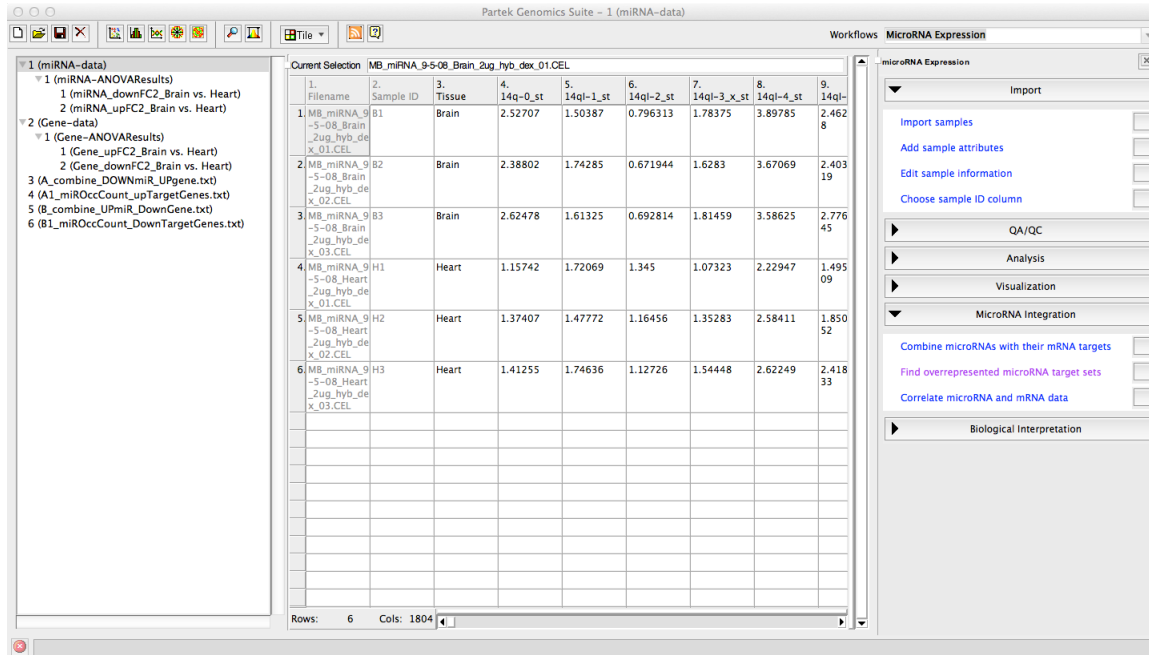
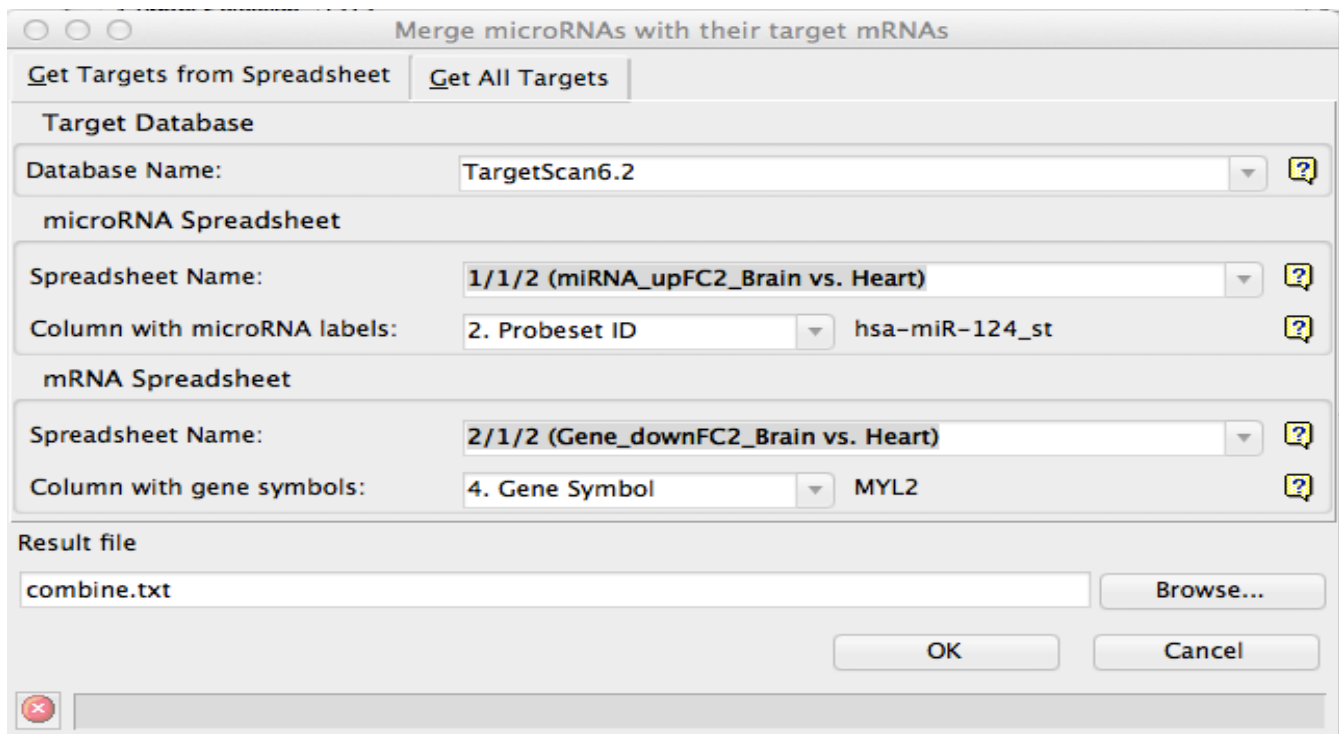


