User Manual and Case Studies

Drivergene.net: A Cytoscape app for the identification of driver nodes of large-scale complex networks and case studies in discovery of drug target genes.

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1. Drivergene.net software interface

Drivergene.net is developed in a Java programming environment and is compiled and packaged separately as a plug-in for Cytoscape. Drivergene.net can be run on any system where Java Virtual Machine is installed, including Windows, Ubuntu, and Mac OS.
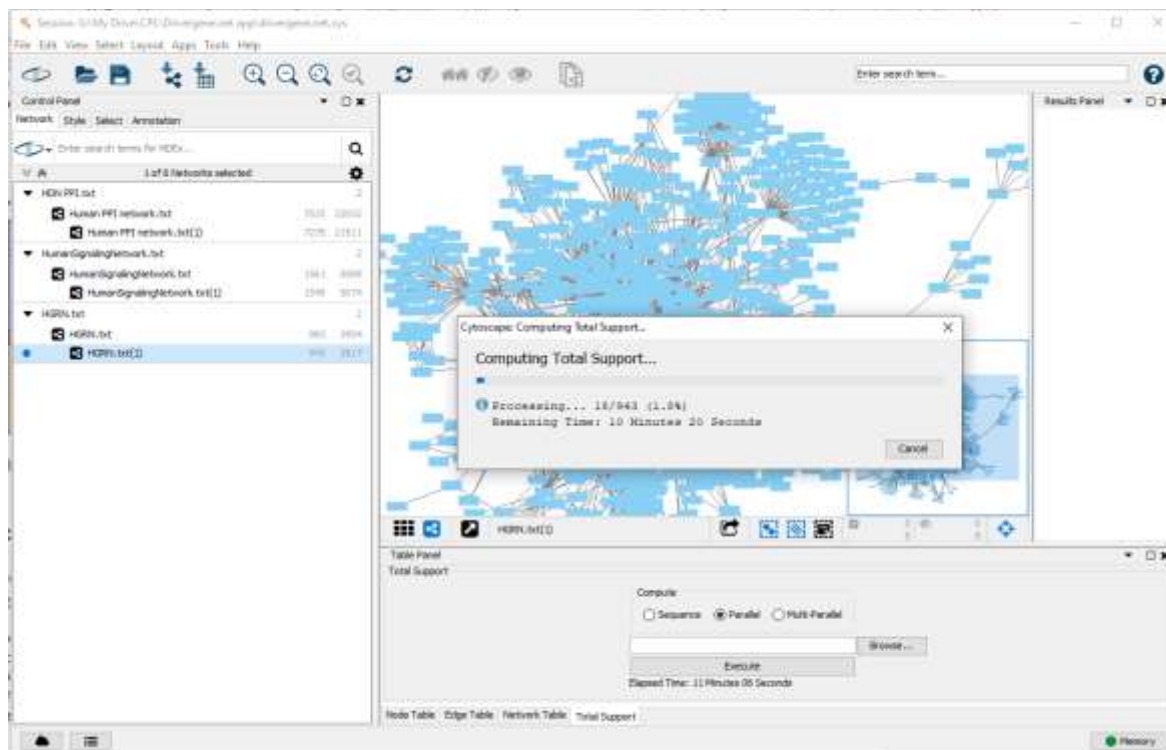

Fig S1. Screenshot of Drivergene.net.

2. Installation

2.1. Install Cytoscape

- Drivergene.net-1.0 can run on Cytoscape 3.7.1 (or later) platform, which has Automation features, therefore the user should download this version at http://cytoscape.org/

- Cytoscape needs JRE to run, therefore download JRE version 8. x or later from

 http://www.oracle.com/technetwork/java/index.html and install it.

- Install Cytoscape to the root folder (e.g., /Applications/Cytoscape_v3.7.1).

