



Investigation of Metabolic Network Analysis in Patients with Acute Lymphoblastic Leukemia

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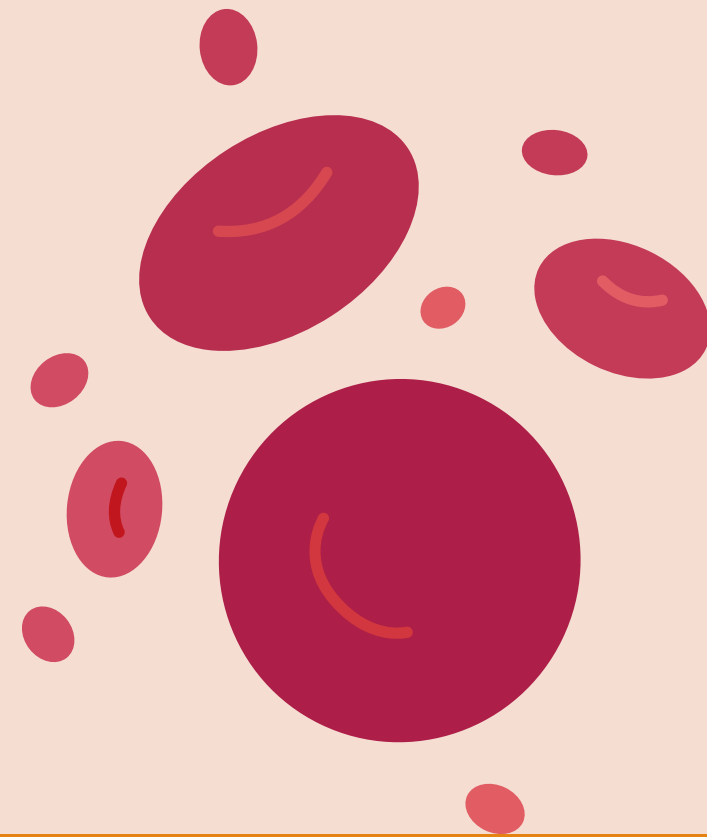
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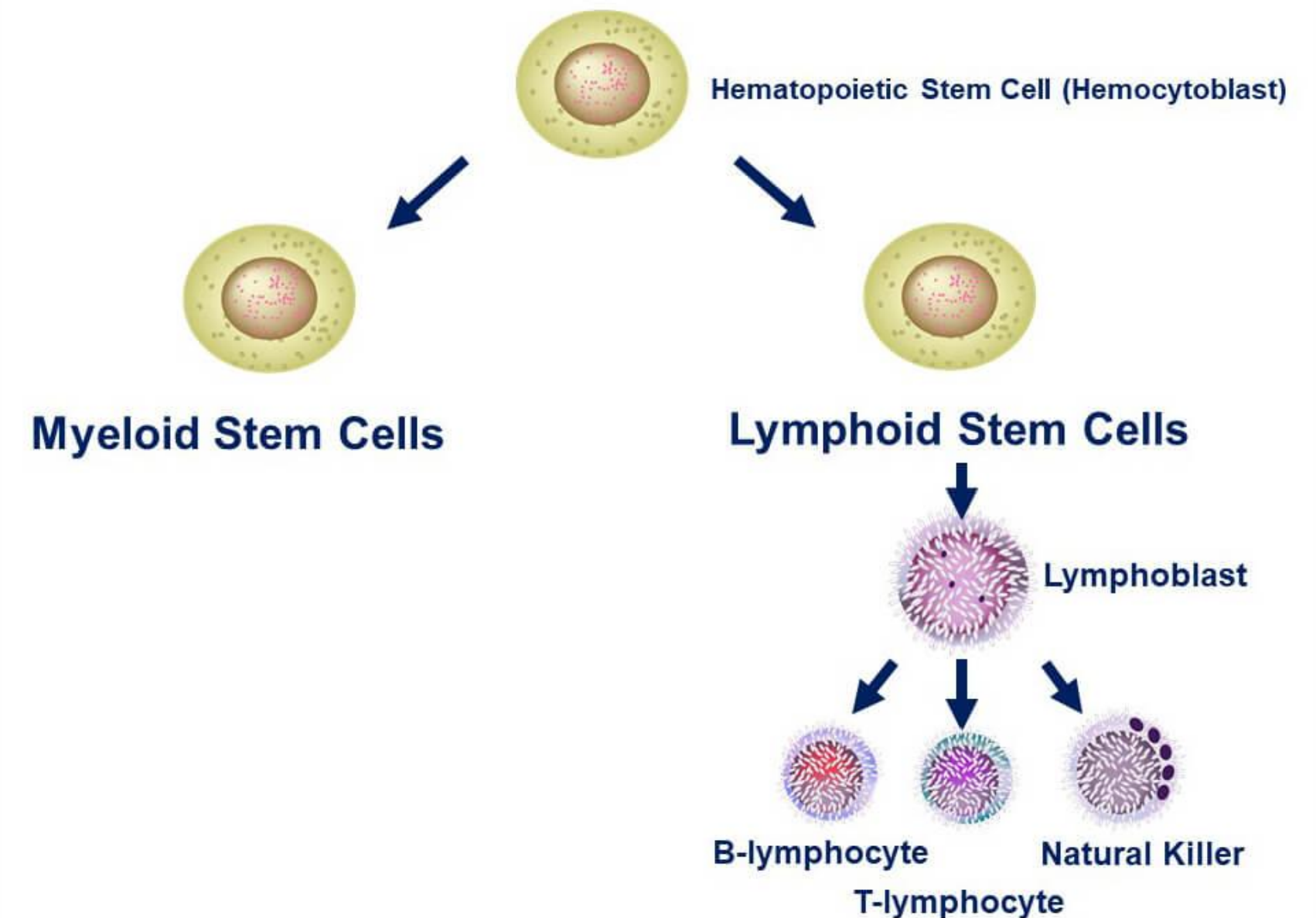
OUTLINES

