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

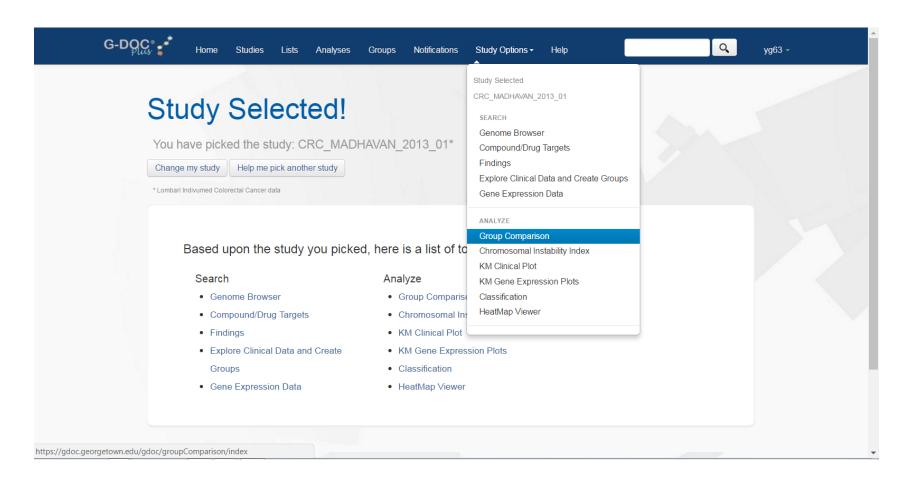
- Step-by-step instructions (for more details see screen shots below):
 - Log in to G-DOC at gdoc.georgetown.edu
 - Find and Select CRC Madhavan 2013 study in G-DOC
 - Follow the initial steps of microRNA expression analysis demo and select and save the same 2 groups of samples that were saved in microRNA 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:

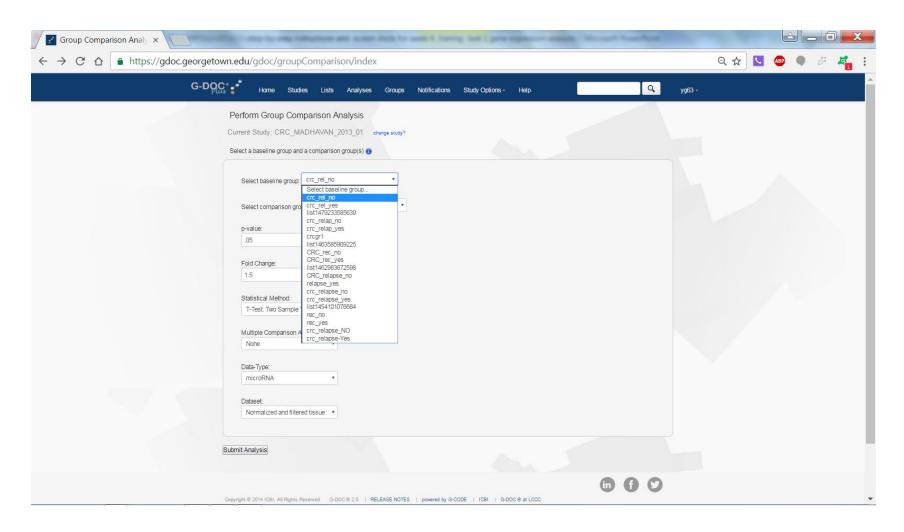
Question 1: what was the total number of micorRNAs in the table? Enter number here: ______

