NaviCenta – Hands on

Required files:

- Gene_GSE177049_1.txt

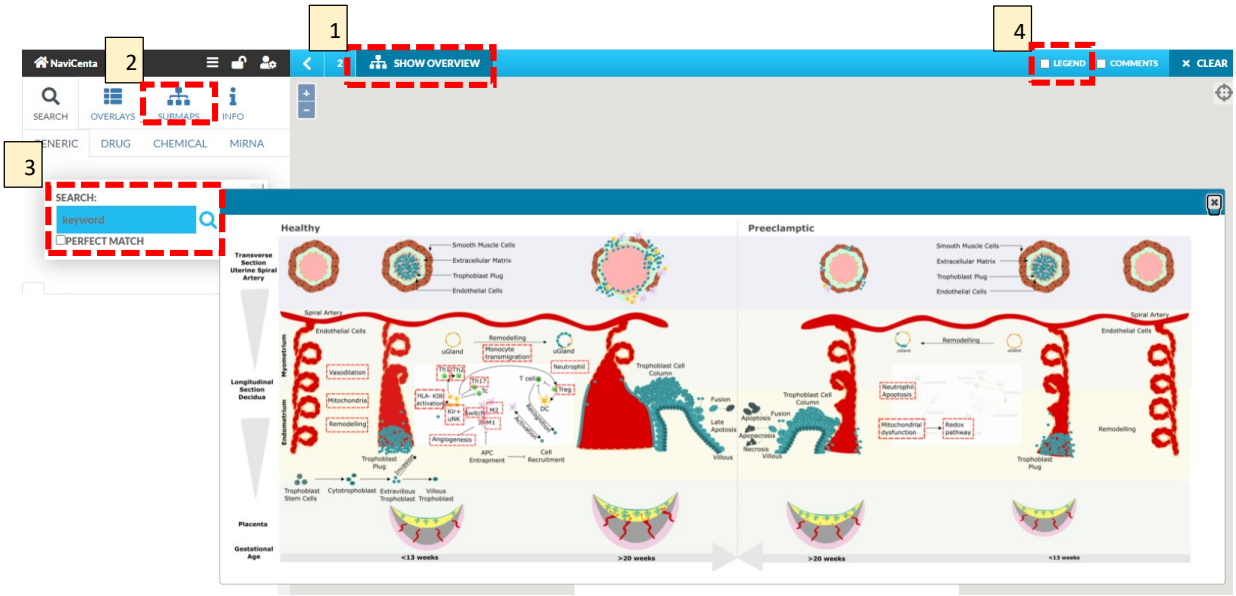
Go to: https://www.sbi.uni-rostock.de/minerva/index.xhtml?id=NaviCenta

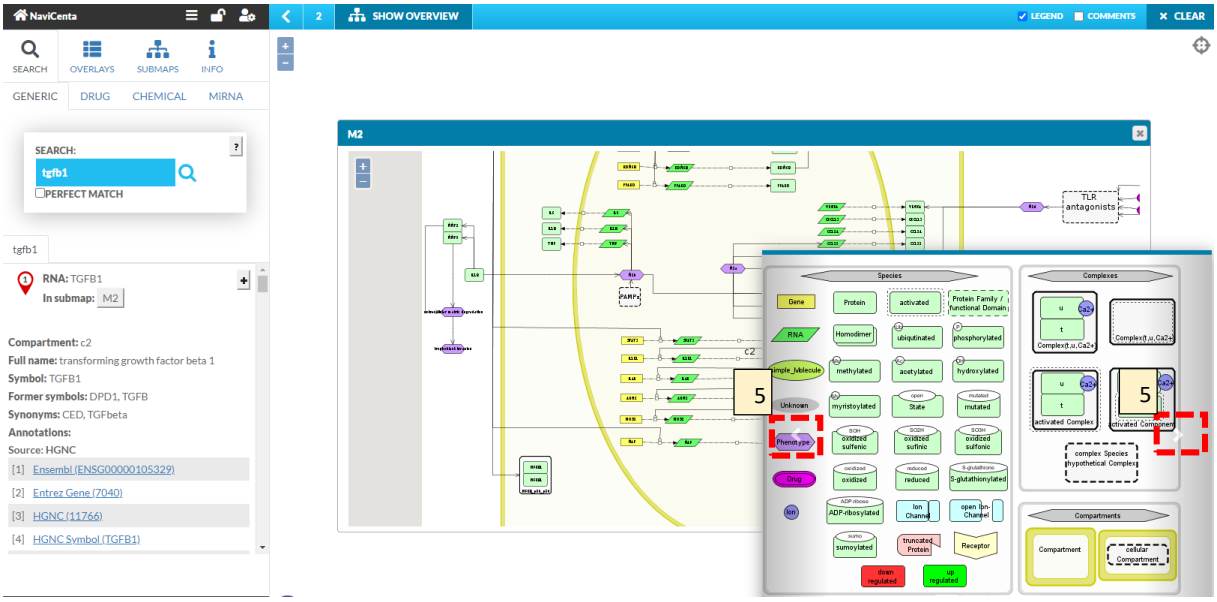
Plugins:

- 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:

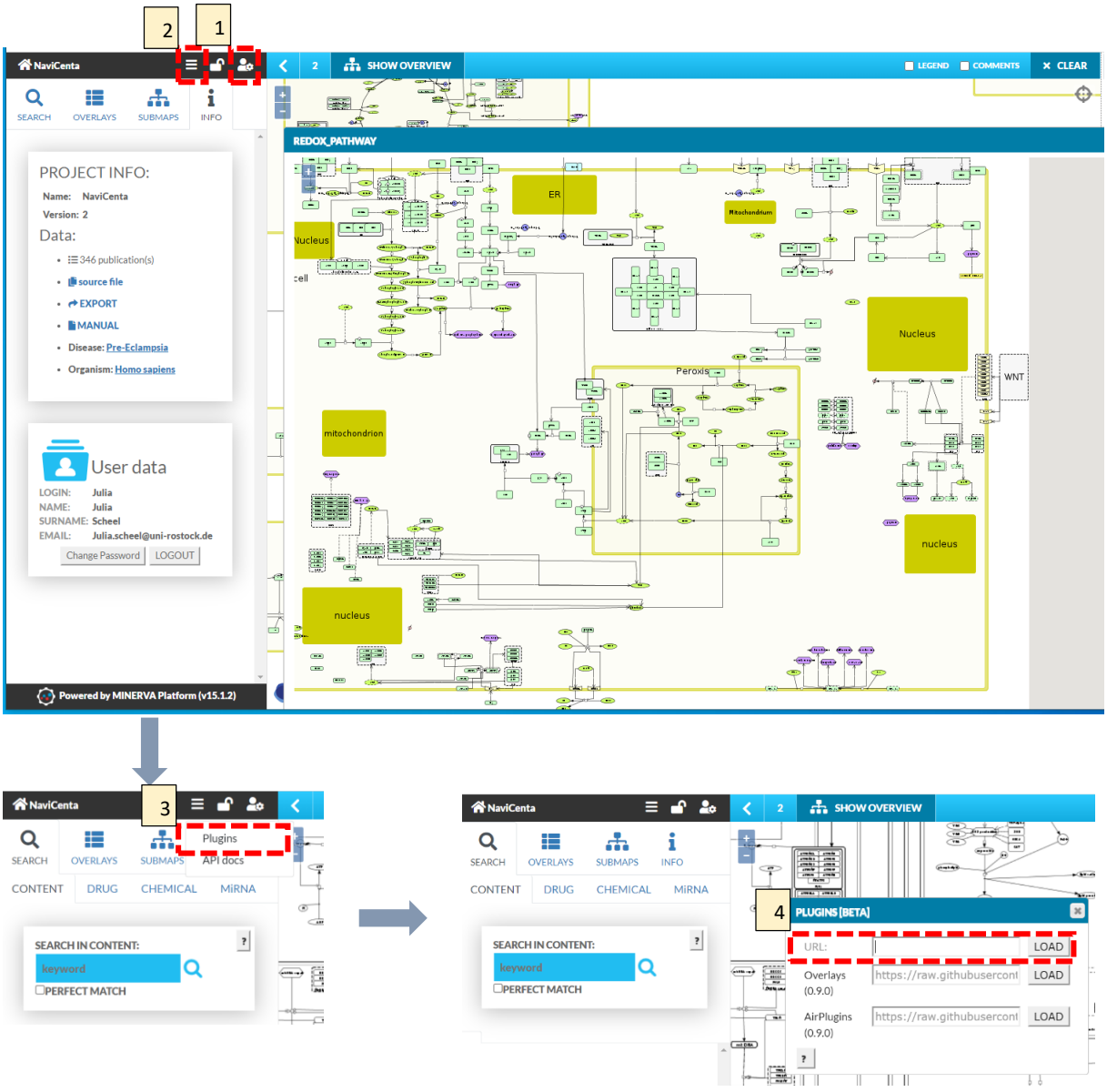
- [2] Click on three dashes on top left of the window
- [3] Click on „plugin“
- [4] Copy: https://raw.githubusercontent.com/sbi-rostock/AIR/master/PlugIns/Overlays.js into the pop up field
- [4] Click “load”

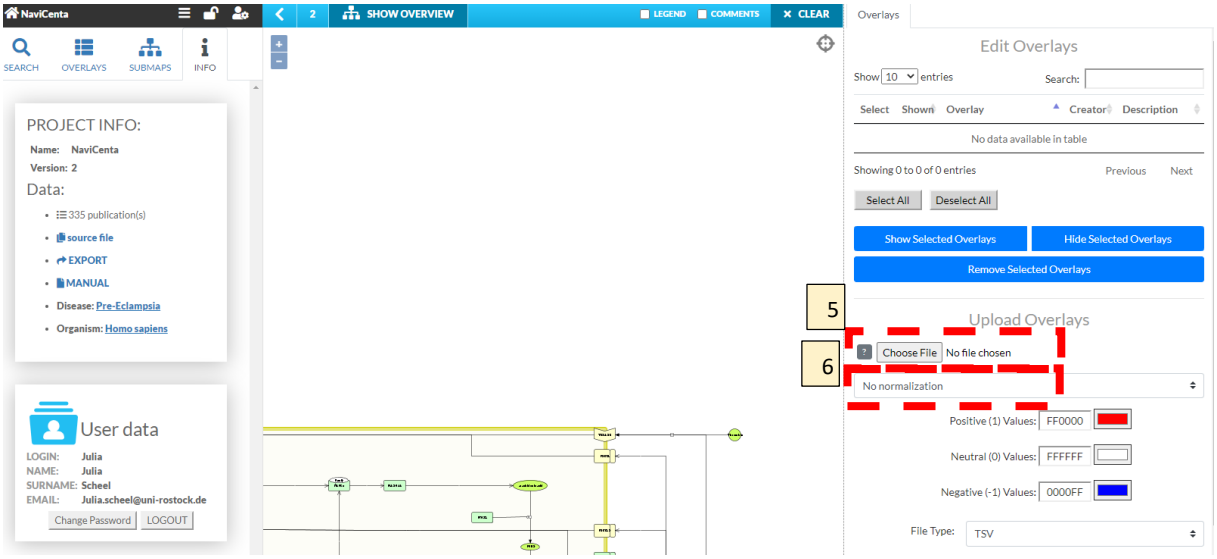
Load gene_GSE177049_1.txt file:

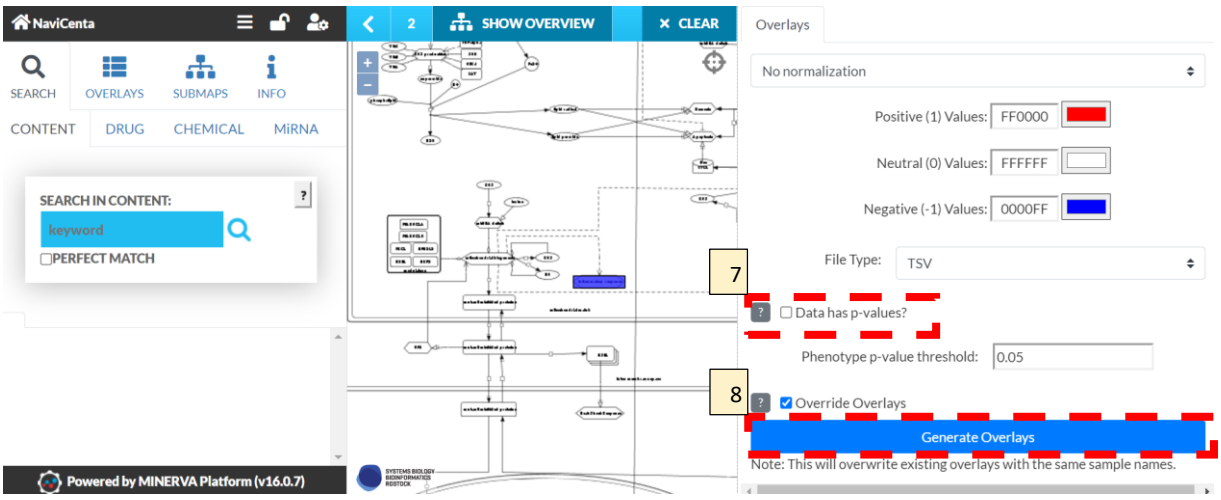
- [5] Click “choose file”
- Select file
- [6] Normalize each sample
- [7] Tick “Data has p-values?”

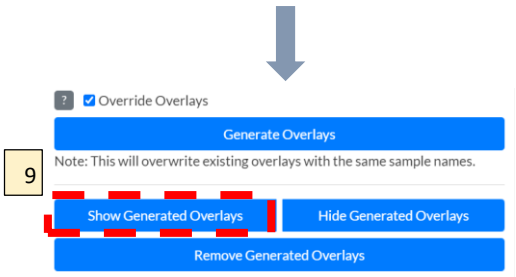
Generate Overlays

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




NaviCenta
SEARCH
OVERLAYS
SUBMAPS
INFO
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
Change Password
LOGOUT
SHOW OVERVIEW
LEGEND
COMMENTS
CLEAR
Overlays
Edit Overlays
Show 10 entries
Search:
Select
Shown
Overlay
Creator
Description
No data available in table
Showing 0 to 0 of 0 entries
Previous
Next
Select All
Deselect All
Show Selected Overlays
Hide Selected Overlays
Remove Selected Overlays
5
Upload Overlays
6
Choose File
No file chosen
No normalization
Positive (1) Values:
FF0000
Neutral (0) Values:
FFFFFF
Negative (-1) Values:
0000FF
File Type:
TSV


NaviCenta
SEARCH
OVERLAYS
SUBMAPS
INFO
CONTENT
DRUG
CHEMICAL
MiRNA
SEARCH IN CONTENT:
keyword
PERFECT MATCH
Powered by MINERVA Platform (v16.0.7)
SHOW OVERVIEW
CLEAR
Overlays
No normalization
Positive (1) Values:
FF0000
Neutral (0) Values:
FFFFFF
Negative (-1) Values:
0000FF
File Type:
TSV
7
Data has p-values?
Phenotype p-value threshold:
0.05
8
Override Overlays
Generate Overlays
Note: This will overwrite existing overlays with the same sample names.


Override Overlays
Generate Overlays
Note: This will overwrite existing overlays with the same sample names.
9
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 – Data Exploration:

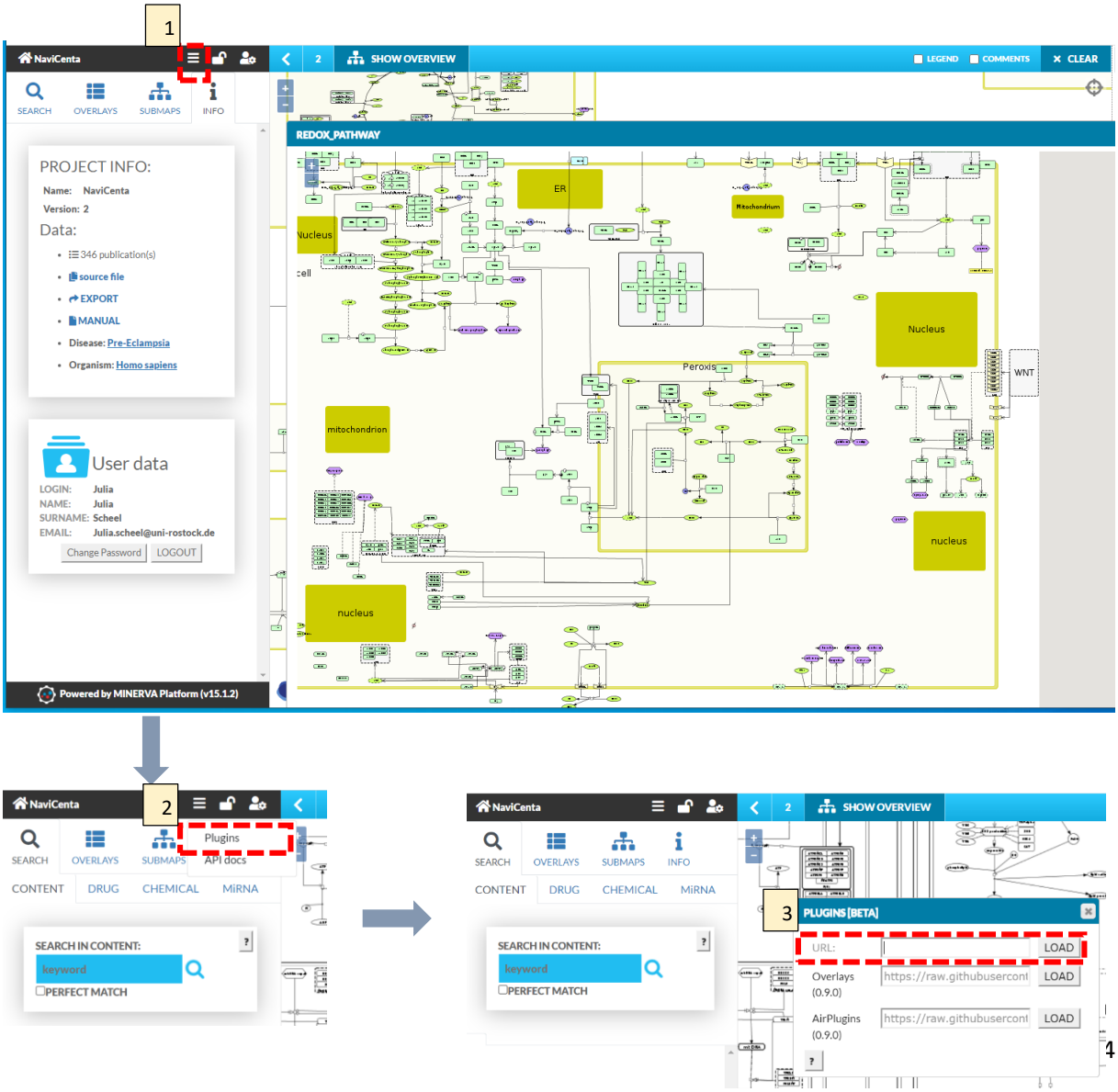
- Select species on map [4] to view regulators [5], targets [6], phenotypes [7],
- Download list of regulators, targets, or phenotypes

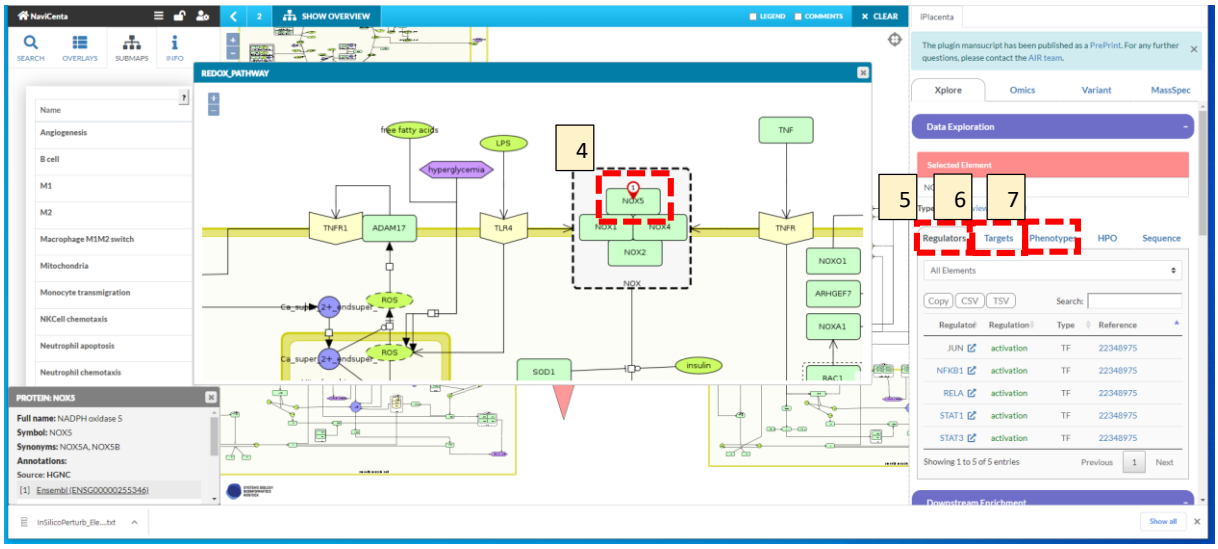
Xplore – Downstream Enrichment

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

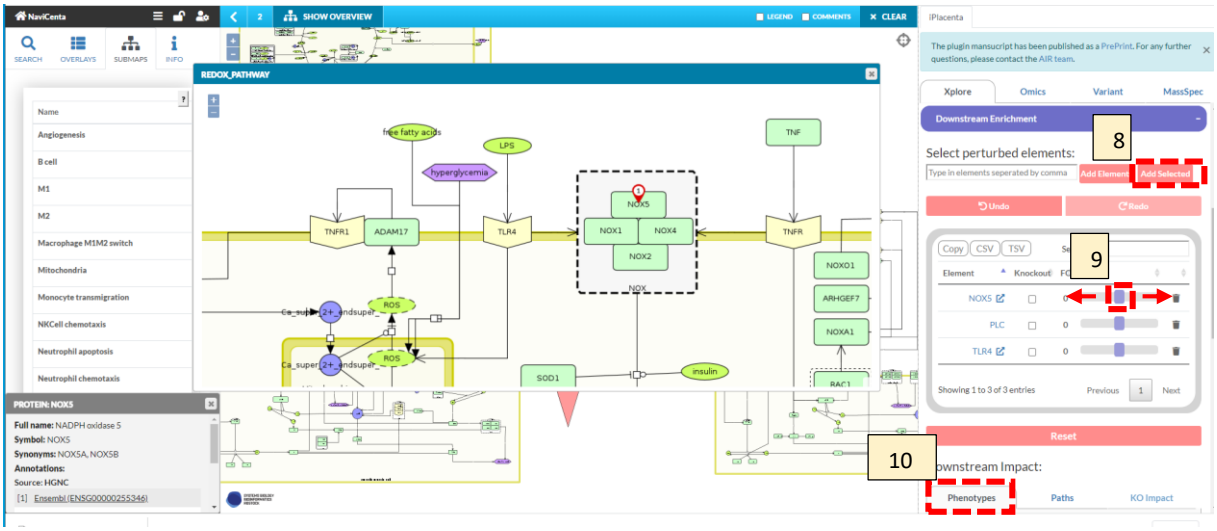
Xplore – Upstream Enrichment

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

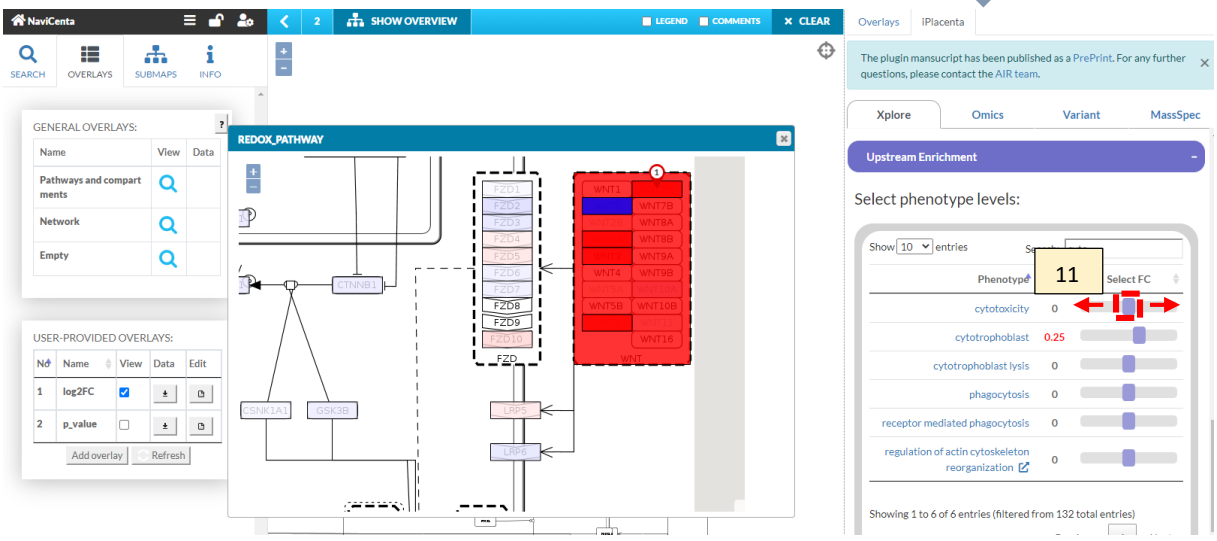




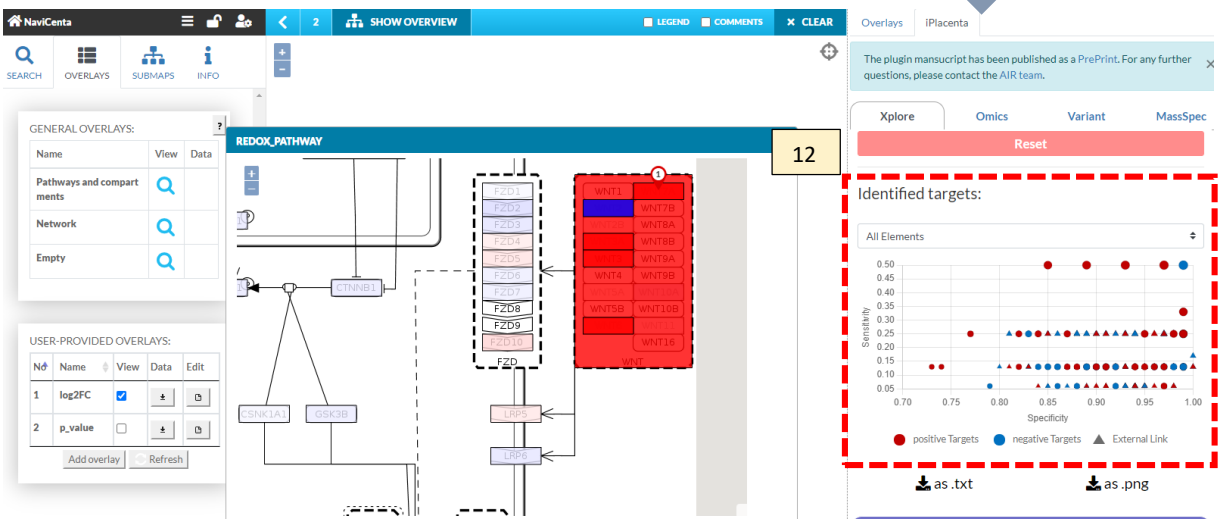
Scroll down



Scroll down



Scroll down



Omics Plugin - Omics

- [1] Navigate to the "Omics" tab

<u>Load Gene_GSE177049_1.txt file</u>

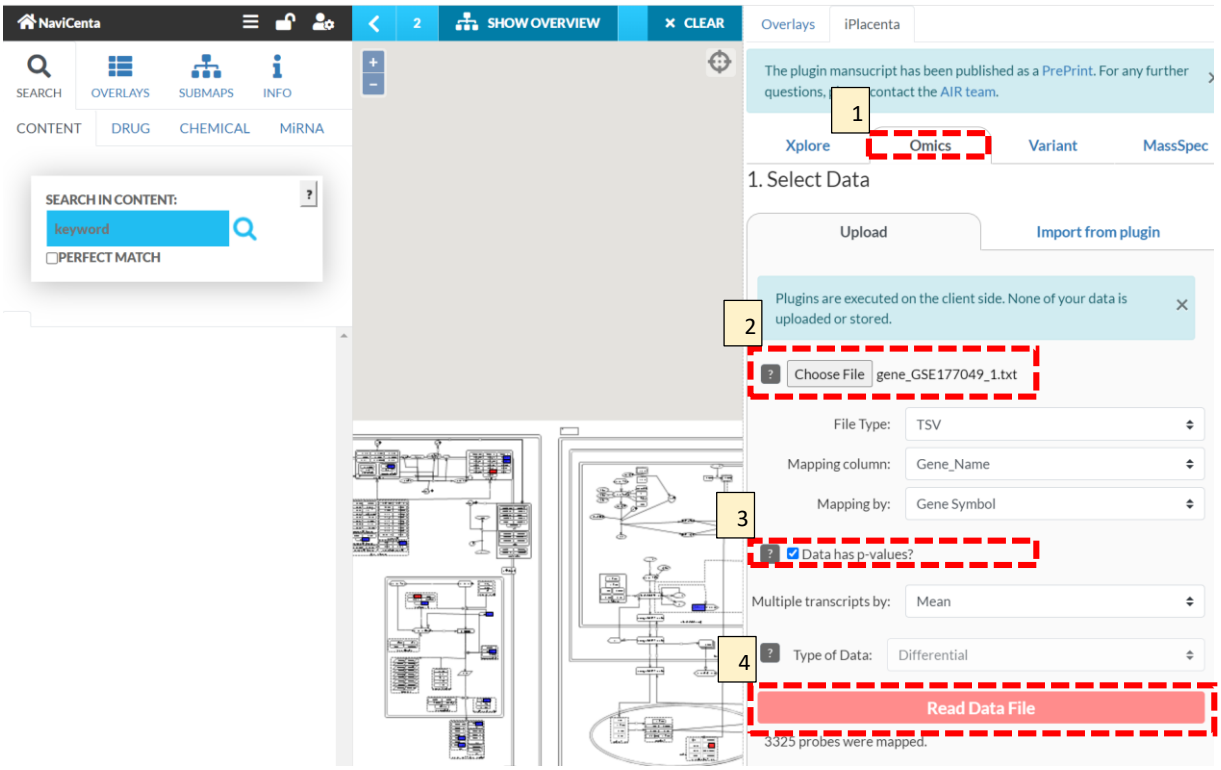
- [2] Click "choose file"
- Select file
- Mapping by:Gene Symbol
- [3] Tick "Data has p-values?"
- [4] Click "Read Data File"

