

A network diagram on a dark background showing relationships between miRNAs. Nodes are represented by small squares (light blue) and circles (orange). The nodes are interconnected by thin white lines. Four specific nodes are highlighted with white text 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' is particularly well-connected to many other nodes.

miRNet Tutorial

Starting with expression data

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

- Perform differential expression analysis of data generated in miRNA functional analysis for miRNet
 - Microarray
 - RNA-seq
 - RT-qPCR

Starting from the expression data

The screenshot displays the miRNet website interface. At the top, the title 'miRNet -- network-based visual analysis of miRNAs, targets and functions' is shown. Below the title, there are navigation links for Home, FAQs, Tutorials, Resources, and About. The main content area is divided into three sections: News & Updates, Overview, and a central diagram. The diagram illustrates the workflow for starting from expression data, with a yellow box highlighting the 'Click here to start with the expression data for mRNA/miRNA' step. The diagram shows a central 'miRNA' node connected to 'mRNA', 'Small molecule', 'Disease', 'IncRNA', and 'Epigenetic modifier'. The 'mRNA' node is further connected to 'Microarray', 'RNAseq', and 'RT-qPCR'. A yellow box with arrows points to the 'Microarray', 'RNAseq', and 'RT-qPCR' nodes, indicating that these are the starting points for the workflow.

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

Home ? FAQs Tutorials Resources About

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

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.

Click on an **expression data** source to start with the expression data for mRNA/miRNA

Microarray RNAseq RT-qPCR mRNA miRNA Small molecule Disease IncRNA Epigenetic modifier

Xia Lab @ McGill (last updated 2017-12-26)

Data Formatting



- Manipulate data headings in a spreadsheet program like MS Excel
- Save as a **tab delimited** .txt file
- The headings **#NAME** and **#CLASS:** (**all capital letters**) must be used
 - **#NAME** is for sample names (first row in your data)
 - **#CLASS** is for the clinical metadata.

The screenshot below shows the labels for the experimental condition.

#NAME	Sample1	Sample2	Sample3	Sample4	Sample5	Sample6	Sample7	Sample8	Sample9
#CLASS	Y	N	N	Y	N	Y	Y	N	N
100_g_at	-3.06	-2.25	-1.15	-6.64	0.4	1.08	1.22	1.02	1.15
1000_at	-1.36	-0.67	-0.17	-0.97	-2.32	-5.06	0.28	1.32	0.73
1002_f_at	1.61	-0.27	0.71	-0.62	0.14		0.11	0.98	0.54
1008_f_at	0.93	1.29	-0.23	-0.74	-2	-1.25	1.07	1.27	1.02

Data Upload

Process your microarray expression data below

① Data Upload 	Upload file	<input type="button" value="Browse..."/> No file selected.	 <input type="button" value="Submit"/>
② Annotation	Specify organism	<input type="text" value="H. sapiens (human)"/>	<input type="button" value="Submit"/>
	ID type	<input type="text" value="Affymetrix Human Genome U95 (chip hgu95av2)"/>	<input type="button" value="Submit"/>

A green check will appear to indicate each step is successfully completed

Step 1 : upload a well formatted file (you can try the example first).

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

Hover over the question marks for more information about each step.

Data Annotation

Annotation ✓	Specify organism	H. sapiens (human)	Submit
	ID type	Affymetrix Human Genome U95 (chip hgu95av2)	
	Tissue (human only)	Bone marrow (598)	

- Specifying the organism type and ID type allows miRNet to annotate your data;
- Eight organisms are supported;
- Entrez ID, Ensembl ID, gene symbol, miRNA ID and miRNA accession are supported for RNA-seq and RT-qPCR analysis;
- Affymetrix, Illumina and Agilent Microarray probe ID are supported for Microarray analysis;
- Supporting 53 tissues for human miRNA annotation.

