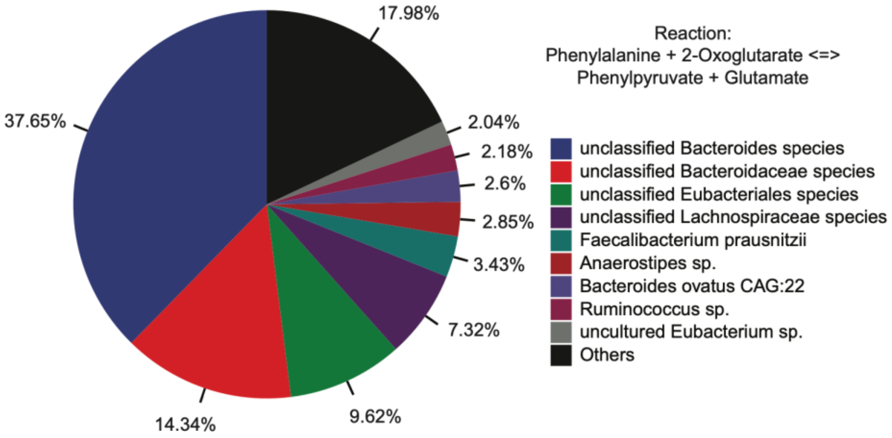
2

Ko00360 Phenylalanine metabolism

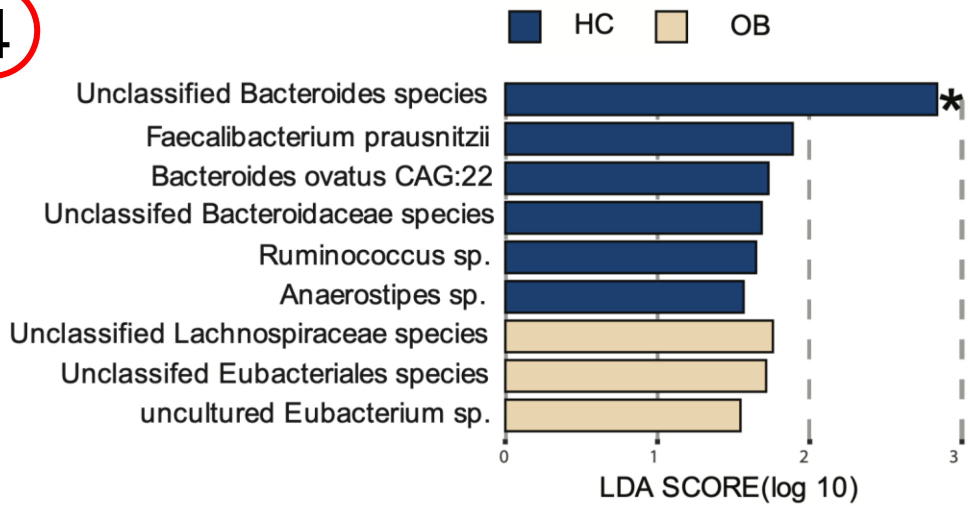


3

K00817 (Enzyme: Histidinol-phosphate transaminase [2.6.1.9])



