



WORKING MANUAL OF MMIP

Notes:

1.  Red arrow and number box indicates additional functionality.
2.  Black dotted arrow indicates feature information.
3. All the comparison and the analyses are between two groups (not more).
4. By the term “significant”, statistical significance is referred to.
5. All the analysis diagrams are made using Plotly and will feature the following tools (as shown below) on the top right corner of each diagram, allowing the user to access features like zoom, edit, download and other interesting tools.



[GET STARTED](#)

Scroll Down the page to get the overview.

MMIP

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Overview

Welcome to MMIP Server.

This server is designed for prediction of the metabolites that could be produced by the microbial community during different health condition by using their metagenomics data (16S-rRNA). Furthermore, it also helps you to compare your real-time metabolomic (untargeted) data with predicted metabolite and helps to see what could be the most probable source of the metabolites.

- ✔ Helps in predicting metabolites from the metagenomic data.
- ✔ Helps in finding the most probable source of the metabolite (microbe responsible for the production).
- ✔ Predict important feature at OTU, Compound, Enzyme level by machine learning approaches.
- ✔ Helps in interlinking important feature.



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Services

Please Select any one of the two module to start your analysis.



MMIP

Perform general prediction of compounds from metagenomic data (16S-rRNA)



MMIP-MASS

Allow user to perform comparative analysis between real-time metabolic data and one being predicted



Click on either of the tabs to go to the respective "upload" pages.

Click on Get Started to use the Respective Services.

(Fig. 1)

MMIP:

Returns to the homepage. ←

MMIP

HOME

MANUAL

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Name

Enter name

Email

Enter Email

Institute Name

Enter Institute Name

Select OTU Table: No files selected.

Download example OTU file 

Select Metadata: No files selected.

Download example Metadata file 

Select Column for Grouping:

Select Group:

Select Database: ☐ 18may2012 ☐ 13_5 ☒ 13_8

By submitting job you agree to our [Terms & Privacy](#).

Submit Job

→ Add the Closed-reference based OTU table.

Select Greengenes database version used.

→ Add the Metadata file (tab-separated, .tsv, format).

(Fig. 2)

Name

Enter name


Email

Enter Email

Institute Name

Enter Institute Name

Select OTU Table: No files selected.


Download example OTU file 

Select Metadata: No files selected.

Download example Metadata file 

Select Column for Grouping: Select Group:

Select Metabolomics Feature table (optional): No files selected.

Look at the example file 

Select Database: ☐ 18may2012 ☐ 13_5 ☒ 13_8

By submitting job you agree to our [Terms & Privacy](#).

Submit Job

(Fig. 3)

RESULT PAGE

USER AND JOB-RELATED INFORMATION:

To search keywords or values within the table.

Each of the tabs take the user to the respective result sections.

MMIP

JOB METABOLITES ALPHA-DIVERSITY TAXONOMY BETA-DIVERSITY PATHWAY FEATURE CONTACT US

Job Summary

Show 10 entries Search:

S.NO	Content	Description
1	Job Id	215
2	User Name	Name of User
3	Biom File Name	otu_table_20000.biom
4	Meta Data File Name	mapping_file.txt
5	Grouping Column	Description
6	Total Number of Sample Group1 (CRC)	20

Showing 1 to 10 of 12 entries Previous 1 2 Next

1

(Fig. 4)

- 1 Scroll the table for additional information including number of samples in group 2, Institute name, email Id, start date, time and status of the job.

METABOLITES:

Add range of desired p values.

Click on the compound ids to get to the KEGG page of the respective compound.

Minimum p-value:

Maximum p-value:

Show entries

Search:

VISUALIZE ALL COMPOUND 2

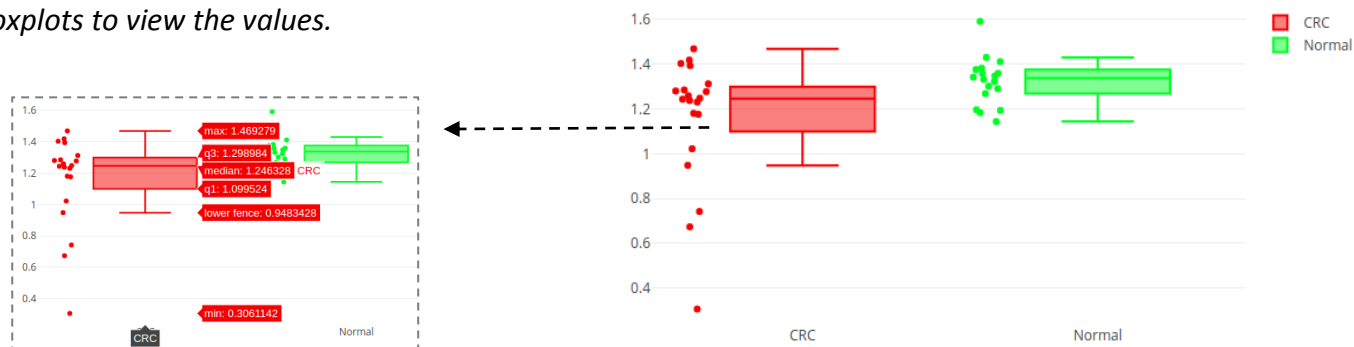
S.NO	KEGG Compound ID	p-value	Box Plot
1	C00064	0.032828	
2	C00117	0.035297	
3	C00120	0.014059	
4	C00167	0.046764	
5	C00185	0.003461	
6	C00194	0.024378	

S.NO	File Name	Download
1	Statistically Significant Compound Detail (kruskal-walis test)	3
2	Statistically Significant Compound Detail (Wilcox test)	
3	Statistically Significant Compound Detail (Anova-1-way test)	
4	Statistically Significant Compound Detail (t-test)	
5	All Compound CMP Score	

