

A network diagram on a dark background showing interactions between miRNAs. Nodes are represented by small squares (light blue) and circles (orange). The nodes are interconnected by thin grey lines. Four specific nodes are highlighted with labels: 'hsa-mir-369-5p' at the top right, 'hsa-mir-29b-3p' in the center, 'hsa-mir-190a-5p' at the bottom left, and 'hsa-mir-23a-3p' at the bottom right. The central node 'hsa-mir-29b-3p' has a high degree of connectivity, with many lines radiating from it to other nodes.

# miRNet Tutorial

## Starting with a list

# Computer and Browser Requirements

- **A modern web browser with Java Script enabled Chrome, Safari, Firefox, and Internet Explorer 9+**
- **For best performance and visualization, use:**
  - Latest Google Chrome
  - At least 4GB of physical RAM
  - A 15-inch screen or bigger

# Goal for this tutorial

- Starting from a list of queries to identify other information related to their functions
  - miRNAs
  - Gene targets
  - Associated diseases
  - Small molecules
  - Long non-coding RNAs (lncRNAs)
  - Epigenetic modifiers

# Starting from a list



miRNet -- network-based visual analysis of miRNAs, targets and functions

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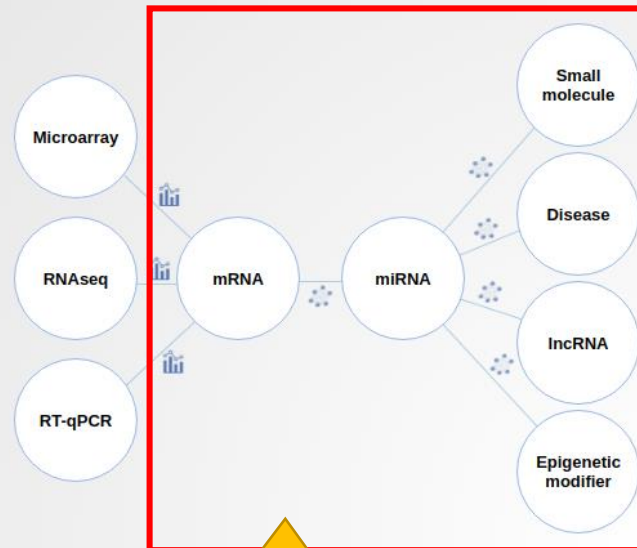
## News & Updates

- Added tissue-specific miRNA annotation for human miRNAs (12/26/2017); **NEW**
- miRNet can now automatically recognize and correct pre-miRNAs to their mature forms (12/16/2017); **NEW**
- Updated miRNA gene targets based on new releases of miRTarbase and TarBase (11/16/2017); **NEW**
- Code refactoring for performance improvement (10/25/2017); **NEW**
- Fixed the issue for broken miRBase links (09/25/2017);
- Added support for reducing node overlap for large network layout (09/22/2017);
- Added Force Atlas layout algorithm to

## Please Cite

Fan Y, Siklenka, K., Arora, SK., Ribeiro, P., Kimmins, S. and Xia, J. (2016) [miRNet - dissecting miRNA-target interactions and functional associations through network-based visual analysis](#). Nucl. Acids Res. 44 W135–141

Click on an input area below to start analysis



Choose one type of list in the red frame.

## Overview

miRNet is an easy-to-use tool with comprehensive support for **statistical analysis** and **functional interpretation** of data generated in miRNAs studies. Its main features include:

- **Support for various inputs & statistics:** miRNet accepts a list of miRNAs or targets, or a data table from microarray, RNAseq or RT-qPCR experiments. miRNet supports differential analysis using limma, edgeR and HTqPCR methods; enrichment analysis using standard hypergeometric tests and unbiased random sampling.
- **Comprehensive functional annotation:** miRNet integrates data from eleven different miRNA databases - [TarBase](#), [miRTarBase](#), [miRecords](#), [miRanda](#) (*S. mansoni* only), [miR2Disease](#), [HMDD](#), [PhenomiR](#), [SM2miR](#), [PharmacomiR](#), [EpimiR](#), and [starBase](#). It currently supports **nine** organisms - Human, Mouse, Rat, Cattle, Chicken, Zebra fish, Fruit fly, *C. elegans* and *S. mansoni*.
- **Creation of miRNA-target interaction networks:** miRNet provides a wide array of options to allow researchers to build miRNA-target interaction networks at different confidence levels. The resulting network can be further optimized using different algorithms to improve visualization and understanding.
- **High-performance network visual analytics:** miRNet offers five types of networks on miRNA-gene, miRNA-disease, miRNA-small molecule, miRNA-lncRNA, and miRNA-epigenetic modifier. The system supports zooming, highlighting, point-and-click, drag-and-drop, enrichment analysis, etc. to enable users to intuitively explore miRNAs, targets and functions.

# Upload a list

This interface performs for miRNA, mRNA and lncRNA

- 8 can be chosen .
- 2 ID types for miRNA (miRBase ID and Accession number.)
- 3 ID types for mRNA (EntrezID, Ensembl ID and gene symbol)
- 56 tissue types for human miRNA

Enter a list of miRNAs below: ?

Organism

ID type

Tissue (human only)

Target type

```
hsa-mir-101-3p
hsa-mir-133b
hsa-mir-147a
hsa-mir-3140-3p
hsa-mir-361-5p
hsa-mir-510-5p
```

Step 1 : Choose the parameters above. Copy and paste a list of miRNA

Step 2 : Click "Submit". A confirm dialog will show on the top right corner.

