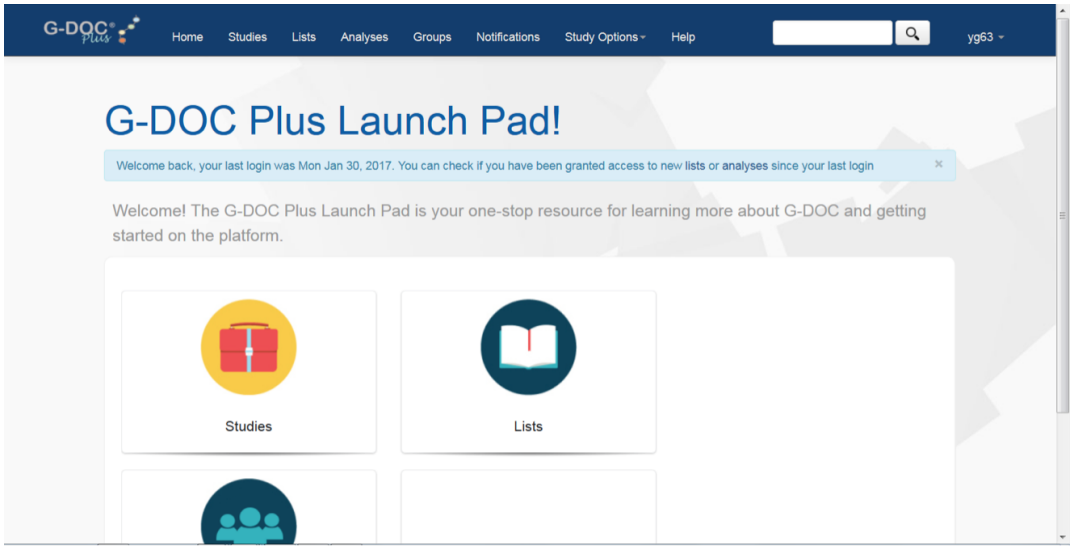
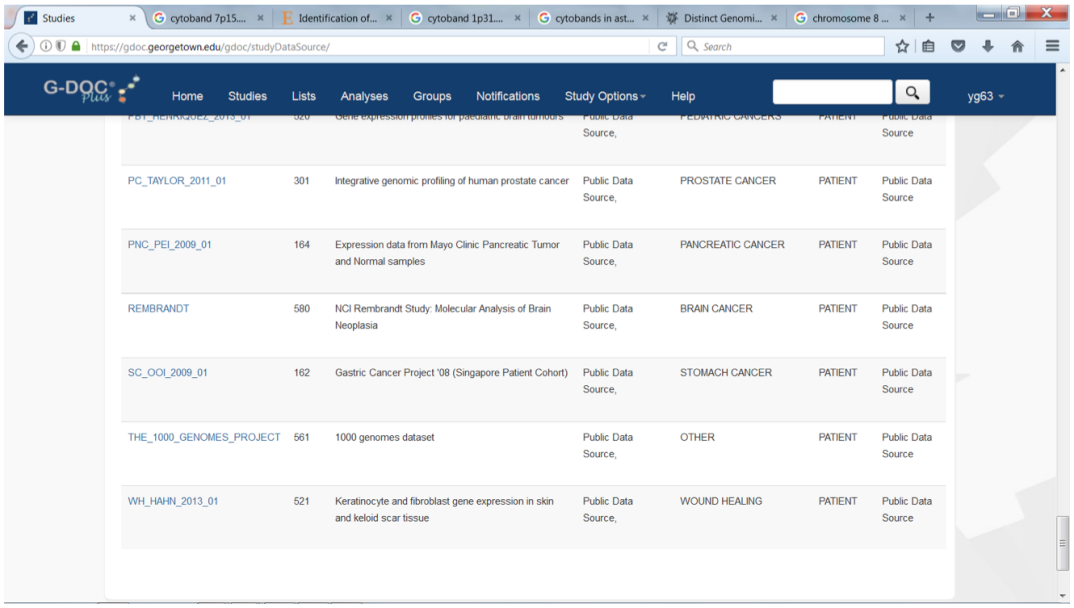
DNA Copy Number Exercise

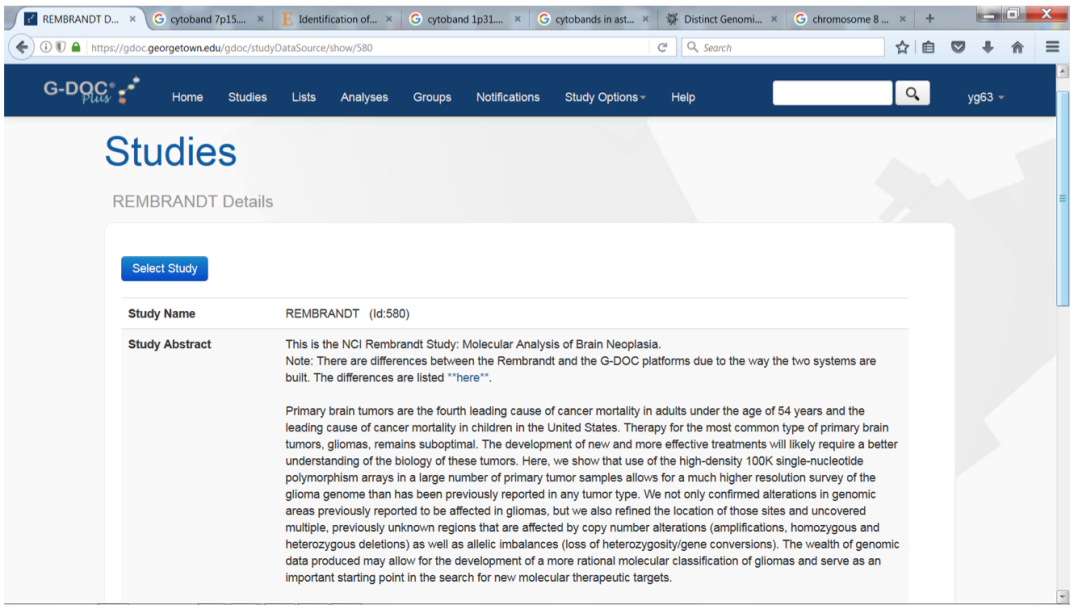
1. Log in to G-DOC (https://gdoc.georgetown.edu) and select "Studies."