2.2. Install the Drivergene.net app

Download the Drivergene.net-1.0.jar file from https://github.com/tinhpd/Drivergene.git

Then, install it by going to Apps →App Manager…. After that, choose Install from file…, then browse the downloaded Drivergene.net-1.0.jar file. (Figure 1).
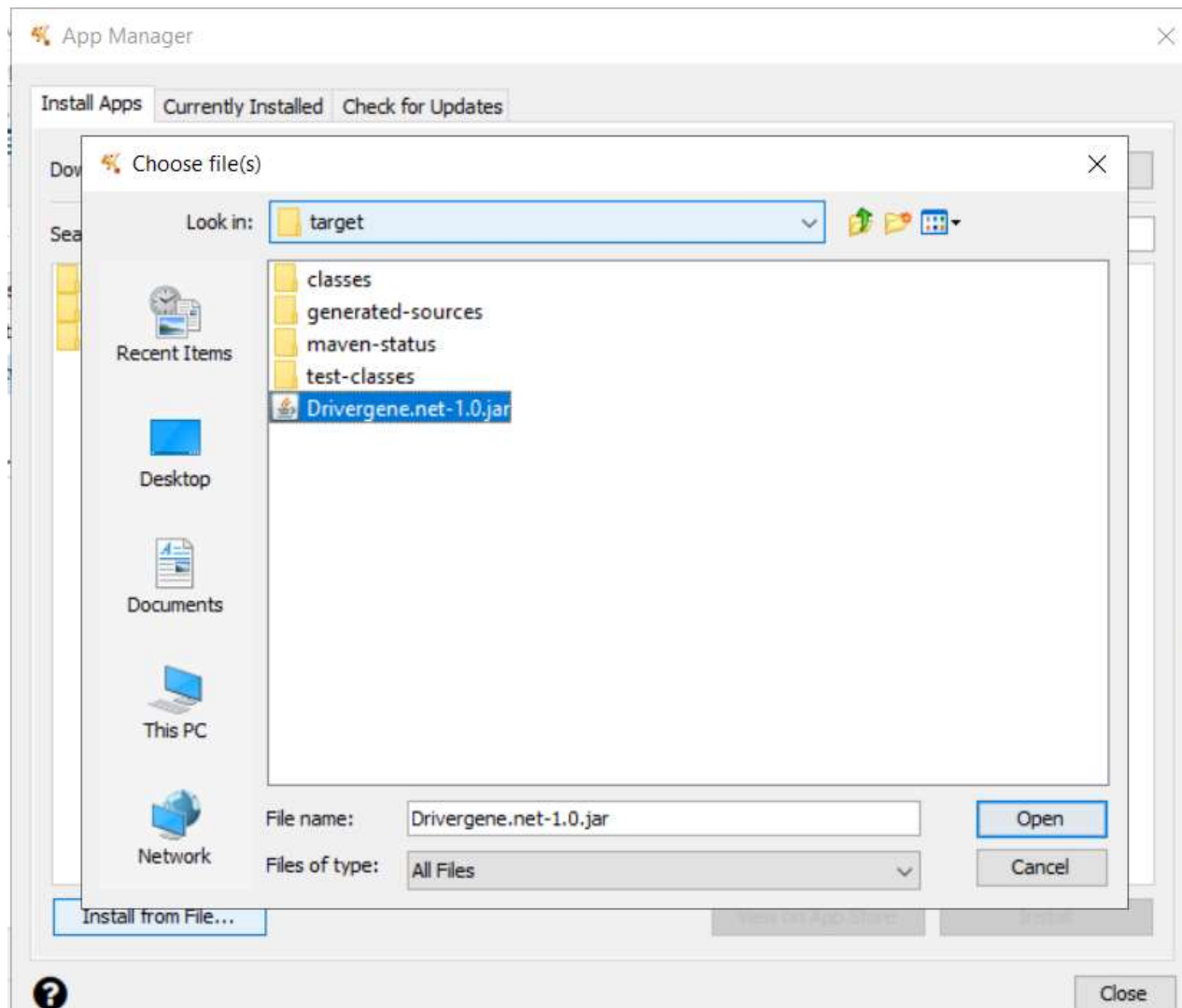
Fig S2. Install Drivergene.net app

Note that: Drivergene.net-1.0 can work on Windows, Ubuntu and Mac OS. The following manual was prepared when running Drivergene.net on Windows.

