

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 app

Drivergene.net is integrated with Cytoscape through Application Programming Interface (API). This software, developed in a Java programming environment, is compiled, and packaged separately as a plug-in for Cytoscape, a popular network analysis software. It can be run on any system with a programming language compiler installed for Java. Details of the features, installation steps, and instructions for use of Drivergene.net software are presented in this document.

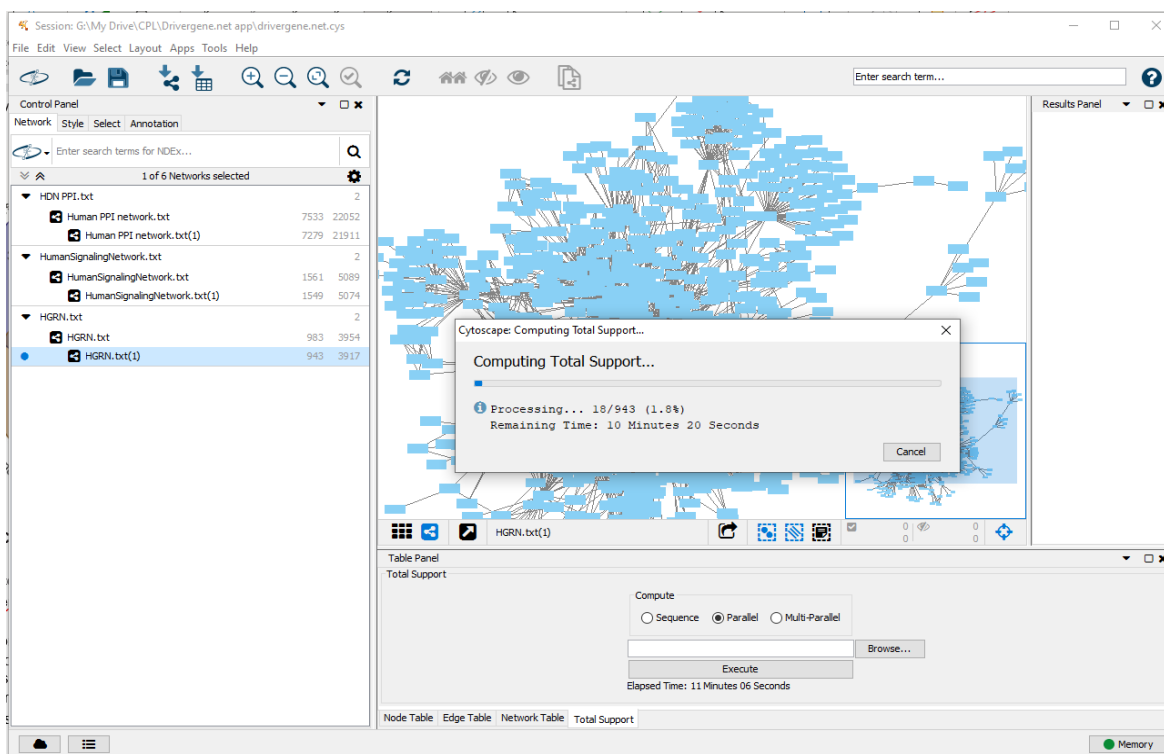


Fig. 1. Screenshot of Drivergene.net.

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).

