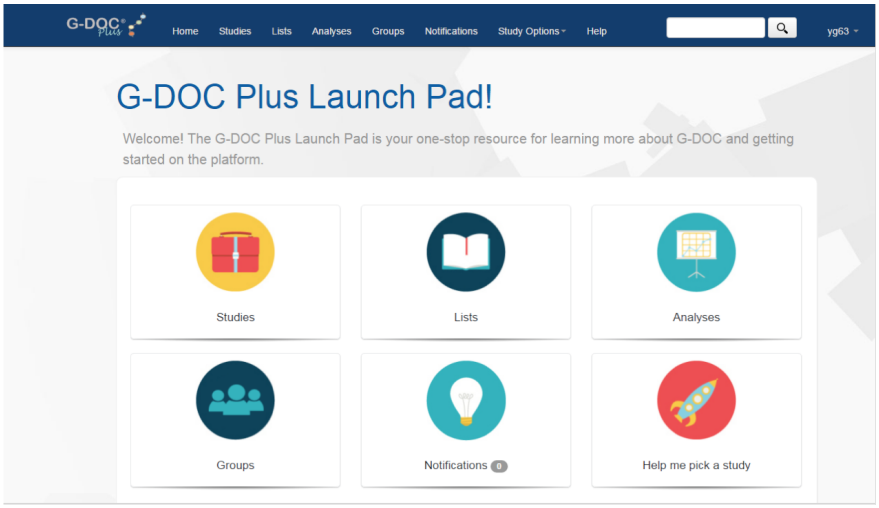
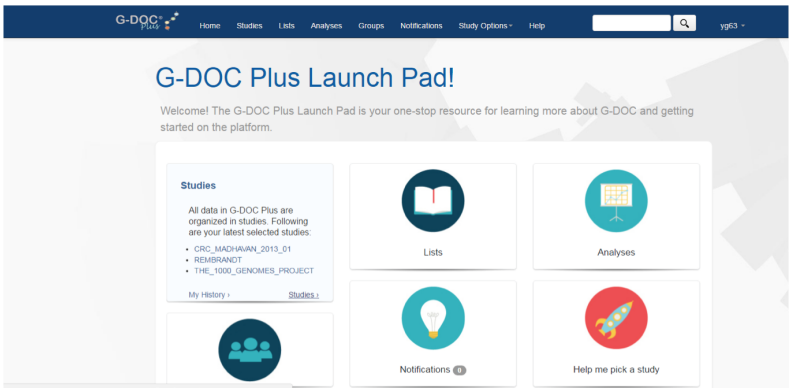
**G-DOC Exercise**

