

FunMappOne Reference Manual

Index

1. Input format
 - a. Data format
 - b. The experiment sheets
 - c. The grouping sheet
2. Input tab
 - a. Input gene lists
 - b. Functional annotation parameters
 - c. Display parameters
3. Plot Maps tab
 - a. Plotting at different levels
 - b. Cluster experiments
 - c. Filter experiments
 - d. Filter rows by level
 - e. Download map

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.

b.

	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	9130409123Rik	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														
	ETP	TCPOBOP	FK506	CA	OA	TCE	BPA	TBTO	DIDP	CSA	CT	DM	MNU	MEN	Grouping	+

d.

	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															
	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 screenshot shows the 'Input' tab of the FunMapOne web application. The interface is divided into three main sections, each with a red arrow and letter annotation:

- a. 1. Input gene lists:** This section contains three sub-sections: '1) Organisms' with radio buttons for 'human' (selected) and 'mouse'; '2) GeneID' with radio buttons for 'symbols' (selected), 'ensemble', and 'entrez'; and '3) Choose Excel File' with a 'Browse...' button and a 'No' button. A red arrow points to the 'Browse...' button with the text 'Upload a file'.
- b. 2. Functional annotation parameters:** This section contains two columns of radio buttons. The left column is 'Select Functional Annotation' with 'KEGG' (selected), 'REACTOME', and 'GO'. The right column is 'Select GO' with 'BP' (selected), 'CC', and 'MF'. Below these is 'Choose Values Type' with 'Pvalue', 'GenesModifications' (selected), and 'GenesModifications_PValue'. To the right is a 'P-value threshold:' dropdown menu set to '0.05'.
- c. 3. Display parameters:** This section contains two columns of radio buttons. The left column is 'Aggregation Function' with 'min', 'max', 'mean' (selected), and 'median'. The right column is 'Correction Method' with 'gSCS' (selected), 'fdr', and 'bonferroni'. Below these is a 'Plot modification' section with 'value' (selected) and 'sign'. A 'Generate Map' button is located at the bottom right of this section.

On the right side of the interface, there is a box that says 'Waiting for input file!' and another empty box below it.

The file has been successfully uploaded

FunMapOne

Input

Plot Maps

1. Input gene lists

1) Organisms

☐ human

☒ mouse

2) GeneID

☒ symbols

☐ ensemble

☐ entrez

3) Choose Excel File

Browse... Ad

Upload complete

2. Functional annotation parameters

Select Functional Annotation

☒ KEGG

☐ REACTOME

☐ GO

Select GO

☒ BP

☐ CC

☐ MF

Choose Values Type

☐ Pvalue

☒ GenesModifications

☐ GenesModifications_PValue

P-value threshold:

0.05

3. Display parameters

Aggregation Function

☐ min

☐ max

☒ mean

☐ median

Correction Method

☒ gSCS

☐ fdr

☐ bonferroni

Plot modification

☒ value

☐ sign

Generate Map

Show 10 entries

Search:

WY	CF	LAC	SAR	CSPT	MMC	ARO	HCE	DEM	TCDD	HCH
Cyp4a10	Cyp4a10	Blvrb	Serpinb9c	Fhit	1700007K13Rik	Cyp1a1	Hmgcs2	Blvrb	Cyp1a1	Cyp2c5l
Acot1	Acot1	Slc1a4	Creb3l3	Immp2l	9230114K14Rik	Cyp1a2	Cyp2c55	Cbr3	Cyp1b1	Ces6
Pdk4	Cyp4a14	Fga	Blvrb	Chchd6	Ccng1	Cyfp2	Hmgcr	Nqo1	Cyfp2	Cyp2c2l
Cyp4a14	Ehhadh	Gclm	Icam1	1700007K13Rik	Gria3	Cyp2c55	Ces6	Gclc	Cyp1a2	493140f
Ehhadh	Pdk4	Igf1bp1	Tnfrap3	Erc2	4632434111Rik	Fgf21	Hyal1	Maoa	Fmo2	Exosc8
Acadl	Acot3	Sgk1	A630038E17Rik	Cadps2	Ercc5	Cyp2c29	5430435G22Rik	Gsta2	Tiparp	Ces3
Acot3	Cyp4a31	Ptpn14	Ddit4	9230114K14Rik	Ddit4l	Tiparp	AA986860	Srxn1	Ereg	Ptges
2310016C08Rik	Fabp1	D16Erd472e	Gclm	Ccng1	Cdc42bpg	Nqo1	Nnt	Cbr1	Sytl2	Pla2g12
Fbp2	Acaa1b	Fgb	1110002E22Rik	Phlda3	Spc25	Hmgcs2	Tnfrap3	Pir	Ins16	Ttc39b
Fabp1	Fbp2	Creb3l3	Cmas	Smyd3	Phlda3	Tns1	Hsd3b3	Icam1	Hsd17b6	Tns1

Showing 1 to 10 of 51 entries

Previous 1 2 3 4 5 6 Next

Number of genes for each sample:

Show 10 entries

Search:

WY	CF	LAC	SAR	CSPT	MMC	ARO	HCE	DEM	TCDD	HCH	PB	ETP	TCPOBOP	FK506	C
49	45	46	48	48	49	48	46	51	49	49	47	51	35	50	38

Showing 1 to 1 of 1 entries

Previous 1 Next

3. Plot Maps tab

- Plotting at different levels:** Enriched pathways and terms can be visualized in multiple levels of hierarchy.
- 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.
- 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.
- 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.
- Download map:** Map view can be downloaded as in pdf format by clicking "Download".

FunMapOne Input Plot Maps

1. Data Selection

Browse hierarchy: choose a level

1

Level 1: All Level 2: All Level 3: All

Select samples: All

2. Plot section

☒ Show categories ☒ Keep aspect ratio Plot Map

3. Download Selection

Width: 15 Height: 30 Download

4. Clustering Selection

Number of clusters: 1 Select aggregation method: complete Select distance method: jaccard

Cluster Samples Reset Cluster

scroll down to see the whole map

Heatmap Clustering

No data to plot

a. d. c. e. b.

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



