The background of the slide features a complex network diagram. It consists of numerous blue circular nodes of varying sizes, interconnected by a dense web of thin, light blue lines. Some nodes are larger and more prominent, while others are smaller and less distinct. The lines represent interactions or connections between the nodes, creating a sense of a dynamic and interconnected system. The overall color scheme is a gradient of blues, from a lighter blue at the top to a darker blue at the bottom.

Reactome Functional Interaction Network and ReactomeFIViz app

Contact: help@reactome.org

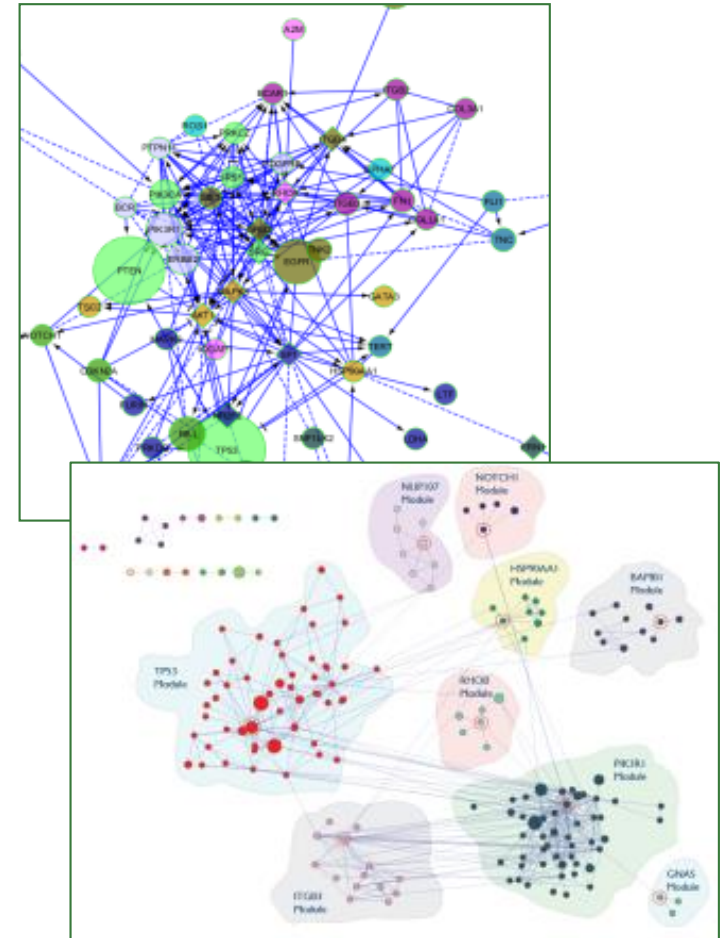


Learning Objectives of Module

- Be able to perform pathway and network-based data analysis using ReactomeFIViz app

Reactome Functional Interaction (FI) Network and ReactomeFIViz app

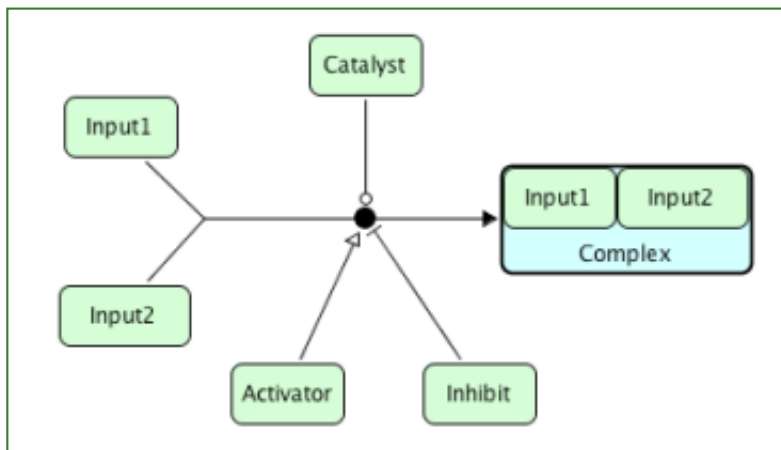
- No single mutated gene is necessary and sufficient to cause cancer.
 - Typically one or two common mutations (e.g. TP53) plus rare mutations.
- Analyzing mutated genes in a network context:
 - reveals relationships among these genes.
 - can elucidate mechanism of action of drivers.
 - facilitates hypothesis generation on roles of these genes in disease phenotype.
- Network analysis reduces hundreds of mutated genes to < dozen mutated pathways.



What is a Functional Interaction?

- Convert reactions in pathways into pair-wise relationships
 - **Functional Interaction:** an interaction in which two proteins are involved in the same reaction as input, catalyst, activator and/or inhibitor, or as components in a complex

Reaction

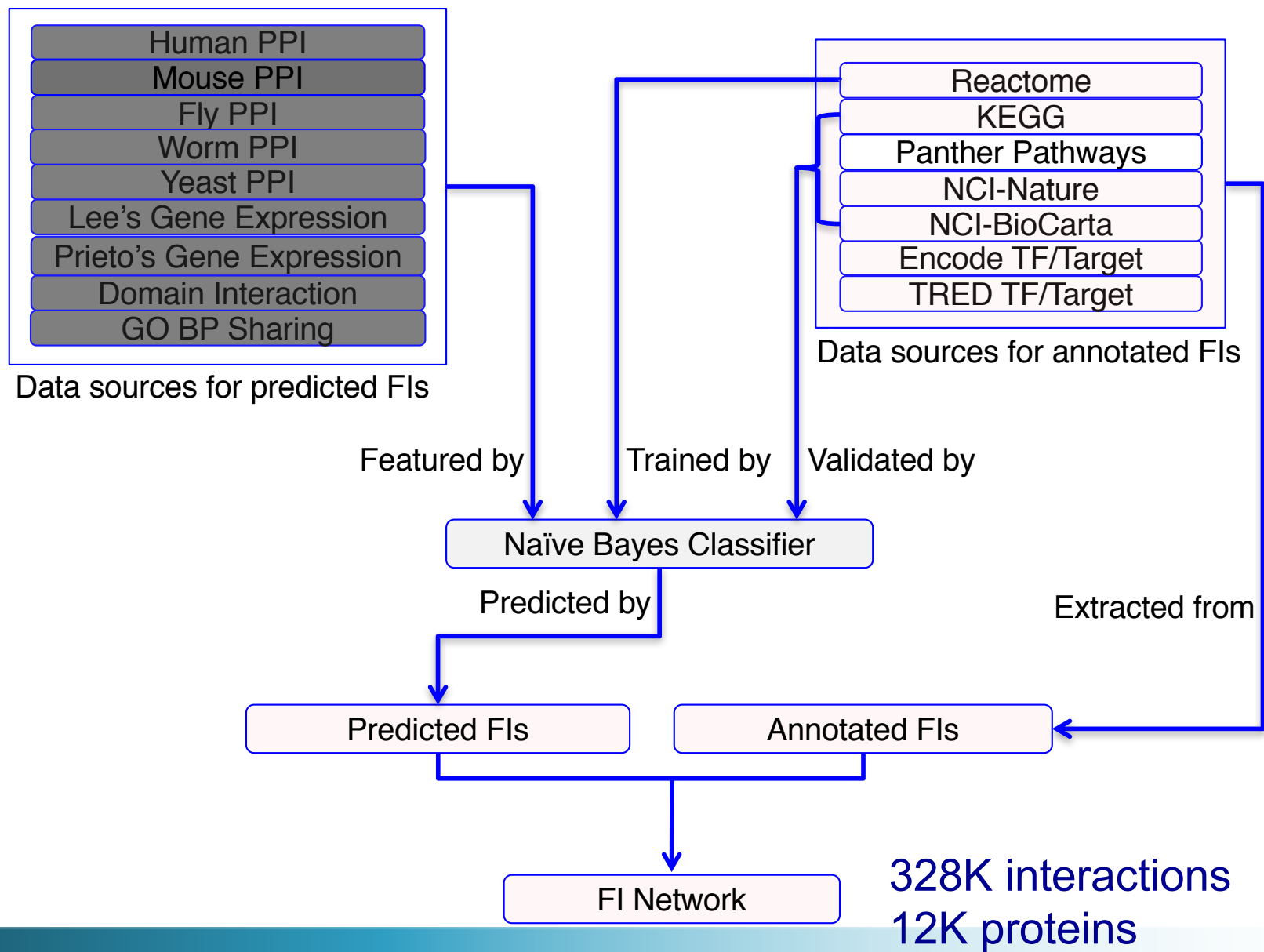


Functional Interactions

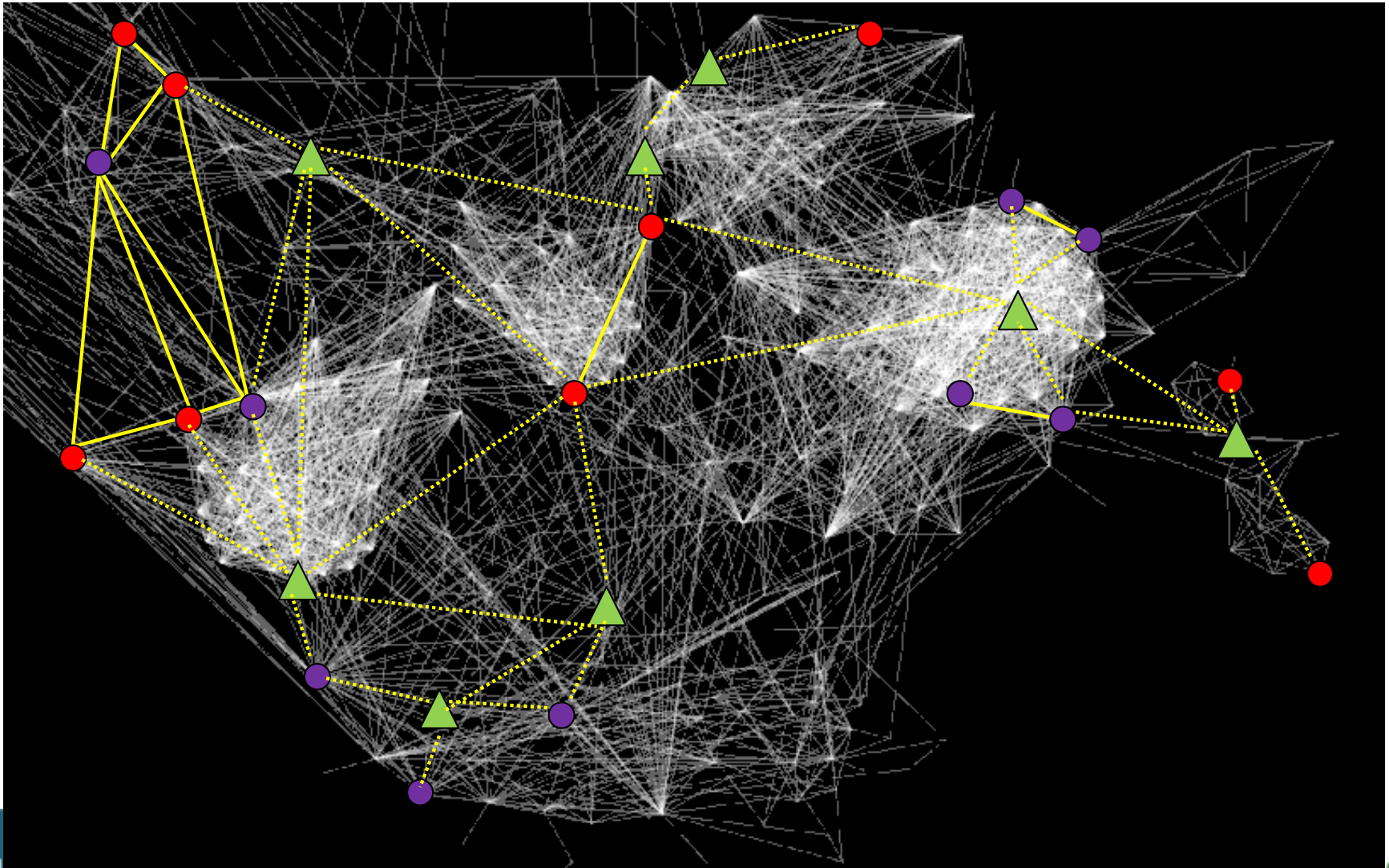
Input1-Input2, Input1-Catalyst,
Input1-Activator, Input1-
Inhibitor, Input2-Catalyst, Input2-
Activator, Input2-Inhibitor,
Catalyst-Activator, Catalyst-
Inhibitor, Activator-Inhibitor

Method and practical application: A human functional protein interaction network and its application to cancer data analysis, [Wu et al. 2010 Genome Biology](#).

