

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."

G-DOC Plus
Home Studies Lists Analyses Groups Notifications Study Options - Help

G-DOC Plus Launch Pad!

Welcome back, your last login was Mon Jan 30, 2017. You can check if you have been granted access to new lists or analyses since your last login

Welcome! The G-DOC Plus Launch Pad is your one-stop resource for learning more about G-DOC and getting started on the platform.

Studies

Lists

Study ID	Sample Size	Description	Data Source	Cancer Type	Patient Status	Public Data Source
PC_TAYLOR_2011_01	301	Integrative genomic profiling of human prostate cancer	Public Data Source,	PROSTATE CANCER	PATIENT	Public Data Source
PNC_PEI_2009_01	164	Expression data from Mayo Clinic Pancreatic Tumor and Normal samples	Public Data Source,	PANCREATIC CANCER	PATIENT	Public Data Source
REMBRANDT	580	NCI Rembrandt Study: Molecular Analysis of Brain Neoplasia	Public Data Source,	BRAIN CANCER	PATIENT	Public Data Source
SC_OOI_2009_01	162	Gastric Cancer Project '08 (Singapore Patient Cohort)	Public Data Source,	STOMACH CANCER	PATIENT	Public Data Source
THE_1000_GENOMES_PROJECT	561	1000 genomes dataset	Public Data Source,	OTHER	PATIENT	Public Data Source
WH_HAHN_2013_01	521	Keratinocyte and fibroblast gene expression in skin and keloid scar tissue	Public Data Source,	WOUND HEALING	PATIENT	Public Data Source

Studies

REMBRANDT Details

Select Study

Study Name	REMBRANDT (Id:580)
Study Abstract	<p>This is the NCI Rembrandt Study: Molecular Analysis of Brain Neoplasia. Note: There are differences between the Rembrandt and the G-DOC platforms due to the way the two systems are built. The differences are listed "here".</p> <p>Primary brain tumors are the fourth leading cause of cancer mortality in adults under the age of 54 years and the leading cause of cancer mortality in children in the United States. Therapy for the most common type of primary brain tumors, gliomas, remains suboptimal. The development of new and more effective treatments will likely require a better understanding of the biology of these tumors. Here, we show that use of the high-density 100K single-nucleotide polymorphism arrays in a large number of primary tumor samples allows for a much higher resolution survey of the glioma genome than has been previously reported in any tumor type. We not only confirmed alterations in genomic areas previously reported to be affected in gliomas, but we also refined the location of those sites and uncovered multiple, previously unknown regions that are affected by copy number alterations (amplifications, homozygous and heterozygous deletions) as well as allelic imbalances (loss of heterozygosity/gene conversions). The wealth of genomic data produced may allow for the development of a more rational molecular classification of gliomas and serve as an important starting point in the search for new molecular therapeutic targets.</p>

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

Browser tabs: Clinical Search R..., cytoband 7p15..., Identification of..., cytoband 1p31..., cytobands in ast..., Distinct Genomi..., chromosome 8...

URL: https://gdoc.georgetown.edu/gdoc/clinical/filter?parent_category_EVENT_OS=EVENT_OS&parent_vocab_EVENT_OS=0&g

G-DOC^{plus} Home Studies Lists Analyses Groups Notifications Study Options Help

Explore Clinical Data and Create Groups

Current Study: REMBRANDT [change study?](#)

Filter [reset] [tips] [advanced search]

Demographics

- ☐ Age range
- ☐ Gender
- ☐ Race

Sample details

- ☐ Anti convulsant status
- ☐ Copy number data
- ☐ Gene expression data
- [view all \(2 more ...\)](#)

Clinical evaluation

- ☐ Disease evaluation by MRI
- ☐ Neurologic exam score
- ☐ Performance Status Score: Karnofsky

Subject Search

Current Split Attribute

Event indicator for overall survival

	Survival	All Subjects
None...		479
Age range		93
Anti convulsant status		572
Copy number data		
Disease evaluation by MRI		
Type of disease		
Event indicator for overall survival		
Gender		
Gene expression data		

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

Browser tabs: Clinical Search R..., cytoband 7p15..., Identification of..., cytoband 1p31..., cytobands in ast..., Distinct Genomi..., chromosome 8...

URL: https://gdoc.georgetown.edu/gdoc/clinical/filter?parent_category_EVENT_OS=EVENT_OS&parent_vocab_EVENT_OS=0&g

G-DOC^{plus} Home Studies Lists Analyses Groups Notifications Study Options Help

Explore Clinical Data and Create Groups

Current Study: REMBRANDT [change study?](#)

Filter [reset] [tips] [advanced search]

Demographics

- ☐ Age range
- ☐ Gender
- ☐ Race

Sample details

- ☐ Anti convulsant status
- ☐ Copy number data
- ☐ Gene expression data
- [view all \(2 more ...\)](#)

Clinical evaluation

- ☐ Disease evaluation by MRI
- ☐ Neurologic exam score
- ☐ Performance Status Score: Karnofsky

Subject Search

Current Split Attribute

Event indicator for overall survival

	Survival	All Subjects
None...		479
Age range		93
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Copy number data		
Disease evaluation by MRI		
Type of disease		
Event indicator for overall survival		
Gender		
Gene expression data		

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

Browser tabs: Clinical Search R..., cytoband 7p15..., Identification of..., cytoband 1p31..., cytobands in ast..., Distinct Genomi..., chromosome 8...

