

## NaviCenta – Hands on

### Required files:

- Gene\_GSE177049\_1.txt

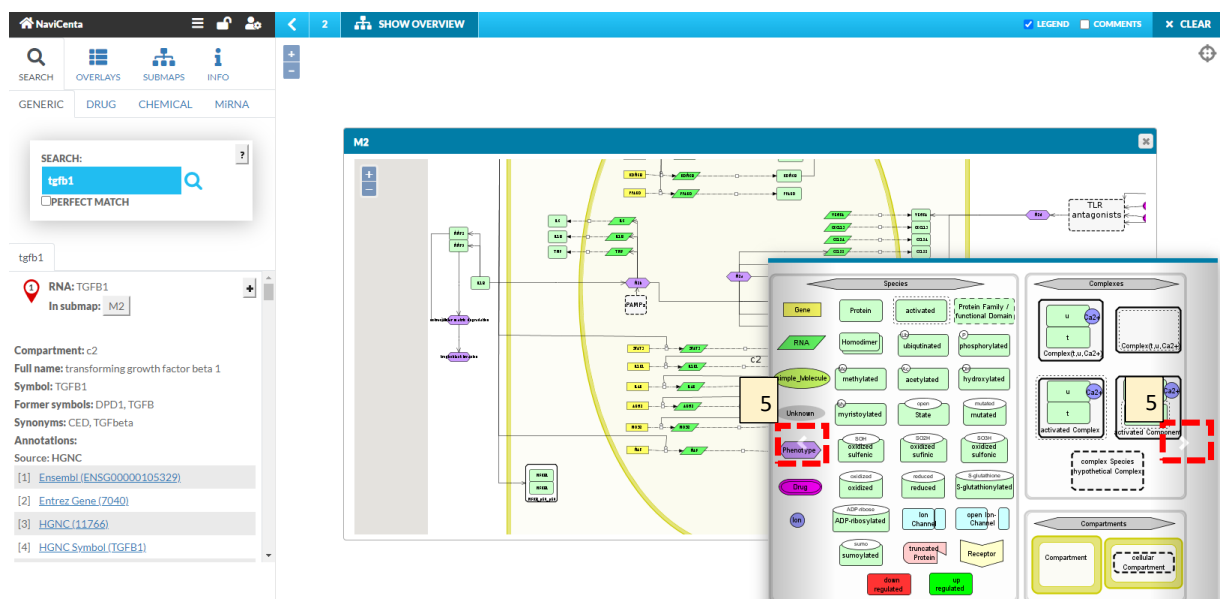
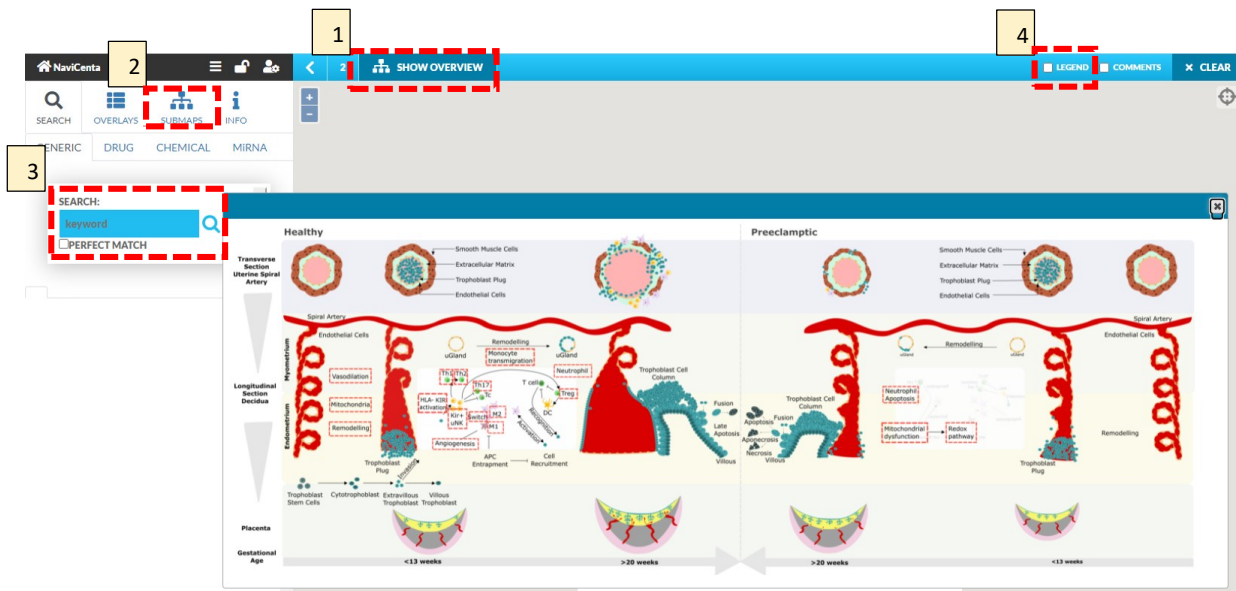
Go to: <https://www.sbi.uni-rostock.de/minerva/index.xhtml?id=NaviCenta>