Data Normalization

Microarray Profiling

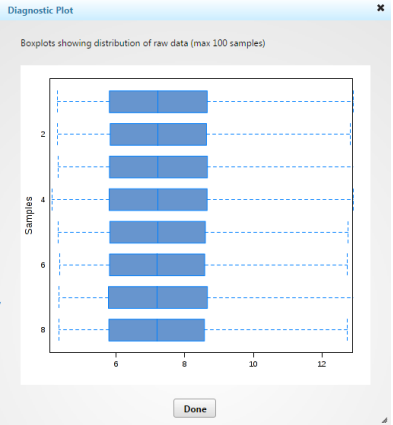
② Annotation ✓

ID type: Affymetrix Human Genome U95 (chip hgu95av2)

③ Normalization ✓

Normalization procedure: -- No normalization --

[View Data](#) [Submit](#)



Diagnostic Plot

Boxplots showing distribution of raw data (max 100 samples)

Samples: 2, 4, 6, 8

Done

The diagnostic plot shows a distribution of raw data for 8 samples. The y-axis is labeled 'Samples' and ranges from 0 to 8. The x-axis ranges from 0 to 12. Each sample has a blue boxplot showing the distribution of raw data. A blue arrow points from the 'View Data' button in the interface to the diagnostic plot.

- This example dataset has been normalized and needed no normalization
- If raw data is uploaded, normalization can be applied
 - Different normalization methods are provided for different data types

Data Analysis

④ Comparisons of Interest	Specify comparison <input type="text" value="absent"/> versus <input type="text" value="present"/>	<input type="button" value="Submit"/>
⑤ Feature Selection	Adjusted p-value: <input type="text" value="0.01"/> Log2 fold change: <input type="text" value="1.0"/> Directions: <input type="text" value="Both directions"/>	<input type="button" value="± Download Result"/> <input type="button" value="Submit"/>
⑥ Specify Network	Choose target <input type="text" value="microRNA"/>	<input type="button" value="Submit"/>

If there is an error with matching your data to our library, please download your result and manually modify your data label. More details in FAQ #5

Both direction
Upregulate only
Downregulate only

If upload data is gene, only miRNA network can be presented. If the data is miRNA, you can choose gene, disease, molecule, lncRNA and epigenetic modifier network

Click "Proceed" to the interaction table

Perform Data Filtering

Data Filter Dialog

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.

Data Filter Dialog

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

Data Filter Dialog

Target Column:	Method
Value Criterion:	(Character) Containing
	CLIP
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

Microarray Profiling > 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.

Only keep the method contains "CLIP"

Data Filter

Reset

Download

miRNA ↕	Link	Tissue	Target:Gene ↕	Link	Method ▾	Literature ↕	Action
<input type="text"/>			<input type="text"/>				
hsa-mir-16-5p	miRBase	Breast cancerous tissues	SLC29A1	Entrez	PAR-CLIP//Proteomics	18668040 , 21572407 , 20371350	Delete
hsa-let-7b-5p	miRBase	Breast cancerous tissues	RRM1	Entrez	PAR-CLIP	23592263	Delete
hsa-let-7e-5p	miRBase	Breast cancerous tissues	CDKN1A	Entrez	PAR-CLIP	21572407	Delete
hsa-let-7e-5p	miRBase	Breast cancerous tissues	RRM1	Entrez	PAR-CLIP	23592263	Delete
hsa-mir-15a-5p	miRBase	Breast cancerous tissues	SLC29A1	Entrez	PAR-CLIP	21572407 , 20371350	Delete
hsa-mir-17-5p	miRBase	Breast cancerous tissues	BTG2	Entrez	PAR-CLIP	23592263 , 21572407	Delete
hsa-mir-20a-5p	miRBase	Breast cancerous tissues	BTG2	Entrez	PAR-CLIP	23592263 , 21572407	Delete
hsa-mir-27a-3p	miRBase	Breast cancerous tissues	FHL2	Entrez	PAR-CLIP	23592263 , 23446348	Delete
hsa-mir-29a-3p	miRBase	Breast cancerous tissues	CCNA2	Entrez	PAR-CLIP	23592263 , 23446348 , 21572407	Delete
hsa-mir-29a-3p	miRBase	Breast cancerous tissues	ID3	Entrez	PAR-CLIP	26701625	Delete
hsa-mir-29a-3p	miRBase	Breast cancerous tissues	BTG2	Entrez	PAR-CLIP	23592263 , 24398324 , 26701625	Delete
hsa-mir-101-3p	miRBase	Breast cancerous tissues	CDKN1A	Entrez	PAR-CLIP	23592263 , 22012620 , 26701625	Delete
hsa-mir-29b-3p	miRBase	Breast cancerous tissues	CCNA2	Entrez	PAR-CLIP	23592263 , 23446348 , 21572407	Delete
hsa-mir-29b-3p	miRBase	Breast cancerous tissues	ID3	Entrez	PAR-CLIP	26701625	Delete
hsa-mir-29b-3p	miRBase	Breast cancerous tissues	BTG2	Entrez	PAR-CLIP	23592263 , 24398324 , 26701625	Delete