*Integration of miR and gene expression data using Partek MicroRNA Expression workflow*

1] Importing the zipped project file should open up the screen below –



2] Combining expression data for miRNA with their gene targets



### 3] Over-represented miRNA target set analysis

- finds miRs that target a disproportionately high number of significant genes

Find enriched target associations

Find microRNAs that target a disproportionately high number of significant mRNAs based on Fisher's exact test. Target associations are taken from the database you specify. The required input is a list of mRNAs of interest, such as a list of differentially expressed mRNAs. This method is based on Creighton et al (RNA 2008. 14: 2290-2296). Optionally, you can combine the results of this analysis with other microRNA data.

Target Database

Database Name: TargetScan6.2

mRNA Spreadsheet

Spreadsheet Name: 2/1/2 (Gene\_downFC2\_Brain vs. Heart)

Column with gene symbols: 4. Gene Symbol MYL2

MicroRNA Spreadsheet (Optional)

Combine enriched microRNA targets with microRNA data

Spreadsheet Name: 1/1/2 (miRNA\_upFC2\_Brain vs. Heart)

Column with microRNA labels: 2. Probeset ID hsa-miR-124\_st

Choose columns from microRNA spreadsheet to merge.

No columns from the microRNA spreadsheet are currently selected.

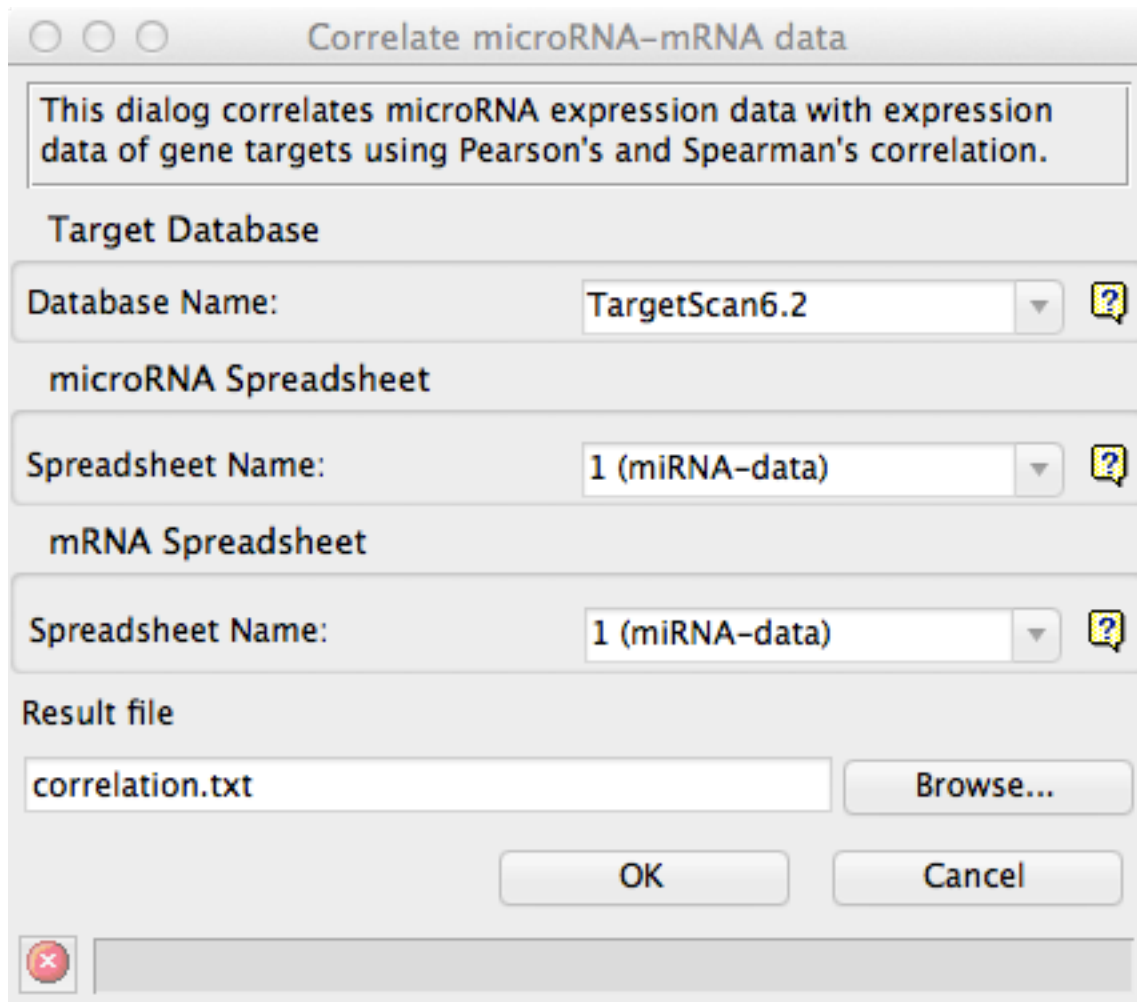
Result file

enrichedAssociations.txt

Browse... OK Cancel

### Columns on the resultant spreadsheet on Partek

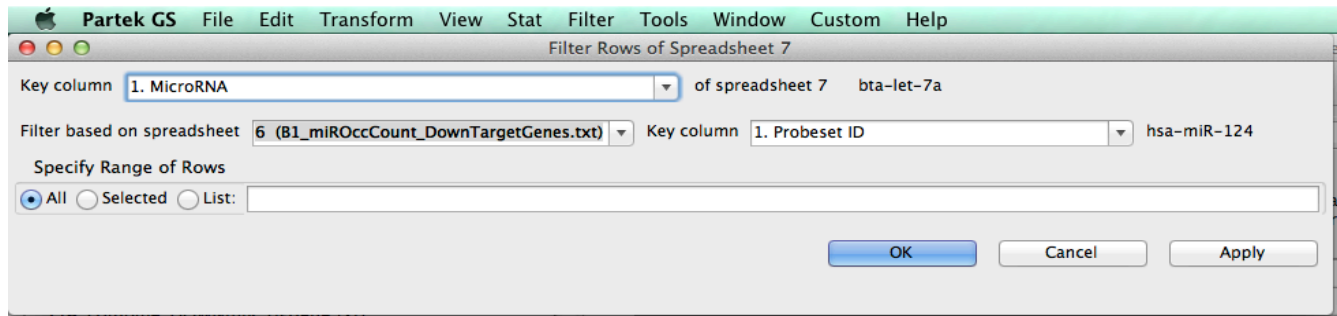
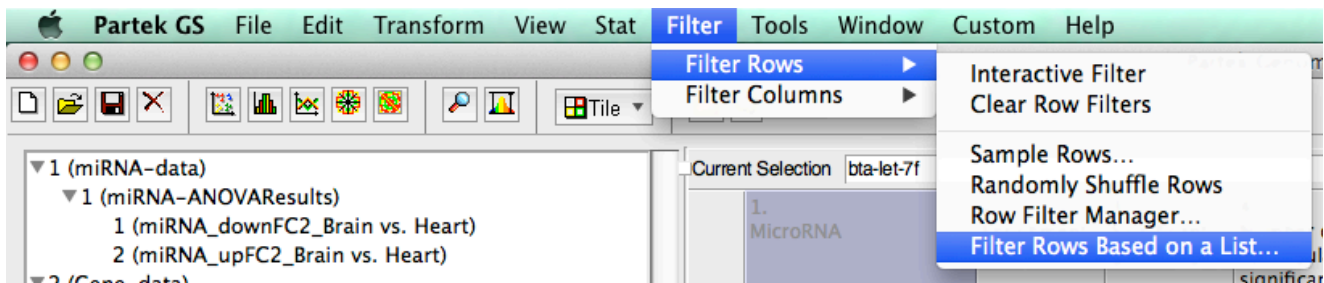
Enrichment p-value >> Fisher's exact test  
 Significant gene targets >> Targeted genes that show differential expression  
 Number of up-regulated significant targets >> Up-regulated gene targets  
 Number of down-regulated significant targets >> Down-regulated gene targets  
 Non-significant gene targets >> Targeted genes that are not differentially expressed  
 Significant non-targeted genes >> Non-targeted genes that are differentially expressed.  
 Non-significant non-targeted genes >> Genes that are not targeted by the microRNA and do not show significant differential expression