### Plugins:

- <https://raw.githubusercontent.com/sbi-rostock/AIR/master/Plugins/Overlays.js>
- <https://raw.githubusercontent.com/sbi-rostock/AIR/master/iPlacenta/iPlacentaPlugin.js>

### Step by step:

- [1] Click “Show Overview”
- [2] Explore sub maps
- [3] Explore search bar
- [4] Tick “Legend” to learn about systems biology symbols
- [5] Explore the legend



## Overlay Plugin (account required)

### Login

- [1] Click on the “person” icon on the top left of the window
- Enter “navicenta” as both user and password

### Load Overlay plugin:

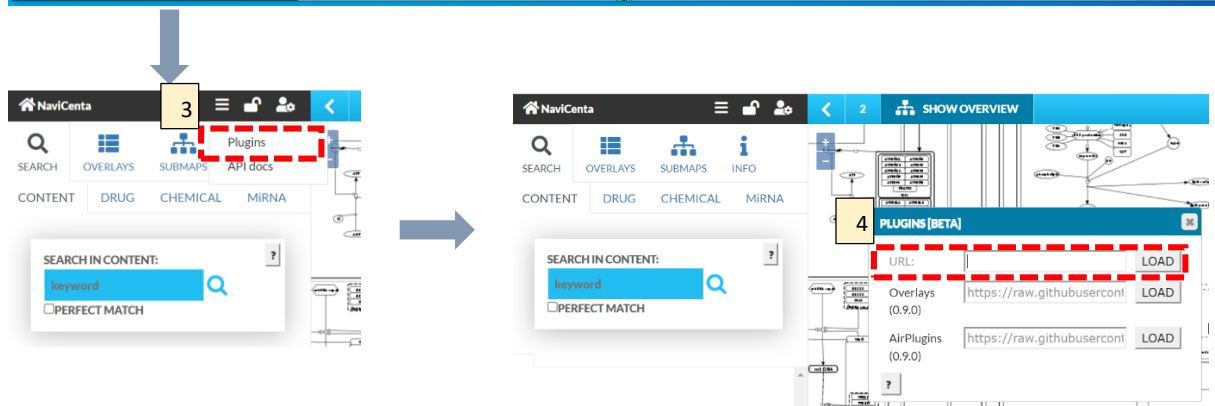
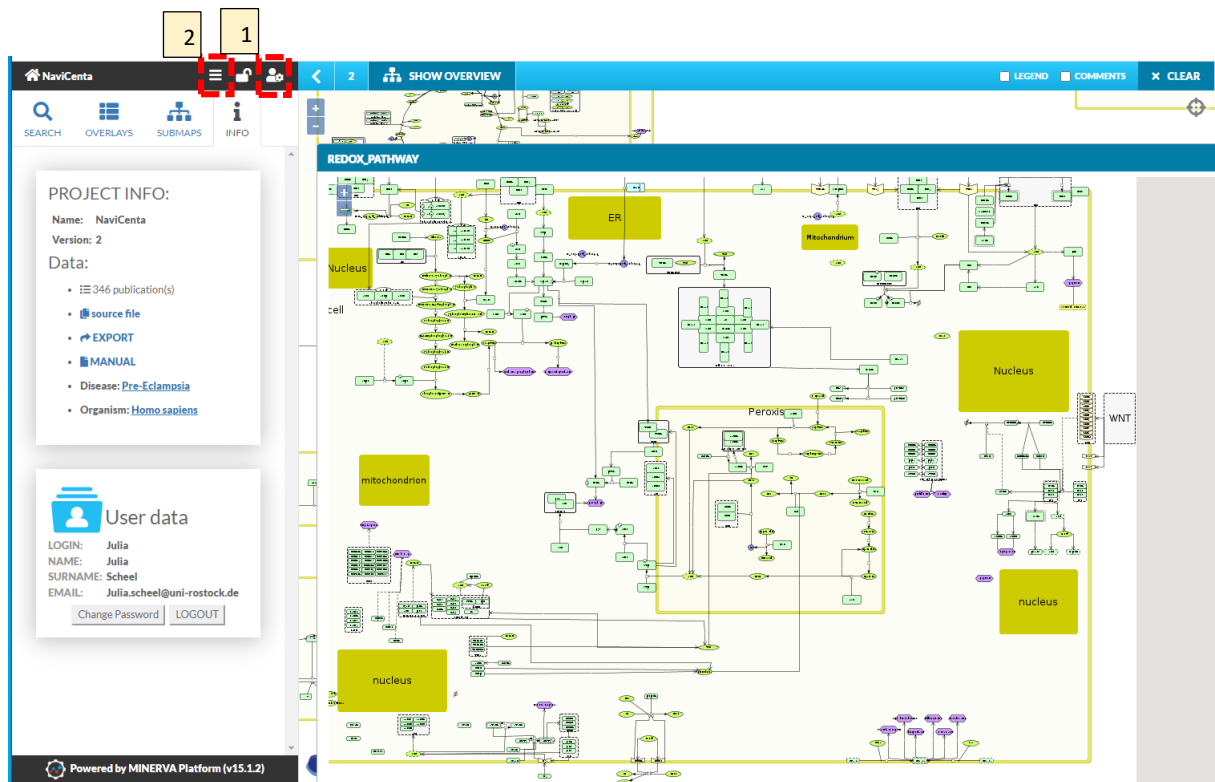
- [2] Click on three dashes on top left of the window
- [3] Click on „plugin“
- [4] Copy: <https://raw.githubusercontent.com/sbi-rostock/AIR/master/Plugins/Overlays.js> into the pop up field
- [4] Click “load”