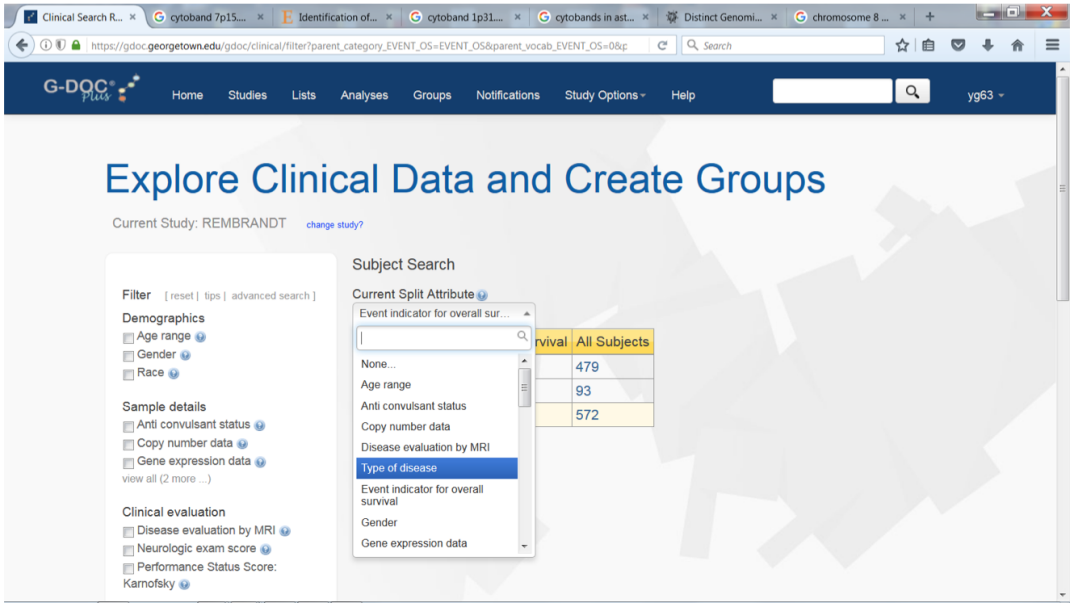
2. Scroll down to the "REMBRANDT" study and click on it.



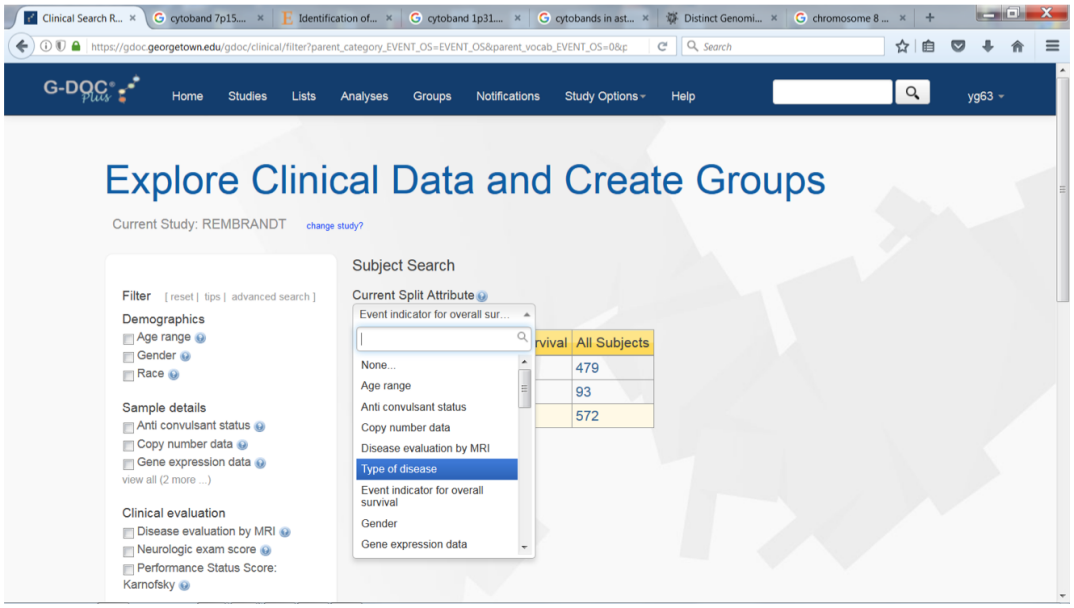
3. Read the study description and click on "Select Study."