Showing 1 to 5 of 5 entries 4

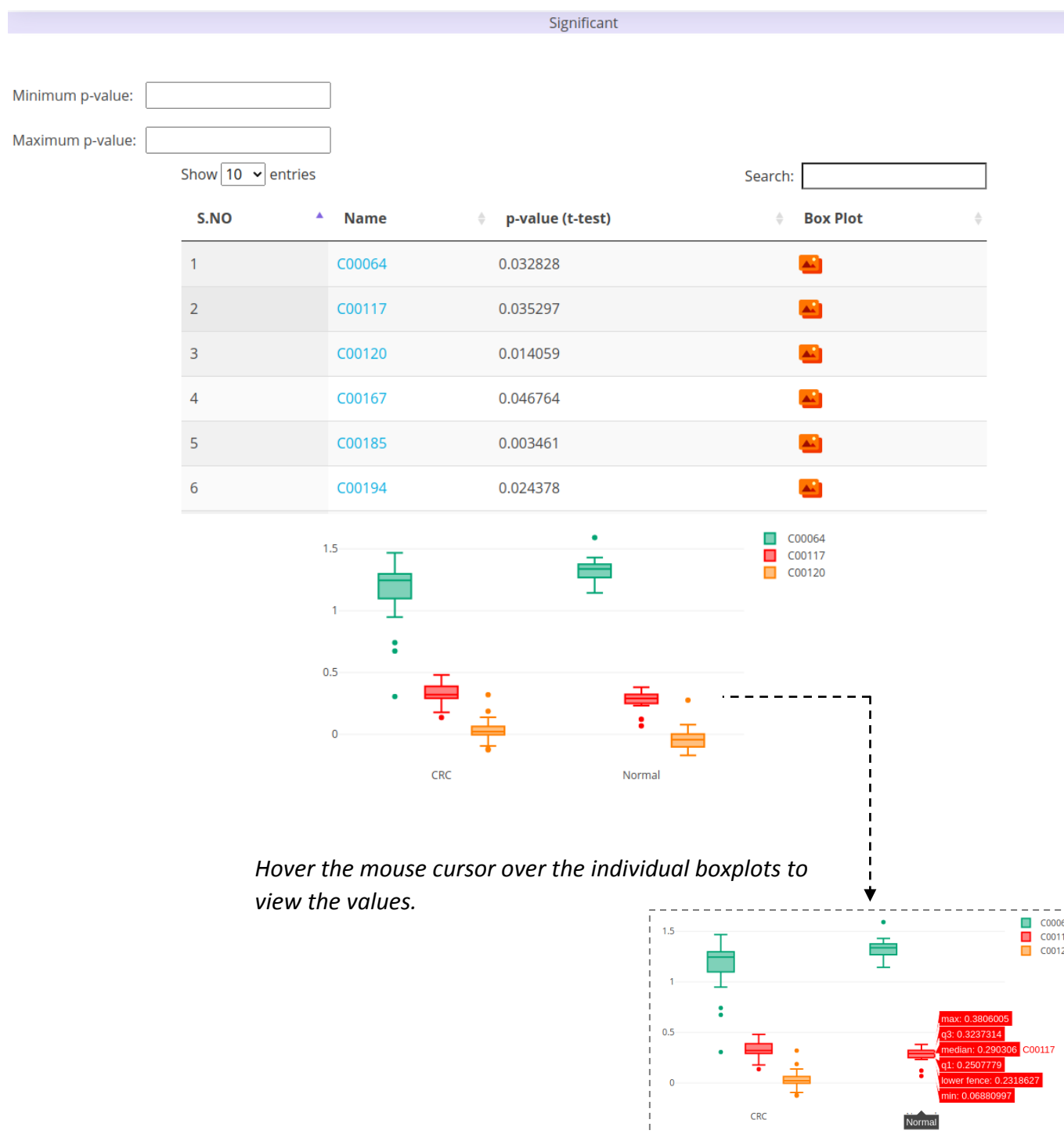
Click to get the boxplot of the compound in the same page (above the table).

Hover the mouse cursor over the individual boxplots to view the values.



(Fig. 5)

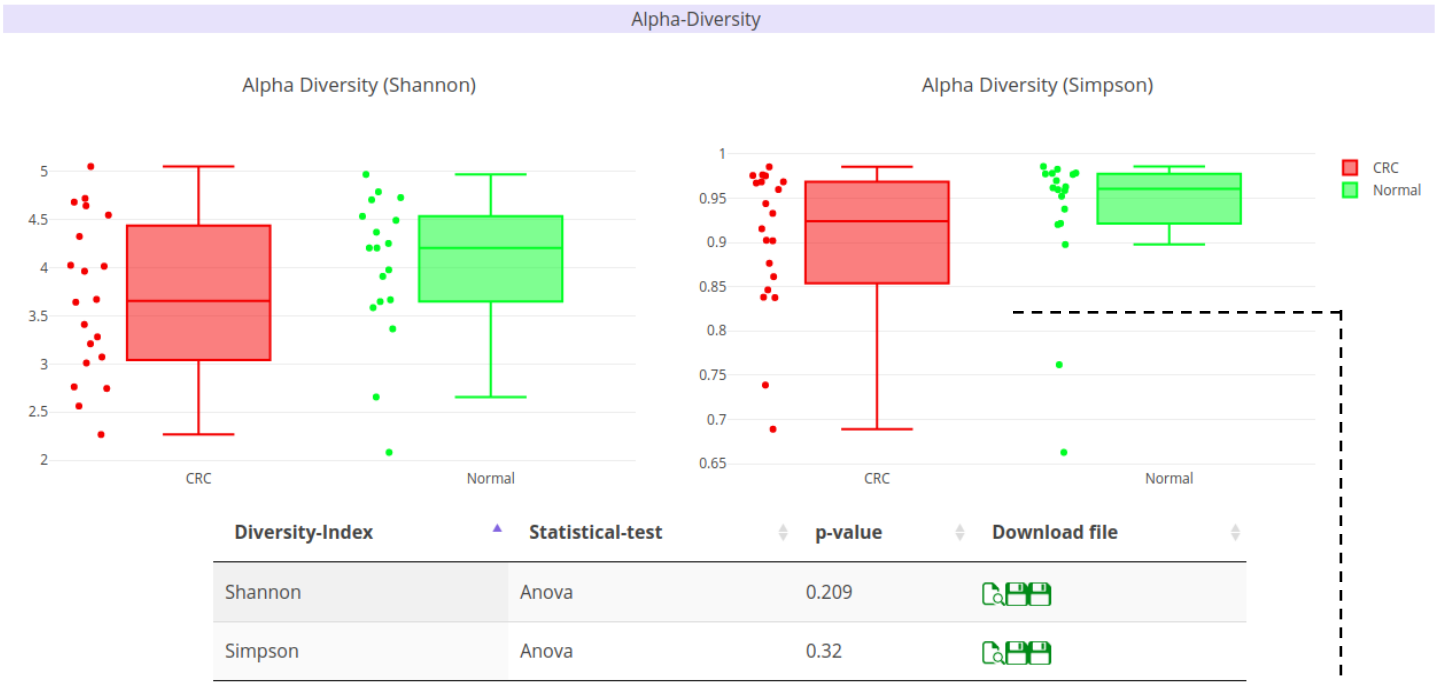
- 2 Click the tab to view all the compounds and more. The following page will open with the significant compounds. The boxplot shows the median values and differences between the two groups.



