FunMappOne Reference Manual

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1. Input format

a. **Data format**: Data should be provided in a single Excel file consisting of a separate sheet for each experimental condition.

b. **The experiment sheets**: Each sheet should be named with a condition id and consist of two columns: the gene names (gene symbols, ensembl, or entrez) and gene modifications (T-statistic, fold change…).

c. **The grouping sheet**: An additional sheet for grouping the conditions is compulsory. It must be the last sheet of the file and consist of two columns: first one with condition ids corresponding to the name of each sheet of the file (**d.**) and the second column for groupings. Groupings are formed by assigning the same number for each condition belonging to the same group (**f.**). If no predefined grouping will be provided, indicate only one number (e.g. fill the rows with number 1) for all conditions.

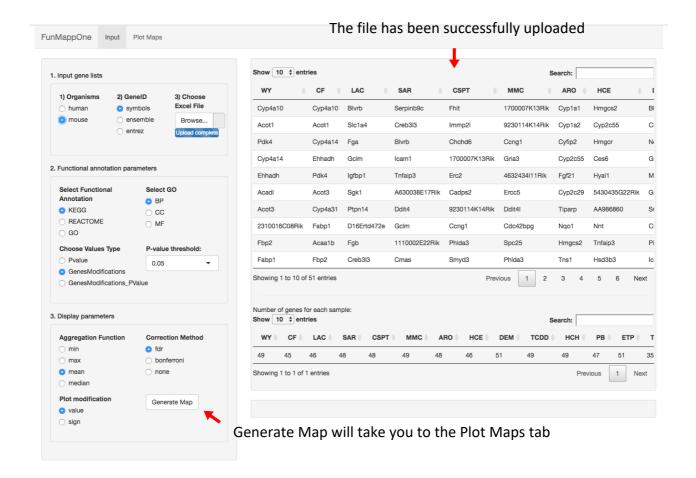|	A	B	C	D	E	F	G	H	I	J	K	L	M
1	**Symbol**	**T-stats**											
2	Lyz1	-10.58											
3	Ces6	9.61											
4	4931406C07Rik	9.56											
5	Gria3	9.19											
6	Cyp2c55	8.92											
7	1700007K13Rik	8.27											
8	9230114K14Rik	7.62											
9	Cyp2c29	7.31											
10	Gpihbp1	-7.31											
11	Gsta4	7.29											
12	9130409I23Rik	7.26											
13	Zfp750	7.01											
14	Nupr1	-6.98											
15	Ces5	6.90											
16	Ccng1	6.81											
17	Ces3	6.78											
18	Exoc4	6.71											
19	Aqp1	-6.62											
20	Upp2	6.56											
21	Aco1	6.43											
22	Cyp3a44	6.32											
23	2210023G05Rik	6.09											
24	Papss2	6.05											
25	6530418L21Rik	6.03											
26	Alas1	6.01											
27	A230058F20Rik	6.00											
28	Cdc42bpg	5.97											
29	Tm7sf3	5.90											
30	Phlda3	5.87											
31	Kcne3	-5.82											
32	Atp13a4	-5.79											
33	D630039A03Rik	5.78											
34	Slc9a3r1	5.77											

Sheet tabs: ETP | TCPOBOP | FK506 | CA | OA | TCE | BPA | TBTO | DIDP | CSA | CT | DM | MNU | MEN | Grouping | +

	A	B	C	D	E	F	G	H	I	J	K
1	**Chemical**	**Grouping**									
2	WY	7									
3	CF	7									
4	LAC	6									
5	SAR	6									
6	CSPT	9									
7	MMC	9									
8	ARO	1									
9	HCE	5									
10	DEM	9									
11	TCDD	1									
12	HCH	5									
13	PB	2									
14	ETP	9									
15	TCPOBOP	2									
16	FK506	4									
17	CA	8									
18	OA	8									
19	TCE	3									
20	BPA	9									
21	TBTO	9									
22	DIDP	9									
23	CSA	4									
24	CT	3									
25	DM	9									
26	MNU	9									
27	MEN	9									
28											

Sheet tabs: TCPOBOP | FK506 | CA | OA | TCE | BPA | TBTO | DIDP | CSA | CT | DM | MNU | MEN | Grouping | +
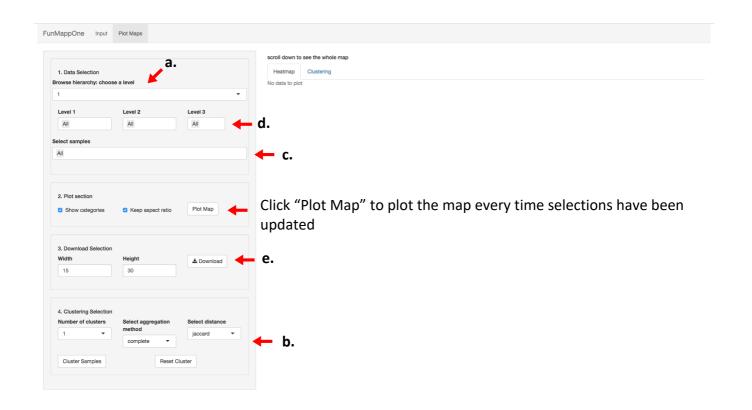
2. Input tab

a. **Input gene lists:** Select the organism, the type of gene names your list consists of and upload the Excel file in the format described above.

