
MicroRNA analysis

Table of Contents

Use the unfiltered Excel data	1
Remove any miRNA that is detected in 3 or fewer samples	1
Replace any undetected value (Inf) with the average of the expression of	2
Print the first 5 row (genes) and first 6 columns (samples) of your data	2
You should end up with data that is the same as the filtered Excel data.	3
For each sample, find the CT0 values by averaging the CT values of RNU44,	3
The result of the previous step will give you normalized deltaCT values.	3
For each miRNA, find the average of all healthy deltaCT values and	3
For each miRNA, subtract the average healthy deltaCT values from the	4
Calculate $2^{\Delta\Delta CT}$, which are the fold change values.	4
Replace any fold change value x that is less than 1, with its negative inverse (-1/x)	4
Print the names and fold changes of the top-10 most changing miRNAs	4
Using the deltaCT values, find the significantly different miRNAs between	5
Print the names and p-values of the top-10 most significantly different	5
The print-out of gene request above are limited to keep your output small.	5
Find which mRNAs are the predicted targets of the significant miRNAs from	6
Perform enrichment of the targets using the DAVID webservice. List the	13
Gene set enrichment with tens of genes will not get any enriched annotations	14

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Use the unfiltered Excel data

matrix is a much more optimizing method to import data

```
data_miRNAs = readmatrix('CRPS_unfiltered.xlsx');
miRNAs = readvars('CRPS_unfiltered.xlsx');
data_miRNAs(:,1) = [];
vars_miRNAs = readcell('CRPS_unfiltered.xlsx');

control = find(contains(vars_miRNAs(1,:), 'control'));
patients = find(contains(vars_miRNAs(1,:), 'patient'));
```

Remove any miRNA that is detected in 3 or fewer samples

```
elimrows = true(size(data_miRNAs,1),1);
for row = 1:size(data_miRNAs,1)
    if size(unique(data_miRNAs(row,:)),2) <= 4
        elimrows(row) = false;
    end
end
data_miRNAs = data_miRNAs(elimrows,:);
miRNAs = miRNAs(elimrows,:);
```

Replace any undetected value (Inf) with the average of the expression of

that miRNA in the rest of the samples

```
temparr = []; tempave = []; TF = [];  
for row = 1:size(data_miRNAs,1)  
    temparr = data_miRNAs(row,:);  
    TF = isinf(temparr);  
    temparr = temparr(~TF);  
    tempave = mean(temparr);  
    for col = 1:size(data_miRNAs,2)  
        if isinf(data_miRNAs(row,col))  
            data_miRNAs(row,col) = tempave;  
        end  
    end  
end  
end
```

Print the first 5 row (genes) and first 6 columns (samples) of your data

of your data

```
T_names = table(miRNAs);  
T_data = array2table(data_miRNAs);  
T = [T_names T_data];  
fprintf('First 5 genes and 6 samples of the filtered data\n')  
disp(T(1:5,1:6))
```

First 5 genes and 6 samples of the filtered data

<i>miRNAs</i>	<i>data_miRNAs1</i>	<i>data_miRNAs2</i>	<i>data_miRNAs3</i>
<i>data_miRNAs4</i>	<i>data_miRNAs5</i>		
{ 'hsa-miR-425' }	18.432	18.539	19.287
17.985	19.948		
{ 'hsa-miR-129-5p' }	33.962	33.675	36.403
33.962	33.962		
{ 'hsa-miR-329' }	33.57	31.332	34.224
29.578	37.798		
{ 'hsa-miR-484' }	14.282	14.232	14.252
13.99	14.676		
{ 'hsa-miR-625' }	25.444	25.188	25.455
24.266	27.167		

You should end up with datda that is the same as the filtered Excel data.

If you get different filtered data, and cannot find out why you are getting different results, abandon your data, use the filtered Excel data.

```
%%%% Filtered Data Matched! %%%%
```

For each sample, find the CT0 values by averaging the CT values of RNU44,

RNU48, and MammU6. Subtract the CT values of that sample with the CT0 of that sample. Finding RNU44 RNU48 & MammU6 data rows

```
expr = 'RNU44|RNU48|MammU6'; indexrow = zeros(size(miRNAs));
for row = 1:size(miRNAs)
    temp = regexp(miRNAs{row},expr, 'once');
    if isempty(temp)
        indexrow(row) = 0;
    else
        indexrow(row) = row;
    end
end
temp = find(indexrow == 0); indexrow(temp,:) = [];
CT0 = mean(data_miRNAs(indexrow,:),1); % get CT0 values
deltaCT_norm = data_miRNAs;
for row = 1:size(deltaCT_norm,1)
    deltaCT_norm(row,:) = deltaCT_norm(row,:) - CT0;
end
```

