TargetedMetaCorePeakTable\_wo\_peakid\_Analysis\_1

# MetaboAnalyst 網頁狀態回饋:

Data Integrity Check:  
Checking sample names - spaces will replaced with underscore, and special characters will be removed;  
Checking the class labels - at least three replicates are required in each class.  
The data (except class labels) must not contain non-numeric values.  
If the samples are paired, the pair labels must conform to the specified format.  
The presence of missing values or features with constant values (i.e. all zeros).  
Data processing information:  
Checking data content ...passed.  
Samples are in columns and features in rows.  
The uploaded file is in comma separated values (.csv) format.  
The uploaded data file contains 6 (samples) by 82 (peaks(mz/rt)) data matrix.  
Samples are not paired.  
2 groups were detected in samples.  
Only English letters, numbers, underscore, hyphen and forward slash (/) are allowed.  
Other special characters or punctuations (if any) will be stripped off.  
All data values are numeric.  
No missing values were detected. Click the Proceed button to the next step.  
Data processing information:  
Checking data content ...passed.  
Samples are in columns and features in rows.  
The uploaded file is in comma separated values (.csv) format.  
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All data values are numeric.  
  
No missing values were detected. Click the Proceed button to the next step.  
Edit Groups  
Proceed  
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Proceed

# LLM檢測分析之結果:

Okay, I'm ready to analyze the MetaboAnalyst output you've provided. Here's a report explaining the data, focusing on the volcano plot and the concepts behind it, presented in a numbered bullet point format:  
  
\*\*Metabolomics Data Analysis Report – Volcano Plot Interpretation\*\*  
  
1. \*\*Volcano Plot Overview:\*\* The image you sent is a volcano plot. This is a common visualization tool in metabolomics (and other 'omics fields) used to display the results of differential metabolite analysis. It simultaneously shows both the \*statistical significance\* and the \*magnitude of change\* (fold change) between two or more groups.  
  
2. \*\*Axes Explanation:\*\*  
 \* \*\*X-axis (Features):\*\* Represents the individual metabolites (or 'features') identified in your study. Each dot corresponds to one metabolite. They are numbered sequentially, from 1 to 85 in this case.  
 \* \*\*Y-axis (-log10(p-value)):\*\* This represents the statistical significance of the difference in abundance of each metabolite between the groups being compared. The negative logarithm (base 10) of the p-value is used because p-values are often very small numbers, making them difficult to visualize on a linear scale. Taking the -log10 transforms small p-values into larger, more manageable values.  
  
3. \*\*Understanding P-value:\*\* The p-value is the probability of observing the obtained results (or more extreme results) if there is \*no real difference\* between the groups being compared. In simpler terms, it tells you how likely it is that the observed differences are due to random chance.  
  
4. \*\*P-value Thresholds for Significance:\*\*  
 \* A p-value of 0.05 is commonly used as a threshold for statistical significance. This means there is a 5% chance of observing the results if there is no real difference.  
 \* However, when performing multiple comparisons (as is the case in metabolomics where you are testing many metabolites simultaneously), it's crucial to adjust the p-value to account for the increased risk of false positives. This is often done using methods like Benjamini-Hochberg (FDR – False Discovery Rate) correction, which appears to be applied here (indicated by the "raw P-value" in the legend).  
 \* A corrected p-value (often called an adjusted p-value or FDR) of 0.05 is a common threshold for significance after multiple comparison correction.  
  
5. \*\*Interpreting the Plot – Significant Metabolites:\*\*  
 \* \*\*Purple Dots:\*\* These represent metabolites that are considered \*statistically significant\* after p-value adjustment. They are located higher on the Y-axis (larger -log10(p-value)), indicating lower p-values. In your plot, there are 4 significant metabolites.  
 \* \*\*Gray Dots:\*\* These represent metabolites that are \*not statistically significant\* after p-value adjustment. They are located lower on the Y-axis.  
  
6. \*\*Fold Change (Not Directly Shown, but Implied):\*\* While the plot doesn't \*directly\* show fold change, the position of the dots along the X-axis \*implies\* the magnitude of the change. Metabolites further to the right (positive X-axis values) are generally more increased in abundance in the comparison group, while those further to the left (negative X-axis values) are generally more decreased. To get the exact fold change values, you would need to refer to the underlying data table generated by MetaboAnalyst.  
  
7. \*\*Focusing on Significant Metabolites:\*\* The metabolites represented by the purple dots are the most interesting ones. Further investigation is needed to understand their biological relevance. This might involve looking up their known functions, pathways they participate in, and potential roles in the biological process being studied.  
  
8. \*\*Limitations:\*\* This plot provides a good overview, but it's important to remember that statistical significance doesn't always equal biological significance. Small but statistically significant changes might not be meaningful in a biological context. Consider the magnitude of the fold change and the biological relevance of the metabolites when interpreting the results.  
  
  
  
To provide a more detailed analysis, I would need the underlying data table from MetaboAnalyst, which includes the fold change values and the raw/adjusted p-values for each metabolite. This would allow me to identify the specific metabolites that are significantly altered and quantify the extent of those changes.

# 圖片結果顯示:









