

Upload [help](#)

 Browse Supplementary file 2 - test data.txt

File format: SAINT

Process

Select columns for analysis [help](#)

Bait column: Bait

Prey column: PreyGene

Abundance column: AvgSpec

Score column: BFDR

Hide advanced

Submit

Parameters [help](#)

Primary filter:

0.01 • Score cutoff for prey inclusion

Secondary filter:

0.05 • Specify middle score boundary for edge colour coding

Minimum abundance value:

0 • Abundance cutoff for prey inclusion

Maximum abundance value:

50 • Abundance cap for visualization

Control subtraction:

yes

Control column:

ctrlCounts

Normalization:

no

Log transform:

no

Color scale:

blue-black

Clustering [help](#)

Clustering to perform:

hierarchical • Options: hierarchical, biclustering, none

Distance metric:

Canberra (default) • Options: binary, Canberra, Euclidean, Manhattan, maximum and Minkowski

Clustering type:

Ward's (default) • Options: average, centroid, complete, McQuitty, median, single and Ward's

Output [help](#)

Output folder name:

RESULTS • Name for output folder

Supplementary Figure 1 | Snapshot of the available parameters for the dot plot analytical tool. Default options are shown; alternative options can be selected through dropdown menus or values can be typed in. SAINT and CRAPome analytical pipeline outputs are explicitly supported (columns are pre-recognized). When inputting another format, the user will be prompted to specify the score directionality. Parameters and clustering options are defined in the text and in the user manuals (available in **Supplementary Note 1**).