

# Step-by-Step screen shots for training task of microRNA expression analysis

Week 4 Task 2

# Perform Groups comparison for Colorectal cancer study CRC\_Madhavan\_2013 using more stringent p-value cutoff

- Step-by-step instructions (for more details see screen shots below):
  - Log in to G-DOC at [gdoc.georgetown.edu](http://gdoc.georgetown.edu)
  - Find and Select CRC\_Madhavan\_2013 study in G-DOC
  - Follow the initial steps of microRNA expression analysis demo and select and save the same 2 groups of samples that were saved in microRNA expression demo (samples with or without relapse)
  - Select “group comparison” option from main menu under “study options” and set up comparison of `crc_rel_no` vs `crc_rel_yes` (make sure that those two groups were saved with corresponding names shown in the demo)
  - To compare those two groups: select two groups for comparison from drop down menus: for base group select `crc_rel_no` and for comparison group select `crc_rel_yes`
  - Change the p-value value to 0.01
  - Do not change fold change - keep it unchanged from the default value of 1.5
  - Select microRNA as data type
  - Run the group comparison
  - When analysis shown as complete on notification page open the result by clicking on hyper link
  - In group comparison results window inspect the table of differentially expressed microRNA. Take a record of total number of genes in the table (shown in the right lower corner under the table).
  - Sort the table by the column “Fold Change” in descending order of fold change values
  - Find the gene name on top row of the sorted table – this is the top overexpressed microRNA in colorectal cancer group with relapse as compared to colorectal cancer group without relapse.
  - Explore information about this top microRNA by left clicking on microRNA name and selecting miRBase
  - In miRBase explore validated targets of this top microRNA by clicking on TarBase link
  - In TarBase - explore KEGG pathways to which validated targets are mapped to.(by clicking on the link to mirPath.

To check if this workflow was executed correctly answer two questions in the quiz:

Question 1: what was the total number of micorRNAs in the table? Enter number here: \_\_\_\_\_

Question 2: What was the name of the top overexpressed microRNA in the sorted table? Enter gene name here: \_\_\_\_\_

# Screen shot 1: select study option “group comparison”

The screenshot shows the G-DOC Plus web application interface. The top navigation bar is dark blue with the G-DOC Plus logo and links for Home, Studies, Lists, Analyses, Groups, Notifications, Study Options, and Help. A search bar and a user profile 'yg63' are also present. The main content area has a large heading 'Study Selected!' and a message 'You have picked the study: CRC\_MADHAVAN\_2013\_01\*'. Below this are two buttons: 'Change my study' and 'Help me pick another study'. A small note indicates '\* Lombardi Individum Colorectal Cancer data'. A dropdown menu is open under 'Study Options', showing a list of analysis options. The 'Group Comparison' option is highlighted in blue. Below the dropdown, there are two columns of links: 'Search' and 'Analyze'. The 'Search' column includes links for Genome Browser, Compound/Drug Targets, Findings, Explore Clinical Data and Create Groups, and Gene Expression Data. The 'Analyze' column includes links for Group Comparison, Chromosomal Instability Index, KM Clinical Plot, KM Gene Expression Plots, Classification, and HeatMap Viewer. The URL at the bottom is 'https://gdoc.georgetown.edu/gdoc/groupComparison/index'.

G-DOC<sup>plus</sup>

Home Studies Lists Analyses Groups Notifications Study Options Help

Study Selected

You have picked the study: CRC\_MADHAVAN\_2013\_01\*

Change my study Help me pick another study

\* Lombardi Individum Colorectal Cancer data

Based upon the study you picked, here is a list of tools to analyze your data

**Search**

- Genome Browser
- Compound/Drug Targets
- Findings
- Explore Clinical Data and Create Groups
- Gene Expression Data

**Analyze**

- Group Comparison
- Chromosomal Instability Index
- KM Clinical Plot
- KM Gene Expression Plots
- Classification
- HeatMap Viewer

Study Selected

CRC\_MADHAVAN\_2013\_01

SEARCH

- Genome Browser
- Compound/Drug Targets
- Findings
- Explore Clinical Data and Create Groups
- Gene Expression Data