(Fig. 6)

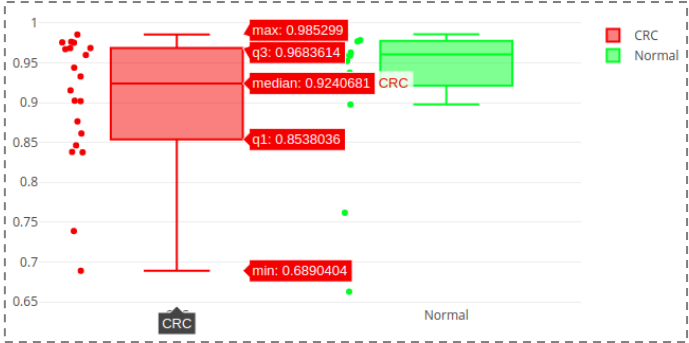
- 3 Click to download the data table (tsv format).
- 4 Click to open the data table in a new webpage (tsv format).

ALPHA DIVERSITY:



Showing 1 to 2 of 2 entries

Hover the mouse cursor over the individual boxplots to view the values.



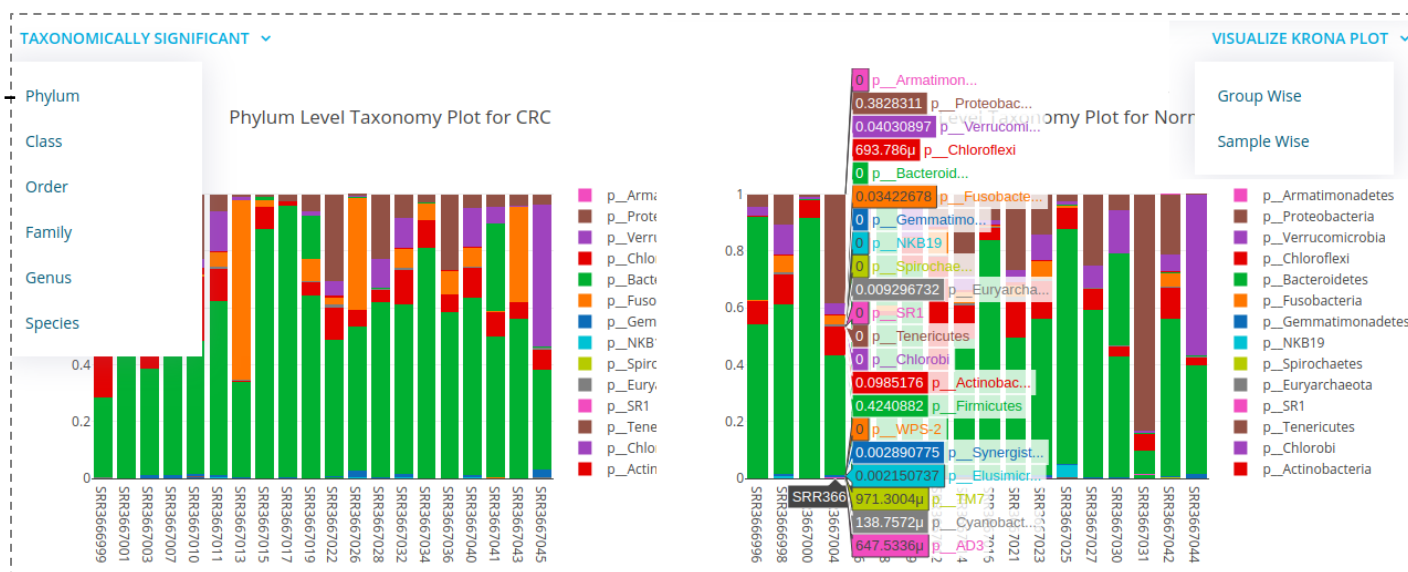
(Fig. 7)

TAXONOMIC DIVERSITY:



(Fig. 8)

5 Click on this tab to find a drop-down list (shown below), from which user can select the desired taxonomic level to check significant ones and is visualized in a new webpage, also depicted below.



(Fig. 9)

Click on one of the taxonomic level to go to the following page showing the taxa that are significant.