### Load gene GSE177049 1.txt file:

- [5] Click “choose file”
- Select file
- [6] Normalize each sample
- [7] Tick “Data has p-values?”

### Generate Overlays

- [8] Click “Generate Overlays”
- [9] Click “Show Generated Overlays”



**PROJECT INFO:**  
Name: NaviCenta  
Version: 2  
Data:  
• 335 publication(s)  
• source file  
• EXPORT  
• MANUAL  
• Disease: [Pre-Eclampsia](#)  
• Organism: [Homo sapiens](#)

**User data**  
LOGIN: Julia  
NAME: Julia  
SURNAME: Scheel  
EMAIL: [Julia.scheel@uni-rostock.de](mailto:Julia.scheel@uni-rostock.de)  
[Change Password](#) [LOGOUT](#)

**Upload Overlays**  
Choose File: No file chosen  
No normalization  
Positive (1) Values: FF0000  
Neutral (0) Values: FFFFFFFF  
Negative (-1) Values: 0000FF  
File Type: TSV

**SEARCH IN CONTENT:**  
keyword  
 PERFECT MATCH

**Upload Overlays**  
No normalization  
Positive (1) Values: FF0000  
Neutral (0) Values: FFFFFFFF  
Negative (-1) Values: 0000FF  
File Type: TSV  
 Data has p-values?  
Phenotype p-value threshold: 0.05  
 Override Overlays  
**Generate Overlays**  
Note: This will over write existing overlays with the same sample names.