Step 3 : Click "Proceed" to the interaction table

You can try our example first

# Upload selected items

The screenshot shows a web interface for disease selection. At the top, there is a breadcrumb 'Disease Selection'. Below it, a dropdown menu is set to 'H. sapiens (human)' with a 'Load Data' button to its right. A 'Tissue:' dropdown is set to 'Bone marrow (598)'. The main area is split into two panes: 'Available' on the left and 'Selected' on the right. The 'Available' pane lists various diseases, including Prion-Jakob Syndrome, Dermatitis, atopic, Diabetic Nephropathies, Diarrhea predominant irritable bowel syndrome (IBS-D), Diffuse large B-cell lymphoma (DLBCL), Down syndrome (DS), Duchenne muscular dystrophy (DMD), Endometrial cancer, Endometriosis, Epithelial ovarian cancer (EOC), Esophageal cancer, Esophageal squamous cell carcinoma, Essential thrombocythemia (ET), Facioscapulohumeral muscular dystrophy (FSHD), Follicular lymphoma (FL), Follicular thyroid carcinoma (FTC), and frontotemporal dementia. The 'Selected' pane lists Acute promyelocytic leukemia (APL), Bladder cancer, Cerebellar neurodegeneration, Dermatomyositis (DM), and Diabetes type 2. Between the panes are four arrow buttons: a right arrow, a right arrow with a plus sign, a left arrow, and a left arrow with a plus sign. A 'Submit' button is located below the 'Available' pane. At the bottom right, there is a 'Proceed' button with a plus sign icon.

1. Choose a source type and choose the items by dragging or selecting or searching

The data for human are available on diseases and epigenetic modifiers. The data for human and mouse are available on small molecules

2. Click "Submit"

3. Click "Proceed" to the interaction table

We proved a list of disease, molecule and epigenetic modifier for users to choose, because there is no standard IDs available and use of free text is error-prone.

# Pruning or Expanding Network Data

miRNA Upload > Interaction Table

For cattle (*B. taurus*), chicken (*G. gallus*) and helminth (*S. mansoni*), the result will be mainly composed of interaction data predicted using miRanda. You can use the "Data Filter" to filter the results based on the miRanda scores to keep more confident predictions.

[Data Filter](#) [Reset](#) [Download](#)

miRNA	Link	Tissue	Target:Gene	Link	Method	Literature	Action
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	ACVR2B	<a href="#">Entrez</a>	Sequencing	<a href="#">20371350</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	AP1G1	<a href="#">Entrez</a>	Sequencing	<a href="#">22263</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	AMD1	<a href="#">Entrez</a>	Sequencing	<a href="#">20371350</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	XIAP	<a href="#">Entrez</a>	Sequencing	<a href="#">20371350</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	BIRC5	<a href="#">Entrez</a>	Sequencing	<a href="#">20371350</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	APP	<a href="#">Entrez</a>	Luciferase reporter assay//qPCR	<a href="#">20395292</a> , <a href="#">21172309</a> , <a href="#">21572407</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	RHOA	<a href="#">Entrez</a>	Luciferase reporter assay//qPCR	<a href="#">28109909</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	ATM	<a href="#">Entrez</a>	Luciferase reporter assay//qPCR	<a href="#">20617180</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	ATP5B	<a href="#">Entrez</a>	qRT-PCR//Reporter assay//Western blot	<a href="#">21291913</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	NKX3-2	<a href="#">Entrez</a>	HITS-CLIP	<a href="#">23824327</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	CCND1	<a href="#">Entrez</a>	Western blot	<a href="#">26286725</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	BCL9	<a href="#">Entrez</a>	Sequencing	<a href="#">20371350</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	PRDM1	<a href="#">Entrez</a>	Chromatin immunoprecipitation	<a href="#">20371350</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	ZFP36L2	<a href="#">Entrez</a>	PAR-CLIP	<a href="#">20371350</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	CAPN2	<a href="#">Entrez</a>	Sequencing	<a href="#">20371350</a>	<a href="#">Delete</a>

[Previous](#) [Proceed](#)

Click here to perform data filtering

Search items by keywords

The experimental methods for validation

Click here to delete individual interaction.

Click "Proceed" to the interaction table

# Perform Data Filtering

The 'Data Filter Dialog' window shows the 'Target Column' dropdown menu open, with 'Method' selected. The 'Value Criterion' dropdown is set to 'Matching'. The 'Action' section has 'Remove' selected. A 'Submit' button is at the bottom.

Target Column:	Method
Value Criterion:	Matching
Action:	<input checked="" type="radio"/> Remove <input type="radio"/> Keep

Submit

Step 1 : Choose a target column which you want to perform the filter.

The 'Data Filter Dialog' window shows the 'Value Criterion' dropdown menu open, with '(Character) Matching' selected. The 'Target Column' is 'Method'. The 'Action' section has 'Remove' selected. A 'Submit' button is at the bottom.

Target Column:	Method
Value Criterion:	(Character) Matching
Action:	<input type="radio"/> Remove <input checked="" type="radio"/> Keep

Submit

Step 2 : Choose the filter option, “Matching” is filtering by the exact words, “Containing” is filtering by keywords, “At least” is filtering by predicted score (only for *S.mansoni*)

The 'Data Filter Dialog' window shows the 'Value Criterion' dropdown set to '(Character) Containing' and the text input field containing 'CLIP'. The 'Action' section has 'Keep' selected. A 'Submit' button is at the bottom.

Target Column:	Method
Value Criterion:	(Character) Containing
Action:	<input type="radio"/> Remove <input checked="" type="radio"/> Keep

Submit

Step 3 : Input the keywords and perform the filtering to keep or remove.



# The table after performing data filter

miRNA Upload > Interaction Table

For cattle (*B. taurus*), chicken (*G. gallus*) and helminth (*S. mansoni*), the result will be mainly composed of interaction data predicted using miRanda. You can use the "Data Filter" to filter the results based on the **miRanda scores** to keep more confident predictions.