Previous

Proceed

Click "Proceed" to the network builder

Pruning or Expanding Network Data

Home > Microarray Profiling > Interaction Table > Network Builder > Network Viewer

Network Overview:

Number of queries:	75
Number of nodes:	1185 (miRNAs: 1142, Targets: 43)
Number of edges:	1738

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"/>	mirnet1	1185	1738	43	± Download

Network Tools:

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

Summary for the nodes of the network

Perform the network management

Click "Proceed" to the network viewer

Previous Proceed

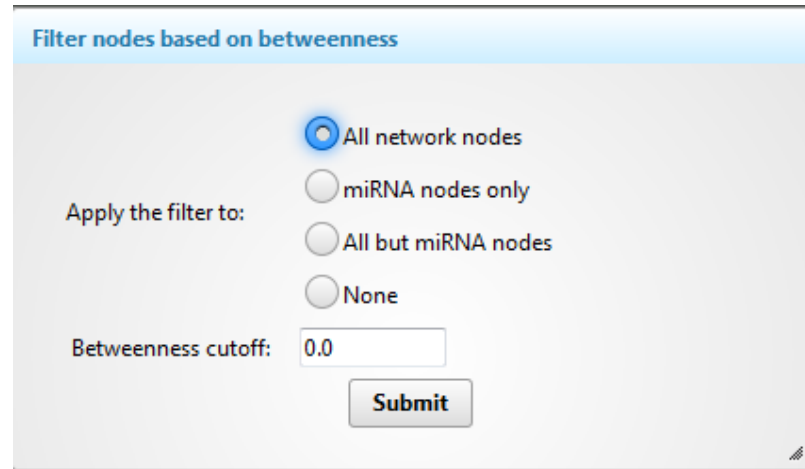
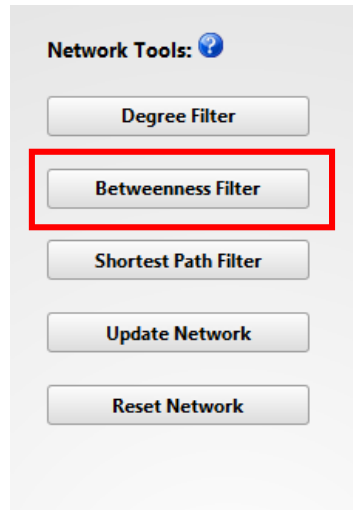
Network tools

The image shows two parts of a web interface. On the left, a sidebar 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 panel 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 a software interface for network analysis. 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 "Shortest Path Filter" callout says "Refresh network as new changes." and the "Reset Network" callout says "Reset the network to default." To the right, a dialog box titled "Reduce connections between densely connected nodes" is open. 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

The screenshot shows a network viewer interface with a central network graph and several side panels. The graph displays a complex network of nodes and edges. Nodes are represented by squares (miRNAs) and circles (targets). The size of the nodes indicates their significance in the network. The interface includes a top navigation bar with options for Background, View, Layout, Scope, and Download. On the left, there is a Node Explorer panel with a search bar and a table of node data. On the right, there is a Function Explorer panel with a query input, algorithm selection, and a table of functional enrichment results. At the bottom, there are panels for Node Effect and Edge Effect settings.

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

Node Explorer

Node ID: Search

Information for nodes and they can be sorted by degree, betweenness and status (only for expression data).