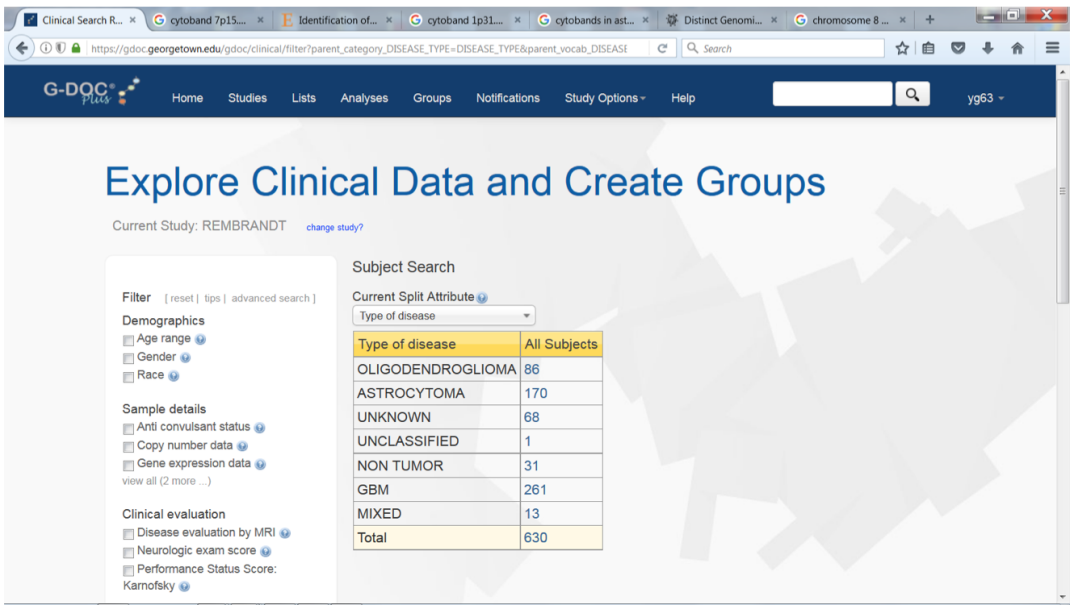
4. Select the next step "Explore Clinical Data" from the list of tools.



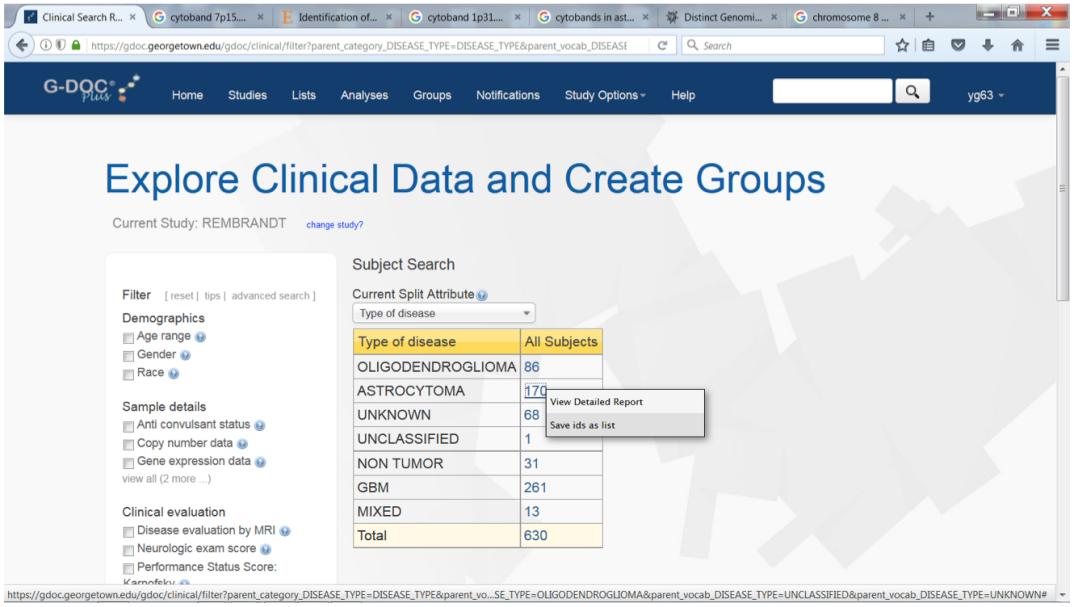
5. Using the explore options, select "Type of disease" as "Current Split Attribute" from the drop down menu.



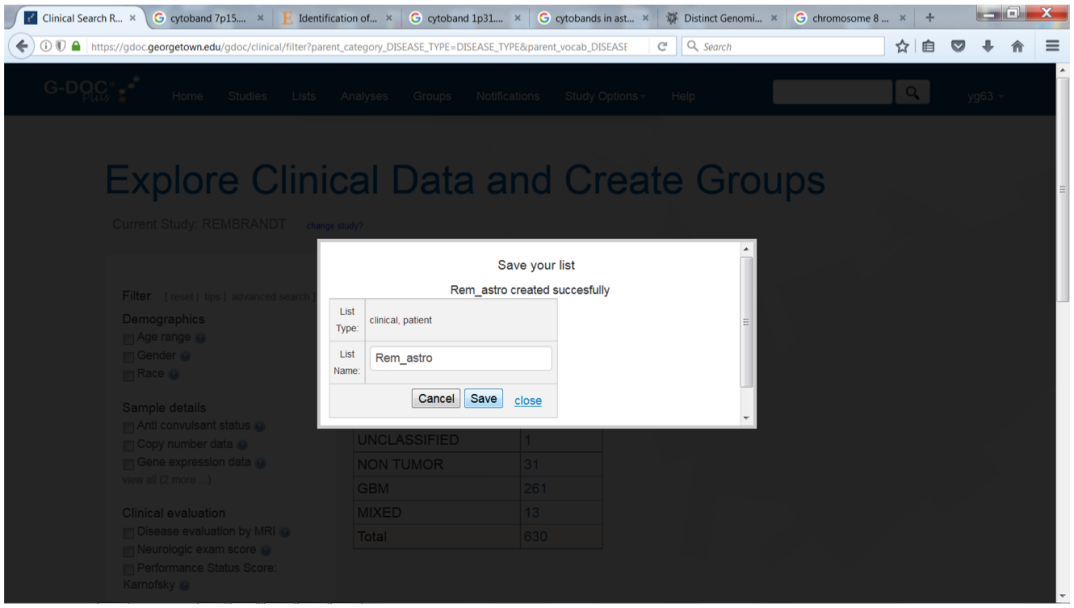
6. In the resulting table, locate two types of brain tumors: OLIGODENDROGLIOMA and ASTROCYTOMA.