Construction of the FI Network



Projecting Experimental Data onto FI Network



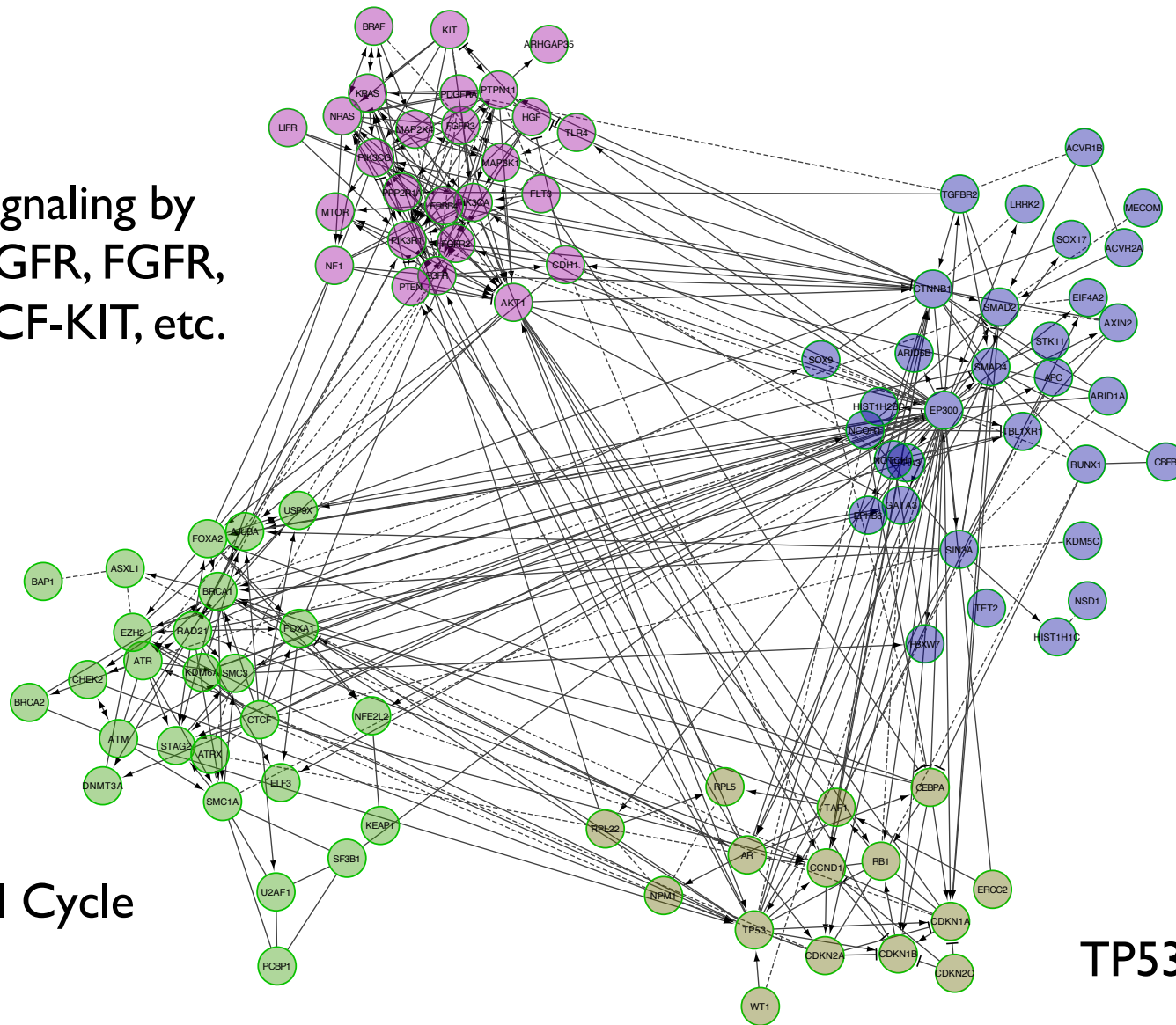
127 Cancer Driver Genes

Signaling by
EGFR, FGFR,
SCF-KIT, etc.

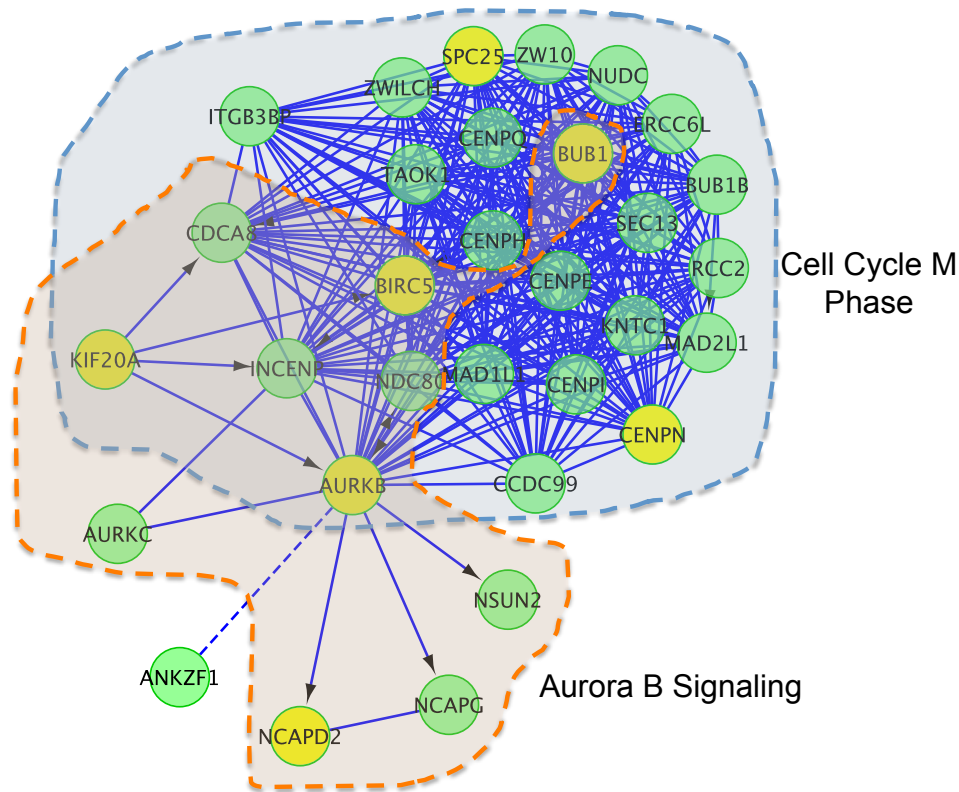
Signaling by
Notch, Wnt,
TGF-beta,
SMAD2/3, etc.

Cell Cycle

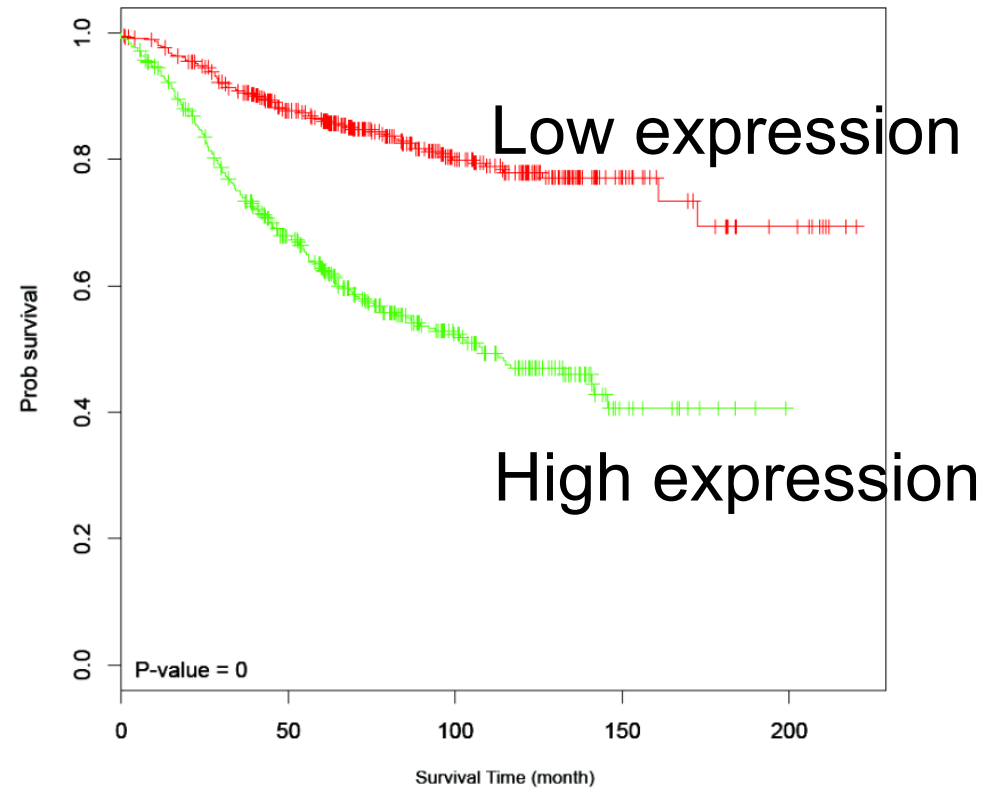
TP53 Pathway



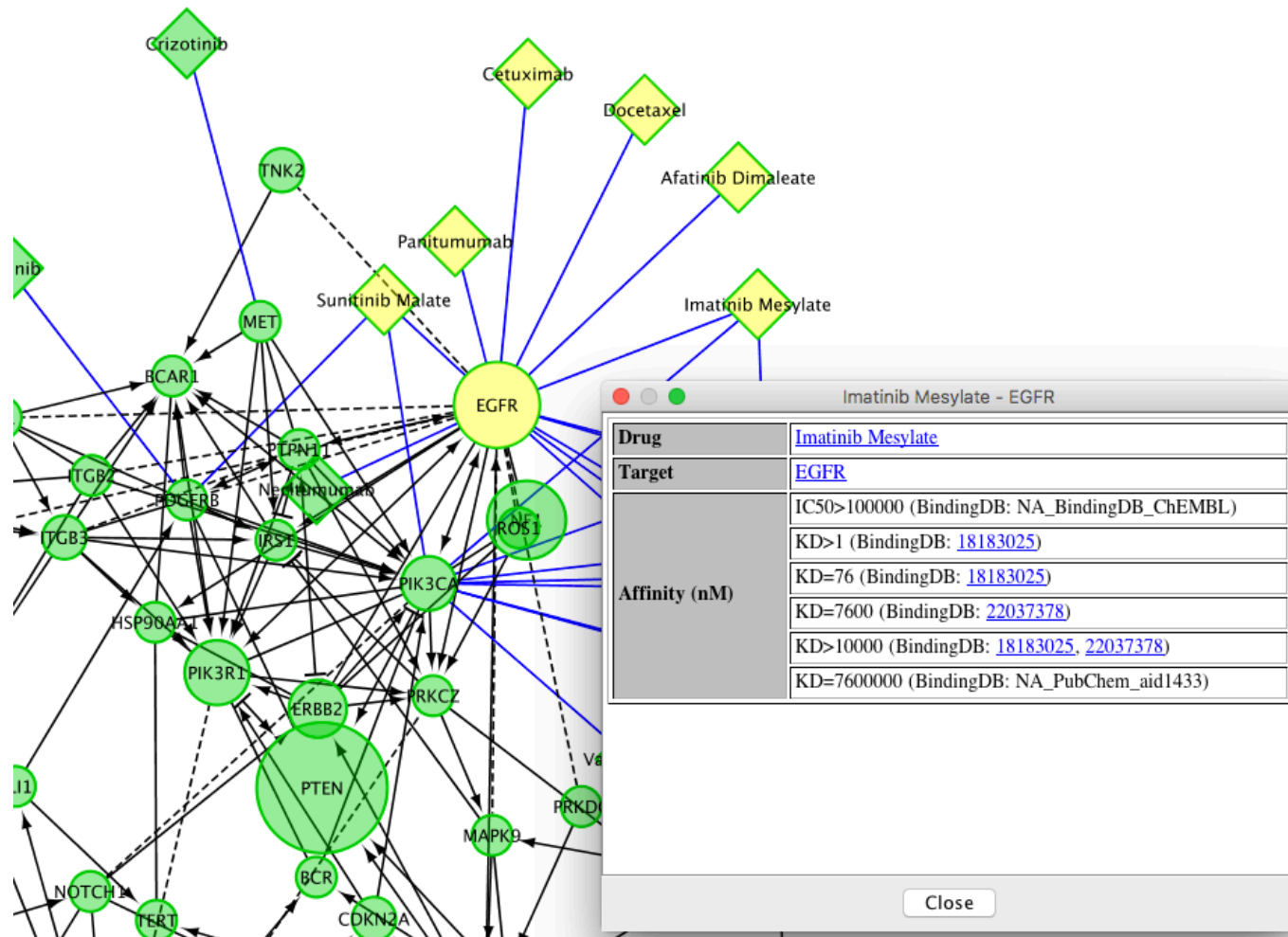
Module-Based Prognostic Biomarker in ER+ Breast Cancer



Measure levels of expression of the genes in this network module



Visualize Cancer Targetome in the Reactome FI Network



TCGA GBM Mutation Profile

3) Pathway-Based Modeling

- Apply list of altered {genes, proteins, RNAs} to biological pathways.
- Preserve detailed biological relationships.
- Attempt to integrate multiple molecular alterations together to yield lists of altered pathway activities.
- Pathway modeling shades into Systems Biology

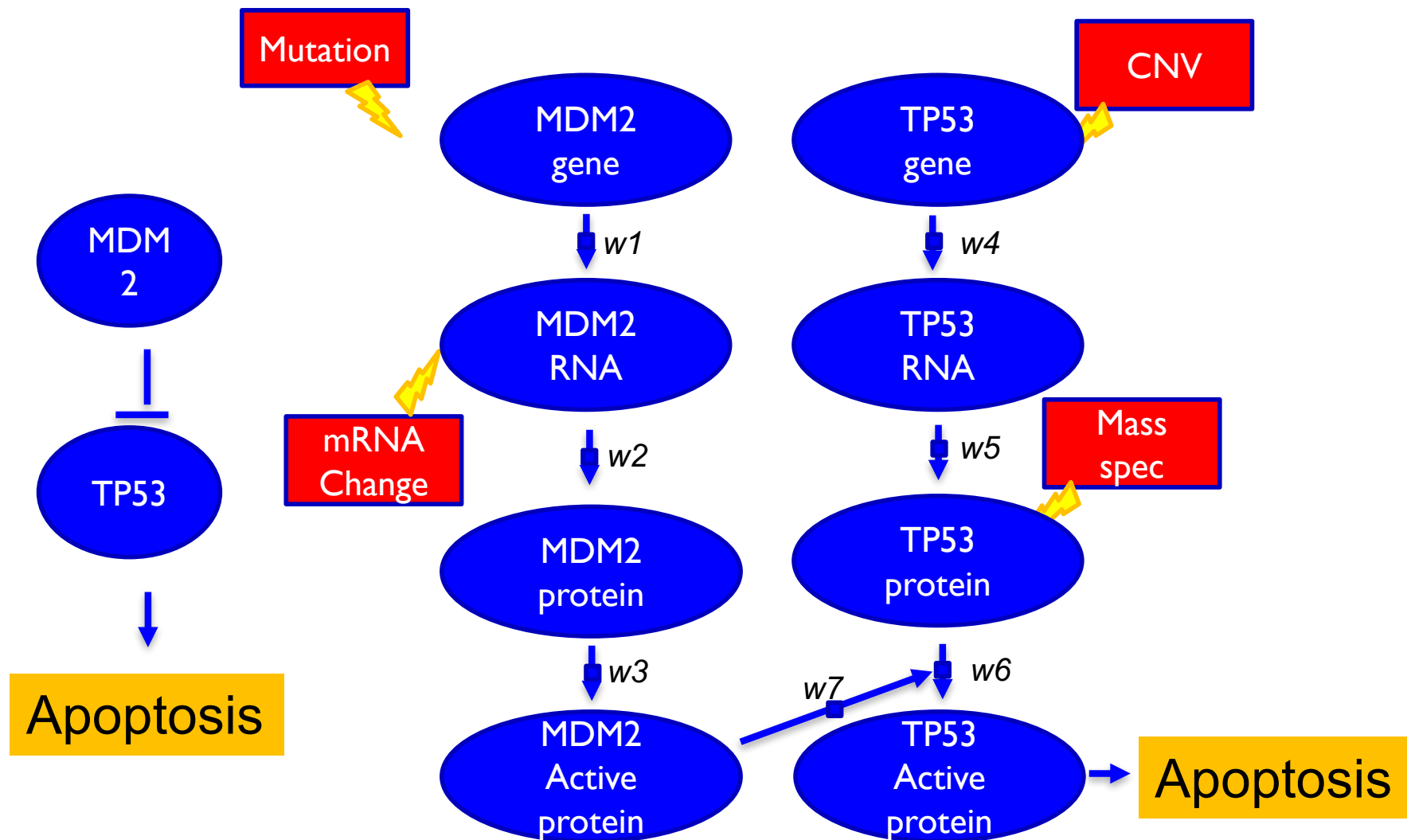
Types of Pathway-Based Modeling

- Partial differential equations/boolean models, e.g. CellNetAnalyzer
 - Mostly suited for biochemical systems (metabolomics)
- Network flow models, e.g. NetPhorest, NetworKIN
 - Mostly suited for kinase cascades (phosphorylation info)
- Transcriptional regulatory network-based reconstruction methods, e.g. ARACNe (expression arrays)
- Probabilistic graph models (PGMs), e.g. PARADIGM
 - Most general form of pathway modeling for cancer analysis at this time.

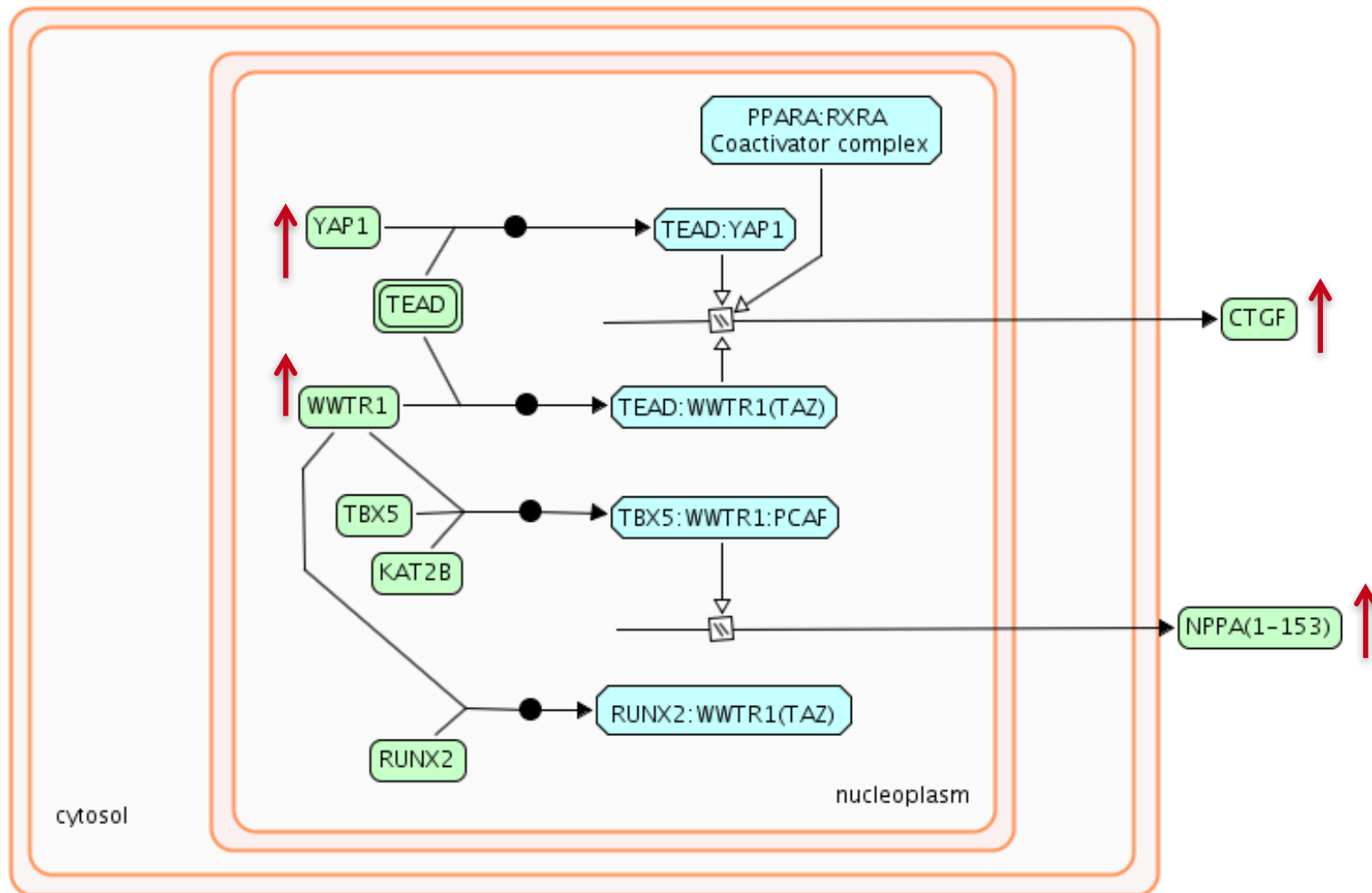
Probabilistic Graphical Model (PGM) based Pathway Analysis

- Attempt to integrate multiple molecular alterations together to yield lists of altered pathway activities.
 - Many omics data types available for one single patient
 - CNV, gene expression, methylation, somatic mutations, etc.
- Pathway and network-based Simulation
 - Find significantly impacted pathways for diseases
 - Link pathway activities to patient phenotypes
 - Predict drug effects: one drug or multiple drugs together?