[Data Filter](#) [Reset](#) [Download](#)

Only keep the method contains "CLIP"

miRNA	Link	Tissue	Target:Gene	Link	Method	Literature	Action
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	AP1G1	<a href="#">Entrez</a>	PAR-CLIP//Sequencing	<a href="#">20371350</a> , <a href="#">23592263</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	AMD1	<a href="#">Entrez</a>	HITS-CLIP	<a href="#">23313552</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	APP	<a href="#">Entrez</a>	Luciferase reporter assay//P	<a href="#">20395292</a> , <a href="#">21172309</a> , <a href="#">2157240</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	NKX3-2	<a href="#">Entrez</a>	HITS-CLIP	<a href="#">23824327</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	ZFP36L2	<a href="#">Entrez</a>	PAR-CLIP	<a href="#">21572407</a> , <a href="#">20371350</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	CAPZB	<a href="#">Entrez</a>	PAR-CLIP	<a href="#">27292025</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	CCNF	<a href="#">Entrez</a>	PAR-CLIP	<a href="#">23592263</a> , <a href="#">26701625</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	CD81	<a href="#">Entrez</a>	PAR-CLIP	<a href="#">23592263</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	CDKN1A	<a href="#">Entrez</a>	PAR-CLIP	<a href="#">23592263</a> , <a href="#">22012620</a> , <a href="#">2670162</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	COX10	<a href="#">Entrez</a>	PAR-CLIP	<a href="#">23592263</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	CPS1	<a href="#">Entrez</a>	PAR-CLIP	<a href="#">23592263</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	DYNC1LI2	<a href="#">Entrez</a>	PAR-CLIP		<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	DSC1	<a href="#">Entrez</a>	PAR-CLIP		<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	EIF4G2	<a href="#">Entrez</a>	PAR-CLIP		<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	ELAVL3	<a href="#">Entrez</a>	HITS-CLIP	<a href="#">27418678</a>	<a href="#">Delete</a>

Click "Proceed" to the network builder

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# Pruning or Expanding Network Data

miRNA Upload > Interaction Table > Network Builder

**Network Overview:**

Number of queries:	6
Number of nodes:	784 (miRNAs: 6, Targets: 778)
Number of edges:	810

In some cases, multiple isolated networks will be generated, with a big 'continent' containing most of queries, and several small 'islands' containing one or a few queries. You can select one or more networks for visual analysis in the next step.

	Networks	Nodes	Edges	Queries	
<input checked="" type="checkbox"/>	mimnet1	784	810	6	± Download

**Network Tools:**

- Degree Filter
- Betweenness Filter
- Shortest Path Filter
- Update Network
- Reset Network

Summary for the nodes of the network

Perform the nodes management

Click "Proceed" to the network viewer

Previous Proceed

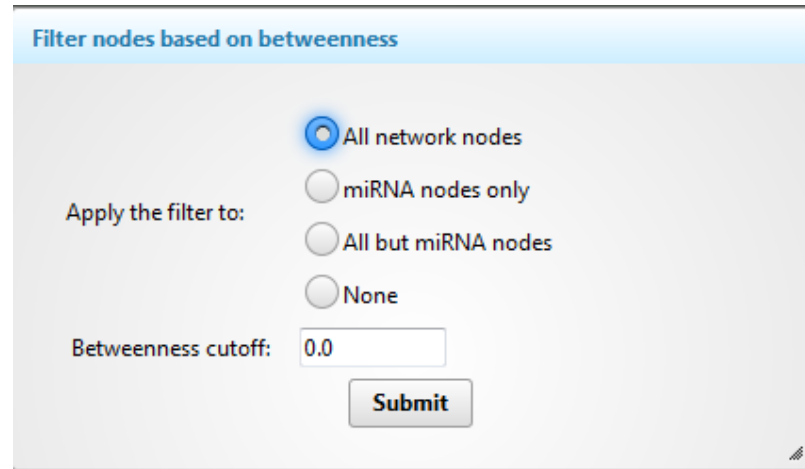
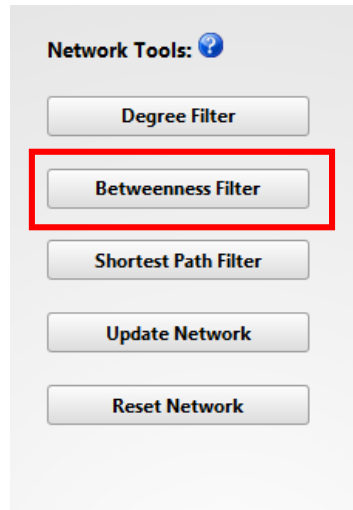
# Network tools

The image shows two parts of a web interface. On the left, a panel titled "Network Tools: ?" contains five buttons: "Degree Filter" (highlighted with a red box), "Betweenness Filter", "Shortest Path Filter", "Update Network", and "Reset Network". On the right, a window titled "Filter nodes based on degree" contains the following controls:

- "Apply the filter to:" with four radio button options:
  - All network nodes
  - miRNA nodes only
  - All but miRNA nodes
  - None
- "Degree cutoff:" with a text input field containing "1.0".
- A "Submit" button.

- The degree of a node is the number of connections it has to other nodes. Nodes with higher node degree act as hubs in a network.
- **Degree cutoff:** default 1.0, the minimal degree you want to choose.
- **All network nodes** : default option, choose all nodes in the network.
- **miRNA nodes only**: the degree filter will only perform in miRNA nodes.
- **All but miRNA nodes** : the degree filter will perform to other nodes except miRNA.
- **None**: Do not perform the filter.

# Network tools



- The **betweenness centrality** measures the number of shortest paths going through the node. It takes into consideration the global network structure. For example, nodes that occur between two dense clusters will have a high betweenness centrality even if their degree centrality values are not high.
- **Degree cutoff**: default 0.0 (all nodes), the minimal betweenness you want to choose.
- **All network nodes** : default option, choose all nodes in the network.
- **miRNA nodes only**: the betweenness filter will only perform in miRNA nodes.
- **All but miRNA nodes** : the betweenness filter will perform to other nodes except miRNA.
- **None**: Do not perform the filter.

