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.*

HOME PAGE

Click to use the respective services.

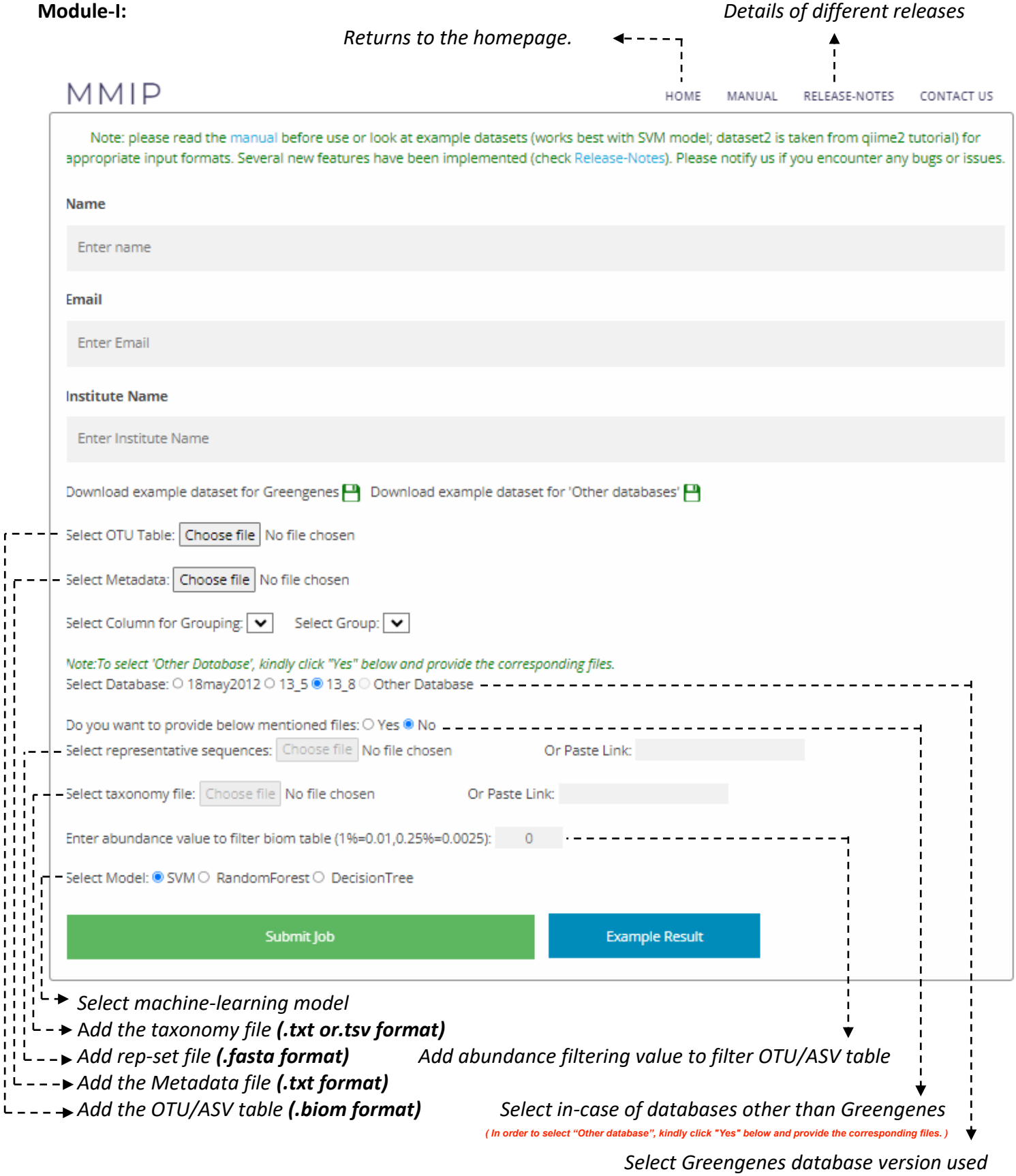
Scroll

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

(Fig. 1)

UPLOAD PAGES

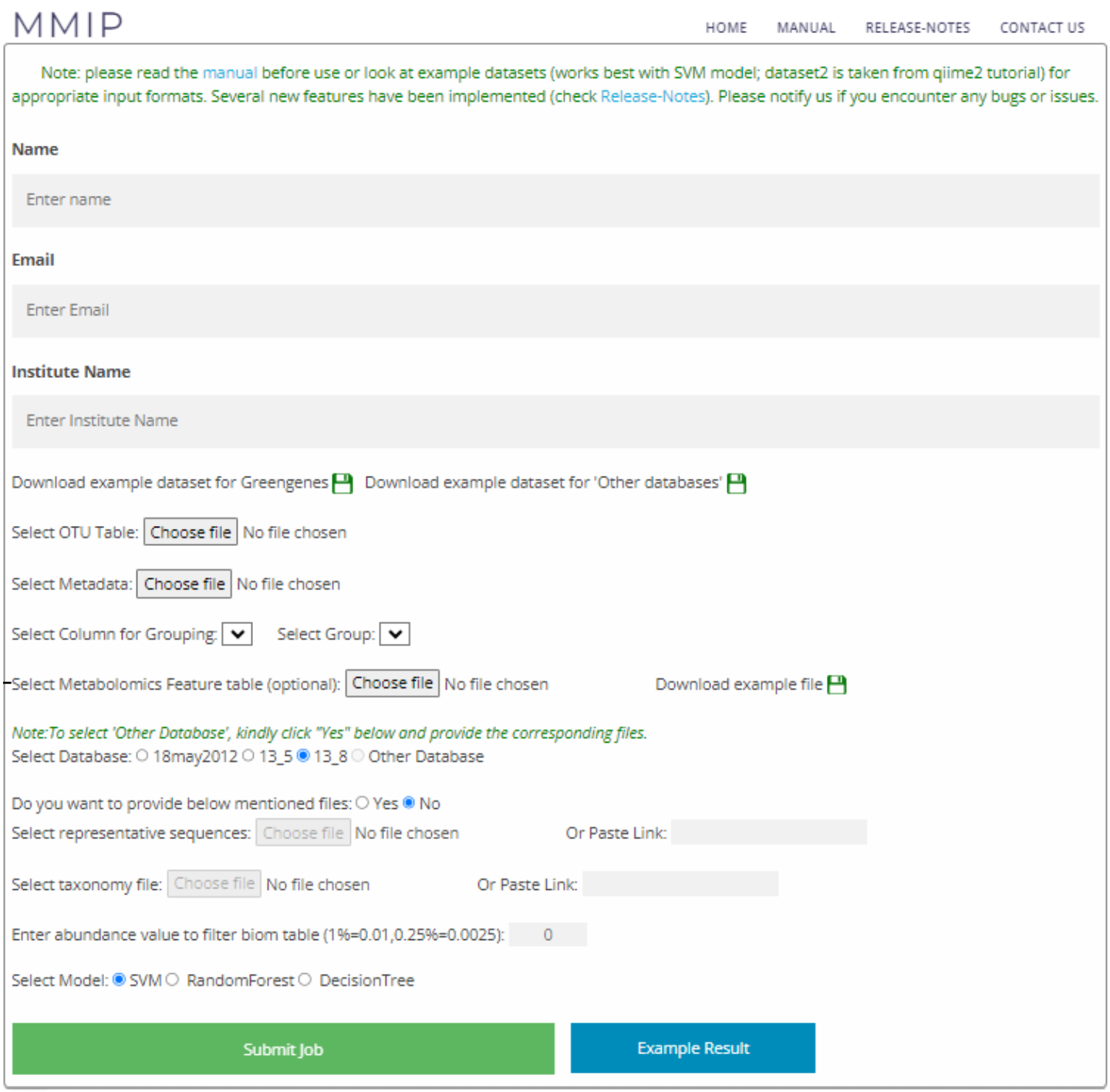
Module-I:



Note: Please maintain the file formats with extensions.

