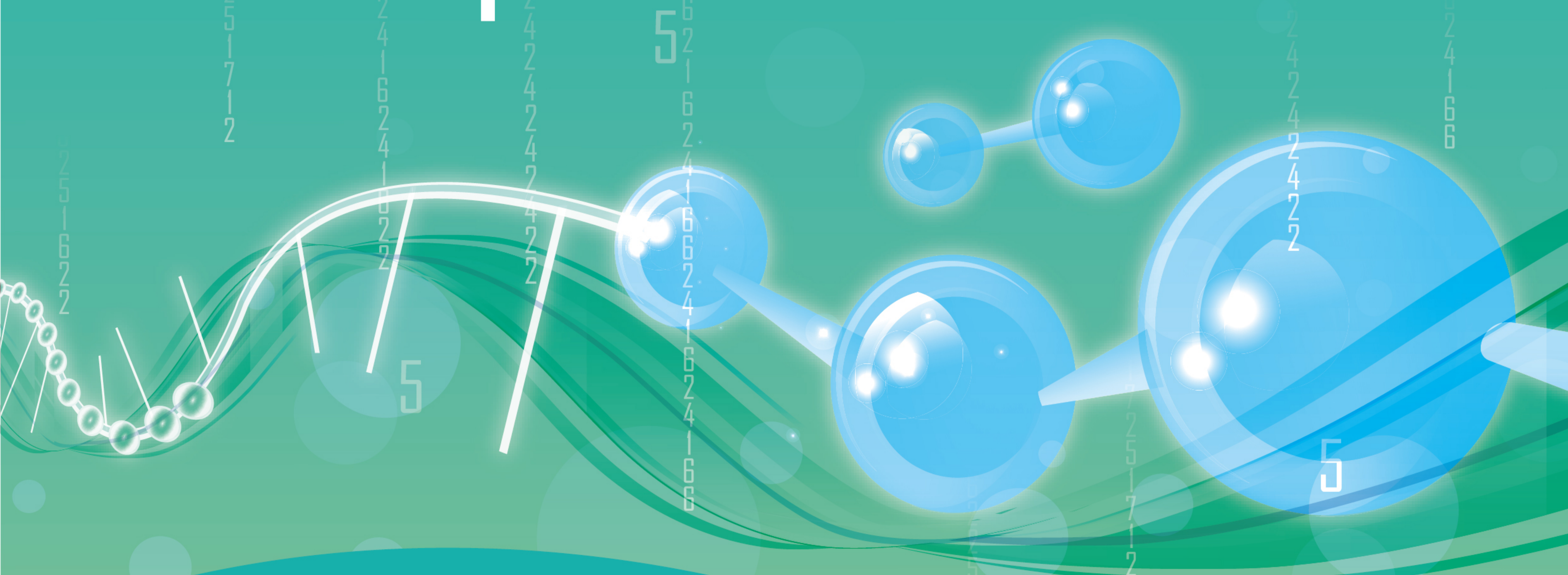






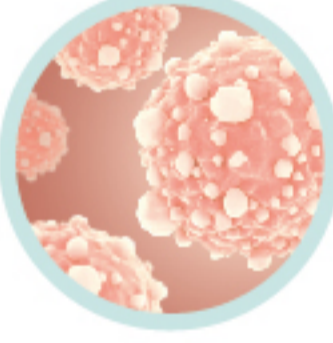




# Transcriptome + Metabolome



## Solutions for Agriculture Research

-  Research on plant growth and development
-  Research on plant biotic stresses
-  Research on plant abiotic stresses
-  Research on the color of fruits and vegetables
-  Research on active ingredients of medicinal plants

## Solutions for Biomedical Research

-  Mechanisms of tumor development
-  Research on the molecular mechanism of complex diseases
-  Drug targets and mechanism of action
-  Embryonic development research
-  Environmental toxicology research

# Multi-omics solution: Transcriptome + Metabolome

In the era of 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. Just as the transcriptome is an important data describing gene expression in a biological system, the metabolome describes the metabolites that result from internal and external regulation of gene/protein expression. Correlating transcriptomic data with differentially expressed genes and metabolomics data with differential metabolites can pinpoint key genes, metabolites, and metabolic pathways that are closely associated with the observed biological system and thereby explaining the biological problems in a more holistic approach.