1. Go to G-DOC at http://gdoc.georgetown.edu/. Please register for an account if you have not already done so.

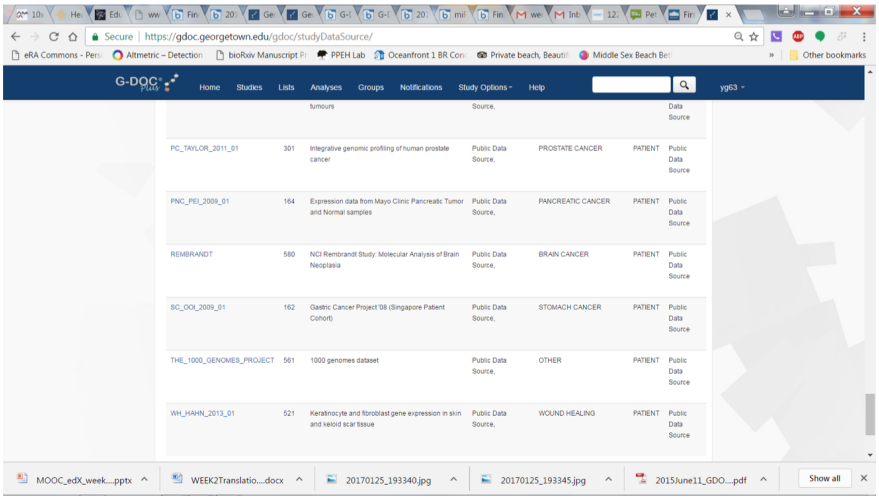



2. Once you have registered successfully and signed in, click on the "Studies" button.

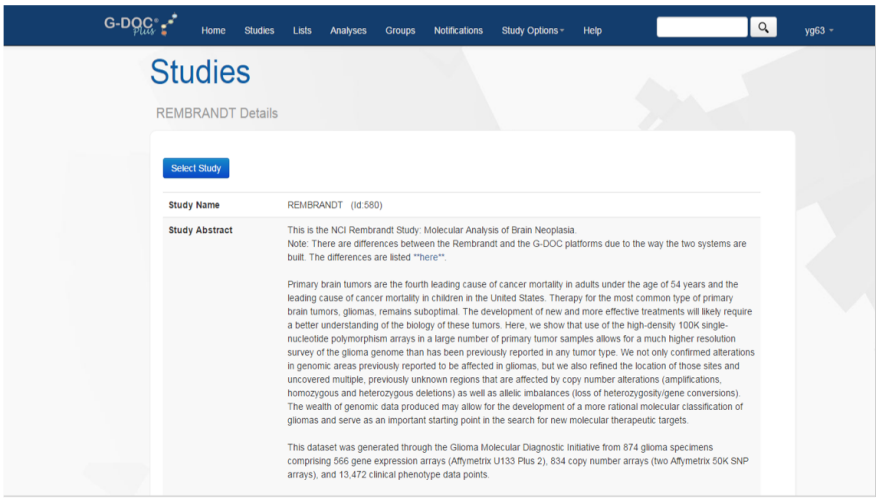
3. Click on the link "Studies."