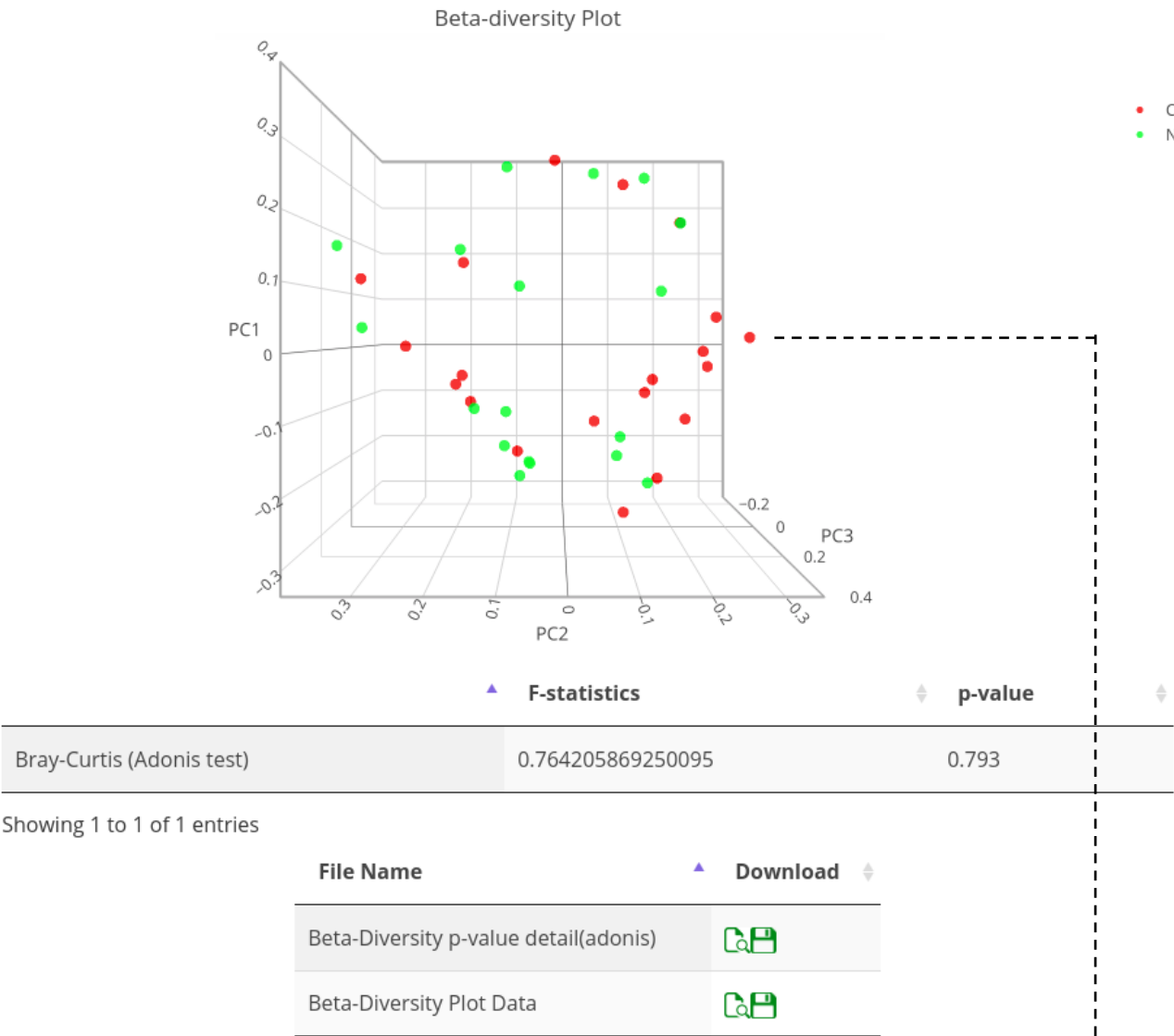
Hover the mouse cursor over the individual samples to view the different taxa and their relative abundance.



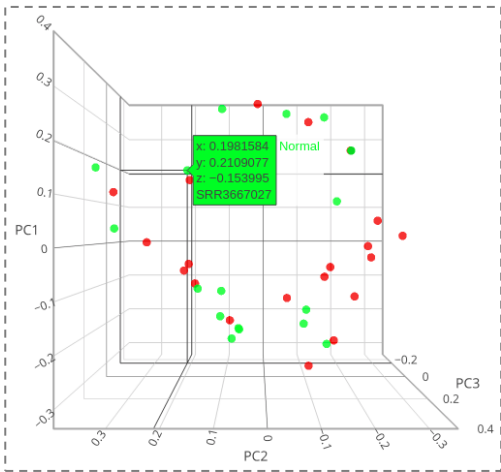
(Fig. 10)

BETA DIVERSITY:

Beta-Diversity

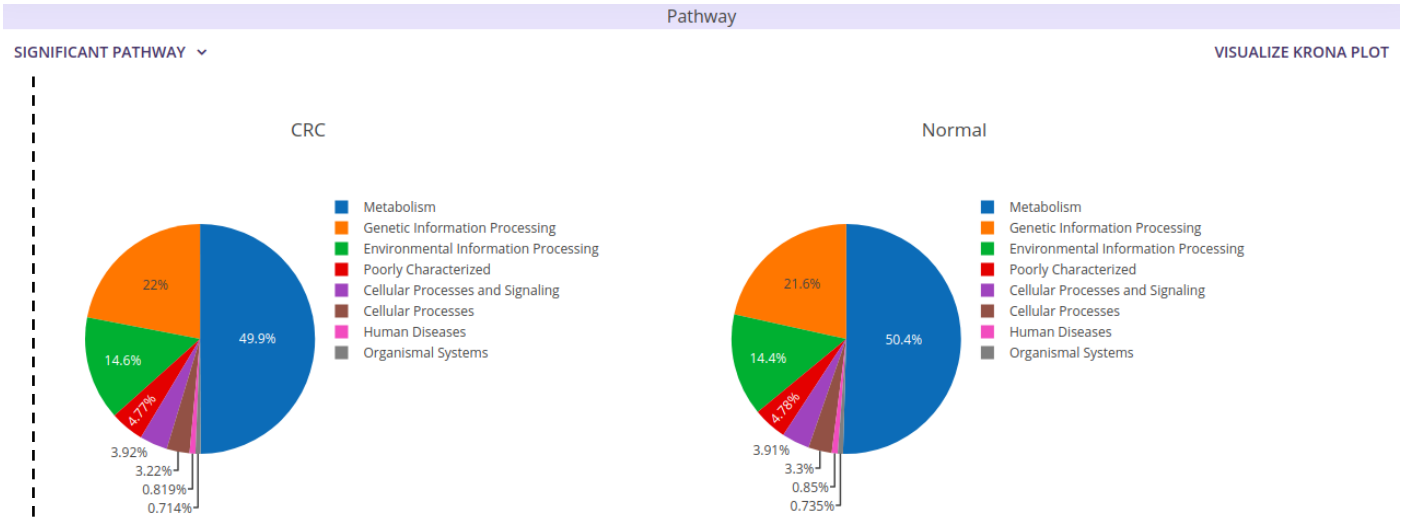


Hover the mouse cursor over the individual dots to view the values and sample number.