## 01 Features

01

Applicable to all sample types.

02

Metabolomics and RNAseq on the same samples.

03

Correlation between gene expression and metabolite quantity.

04

RNAseq with 20M reads using PE150.

05

Detects >1300 metabolites on average.

## 02 Transcriptome analysis approach and platforms

High-throughput approaches to studying gene expression include microarray and sequencing. In particular, sequencing (RNAseq) is the most versatile and comprehensive to examine the expression of known and unknown transcripts. As part of our multi-omics service, we will use paired-end sequencing to obtain 20 million reads. Data analysis will provide differentially expressed genes and enriched biological pathways\*.



## 03 Metabolome detection approaches and platforms

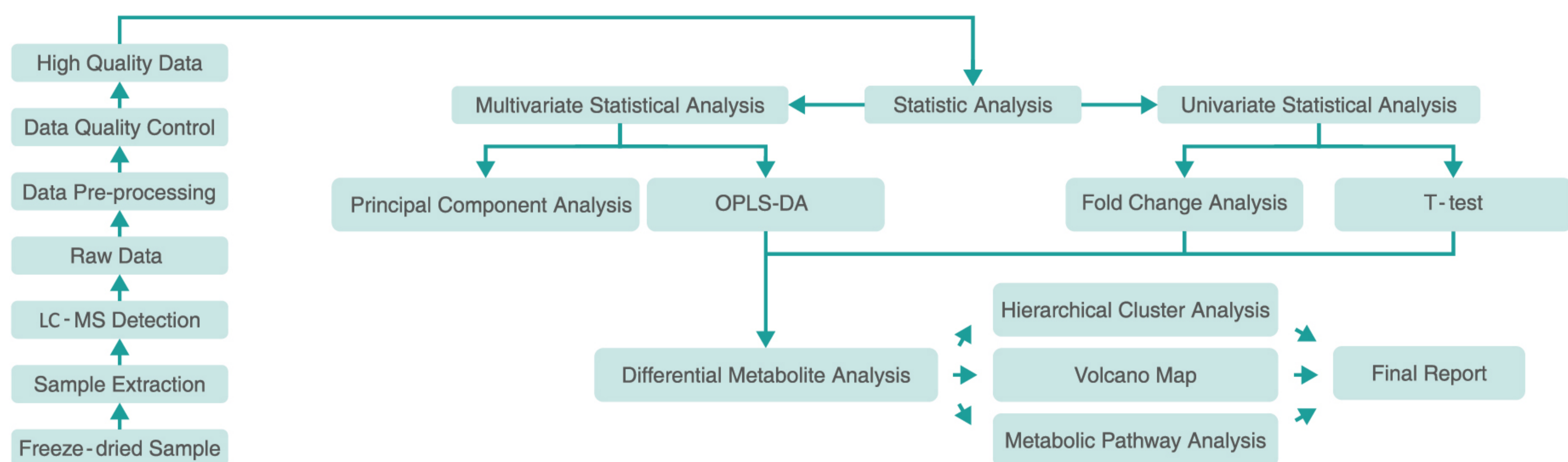
Gene expression can be correlated to many forms of metabolomics data, depending on the research needs. Metware offers a complete suite of metabolomics services that can be paired with RNAseq.

### Widely-Targeted Metabolomics

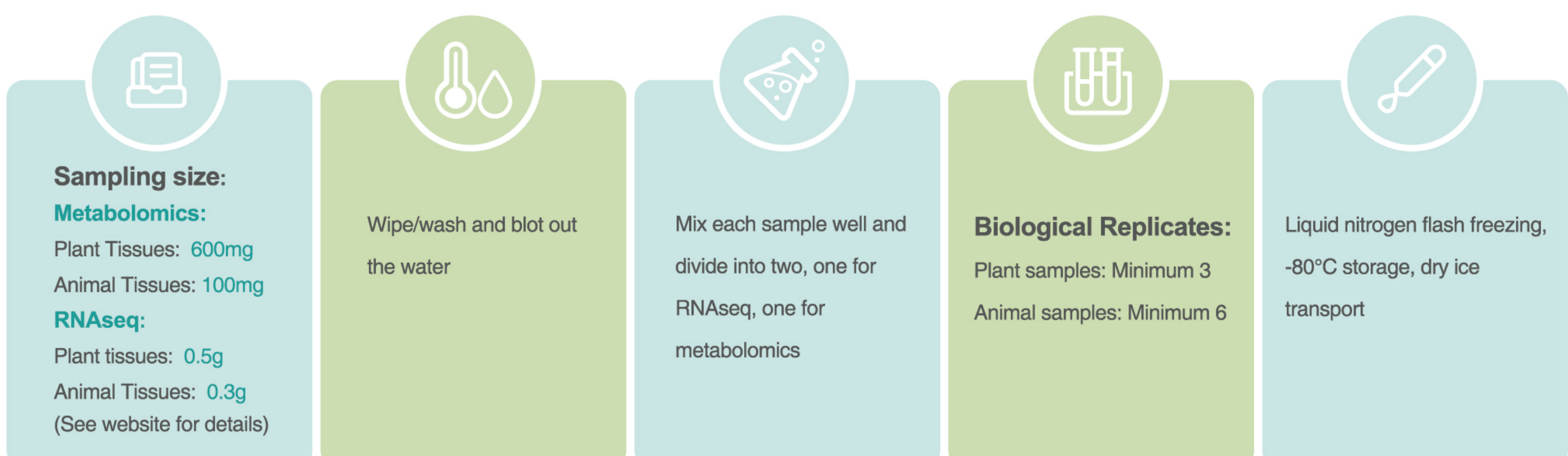
A unique assay that uses UPLC-QTOF-MS/MS platform followed by QqQ MRM scanning mode to efficiently obtain both the qualitative and quantitative amounts of metabolites in the sample. Our in-house metabolite database empowers the extensive annotation from the high-resolution mass spec and allows precise tuning of QqQ for the quantification of these annotated metabolites. In essence, Metware's Widely-Targeted Metabolomics process combines the benefit of untargeted metabolomics and targeted metabolomics to achieve high-throughput, high-sensitivity, and wide-coverage. Services that uses this approach includes TM Widely-Targeted Metabolomics, Widely-Targeted Metabolomics for Plants, and Flavonoid Metabolomics.