# Network tools

The image shows two parts of a software interface. On the left, a panel titled "Network Tools: ?" contains five buttons: "Degree Filter", "Betweenness Filter", "Shortest Path Filter" (highlighted with a red box), "Update Network", and "Reset Network". Two blue callout boxes point to the "Shortest Path Filter" and "Reset Network" buttons. The first callout says "Refresh network as new changes." and the second says "Reset the network to default." On the right, a dialog box titled "Reduce connections between densely connected nodes" is shown. It contains the text "Apply the filter to:" followed by four radio button options: "All network nodes" (selected), "miRNA nodes only", "All but miRNA nodes", and "None". A "Submit" button is located at the bottom right of the dialog box.

- **Shortest Path Filter** : If there are multiple paths that can link two nodes together, only one shortest path will be chose to reduce dense networks.
- **All network nodes** : default option, choose all nodes in the network.
- **miRNA nodes only**: the filter will only perform in miRNA nodes.
- **All but miRNA nodes** : the filter will perform to other nodes except miRNA.
- **None**: Do not perform the filter.

# Understanding the Network Viewer

Background: Black View: Default Layout: Default Layout Scope: -- Specify -- Download: -- Specify --

**Node Explorer**

Node ID: Search

Locating nodes in the network by click IDs and they can be sorted by degree, betweenness and status (only for expression data).

<input type="checkbox"/>	KIAA1210	2	10814
<input type="checkbox"/>	ZNF281	2	10814
<input type="checkbox"/>	PLAG1	2	10598
<input type="checkbox"/>	PFAFH1B2	2	6200
<input type="checkbox"/>	FSCN1	2	6193.2
<input type="checkbox"/>	INSIG1	2	6193.2
<input type="checkbox"/>	RAB11FIP1	2	6193.2
<input type="checkbox"/>	C1QTNF6	2	6193.2
<input type="checkbox"/>	CCDC117	2	6193.2
<input type="checkbox"/>	LIMS1	2	6193.2

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**Current Selections**

- Node: hsa-mir-23a-3p
- Link: mirBase
- Degree: 121
- Betweenness: 82671

**Functional enrichment analysis**

Query: All genes  
Algorithm: Hypergeometric test  
Database: KEGG Submit

Name	Hits	Pval	Color
p53 signaling pathway	10	0.0957	
Glycolysis / Gluconeogenesis	3	1	
Citrate cycle (TCA cycle)	1	1	
Pentose phosphate pathwa:	1	1	
Pentose and glucuronate in	2	1	
Fructose and mannose met:	2	1	
Ascorbate and aldarate met	1	1	
Fatty acid elongation	2	1	
Fatty acid degradation	4	1	
Synthesis and degradation	1	1	
Steroid biosynthesis	1	1	
Ubiquinone and other terpe	1	1	
Steroid hormone biosynthes	2	1	
Oxidative phosphorylation	0	1	

View Options Path Finder Batch Hit

**Node Effect**

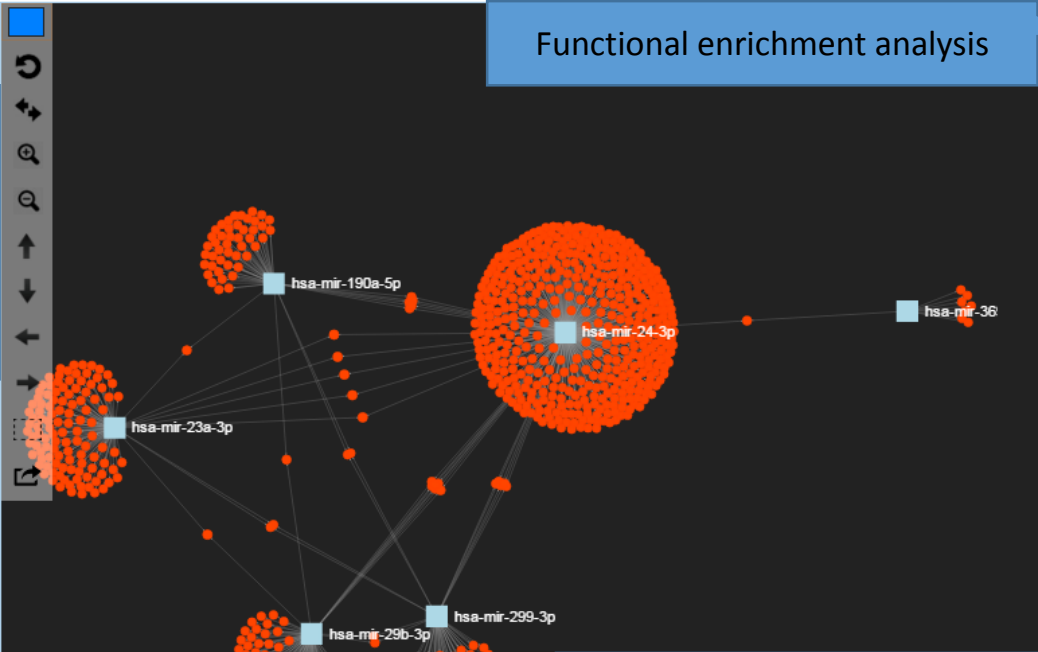
Set size for: All nodes  
Increase ++ Submit  
Note: you can increase size of any particular node by repeatedly clicking on it

**Edge Effect**

Edge shape: Line  
Edge width: Default Submit

In the network, the square nodes are miRNAs and the round nodes are the targets. The size of the node indicate its significance in the network.