- 1. Acute Lymphoblastic Leukemia**
- 2. Gaps in Literature & Research Opportunities**
- 3. Metabolomics**
- 4. Aim of Research**
- 5. Method**
- 6. Results**
- 7. Conclusion**



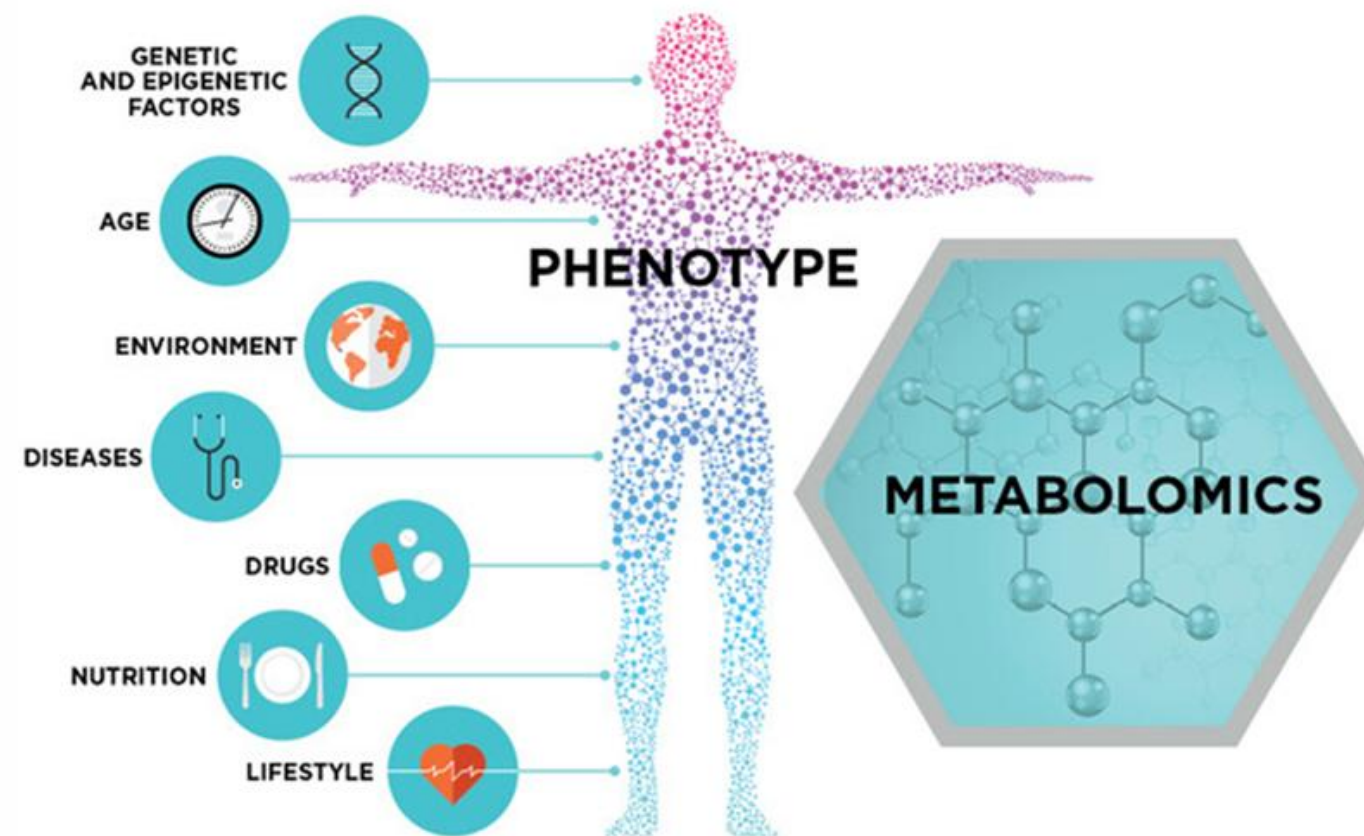
Acute Lymphoblastic Leukemia (ALL)

- ALL is the malignant transformation and proliferation of lymphoid progenitor cells in the bone marrow, blood and extramedullary areas.
- It is the most common type of childhood cancer, accounting for 25% of all pediatric cancers.