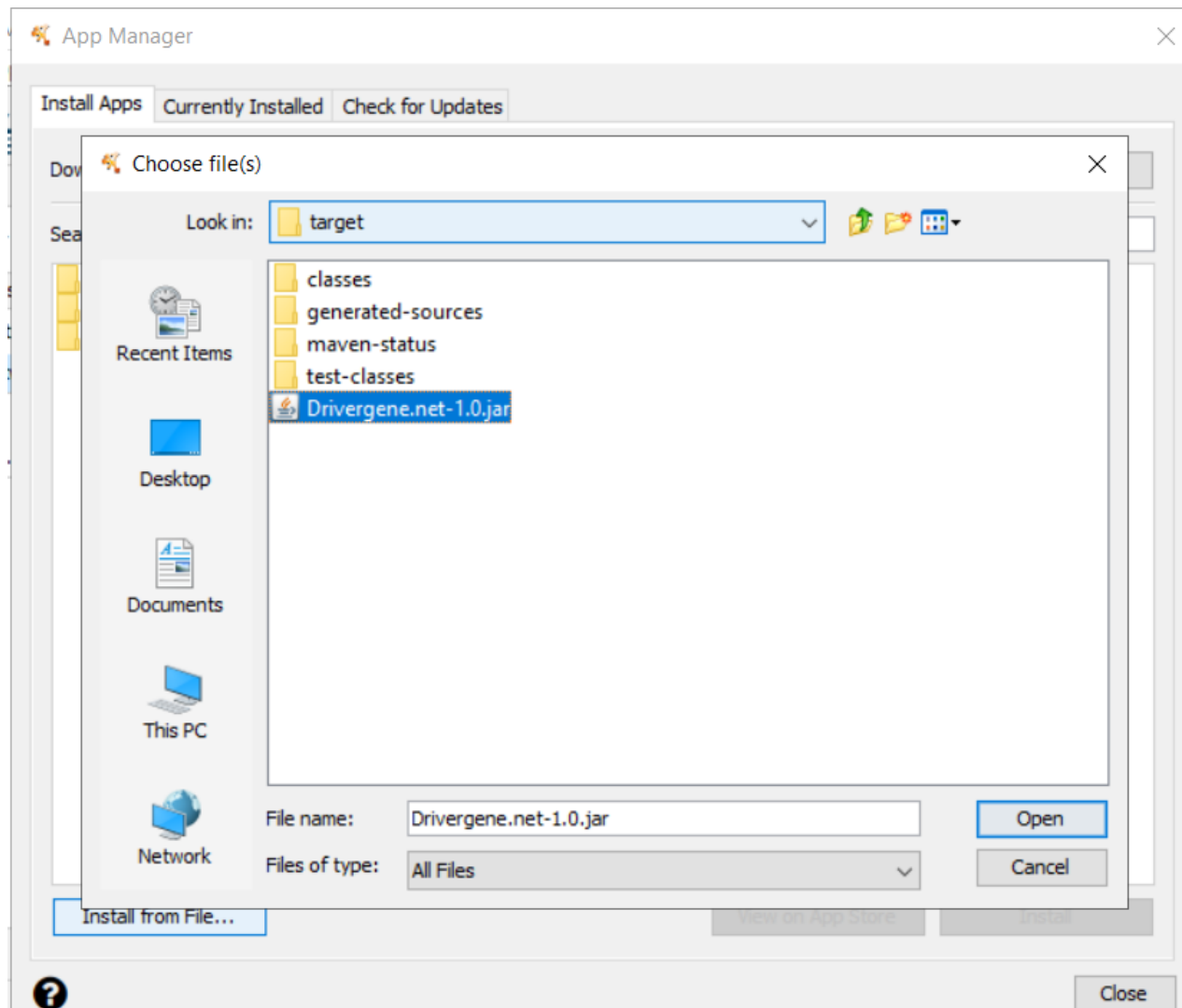


Figure 1. Install Drivergene.net app

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)