### Targeted Metabolomics

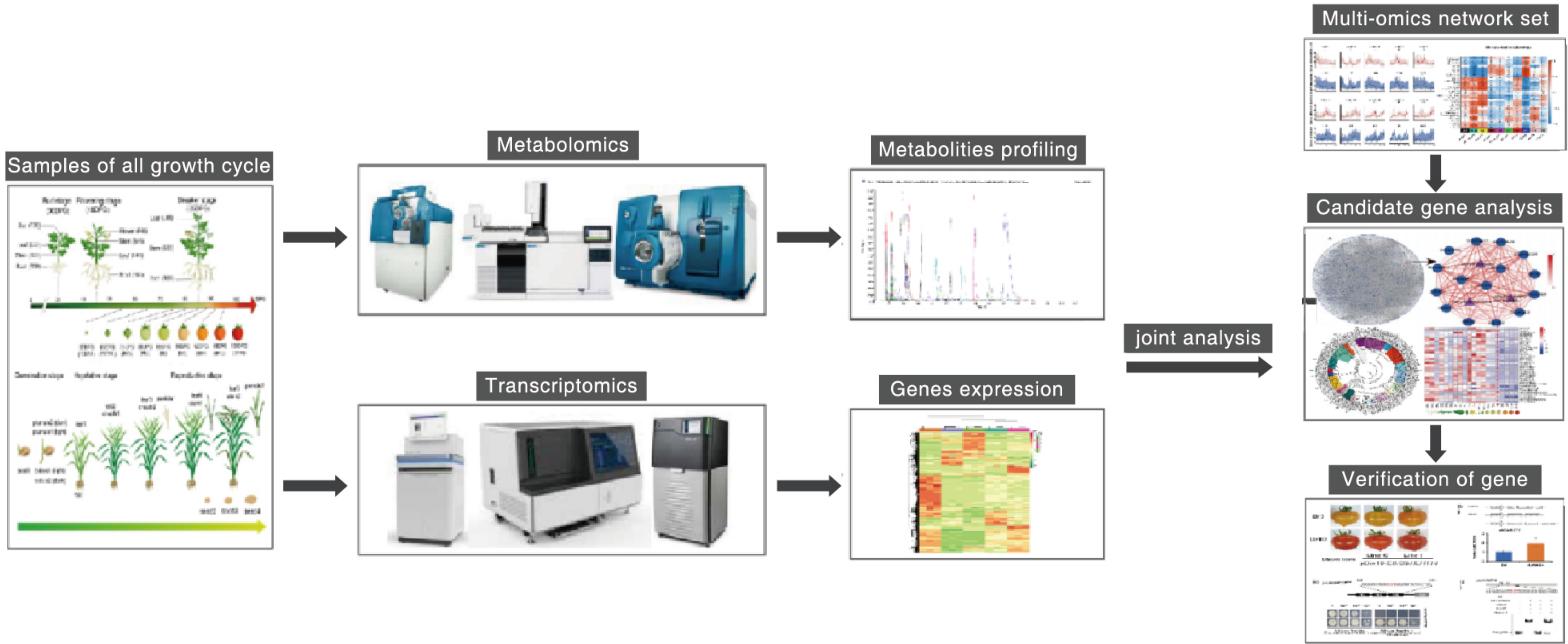
Targeted Metabolomics will provide the most accurate quantification, especially when absolute quantification is needed. The process uses QqQ mass spectrometry with external reference standards of known compounds and known concentrations to build a standard curve. The same specific compounds from the sample are matched to the reference standard and quantified based on the standard curve. Targeted Metabolomics services that are offered at Metware include T500 Targeted Assay, Anthocyanin Targeted Assay, and Plant Hormone Targeted Assay.