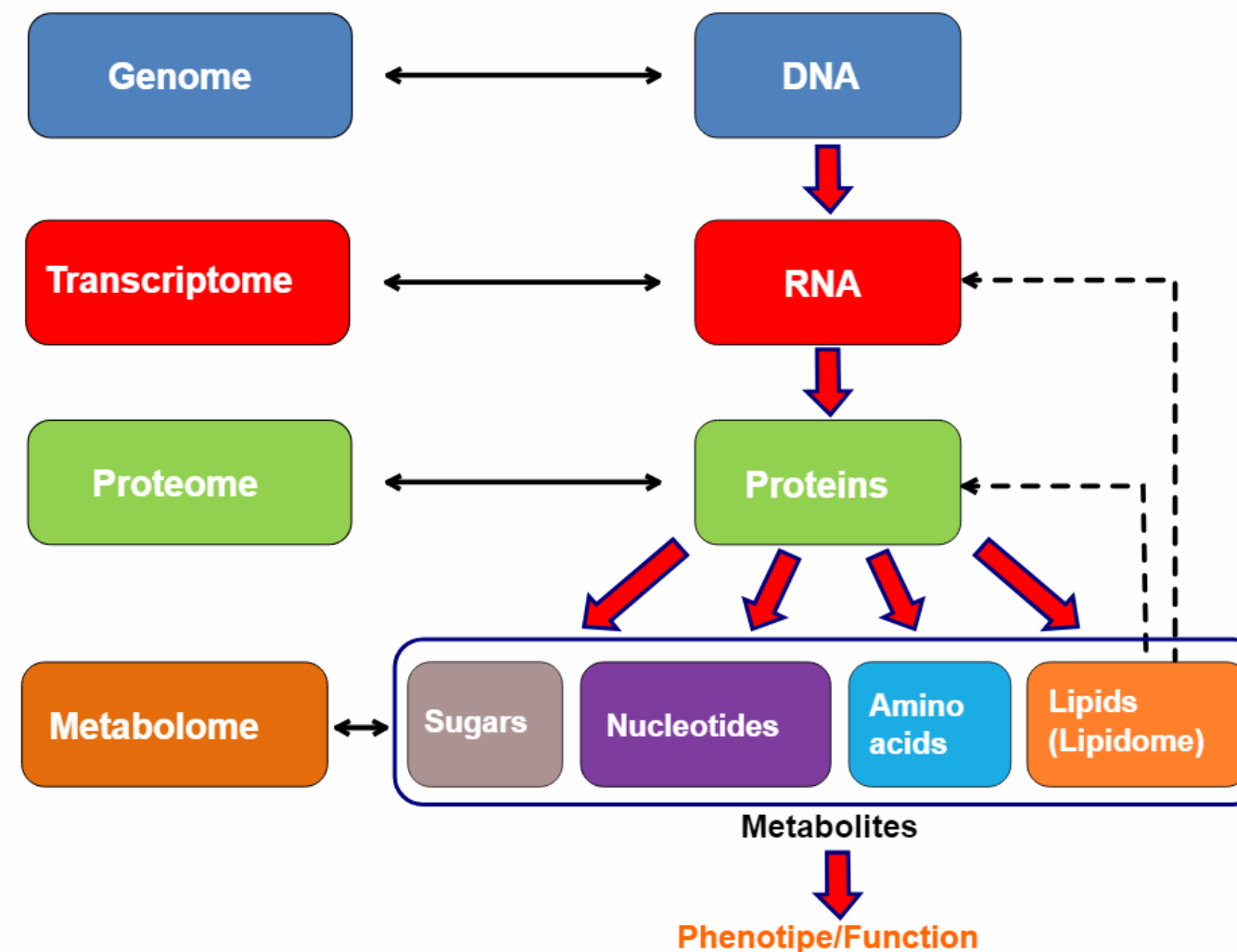
Gaps in Literature & Research Opportunities

- Our understanding of the specific details of metabolism in ALL **remains far from complete**. New studies are **necessary to explain** the findings in the literature and **to discover** new metabolites that can help us understand the pathophysiology of the disease.



Metabolomics

- Metabolomics involves the **comprehensive analysis of metabolites**, the small molecules resulting from cellular processes.
- This method allows the examination of pathomechanisms of the disease and the investigation for possible early biomarkers.