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

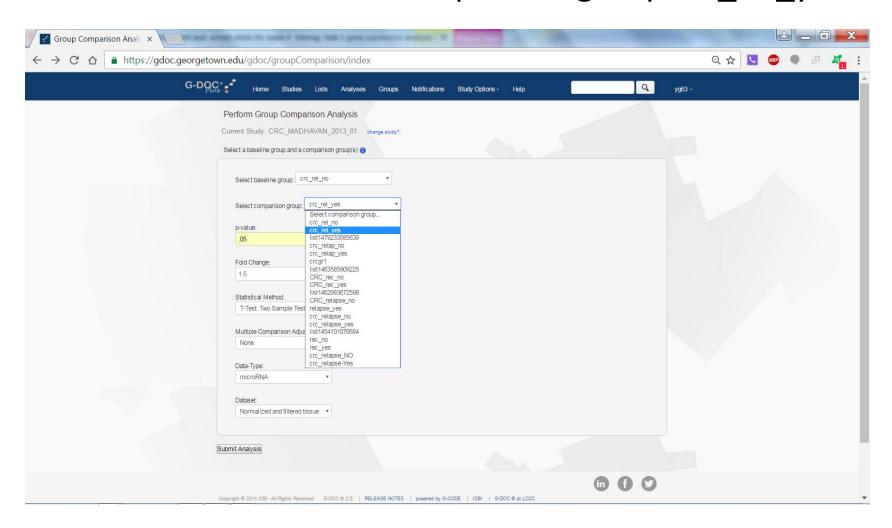
Screen shot 1: select study option "group comparison"



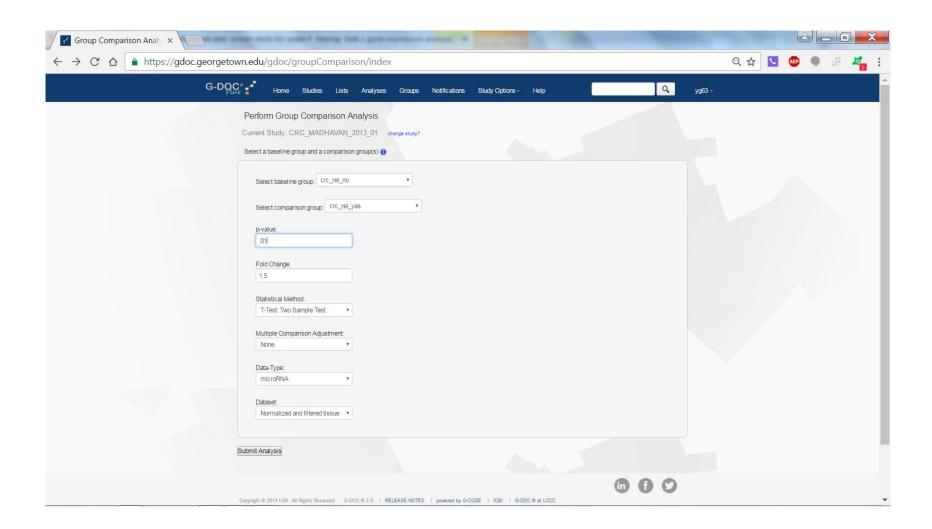
Screen shot 2: select baseline group crc_rel_no



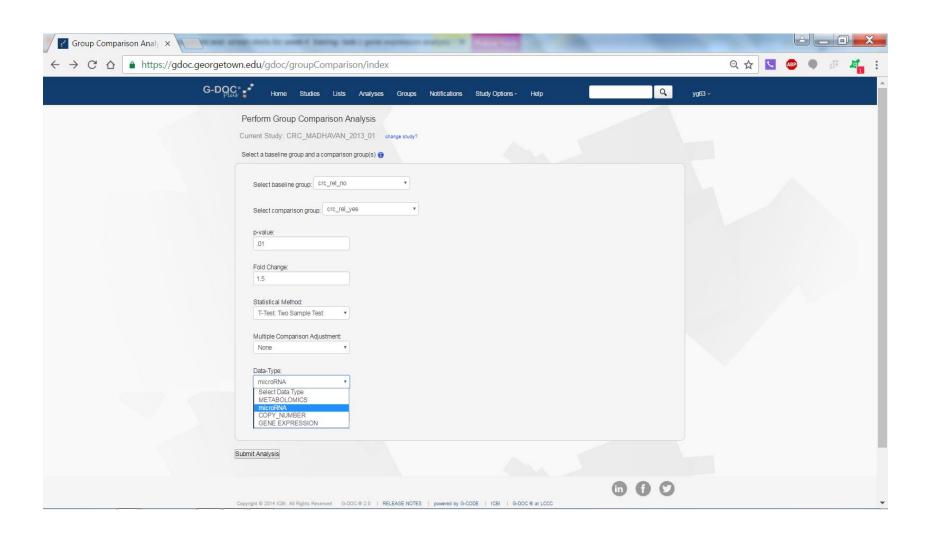
Screen shot 3: select comparison group crc_rel_yes