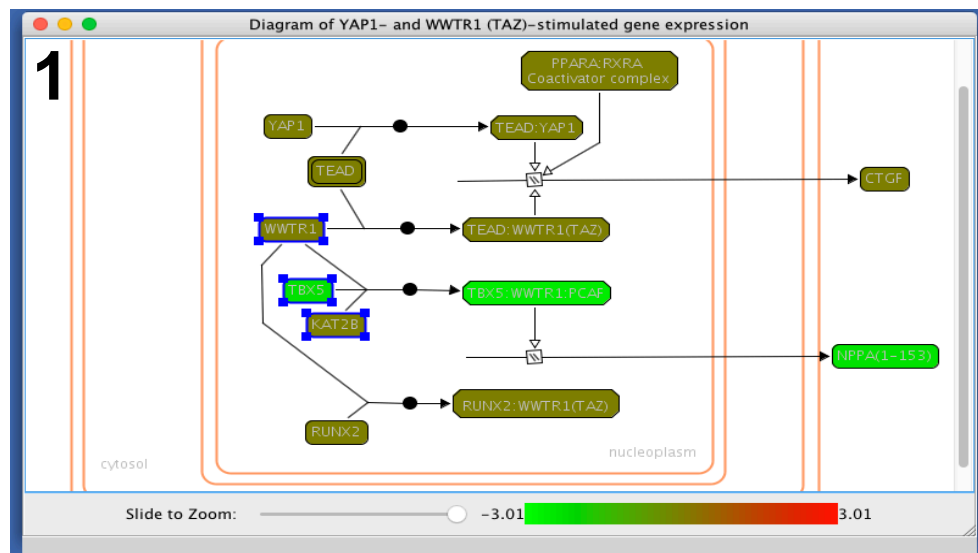
PARADIGM



Probabilistic Graphical Models (PGMs) for Reactome Pathways



PGM-based Single Patient Pathway View



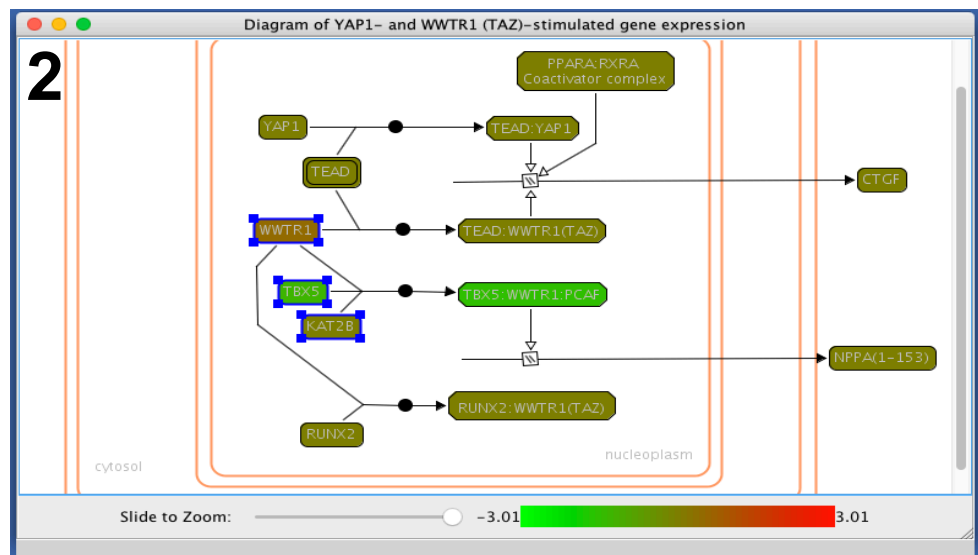
Results Panel

Sample List

Choose sample: TCGA-09-0366

Name	Value	p-value	FDR
TBL1X_CN...	1	0.94	0.98
TBL1X_mRNA...	1	1	1
TBL1XR1_CN...	1	0.96	0.98
TBL1XR1_mRN...	1	1	1
TBX5_CN...	1	0.96	0.98
TBX5_mRNA_EXP	0	0	0.238
TEAD1_CN...	1	0.93	0.98
TEAD1_mRNA...	1	0.99	0.99
TEAD2_CN...	1	0.97	0.98
TEAD2_mRNA...	1	1	1
TEAD3_CN...	1	0.98	0.98
TEAD3_mRNA...	1	0.98	0.98
TEAD4_CN...	1	0.93	0.98
TEAD4_mRNA...	1	0.99	0.99
TGS1_CN...	1	0.94	0.98
TGS1_mRNA_EXP	1	0.99	0.99
WWTR1_CN...	1	0.96	0.98
WWTR1_mRNA...	1	1	1
YAP1_CN...	1	0.96	0.98
YAP1_mRNA_EXP	1	1	1

Inference Observation



Results Panel

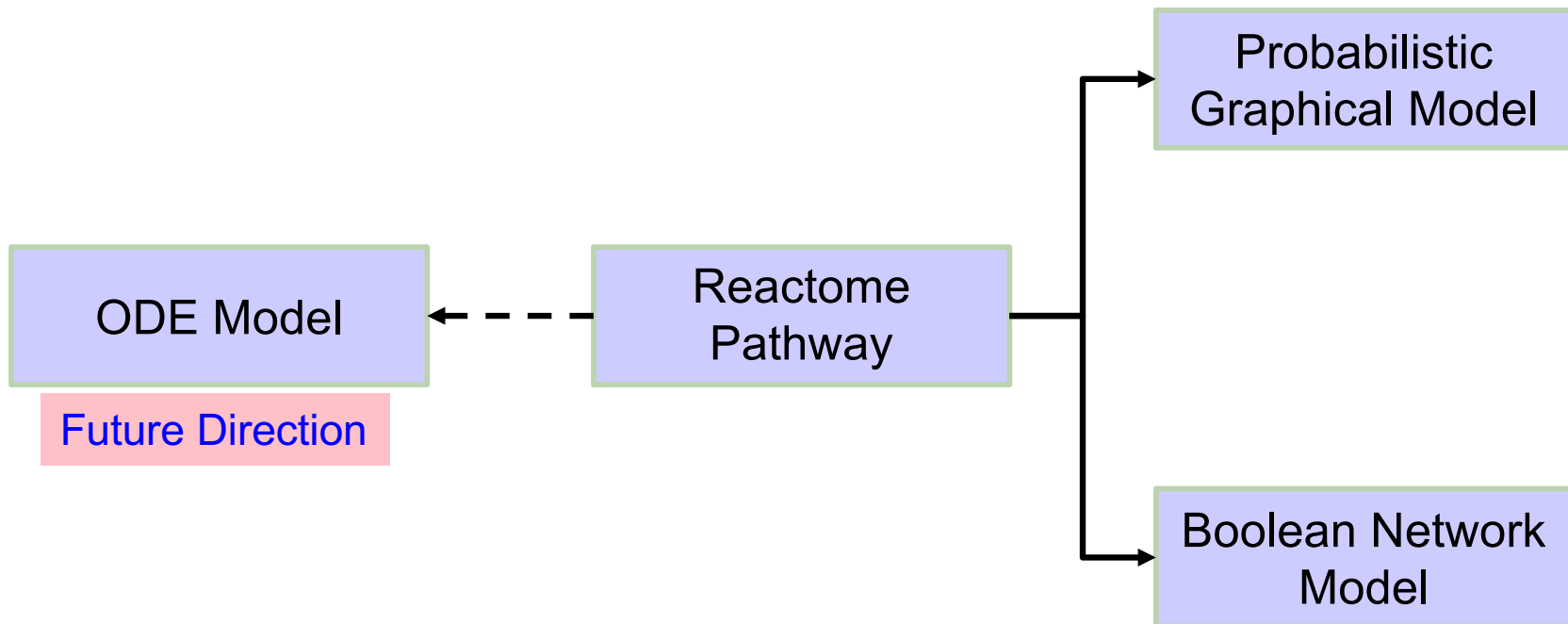
Sample List

Choose sample: TCGA-09-1668

Name	Value	p-value	FDR
TBL1X_CN...	1	0.94	0.98
TBL1X_mRNA...	1	1	1
TBL1XR1_CN...	2	0.04	0.64
TBL1XR1_mRN...	1	1	1
TBX5_CN...	1	0.96	0.98
TBX5_mRNA_EXP	0	0	0.475
TEAD1_CN...	1	0.93	0.98
TEAD1_mRNA...	1	0.99	0.99
TEAD2_CN...	1	0.97	0.98
TEAD2_mRNA...	1	1	1
TEAD3_CN...	1	0.98	0.98
TEAD3_mRNA...	1	0.98	0.98
TEAD4_CN...	1	0.93	0.98
TEAD4_mRNA...	1	0.99	0.99
TGS1_CN...	1	0.94	0.98
TGS1_mRNA_EXP	1	0.99	0.99
WWTR1_CN...	2	0.04	0.64
WWTR1_mRNA...	1	1	1
YAP1_CN...	1	0.96	0.98
YAP1_mRNA_EXP	1	1	1