(*Fig. 2*)

Module-II:



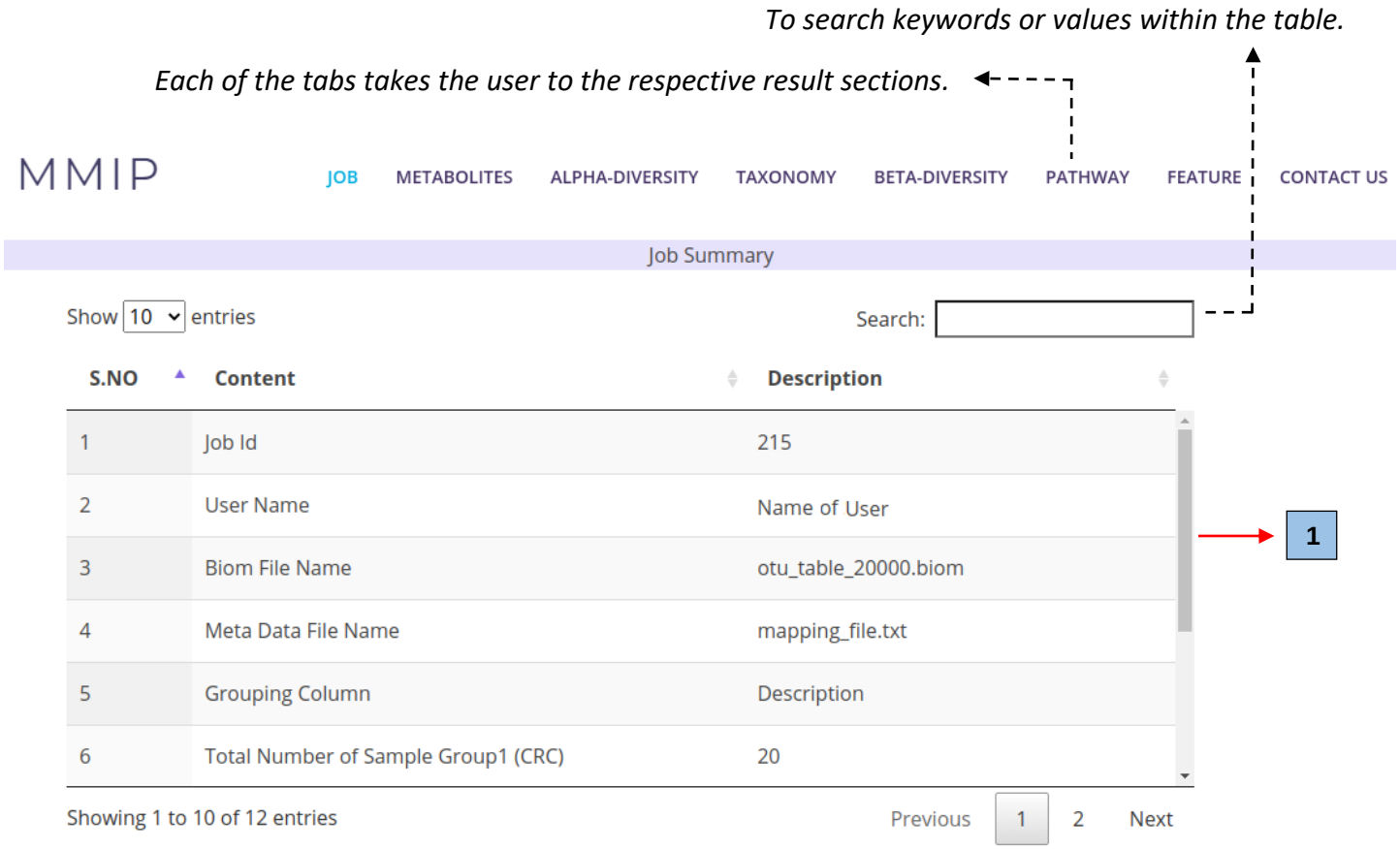
→ *Add metabolite table from metabolomic processing* ***(.txt format)***

Note: Please maintain the file format with extension.

(*Fig. 3)*

RESULT PAGES

USER AND JOB RELATED INFORMATION:



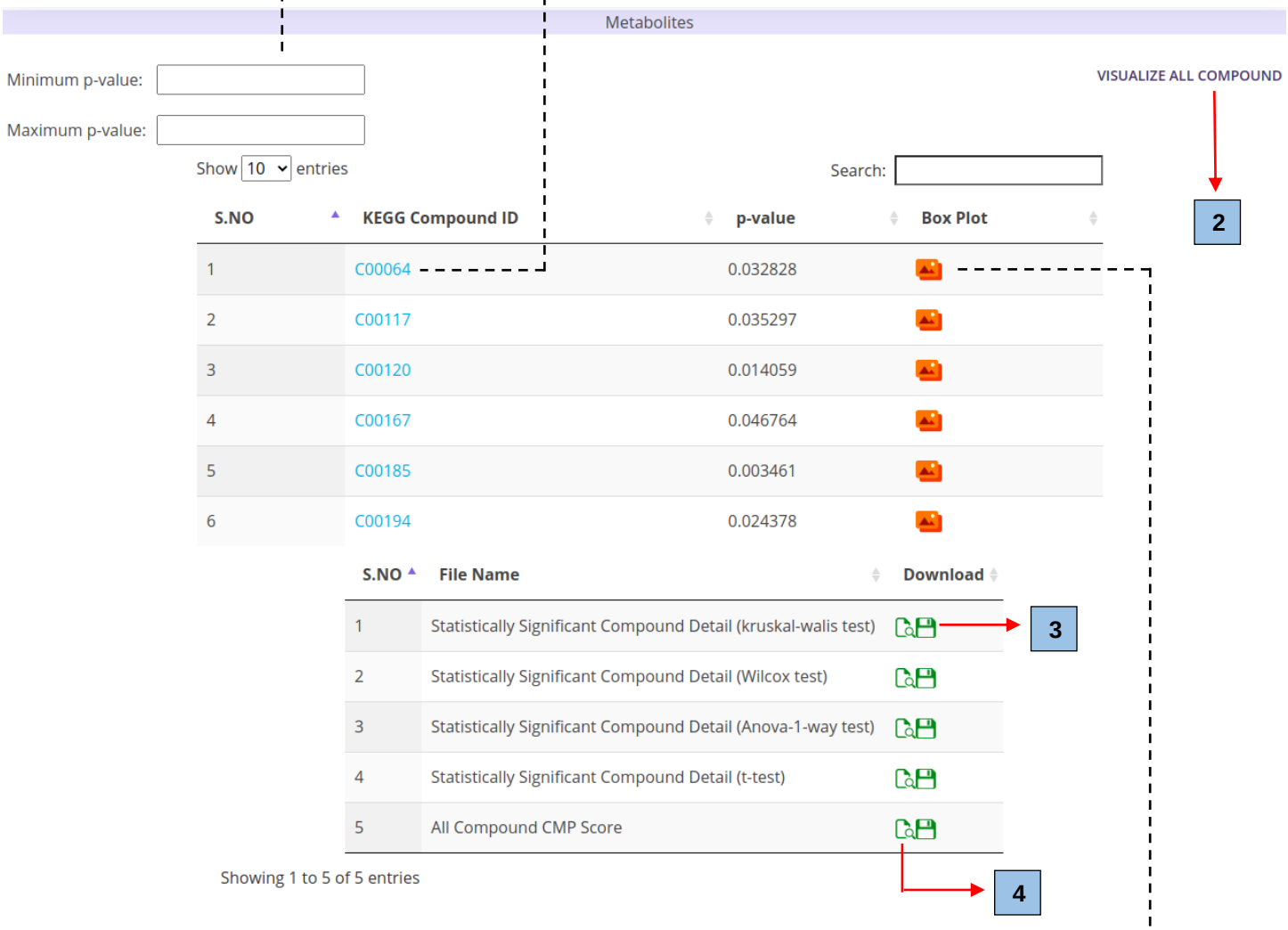
(*Fig. 4*)

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.*

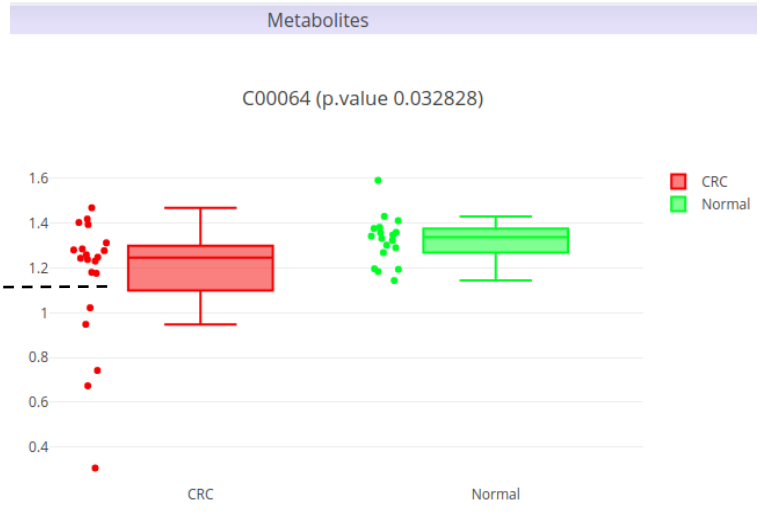
METABOLITES:

Add range of desired p values.