Override Overlays  
**Generate Overlays**  
Note: This will overwrite existing overlays with the same sample names.  
**Show Generated Overlays** **Hide Generated Overlays**  
**Remove Generated Overlays**

## Omics Plugin - Xplore (no account required)

### Load iPlacenta plugin:

- [1] Click on three dashes on top left of the window
- [2] Click on „plugin“
- [3] Copy:  
<https://raw.githubusercontent.com/sbi-rostock/AIR/master/iPlacenta/iPlacentaPlugin.js> into the pop up field
- [3] Click “load”

### Xplore – Downstream Enrichment

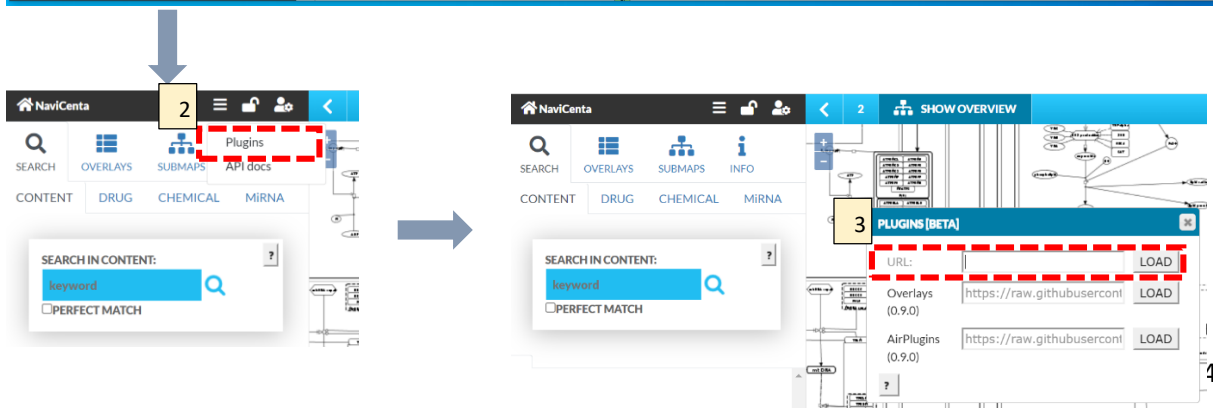
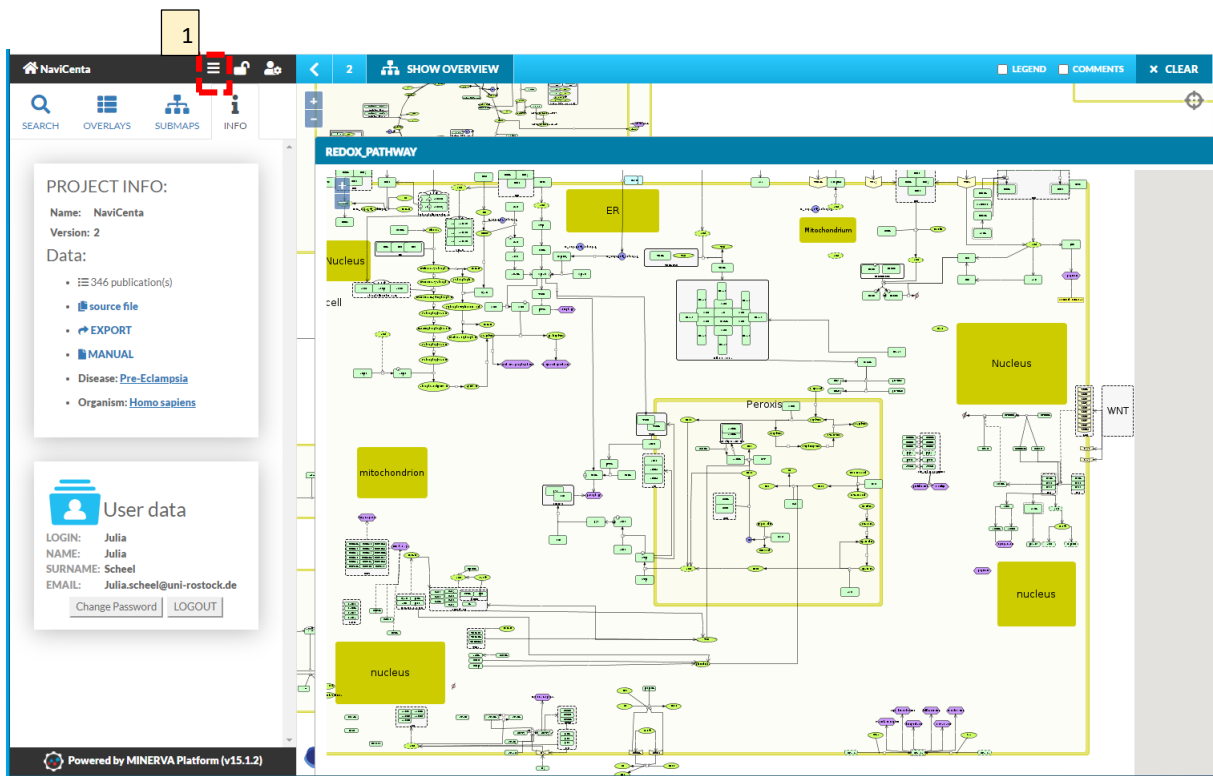
- [8] Select species (add selected)
- [9] Manipulate
- [10] Which phenotypes are affected?