The result of the previous step will give you normalized deltaCT values.

```
%%%% Normalized deltaCT values obtained! %%%%
```

For each miRNA, find the average of all healthy deltaCT values and

separately, find the average of the patient deltaCT values

```
deltaCT_ctrl = zeros(size(deltaCT_norm,1),1); % preallocation for
healthy values
deltaCT_pat = zeros(size(deltaCT_norm,1),1); % preallocation for
patients values
for row = 1:size(deltaCT_norm,1)
    deltaCT_ctrl(row) = mean(deltaCT_norm(row,control-1));
    deltaCT_pat(row) = mean(deltaCT_norm(row,patients-1));
end
```

For each miRNA, subtract the average healthy deltaCT values from the

average patient deltaCT values. This gives you the deltadelta CT.

```
deltadeltaCT = deltaCT_pat - deltaCT_ctrl;
```

Calculate $2^{\text{deltadeltaCT}}$, which are the fold change values.

```
FC = 2.^(-deltadeltaCT);
```

Replace any fold change value x that is less than 1, with its negative inverse (-1/x)

```
for row = 1:size(FC,1)
    if FC(row) < 1
        FC(row) = (-1/FC(row));
    end
end
```

Print the names and fold changes of the top-10 most changing miRNAs

```
%(either up or down regulation, i.e., order by descending
%absolute fold change)
[~,FCindex] = sort(abs(FC),'descend');
T_namesFC = table(miRNAs(FCindex));
T_namesFC.Properties.VariableNames{1} = 'miRNAs'; %rename column
T_FC = array2table(FC(FCindex));
T_FC.Properties.VariableNames{1} = 'Fold Changes Values'; % rename
column
TFC = [T_namesFC T_FC];
TFC.Properties.Description = 'Top 10 Most Changing miRNAs';
fprintf('Top 10 Most Changing miRNAs\n')
disp(TFC(1:10,:))
```

Top 10 Most Changing miRNAs

<i>miRNAs</i>	<i>Fold Changes Values</i>
{ 'hsa-miR-939' }	-5.7578
{ 'hsa-miR-25#' }	-5.0779
{ 'hsa-miR-17#' }	-4.2824
{ 'hsa-miR-223' }	-3.8947
{ 'hsa-miR-29b' }	-3.5807
{ 'hsa-let-7c' }	-3.2294
{ 'hsa-miR-133b' }	-3.1393

```
{ 'hsa-miR-18b' }      -3.1148
{ 'hsa-let-7b'  }      -3.0898
{ 'hsa-miR-190' }      -3.0596
```

Using the deltaCT values, find the significantly different miRNAs between

```
%controls and patients.
pvals = mattest(deltaCT_norm(:,control-1),deltaCT_norm(:,patients-1));
```

Print the names and p-values of the top-10 most significantly different

miRNAs (ordered by pvalue)

```
[~,pindex] = sort(pvals,'descend');
T_namesp = table(miRNAs(pindex));
T_namesp.Properties.VariableNames{1} = 'miRNAs'; %rename column
T_pvals = array2table(pvals(pindex));
T_pvals.Properties.VariableNames{1} = 'P-Values'; % rename column
TFC = [T_namesp T_pvals];
TFC.Properties.Description = 'Top 10 Most Significantly Different
    miRNAs';
fprintf('Top 10 Most Significantly Different miRNAs\n')
disp(TFC(1:10,:))
```

```
Top 10 Most Significantly Different miRNAs
      miRNAs      P-Values
```

{ 'hsa-miR-589' }	0.99683
{ 'hsa-miR-27b#' }	0.99166
{ 'hsa-miR-1260' }	0.98559
{ 'hsa-miR-151-3p' }	0.97488
{ 'hsa-miR-551b#' }	0.97481
{ 'hsa-miR-218' }	0.96783
{ 'hsa-miR-30d' }	0.96188
{ 'hsa-miR-29b-1#' }	0.94585
{ 'hsa-miR-1200' }	0.92948
{ 'hsa-miR-149' }	0.92443

The print-out of gene request above are limited to keep your output small.