Gene	Count	Score	Value
BTG1	105	108970	1.9003
FHL2	85	82136	-1.5401
SLC29A1	83	67482	-1.3441
POLA2	73	84597	-1.6136
BAK1	73	62451	1.7522
EFNA1	66	68793	1.3762
CSE1L	65	52367	-1.1473
MTHFD1	64	57698	-1.5063
TFPI	64	71220	1.901
IGFBP4	60	45883	-1.4207
CDT1	55	67225	-1.0018
MCM7	50	41668	-2.1023
H2AFX	42	47479	-1.6104

Page 1 of 49

Current Selections

- Node: BTG2
- Link: Entrez
- Degree: 275
- Betweenness: 383380

Functional enrichment analysis

Function Explorer

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

Name	Hits	Pval	Color
DNA replication	5	0.0000769	
Cell cycle	7	0.0000769	
Base excision repair	3	0.0311	
Hepatitis B	4	0.209	
Pyrimidine metabolism	3	0.464	
Viral carcinogenesis	4	0.464	
Bladder cancer	2	0.508	
HTLV-I infection	4	0.754	
p53 signaling pathway	2	0.808	
MicroRNAs in cancer	4	0.808	
Glioma	2	0.808	
Melanoma	2	0.808	
Chronic myeloid leukemia	2	0.808	
DNA replication	2	0.808	

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

The detail for selected node

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

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

Background: Black View: Default Layout: Default Layout

Node Explorer

Node ID: Search

Highlight miRNA targets: All Submit

ID	Degree	Betweenness	Status
<input checked="" type="checkbox"/> BTG2	275	383380	1.2725
<input checked="" type="checkbox"/> CCND1	203	238610	-1.1596
<input checked="" type="checkbox"/> SLC7A5	153	181220	-1.5115
<input checked="" type="checkbox"/> CDKN1A	113	129780	1.416
<input checked="" type="checkbox"/> BTG1	105	108970	1.9003

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

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

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

Function Explorer

Query: Highlighted genes

Algorithm: Hypergeometric test

Database: KEGG Submit

Name	Hits	Pval	Color
RNA degradation	2	0.0564	
p53 signaling pathway	2	0.0564	
Glioma	2	0.0564	
Melanoma	2	0.0564	
Bladder cancer	2	0.0564	
Chronic myeloid leukemia	2	0.0564	
Prostate cancer	2	0.0645	
Cell cycle	2	0.109	
FoxO signaling pathway	2	0.113	
Jak-STAT signaling pathway	2	0.117	
Oxytocin signaling pathway	2	0.117	
Hepatitis B	2	0.117	
Viral carcinogenesis	2	0.166	

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: hsa-let-7g-5p
- Link: [mirBase](#)
- Degree: 3
- Betweenness: 1288.5

Enrichment analysis by selecting pathway

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

Layout: Default Layout Scope: -- Specify -- Download: -- Specify --

Function Explorer

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

Name	Hits	Pval	Color
DNA replication	5	0.0000769	
Cell cycle	7	0.0000769	
Base excision repair	3	0.0311	Blue
Hepatitis B	4	0.209	
Pyrimidine metabolism	3	0.464	Yellow
Viral carcinogenesis	4	0.464	
Bladder cancer	2	0.508	Green
HTLV/Infection	1	0.54	