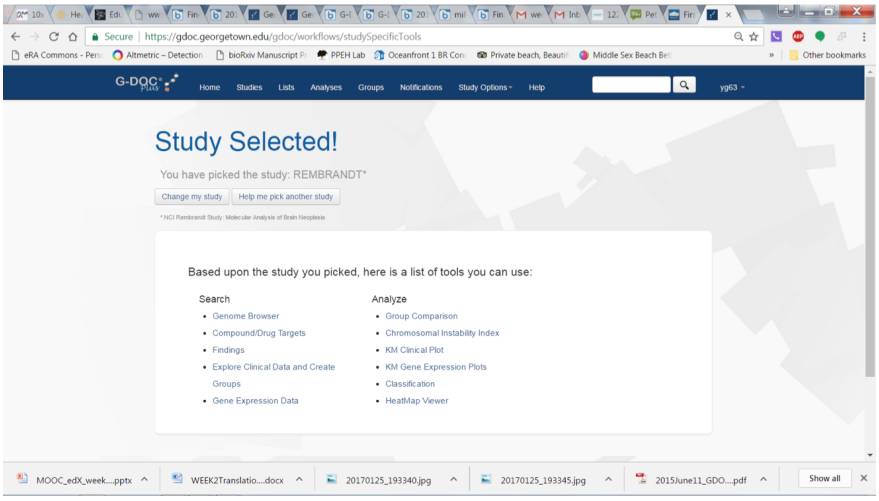

4. The Studies list is organized by names in alphabetical order. Scroll down to "REMBRANDT" and click on the name.




5. On the Study page, click on "Select Study."

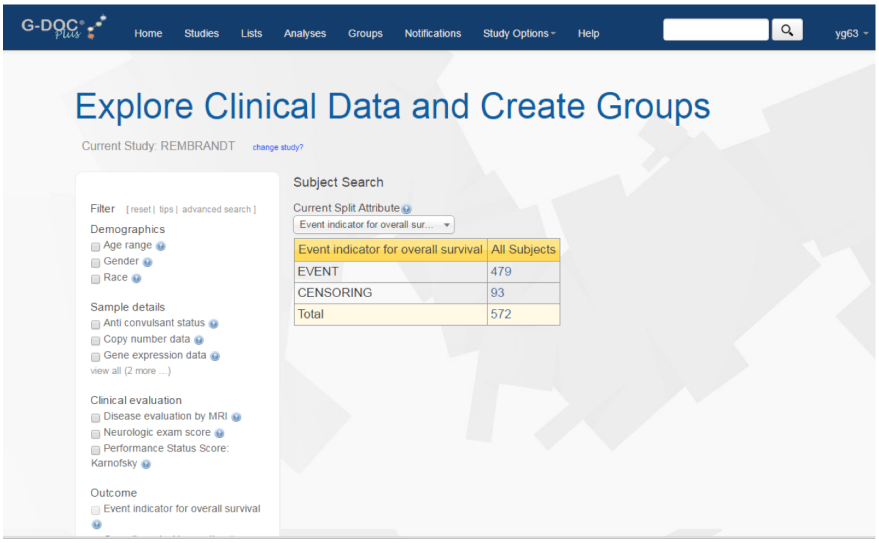



6. Based on selected study, a list of tools appears on the next page that can be used to explore data in this particular study. Under the Search column, select "Explore Clinical Data and Create Groups."

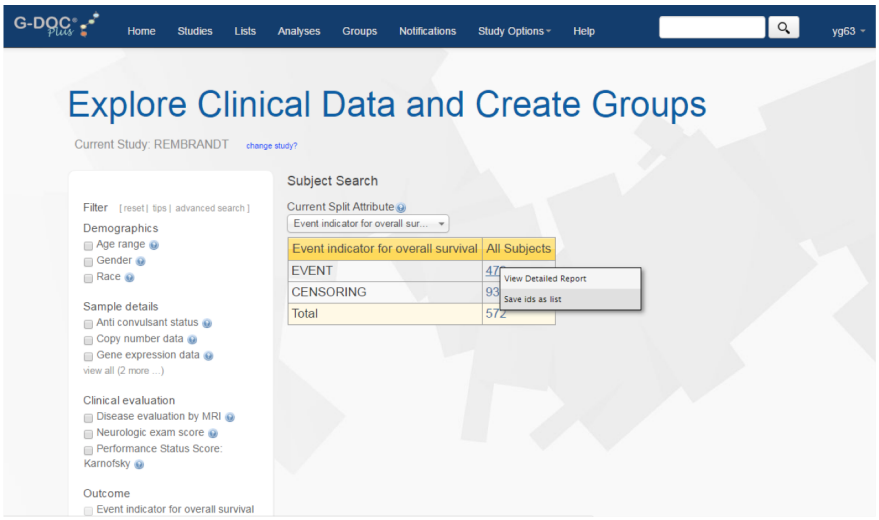



By selecting the event indicator for overall survival, you are selecting those patients from the study who have been reported as having died at a certain point within the duration of the study.

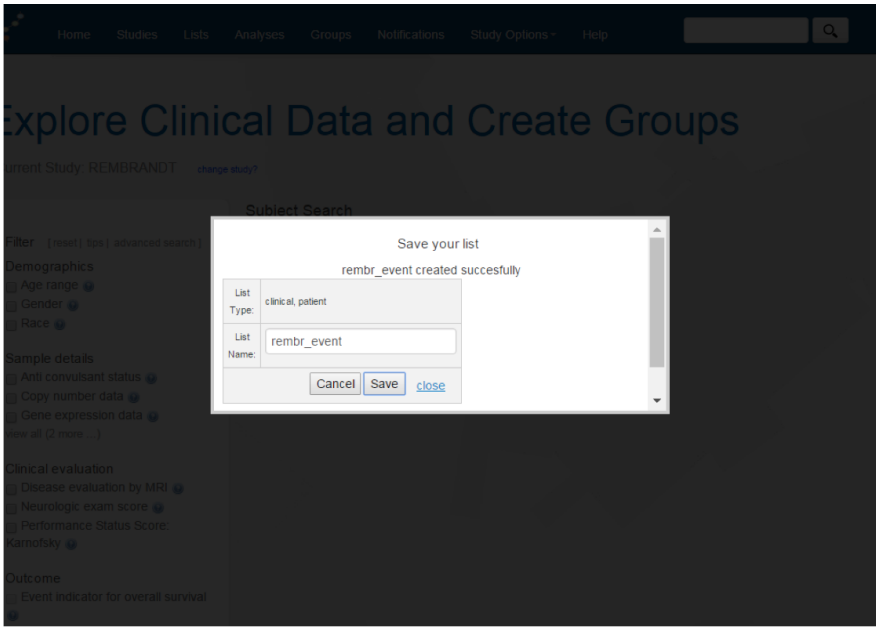
7. When on "Explore Clinical Data and Create Groups," check the Current Split Attribute window, and make sure that "Event indicator for overall survival" is selected. Check the table in the middle of the screen, then point and click at hyperlinked number in the upper row in the table.