ANALYZE

- Group Comparison
- Chromosomal Instability Index
- KM Clinical Plot
- KM Gene Expression Plots
- Classification
- HeatMap Viewer

https://gdoc.georgetown.edu/gdoc/groupComparison/index

# Screen shot 2: select baseline group crc\_rel\_no

Group Comparison Analysis

https://gdoc.georgetown.edu/gdoc/groupComparison/index

G-DOC<sup>plus</sup> Home Studies Lists Analyses Groups Notifications Study Options - Help

Perform Group Comparison Analysis

Current Study: CRC\_MADHAVAN\_2013\_01 [change study?](#)

Select a baseline group and a comparison group(s) [?](#)

Select baseline group:

Select comparison group:

p-value:

Fold Change:

Statistical Method:

Multiple Comparison Adjustment:

Data-Type:

Dataset:

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# Screen shot 3: select comparison group crc\_rel\_yes

Group Comparison Analy x

https://gdoc.georgetown.edu/gdoc/groupComparison/index

G-DOC<sup>plus</sup> Home Studies Lists Analyses Groups Notifications Study Options - Help

Perform Group Comparison Analysis

Current Study: CRC\_MADHAVAN\_2013\_01 [change study?](#)

Select a baseline group and a comparison group(s) [?](#)

Select baseline group:

Select comparison group:

p-value:

Fold Change:

Statistical Method:

Multiple Comparison Adjustment:

Data-Type:

Dataset:

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# Screen shot 4: change p-value to 0.01

Group Comparison Analysis

https://gdoc.georgetown.edu/gdoc/groupComparison/index

G-DOC<sup>plus</sup> Home Studies Lists Analyses Groups Notifications Study Options - Help

Perform Group Comparison Analysis

Current Study: CRC\_MADHAVAN\_2013\_01 [change study?](#)

Select a baseline group and a comparison group(s) [?](#)

Select baseline group:

Select comparison group:

p-value:

Fold Change:

Statistical Method:

Multiple Comparison Adjustment:

Data-Type:

Dataset:

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# Screen shot 5: Select Data Type “microRNA”

Group Comparison Analysis x

https://gdoc.georgetown.edu/gdoc/groupComparison/index

G-DOC<sup>plus</sup> Home Studies Lists Analyses Groups Notifications Study Options - Help

Perform Group Comparison Analysis

Current Study: CRC\_MADHAVAN\_2013\_01 [change study?](#)

Select a baseline group and a comparison group(s) [?](#)

Select baseline group:

Select comparison group:

p-value:

Fold Change:

Statistical Method:

Multiple Comparison Adjustment:

Data-Type:

- Select Data Type
- METABOLOMICS
- microRNA
- COPY\_NUMBER
- GENE EXPRESSION

Submit Analysis

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# Screen shot 6: Select Data Set “normalized and filtered tissue”

Group Comparison Analysis x

https://gdoc.georgetown.edu/gdoc/groupComparison/index

G-DOC<sup>plus</sup> Home Studies Lists Analyses Groups Notifications Study Options - Help

Perform Group Comparison Analysis

Current Study: CRC\_MADHAVAN\_2013\_01 [change study?](#)

Select a baseline group and a comparison group(s) [?](#)

Select baseline group:

Select comparison group:

p-value:

Fold Change:

Statistical Method:

Multiple Comparison Adjustment:

Data-Type:

Dataset:

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# Screen shot 7: Check Notifications for completion of analysis

The screenshot shows a web browser window with the address bar displaying <https://gdoc.georgetown.edu/gdoc/notification/index>. The page title is "Notifications". Below the title, a message states: "Below are your latest running analyses. Once completed, click on the Analysis name to see detailed results." A white box contains a list of analyses, all marked as "Complete".