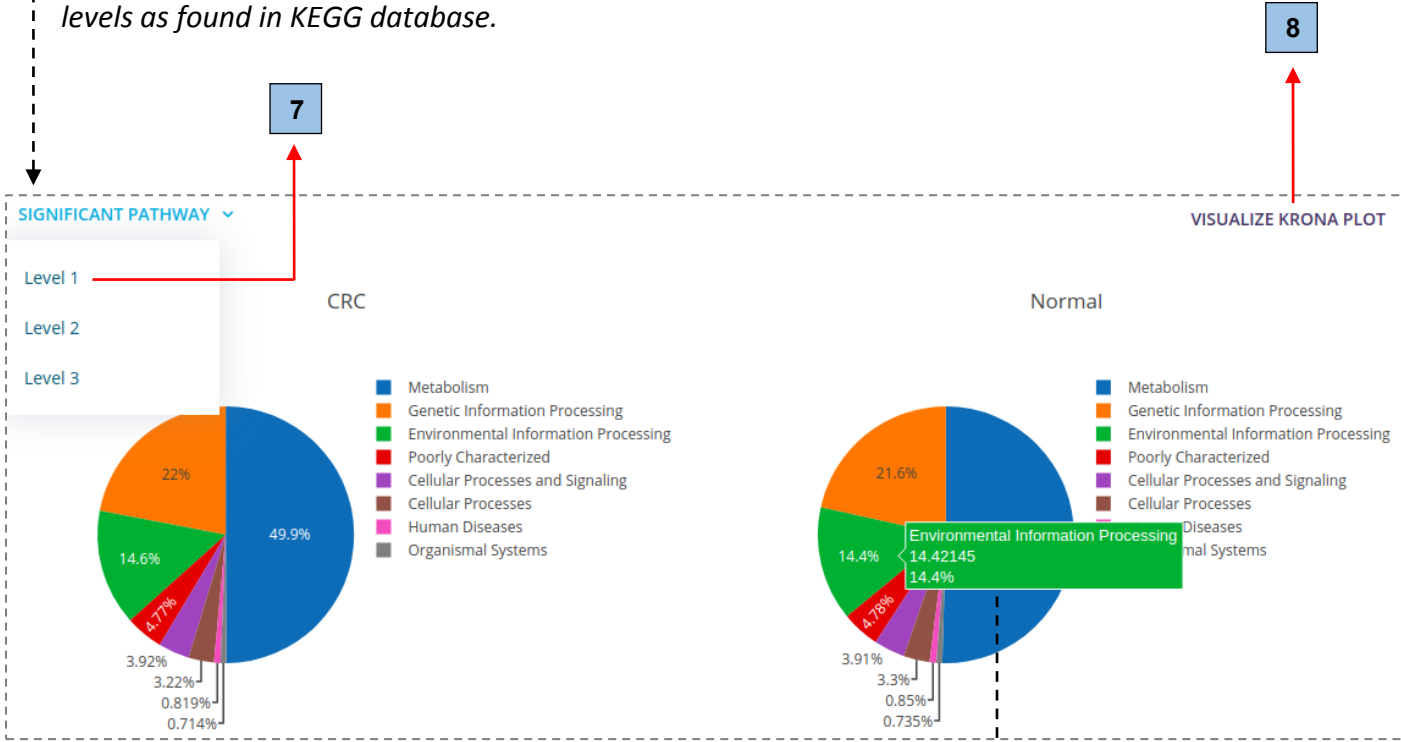


(Fig. 12)

PATHWAY ANALYSIS:



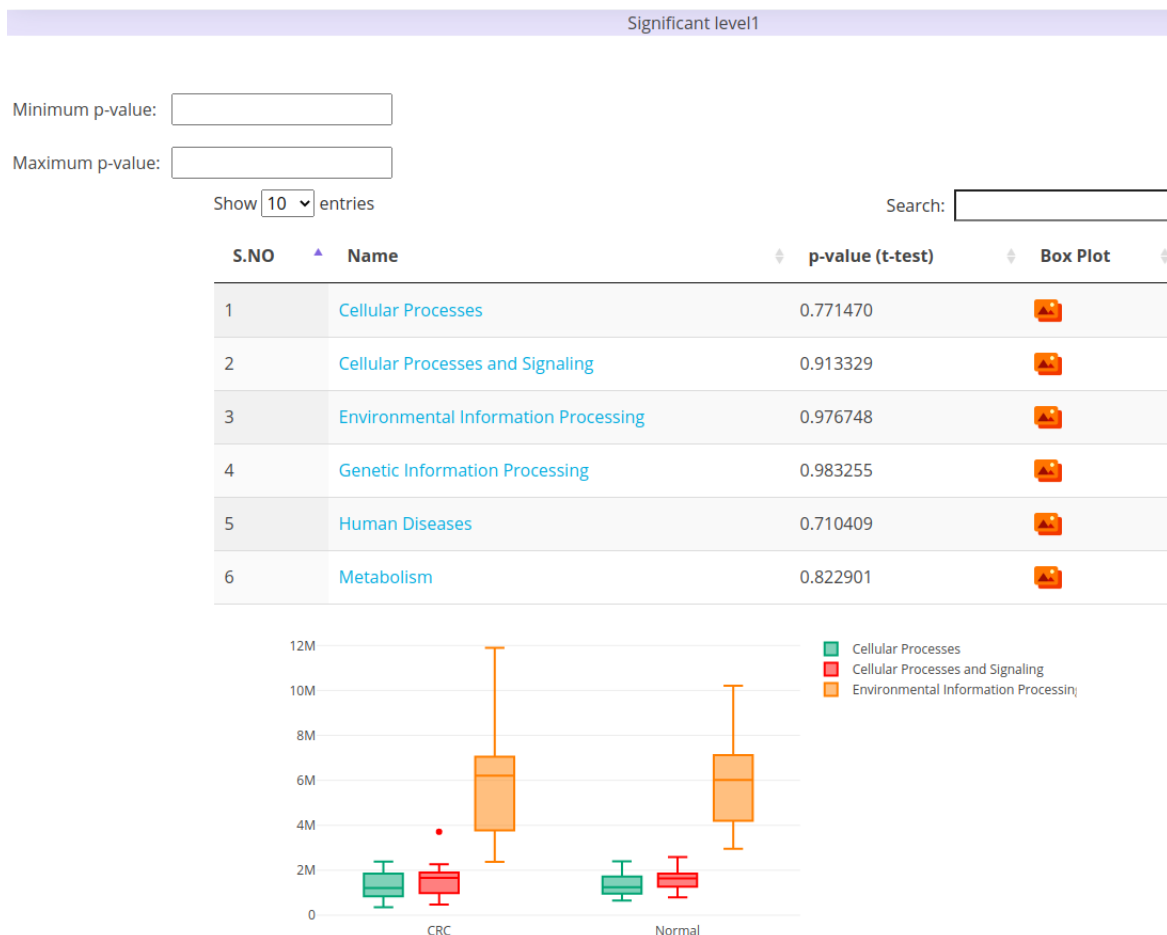
Click on the tab for a drop-down list showing the different pathway levels as found in KEGG database.



Hover the mouse cursor over the different section to view the pathway name and the percentage of its contribution to overall metabolism in that group.

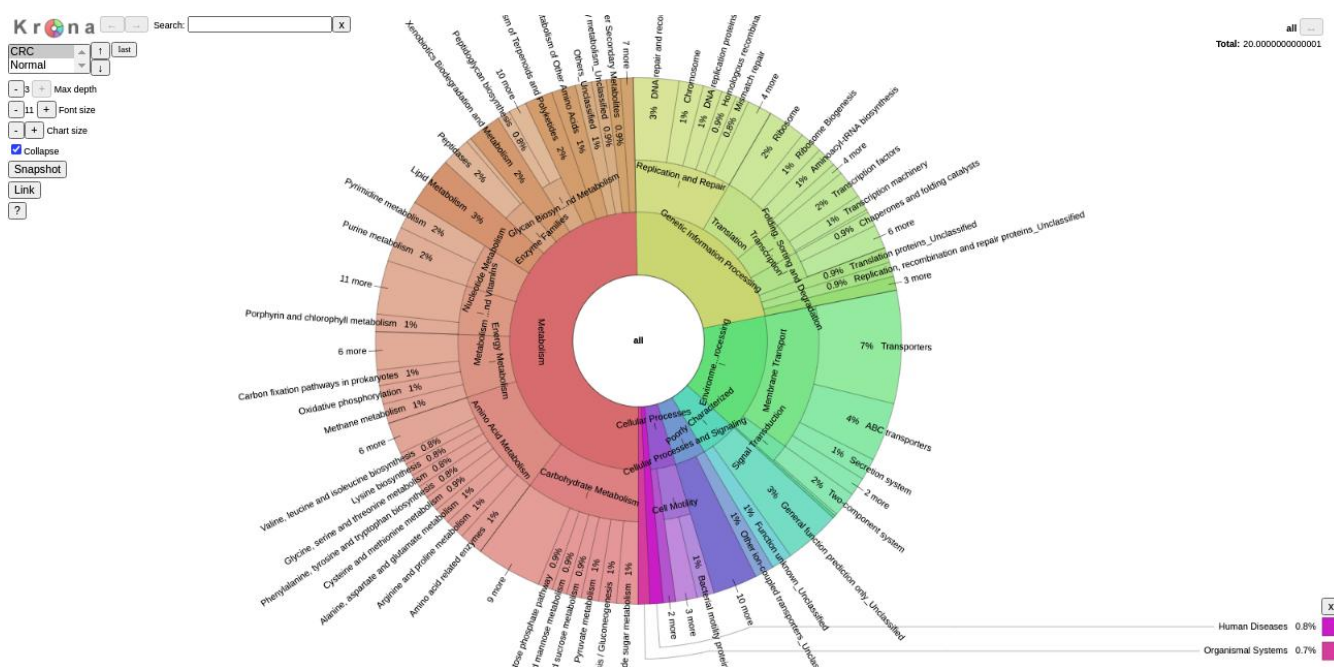
(Fig. 13)

7 Click on one of the levels to check the significant pathways in that level and it opens in a new page.



(Fig. 14)

8 Click on this tab to visualize the Krona plot for metabolic pathway abundances between two groups.



(Fig. 15)

REAL TIME V/S PREDICTED METABOLITES:

In case of MMIP MASS this additional tab is observed.