The detail for selected node



# Choose different algorithms

- **Hypergeometric tests :**

Using the hypergeometric distribution to measure the statistical significance of those genes are identified from the miRNA target analysis.

- **Unbiased Empirical tests (only for miRNA):**

Being used to estimate the null distribution of the target genes as selected based on the input miRNAs. The procedures can be divided into three steps:

- 1) A list of miRNAs of the same size are randomly selected from all the miRNAs with known targets in the database;
- 2) The functional annotations (i.e. GO or KEGG) are then performed for the list;
- 3) The process is repeated 1000 times (default);
- 4) Compare the hits in each GO or KEGG pathways and the empirical p (Emp. p) values are calculated as the proportion of overlaps (with pathways or GO) from 1000 random process that equal or larger than the original.
- 5) User can perform the functional analysis again under the same parameters, the results will be combined. i.e. clicking five times will generate empirical p values based on 5000 random samplings.

# Enrichment analysis by highlighting nodes

1. Locate the node by clicking IDs, the size of nodes will be increased and zoom in. (they are sorted by the betweenness).

<input type="checkbox"/>	hsa-mir-29b-3	100	67337	-
<input type="checkbox"/>	hsa-mir-299-3	57	37315	-
<input type="checkbox"/>	hsa-mir-190a-1	54	35637	-
<input checked="" type="checkbox"/>	SSR1	2	10814	
<input checked="" type="checkbox"/>	ADAM17	2	10814	
<input checked="" type="checkbox"/>	CEP57L1	2	10814	
<input checked="" type="checkbox"/>	KIAA1210	2	10814	
<input checked="" type="checkbox"/>	ZNF281	2	10814	
<input type="checkbox"/>	PLAG1	2	10598	
<input type="checkbox"/>	PAFAH1B2	2	6200	
<input type="checkbox"/>	FSCN1	2	6193.2	
<input type="checkbox"/>	INSIG1	2	6193.2	
<input type="checkbox"/>	RAB11FIP1	2	6193.2	
<input type="checkbox"/>	C1QTNF6	2	6193.2	
<input type="checkbox"/>	CCDC117	2	6193.2	
<input type="checkbox"/>	LIMS1	2	6193.2	

Current Selections

- Node: ADAM17
- Link: [Entrez](#)
- Degree: 2
- Betweenness: 10814

3. Choose "Highlighted nodes", algorithm (hypergeometric test or empirical test) and pathway (KEGG, GO and Reactome). Click "submit".

Function Explorer

Query:  Algorithm:  Database:

Name	Hits	Pval	Color
Signaling by ERBB4	1	1	
Nuclear signaling by ERBB4	1	1	
Cytokine Signaling in Immune	1	1	
Collagen degradation	1	1	
Degradation of the extracell	1	1	
Extracellular matrix organiz	1	1	
Signal Transduction	1	1	
Signalling by NGF	1	1	
Immune System	1	1	
Signaling by EGFR	1	1	
SRP-dependent cotranslatic	1	1	
Regulated proteolysis of p7	1	1	
p75 NTR receptor-mediated	1	1	
YRB1(S) activates chaperon	1	1	

Node Effect

Set size for:

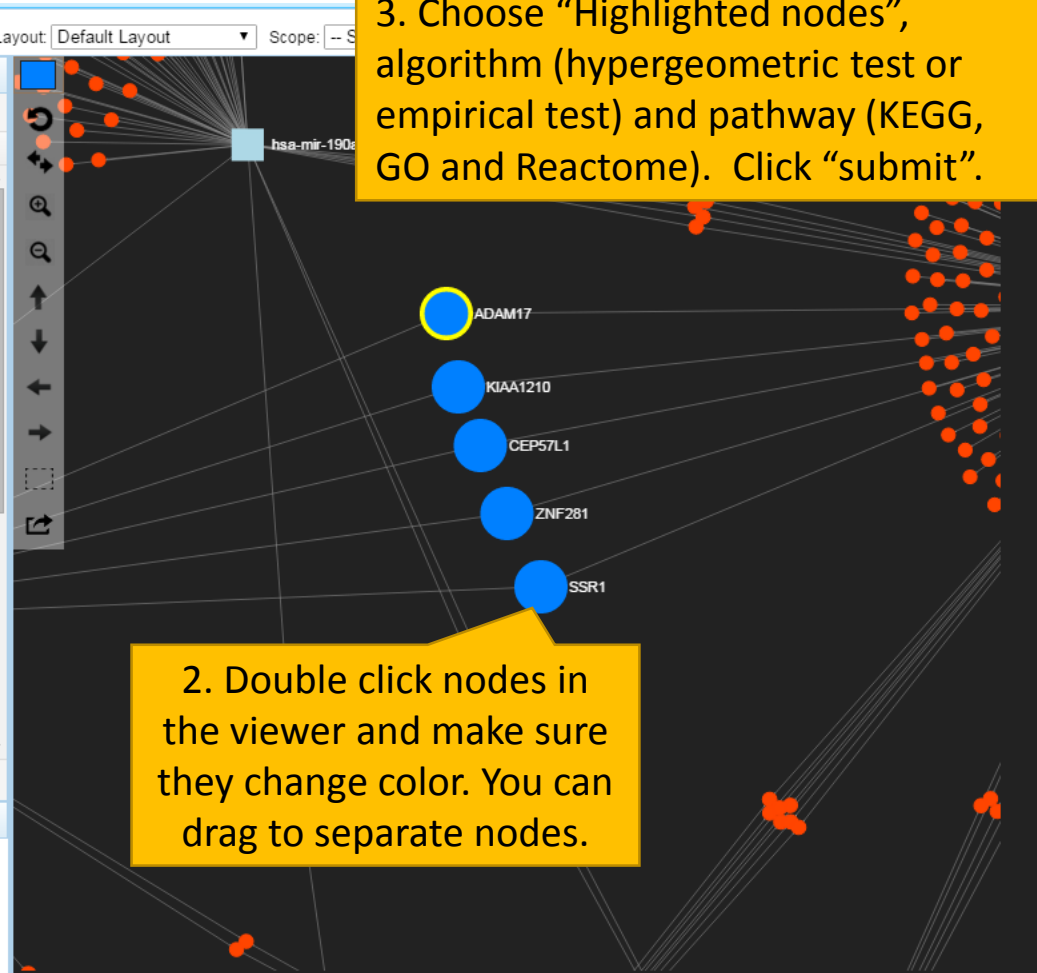
Note: you can increase size of any particular node by repeatedly clicking on it