Analysis Name	Status
<a href="#">GROUP_COMPARISON (5:53 12/19/2016)</a>	Complete
<a href="#">GROUP_COMPARISON (5:31 12/19/2016)</a>	Complete
<a href="#">GROUP_COMPARISON (5:30 12/19/2016)</a>	Complete
<a href="#">GROUP_COMPARISON (5:10 12/19/2016)</a>	Complete
<a href="#">GROUP_COMPARISON (4:08 12/19/2016)</a>	Complete
<a href="#">GROUP_COMPARISON (3:24 12/19/2016)</a>	Complete
<a href="#">GROUP_COMPARISON (3:21 12/19/2016)</a>	Complete

The footer of the page includes copyright information: "Copyright © 2014 ICBi. All Rights Reserved", version "G-DQC © 2.0", and links to "RELEASE NOTES", "powered by G-CODE", "ICBi", and "G-DQC @ LOCC". It also lists "SYSTEM REQUIREMENTS", "CITATION POLICY", "PUBLICATIONS USING G-DQC", "DATA ACCESS POLICY", "LICENSE INFO", "CONTACT US", and "G-DQC @ TEAM". Social media icons for LinkedIn, Facebook, and Twitter are present. The bottom of the page shows the URL <https://gdoc.georgetown.edu/gdoc/groupComparison/view/1249586>, the Georgetown University logo, and "Georgetown MEDICAL CENTER".

# Screenshot 8: Open analysis results of the group comparison

G-DQC<sup>plus</sup> Home Studies Lists Analyses Groups Notifications Study Options Help   yg63

Analysis Results  
Current Study: CRC\_MADHAVAN\_2013\_01

Analysis Results

Statistical Method	TTest
Adjustment	NONE
Fold Change	1.5
Pvalue	.01
Study	CRC_PILOT_01
Data File	CRC_PILOT_01_microRNA.Rda
Baseline Group	crc_rel_no
Groups	crc_rel_yes

List Name:

[View HeatMap for selected reporters](#)

Analysis Results

<input type="checkbox"/>	Reporter ID	microRNA	p-value	Fold Change	Mean Baseline (log)	Mean Group (log2)	Std Baseline	Std Group
<input type="checkbox"/>	hsa-miR-147-437	hsa-miR-147	$3.424 \times 10^{-4}$	-7.260	-16.327	-19.186	1.987	1.934
<input type="checkbox"/>	hsa-miR-223#-00	hsa-miR-223#	$6.437 \times 10^{-4}$	-2.663	-7.261	-8.675	1.310	1.083
<input type="checkbox"/>	hsa-miR-148b-43	hsa-miR-148b	$9.463 \times 10^{-4}$	8.279	-9.467	-6.418	2.666	2.713
<input type="checkbox"/>	hsa-miR-23a-437	hsa-miR-23a	$1.227 \times 10^{-3}$	-11.174	-14.592	-18.074	2.174	3.520
<input type="checkbox"/>	hsa-miR-493-439	hsa-miR-493	$1.347 \times 10^{-3}$	-9.335	-9.966	-13.189	2.606	3.249
<input type="checkbox"/>	hsa-let-7a-43731	hsa-let-7a	$1.866 \times 10^{-3}$	2.215	-6.740	-5.592	1.076	1.094
<input type="checkbox"/>	hsa-miR-370-439	hsa-miR-370	$2.582 \times 10^{-3}$	-2.141	-7.731	-8.829	0.992	1.129
<input type="checkbox"/>	hsa-miR-548d-5p	hsa-miR-548d	$2.748 \times 10^{-3}$	-4.028	-12.230	-14.240	2.063	1.834
<input type="checkbox"/>	hsa-miR-542-5p	hsa-miR-542	$2.823 \times 10^{-3}$	-5.661	-10.778	-13.279	1.378	3.130
<input type="checkbox"/>	hsa-miR-342-5p	hsa-miR-342	$4.134 \times 10^{-3}$	-5.113	-13.461	-15.816	2.361	1.654
<input type="checkbox"/>	hsa-miR-1226#-0	hsa-miR-1226#	$4.657 \times 10^{-3}$	-4.108	-10.842	-12.881	1.846	2.405
<input type="checkbox"/>	hsa-miR-218-2#	hsa-miR-218	$5.102 \times 10^{-3}$	-3.087	-14.766	-16.392	1.273	1.798
<input type="checkbox"/>	hsa-miR-934-002	hsa-miR-934	$5.303 \times 10^{-3}$	-13.240	-17.030	-20.756	1.466	2.116
<input type="checkbox"/>	hsa-miR-101#-00	hsa-miR-101#	$5.908 \times 10^{-3}$	-19.260	-15.181	-19.449	3.514	1.811