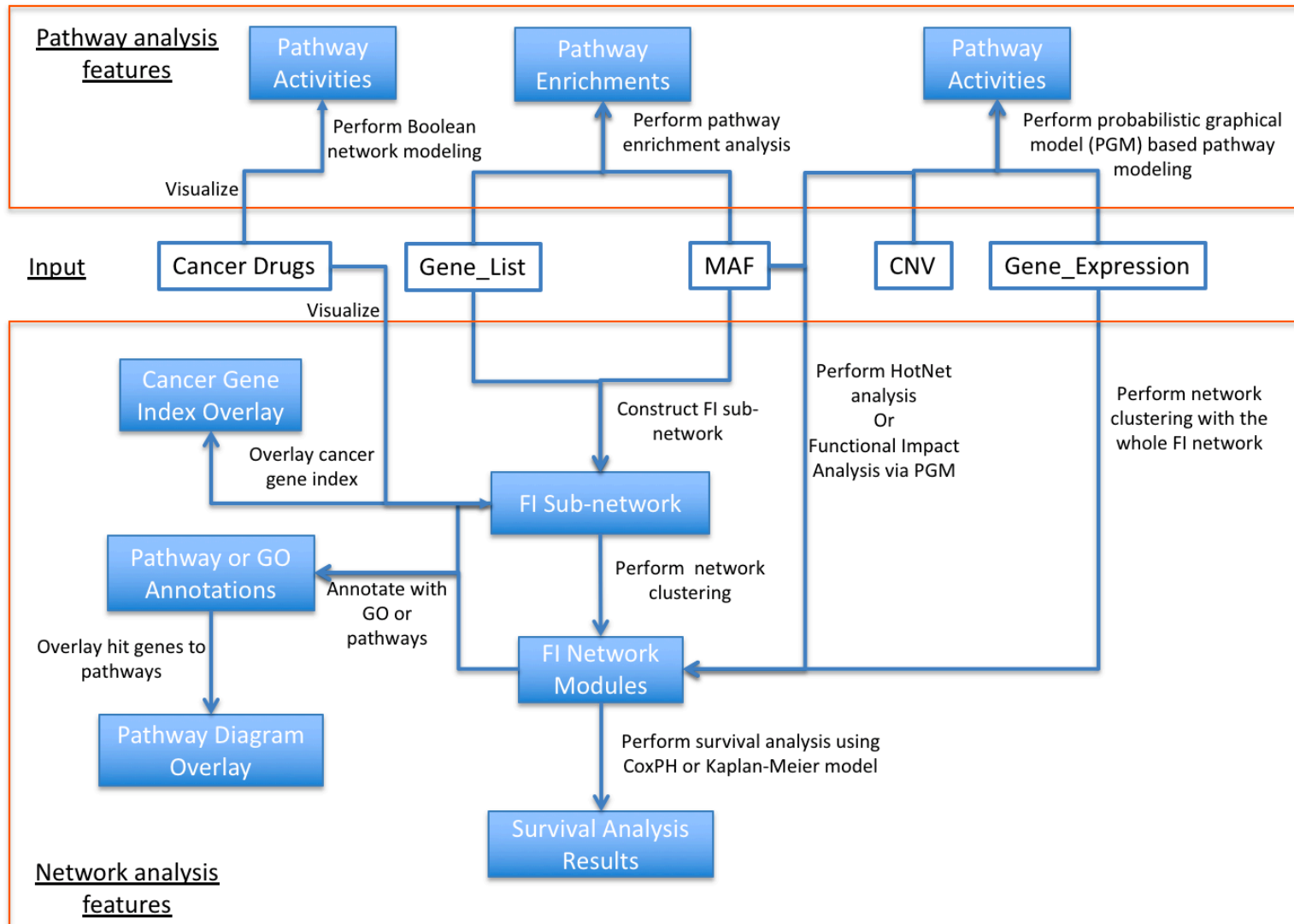
Inference Observation

Building Quantitative Models for Reactome Pathways

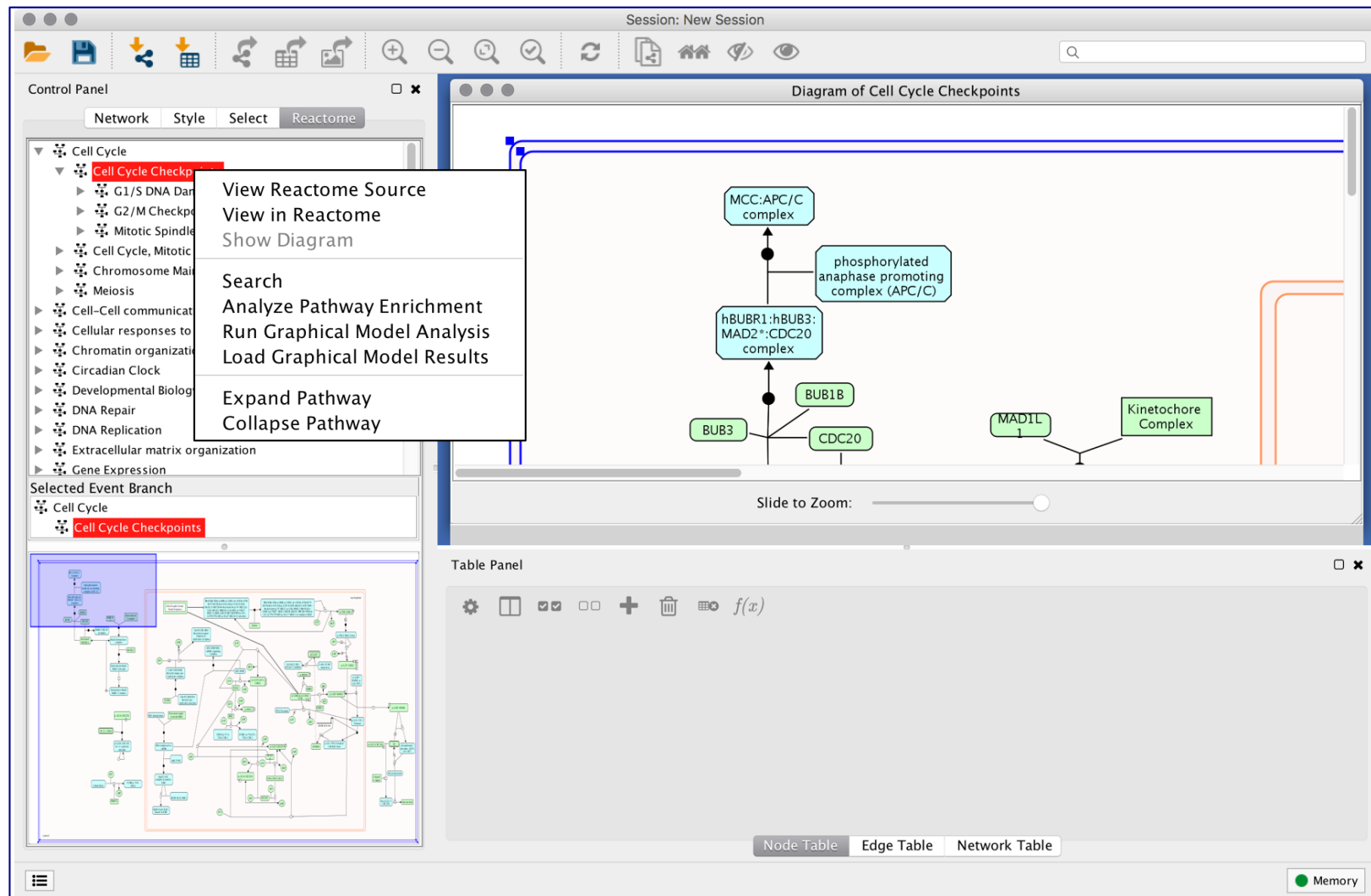


Tutorial

Major Features in ReactomeFIViz



AI) Reactome Pathway Enrichment Analysis



Displaying Reactome Pathways in the FI Network View

Session: New Session

Control Panel

Network Style Select Reactome

Cell Cycle

- Cell Cycle Checkpoints
 - G1/S DNA Damage Checkpoints
 - G2/M Checkpoints
 - Mitotic Spindle Checkpoint**
- Cell Cycle, Mitotic
- Chromosome Maintenance
- Meiosis
- Cell-Cell communication
- Cellular responses to stress
- Chromatin organization
- Circadian Clock
- Developmental Biology
- DNA Repair
- DNA Replication
- Extracellular matrix organization

Selected Event Branch

Cell Cycle

- Cell Cycle Checkpoints
 - Mitotic Spindle Checkpoint**

Slide to Zoom:

FI Network for Diagram of Cell Cycle Checkpoints

Convert to FI Network

Run Boolean Network Analysis

Remove Analysis Results

Run Graphical Model Analysis

Show Gene Level Analysis Results

Show Observation

Save Analysis Results

Open Analysis Results

Fetch Cancer Drugs

Filter Cancer Drugs

Search Entities

Search Reactions

Export Diagram

Table Panel

shared name	name	module	commonName
BABAM1	BABAM1		BABAM1
BRCA1	BRCA1		BRCA1
PSMB1	PSMB1		PSMB1
PSME2	PSME2		PSME2
HERC2	HERC2		HERC2
HIST3H2BB	HIST3H2BB		HIST3H2BB
PSME1	PSME1		PSME1
HIST1H2BO	HIST1H2BO		HIST1H2BO
KDM4B	KDM4B		KDM4B

Node Table Edge Table

Pathway Enrichment Analysis

Session: New Session

Control Panel

Network Style Select Reactome

FDR: ☐ ≥ 0.1 ☐ ≥ 0.01 ☐ ≥ 0.001 ☐ < 0.001

Interleukin-7 signaling (FDR: 0.091)

- IL7 binds HGF(495-728) to form PPBSF
- IL7R binds JAK1
- IL2RG binds JAK3
- IL7 binds IL7R:JAK1
- IL7:IL7R:JAK1 binds IL7
- IL7R is phosphorylated
- IL7:p-Y449-IL7R:JAK1
- IL7:p-Y449-IL7R:JAK1
- IL7:p-Y449-IL7R:JAK1
- Interleukin-11 receptor a
- Interleukin-11 receptor a
- IL27 is a dimer of IL27A a
- IL27 binds IL27RA:gp130

View Reactome Source
View in Reactome
Show Diagram

Search
Analyze Pathway Enrichment
Run Graphical Model Analysis
Load Graphical Model Results

Expand Pathway
Collapse Pathway

Diagram of Interleukin-7 signaling and JAK3 deficiency causes SCID (IL7R)

Reactome Pathway Enrichment Analysis

Gene Set Loading

Choose a gene set file:

Specify file format: ☒ One gene per line
☐ Comma delimited (e.g. TP53, EGFR)
☐ Tab delimited (e.g. TP53 EGFR)

OK Cancel

Table Panel

Apply Filters: FDR 1.0

ReactomePathway	RatioOfProteinInPat...	NumberOfProteinIn...	ProteinFromGeneSet	P-value	FDR	HitGenes
Laminin interactions	0.0032	23	5	0.0111	0.0890	ITGA6,LAMC1,LAMB...
Activation of Rac	0.0011	8	3	0.0114	0.0911	ROBO1,SOS1,SLIT2
Interleukin-7 signali...	0.0011	8	3	0.0114	0.0911	IL7R,HGF,JAK1
CREB phosphorylati...	0.0021	15	4	0.0115	0.0917	GRIN2B,GRIN2A,AKA...
Mismatch Repair	0.0021	15	4	0.0115	0.0917	RPA1,POLD3,MLH1,...
M Phase	0.0315	225	22	0.0117	0.0937	KNTC1,NDE1,UBC,A...
GABA receptor activ...	0.0074	53	8	0.0124	0.0993	GABBR2,GNAT3,GAB...
Mitotic Prometaphase	0.0139	99	12	0.0131	0.1016	KNTC1,NDE1,PDS5B,...
Digestion of dietary ...	0.0004	3	2	0.0132	0.1016	MGAM,LCT
Mitotic Anaphase	0.0227	162	17	0.0136	0.1016	KNTC1,NDE1,UBC,A...
TGF-beta receptor s...	0.0022	16	4	0.0142	0.1016	UBC,PARD3,TGFB2,...

Node Table Edge Table Network Table Reactome Pathway Enrichment

Memory

Visualize Cancer Targetome in Reactome Pathways

Session: New Session

Control Panel

Network Style Select

Cell Cycle

- Cell Cycle Checkpoints
 - G1/S DNA Damage Checkpoints
 - G2/M Checkpoints
 - G2/M DNA damage checkpoint
 - G2/M DNA replication checkpoint
 - Activation of ATR in response to replication stress
 - Stalling of DNA replication fork and RPA binding
 - Binding of ATR-ATRIP to the RPA-ssDNA complex
 - Recruitment of Rad17-RFC complex to DNA
 - Loading of claspin onto DNA during replication or
 - Activation of claspin
 - Recruitment and activation of Chk1
 - Phosphorylation of Cdc25A at Ser-123 by Chk1
 - Phosphorylation of Cdc25C at Ser 216 by Chk1
 - GTSE1 binds TP53
 - GTSE1 promotes translocation of TP53 to the cytosol
 - GTSE1 facilitates proteasome-mediated degradation of
- Mitotic Spindle Checkpoint
- Cell Cycle, Mitotic
- Chromosome Maintenance
- Meiosis
- Cell-Cell communication
- Cellular responses to stress
- Chromatin organization
- Circadian Clock
- Developmental Biology
- DNA Repair
- DNA Replication
- Extracellular matrix organization
- Gene Expression
- Hemostasis
- Immune System
- Mitophagy
- Metabolism

Selected Event Branch

- Cell Cycle
 - Cell Cycle Checkpoints

Diagram of Cell Cycle Checkpoints

Slide to Zoom:

Table Panel

Drag table files here

Node Table Edge Table

Memory

Convert to FI Network

Run Boolean Network Analysis

Remove Analysis Results

Run Graphical Model Analysis

Show Gene Level Analysis Results

Show Observation

Save Analysis Results

Open Analysis Results

Fetch Cancer Drugs

Filter Cancer Drugs

Load Mechismo Results

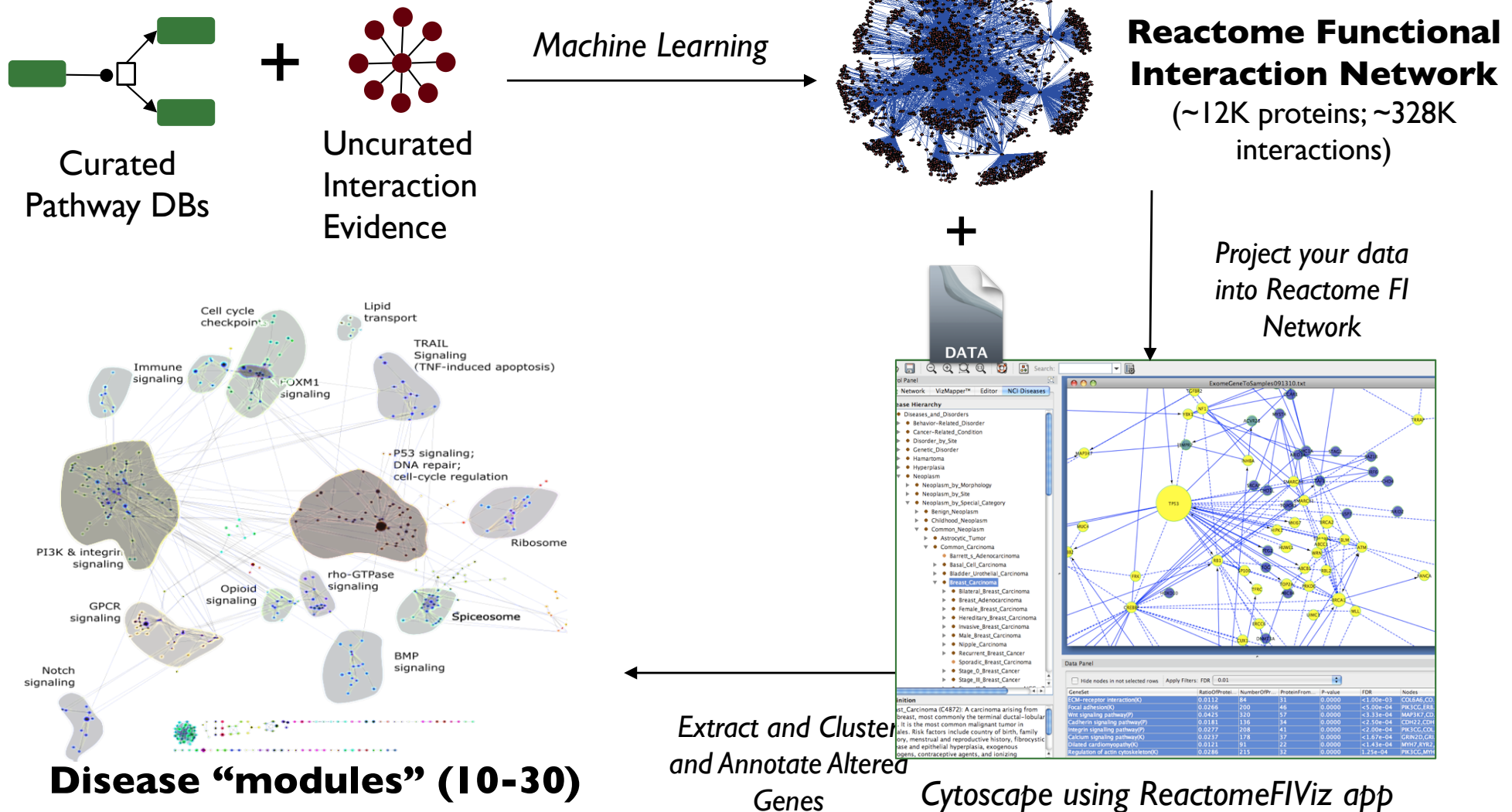
Remove Mechismo Results

Search Entities

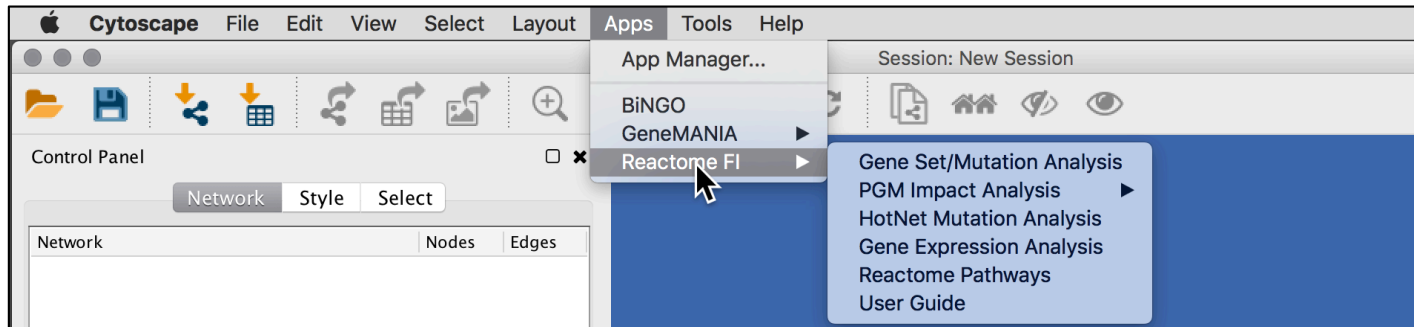
Search Reactions

Export Diagram

A2) De Novo Subnetwork Construction & Clustering



Upload your data



- FI plug-in supports four file formats:
 - Simple gene set: one line per gene
 - Gene/sample number pair. Contains two required columns, gene and number of samples having gene mutated, and an optional third column listing sample names (delimited by semi-colon ;)
 - NCI MAF (mutation annotation file)
 - Sample Gene Expression data file

File Formats

- Choose Plugins, Reactome FIs.
- FI plug-in supports four file formats:
 - Gene list
 - Gene-Sample gene
 - NCI Mutation Annotation File
 - Microarray Expression Data

Gene Set-based Analysis

The image shows a screenshot of the Cytoscape software interface. The top menu bar includes File, Edit, View, Select, Layout, Apps, Tools, and Help. The 'Apps' menu is open, showing options: App Manager..., CyBrowser, and Reactome FI. The 'Reactome FI' sub-menu is also open, listing: Gene Set/Mutation Analysis, PGM Impact Analysis, HotNet Mutation Analysis, Gene Expression Analysis, Reactome Pathways, and User Guide. The 'Gene Set/Mutation Analysis' option is highlighted. In the foreground, the 'Reactome FI Network Version' dialog box is open. It has three tabs: 'Reactome FI Network Version', 'Gene Set Parameters', and 'FI Network Construction Parameters'. The 'Reactome FI Network Version' tab is active, showing radio buttons for 2016 (selected), 2015, and 2014. Below this is a note: '* Different versions of the FI network may produce different results.' The 'Gene Set Parameters' tab is also visible, showing fields for 'Choose data file:', 'Or enter gene set:' (with '127 Genes Entered' entered), 'Specify format:' (with 'Gene set' selected), and 'Choose sample cutoff:' (with '2' entered). There is also a checkbox for 'Choose genes mutated at both alleles'. The 'FI Network Construction Parameters' tab is partially visible at the bottom, showing checkboxes for 'Fetch FI annotations', 'Use linker genes', and 'Show genes not linked to others'. At the bottom of the dialog box are 'OK' and 'Cancel' buttons. A black arrow points from the 'Gene Set/Mutation Analysis' option in the 'Reactome FI' sub-menu to the 'Gene Set Parameters' tab of the dialog box.

Cytoscape File Edit View Select Layout Apps Tools Help

App Manager...
CyBrowser
Reactome FI

Gene Set/Mutation Analysis
PGM Impact Analysis
HotNet Mutation Analysis
Gene Expression Analysis
Reactome Pathways
User Guide

Reactome FI Network Version

☒ 2016 ☐ 2015 ☐ 2014

* Different versions of the FI network may produce different results.

Gene Set Parameters

Choose data file: Browse

Or enter gene set:

Specify format: ☒ Gene set
☐ Gene/sample number pair
☐ NCI MAF (Mutation Annotation File)

Choose sample cutoff:

* Genes altered in 2 or more samples will be chosen if '2' is entered.

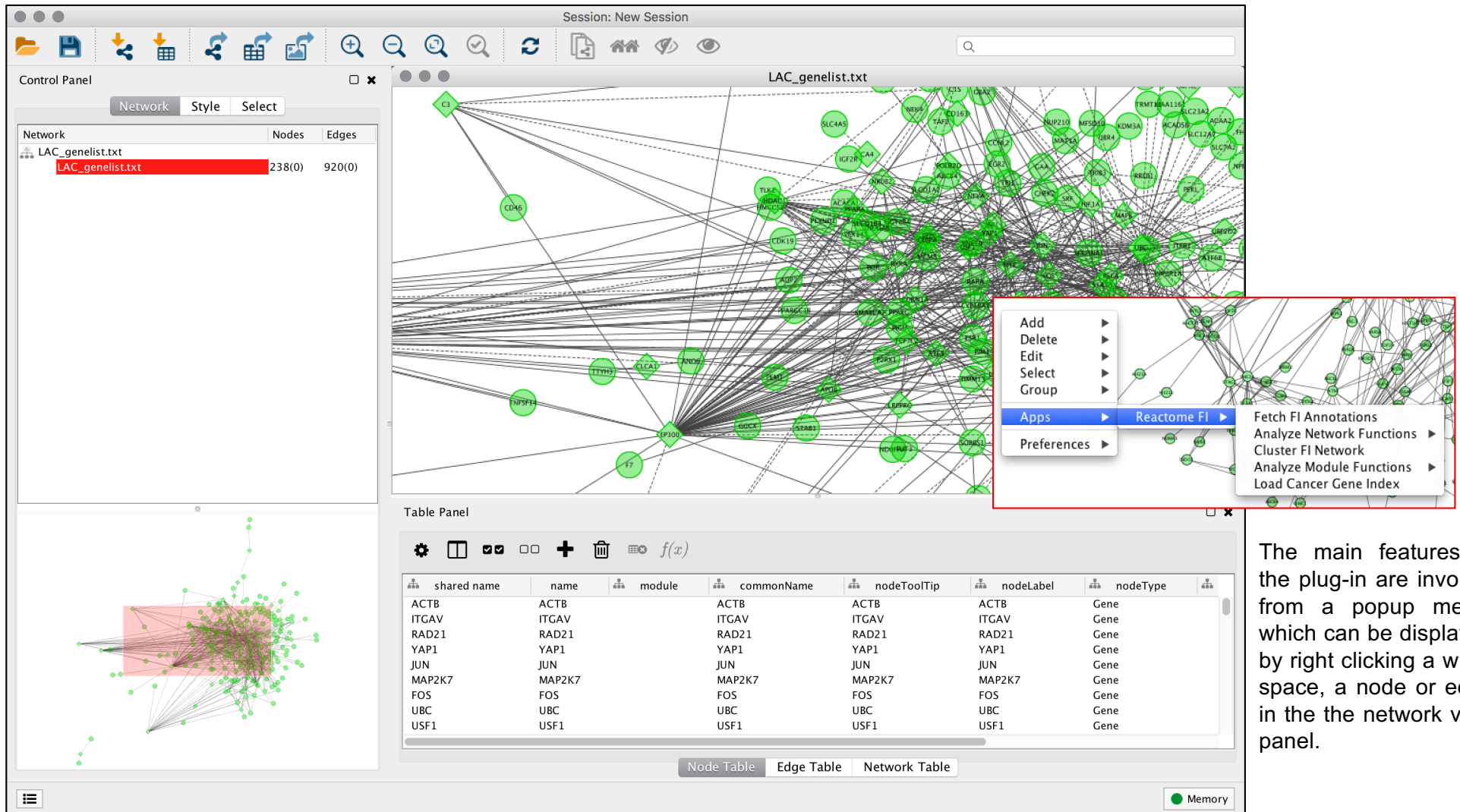
☐ Choose genes mutated at both alleles

FI Network Construction Parameters

☐ Fetch FI annotations
* Annotations may be fetched later.
☐ Use linker genes
☐ Show genes not linked to others

OK Cancel

FI Results Display

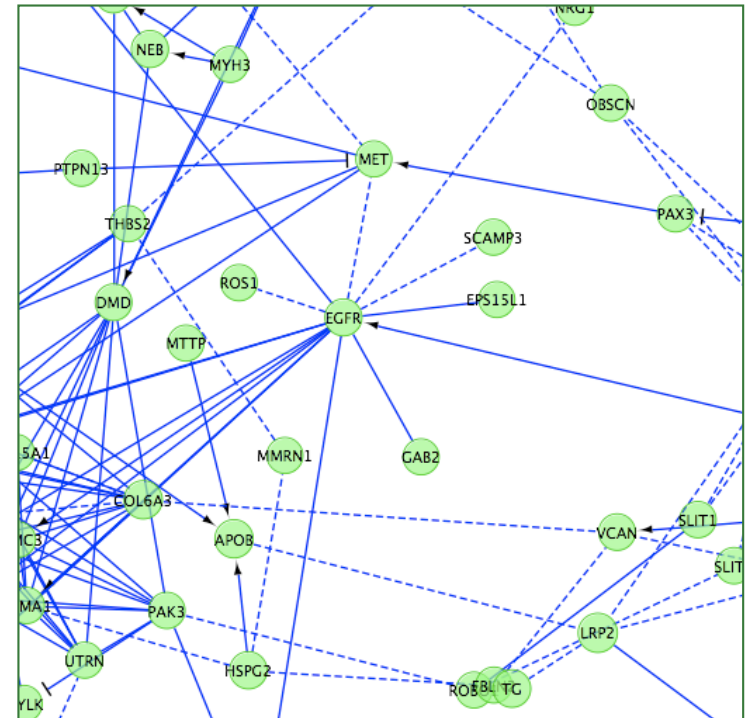


The main features of the plug-in are invoked from a popup menu, which can be displayed by right clicking a white space, a node or edge in the the network view panel.