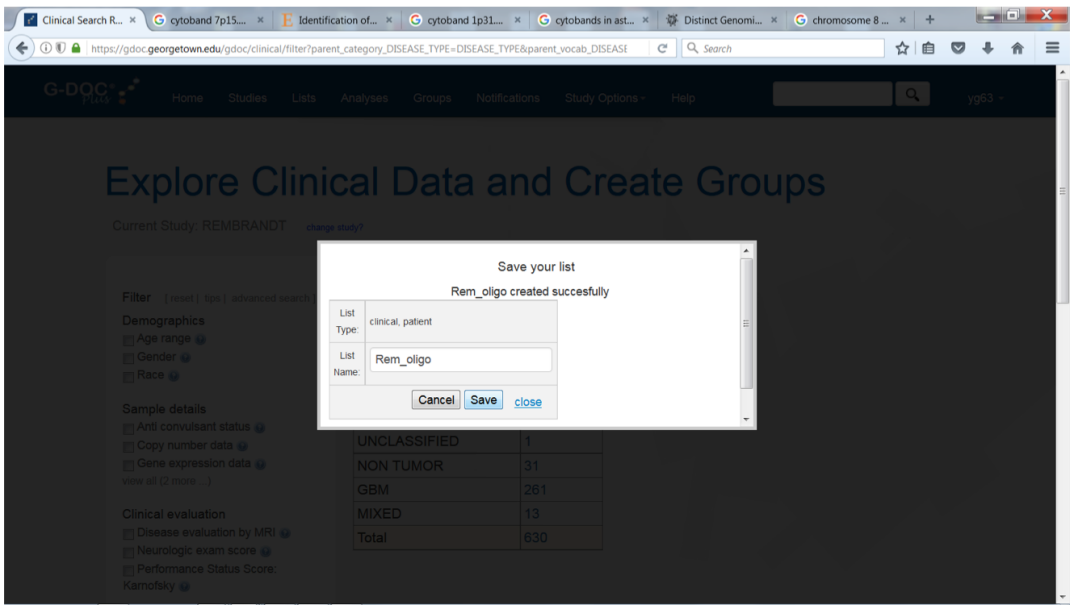
7. Find ASTROCYTOMA on the list, click on the number "170," and then select the option "Save IDs as a list."



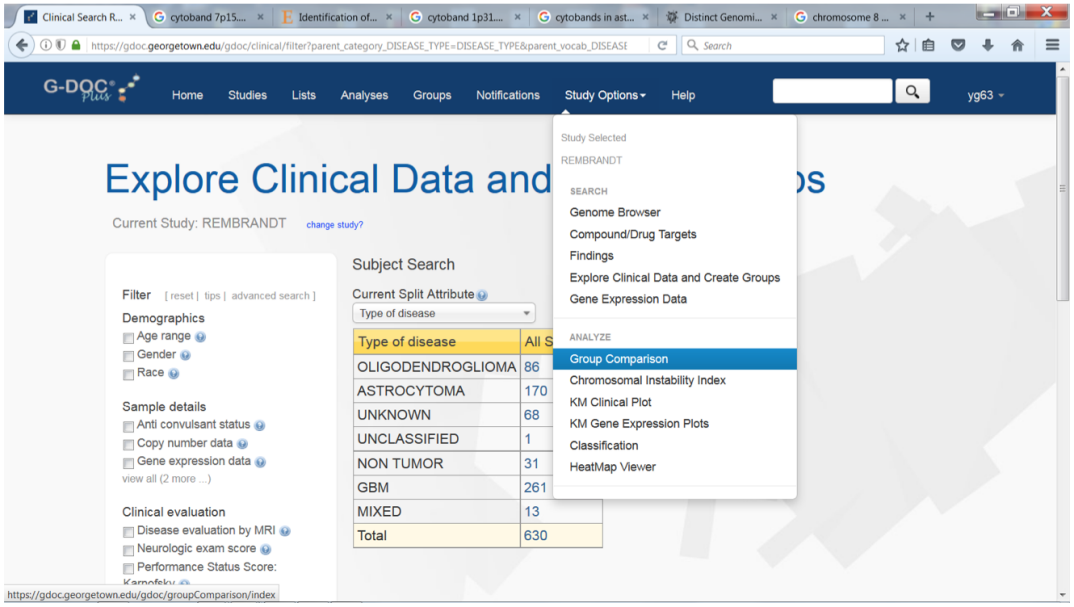
8. When the small window opens, type in a name of the group "Rem_astro," then click "Save." When the message "created successfully" appears, click on "close."