Page 1 of 1 50 View

# Screenshot 9: Check the table with the analysis results of the group comparison – find a total number of differentially expressed microRNAs (lower right corner under the table)

**G-DOC<sup>plus</sup>** Home Studies Lists Analyses Groups Notifications Study Options Help

Analysis Results  
Current Study: CRC\_MADHAVAN\_2013\_01

**Analysis Results**

Statistical Method	TTest
Adjustment	NONE
Fold Change	1.5
Pvalue	.01
Study	CRC_PILOT_01
Data File	CRC_PILOT_01_microRNA.Rda
Baseline Group	crc_rel_no
Groups	crc_rel_yes

List Name:  
 Save Selected

[View HeatMap for selected reporters](#)

**Analysis Results**

	Reporter ID	microRNA	p-value	Fold Change	Mean Baseline (log)	Mean Group (log2)	Std Baseline	Std Group
<input type="checkbox"/>	hsa-miR-147-437	hsa-miR-147	$3.424 \times 10^{-4}$	-7.260	-16.327	-19.186	1.987	1.934
<input type="checkbox"/>	hsa-miR-223#-00	hsa-miR-223#	$6.437 \times 10^{-4}$	-2.663	-7.261	-8.675	1.310	1.083
<input type="checkbox"/>	hsa-miR-148b-43	hsa-miR-148b	$9.463 \times 10^{-4}$	8.279	-9.467	-6.418	2.666	2.713
<input type="checkbox"/>	hsa-miR-23a-437	hsa-miR-23a	$1.227 \times 10^{-3}$	-11.174	-14.592	-18.074	2.174	3.520
<input type="checkbox"/>	hsa-miR-493-439	hsa-miR-493	$1.347 \times 10^{-3}$	-9.335	-9.966	-13.189	2.606	3.249
<input type="checkbox"/>	hsa-let-7a-43731	hsa-let-7a	$1.866 \times 10^{-3}$	2.215	-6.740	-5.592	1.076	1.094
<input type="checkbox"/>	hsa-miR-370-439	hsa-miR-370	$2.582 \times 10^{-3}$	-2.141	-7.731	-8.829	0.992	1.129
<input type="checkbox"/>	hsa-miR-548d-5p	hsa-miR-548d	$2.748 \times 10^{-3}$	-4.028	-12.230	-14.240	2.063	1.834
<input type="checkbox"/>	hsa-miR-542-5p	hsa-miR-542	$2.823 \times 10^{-3}$	-5.661	-10.778	-13.279	1.378	3.130
<input type="checkbox"/>	hsa-miR-342-5p	hsa-miR-342	$4.134 \times 10^{-3}$	-5.113	-13.461	-15.816	2.361	1.654
<input type="checkbox"/>	hsa-miR-1226#-0	hsa-miR-1226#	$4.657 \times 10^{-3}$	-4.108	-10.842	-12.881	1.846	2.405
<input type="checkbox"/>	hsa-miR-218-2#	hsa-miR-218	$5.102 \times 10^{-3}$	-3.087	-14.766	-16.392	1.273	1.798
<input type="checkbox"/>	hsa-miR-934-002	hsa-miR-934	$5.303 \times 10^{-3}$	-13.240	-17.030	-20.756	1.466	2.116
<input type="checkbox"/>	hsa-miR-101#-00	hsa-miR-101#	$5.908 \times 10^{-3}$	-19.260	-15.181	-19.449	3.514	1.811

Export results Page 1 of 1 50 View 1

# Screenshot 10: Sort a table with the analysis results by column “Fold Change” in descending order (by clicking once on column label); Record of the name of the top overexpressed microRNA (top row, second column)