After installing, Drivergene.net will be automatically loaded in the App menu of Cytoscape. (Figure 2)
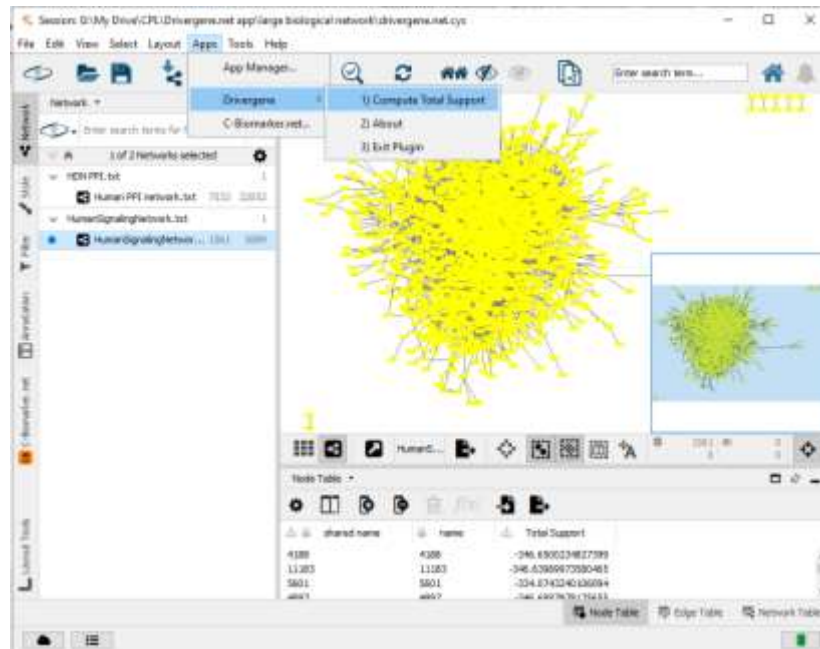
Fig S3. Drivergene.net loaded in the App menu of Cytoscape

3. Import example data

The example data are made available at https://github.com/tinhpd/Drivergene.git

Step 1. Open Cytoscape

Step 2: Load data sets (target gene interactions network)

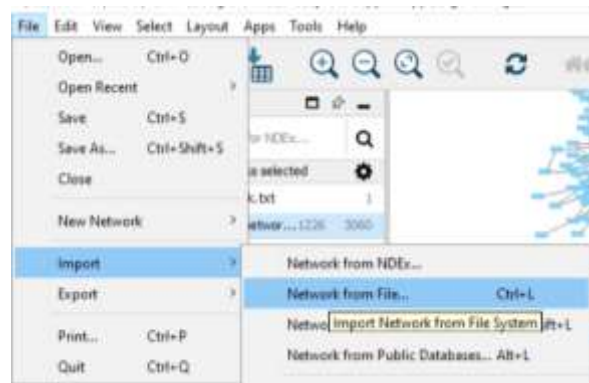- From the Cytoscape menu, select submenu File -> Import -> Network from file (Figure 3)

Fig S4. Load data sets

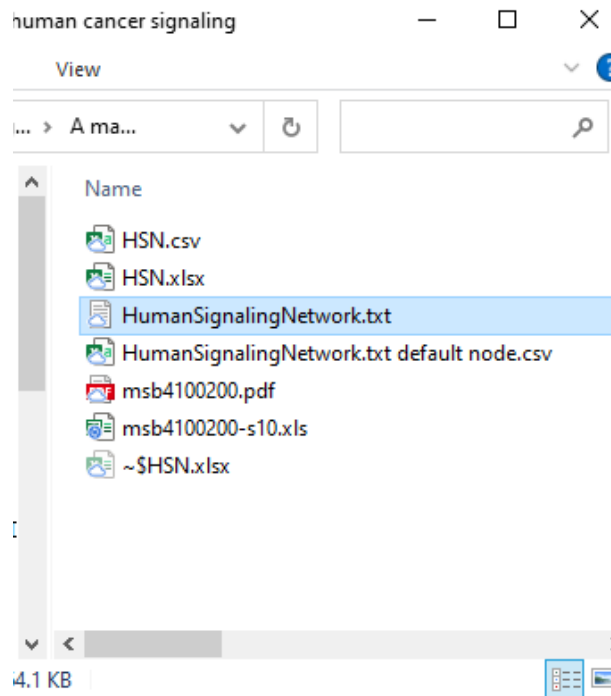- Select file → Open. (Figure 4)