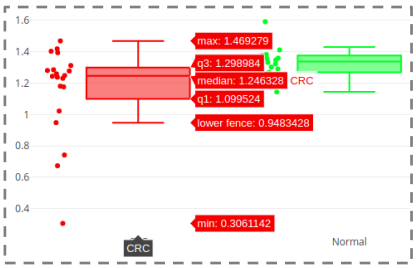
Click on the compound Ids to get to the KEGG page of the respective compound.



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

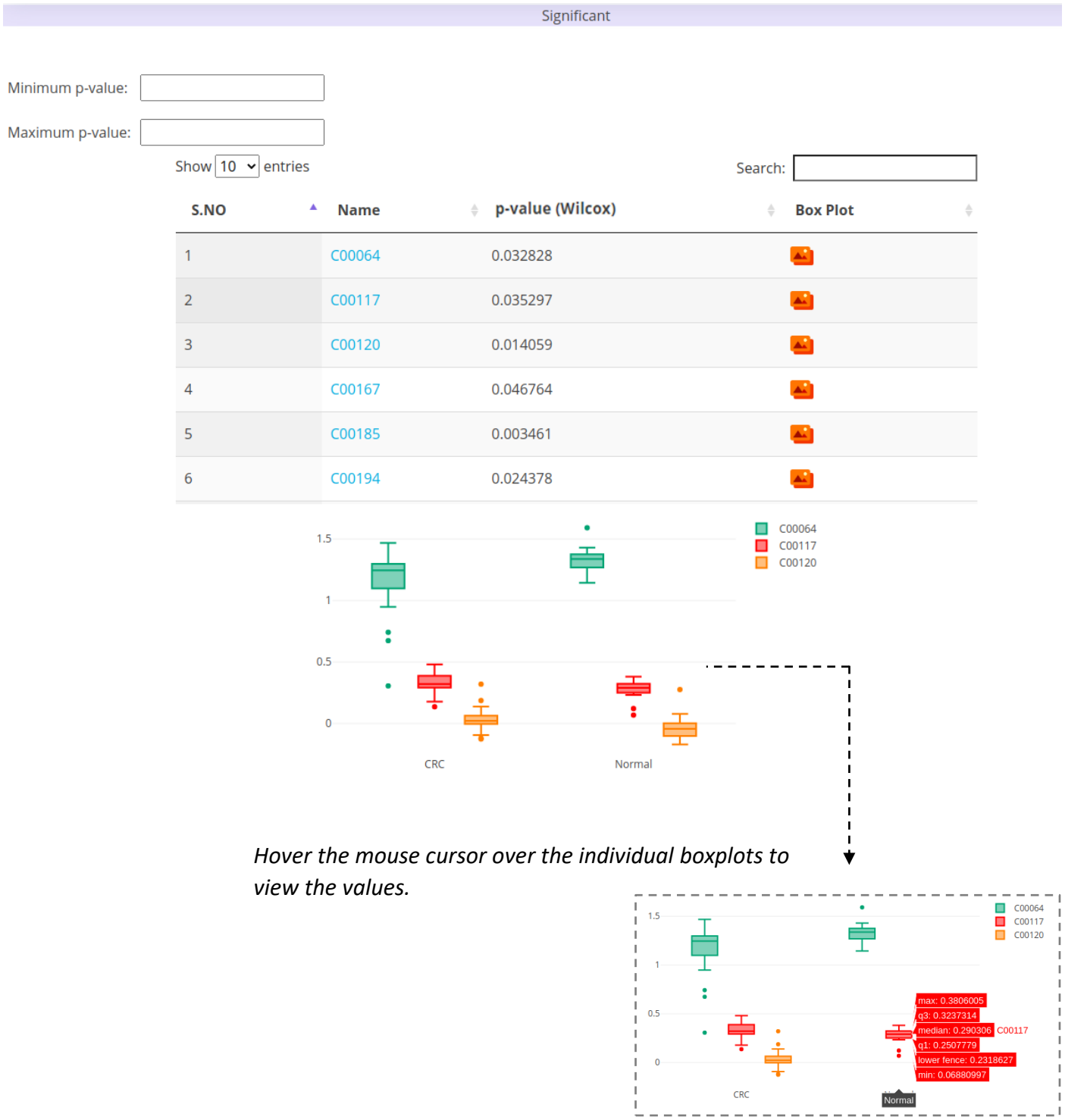


Hover the mouse cursor over the individual boxplots to view the values.



(*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.*

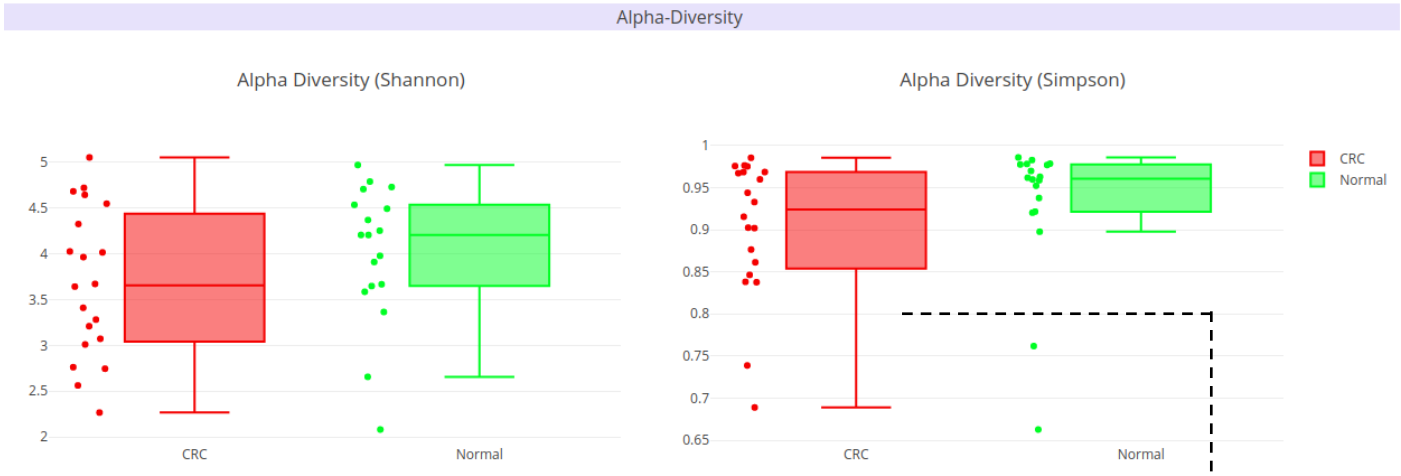


(*Fig. 6*)

3 *Click to download the data table (tsv format).*

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

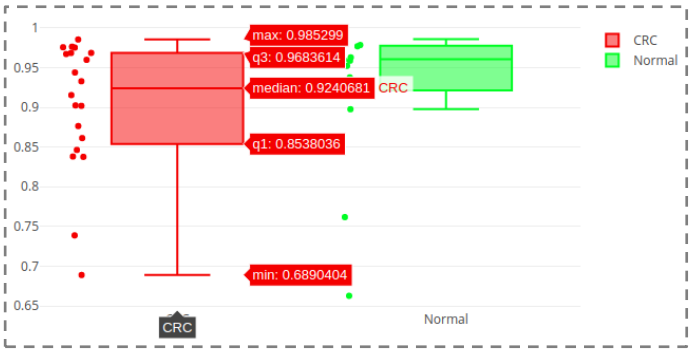
ALPHA DIVERSITY:



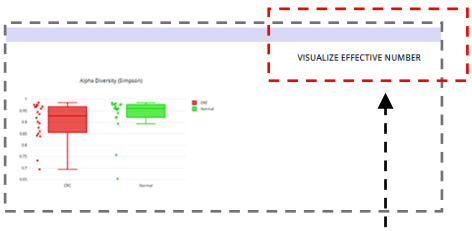
Diversity-Index	Anova	Tukey(p-value (Anova))	Mann-Whitney/Wilcoxon rank sum test	Kruskal-Wallis	Download file
Shannon	0.223	0.223	0.193	0.188	
Simpson	0.352	0.352	0.132	0.128	