8. Click on Number in the table in a row "EVENT" and select option "Save as ID List."

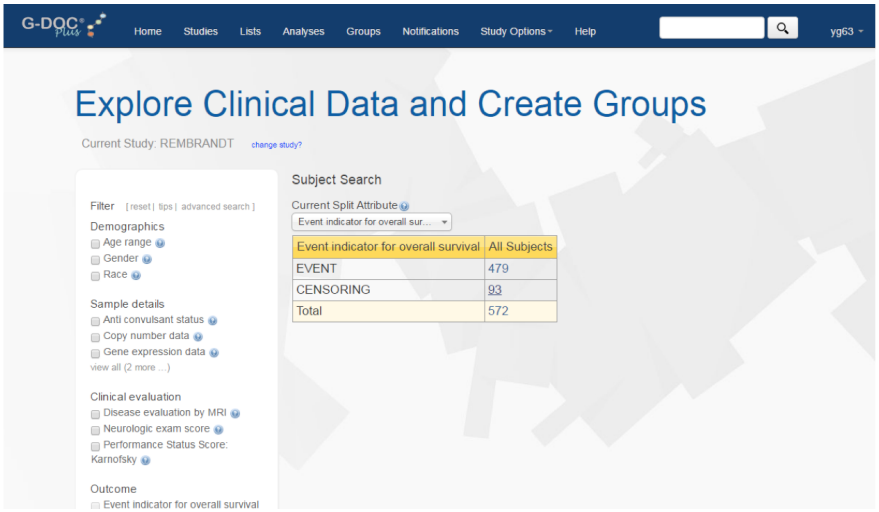



9. Type in a name for this list of IDs: rembr_event and click on "Save." After confirmation message is shown, click on "close."




10. Repeat saving of the IDs list one more time for a second group, "CENSORING."

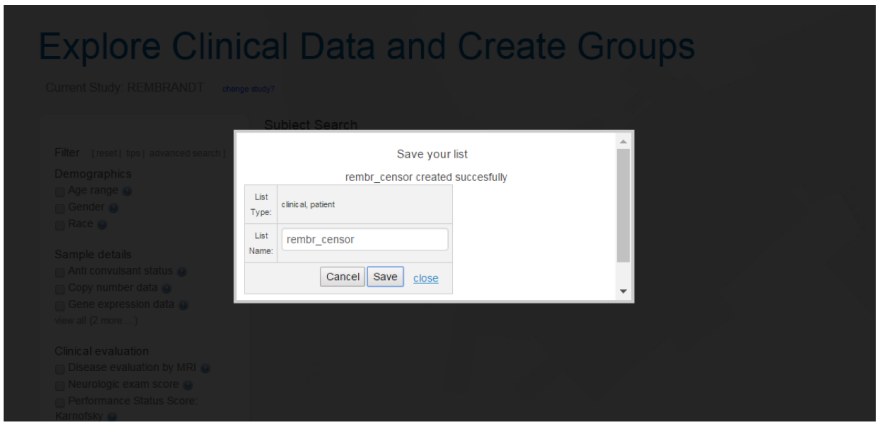
By selecting and saving a group of patient IDs in a category "censoring," you are selecting those patients who did not die during the course of the study.




11. Type in a name for this list of IDs: "rembr_censor" and click on "Save." After confirmation message is shown, click on "close."