Fig S5. Select and open file

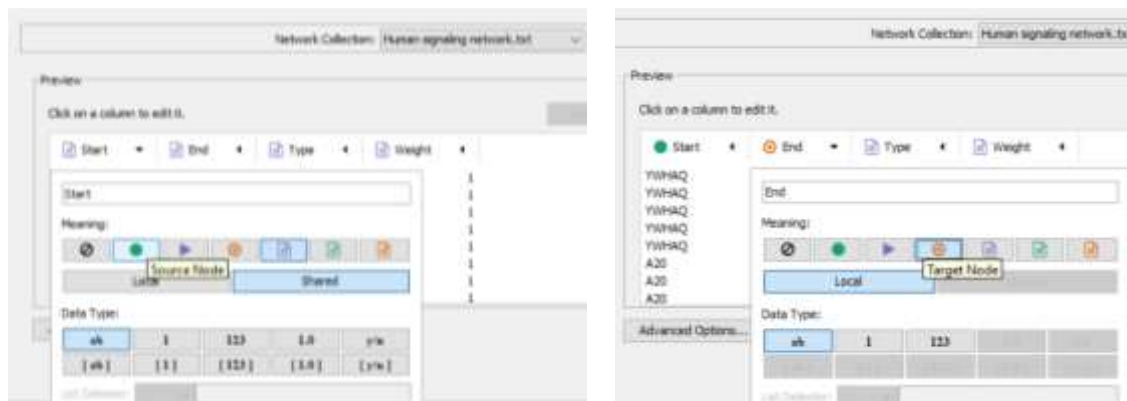- Next, specify the Start and End columns for the data. (Figure 5)

Fig S6. Specify the Start and End columns for the data

4. Compute total support by Drivergene.net

Step 1. Select an example data set from the left panel

Step 2. Select Apps menu of Cytoscape→ submenu Drivergene → 1) Compute Total Support. (Figure 6)

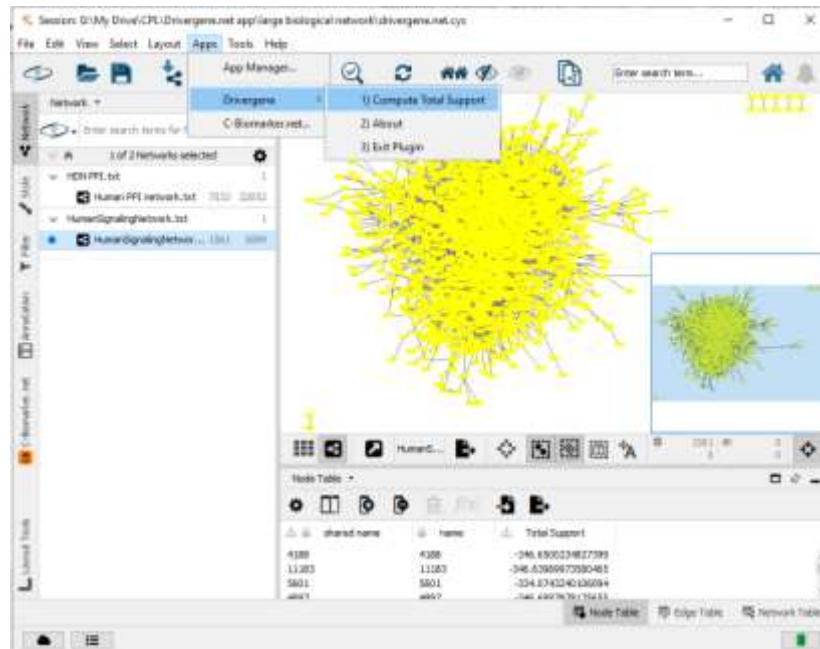**Fig S7**. Drivergene.net loaded in the App menu of Cytoscape

Step 3. Choose an execution mode. (Figure 7)