Showing 1 to 2 of 2 entries

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

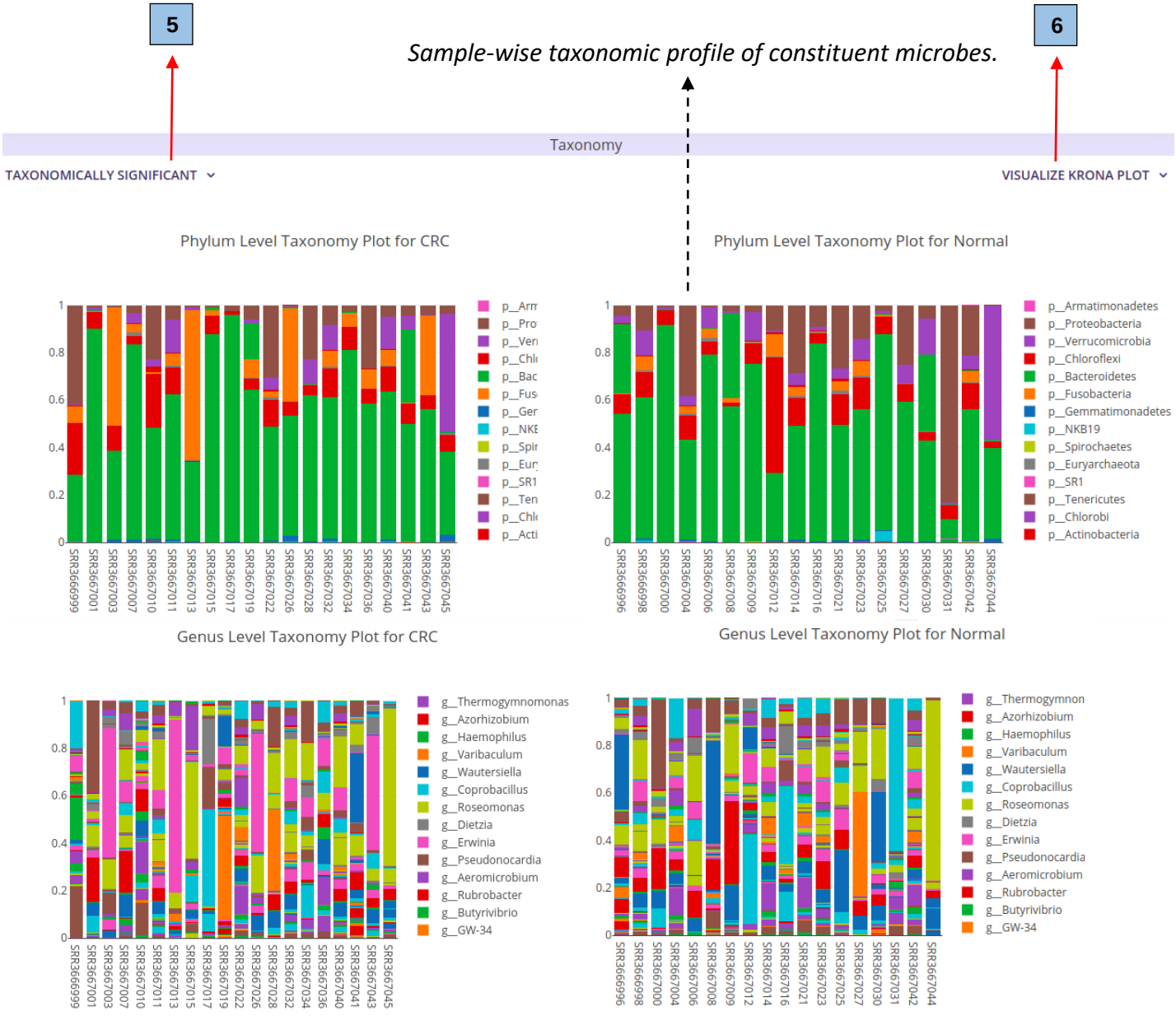


Note: **EFFECTIVE NUMBER** added.
(Click to go to a new page and view.)



(*Fig. 7)*

TAXONOMIC DIVERSITY:

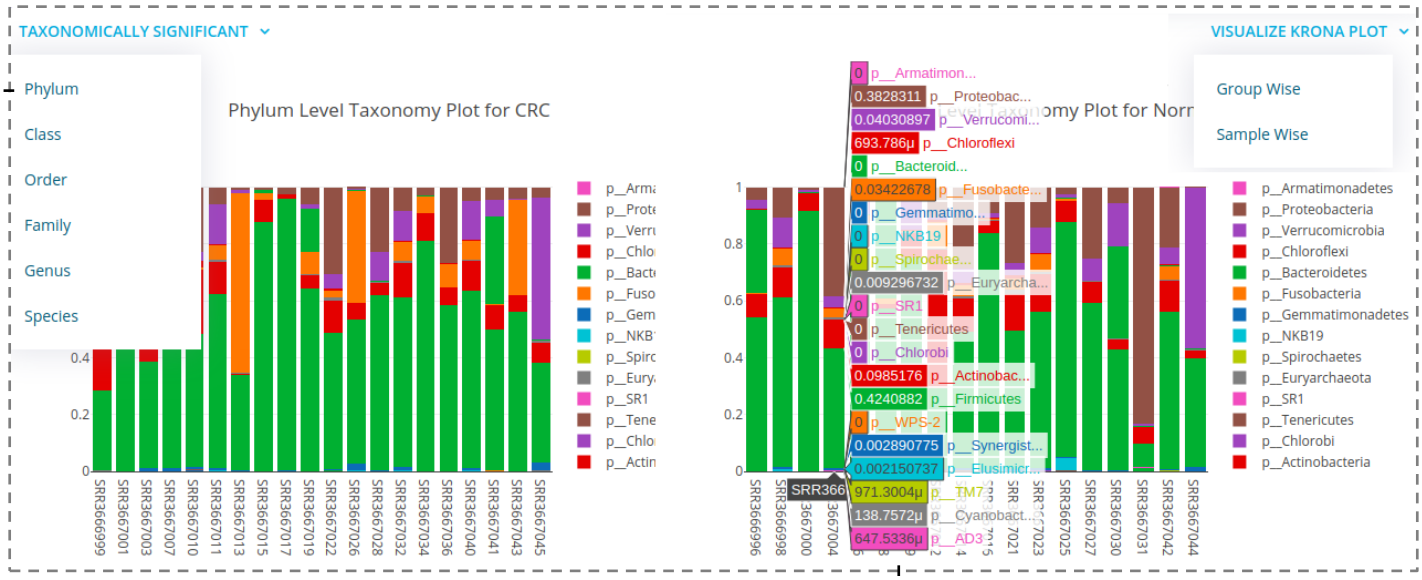


S.No	File Description	Download File
1	Phylum Level Taxonomy Data Group1	
2	Phylum Level Taxonomy Data Group2	
3	Genus Level Taxonomy Data Group1	
4	Genus Level Taxonomy Data Group2	
5	Statistically Significant OTUs Group1	
6	Statistically Significant OTUs Group2	

Showing 1 to 6 of 6 entries

(*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)

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

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

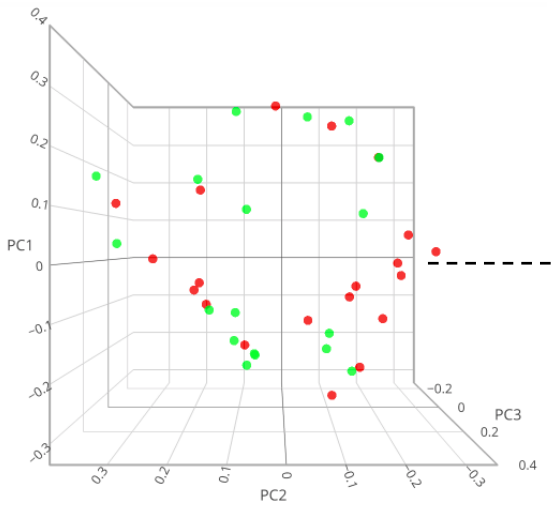
(*Fig. 10*)

6 *Click on this tab to open the Krona plots representing the taxonomic abundance profile, both group-wise and sample-wise (as shown in fig. 9). This is an interactive plot, and is another way of depicting the taxonomic profiles.*

Click on the different segments to see its constituent taxa and at different levels. The ring can be collapsed back into its higher levels of taxa.