Aim of Research

We **hypothesized** that there may be different types of metabolites between the blood samples of ALL patients and healthy controls. We **aim to** investigate which metabolic networks are associated with the disease.

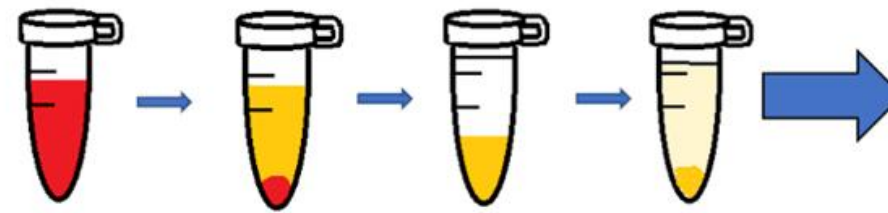
Method

A total of **36 participants** were included in the study, with **18 patients** diagnosed with ALL and **18 healthy controls**.



Sample collection

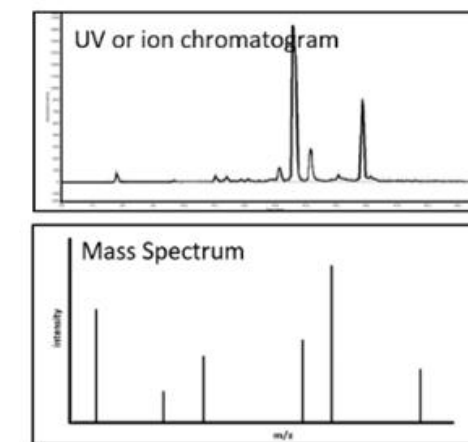
Fasting blood samples were collected, processed, and stored at **-86°C** prior to analysis



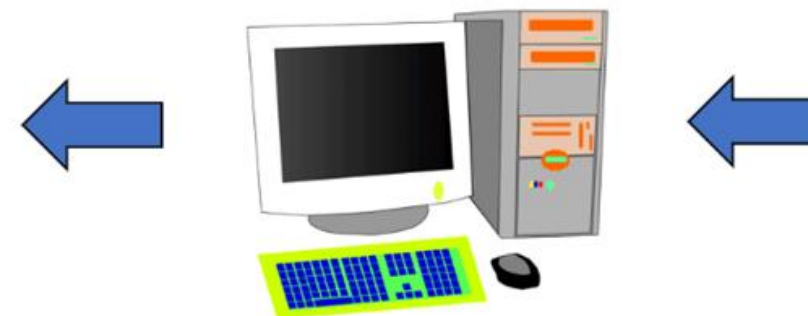
Sample preparation



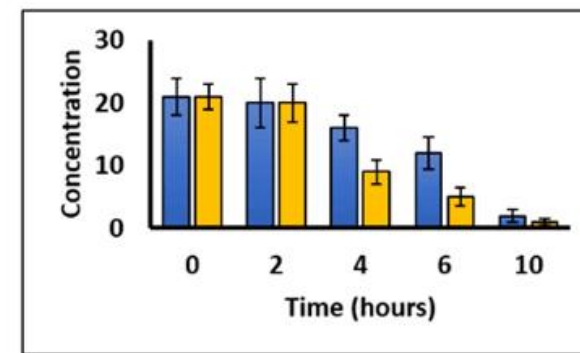
Samples were analyzed using **high-resolution mass spectrometry (LC-MS/MS)**