- Constructed network is displayed in the Network View panel using an FI specific visual style

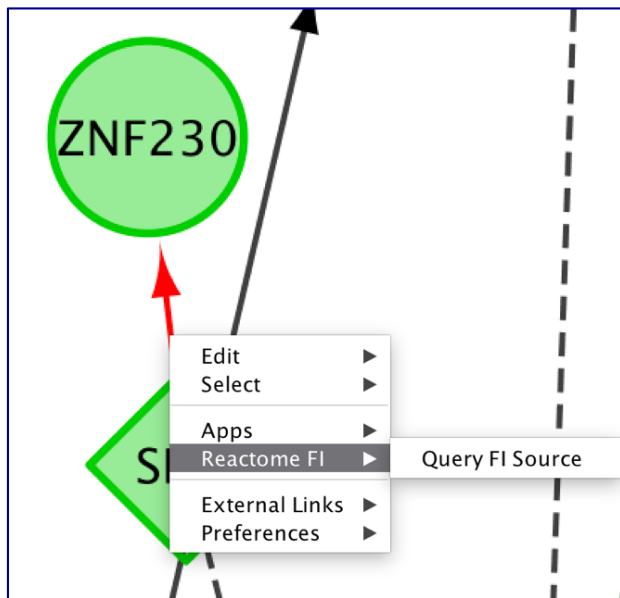
FI Annotations

- Provides detailed information on selected FIs.
- Three edge attributes are created:
 - FI Annotation.
 - FI Direction.
 - FI Score (for predicted FI).
- Edges display direction attribute values.
 - --> for activating/catalyzing.
 - --| for inhibition.
 - solid line for complexes or inputs.
 - --- for predicted FIs.



The main features of the plug-in are invoked from a popup menu, which can be displayed by right clicking a node or edge in the the network view panel.

Query FI Source



Annotated FIs

Reactome Sources

Reactome ID	Type	Data Source
6951674	TARGETED_INTERAC	ENCODE

View Reactome Source

Reactome Instance View

classType	TargetedInteraction
dbId	6951674
displayName	SIX5 ZNF230
dataSource	ENCODE
definition	ENCODE proximal_filtered TF/target interaction; supported by GO BP sharing
factor	SIX5
species	Homo sapiens
target	ZNF230

Close

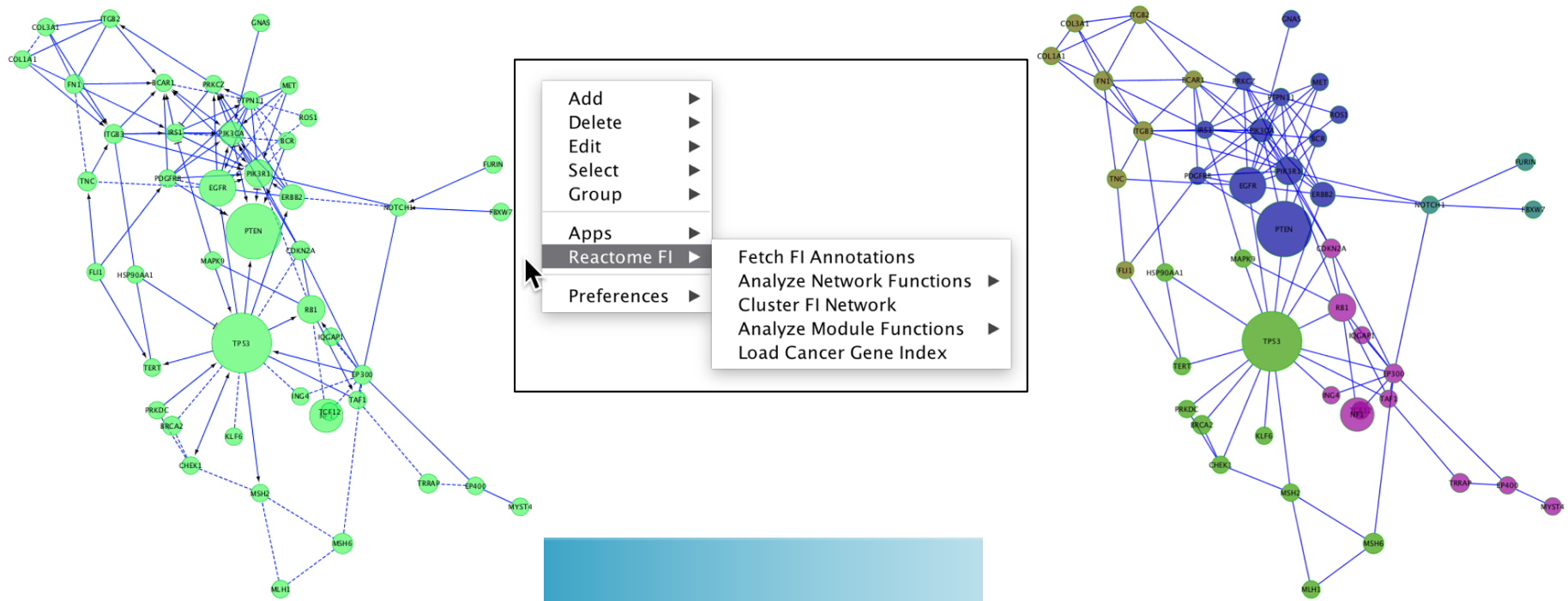
Predicted FIs

Support Evidence

Predictor	Value
Human Interaction	true
Yeast Interaction	false
Fly Interaction	false
Worm Interaction	false
Mouse Interaction	false
Pavlidis Gene Exp	false
Carlos Gene Exp	false
PfamDomain Interaction	true
GO BP Sharing	true
Score	0.9642255584531738

Cluster FI Network

- Runs spectral partition based network clustering ([Newman, 2006](#)) on the displayed FI network.
- Nodes in different network modules will be shown in different colours (max 15 colours).
- Analyze cancer mutation data with HotNet algorithm ([Vandin, 2012](#))



Analyze Module Functions

- Pathway or GO term enrichment analysis on individual network modules.
 - Use filter to remove small network modules
 - Filter by FDR

The screenshot shows the 'Reactome FI' menu with the following options:

- Add
- Delete
- Edit
- File
- Group
- Apps
 - Reactome FI
 - Fetch FI Annotations
 - Analyze Network Functions
 - Cluster FI Network
 - Analyze Module Functions (highlighted)
 - Load Cancer Gene Index
- Layout
- Select

On the right, a list of analysis types is shown:

- Pathway Enrichment
- GO Cell Component
- GO Biological Process
- GO Molecular Function
- Survival Analysis

Data Panel

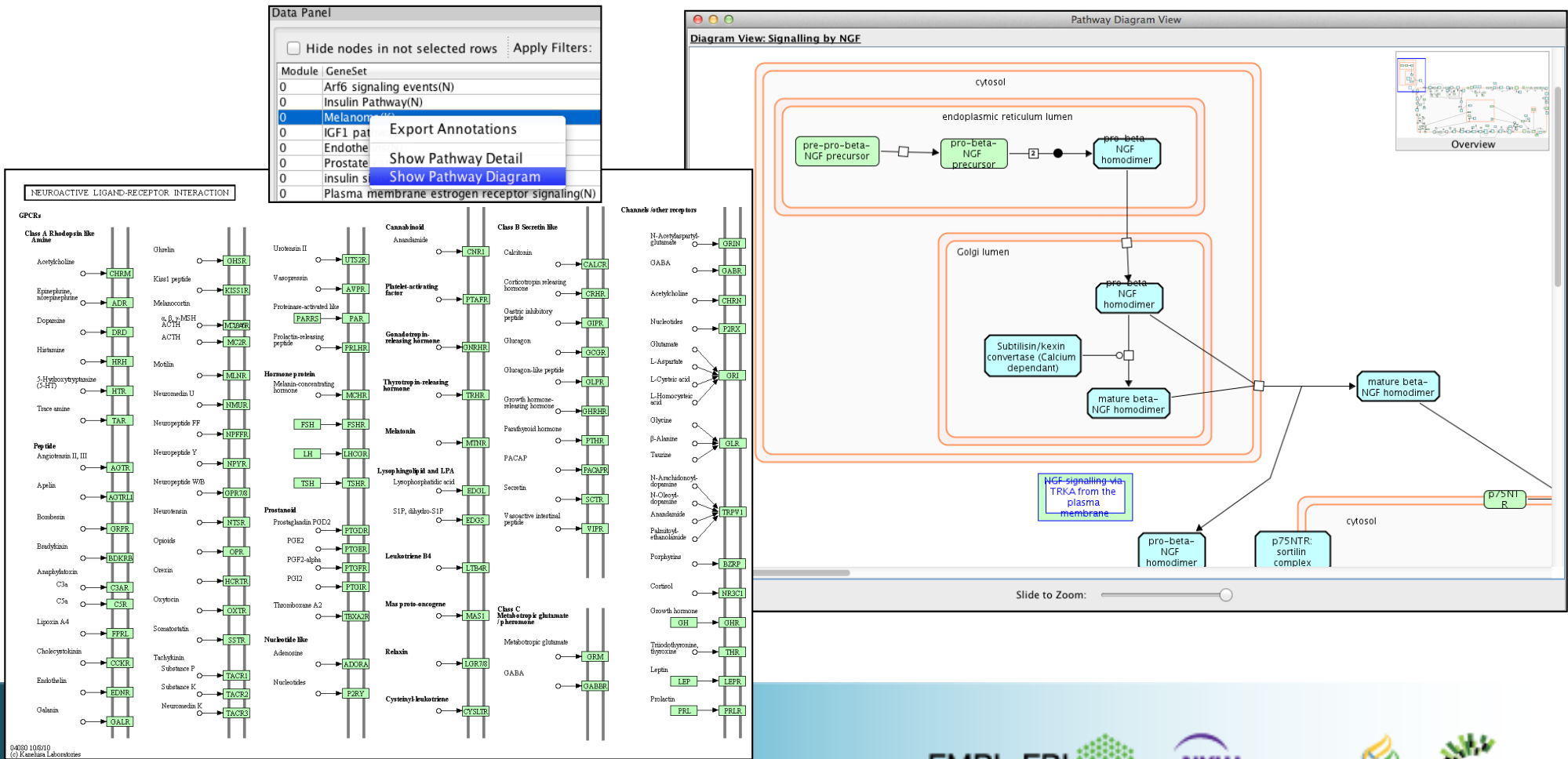
☐ Hide nodes in not selected rows Apply Filters: FDR 0.01 Module Size 10

Module	GeneSet	RatioOfProteinIn	NumberOfProteinInGe...	ProteinIn	mModule	P	FDR	Nodes
0	Translation(R)	0.0158	0.0010					RPL18,RPL17,RPL36...
0	Influenza Life Cycle(R)	0.0249	0.0050				<2.50e-04	RPL18,RPL17,RPL36...
0	Ribosome(K)	0.0117	✓ 0.01				<2.50e-04	RPL18,RPL17,RPL36...
0	Metabolism of protei...	0.0267	0.05				<2.50e-04	RPL18,RPL17,RPL36...
1	M Phase(R)	0.0128	0.25	119	64		<2.50e-04	ITGB3BP,MAD1L1,CC...
1	Aurora B signaling(N)	0.0052	0.5	187	60		<5.00e-04	AURKC,AURKB,CDCA...
1	Signaling by Aurora k...	0.0125	1.0	88	58		<3.33e-04	AURKC,AURKB,CDCA...
2	Glucose Regulation of...	0.0197		148	16	0.0000	<1.67e-04	NDUF84,NDUFA2,ND...
2	Parkinson's disease(K)	0.0176		132	15	0.0000	<1.67e-04	NDUF84,NDUFA2,ND...
2	Alzheimer's disease(K)	0.0223		168	15	0.0000	<1.67e-04	NDUF84,NDUFA2,ND...
2	Huntington's disease(K)	0.0246		185	15	0.0000	<1.67e-04	NDUF84,NDUFA2,ND...
2	Oxidative phosphoryl...	0.0178		134	15	0.0000	<1.67e-04	NDUF84,NDUFA2,ND...
2	Electron Transport C...	0.0101		76	16	0.0000	<1.67e-04	NDUF84,NDUFA2,ND...
2	Metabolic pathways(K)	0.1489		1120	16	0.0000	<1.43e-04	NDUF84,NDUFA2,ND...
3	Antigen processing a...	0.0104		78	9	0.0000	<1.00e-03	KLRC2,KIR2DS1,HLA...
3	Immunoregulatory int...	0.0153		115	8	0.0000	<5.00e-04	KIR2DS1,HLA-B,HLA...
3	Natural killer cell me...	0.0182		137	7	0.0000	<3.33e-04	KLRC2,KIR2DS1,HLA...