(*Fig. 11)*

BETA DIVERSITY:

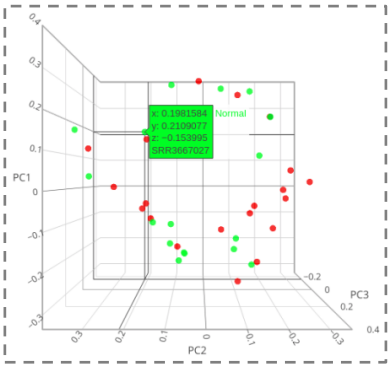


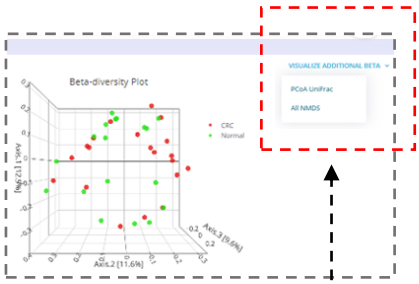
..	F.Model	p-value
Bray-Curtis (Adonis test)	0.760695687284777	0.797

Showing 1 to 1 of 1 entries

File Name	Download
Beta-Diversity p-value detail (adonis)	
Beta-Diversity Plot Data & Distance Matix	

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

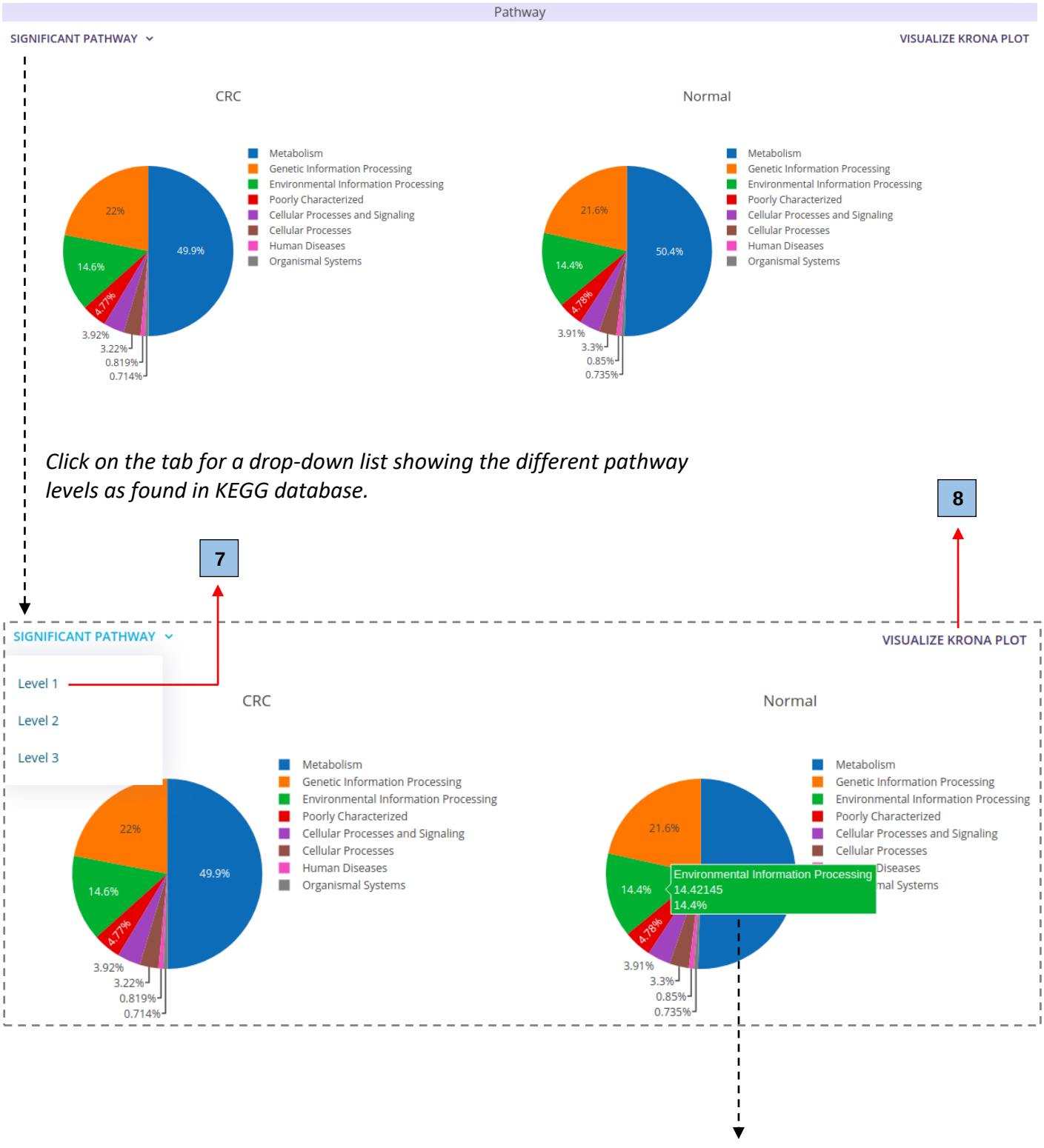




Note: **UNIFRAC (WEIGHTED/UNWEIGHTED)** added.
(Click to go to a new page and view.)

(Fig. 12)

PATHWAY ANALYSIS:

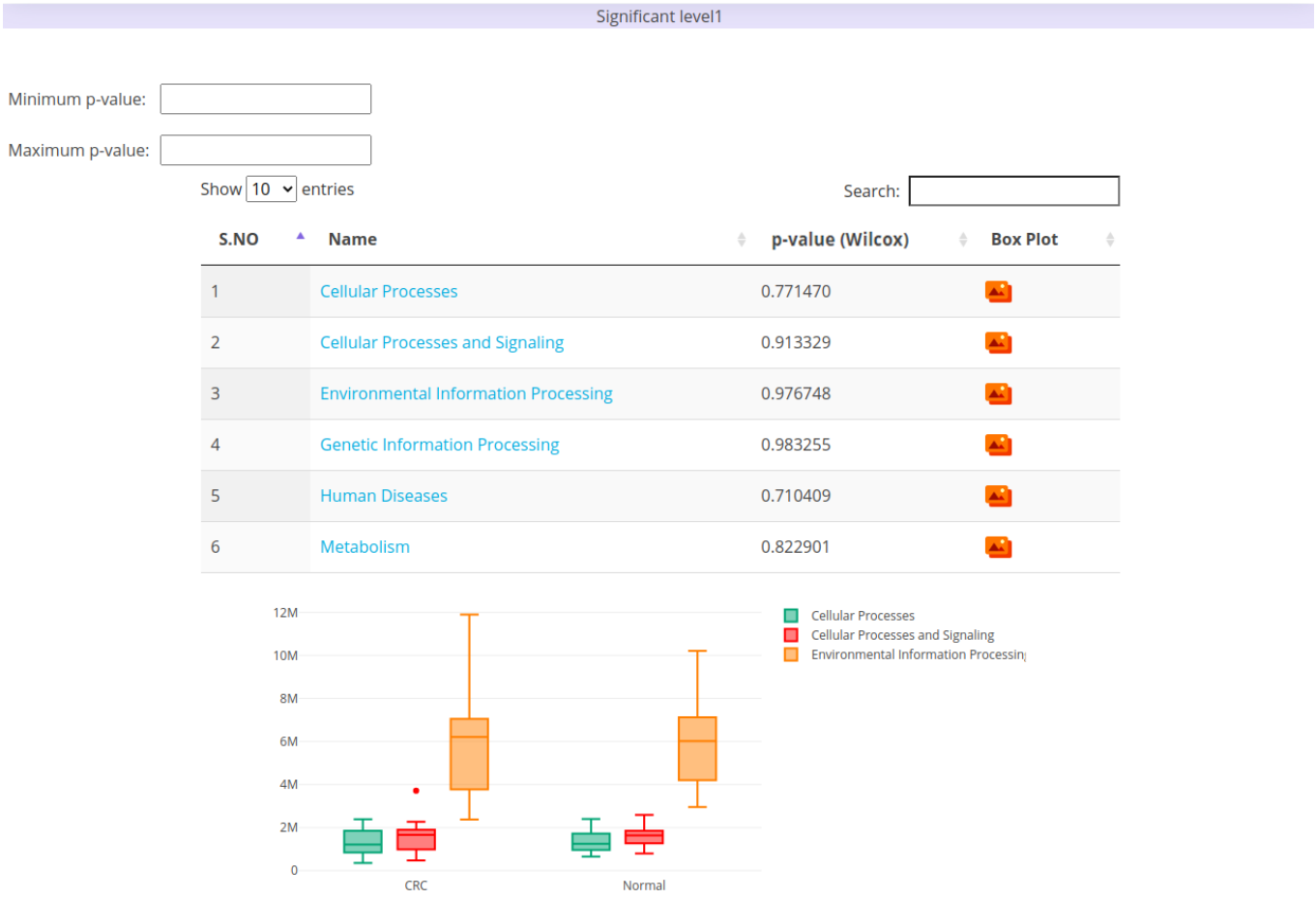


Click on the tab for a drop-down list showing the different pathway levels as found in KEGG database.