Data acquisition



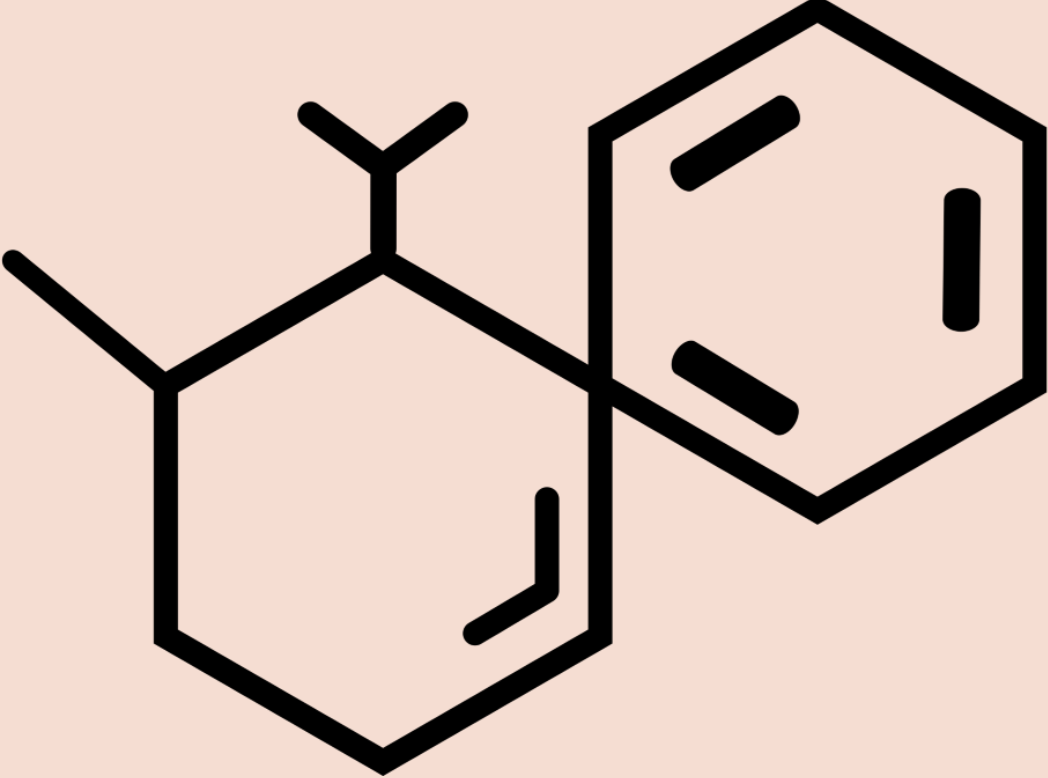
Data analysis



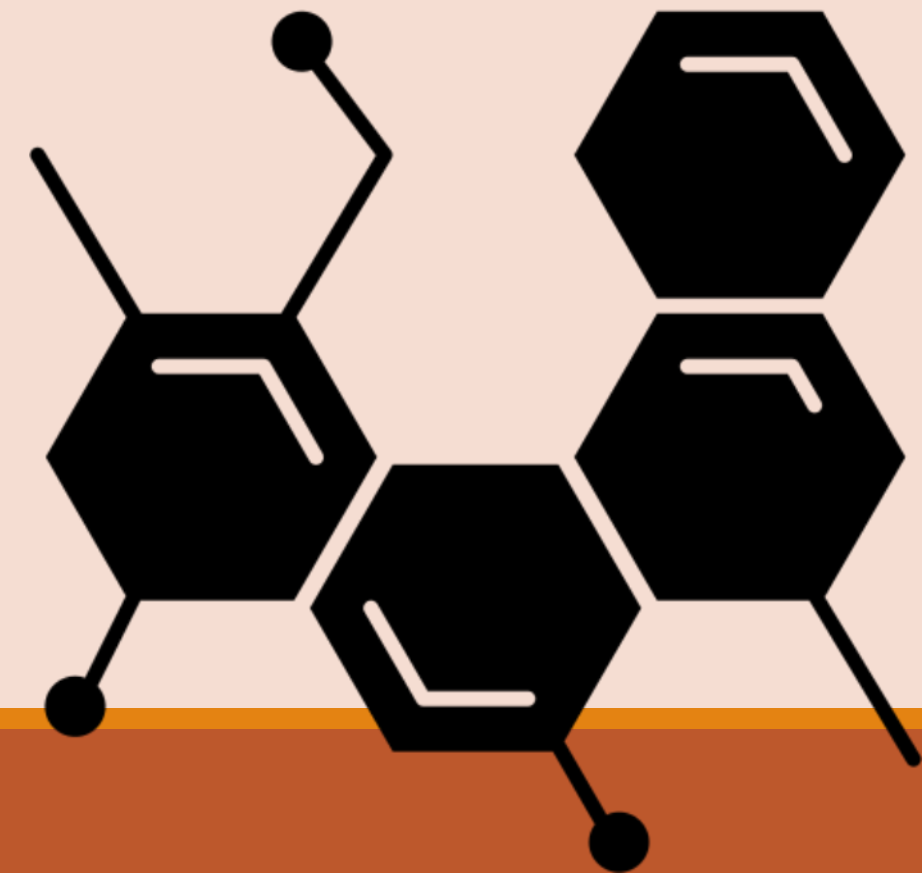
Results

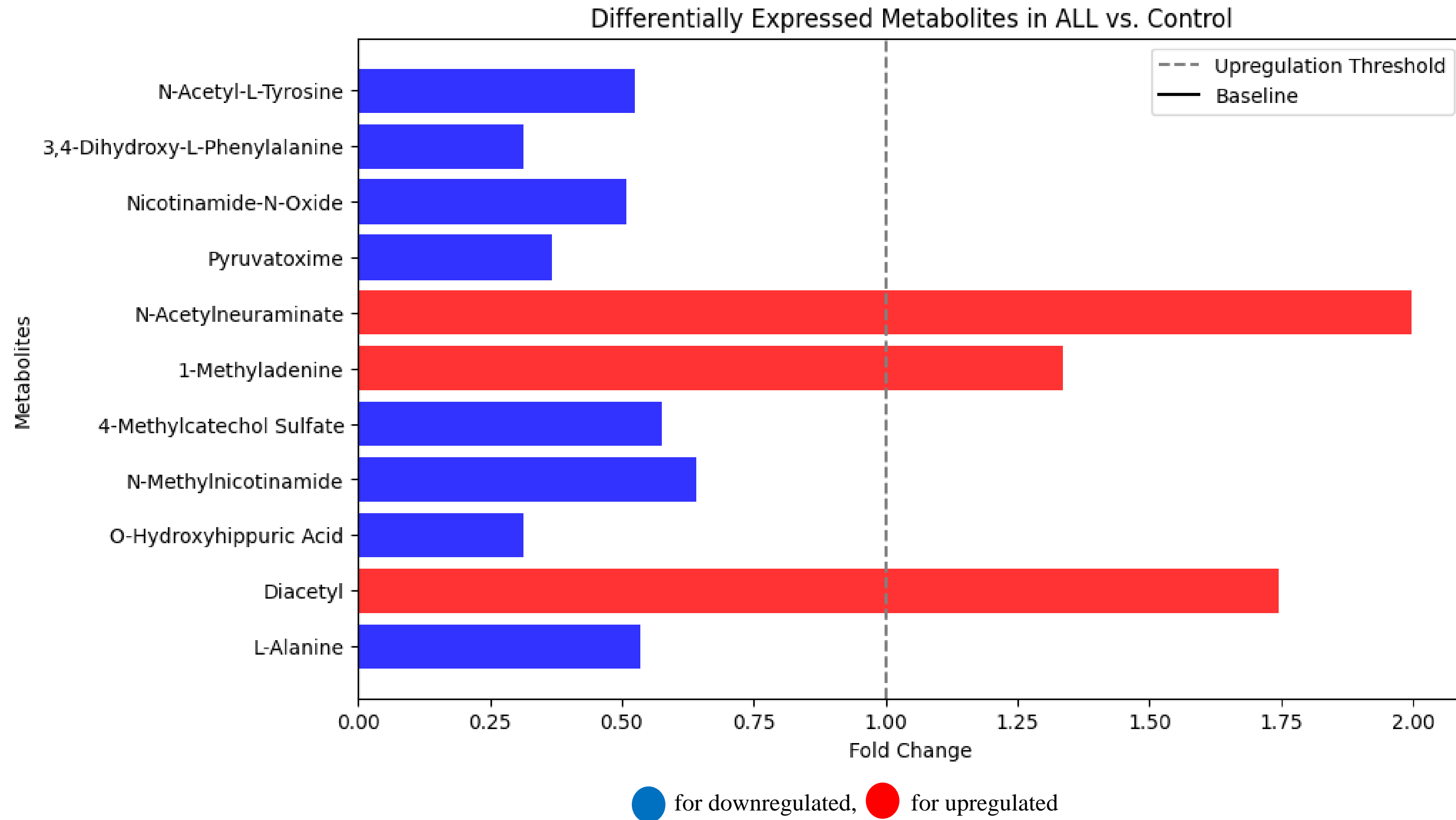
Statistical analyses, including t-tests, Principal Component Analysis (PCA), and Random Forests, were performed via MetaboAnalyst.