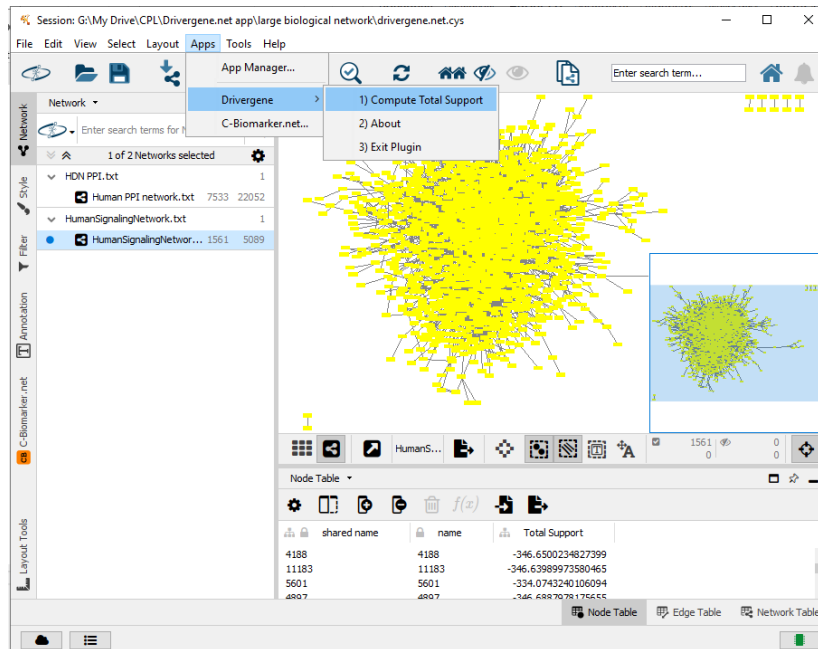


Figure 2. Drivergene.net loaded in the App menu of Cytoscape

2.3. 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)

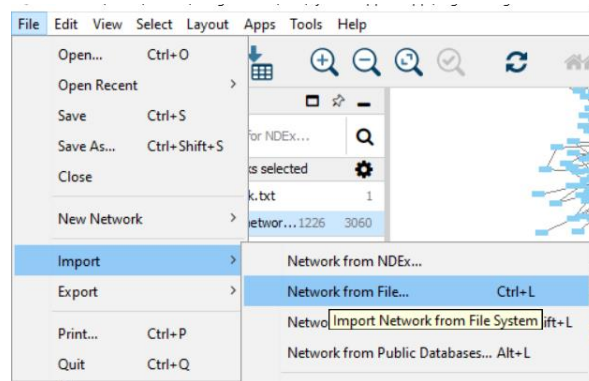


Figure 3. Load data sets

- Select file → Open. (Figure 4)