you will need to define you own p value and or fold change thresholds to be used for selecting significantly different miRNAs for the steps below. Use all differentially expressed genes for the steps below, not just the ones you printed above.

```
newdata = cat(2,miRNAs,num2cell(FC));
newdata = cat(2,newdata,num2cell(pvals));
TF_miRNA = false(size(newdata,1),1);
for row = 1:size(newdata,1)
    if (abs(newdata{row,2}) >= 1.5) && (newdata{row,3} <= 0.01)
        TF_miRNA(row) = true;
    end
end

signf_miRNA = newdata(TF_miRNA,:);
```

Find which mRNAs are the predicted targets of the significant miRNAs from

the CRPS study using TargetScan. Sequelquery

```
targettemp = [];newlist = {};
for row = 1:size(signf_miRNA,1)
    tempstruct = bmes_targetscandb_mir2target(newdata{row,1},0.9);
    if isempty(tempstruct) ~= true
        for row = 1:size(tempstruct)
            newlist = [newlist; tempstruct{row}];
        end
    end
end
newlist = unique(string(newlist));
fprintf('Number of genes from gene list found in pathways is
      %d',length(newlist))

--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
      score>=0.900000 AND mirna IN ("hsa-miR-425","hsa-miR-425-3p","hsa-
miR-425-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
      WHERE score>=0.900000 AND mirna IN ("hsa-miR-129-5p","hsa-
miR-129-5p-3p","hsa-miR-129-5p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
      score>=0.900000 AND mirna IN ("hsa-miR-329","hsa-miR-329-3p","hsa-
miR-329-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
      score>=0.900000 AND mirna IN ("hsa-miR-484","hsa-miR-484-3p","hsa-
miR-484-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
      score>=0.900000 AND mirna IN ("hsa-miR-625","hsa-miR-625-3p","hsa-
miR-625-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
      score>=0.900000 AND mirna IN ("hsa-miR-198","hsa-miR-198-3p","hsa-
miR-198-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
      score>=0.900000 AND mirna IN ("hsa-miR-133b","hsa-miR-133b-3p","hsa-
miR-133b-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
      WHERE score>=0.900000 AND mirna IN ("hsa-miR-193a-5p","hsa-
miR-193a-5p-3p","hsa-miR-193a-5p-5p")
```

```

--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-541","hsa-miR-541-3p","hsa-
miR-541-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
    WHERE score>=0.900000 AND mirna IN ("hsa-miR-483-5p","hsa-
miR-483-5p-3p","hsa-miR-483-5p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-215","hsa-miR-215-3p","hsa-
miR-215-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-99a","hsa-miR-99a-3p","hsa-
miR-99a-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-222","hsa-miR-222-3p","hsa-
miR-222-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
    WHERE score>=0.900000 AND mirna IN ("hsa-miR-518d-5p","hsa-
miR-518d-5p-3p","hsa-miR-518d-5p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-125b","hsa-miR-125b-3p","hsa-
miR-125b-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-196b","hsa-miR-196b-3p","hsa-
miR-196b-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-660","hsa-miR-660-3p","hsa-
miR-660-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-27a","hsa-miR-27a-3p","hsa-
miR-27a-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-218","hsa-miR-218-3p","hsa-
miR-218-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-105","hsa-miR-105-3p","hsa-
miR-105-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
    WHERE score>=0.900000 AND mirna IN ("hsa-miR-199b-5p","hsa-
miR-199b-5p-3p","hsa-miR-199b-5p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-18b","hsa-miR-18b-3p","hsa-
miR-18b-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
    WHERE score>=0.900000 AND mirna IN ("hsa-miR-423-5p","hsa-
miR-423-5p-3p","hsa-miR-423-5p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
    WHERE score>=0.900000 AND mirna IN ("hsa-miR-576-5p","hsa-
miR-576-5p-3p","hsa-miR-576-5p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-301a","hsa-miR-301a-3p","hsa-
miR-301a-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-381","hsa-miR-381-3p","hsa-
miR-381-5p")