Node Attribute Browser Edge Attribute Browser Network Attribute Browser MCL Module Browser Pathways in Modules

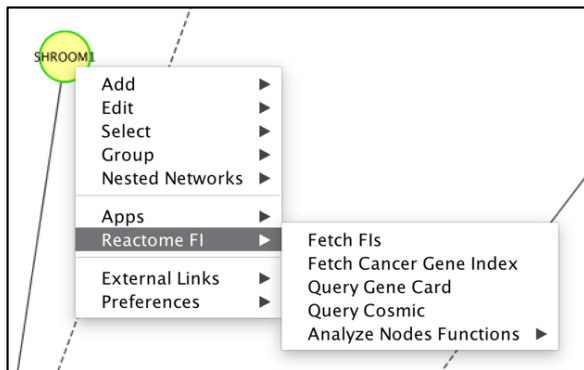
Other Features – Show Pathway Diagrams

- Select a pathway in "Pathways in Network/Modules" tabs, right click, select "Show Pathway Diagram"



Other Features – NCI Cancer Gene Index

- View detailed annotations for the selected gene or protein.
- Annotations are sortable by PubMed ID, Cancer type, status, and other criteria.



Cancer Index Annotations

Cancer Gene Index Annotations for "MAF"

Order by: PubMedID Set Filters Current filters: None

Results: 1 to 8 of 8 Page 1

Cancer type: tumors
Primary NCI role code: Gene_Has_Anormally
Other roles: not_assigned
Evidence code: EV-AS-TAS
Negation indicator: no
Cellline indicator: no
Status: finished
PubMedID: [16155016](#)
Comment: Anomalie_Detail: Chromosomal_Translocation

Nearly half of tumors are nonhyperdiploid, and mostly have one of five recurrent IgH translocations: 16% 11q13 (CCN D1), 3% 6p21 (CCN D3), 5% 16q23 (MAF), 2% 20q12 (MAFB), and 15% 4p16 (FGFR3 and MMSET).

Cancer type: tumors
Primary NCI role code: Gene_is_Biomarker_of
Other roles: not_assigned
Evidence code: EV-EXP-IEP, EV-EXP-IDA
Negation indicator: no
Cellline indicator: no
Status: finished
PubMedID: [15755896](#)

Using gene expression profiling to identify 5 recurrent translocations, specific trisomies, and expression of cyclin D genes, MM tumors can be divided into 8 TC (translocation/cyclin D) groups (11q13, 6p21, 4p16, maf, D1, D1+D2, D2, and none) that appear to be defined by early, and perhaps initiating, oncogenic events.

Cancer type: plasma-cell leukemias (pcl)
Negation indicator: no
Cellline indicator: no
Status: no_fact
PubMedID: [15543617](#)

We investigated the expression profiles of the FGFR3/MMSET, CCND1, CCND3, MAF, and MAFB genes, which

Other Features – Overlay Cancer Gene Index

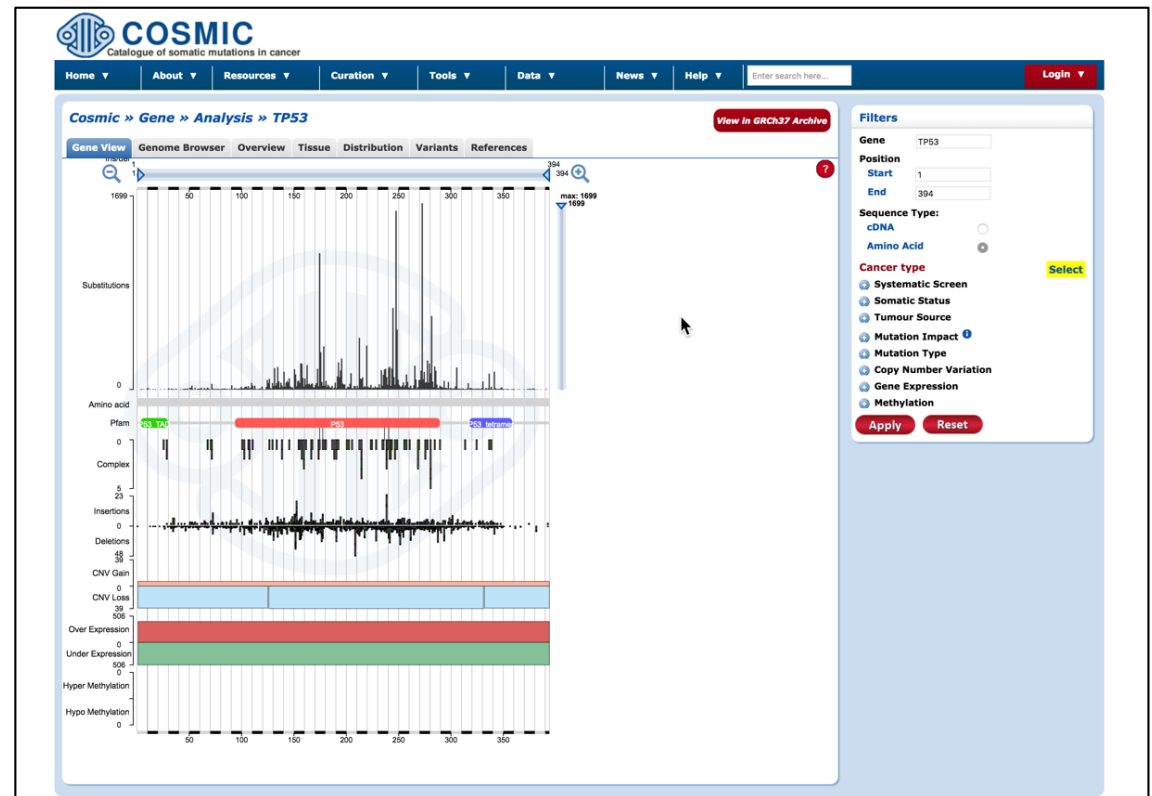
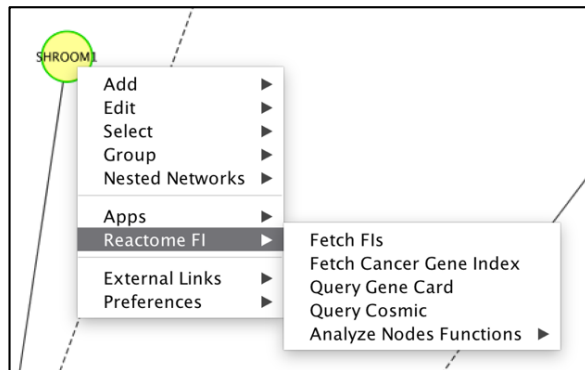
- Load the NCI disease terms hierarchy in the left panel.
- Select a disease term in the tree to select all nodes that have this annotation or one of its sub-terms.

The screenshot displays the Reactome VizMapper interface. On the left, the 'Control Panel' shows the 'Disease Hierarchy' with 'Papillary_Breast_Neoplasm' selected. The main area shows a network diagram with nodes and edges. A context menu is open over the network, showing options like 'Add', 'Edit', 'Select', 'Group', 'Nested Networks', 'Apps', 'Reactome FI', 'External Links', and 'Preferences'. The 'Reactome FI' option is highlighted, showing a sub-menu with 'Fetch FIS', 'Fetch Cancer Gene Index', 'Query Cosmic', and 'Analyze Nodes Functions'. At the bottom, the 'Table Panel' displays a table of gene sets with columns for Module, GeneSet, RatioOfProteinIn..., NumberOfProtei..., ProteinFromMod..., P-value, FDR, and Nodes.

Module	GeneSet	RatioOfProteinIn...	NumberOfProtei...	ProteinFromMod...	P-value	FDR	Nodes
0	Bladder cancer(K)	0.0038	38	2	0.0063	2.026e-01	E2F3,CDKN2A...
0	Lysosome(K)	0.0123	122	3	0.0065	1.906e-01	ARSG,NEU1,SCA...
0	HTLV-I infection...	0.0262	260	4	0.0084	2.256e-01	E2F3,CDKN2A...
0	Validated trans...	0.0049	49	2	0.0103	2.498e-01	PMAIP1,CDKN2A...
1	Focal adhesion(K)	0.0208	206	8	0.0000	<1.000e-03	TLN2,TNC,BCA...
1	Integrins in angi...	0.0047	47	4	0.0000	4.000e-03	BCAR1,PTK2B,I...
1	Type II diabetes...	0.0048	48	4	0.0000	2.667e-03	KCNJ11,PRKCE...
1	Signaling by EG...	0.0172	171	6	0.0000	3.000e-03	FGF9,LRIG1,SPR...
1	Endothelins(N)	0.0063	62	4	0.0001	4.400e-03	BCAR1,PTK2B,P...

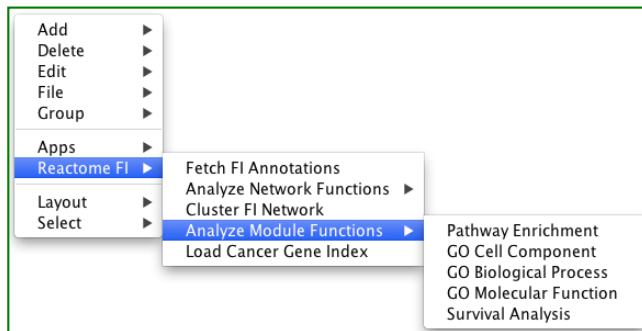
Other Features – COSMIC

- View detailed variant annotations for the selected gene or protein from COSMIC database.



Module Based Survival Analysis

- Discover Prognostic Signatures in Disease Module Datasets.
- Based on a server-side R script that runs either CoxPH or Kaplan-Meier survival analysis.
- Requires appropriate clinical data file.



Results Panel

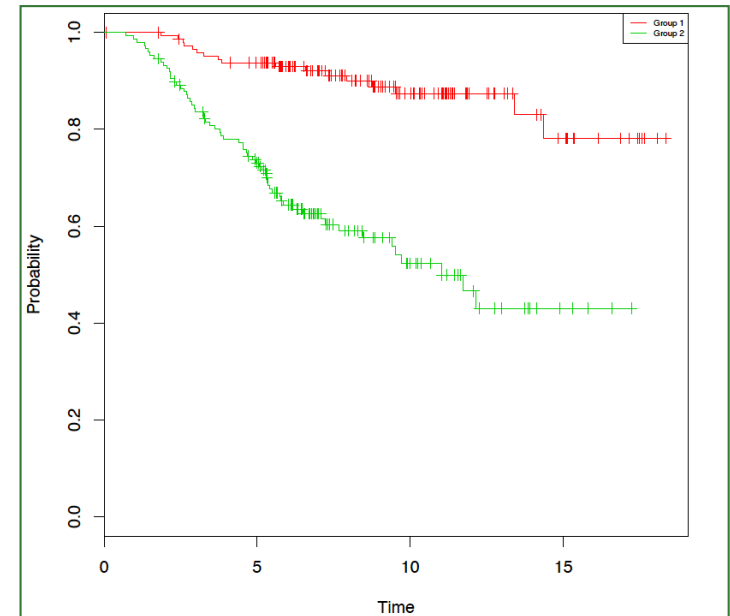
Survival Analysis

Analysis: Coxph (all modules)

----Output----

Note: Click underlined modules in blue for single module-based analysis. You may not see any underlined module if all p-values > 0.05.

Module	Coefficient	P-value
<u>0</u>	<u>-0.6142421</u>	<u>0.0015</u>
<u>1</u>	<u>1.308675</u>	<u>2.7e-10</u>
<u>2</u>	<u>0.4908374</u>	<u>0.015</u>
3	0.3854999	0.071
4	0.1916897	0.38
<u>5</u>	<u>1.015691</u>	<u>4.4e-07</u>
6	-0.06630745	0.71
7	-0.01376751	0.94
8	0.4978022	0.053
<u>9</u>	<u>0.948809</u>	<u>3.8e-06</u>
<u>10</u>	<u>0.6773846</u>	<u>0.024</u>
11	0.09736692	0.61
<u>12</u>	<u>-0.6155788</u>	<u>0.00033</u>



For any questions or feedback, please contact
help@reactome.org