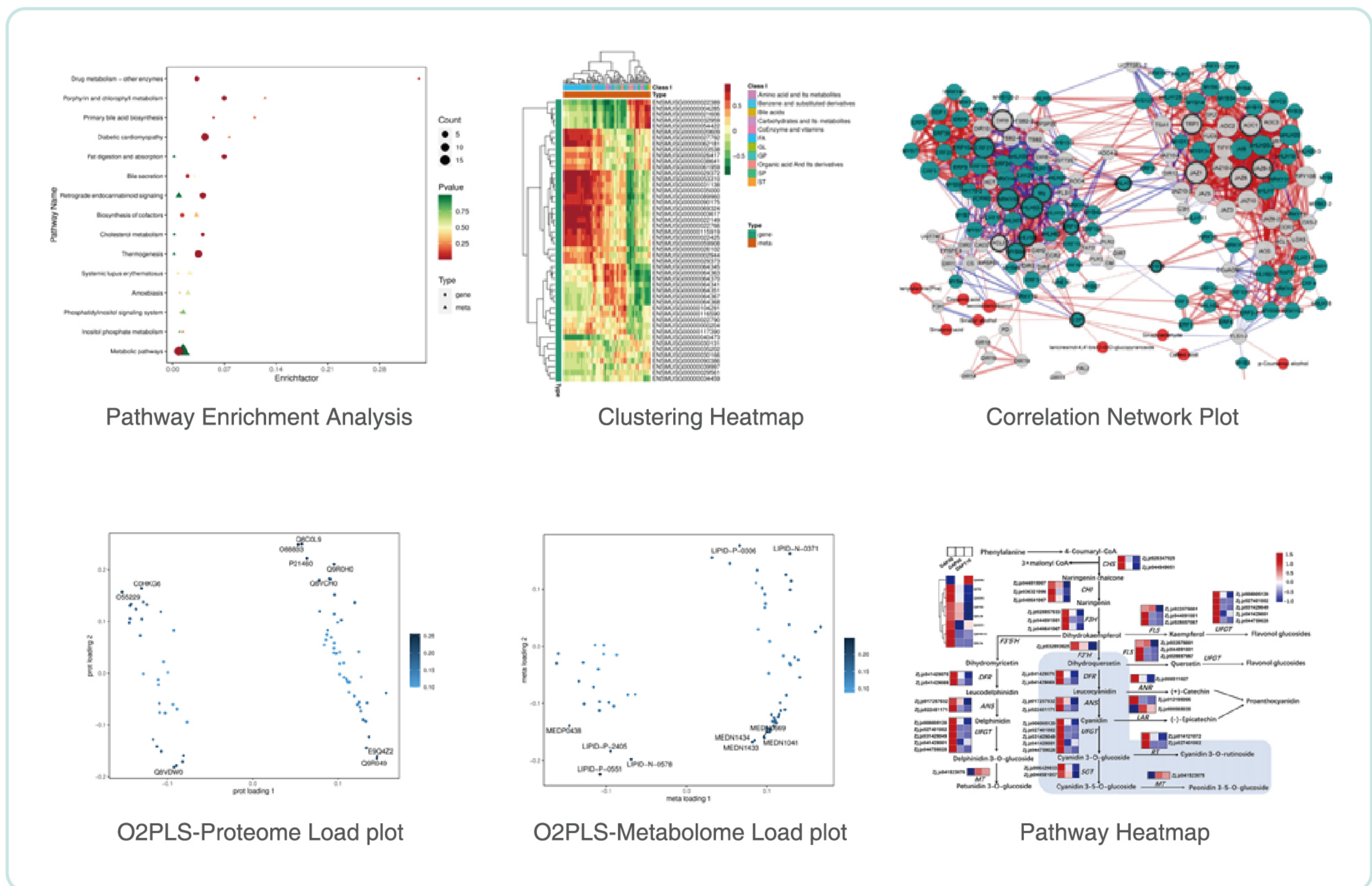
## 04 Sample requirements



# 05 Project workflow



# 06 Data analysis



# 07 Participated Studies

## 1. Evaluation of the influences of low dose polybrominated diphenyl ethers exposure on human early retinal development