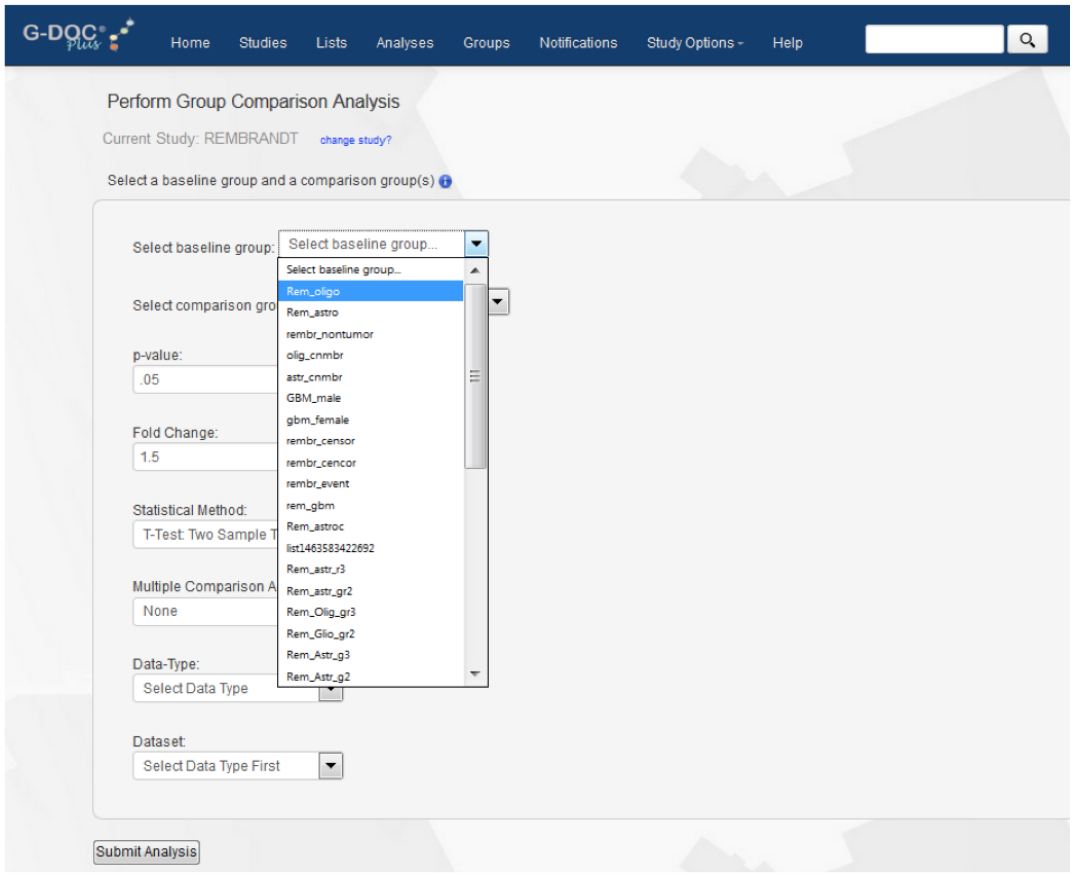
9. Repeat the same steps for the second group, OLIGODENDROGLIOMA. Click on the number in the table. When the small window opens, type in the name of the group ("Rem_oligo"), then click "save." When the message "created successfully" appears, click on "close."



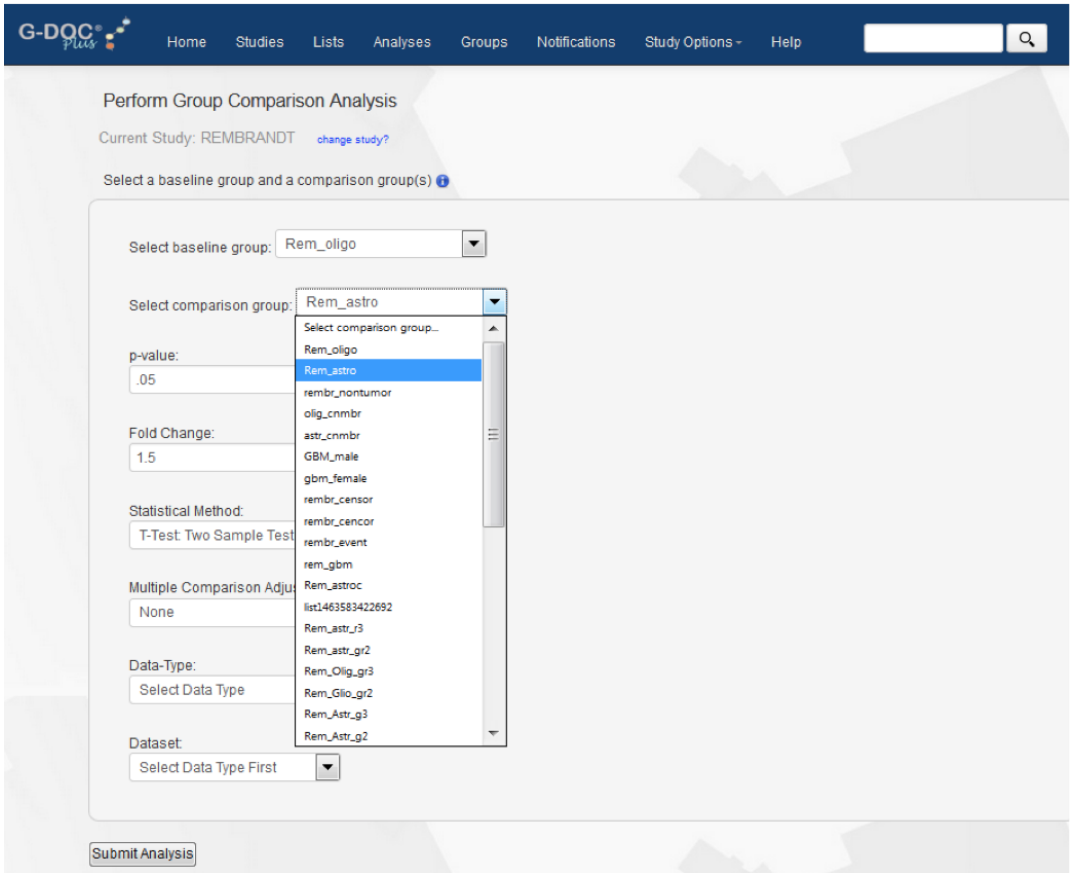
10. Once two groups are selected and saved, use the main menu to select "Study Options," then "Group Comparison."