<u>Phenotype Inference</u>

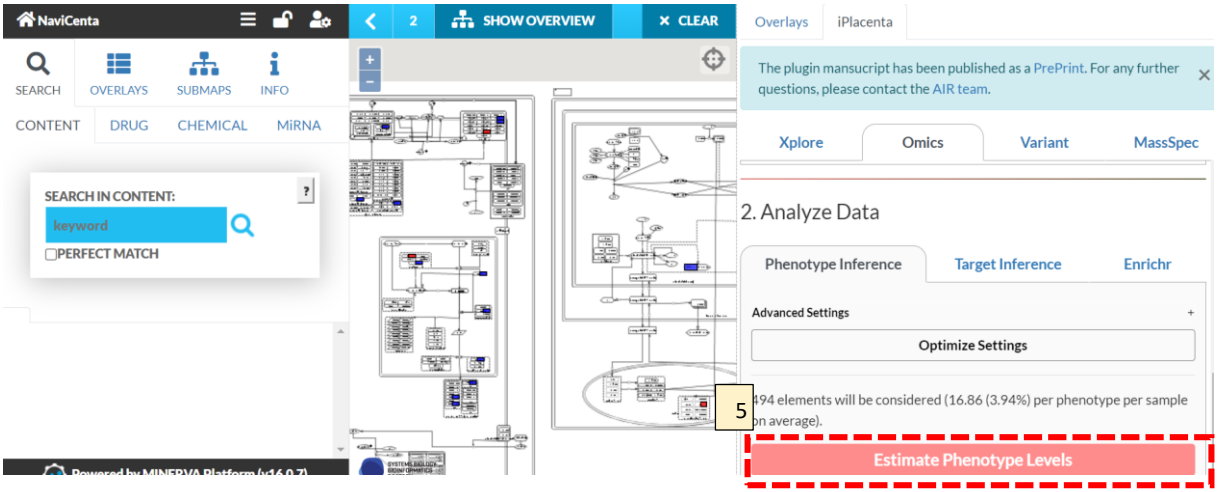
- [5] Click "Estimate Phenotype Levels
- [6] view phenotype estimation results

<u>Create Overlay</u>

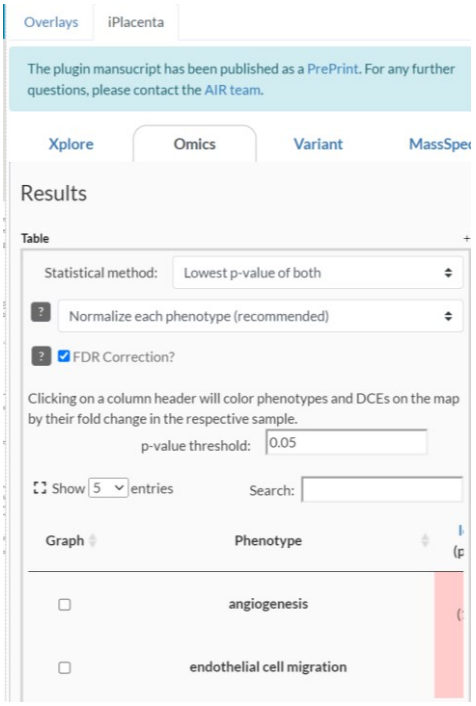
- [7] Scroll down the „Omics" tab and click „Create Overlays"
- [8] Click „Show Overlays"