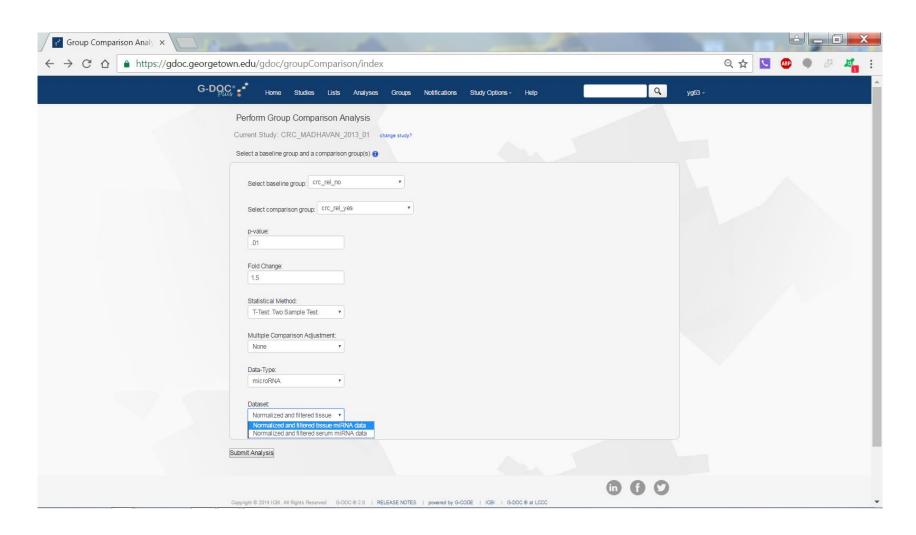
Screen shot 4: change p-value to 0.01



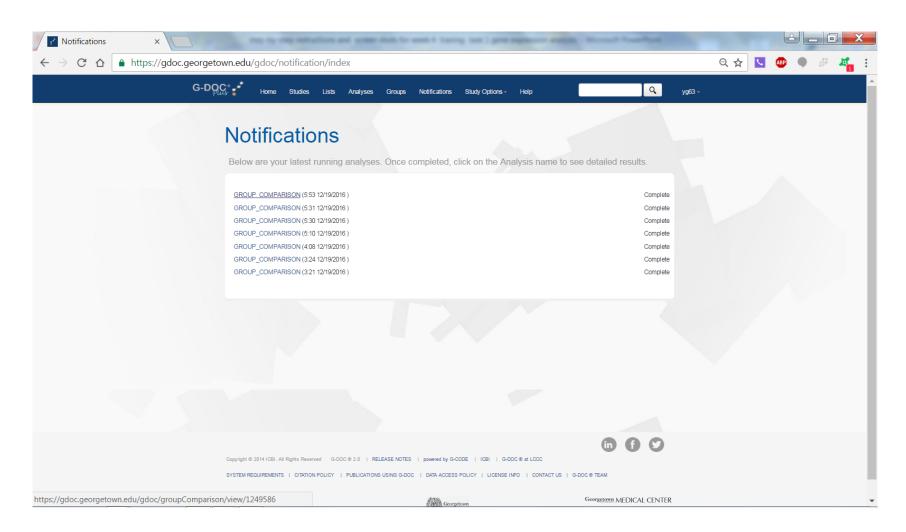
Screen shot 5: Select Data Type "microRNA"