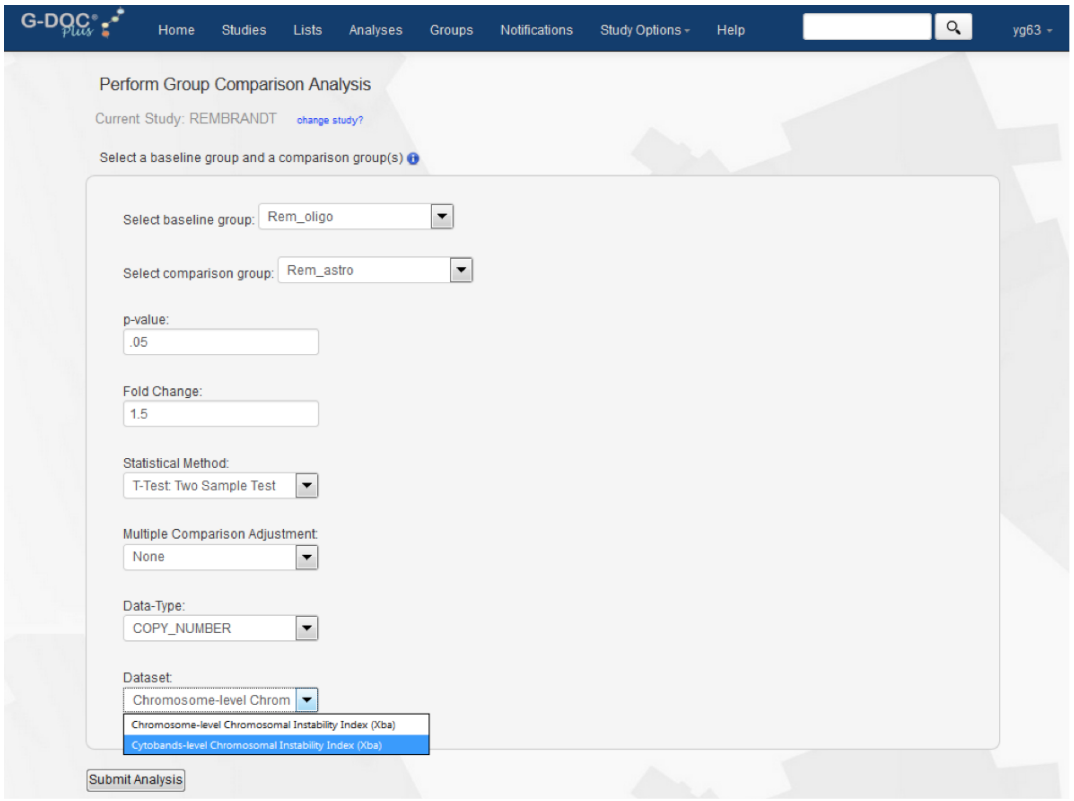
11. In the "Perform Group Comparison Analysis" window, Select baseline group: "Rem_oligo."



12. In the "Perform Group Comparison Analysis" window, Select comparison group: "Rem_astro."

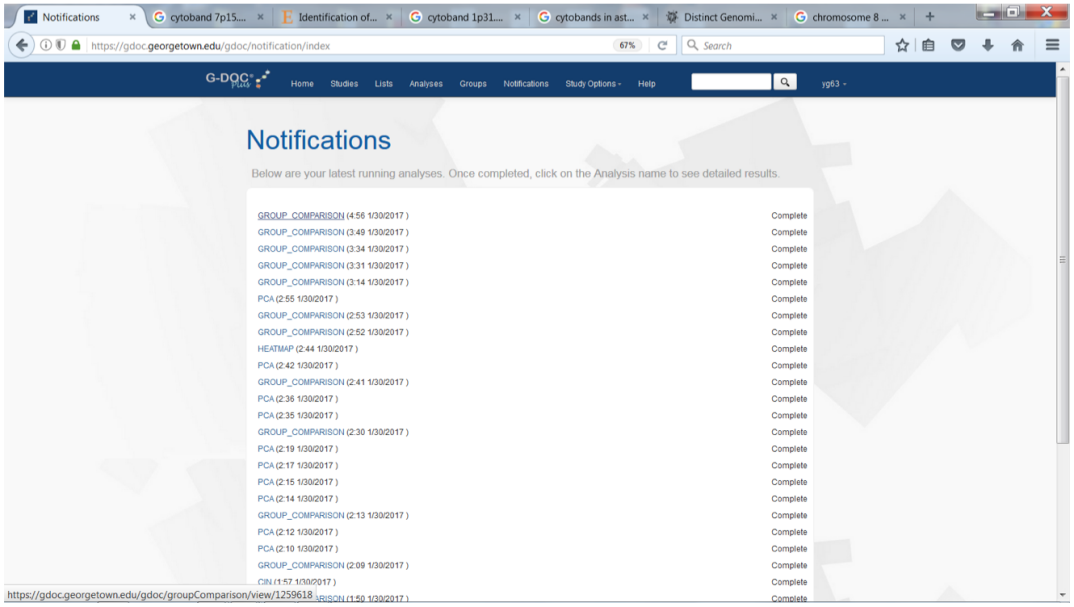


13. For data type, select "COPY_NUMBER." For dataset, select "Cytoband-level Chromosomal Instability Index," then click on "Submit Analysis."