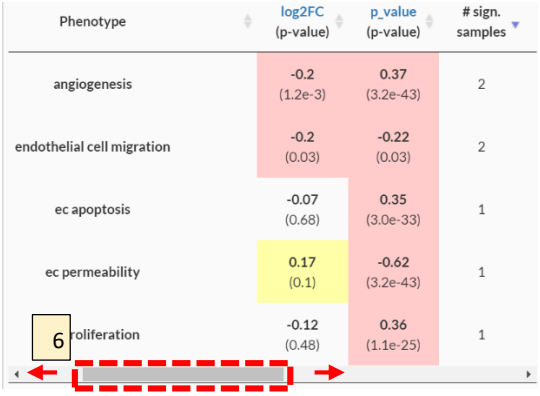


Scroll down

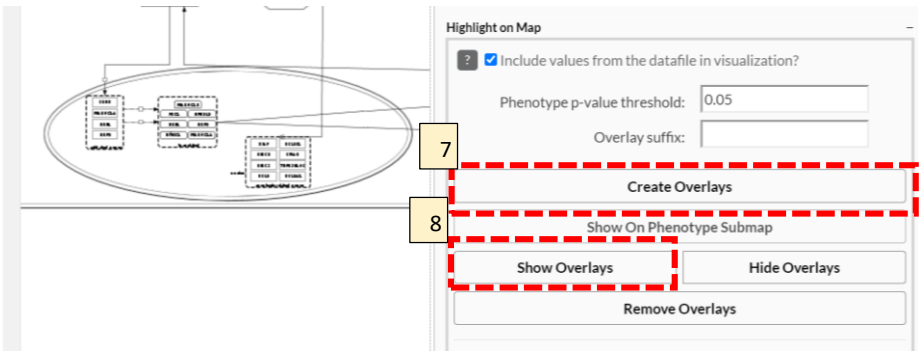


Scroll down





Scroll down



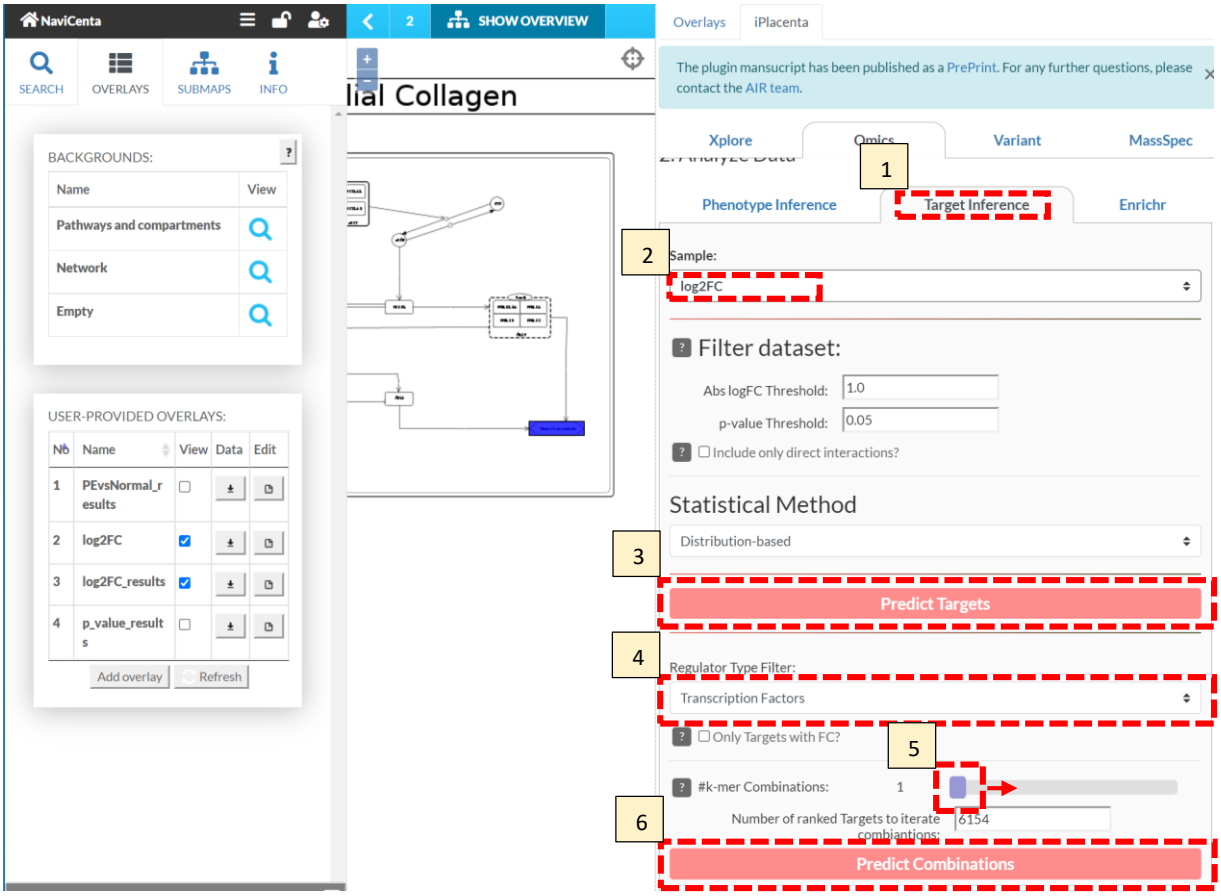
Omics Plugin - Omics II

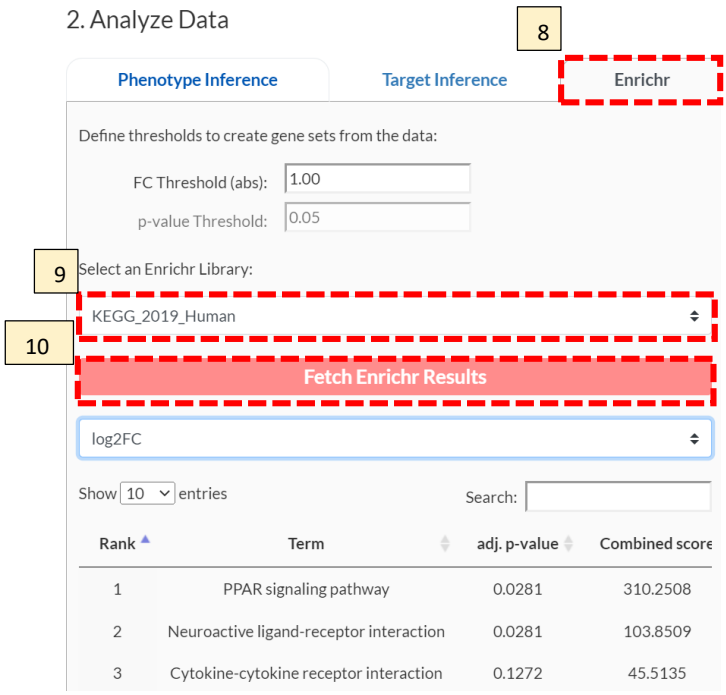
Target Inference:

- [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:

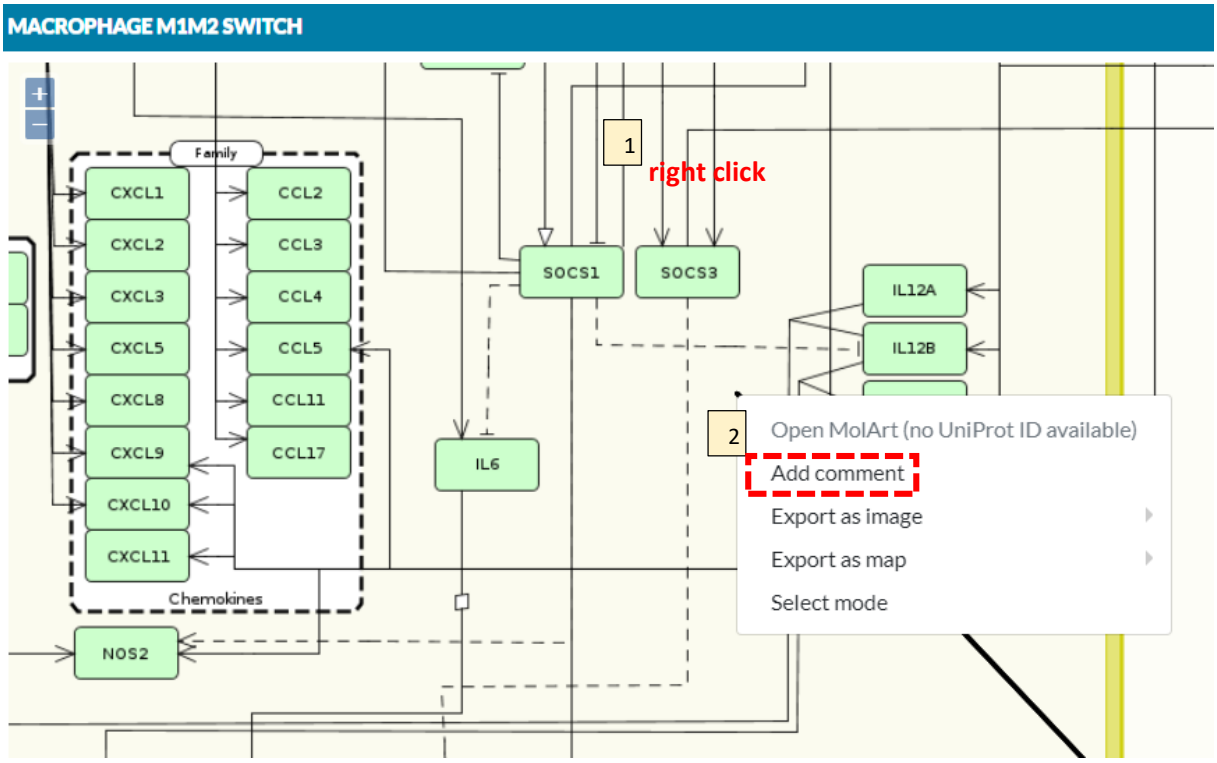
- [8] Navigate to „EnrichR“ tab within the Omics plugin
- [9] Select EnrichR Library
- [10] click “Fetch EnrichR Results”

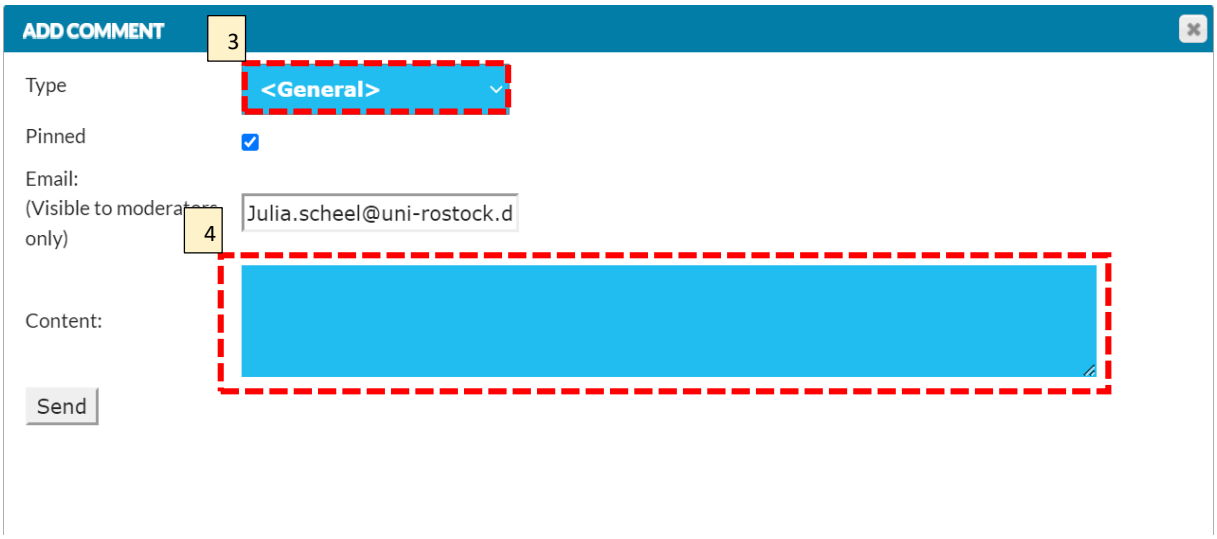



2. Analyze Data
8
Phenotype Inference
Target Inference
Enrichr
Define thresholds to create gene sets from the data:
FC Threshold (abs):
1.00
p-value Threshold:
0.05
9
Select an Enrichr Library:
KEGG_2019_Human
10
Fetch Enrichr Results
log2FC
Show 10 entries
Search:
Rank
Term
adj. p-value
Combined score
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

NaviCenta – 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





Contact: navicenta@uni-rostock.de