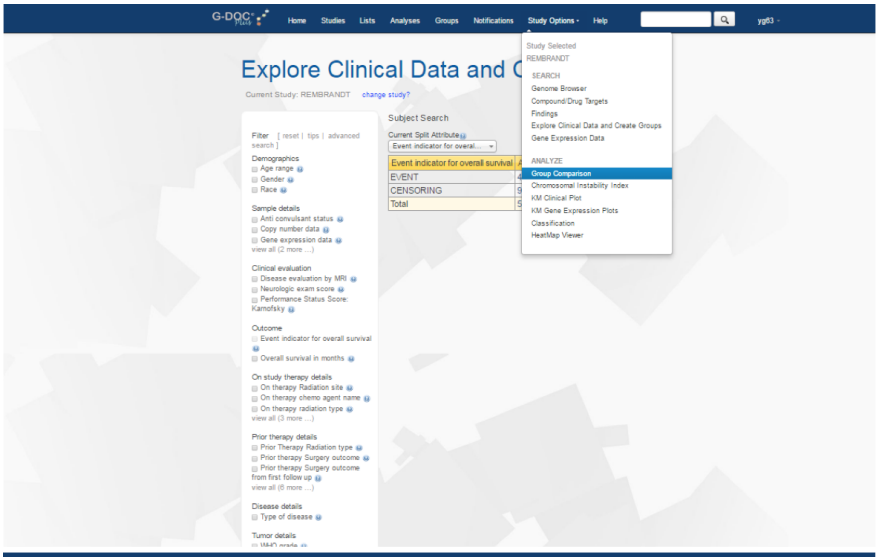
Note: by creating these two groups, you have selected two cohorts of patients for comparison, and the G-DOC system will automatically pull the molecular profiling data for each of those patients from the

database and will have them ready for comparative analysis and exploration in the next few steps.



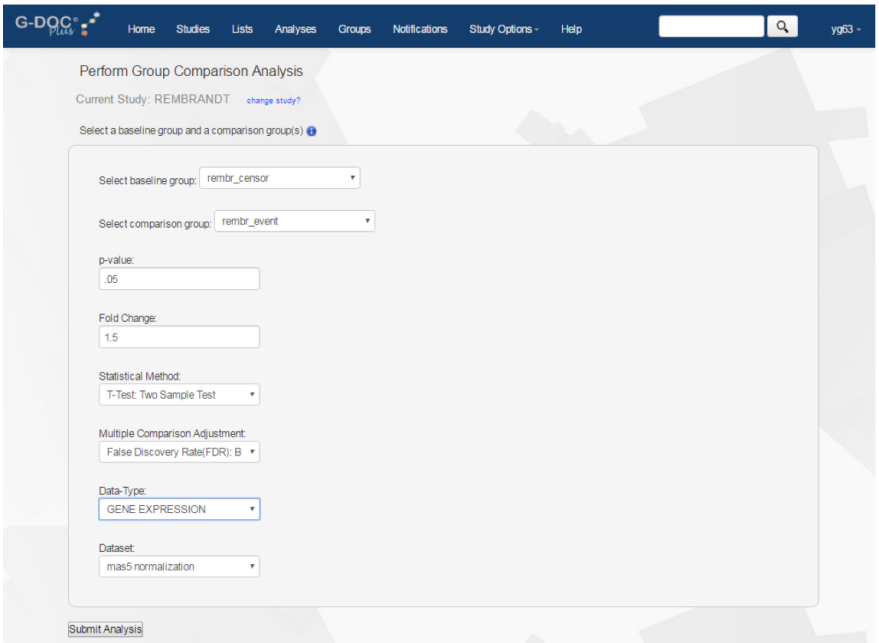

12. Select "Group Comparison" from the main menu.

A group comparison allows you to compare average trends in gene expression across all known genes between two groups of cancer patients to find out what the average molecular differences in level of activity of all the known genes are that might have contributed to overall survival of cancer patients.




13. Select "rembr_censor" as a baseline group from dropdown list. Then select "rembr_event" as a comparison group. Keep the settings for p-value and fold change, as well as for statistical method. Select False discovery rate option for Multiple comparison adjustment, then select Gene expression for Data Type, and finally click on "Submit Analysis."