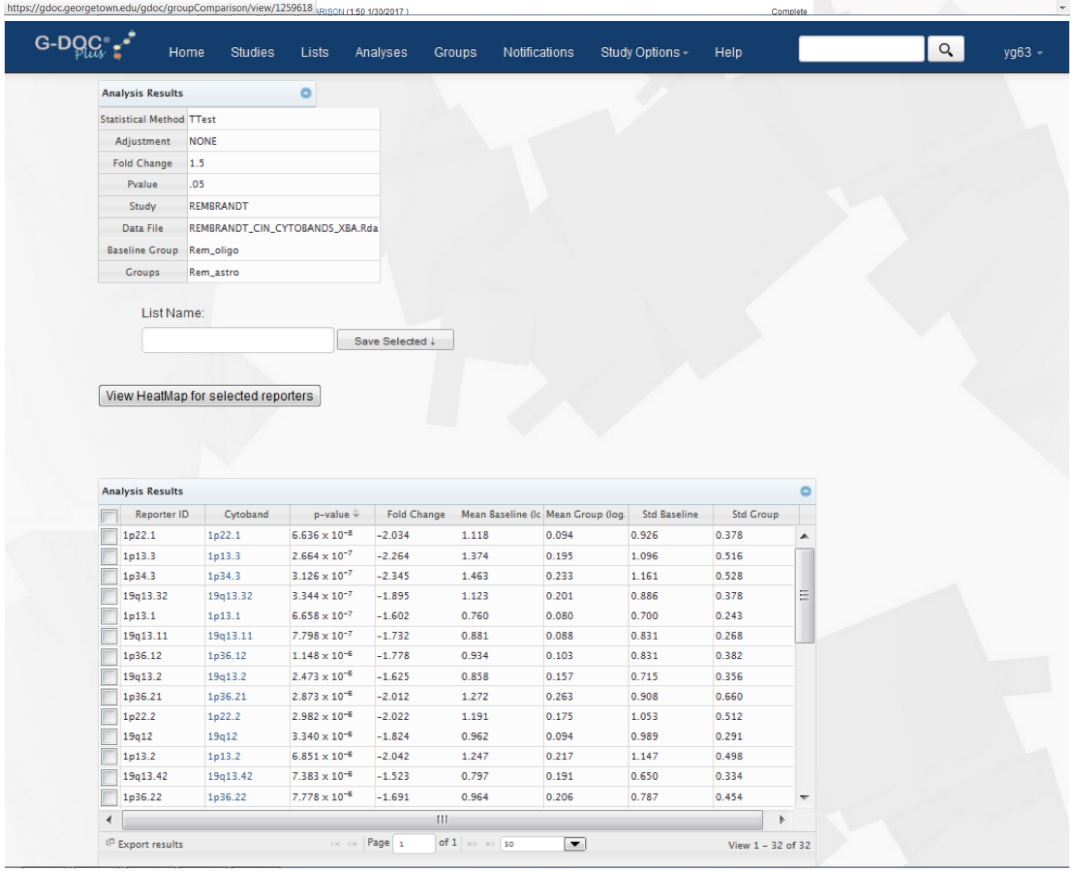


14. When you reach the notification

page, click on "GROUP_COMPARISON" when it is completed.