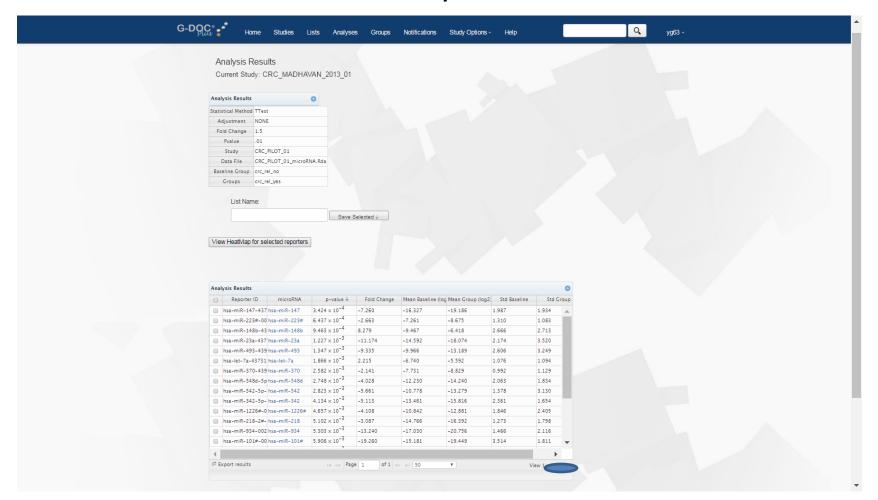
Screen shot 6: Select Data Set "normalized and filtered tissue"



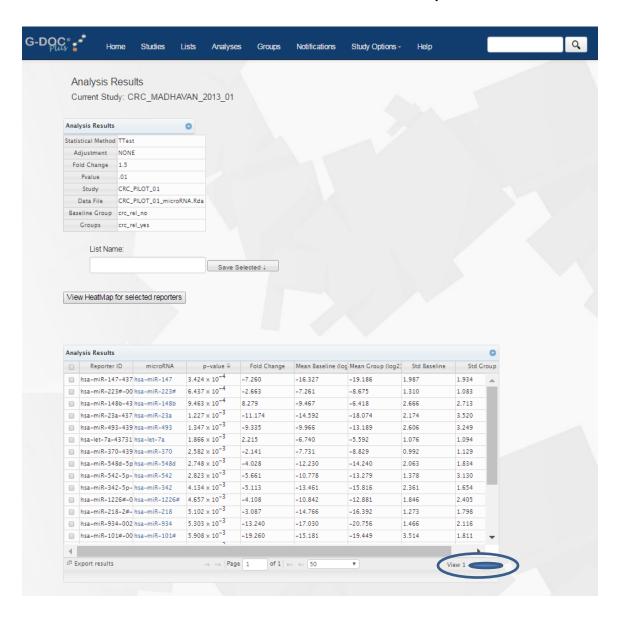
Screen shot 7: Check Notifications for completion of analysis



Screenshot 8: Open analysis results of the group comparison

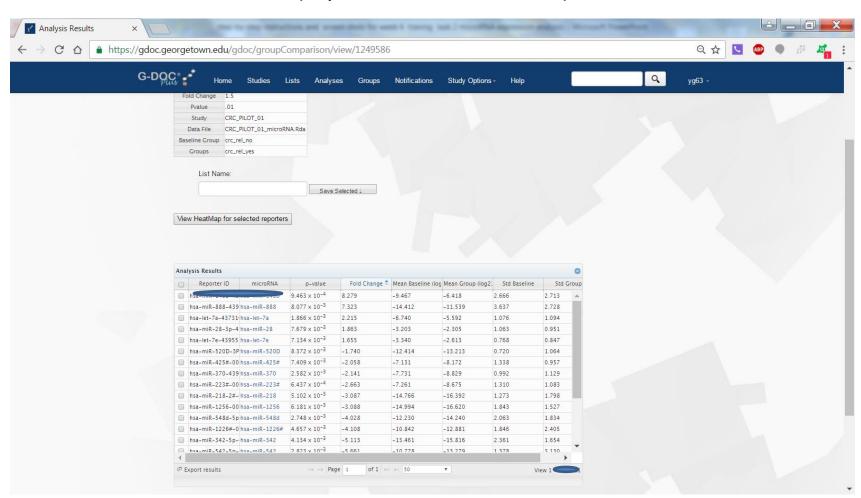


Screenshot 9: Check the table with the analysis results of the group comparison – find a total number of differentially expressed microRNAs (lower right corner under the table)