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

- Bladder cancer
 - CCND1
 - CDKN1A

The genes in this pathway

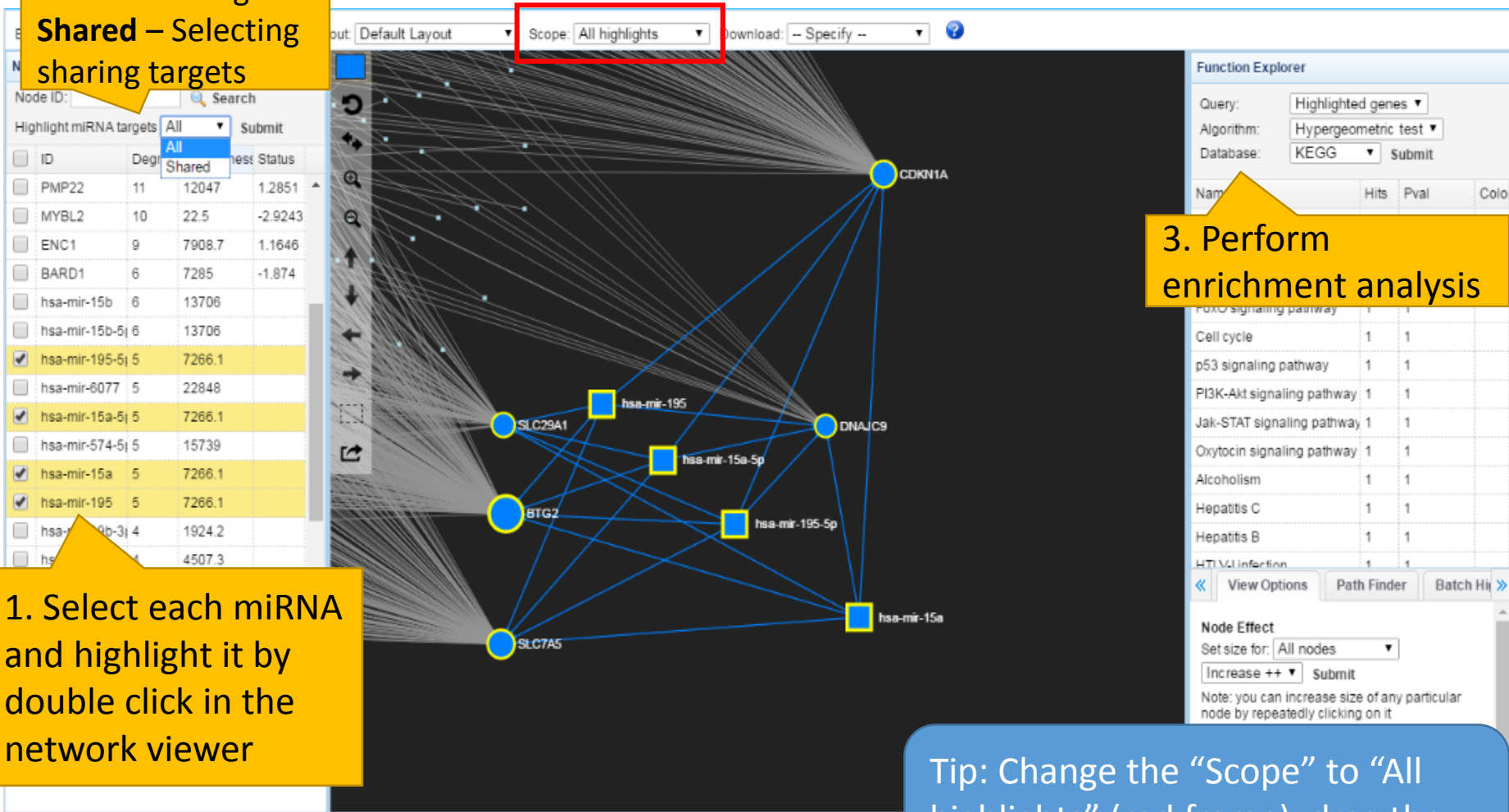
1. Choose an algorithm and a pathway then perform for all genes

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

Enrichment analysis by associated targets

2. All – Selecting all associated targets
Shared – Selecting sharing targets

1. Select each miRNA and highlight it by double click in the network viewer



3. Perform enrichment analysis

Tip: Change the "Scope" to "All highlights" (red frame), drag the whole group aside and zoom in.

Dragging nodes-Current highlights

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

Node Explorer

Node ID: Search

Highlight miRNA targets: All Submit

ID	Degree	Betweenness	Status
<input type="checkbox"/> BTG2	275	383380	1.2725
<input type="checkbox"/> CCND1	203	238610	-1.1596
<input type="checkbox"/> SLC7A5	153	181220	-1.5115
<input type="checkbox"/> CDKN1A	113	129780	1.416
<input type="checkbox"/> BTG1	105	108970	1.9003
<input type="checkbox"/> FHL2	85	82136	-1.5401
<input type="checkbox"/> SLC29A1	83	67482	-1.3441
<input type="checkbox"/> POLA2	73	84597	-1.6136
<input type="checkbox"/> BAK1	73	62451	1.7522
<input type="checkbox"/> EFNA1	66	68793	1.3762
<input type="checkbox"/> CSE1L	65	52367	-1.1473
<input type="checkbox"/> MTHFD1	64	57698	-1.5063
<input type="checkbox"/> TFPI	64	71220	1.901
<input type="checkbox"/> IGFBP4	60	45883	-1.4207
<input type="checkbox"/> CDT1	55	67225	-1.0018
<input type="checkbox"/> MCM7	50	41668	-2.1023