MMIP

JOB

METABOLITES

ALPHA-DIVERSITY

TAXONOMY

BETA-DIVERSITY

PATHWAY

R VS P

FEATURE

CONTACT US











RealTime Vs Predicted Metabolites

Minimum p-value:

Maximum p-value:

Show 10 entries

Search:

S.NO	KEGG Compound ID	p-value	Mantel Statistic R	Visualize
1	C00021	0.461000	-0.017709	
2	C00022	0.643000	-0.049009	
3	C00025	0.823000	-0.093974	
4	C00026	0.892000	-0.104520	
5	C00031	0.434000	0.004802	
6	C00036	0.339000	0.018716	
7	C00037	0.601000	-0.022063	
8	C00041	0.712000	-0.051428	
9	C00042	0.810000	-0.088605	
10	C00046	0.409000	0.009349	


Showing 1 to 10 of 20 entries

Previous

1

2

Next

File Name	Statistical-test	Download file
Mantel Correlation Detail	Mantel	

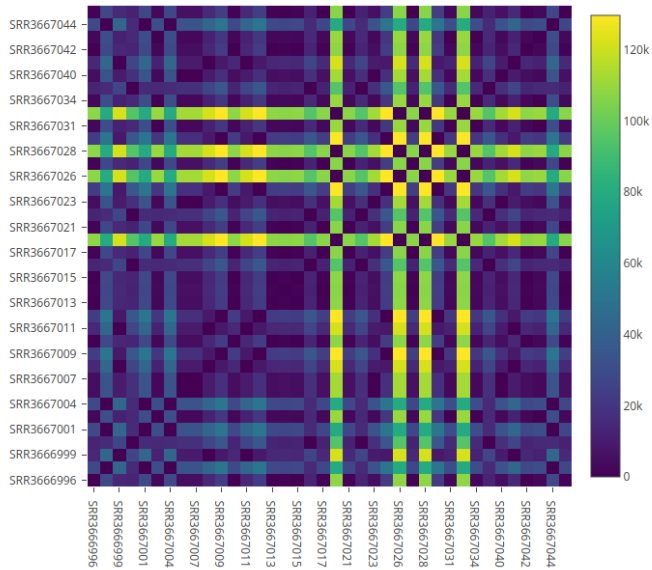
Showing 1 to 1 of 1 entries

Click to open the correlation results of this metabolite in a new page (as shown in fig 17).

(Fig. 16)

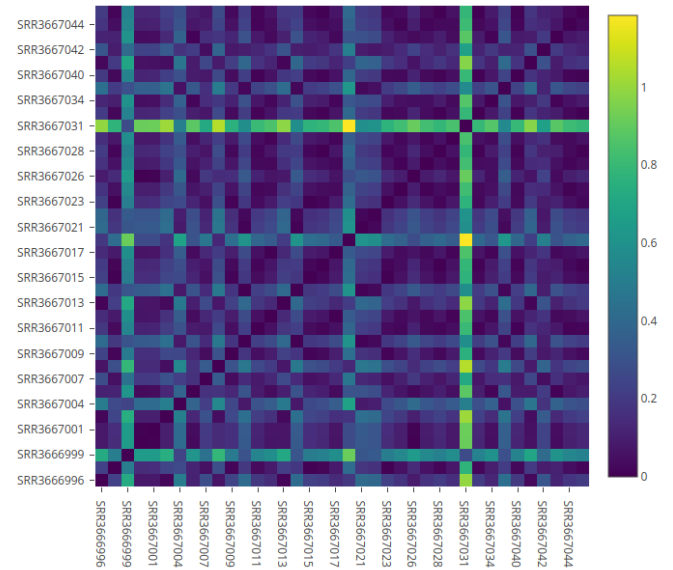
Correlation Result For C00021

Distance Matrix For Real Time Metabolite (C00021 Method=Euclidean)



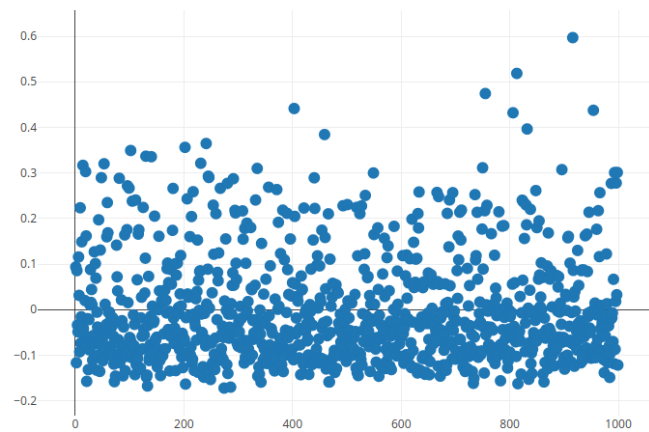
[Download Distance Matrix Data for Above Plot](#)

Distance Matrix For Predicted Time Metabolite (C00021 Method=Euclidean)



[Download Distance Matrix Data for Above Plot](#)

Mantel Test (Pvalue= 0.461, R-Statistics=-0.0177093134075238)



[Download All Permuataion Data For Above Plot](#)

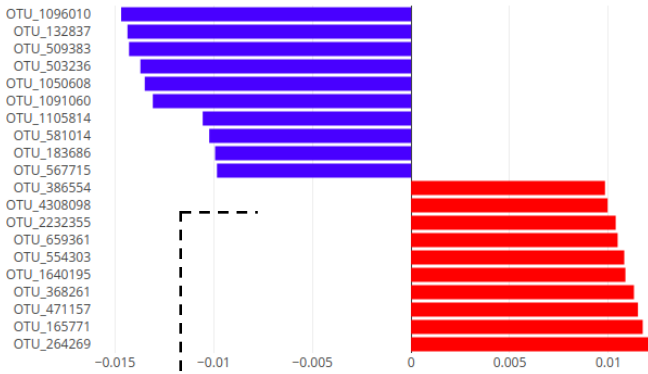
(Fig. 17)

FEATURE PREDICTION:



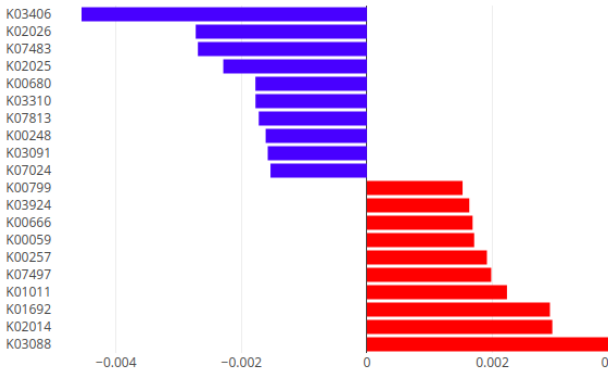
Feature Identified

Community Structure



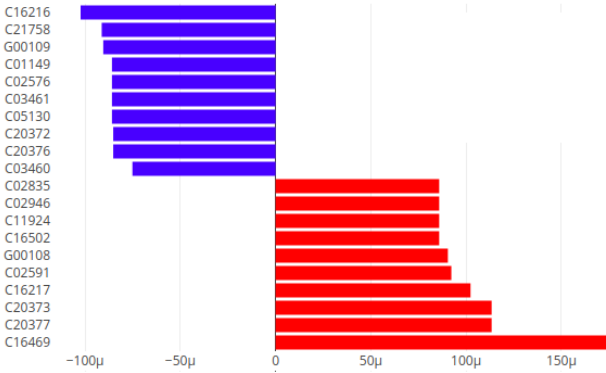
[Download All Feature For Community Structure](#)

KEGG



[Download All Feature For KEGG](#)

CMP



[Download All Feature For CMP](#)

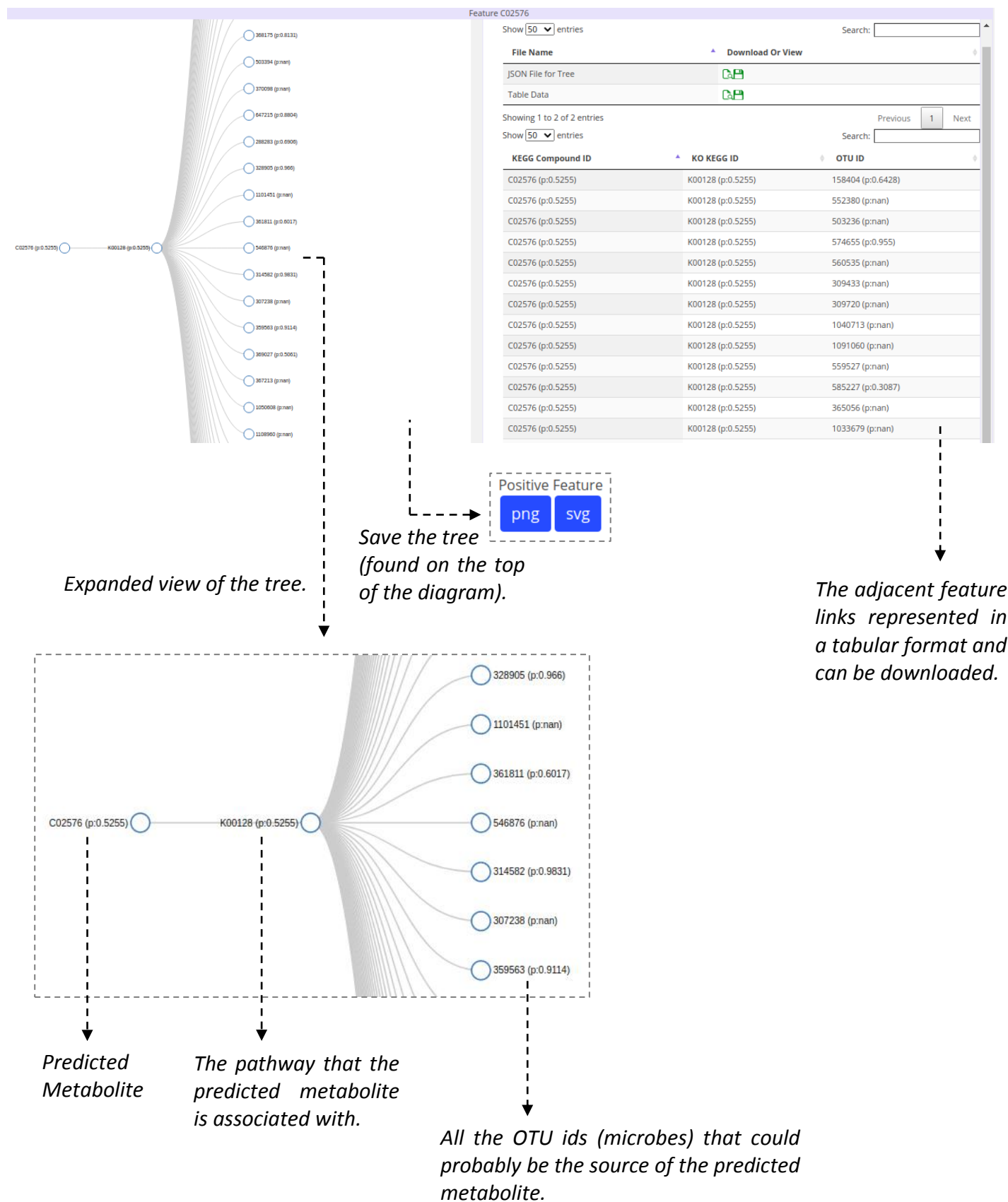
The top 10 features each of positive (in red) and of negative (in blue) are shown here. Also hover mouse over diagram to view values.

The feature table can be downloaded (tsv format).

Feature Category					
Positive Feature			Negative Feature		
Show <input type="text" value="10"/> entries		Search	Show <input type="text" value="10"/> entries		Search
KEGG Compound ID	p-value (Anova)	Visualize cor	KEGG Compound ID	p-value (Anova)	Visualize cor
C02591	0.56764712027688	LINK	C01149	0.5254858214149752	LINK
C02835	0.5254858214149772	LINK	C02576	0.5254858214149752	LINK
C02946	0.5254858214149772	LINK	C03460	0.6294221232575476	LINK
C11924	0.5254858214149772	LINK	C03461	0.5254858214149752	LINK
C16217	0.5107272046458358	LINK	C05130	0.5254858214149752	LINK
C16469	0.6895104179008892	LINK	C16216	0.5107272046458358	LINK

(Fig. 19)

- 9 Click on the link to visualize the following page which shows the predicted microbial source of metabolites (predicted as feature by our algorithm), in a tree as well as tabular form. [all p values provided in adjacent brackets]



(Fig. 20)