4



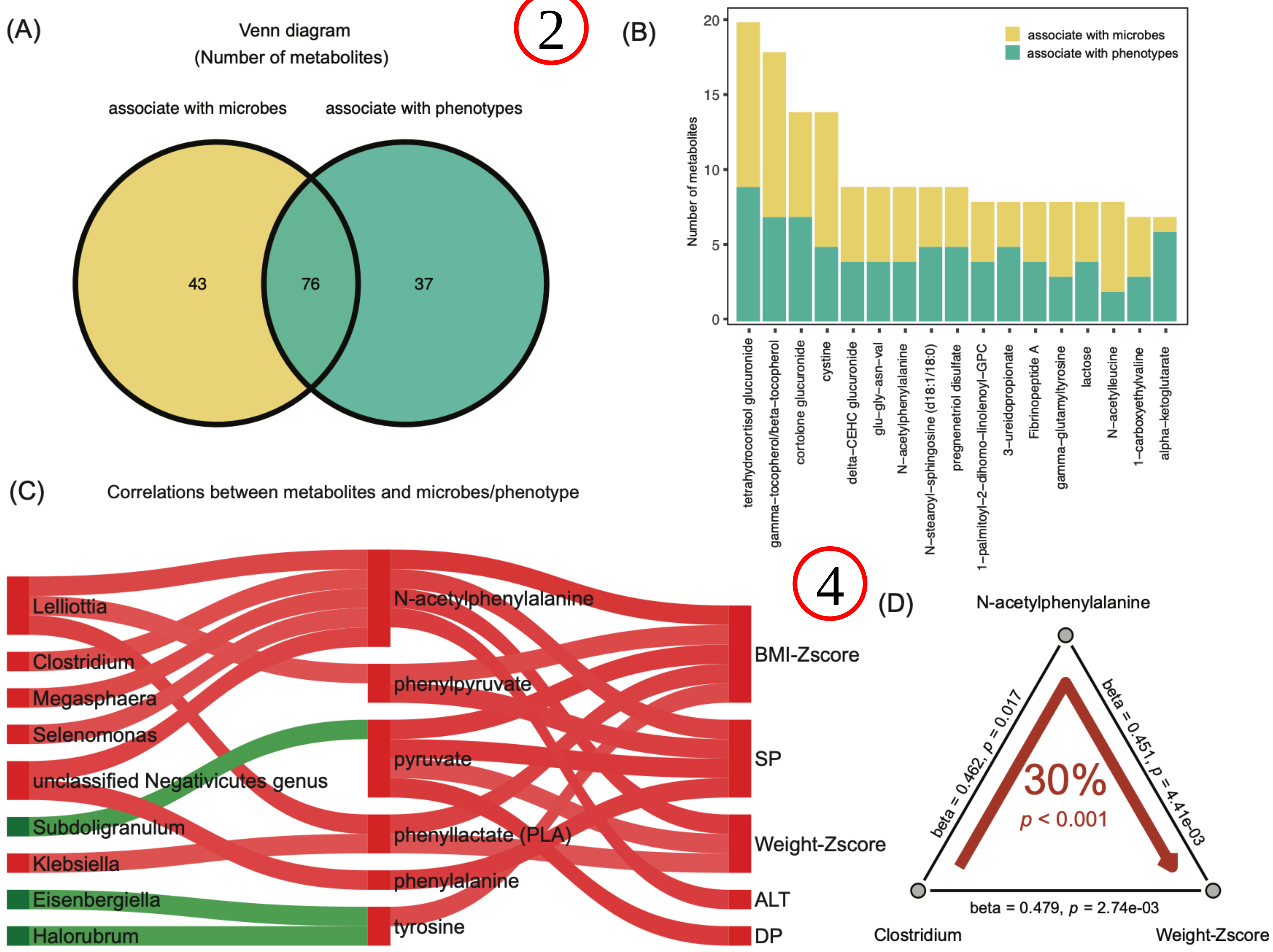
中介分析

1

2

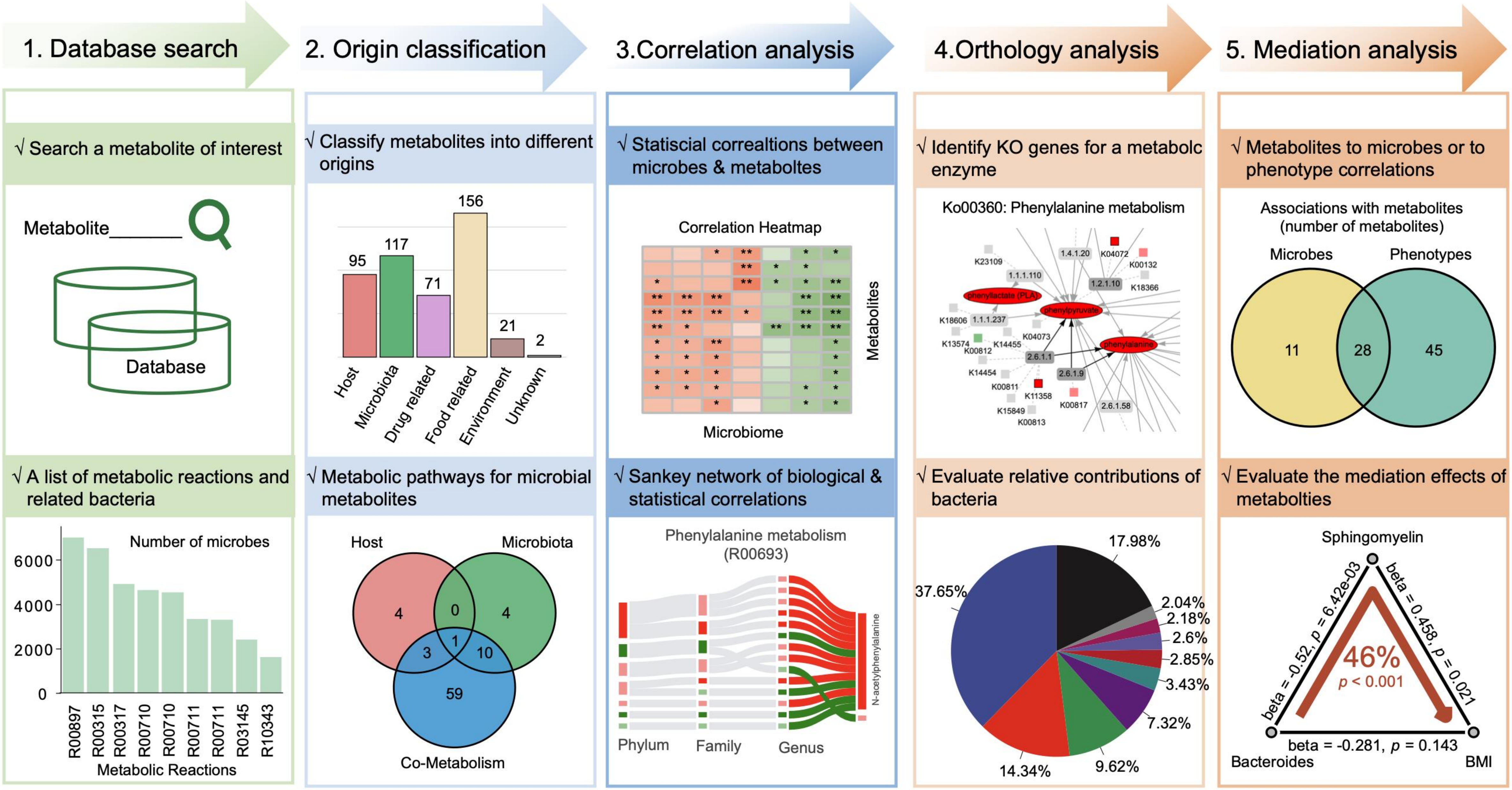
3

4

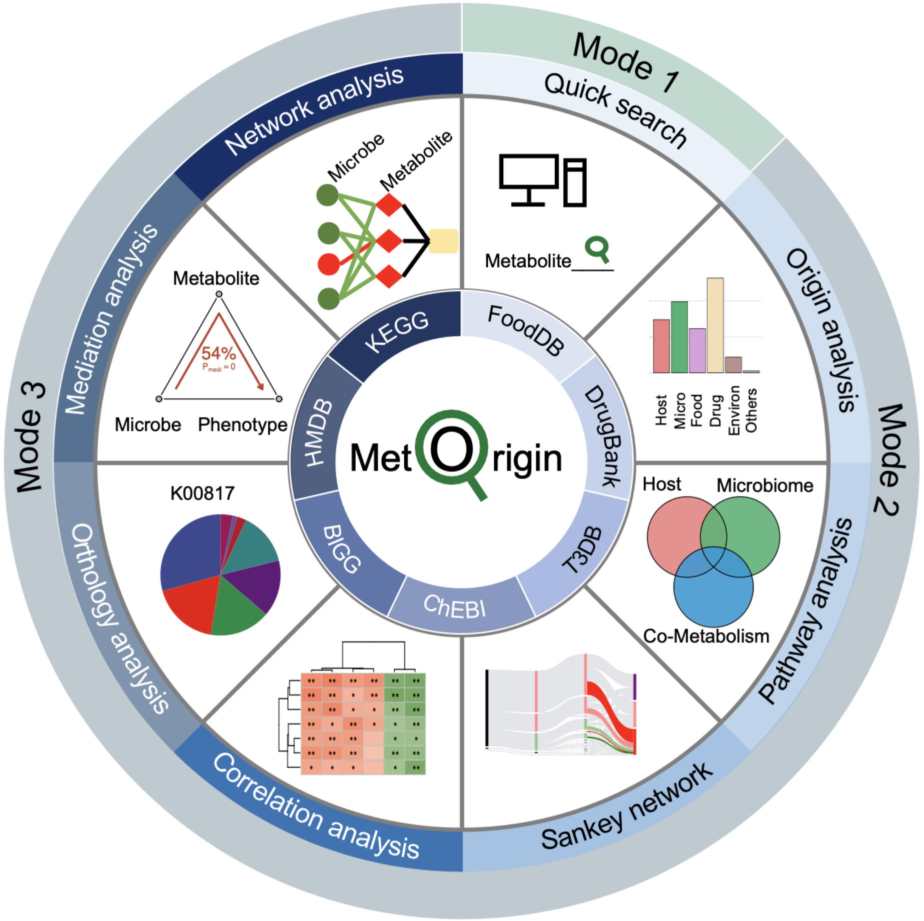


(A)
Venn diagram
(Number of metabolites)
associate with microbes
associate with phenotypes
43
76
37
(B)
associate with microbes
associate with phenotypes
Number of metabolites
20
15
10
5
0
tetrahydrocortisol glucuronide
gamma−tocopherol/beta−tocopherol
cortolone glucuronide
cystine
delta−CEHC glucuronide
glu−gly−asn−val
N−acetylphenylalanine
N−stearoyl−sphingosine (d18:1/18:0)