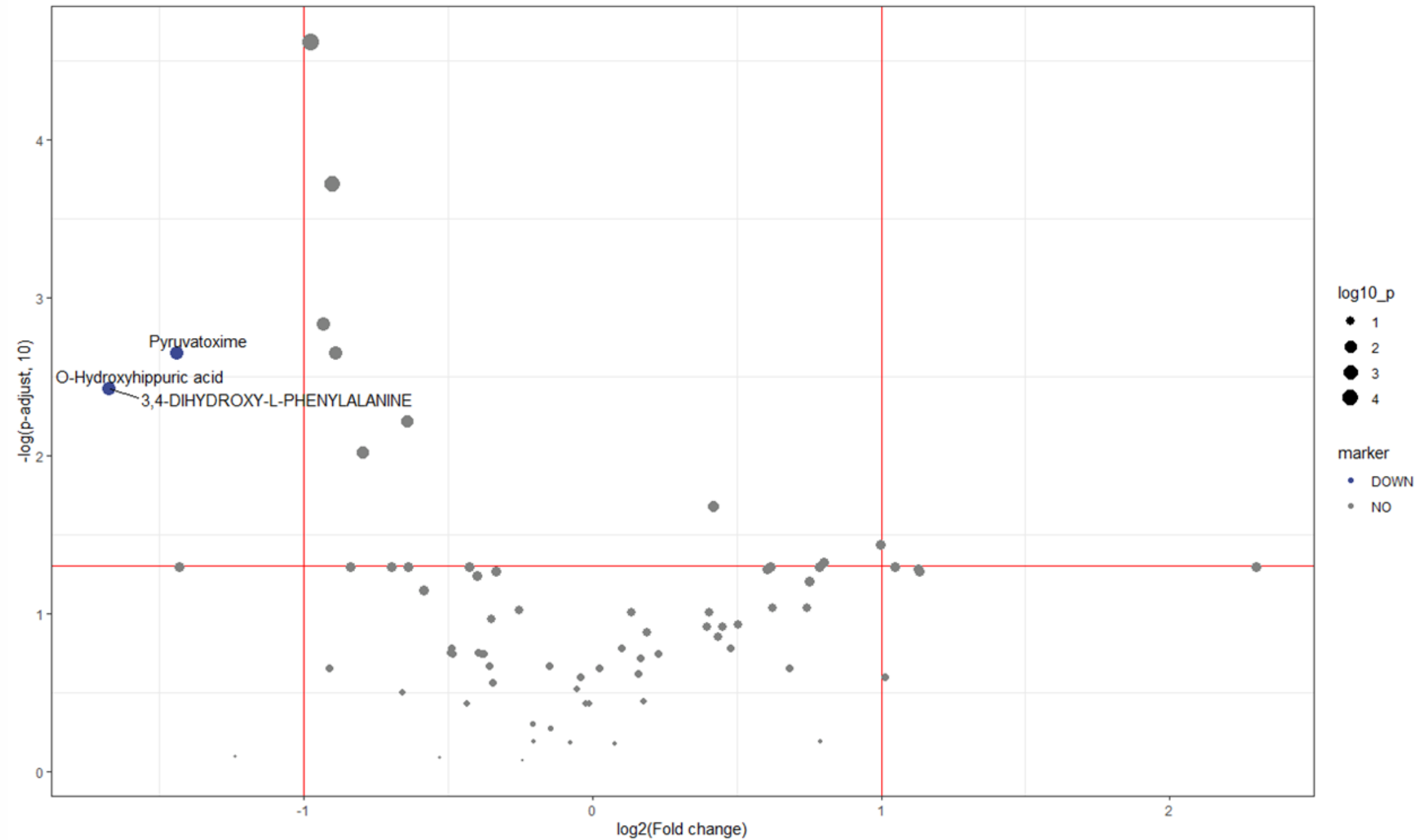
- The spectral data were processed through software tools.
- Metabolite identification was conducted using databases.