**4] Correlation between miR-gene – needs common Sample ID for look up**

**5] Post-integration processing and filtering of combined data sheets**

**[a] Generating a subset of only Human miRs(spreadsheet 7a) that have significant enriched associations**

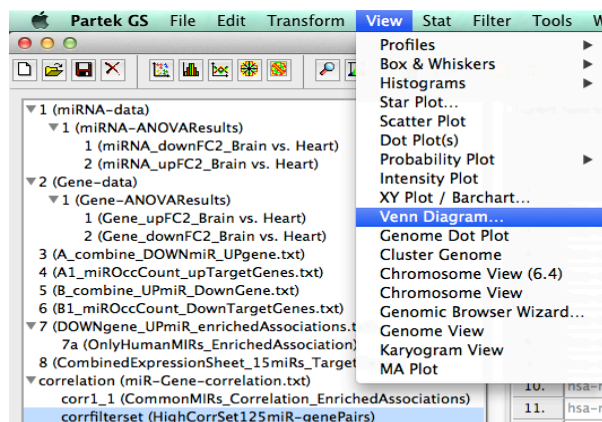
- Click on Spreadsheet 7 (DOWNgene\_UPmiR\_enrichedAssociations.txt)
- Go to Toolbar→Filter→Choose Spreadsheet 6 (Occurrence Count) – same miR ID

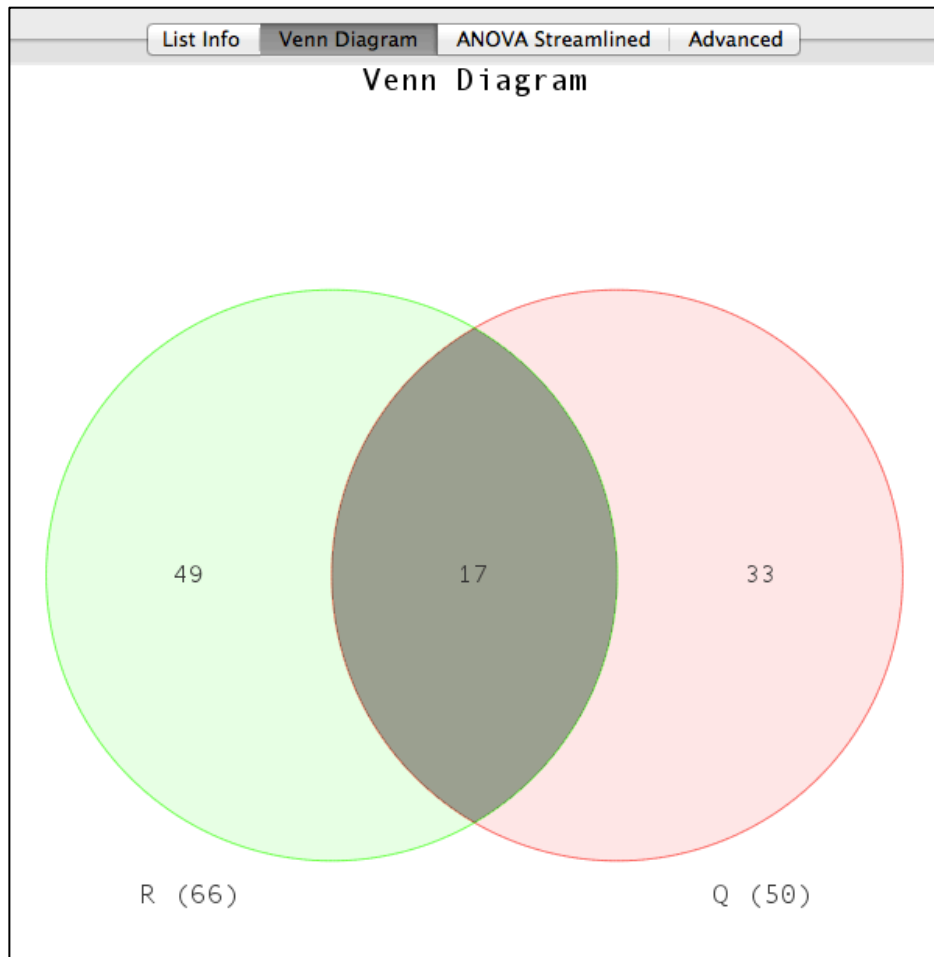


**[b] Generating a subset of highly correlated miRs**

- Based on Pearson and Spearman’s Rank Correlation Coefficients
- Correlation values less than -0.995 or more than 0.995
- Exclude rows that do not meet this criteria
- Resultant subset of 125 miRs with high correlation

**[c] Create Gene list for miRs common to both lists from [a] and [b] above**





**[d] Merging spreadsheets to obtain a final integrated data file**

*Significant\_miR-gene\_IntegratedDataFile.txt*

**Homework:**

Upload the integrated data text file onto IPA and understand the enrichment profiles that are generated.

**Thanks and good luck!**