Edge Effect

Edge shape:

Edge width:

2. Double click nodes in the viewer and make sure they change color. You can drag to separate nodes.





# Enrichment analysis by selecting pathway

2. Choose a color here, you can change different colors to perform selection

1. Choose an algorithm and a pathway then perform for all genes

3. Click a pathway, the genes inside will be highlighted by selected color.

The genes in this pathway

The screenshot displays a bioinformatics software interface for pathway enrichment analysis. On the left, a list of genes is shown with checkboxes. In the center, a network diagram features several clusters of nodes (miRNAs) connected to a larger network of genes. A color selection tool is overlaid on the network, showing a color gradient and a text input field with the value 'rgb(0, 128, 255)'. On the right, a 'Function Explorer' window shows a table of enriched pathways. A yellow callout points to the 'Activation of BH3-only proteins' pathway, which is highlighted in blue in the table. A blue callout points to the 'Current Selections' list at the bottom left, which contains genes associated with the selected pathway.

Name	Hits	Pval	Color
Gene Expression	57	0.0555	
Intrinsic Pathway for Apopto	7	0.129	
SMAD2/SMAD3:SMAD4 hel	6	0.129	Magenta
Oxidative Stress Induced Se	11	0.129	
XBP1(S) activates chaperon	9	0.129	
IRE1alpha activates chaper	9	0.129	
Unfolded Protein Response	10	0.129	Green
Apoptosis	12	0.887	
Hemostasis	27	0.887	
Activation of BH3-only prote	4	0.887	Blue
Glycosphingolipid metabolis	5	0.887	
Signaling by TGF-beta Recc	7		

**Current Selections**

- Activation of BH3-only proteins
- BCL2L11
- DYNLL2
- YWHAZ
- BBC3

# Dragging nodes-Current highlights

Background: Black View: Default Layout: Graphopt Layout Scope: Current highlights Download: -- Specify --

**Node Explorer**

Node ID:  Search

Highlight miRNA targets: All Submit

ID	Degree	Betweenness	Status
<input type="checkbox"/> hsa-mir-24-3p	470	256970	-
<input type="checkbox"/> hsa-mir-23a-3p	121	82671	-
<input type="checkbox"/> hsa-mir-29b-3p	100	67337	-
<input type="checkbox"/> hsa-mir-299-3p	57	37315	-
<input type="checkbox"/> hsa-mir-190a-1	54	35637	-
<input type="checkbox"/> hsa-mir-369-5p	8	5453	-
<input type="checkbox"/> ATXN7L3B	2	5518.9	
<input type="checkbox"/> CEP57L1	2	10814	
<input type="checkbox"/> KIAA1210	2	10814	
<input type="checkbox"/> NUFIP2	2	2946.7	
<input type="checkbox"/> PLAG1	2	10598	
<input type="checkbox"/> PTPN14	2	2946.7	
<input type="checkbox"/> SSR1	2	10814	
<input type="checkbox"/> ZNF281	2	10814	
<input type="checkbox"/> C1QTNF6	2	6193.2	
<input type="checkbox"/> CCDC117	2	6193.2	
<input type="checkbox"/> COX20	2	4673.9	

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**Current Selections**

- Node: YWHAZ
- Link: Entrez
- Degree: 1
- Betweenness: 0

**Function Explorer**

Query: All genes  
Algorithm: Hypergeometric test  
Database: Reactome Submit

Name	Hits	Pval	Color
Gene Expression	57	0.0555	
Intrinsic Pathway for Apopto	7	0.129	
SMAD2/SMAD3:SMAD4 hel	6	0.129	Blue
Oxidative Stress Induced Se	11	0.129	
XBP1(S) activates chaperon	9	0.129	
IRE1alpha activates chaper	9	0.129	
Unfolded Protein Response	10	0.129	Magenta
Apoptosis	12	0.887	
Hemostasis	27	0.887	
Activation of BH3-only prote	4	0.887	Green
Cholesterol and lipid metabolis	5	0.887	

Increase ++ Submit  
Note: you can increase size of any particular node by repeatedly clicking on it

**Edge Effect**  
Edge shape: Line  
Edge width: Default Submit

**1. Choose "Current highlights"**

**2. Click a pathway, the current selected nodes are circled by golden line.**

**3. Drag current highlighted nodes aside and zoom in.**

# Dragging nodes-All highlights

Background: Black View: Default Layout: Graphopt Layout Scope: All highlights Download: -- Specify --

**Node Explorer**

Node ID: Search

Highlight miRNA targets: All Submit

ID	Degree	Betweenness	Status
hsa-mir-24-3p	470	256970	-
hsa-mir-23a-3p	121	82671	-
hsa-mir-29b-3p	100	67337	-
hsa-mir-299-3p	57	37315	-
hsa-mir-190a-1	54	35637	-
hsa-mir-369-5p	8	5453	-
ATXN7L3B	2	5518.9	
CEP57L1	2	10814	
KIAA1210	2	10814	
NUFIP2	2	2946.7	
PLAG1	2	10598	
PTPN14	2	2946.7	
SSR1	2	10814	
ZNF281	2	10814	
C1QTNF6	2	6193.2	
CCDC117	2	6193.2	
COX20	2	4673.9	