Page 1 of 49

Current Selections

- Node: CCND1
- Link: [Entrez](#)
- Degree: 203
- Betweenness: 238610

Function Explorer

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

Name	Hits	Pval	Color
DNA replication	5	0.0000769	
Cell cycle	7	0.0000769	
Base excision repair	3	0.0311	Blue
Hepatitis B	4	0.209	
Pyrimidine metabolism	3	0.464	Yellow
Viral carcinogenesis	4	0.464	
Bladder cancer	2	0.508	Green
HT infection pathway	4	0.754	
	2	0.808	

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 "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: Default Layout Scope: All highlights Download: -- Specify --

1. Choose "All highlights"

2. Drag all highlighted nodes aside and zoom in.

Node Explorer

Node ID: Search

Highlight miRNA targets All Submit

ID	Degree	Betweenness	Status
<input type="checkbox"/> BTG2	275	383380	1.2725
<input type="checkbox"/> CCND1	203	238610	-1.1596
<input type="checkbox"/> SLC7A5	153	181220	-1.5115
<input type="checkbox"/> CDKN1A	113	129780	1.416
<input type="checkbox"/> BTG1	105	108970	1.9003
<input type="checkbox"/> FHL2	85	82136	-1.5401
<input type="checkbox"/> SLC29A1	83	67482	-1.3441
<input type="checkbox"/> POLA2	73	84597	-1.6136
<input type="checkbox"/> BAK1	73	62451	1.7522
<input type="checkbox"/> EFNA1	66	68793	1.3762
<input type="checkbox"/> CSE1L	65	52367	-1.1473
<input type="checkbox"/> MTHFD1	64	57698	-1.5063
<input type="checkbox"/> TFPI	64	71220	1.901
<input type="checkbox"/> IGFBP4	60	45883	-1.4207
<input type="checkbox"/> CDT1	55	67225	-1.0018
<input type="checkbox"/> MCM7	50	41668	-2.1023
<input type="checkbox"/> H2AFX	42	47479	-1.6104

Current Selections

- Bladder cancer
 - CCND1
 - CDKN1A

Function Explorer

Query: All genes

Algorithm: Hypergeometric test

Database: KEGG Submit

Name	Hits	Pval	Color
DNA replication	5	0.000769	
Cell cycle	7	0.000769	
Base excision repair	3	0.0311	Blue
Hepatitis B	4	0.209	
Pyrimidine metabolism	3	0.464	Yellow
Viral carcinogenesis	4	0.464	
Bladder cancer	2	0.508	Green
HTLV-I infection	4	0.754	
p53 signaling pathway	2	0.808	
MicroRNAs in cancer	4	0.808	
Glioma	2	0.808	
Melanoma	2	0.808	
Chronic myeloid leukemia	2	0.808	
RNA degradation	2	0.827	

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

Expression analysis in network

The screenshot displays a network analysis software interface. The central part is a network graph with nodes of various sizes and colors (red, green, grey) connected by edges. The background is black. The interface includes several panels:

- Node Explorer:** A table with columns for gene IDs and expression values. It lists genes like ID3, CDKN1A, EFNA1, PMP22, and BTG1.
- Function Explorer:** A panel on the right showing a query for "Highlighted genes" using the "Hypergeometric test" algorithm from the "KEGG" database. It displays a list of biological pathways such as "RNA degradation", "Ras signaling pathway", and "Rap1 signaling pathway".
- View Options:** A panel at the bottom right for adjusting node size and edge effects.

Four yellow callout boxes provide instructions:

1. Choose "Expression" here. In the network, red nodes are upregulated and green nodes are downregulated
2. Locate the nodes by clicking each ID or you can skip this step and directly highlight nodes in the network.
3. Double click node and make sure the color has been changed.
4. Choose "Highlighted genes" and pathway. Click "submit"

Selecting a group in the network

1. Choose a color

2A. Choose "Node-neighbours"

2B. Click here

3A. Double click the center node.

3B. Circle a group of nodes and they will be highlighted.