```

```
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
  score>=0.900000 AND mirna IN ("hsa-miR-19b","hsa-miR-19b-3p","hsa-
miR-19b-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
  score>=0.900000 AND mirna IN ("hsa-miR-195","hsa-miR-195-3p","hsa-
miR-195-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
  score>=0.900000 AND mirna IN ("hsa-miR-874","hsa-miR-874-3p","hsa-
miR-874-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
  score>=0.900000 AND mirna IN ("hsa-miR-496","hsa-miR-496-3p","hsa-
miR-496-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
  WHERE score>=0.900000 AND mirna IN ("hsa-miR-193a-3p","hsa-
miR-193a-3p-3p","hsa-miR-193a-3p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
  WHERE score>=0.900000 AND mirna IN ("hsa-miR-139-3p","hsa-
miR-139-3p-3p","hsa-miR-139-3p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
  score>=0.900000 AND mirna IN ("hsa-miR-517b","hsa-miR-517b-3p","hsa-
miR-517b-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
  score>=0.900000 AND mirna IN ("hsa-miR-449b","hsa-miR-449b-3p","hsa-
miR-449b-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
  score>=0.900000 AND mirna IN ("hsa-miR-320","hsa-miR-320-3p","hsa-
miR-320-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
  score>=0.900000 AND mirna IN ("hsa-miR-217","hsa-miR-217-3p","hsa-
miR-217-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
  score>=0.900000 AND mirna IN ("hsa-miR-616","hsa-miR-616-3p","hsa-
miR-616-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
  score>=0.900000 AND mirna IN ("hsa-miR-98","hsa-miR-98-3p","hsa-
miR-98-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
  WHERE score>=0.900000 AND mirna IN ("hsa-miR-501-5p","hsa-
miR-501-5p-3p","hsa-miR-501-5p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
  WHERE score>=0.900000 AND mirna IN ("hsa-miR-486-5p","hsa-
miR-486-5p-3p","hsa-miR-486-5p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
  score>=0.900000 AND mirna IN ("hsa-miR-335","hsa-miR-335-3p","hsa-
miR-335-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
  score>=0.900000 AND mirna IN ("hsa-miR-374b","hsa-miR-374b-3p","hsa-
miR-374b-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
  score>=0.900000 AND mirna IN ("hsa-miR-130a","hsa-miR-130a-3p","hsa-
miR-130a-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
  score>=0.900000 AND mirna IN ("hsa-miR-570","hsa-miR-570-3p","hsa-
miR-570-5p")
```

```

--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-100","hsa-miR-100-3p","hsa-
miR-100-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-let-7e","hsa-let-7e-3p","hsa-
let-7e-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-410","hsa-miR-410-3p","hsa-
miR-410-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
    WHERE score>=0.900000 AND mirna IN ("hsa-miR-188-3p","hsa-
miR-188-3p-3p","hsa-miR-188-3p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-190","hsa-miR-190-3p","hsa-
miR-190-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
    WHERE score>=0.900000 AND mirna IN ("hsa-miR-219-5p","hsa-
miR-219-5p-3p","hsa-miR-219-5p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-340","hsa-miR-340-3p","hsa-
miR-340-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-27b","hsa-miR-27b-3p","hsa-
miR-27b-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-629","hsa-miR-629-3p","hsa-
miR-629-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
    WHERE score>=0.900000 AND mirna IN ("hsa-miR-450b-5p","hsa-
miR-450b-5p-3p","hsa-miR-450b-5p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
    WHERE score>=0.900000 AND mirna IN ("hsa-miR-671-3p","hsa-
miR-671-3p-3p","hsa-miR-671-3p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-494","hsa-miR-494-3p","hsa-
miR-494-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
    WHERE score>=0.900000 AND mirna IN ("hsa-miR-548d-3p","hsa-
miR-548d-3p-3p","hsa-miR-548d-3p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
    WHERE score>=0.900000 AND mirna IN ("hsa-miR-532-5p","hsa-
miR-532-5p-3p","hsa-miR-532-5p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
    WHERE score>=0.900000 AND mirna IN ("hsa-miR-509-5p","hsa-
miR-509-5p-3p","hsa-miR-509-5p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-182","hsa-miR-182-3p","hsa-
miR-182-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-132","hsa-miR-132-3p","hsa-
miR-132-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-29b","hsa-miR-29b-3p","hsa-
miR-29b-5p")