Analysis Results

https://gdoc.georgetown.edu/gdoc/groupComparison/view/1249586

G-DOC<sup>plus</sup> Home Studies Lists Analyses Groups Notifications Study Options - Help

Fold Change 1.5  
Pvalue .01  
Study CRC\_PILOT\_01  
Data File CRC\_PILOT\_01\_microRNA.Rda  
Baseline Group crc\_rel\_no  
Groups crc\_rel\_yes

List Name:  
  
Save Selected

View HeatMap for selected reporters

Analysis Results

Reporter ID	microRNA	p-value	Fold Change	Mean Baseline (log)	Mean Group (log2)	Std Baseline	Std Group
hsa-miR-218-2#-hsa-miR-218	hsa-miR-218-2#-hsa-miR-218	9.463 x 10 <sup>-4</sup>	8.279	-9.467	-6.418	2.666	2.713
hsa-miR-888-439 hsa-miR-888	hsa-miR-888-439 hsa-miR-888	8.077 x 10 <sup>-3</sup>	7.323	-14.412	-11.539	3.637	2.728
hsa-let-7a-43731 hsa-let-7a	hsa-let-7a-43731 hsa-let-7a	1.866 x 10 <sup>-3</sup>	2.215	-6.740	-5.592	1.076	1.094
hsa-miR-28-3p-4 hsa-miR-28	hsa-miR-28-3p-4 hsa-miR-28	7.679 x 10 <sup>-3</sup>	1.863	-3.203	-2.305	1.063	0.951
hsa-let-7e-43955 hsa-let-7e	hsa-let-7e-43955 hsa-let-7e	7.134 x 10 <sup>-3</sup>	1.655	-3.340	-2.613	0.768	0.847
hsa-miR-520D-3P hsa-miR-520D	hsa-miR-520D-3P hsa-miR-520D	8.372 x 10 <sup>-3</sup>	-1.740	-12.414	-13.213	0.720	1.064
hsa-miR-425#-00 hsa-miR-425#	hsa-miR-425#-00 hsa-miR-425#	7.409 x 10 <sup>-3</sup>	-2.058	-7.131	-8.172	1.338	0.957
hsa-miR-370-439 hsa-miR-370	hsa-miR-370-439 hsa-miR-370	2.582 x 10 <sup>-3</sup>	-2.141	-7.731	-8.829	0.992	1.129
hsa-miR-223#-00 hsa-miR-223#	hsa-miR-223#-00 hsa-miR-223#	6.437 x 10 <sup>-4</sup>	-2.663	-7.261	-8.675	1.310	1.083
hsa-miR-218-2#-hsa-miR-218	hsa-miR-218-2#-hsa-miR-218	5.102 x 10 <sup>-3</sup>	-3.087	-14.766	-16.392	1.273	1.798
hsa-miR-1256-00 hsa-miR-1256	hsa-miR-1256-00 hsa-miR-1256	6.181 x 10 <sup>-3</sup>	-3.088	-14.994	-16.620	1.843	1.527
hsa-miR-548d-5p hsa-miR-548d	hsa-miR-548d-5p hsa-miR-548d	2.748 x 10 <sup>-3</sup>	-4.028	-12.230	-14.240	2.063	1.834
hsa-miR-1226#-0 hsa-miR-1226#	hsa-miR-1226#-0 hsa-miR-1226#	4.657 x 10 <sup>-3</sup>	-4.108	-10.842	-12.881	1.846	2.405
hsa-miR-342-5p hsa-miR-342	hsa-miR-342-5p hsa-miR-342	4.134 x 10 <sup>-3</sup>	-5.113	-13.461	-15.186	2.361	1.654
hsa-miR-542-5p hsa-miR-542	hsa-miR-542-5p hsa-miR-542	2.823 x 10 <sup>-3</sup>	-4.661	-10.778	-13.279	1.278	1.120

Export results Page 1 of 1 50 View 1

# Screenshot 11. Explore the function of the top over-expressed microRNA by left-clicking on microRNA name in top row and selecting “miRBase” from the drop down menu