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.

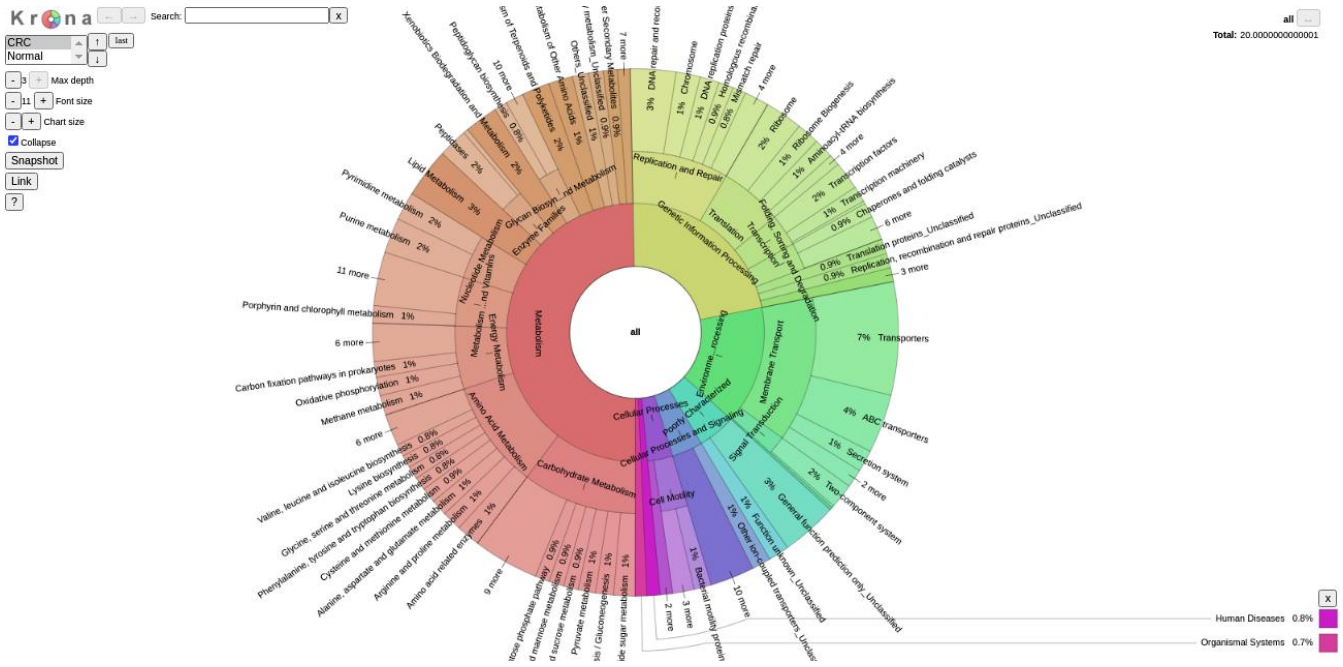
(Fig. 13)

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



(Fig. 14)

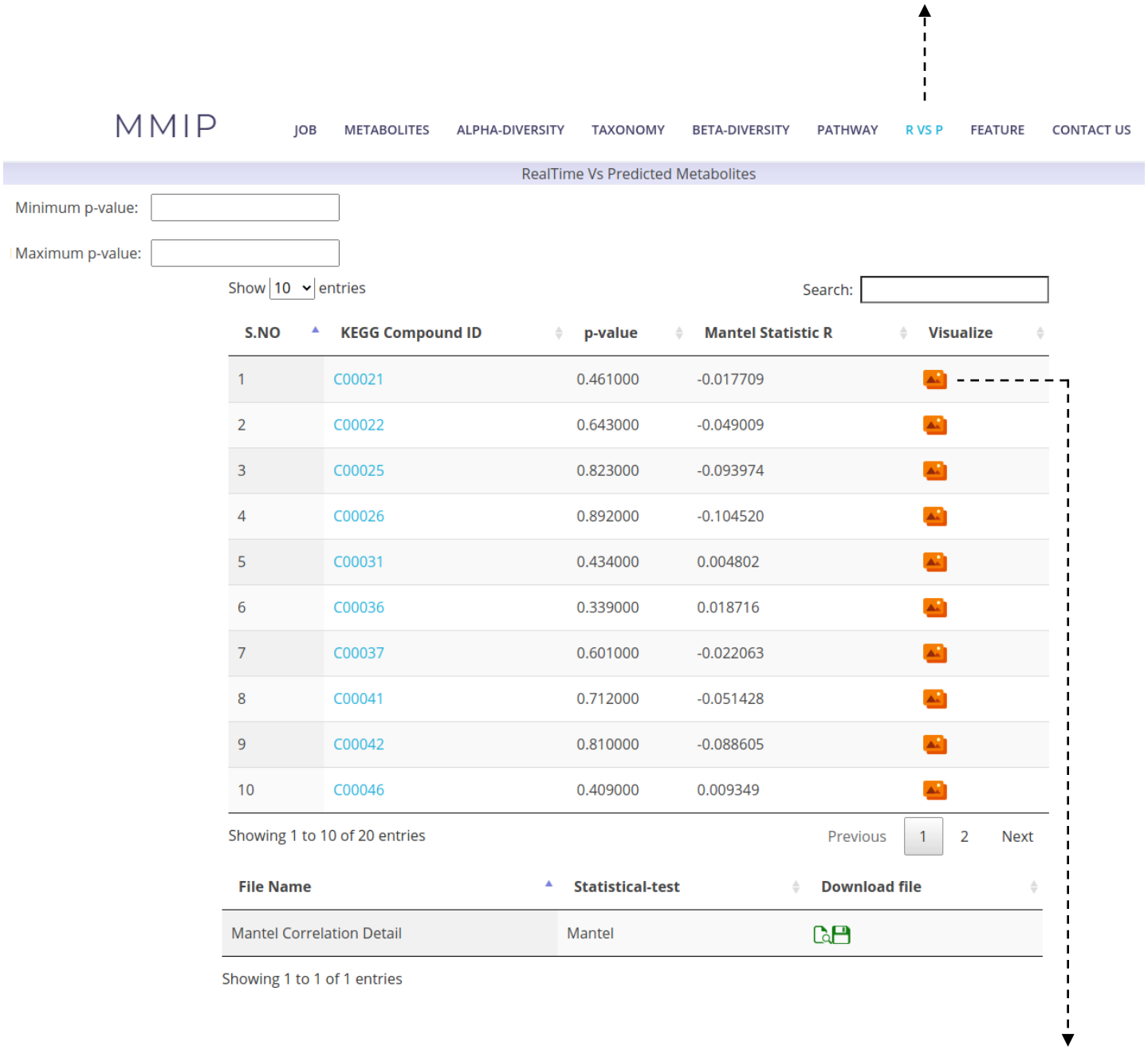
8 *Click on this tab to visualize the Krona plot for metabolic pathway abundances between two groups.*



(Fig. 15)