**Journal:** Environment International

**Date:** Mar 2022

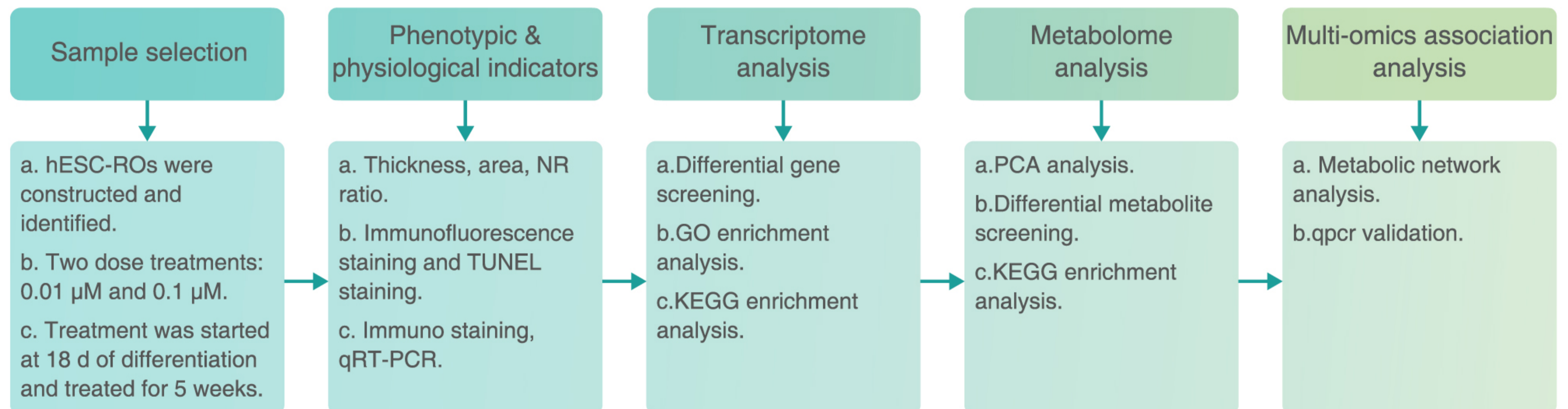
### Research background

01 There is a great need for studies on retinal toxicity from environmental chemicals.

02 PBDEs (Polybrominated Diphenyl Ethers) have been found to cause retinal toxicity in animal models, and fewer studies have been done in humans.

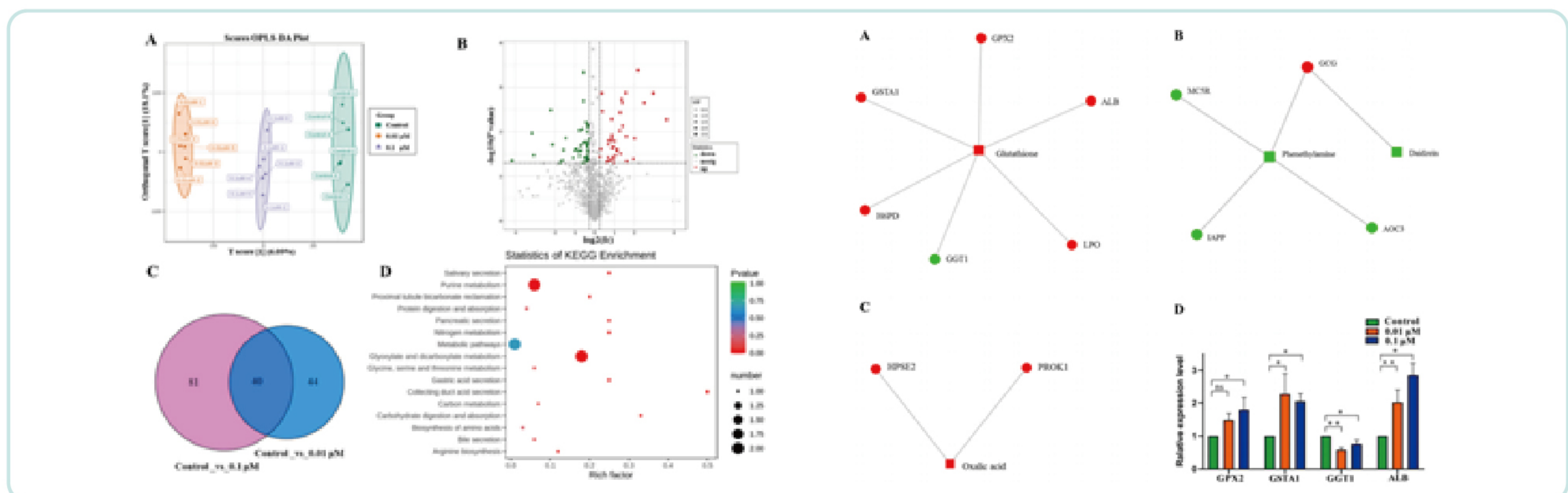
03 The hESC-ROs (human embryonic stem cell-retinal organoid) are good models to study retinal development.

### Project workflow



### Conclusion

This study reveals the potential early human retinal developmental toxicity of PBDEs (Polybrominated Diphenyl Ethers) through the hESC-RO model. This paper demonstrates that low doses of PBDEs may produce multifaceted early developmental toxicity, affecting the proliferation, migration, and differentiation of retinal progenitor cells. Metabolomic and transcriptomic analyses are powerful tools to identify molecular markers and demonstrate the involvement of extracellular matrix organization and metabolism of purines and glutathione in the retinal toxicity of PBDEs. Future studies are still needed to further elucidate the complete molecular mechanism of PBDE-induced retinal developmental toxicity.