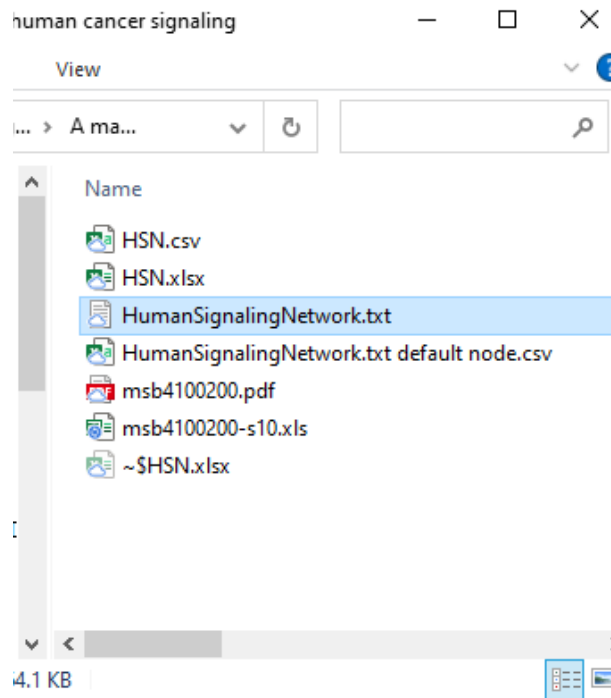


Figure 4. Select and open file

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

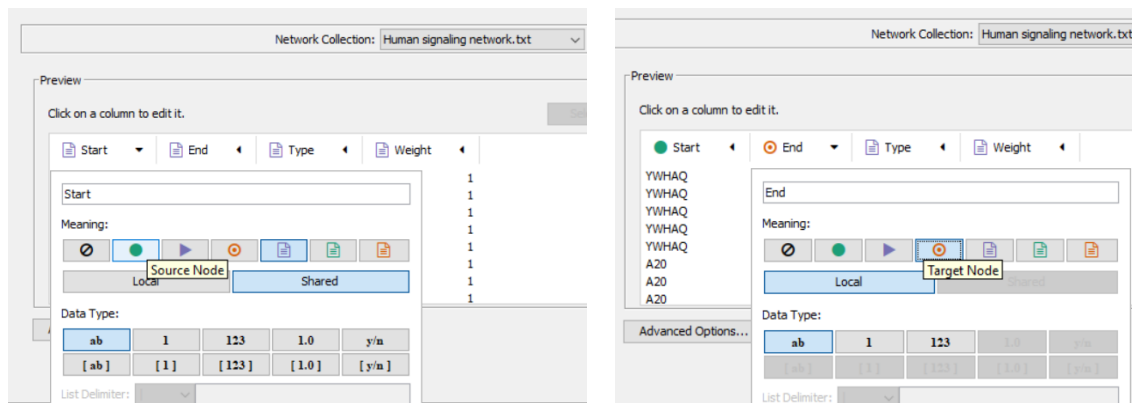


Figure 5. Specify the Start and End columns for the data

2.4. 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)