```

```

--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-370","hsa-miR-370-3p","hsa-
miR-370-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-183","hsa-miR-183-3p","hsa-
miR-183-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-32","hsa-miR-32-3p","hsa-
miR-32-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-382","hsa-miR-382-3p","hsa-
miR-382-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-92a","hsa-miR-92a-3p","hsa-
miR-92a-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-379","hsa-miR-379-3p","hsa-
miR-379-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-145","hsa-miR-145-3p","hsa-
miR-145-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
    WHERE score>=0.900000 AND mirna IN ("hsa-miR-369-3p","hsa-
miR-369-3p-3p","hsa-miR-369-3p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
    WHERE score>=0.900000 AND mirna IN ("hsa-miR-361-5p","hsa-
miR-361-5p-3p","hsa-miR-361-5p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
    WHERE score>=0.900000 AND mirna IN ("hsa-miR-491-3p","hsa-
miR-491-3p-3p","hsa-miR-491-3p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-29c","hsa-miR-29c-3p","hsa-
miR-29c-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-let-7a","hsa-let-7a-3p","hsa-
let-7a-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-504","hsa-miR-504-3p","hsa-
miR-504-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-29a","hsa-miR-29a-3p","hsa-
miR-29a-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-137","hsa-miR-137-3p","hsa-
miR-137-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-651","hsa-miR-651-3p","hsa-
miR-651-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-130b","hsa-miR-130b-3p","hsa-
miR-130b-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-506","hsa-miR-506-3p","hsa-
miR-506-5p")

```

```

--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
      WHERE score>=0.900000 AND mirna IN ("hsa-miR-339-5p","hsa-
miR-339-5p-3p","hsa-miR-339-5p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
      WHERE score>=0.900000 AND mirna IN ("hsa-miR-574-3p","hsa-
miR-574-3p-3p","hsa-miR-574-3p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
      score>=0.900000 AND mirna IN ("hsa-miR-99b","hsa-miR-99b-3p","hsa-
miR-99b-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
      score>=0.900000 AND mirna IN ("hsa-miR-187","hsa-miR-187-3p","hsa-
miR-187-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
      score>=0.900000 AND mirna IN ("hsa-miR-223","hsa-miR-223-3p","hsa-
miR-223-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
      score>=0.900000 AND mirna IN ("hsa-miR-193b","hsa-miR-193b-3p","hsa-
miR-193b-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
      score>=0.900000 AND mirna IN ("hsa-miR-34a","hsa-miR-34a-3p","hsa-
miR-34a-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
      score>=0.900000 AND mirna IN ("hsa-miR-93","hsa-miR-93-3p","hsa-
miR-93-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
      WHERE score>=0.900000 AND mirna IN ("hsa-miR-654-5p","hsa-
miR-654-5p-3p","hsa-miR-654-5p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
      score>=0.900000 AND mirna IN ("hsa-miR-523","hsa-miR-523-3p","hsa-
miR-523-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
      score>=0.900000 AND mirna IN ("hsa-miR-495","hsa-miR-495-3p","hsa-
miR-495-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
      score>=0.900000 AND mirna IN ("hsa-miR-412","hsa-miR-412-3p","hsa-
miR-412-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
      WHERE score>=0.900000 AND mirna IN ("hsa-miR-486-3p","hsa-
miR-486-3p-3p","hsa-miR-486-3p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
      score>=0.900000 AND mirna IN ("hsa-miR-598","hsa-miR-598-3p","hsa-
miR-598-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
      score>=0.900000 AND mirna IN ("hsa-miR-26a","hsa-miR-26a-3p","hsa-
miR-26a-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
      WHERE score>=0.900000 AND mirna IN ("hsa-miR-491-5p","hsa-
miR-491-5p-3p","hsa-miR-491-5p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
      score>=0.900000 AND mirna IN ("hsa-let-7d","hsa-let-7d-3p","hsa-
let-7d-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
      score>=0.900000 AND mirna IN ("hsa-miR-214","hsa-miR-214-3p","hsa-
miR-214-5p")