### Xplore – Upstream Enrichment

- [11] Manipulate phenotypes of interest
- [12] View targets

### Xplore – Data Exploration:

- Select species on map [4] to view regulators [5], targets [6], phenotypes [7],
- Download list of regulators, targets, or phenotypes



**PROTEIN: NOX5**  
Full name: NADPH oxidase 5  
Symbol: NOX5  
Synonyms: NOX5A, NOX5B  
Annotations:  
Source: HGNC  
[1] Ensembl (ENSG00000255346)

Regulator	Regulation	Type	Reference
JUN	activation	TF	22348975
NFKB1	activation	TF	22348975
RELA	activation	TF	22348975
STAT1	activation	TF	22348975
STAT3	activation	TF	22348975

↓ Scroll down

**Downstream Enrichment**

Select perturbed elements: 8

Element	Knockout	FC
NOX5	<input checked="" type="checkbox"/>	0
PLC	<input type="checkbox"/>	0
TLR4	<input type="checkbox"/>	0

Showing 1 to 3 of 3 entries

**Downstream Impact:**  
Phenotypes Paths KO Impact

↓ Scroll down

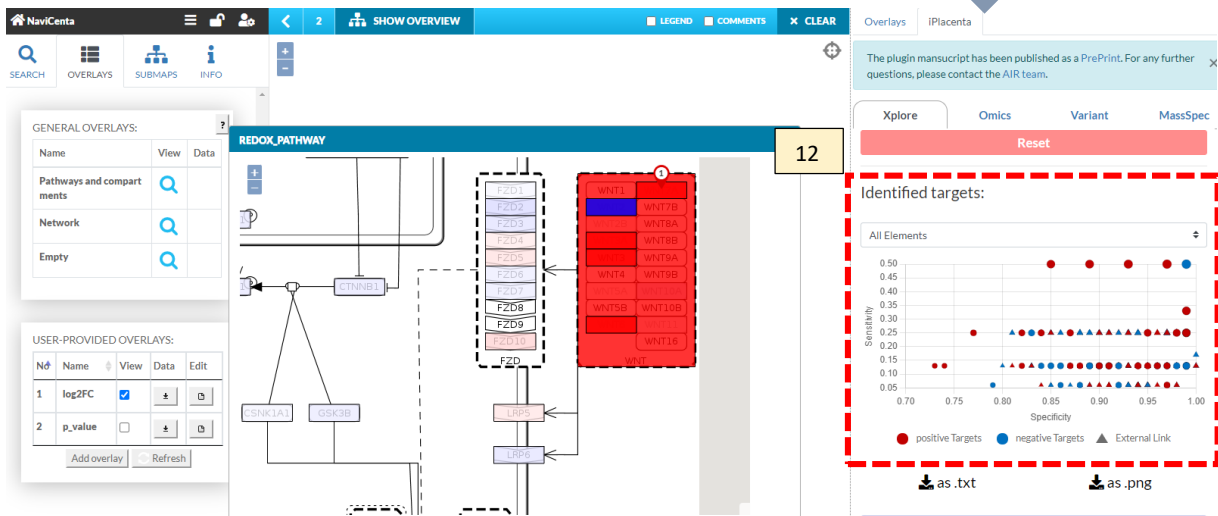
**Upstream Enrichment**

Select phenotype levels: 11

Phenotype#	Level
cytotoxicity	0
cytotrophoblast	0.25
cytotrophoblast lysis	0
phagocytosis	0
receptor mediated phagocytosis	0
regulation of actin cytoskeleton reorganization	0