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**Current Selections**

- Node: BBC3
- Link: Entrez
- Degree: 1
- Betweenness: 0

**Function Explorer**

Query: All genes

Algorithm: Hypergeometric test

Database: Reactome Submit

Name	Hits	Pval	Color
Gene Expression	57	0.0555	
Intrinsic Pathway for Apopto	7	0.129	
SMAD2/SMAD3:SMAD4 hel 6	6	0.129	Blue
Oxidative Stress Induced Se	11	0.129	
XBP1(S) activates chaperon	9	0.129	
IRE1alpha activates chaper	9	0.129	
Unfolded Protein Response	10	0.129	Magenta
Apoptosis	12	0.887	
Hemostasis	27	0.887	
Activation of BH3-only prote	4	0.887	Green
Glycosphingolipid metabolis	5	0.887	
Signaling by TGF-beta Recc	7	0.887	
Negative regulation of the P	2	0.887	
HS GAG biosynthesis	4	0.887	

View Options Path Finder Batch Hi

**Node Effect**

Set size for: All nodes

Increase ++ Submit

Note: you can increase size of any particular node by repeatedly clicking on it

**Edge Effect**

Edge shape: Line

Edge width: Default Submit

1. Choose "All highlights"

2. Drag all highlighted nodes aside and zoom in.

# Selecting a group in the network

The screenshot shows a network visualization tool with several panels and a central network graph. The interface includes a Node Explorer table, a Function Explorer table, and a Node Effect section. Four yellow callout boxes provide instructions:

- 1. Choose a color**: Points to a green color selection button in the Node Explorer panel.
- 2A. Choose "Node-neighbours"**: Points to the "Node-neighbours" dropdown menu in the top navigation bar.
- 2B. Click here**: Points to a dashed selection box in the Node Explorer panel.
- 3A. Double click the center node.**: Points to a blue node in the network graph.
- 3B. Circle a group of nodes and they will be highlighted.**: Points to a green circle around a cluster of nodes in the network graph.
- 4. Choose "Highlighted nodes", algorithm and pathway, click "submit" to perform the enrichment analysis.**: Points to the Function Explorer panel, specifically the "Submit" button.

**Node Explorer Table:**

ID	Degree	Betweenness	Status
hsa-mir-24-3p	470	256970	-
hsa-mir-23a-3p	121	82671	-
hsa-mir-29b-3p	100	67337	-
hsa-mir-299-3p	57	37315	-
hsa-mir-190a-5p	54	35637	-
hsa-mir-369-5p	8	5453	-
ATXN7L3B	2	5518.9	
CEP57L1	2	10814	
KIAA1210	2	10814	
NUFIP2	2	2946.7	
PLAG1	2	10598	
PTPN14	2	2946.7	
SSR1	2	10814	
ZNF281	2	10814	
C1QTNF6	2	6193.2	
CCDC117	2	6193.2	
COX20	2	4673.9	
CPT1A	2	4673.9	

**Function Explorer Table:**

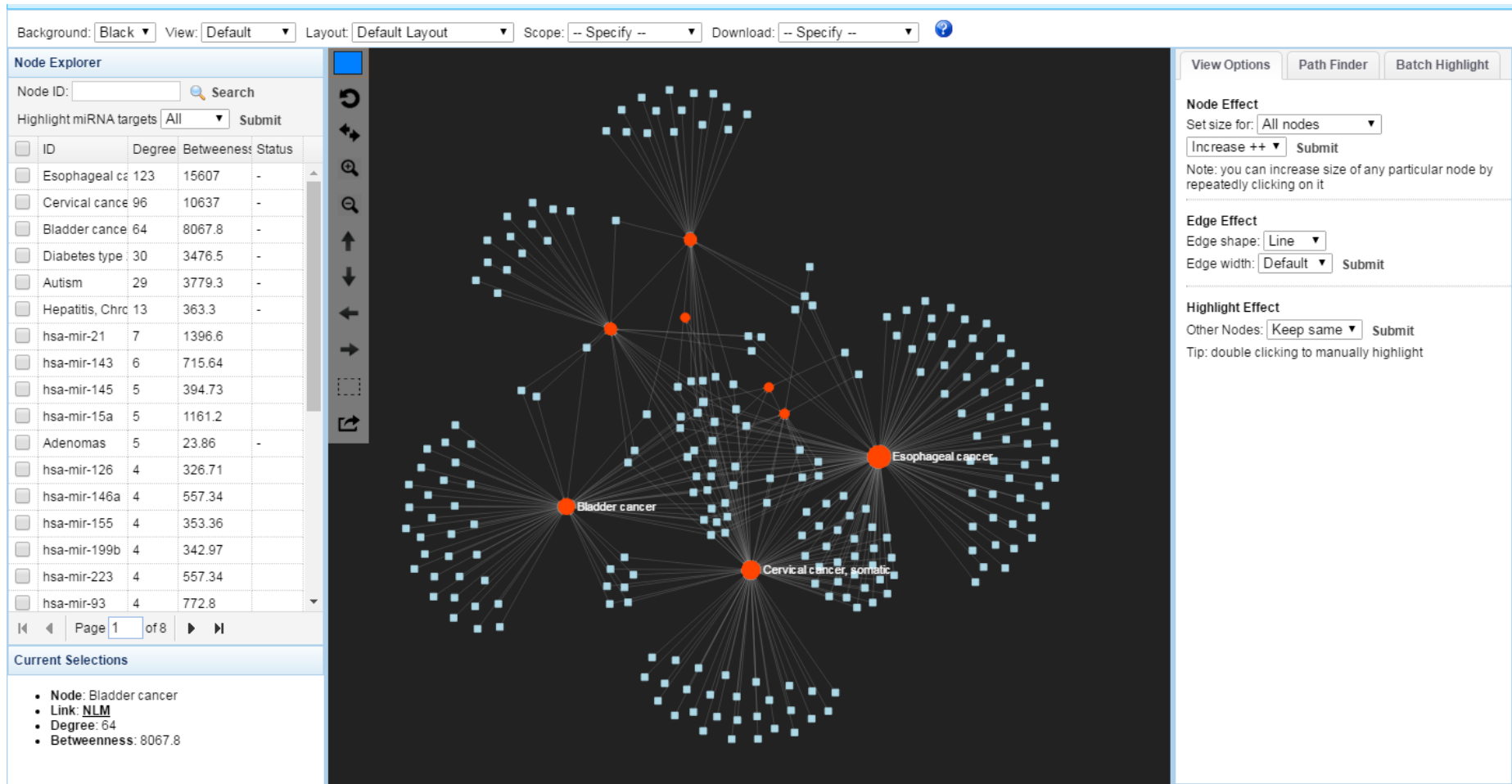
Name	Hits	Pval	Color
MAP kinase kinase kinase a 2		0.633	
nucleotide binding		1	
magnesium ion binding			