pregnenetriol disulfate
1−palmitoyl−2−dihomo−linolenoyl−GPC
3−ureidopropionate
Fibrinopeptide A
gamma−glutamyltyrosine
lactose
N−acetylleucine
1−carboxyethylvaline
alpha−ketoglutarate
(C)
Correlations between metabolites and microbes/phenotype
Lelliottia
Clostridium
Megasphaera
Selenomonas
unclassified Negativicutes genus
Subdoligranulum
Klebsiella
Eisenbergiella
Halorubrum
N-acetylphenylalanine
phenylpyruvate
pyruvate
phenyllactate (PLA)
phenylalanine
tyrosine
BMI-Zscore
SP
Weight-Zscore
ALT
DP
(D)
N-acetylphenylalanine
beta = 0.462, p = 0.017
beta = 0.451, p = 4.41e-03
30%
p < 0.001
beta = 0.479, p = 2.74e-03
Clostridium
Weight-Zscore

MetOrigin 2.0 系统分析流程



总结



欢迎使用MetOrigin 2.0
http://metorigin.met-bioinformatics.cn

- MetOrigin 2.0整合了三种分析模式和八个独立分析功能，推进更系统、深入的微生物代谢物鉴定分析。
- 数据库更新、快速搜索、同源分析、和中介分析等新功能，显著拓展分析平台的多样性和功能性。
- MetOrigin 2.0 作为一个全面的网络服务器，旨在整合微生物组和代谢组数据，加快微生物代谢物的发现和溯源。

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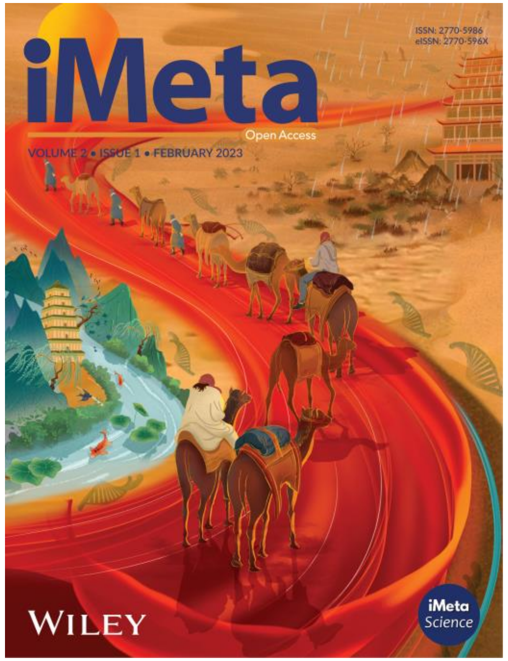

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