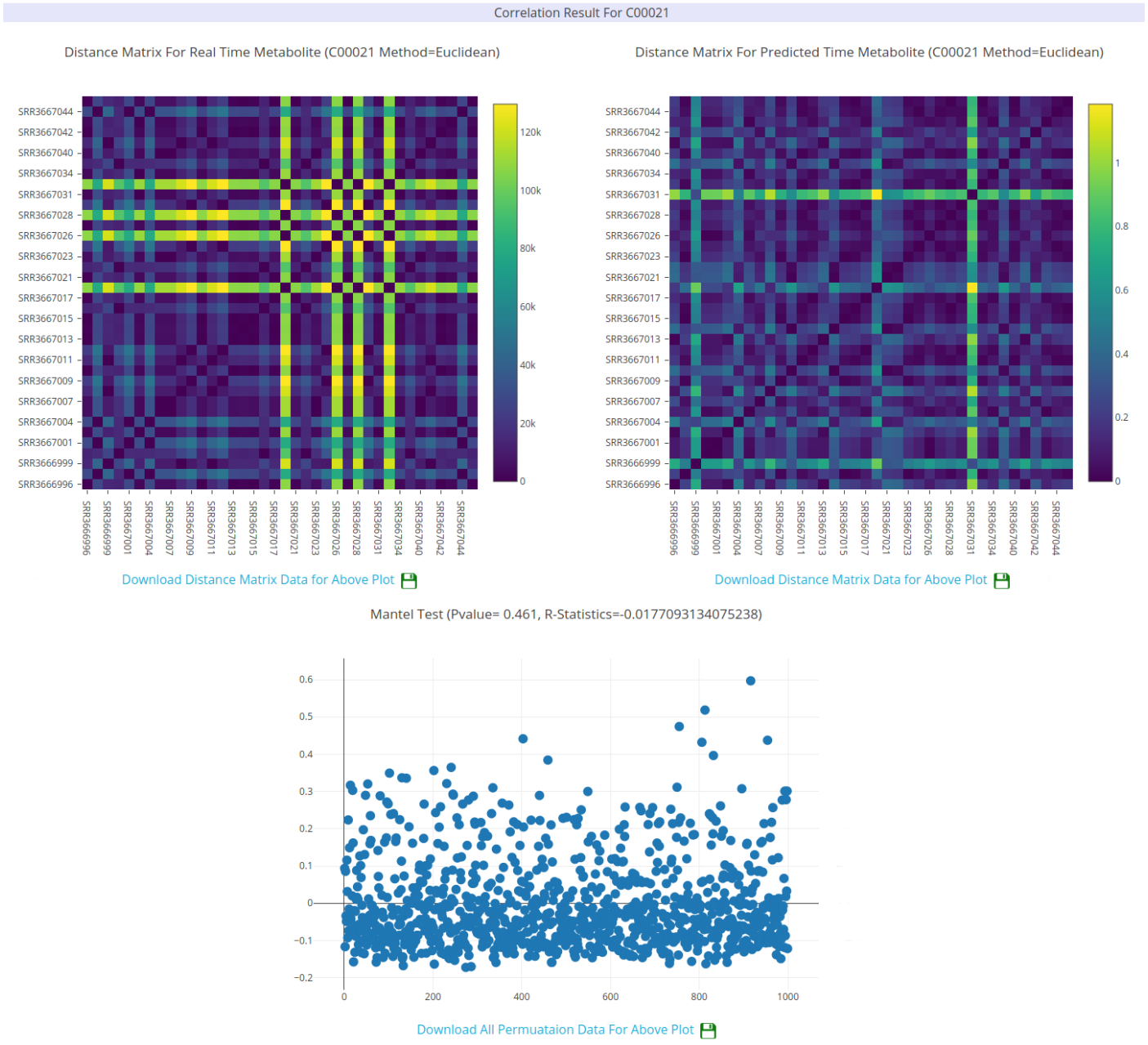
REAL TIME V/S PREDICTED METABOLITES:

In case of MMIP Module-II this additional tab is observed.



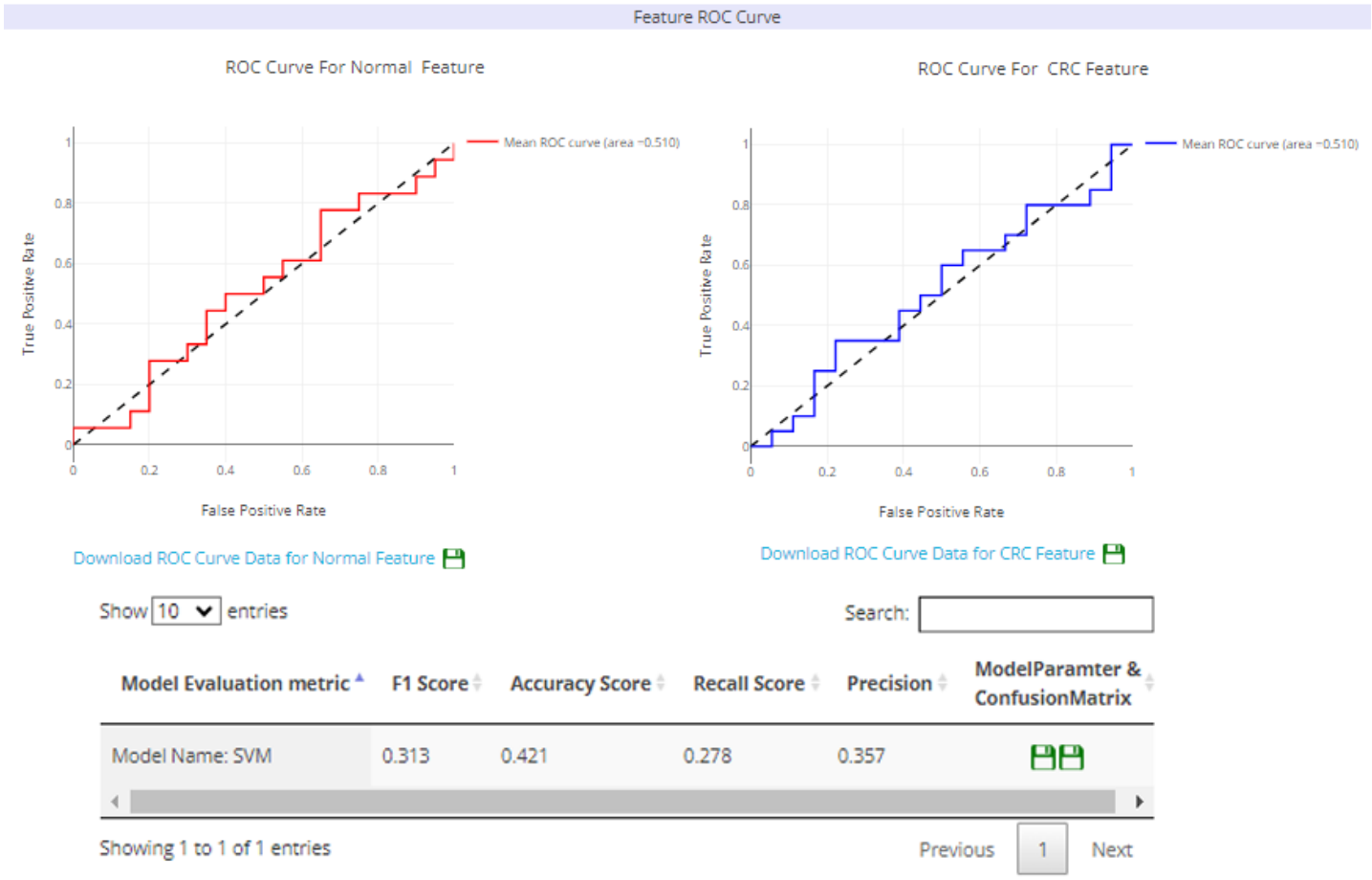
Click to open the correlation results of this metabolite in a new page (as shown in fig 17).