b. **Functional annotation parameters:** In this section you can select the functional annotation between KEGG and Reactome pathways as well as GO and its aspects (Biological Processes, Cellular Components, Molecular Function). Select the value type for the annotation between the P-value of the enriched pathway, the gene modification provided in the input list, or the combination of the two. You can also adjust the threshold for the P-value.

c. **Display parameters:** Select the display parameters. Choosing to plot based on the value will provide a colour scale of the chosen values while "sign" only indicates the direction of the modification.
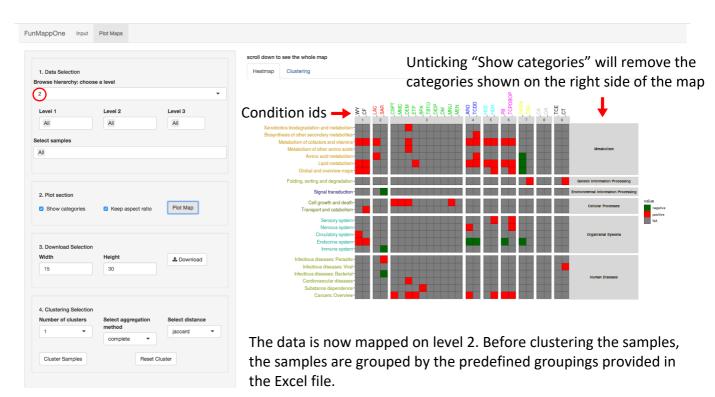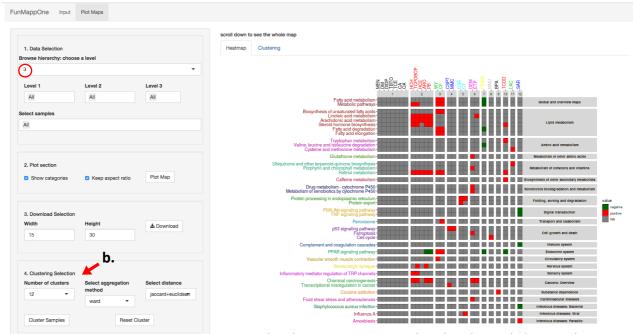
The file has been successfully uploaded

Generate Map will take you to the Plot Maps tab

3. Plot Maps tab

a. **Plotting at different levels:** Enriched pathways and terms can be visualized in multiple levels of hierarchy.

b. **Cluster experiments:** In Clustering Selection the experiments can be clustered into desired number of clusters with three different clustering methods and distances. Click "Cluster Samples" to activate clustering.

c. **Filter experiments:** Experimental conditions (condition ids) can be filtered and only selected experiments will be mapped. Remove "All" from the selections to only plot the selected experiments.

d. **Filter rows by level:** Pathways and processes can be filtered based on the level to only visualize the selected rows. Remove "All" from the selections to only plot the selected experiments.

e. **Download map:** Map view can be downloaded as in pdf format by clicking "Download".

a.

1. Data Selection

Browse hierarchy: choose a level

`1`

Level 1	Level 2	Level 3
All	All	All

d.

Select samples

`All`

c.

scroll down to see the whole map

Heatmap   Clustering

No data to plot

2. Plot section

☑ Show categories   ☑ Keep aspect ratio   [Plot Map]

Click "Plot Map" to plot the map every time selections have been updated

3. Download Selection

Width	Height
15	30

[⬇ Download]

e.

4. Clustering Selection

Number of clusters	Select aggregation method	Select distance
1	complete	jaccard

[Cluster Samples]   [Reset Cluster]

b.

---

scroll down to see the whole map

Heatmap   Clustering

Unticking "Show categories" will remove the categories shown on the right side of the map

Condition ids →

Xenobiotics biodegradation and metabolism
Biosynthesis of other secondary metabolites
Metabolism of cofactors and vitamins
Metabolism of other amino acids
Amino acid metabolism
Lipid metabolism
Global and overview maps

Metabolism

Folding, sorting and degradation

Genetic Information Processing

Signal transduction

Environmental Information Processing

Cell growth and death
Transport and catabolism

Cellular Processes

Sensory system
Nervous system
Circulatory system
Endocrine system
Immune system

Organismal Systems

Infectious diseases: Parasitic
Infectious diseases: Viral
Infectious diseases: Bacterial
Cardiovascular diseases
Substance dependence
Cancers: Overview

Human Diseases

value
■ negative
■ positive
■ NA

The data is now mapped on level 2. Before clustering the samples, the samples are grouped by the predefined groupings provided in the Excel file.

The data is now mapped on level 3 and clustered into 12 clusters.

Cluster dendrogram can be visualized by clicking the Clustering tab