**Node Effect Section:**

Set size for: All nodes  
Increase ++ Submit  
Note: you can increase size of any particular node by repeatedly clicking on it

Edge shape: Line  
Edge width: Default Submit

# Network for other targets



- For diseases, small molecules, lncRNAs and epigenetic modifiers, miRNet does not perform the functional enrichment analysis

# Configuring the general visualization feature

Background: White View: Default Layout: Large Graph Layout Scope: -- Specify -- Download: -- Specify --

Node Explorer

Change to white background

Change different layouts

Download the network in different formats.

Function Explorer

All genes  
Hypergeometric test  
KEGG Submit

Name	Hits	Pval	Color
Epstein-Barr virus infection	3	0.125	
Cell cycle	2	0.444	
Hepatitis B	2	0.444	
Measles	2	0.444	
Transcriptional misregulation of gene expression	2	0.527	
Viral carcinogenesis	2	0.571	
Glycolysis / Gluconeogenesis	1	1	
Cysteine and methionine metabolism	1	1	
Pyruvate metabolism	1	1	
Propanoate metabolism	1	1	
Metabolic pathways	1	1	
RNA degradation	1	1	
Spliceosome	1	1	
ErbB signaling pathway	1	1	

View Options Path Finder Batch Hit

Node Effect  
Set size for: All nodes  
Increase ++ Submit  
Note: you can increase size of any particular node by repeatedly clicking on it

Edge Effect  
Edge shape: Line  
Edge width: Default Submit

Current Selections

- Node: DDX5
- Link: Entrez
- Degree: 2
- Betweenness: 5.7342



# View Options

View Options Path Finder Highlight

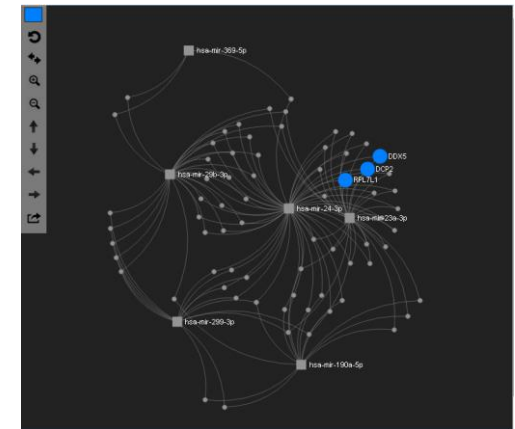
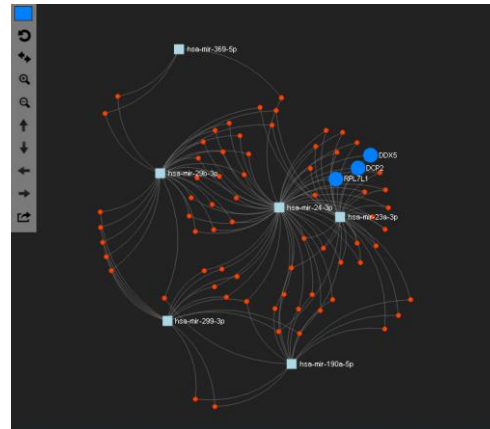
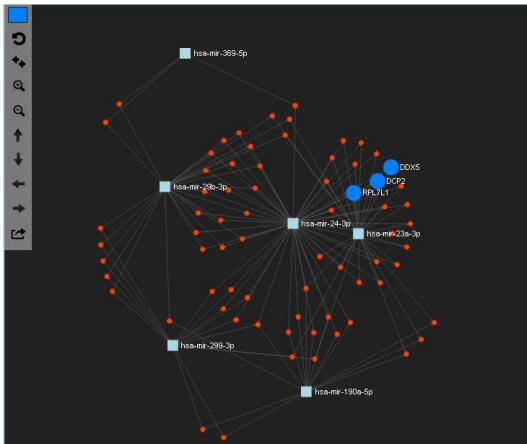
**Node Effect**  
Set size for: Selected Nodes ▾  
Increase ++ ▾ Submit  
Note: you can increase size of any particular node by repeatedly clicking on it

View Options Path Finder Highlight

**Edge Effect**  
Edge shape: Curve ▾  
Edge width: Thick ▾ Submit

View Options Path Finder Highlight

**Highlight Effect**  
Other Nodes: Dim down ▾ Submit  
Tip: double clicking to manually highlight



Node Effect: adjust the node size. You can increase or decrease the nodes.

Edge Effect : change the edge shape as curve or line. And the edge width as thin, medium and thick

Highlight Effect : for other nodes you can choose dim down or hide.

**==END==**