```

```
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
    WHERE score>=0.900000 AND mirna IN ("hsa-miR-886-3p","hsa-
miR-886-3p-3p","hsa-miR-886-3p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-451","hsa-miR-451-3p","hsa-
miR-451-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
    WHERE score>=0.900000 AND mirna IN ("hsa-miR-199a-3p","hsa-
miR-199a-3p-3p","hsa-miR-199a-3p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
    WHERE score>=0.900000 AND mirna IN ("hsa-miR-369-5p","hsa-
miR-369-5p-3p","hsa-miR-369-5p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-141","hsa-miR-141-3p","hsa-
miR-141-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
    WHERE score>=0.900000 AND mirna IN ("hsa-miR-125a-5p","hsa-
miR-125a-5p-3p","hsa-miR-125a-5p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-505","hsa-miR-505-3p","hsa-
miR-505-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-545","hsa-miR-545-3p","hsa-
miR-545-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-500","hsa-miR-500-3p","hsa-
miR-500-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-200b","hsa-miR-200b-3p","hsa-
miR-200b-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
    WHERE score>=0.900000 AND mirna IN ("hsa-miR-628-5p","hsa-
miR-628-5p-3p","hsa-miR-628-5p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-10a","hsa-miR-10a-3p","hsa-
miR-10a-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-148a","hsa-miR-148a-3p","hsa-
miR-148a-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-363","hsa-miR-363-3p","hsa-
miR-363-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-19a","hsa-miR-19a-3p","hsa-
miR-19a-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-511","hsa-miR-511-3p","hsa-
miR-511-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target"
    WHERE score>=0.900000 AND mirna IN ("hsa-miR-28-5p","hsa-
miR-28-5p-3p","hsa-miR-28-5p-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-22","hsa-miR-22-3p","hsa-
miR-22-5p")
```

```

--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-134","hsa-miR-134-3p","hsa-
miR-134-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-422a","hsa-miR-422a-3p","hsa-
miR-422a-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-221","hsa-miR-221-3p","hsa-
miR-221-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-487a","hsa-miR-487a-3p","hsa-
miR-487a-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-520f","hsa-miR-520f-3p","hsa-
miR-520f-5p")
--- SQL: SELECT distinct("generefseqid") FROM "mir2target" WHERE
    score>=0.900000 AND mirna IN ("hsa-miR-383","hsa-miR-383-3p","hsa-
miR-383-5p")
Number of genes from gene list found in pathways is 2736

```

Perform enrichment of the targets using the DAVID webservice. List the

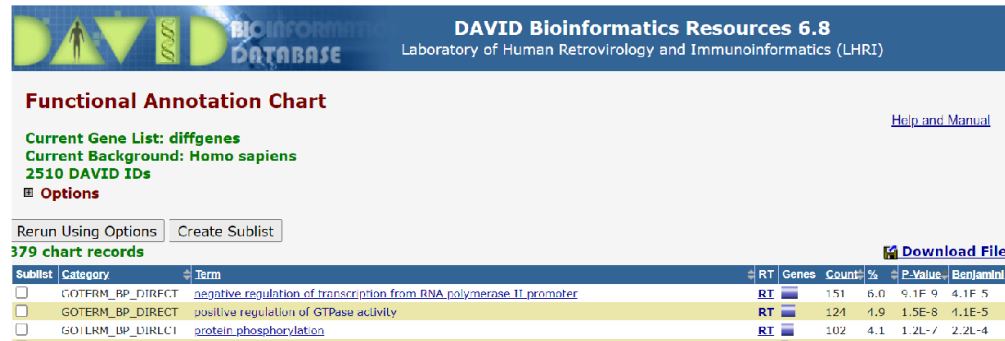
top 3 most significantly enriched pathways and top 3 most significantly enriched Gene Ontology terms, along with their p-values and the number of genes from your gene list found in these pathways and terms.

```

figure(1)
imshow(imread('enriched_pathways.png'))
figure(2)
imshow(imread('Gene_Ontology_terms.png'))

```

DAVID Bioinformatics Resources 6.8 Laboratory of Human Retrovirology and Immunoinformatics (LHRI)									
Functional Annotation Chart									
Current Gene List: diffgenes									
Current Background: Homo sapiens									
2510 DAVID IDs									
Options									
Rerun Using Options Create Sublist									
91 chart records									
Download File									
Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini	
<input type="checkbox"/>	KEGG_PATHWAY	Axon guidance	RT	44	1.8	1.0E-9	2.8E-7		
<input type="checkbox"/>	KEGG_PATHWAY	Insulin signaling pathway	RT	42	1.7	1.7E-7	2.3E-5		
<input type="checkbox"/>	KEGG_PATHWAY	Focal adhesion	RT	54	2.2	5.1E-7	4.6E-5		



Gene set enrichment with tens of genes will not get any enriched annotations

%and the annotations from many thousands of genes will not be meaningful.

%For targets can be, you can additionally adjust the confidence score threshold to control how many genes you get. You can also adjust pvalue or fold change thresholds above to control the number of most-different micrornas and this to limit the resulting gene set.

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