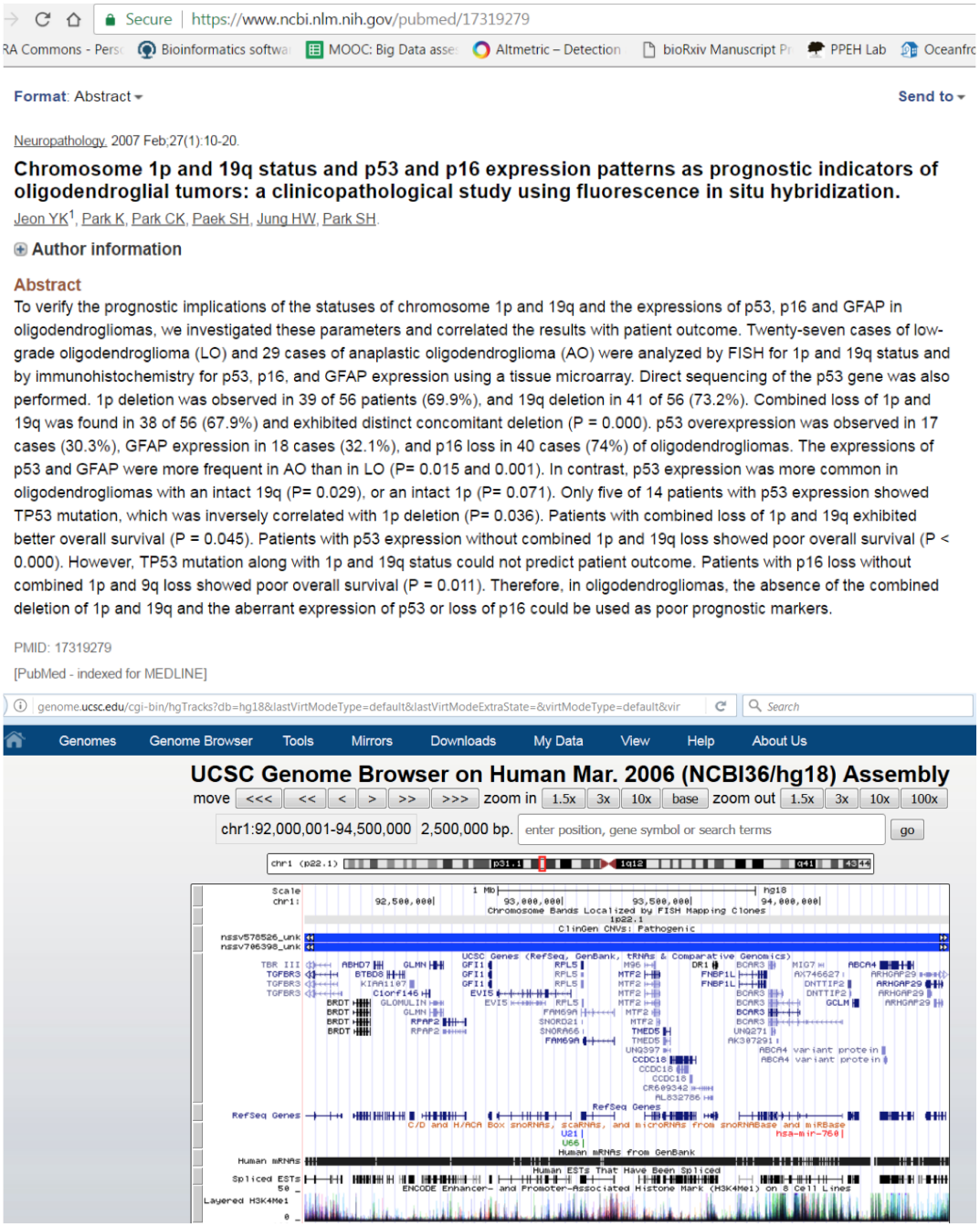


15. When the new window "Analysis Results" is fully displayed, inspect the table with the results. Find the top entry in the table, record the ID of "Cytoband." This is the answer to the first question. Find the total number of table entries (lower right corner), then record the total number of cytobands.



16. Compare the top 10 results in the table (column 2: cytobands/chromosome arms) with the published results on copy number status as prognostic indicators of oligodendrogliomas. Are the findings in this exercise very similar to cytoband changes reported in this paper?

17. You can further explore analysis of top findings using external links. Click on the cytoband ID in the table and look up cytobands (from the table) in the UCSC Genome browser. For example, you could look up Cytoband 1p22.1 genomic map with genes and microRNA locations.



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Neuropathology. 2007 Feb;27(1):10-20.

Chromosome 1p and 19q status and p53 and p16 expression patterns as prognostic indicators of oligodendroglial tumors: a clinicopathological study using fluorescence in situ hybridization.

Jeon YK[1], Park K, Park CK, Paek SH, Jung HW, Park SH.

Author information

Abstract

To verify the prognostic implications of the statuses of chromosome 1p and 19q and the expressions of p53, p16 and GFAP in oligodendrogliomas, we investigated these parameters and correlated the results with patient outcome. Twenty-seven cases of low-grade oligodendroglioma (LO) and 29 cases of anaplastic oligodendroglioma (AO) were analyzed by FISH for 1p and 19q status and by immunohistochemistry for p53, p16, and GFAP expression using a tissue microarray. Direct sequencing of the p53 gene was also performed. 1p deletion was observed in 39 of 56 patients (69.9%), and 19q deletion in 41 of 56 (73.2%). Combined loss of 1p and 19q was found in 38 of 56 (67.9%) and exhibited distinct concomitant deletion (P = 0.000). p53 overexpression was observed in 17 cases (30.3%), GFAP expression in 18 cases (32.1%), and p16 loss in 40 cases (74%) of oligodendrogliomas. The expressions of p53 and GFAP were more frequent in AO than in LO (P= 0.015 and 0.001). In contrast, p53 expression was more common in oligodendrogliomas with an intact 19q (P= 0.029), or an intact 1p (P= 0.071). Only five of 14 patients with p53 expression showed TP53 mutation, which was inversely correlated with 1p deletion (P= 0.036). Patients with combined loss of 1p and 19q exhibited better overall survival (P = 0.045). Patients with p53 expression without combined 1p and 19q loss showed poor overall survival (P < 0.000). However, TP53 mutation along with 1p and 19q status could not predict patient outcome. Patients with p16 loss without combined 1p and 9q loss showed poor overall survival (P = 0.011). Therefore, in oligodendrogliomas, the absence of the combined deletion of 1p and 19q and the aberrant expression of p53 or loss of p16 could be used as poor prognostic markers.

PMID: 17319279

[PubMed - indexed for MEDLINE]

genome.ucsc.edu/cgi-bin/hgTracks?db=hg18&lastVirtModeType=default&lastVirtModeExtraState=&virtModeType=default&vir

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UCSC Genome Browser on Human Mar. 2006 (NCBI36/hg18) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

chr1:92,000,001-94,500,000 2,500,000 bp. enter position, gene symbol or search terms go

chr1 (p22.1) p31.1 q12 q41

Scale
chr1:
92,500,000
93,000,000
93,500,000
94,000,000
Chromosome Bands Localized by FISH Mapping Clones
1p22.1
ClinGen CNVs: Pathogenic
nssv578526_unk
nssv706398_unk
UCSC Genes (RefSeq, GenBank, tRNAs & Comparative Genomics)
RefSeq Genes
C/D and H/ACA Box snoRNAs, scaRNAs, and microRNAs from snoRNABase and miRBase
Human mRNAs
Human mRNAs from GenBank
Spliced ESTs
Human ESTs That Have Been Spliced
Layered H3K4Me1
ENCODE Enhancer- and Promoter-Associated Histone Mark (H3K4Me1) on 8 Cell Lines