(Fig. 16)


Correlation Result For C00021
Distance Matrix For Real Time Metabolite (C00021 Method=Euclidean)
Distance Matrix For Predicted Time Metabolite (C00021 Method=Euclidean)
Download Distance Matrix Data for Above Plot
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)

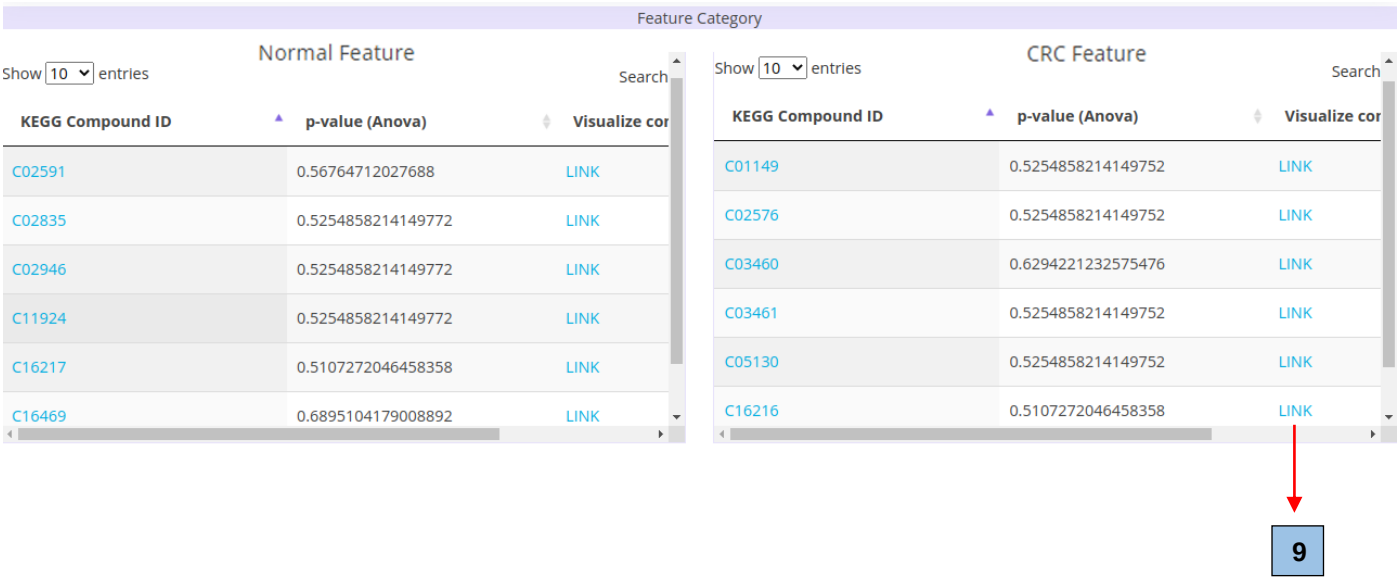
FEATURE PREDICTION:



ROC curve and evaluation metrics of the selected machine learning model shown.

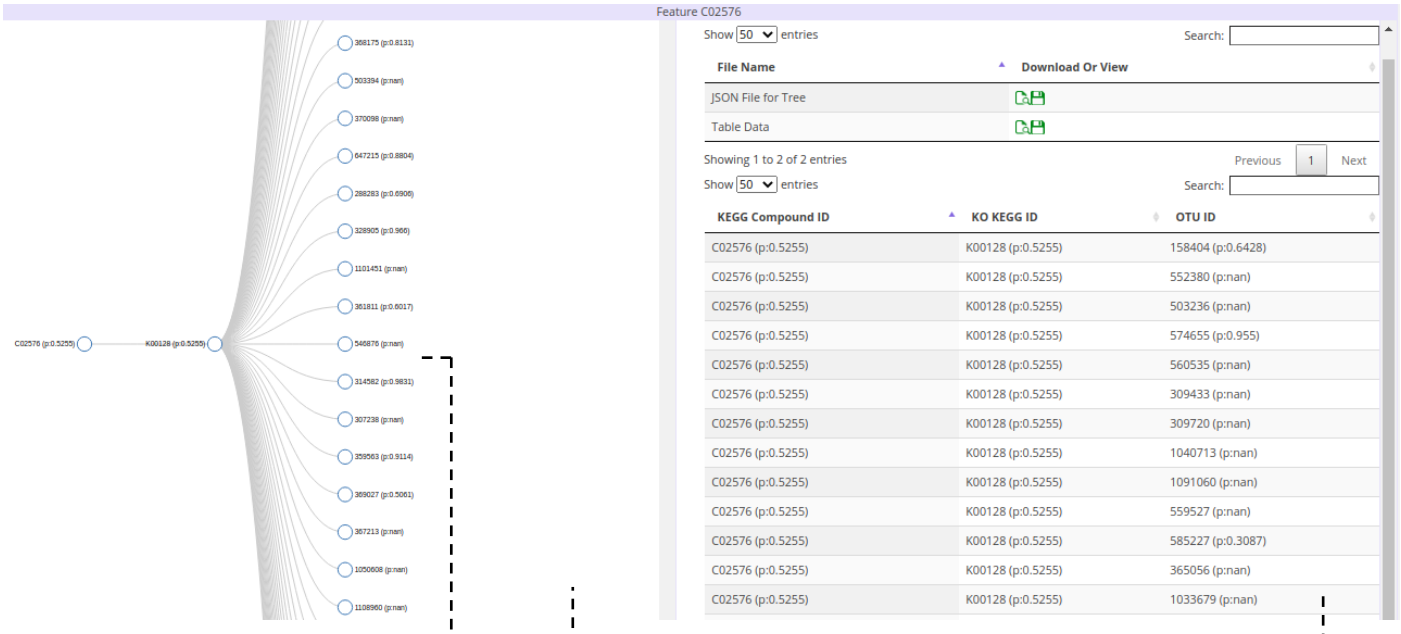
(Fig. 18)


Feature Identified
Community Structure
OTU_1096010
OTU_132837
OTU_509383
OTU_503236
OTU_1050608
OTU_1091060
OTU_1105814
OTU_581014
OTU_183686
OTU_567715
OTU_386554
OTU_4308098
OTU_2232355
OTU_659361
OTU_554303
OTU_1640195
OTU_368261
OTU_471157
OTU_165771
OTU_264269
−0.015
−0.01
−0.005
0
0.005
0.01
Download All Feature For Community Structure
KEGG
K03406
K02026
K07483
K02025
K00680
K03310
K07813
K00248
K03091
K07024
K00799
K03924
K00666
K00059
K00257
K07497
K01011
K01692
K02014
K03088
−0.004
−0.002
0
0.002
0
Download All Feature For KEGG
CMP
C16216
C21758
G00109
C01149
C02576
C03461
C05130
C20372
C20376
C03460
C02835
C02946
C11924
C16502
G00108
C02591
C16217
C20373
C20377
C16469
−100µ
−50µ
0
50µ
100µ
150µ
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
Normal Feature
Show 10 entries
Search
KEGG Compound ID
p-value (Anova)
Visualize cor
C02591 0.56764712027688 LINK
C02835 0.5254858214149772 LINK
C02946 0.5254858214149772 LINK
C11924 0.5254858214149772 LINK
C16217 0.5107272046458358 LINK
C16469 0.6895104179008892 LINK
CRC Feature
Show 10 entries
Search
KEGG Compound ID
p-value (Anova)
Visualize cor
C01149 0.5254858214149752 LINK
C02576 0.5254858214149752 LINK
C03460 0.6294221232575476 LINK
C03461 0.5254858214149752 LINK
C05130 0.5254858214149752 LINK
C16216 0.5107272046458358 LINK
9

(Fig. 19)

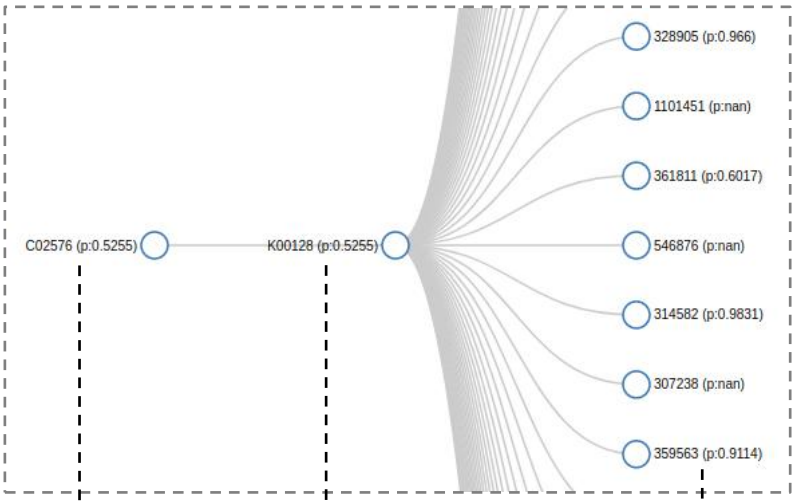
9 *Click on the link to visualize the following page which shows the predicted microbial source of metabolites (predicted as feature by our algorithm), in a tree as well as tabular form. [all p values provided in adjacent brackets]*



Save the tree (found on the top of the diagram).

The adjacent feature links represented in a tabular format and can be downloaded.

Expanded view of the tree.



Predicted Metabolite

The pathway that the predicted metabolite is associated with.

All the OTU ids (microbes) that could probably be the source of the predicted metabolite.

(Fig. 20)