Drivergene.net provides three execution modes

- Sequence: executing in sequential on CPU

- Parallel: executing in parallel on CPUs

- Multi-Parallel: executing in parallel on all computing devices
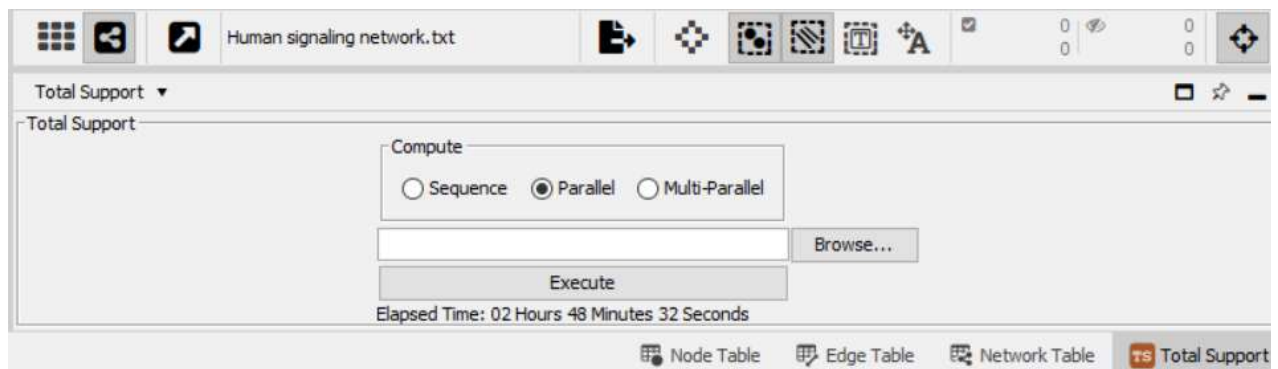
Fig S8. Choose execution modes

Step 4. Click execute for computing
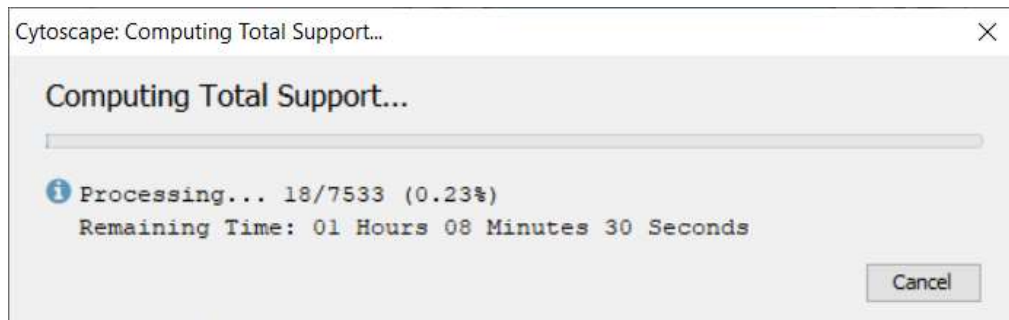
Fig S9. Computing the total support of nodes on the network to each network node.

The actual computing time for the entire network is displayed after the computing is finished. (Figure 9).

Fig S10. The actual computing time for the entire network is displayed

5. Output computation results

After the computing is finished, click Node table tap → Export Table to file. (Figure 10)

Fig S11. Export computation results

Select the path and set the file name, the default file name is the import data file name with the extension is csv. (Figure 11)