Showing 1 to 6 of 6 entries (filtered from 132 total entries)

Scroll down 5



## Omics Plugin - Omics

- [1] Navigate to the “Omics” tab

Load Gene\_GSE177049\_1.txt file

- [2] Click “choose file”
- Select file
- Mapping by: Gene Symbol
- [3] Tick “Data has p-values?”
- [4] Click “Read Data File”

## Phenotype Inference

- [5] Click “Estimate Phenotype Levels”
- [6] view phenotype estimation results

## Create Overlay

- [7] Scroll down the „Omics“ tab and click „Create Overlays“
- [8] Click „Show Overlays“

The figure shows the NaviCenta software interface with the 'Omics' tab selected. The 'Omics' tab is highlighted with a red dashed box and labeled with a yellow box containing the number '1'. Below the tab, there is a section titled '1. Select Data' with two sub-sections: 'Upload' and 'Import from plugin'. The 'Upload' section is active, showing a 'Choose File' button (labeled with a yellow box containing the number '2') that has selected the file 'gene\_GSE177049\_1.txt'. Below this, there are dropdown menus for 'File Type' (set to TSV), 'Mapping column' (set to Gene\_Name), and 'Mapping by' (set to Gene Symbol). A checkbox labeled 'Data has p-values?' (labeled with a yellow box containing the number '3') is checked. Below this, there is a dropdown menu for 'Multiple transcripts by' (set to Mean) and another dropdown menu for 'Type of Data' (set to Differential, labeled with a yellow box containing the number '4'). At the bottom of the configuration panel, there is a red button labeled 'Read Data File' (labeled with a yellow box containing the number '4') and the text '3325 probes were mapped.' A red dashed box highlights the 'Read Data File' button and the text below it.

↓ Scroll down

SEARCH IN CONTENT: keyword  
 PERFECT MATCH

2. Analyze Data

Phenotype Inference Target Inference Enrich

Advanced Settings

Optimize Settings

94 elements will be considered (16.86 (3.94%) per phenotype per sample on average).

**Estimate Phenotype Levels**

Scroll down

Results

Table

Statistical method: Lowest p-value of both

Normalize each phenotype (recommended)

FDR Correction?

Clicking on a column header will color phenotypes and DCEs on the map by their fold change in the respective sample.

p-value threshold: 0.05

Show 5 entries

Phenotype	log2FC (p-value)	p_value (p-value)	# sign. samples
angiogenesis	-0.2 (1.2e-3)	0.37 (3.2e-43)	2
endothelial cell migration	-0.2 (0.03)	-0.22 (0.03)	2
ec apoptosis	-0.07 (0.68)	0.35 (3.0e-33)	1
ec permeability	0.17 (0.1)	-0.62 (3.2e-43)	1
<b>6 Proliferation</b>	-0.12 (0.48)	0.36 (1.1e-25)	1

Scroll down

Highlight on Map

Include values from the datafile in visualization?

Phenotype p-value threshold: 0.05

Overlay suffix:

**7 Create Overlays**

8 Show On Phenotype Submap

Show Overlays Hide Overlays

Remove Overlays

## Omics Plugin - Omics II

### Target Inference:

- [1] Navigate to “Target Inference” tab within the Omics plugin
- [2] select sample group for target inference
- [3] click “Predict Targets”
- [4] select regulator type (all elements, proteins, receptors, miRNAs, lncRNAs, transcription factors)
- [5] select number of elements for target combination prediction

- [6] click “Predict Combinations”
- [7] scroll down to view results

### Fetch EnrichR KEGG results:

- [8] Navigate to „EnrichR” tab within the Omics plugin
- [9] Select EnrichR Library
- [10] click “Fetch EnrichR Results”

The screenshot displays the NaviCentra Omics plugin interface. The main control panel on the right contains the following elements:

- 1**: Target Inference tab selected.
- 2**: Sample dropdown menu set to log2FC.
- 3**: Predict Targets button.
- 4**: Regulator Type Filter dropdown menu set to Transcription Factors.
- 5**: #k-mer Combinations slider set to 1.
- 6**: Predict Combinations button.
- 7**: Scroll down arrow indicating the next step.