Results





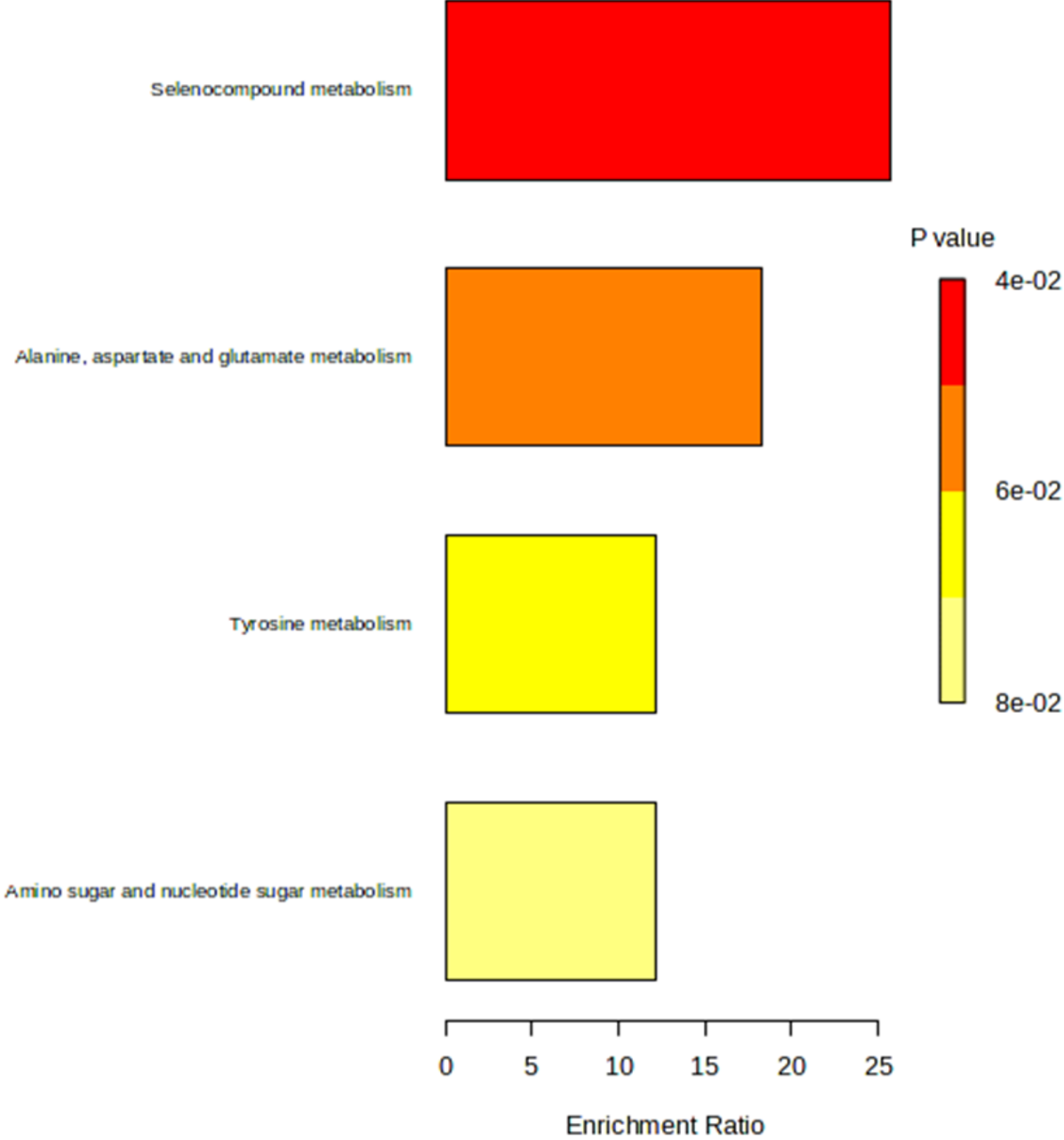


Volcano Plot:

The volcano plot visually displays the metabolite changes between the two groups, highlighting significant up- and downregulated metabolites.

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- **O-Hydroxyhippuric Acid:** Displayed a significant reduction in ALL patients. This may reflect compromised **detoxification pathways in leukemia cells**.
 - **Pyruvatoxime:** Notably downregulated, indicating a disruption in **energy production pathways**.
 - **3,4-Dihydroxy-L-Phenylalanine (L-DOPA):** A significant decrease suggests alterations in phenylalanine metabolism, which may impact **cancer cell survival**.

Metabolite Sets Enrichment Overview



Pathway Enrichment Analysis

Pathway	Key Findings	Implications in Leukemia
Selenocompound Metabolism	Most enriched pathway (enrichment ratio ~25 , $p < 0.04$)	Involved in redox balance & antioxidant defense , potentially aiding leukemia cell survival
Alanine, Aspartate, and Glutamate Metabolism	Disruptions suggest altered amino acid utilization	Supports cancer cell growth by providing building blocks for proliferation
Tyrosine Metabolism	Linked to phenylalanine and catecholamine synthesis	May contribute to ALL oncogenesis via metabolic reprogramming
Amino Sugar and Nucleotide Sugar Metabolism	Altered glycoprotein and nucleotide metabolism	Impacts DNA repair and replication , essential for leukemia progression

Conclusion

Summary:

This study revealed key **metabolomic changes** in ALL patients, particularly in pathways related to **oxidative stress, amino acid metabolism, and energy production**.

Strengths:

- Many significant metabolite differences were found in our study.
- When the results of our study were compared with the studies in the literature, the metabolites that we found are rare metabolites. This allows new validation studies to be conducted.

Conclusion

Limitations:

Small Sample Size: The study includes **only 36 participants**, which may limit the generalizability of the findings.

Not evaluate the relationship of metabolic changes to disease stage.

Future Directions:

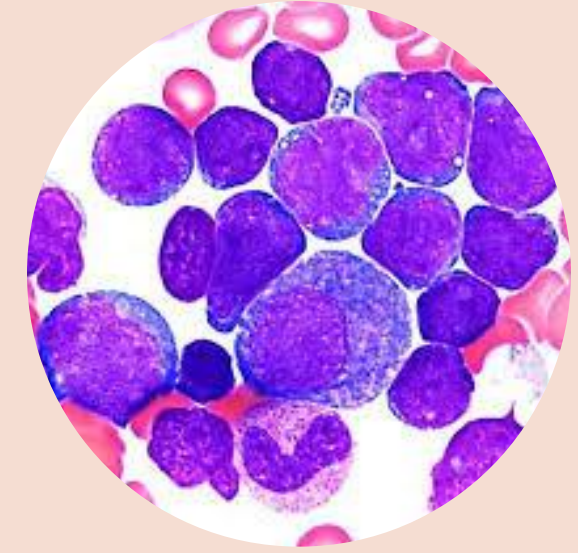
Further research with **larger cohorts** and **longitudinal studies** is necessary to validate these findings. Biomarker studies can be conducted with the metabolites we found. The metabolic pathways we discovered may help in studies to understand the pathomechanism of ALL.

References

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Thank you for listening!