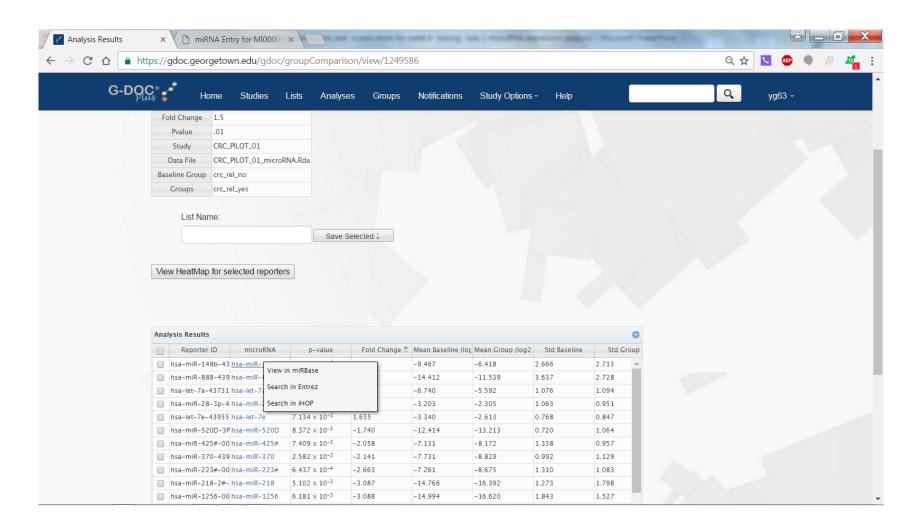


Screenshot 10: Sort a table with the analysis results by column "Fold Change" in descending order (by clicking once on column label);

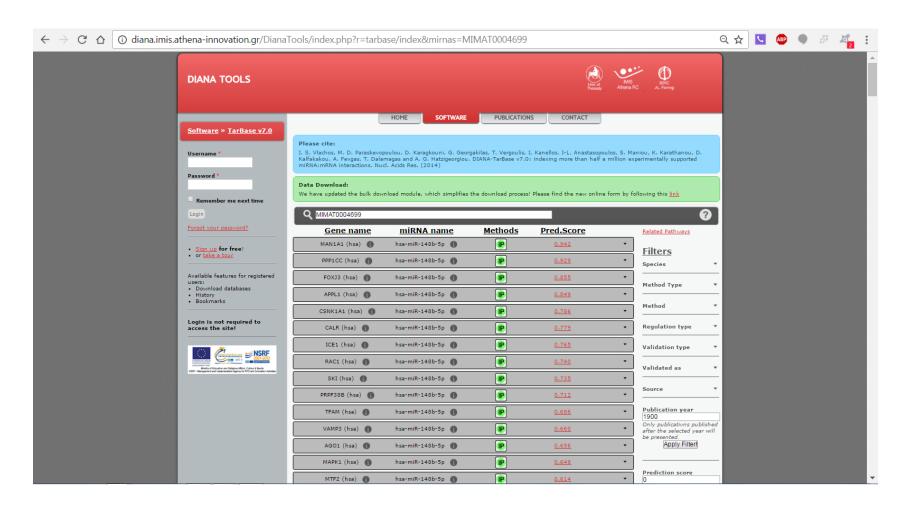
Record of the name of the top overexpressed microRNA (top row, second column)



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



Screnshot 13: explore validated targets for top overexpressed miroRNA in TarBase 7.0



Screnshot 14: explore KEGG pathways for validated targets of top overexpressed miroRNA in mirPath 3.0