Export Table   ✕

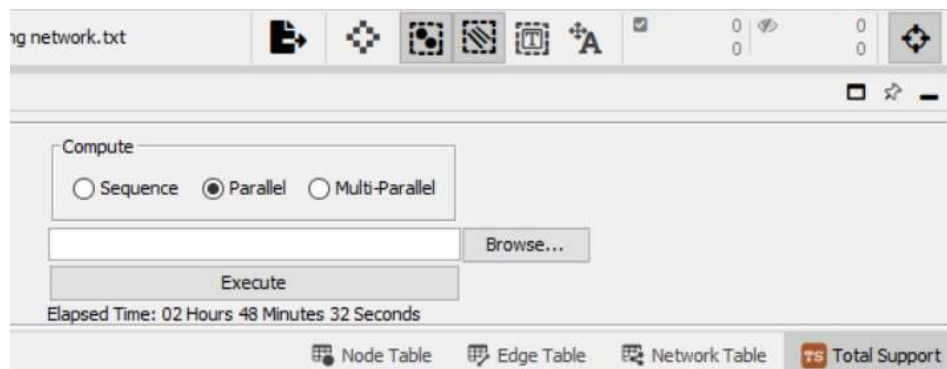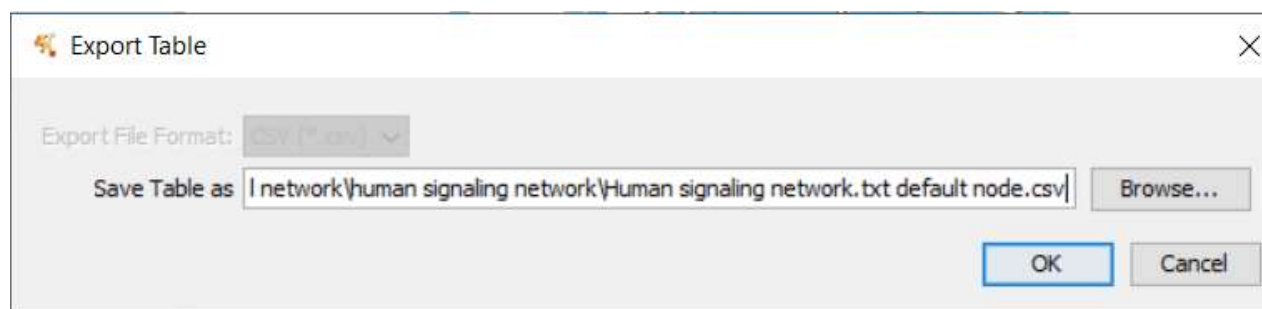Export File Format: csv (*.csv) ▾

Save Table as I network\human signaling network\Human signaling network.txt default node.csv   Browse...

                                                          OK   Cancel

Fig S12. Set the path and file name

6. Output data processing

Step 1. Open file .csv

Step 2. Split data into columns: Select column data → select menu Data → Text to columns → Dilimited → Next → Other → input ';' →Next → Finish

Step 3. Sort data descesding by total support columns value

	B	C
1	Gene nam	Total Support
2	Ca++	-223.4447584
3	AR	-307.1771514
4	SRC	-310.1332151
5	AKT	-315.0082959
6	SHC	-317.6586278
7	SMAD3	-317.8635362
8	GAB2	-317.8745088
9	RAC1	-318.9578427
10	PI3K	-320.6718161
11	SMAD4	-321.9607696
12	PKA	-322.0440754
13	CASP3	-323.5045572
14	ERK2	-323.7599229
15	GRB2	-324.3413582
16	CAMK2A	-324.7593049
17	PKCA	-325.1096534
18	PLCγ	-325.4381322
19	KIT	-325.6493678
20	MEK1	-326.076013
21	p38	-326.2331629
	Human signa	

A

	F	G
1	Name	Totalsupport
2	TP53	-2028.569556
3	GRB2	-2049.635234
4	PXN	-2060.820722
5	TRAF2	-2078.312998
6	CCDC85B	-2078.613248
7	SMAD2	-2080.41373
8	VCL	-2082.345592
9	EGFR	-2090.558222
10	SRC	-2092.64132
11	SMAD3	-2092.666055
12	JUN	-2098.863192
13	LRIF1	-2099.131048
14	FYN	-2099.192528
15	PIK3R1	-2099.822733
16	EWSR1	-2103.868235
17	SMAD9	-2104.398201
18	ESR1	-2104.63275
19	SHC1	-2106.156937
20	AR	-2106.477537
21	MDFI	-2106.745768
	Human PPI netw	

B

	A	B
1	Name	Total Support
2	NFKB1	-104.2534064
3	RELA	-104.5543247
4	JUN	-112.2052259
5	FOS	-128.5002097
6	MYC	-133.259786
7	STAT1	-145.4639074
8	CCND1	-151.3011277
9	CREB1	-151.7486813
10	STAT3	-157.1836446
11	HIF1A	-159.6569218
12	ATF2	-166.9532088
13	RXRA	-167.6705421
14	NFATC1	-170.4160488
15	RXRB	-171.7804319
16	RXRG	-171.7812598
17	EP300	-173.0926174
18	CREBBP	-173.0926175
19	CDKN1A	-174.9512694
20	NFKB2	-175.1906035
21	CREB3L1	-175.2550116
22	CREB3	-175.2550118

C

Fig S13. Sort data descesding by total support value

A) Molecule Signal Network. B) Protein-protein Interaction Network. C) Gene Regulatory Network