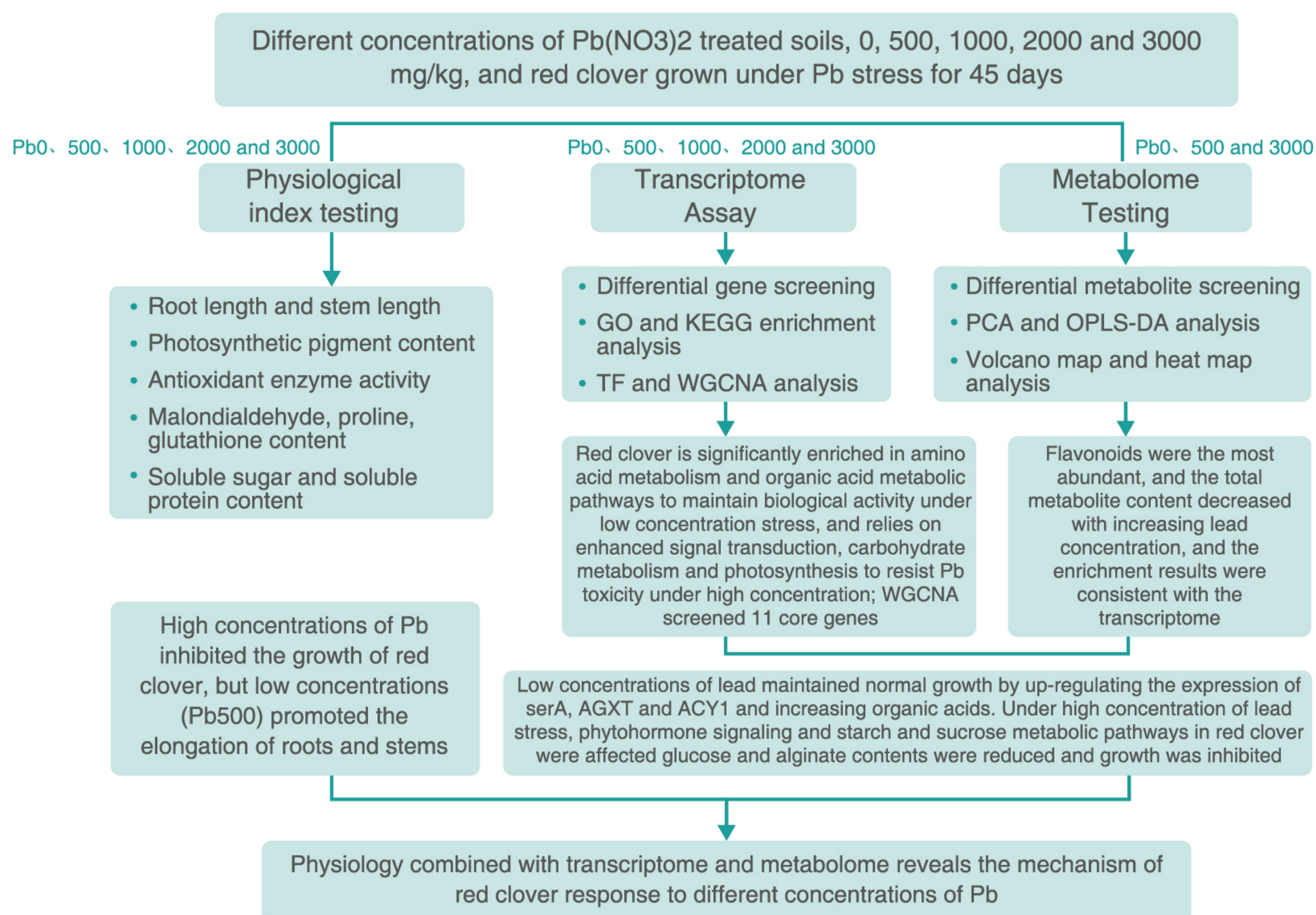
### Reference

Li M, Zeng Y, Ge L, Gong J, Weng C, Yang C, Yang J, Fang Y, Li Q, Zou T, Xu H. Evaluation of the influences of low dose polybrominated diphenyl ethers exposure on human early retinal development. *Environ Int.* 2022 May;163:107187. doi: 10.1016/j.envint.2022.107187. Epub 2022 Mar 18. PMID: 35313214.

## 2. Integrated physiological, transcriptomic and metabolomic analysis of the response of *Trifolium pratense* L. to Pb toxicity

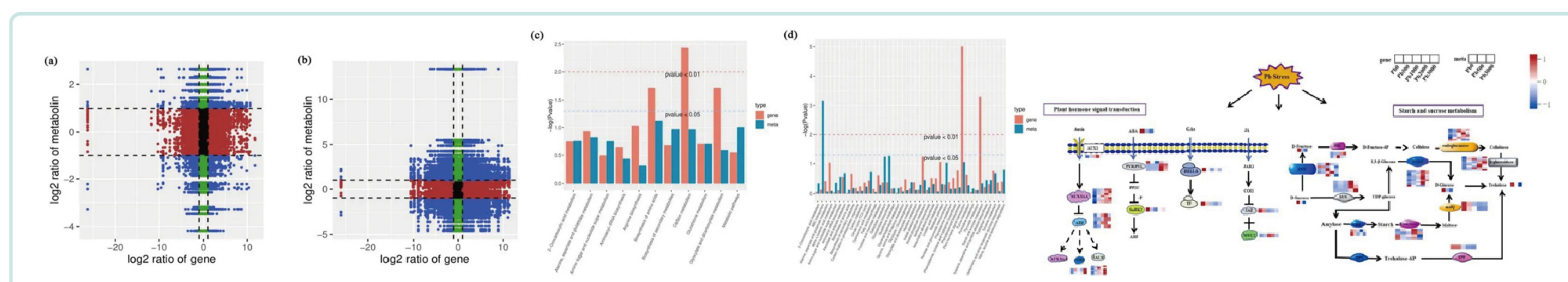
**Journal:** Journal of Hazardous Materials **Date:** May 2022

### Project workflow



### Conclusion

In this study, red clover was treated with different concentrations of Pb. Growth and physiological metabolite levels showed a positive and complex stress response when the stress dose was 500 mg/kg. Pb concentrations greater than 1000 mg/kg damaged photosynthetic pigments and altered the content of antioxidant enzymes, malondialdehyde, proline, and soluble substances, which resulted in toxicity to red clover. In addition, transcriptomics and metabolomics analyses showed that low concentrations (500 mg/kg) of Pb increased organic acid, especially citric acid and amino acid levels by upregulating the expression of serA, AGXT, and ACY1, and regulated changes in carbon metabolism, glycine and dicarboxylic acid metabolism and amino acid biosynthetic pathways in red clover to maintain normal growth. The phytohormone signaling and starch and sucrose metabolic pathways of red clover were affected under high concentration (3000 mg/kg) of Pb stress. Changes in phytohormone signaling compounds altered the growth strategy of red clover with reduced glucose and alginate content under Pb stress. The results of this study are expected to provide new ideas for studying the growth, physiological and molecular responses of red clover under Pb stress. In addition, the method can be used to study the molecular mechanism of plant response to different heavy metals.



### Reference

Meng L, Yang Y, Ma Z, Jiang J, Zhang X, Chen Z, Cui G, Yin X. Integrated physiological, transcriptomic and metabolomic analysis of the response of *Trifolium pratense* L. to Pb toxicity. *J Hazard Mater.* 2022 Aug 15;436:129128. doi: 10.1016/j.jhazmat.2022.129128. Epub 2022 May 13. PMID: 35594664.