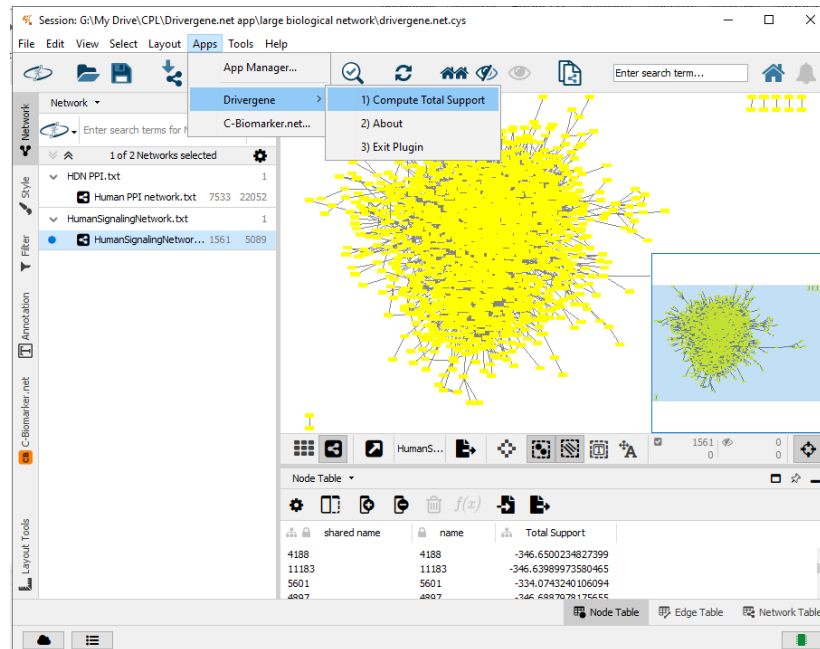


Figure 6. Drivergene.net loaded in the App menu of Cytoscape

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

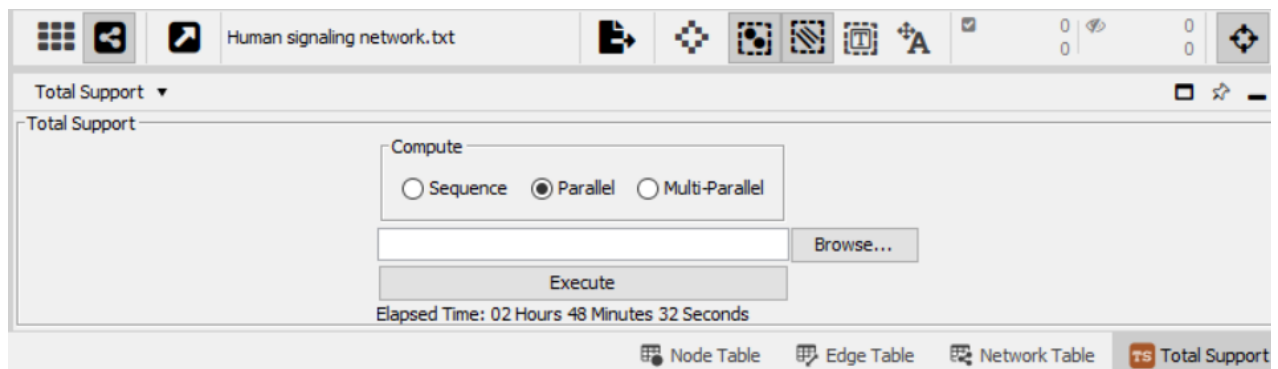


Figure 7. Choose execution modes

Step 4. Click execute for computing



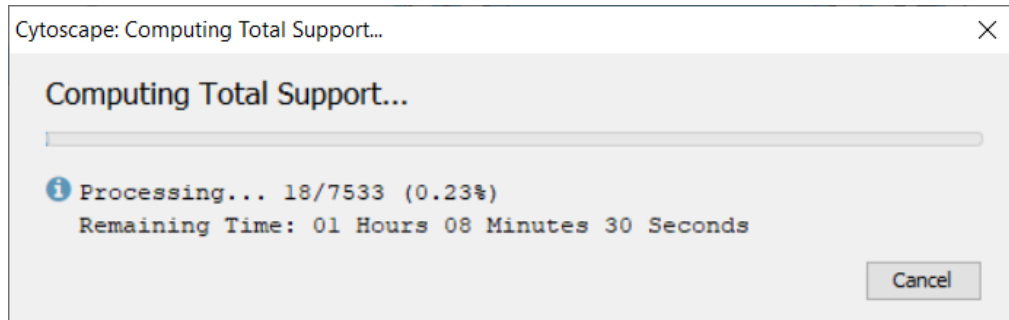
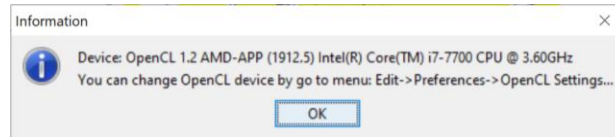


Figure 8. Computing the total support of nodes on the network to each network node.

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

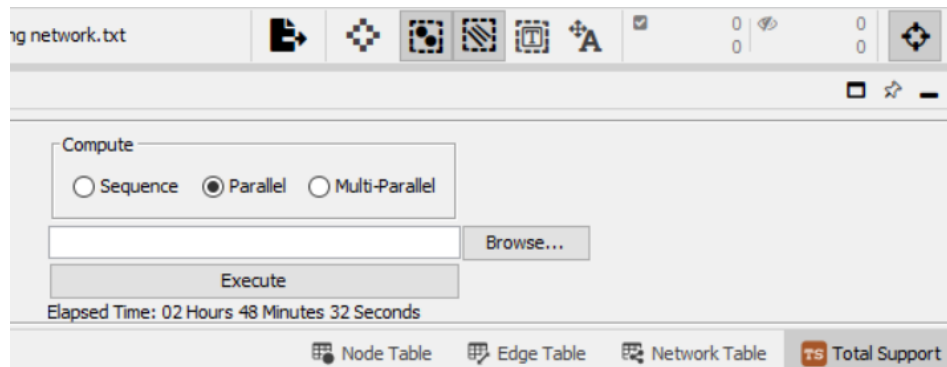


Figure 9. The actual computing time for the entire network is displayed

2.5. Output computation results

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

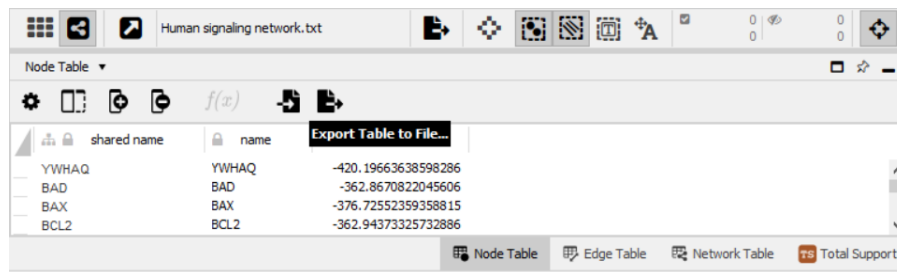


Figure 10. Export computation results

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)