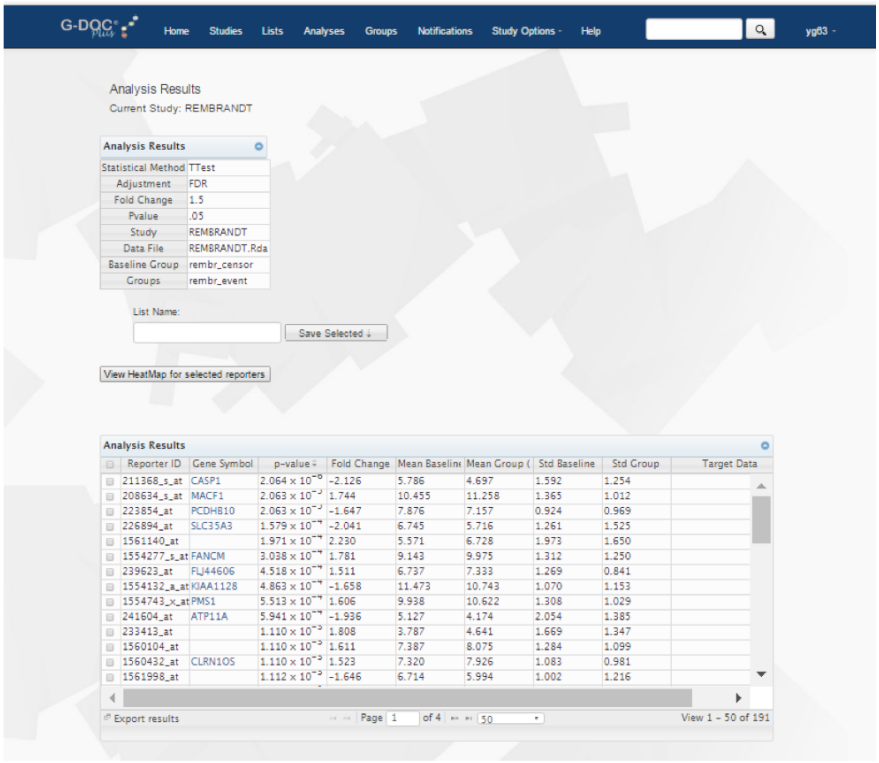
A program will now compare two sets of gene expression matrices and determine those genes that are showing significantly different levels of activity (expression) in the comparison group (deceased) as opposed to the baseline group (alive).



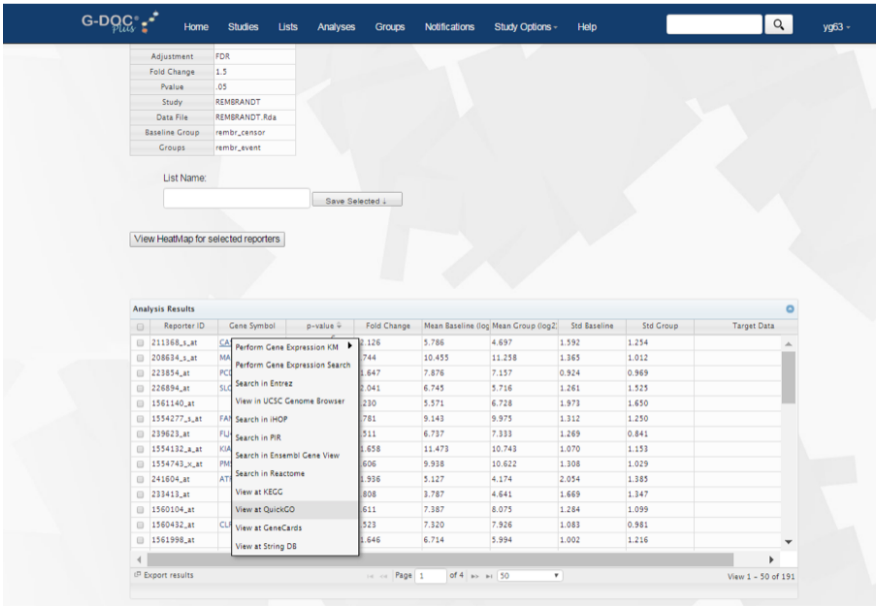

14. Check the analysis results table. Find the total number of differentially expressed genes (listed on the lower right corner of the table). Then find the gene

symbol for the gene at the top of the table (which has the lowest p-value).

The resulting table contains a short list of only those genes that on average are significantly more activated (up-regulated) or inhibited (down-regulated) in one group of patients (deceased) when compared to a baseline group (alive).




15. Explore the biological function of a gene in the top row of the table. (Click on gene symbol and click on GeneCards option from drop-down list.)




16. Explore annotation and function of top significant gene in GeneCards.