4. Choose "Highlighted nodes", algorithm and pathway, click "submit" to perform the enrichment analysis.

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

Node Explorer

No	ID	Degree	Betweenness	Status
<input type="checkbox"/>	BTG2	221	252550	1.2725
<input type="checkbox"/>	CCND1	157	152620	-1.1596
<input type="checkbox"/>	SLC7A5	121	117090	-1.5115
<input type="checkbox"/>	CDKN1A	87	82222	1.416
<input type="checkbox"/>	BTG1	81	72045	1.9003
<input type="checkbox"/>	POLA2	58	55530	-1.6136
<input type="checkbox"/>	FHL2	68	55278	-1.5401
<input type="checkbox"/>	TFPI	53	48783	1.901
<input type="checkbox"/>	SLC29A1	68	47401	-1.3441
<input type="checkbox"/>	EFNA1	54	45821	1.3762
<input type="checkbox"/>	CDT1	45	43079	-1.0018
<input type="checkbox"/>	BAK1	56	40929	1.7522
<input type="checkbox"/>	MTHFD1	55	40201	-1.5063
<input type="checkbox"/>	CSE1L	55	35628	-1.1473
<input type="checkbox"/>	FEN1	30	32802	-2.1068
<input type="checkbox"/>	H2AFX	34	31430	-1.6104
<input type="checkbox"/>	IGFBP4	51	30794	-1.4207
<input type="checkbox"/>	GREB1	32	26327	-2.1884

Page 1 of 40

Current Selections

Manual Selection

- hsa-let-7d-5p
- hsa-let-7f-5p
- hsa-mir-18a-5p
- hsa-mir-95-3p
- hsa-mir-96-5p
- hsa-mir-101-2p

Function Explorer

Query: Highlighted genes

Algorithm: Hypergeometric test

Database: Reactome Submit

Name	Hits	Color
Signaling by NOTCH	1	
Signal Transduction	1	

Cyclin D associated events 1 1

G1 Phase 1 1

S Phase 1 1

Cell Cycle Mitotic 1 1

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

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

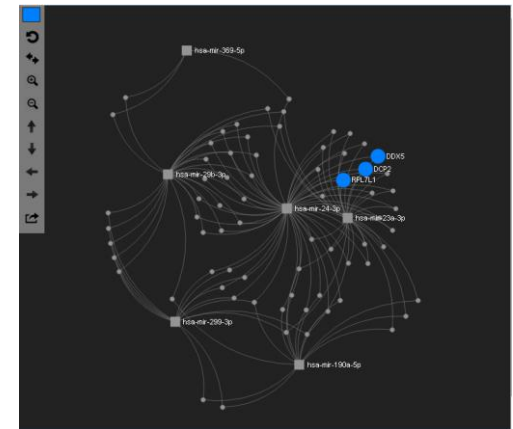
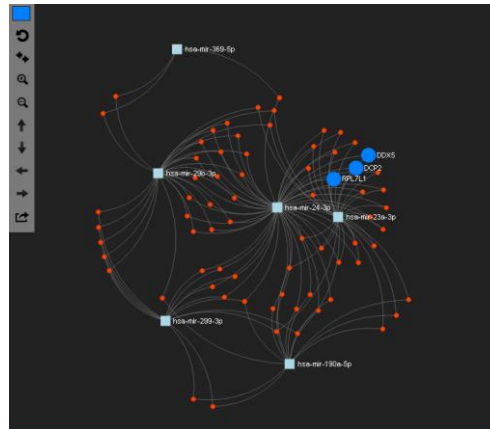
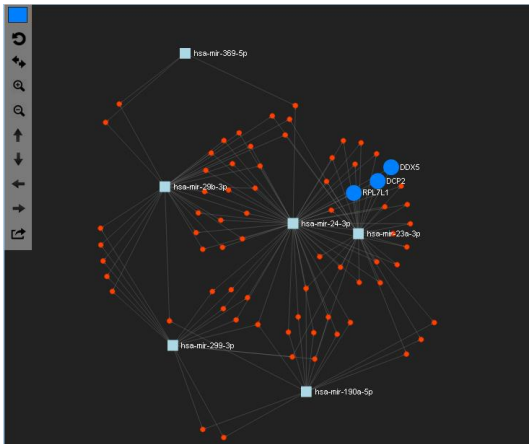
Node Effect
Set size for: Selected Nodes ▾
Increase ++ ▾ Submit
Note: you can increase size of any particular node by repeatedly clicking on it

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==