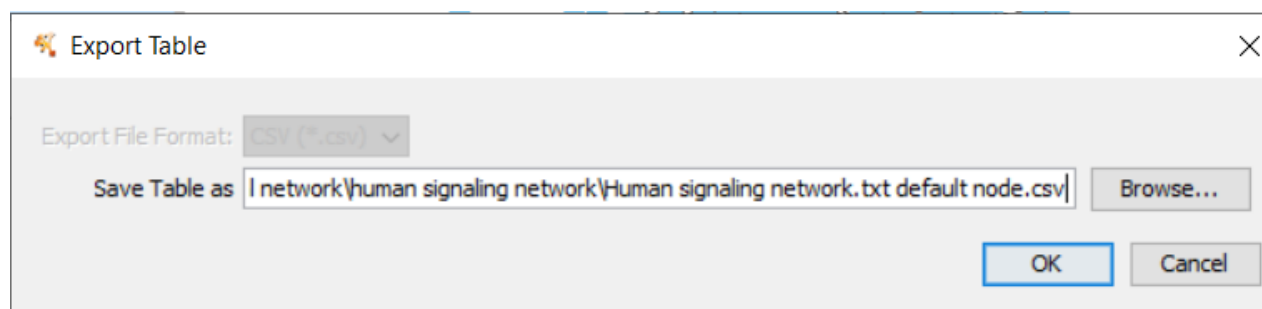


Figure 11. Set the path and file name

2.6. 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 descending by total support columns value

	B	C		F	G		A	B
1	Gene name	Total Support	1	Name	Totalsupport	1	Name	Total Support
2	Ca++	-223.4447584	2	TP53	-2028.569556	2	NFKB1	-104.2534064
3	AR	-307.1771514	3	GRB2	-2049.635234	3	RELA	-104.5543247
4	SRC	-310.1332151	4	PXN	-2060.820722	4	JUN	-112.2052259
5	AKT	-315.0082959	5	TRAF2	-2078.312998	5	FOS	-128.5002097
6	SHC	-317.6586278	6	CCDC85B	-2078.613248	6	MYC	-133.259786
7	SMAD3	-317.8635362	7	SMAD2	-2080.41373	7	STAT1	-145.4639074
8	GAB2	-317.8745088	8	VCL	-2082.345592	8	CCND1	-151.3011277
9	RAC1	-318.9578427	9	EGFR	-2090.558222	9	CREB1	-151.7486813
10	PI3K	-320.6718161	10	SRC	-2092.64132	10	STAT3	-157.1836446
11	SMAD4	-321.9607696	11	SMAD3	-2092.666055	11	HIF1A	-159.6569218
12	PKA	-322.0440754	12	JUN	-2098.863192	12	ATF2	-166.9532088
13	CASP3	-323.5045572	13	LRIF1	-2099.131048	13	RXRA	-167.6705421
14	ERK2	-323.7599229	14	FYN	-2099.192528	14	NFATC1	-170.4160488
15	GRB2	-324.3413582	15	PIK3R1	-2099.822733	15	RXRB	-171.7804319
16	CAMK2A	-324.7593049	16	EWSR1	-2103.868235	16	RXRG	-171.7812598
17	PKCA	-325.1096534	17	SMAD9	-2104.398201	17	EP300	-173.0926174
18	PLCy	-325.4381322	18	ESR1	-2104.63275	18	CREBBP	-173.0926175
19	KIT	-325.6493678	19	SHC1	-2106.156937	19	CDKN1A	-174.9512694
20	MEK1	-326.076013	20	AR	-2106.477537	20	NFKB2	-175.1906035
21	p38	-326.2331629	21	MDFI	-2106.745768	21	CREB3L1	-175.2550116
						22	CREB3	-175.2550118

Figure 13. Sort data descending by total support value

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