Below the scroll down arrow, a scatter plot (Chart) is shown with the following data series:

- positive Targets**: Red triangles
- negative Targets**: Blue triangles
- combined**: Grey circles

The plot shows Sensitivity on the y-axis (0 to 0.35) and Specificity on the x-axis (0.88 to 1.00). The data points are clustered in the upper right quadrant, indicating high specificity and sensitivity for the predicted targets.



## 2. Analyze Data

8

Phenotype Inference   Target Inference   **Enrichr**

Define thresholds to create gene sets from the data:

FC Threshold (abs):

p-value Threshold:

9 Select an Enrichr Library:

KEGG\_2019\_Human

10 **Fetch Enrichr Results**

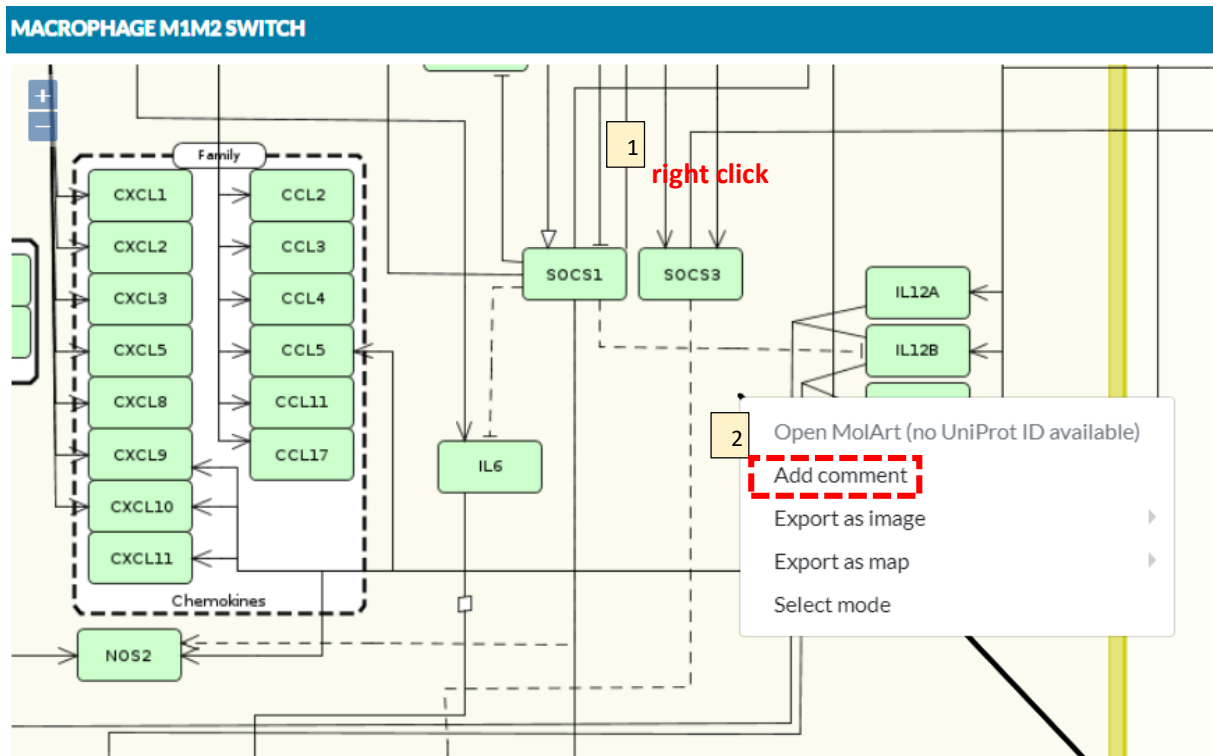
log2FC

Show  entries   Search:

Rank	Term	adj. p-value	Combined score
1	PPAR signaling pathway	0.0281	310.2508
2	Neuroactive ligand-receptor interaction	0.0281	103.8509
3	Cytokine-cytokine receptor interaction	0.1272	45.5135

## NaviCentra – How to Leave Feedback

- [1] Right click on the species of interest
- [2] Select “add comment”
- [3] select Type (i.e. specific species, reaction, or general)
- [4] add comment in the “Content” box



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