Analysis Results x miRNA Entry for MI0000 x

https://gdoc.georgetown.edu/gdoc/groupComparison/view/1249586

G-DOC<sup>plus</sup> Home Studies Lists Analyses Groups Notifications Study Options Help

yg63

Fold Change	1.5
Pvalue	.01
Study	CRC_PILOT_01
Data File	CRC_PILOT_01_microRNA.Rda
Baseline Group	crc_rel_no
Groups	crc_rel_yes

List Name:

Save Selected ↓

View HeatMap for selected reporters

Analysis Results

<input type="checkbox"/>	Reporter ID	microRNA	p-value	Fold Change	Mean Baseline (log)	Mean Group (log2)	Std Baseline	Std Group
<input type="checkbox"/>	hsa-miR-148b-43	<a href="#">hsa-miR-148b-43</a>			-9.467	-6.418	2.666	2.713
<input type="checkbox"/>	hsa-miR-888-439	hsa-miR-888-439			-14.412	-11.539	3.637	2.728
<input type="checkbox"/>	hsa-let-7a-43731	hsa-let-7a-43731			-6.740	-5.592	1.076	1.094
<input type="checkbox"/>	hsa-miR-28-3p-4	hsa-miR-28-3p-4			-3.203	-2.305	1.063	0.951
<input type="checkbox"/>	hsa-let-7e-43955	hsa-let-7e-43955	$7.134 \times 10^{-3}$	1.655	-3.340	-2.613	0.768	0.847
<input type="checkbox"/>	hsa-miR-520D-3P	hsa-miR-520D-3P	$8.372 \times 10^{-3}$	-1.740	-12.414	-13.213	0.720	1.064
<input type="checkbox"/>	hsa-miR-425#-00	hsa-miR-425#-00	$7.409 \times 10^{-3}$	-2.058	-7.131	-8.172	1.338	0.957
<input type="checkbox"/>	hsa-miR-370-439	hsa-miR-370	$2.582 \times 10^{-3}$	-2.141	-7.731	-8.829	0.992	1.129
<input type="checkbox"/>	hsa-miR-223#-00	hsa-miR-223#	$6.437 \times 10^{-4}$	-2.663	-7.261	-8.675	1.310	1.083
<input type="checkbox"/>	hsa-miR-218-2#	hsa-miR-218	$5.102 \times 10^{-3}$	-3.087	-14.766	-16.392	1.273	1.798
<input type="checkbox"/>	hsa-miR-1256-00	hsa-miR-1256	$6.181 \times 10^{-3}$	-3.088	-14.994	-16.620	1.843	1.527

View in miRBase  
Search in Entrez  
Search in iHOP

# Screenshot 13: explore validated targets for top overexpressed miRNA in TarBase 7.0

The screenshot displays the TarBase 7.0 web interface. The top navigation bar includes links for HOME, SOFTWARE, PUBLICATIONS, and CONTACT. The left sidebar contains a login section with fields for Username and Password, a 'Remember me next time' checkbox, and a 'Login' button. Below the login section, there are links for 'Forgot your password?' and 'Sign up for free! or take a tour'. The main content area features a search bar with the query 'MIMAT0004699'. Below the search bar, a table lists validated targets for the miRNA. The table has four columns: Gene name, miRNA name, Methods, and Pred.Score. The targets are listed in descending order of prediction score. To the right of the table, there is a 'Related Pathways' section and a 'Filters' section with various dropdown menus for filtering the results.

**DIANA TOOLS**

HOME SOFTWARE PUBLICATIONS CONTACT

**Software » TarBase v7.0**

**Please cite:**  
I. S. Vlachos, M. D. Paraskevopoulou, D. Karagkouni, G. Georgakilas, T. Vergoulis, I. Kanellos, I.-L. Anastasopoulos, S. Manioui, K. Karathanou, D. Kalfakakou, A. Fevgas, T. Dalamagas and A. G. Hatzigeorgiou. DIANA-TarBase v7.0: indexing more than half a million experimentally supported miRNA:mRNA interactions. Nucleic Acids Res. (2014)

**Data Download:**  
We have updated the bulk download module, which simplifies the download process! Please find the new online form by following this [link](#)

Search: MIMAT0004699

Gene name	miRNA name	Methods	Pred.Score
MAN1A1 (hsa)	hsa-miR-148b-5p	IP	0.842
PPP1CC (hsa)	hsa-miR-148b-5p	IP	0.832
FOXJ3 (hsa)	hsa-miR-148b-5p	IP	0.825
APPL1 (hsa)	hsa-miR-148b-5p	IP	0.849
CSNK1A1 (hsa)	hsa-miR-148b-5p	IP	0.786
CALR (hsa)	hsa-miR-148b-5p	IP	0.779
ICE1 (hsa)	hsa-miR-148b-5p	IP	0.765
RAC1 (hsa)	hsa-miR-148b-5p	IP	0.740
SKI (hsa)	hsa-miR-148b-5p	IP	0.735
PRPF38B (hsa)	hsa-miR-148b-5p	IP	0.712
TFAM (hsa)	hsa-miR-148b-5p	IP	0.686
VAMP3 (hsa)	hsa-miR-148b-5p	IP	0.660
AGO1 (hsa)	hsa-miR-148b-5p	IP	0.656
MAPK1 (hsa)	hsa-miR-148b-5p	IP	0.642
MTF2 (hsa)	hsa-miR-148b-5p	IP	0.614

**Related Pathways**

**Filters**

- Species
- Method Type
- Method
- Regulation type
- Validation type
- Validated as
- Source
- Publication year: 1900
- Only publications published after the selected year will be presented.
- [Apply Filter!](#)
- Prediction score: 0

# Screenshot 14: explore KEGG pathways for validated targets of top overexpressed miRNA in mirPath 3.0

Analysis Results x iHOP - Information Hype x Homo sapiens microRNA x DIANA TOOLS - TarBase x DIANA TOOLS - mirPath x

snf-515788.vm.oceanos.gnet.gr/#mirnas=hsa-miR-148b-5p&methods=Tarbase&selection=0

mirPath v.3

New search

KEGG analysis

Species: Human

Gene filter: [determine genes \(optional\)](#)

Add miRNAs:  TarBase v7.0 or [upload a file](#)

[Reverse Search](#)

[Run example](#)

Hide lists added ^

hsa-miR-148b-5p TarBase [disable](#) [see genes](#) (370)

Select the way to merge results: [genes union](#) [genes intersection](#) [pathways union](#) [pathways intersection](#)

P-value threshold: 0.05 Apply default

In order to see HeatMap select pathway intersection or pathway union.

[Show Heatmap](#) [Show microRNA/Pathway Clusters](#)

☒ Significance Clusters/Heatmap  
☐ Targeted Pathways Clusters/Heatmap

# KEGG pathway	p-value	#genes	#miRNAs	<a href="#">download results</a>
1. <a href="#">Proteoglycans in cancer</a> (hsa05205)	8.91841509156e-05	12 <a href="#">see genes</a>	1 <a href="#">details</a>	
2. <a href="#">Huntington's disease</a> (hsa05016)	0.00315727751792	7 <a href="#">see genes</a>	1 <a href="#">details</a>	
3. <a href="#">Arrhythmogenic right ventricular cardiomyopathy (ARVC)</a> (hsa05412)	0.00485062767494	3 <a href="#">see genes</a>	1 <a href="#">details</a>	
4. <a href="#">Glioma</a> (hsa05214)	0.00556691883448	7 <a href="#">see genes</a>	1 <a href="#">details</a>	
5. <a href="#">Other glycan degradation</a> (hsa00511)	0.00803852967179	1 <a href="#">see genes</a>	1 <a href="#">details</a>	
6. <a href="#">TGF-beta signaling pathway</a> (hsa04350)	0.0244544674713	5 <a href="#">see genes</a>	1 <a href="#">details</a>	
7. <a href="#">mTOR signaling pathway</a> (hsa04150)	0.0324731898171	8 <a href="#">see genes</a>	1 <a href="#">details</a>	
8. <a href="#">Adherens junction</a> (hsa04520)	0.0456017285821	8 <a href="#">see genes</a>	1 <a href="#">details</a>	

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