URL: https://gdoc.georgetown.edu/gdoc/clinical/filter?parent_category_DISEASE_TYPE=DISEASE_TYPE&parent_vocab_DISEASE

G-DOC^{plus} Home Studies Lists Analyses Groups Notifications Study Options Help

Explore Clinical Data and Create Groups

Current Study: REMBRANDT [change study?](#)

Filter [reset] [tips] [advanced search]

Demographics

- ☐ Age range
- ☐ Gender
- ☐ Race

Sample details

- ☐ Anti convulsant status
- ☐ Copy number data
- ☐ Gene expression data
- [view all \(2 more ...\)](#)

Clinical evaluation

- ☐ Disease evaluation by MRI
- ☐ Neurologic exam score
- ☐ Performance Status Score: Karnofsky

Subject Search

Current Split Attribute

Type of disease

Type of disease	All Subjects
OLIGODENDROGLIOMA	86
ASTROCYTOMA	170
UNKNOWN	68
UNCLASSIFIED	1
NON TUMOR	31
GBM	261
MIXED	13
Total	630

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

Current Study: REMBRANDT

Filter [reset] [tips] [advanced search]

Demographics

- Age range
- Gender
- Race

Sample details

- Anti convulsant status
- Copy number data
- Gene expression data
- view all (2 more ...)

Clinical evaluation

- Disease evaluation by MRI
- Neurologic exam score
- Performance Status Score: Karnofsky

Subject Search

Current Split Attribute: Type of disease

Type of disease	All Subjects
OLIGODENDROGLIOMA	86
ASTROCYTOMA	170
UNKNOWN	68
UNCLASSIFIED	1
NON TUMOR	31
GBM	261
MIXED	13
Total	630

View Detailed Report
Save ids as 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."

Save your list

Rem_astro created successfully

List Type: clinical_patient

List Name: Rem_astro

Cancel Save close

UNCLASSIFIED	1
NON TUMOR	31
GBM	261
MIXED	13
Total	630

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."

Save your list

Rem_oligo created successfully

List Type: clinical_patient

List Name: Rem_oligo

Cancel Save close

UNCLASSIFIED	1
NON TUMOR	31
GBM	261
MIXED	13
Total	630

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

The screenshot shows the G-DOC Plus web application interface. The top navigation bar includes links for Home, Studies, Lists, Analyses, Groups, Notifications, Study Options, and Help. The 'Study Options' menu is currently open, displaying a list of options: Study Selected, REMBRANDT, SEARCH, Genome Browser, Compound/Drug Targets, Findings, Explore Clinical Data and Create Groups, Gene Expression Data, ANALYZE, Group Comparison (highlighted), Chromosomal Instability Index, KM Clinical Plot, KM Gene Expression Plots, Classification, and HeatMap Viewer. The main content area shows the 'Explore Clinical Data and Analysis' page for the current study 'REMBRANDT'. It includes a filter section on the left with categories like Demographics, Sample details, and Clinical evaluation. A 'Subject Search' table is displayed, showing the 'Type of disease' and the number of samples for each category.

Type of disease	All S
OLIGODENDROGLIOMA	86
ASTROCYTOMA	170
UNKNOWN	68
UNCLASSIFIED	1
NON TUMOR	31
GBM	261
MIXED	13
Total	630

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

The screenshot shows the 'Perform Group Comparison Analysis' window in the G-DOC Plus web application. The current study is 'REMBRANDT'. The user is prompted to 'Select a baseline group and a comparison group(s)'. The 'Select baseline group' dropdown is open, showing a list of groups: Rem_oligo (selected), Rem_astro, rembr_nontumor, olig_cnmb, astr_cnmb, GBM_male, gbm_female, rembr_censor, rembr_cencor, rembr_event, rem_gbm, Rem_astroc, list1463583422692, Rem_ast_r3, Rem_ast_r2, Rem_Olig_gr3, Rem_Glio_gr2, Rem_Astr_g3, and Rem_Astr_g2. Other fields include p-value (0.05), Fold Change (1.5), Statistical Method (T-Test: Two Sample T), Multiple Comparison Adjustment (None), Data-Type (Select Data Type), and Dataset (Select Data Type First). A 'Submit Analysis' button is at the bottom.

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

G-DOC^{plus} Home Studies Lists Analyses Groups Notifications Study Options - Help

Perform Group Comparison Analysis

Current Study: REMBRANDT [change study?](#)

Select a baseline group and a comparison group(s) [?](#)

Select baseline group: Rem_oligo

Select comparison group: Rem_astro

p-value: .05

Fold Change: 1.5

Statistical Method: T-Test: Two Sample Test

Multiple Comparison Adjustment: None

Data-Type: Select Data Type

Dataset: Select Data Type First

[Submit Analysis](#)

G-DOC^{plus} Home Studies Lists Analyses Groups Notifications Study Options - Help

Perform Group Comparison Analysis

Current Study: REMBRANDT [change study?](#)

Select a baseline group and a comparison group(s) [?](#)

Select baseline group: Rem_oligo

Select comparison group: Rem_astro

p-value: .05

Fold Change: 1.5

Statistical Method: T-Test: Two Sample Test

Multiple Comparison Adjustment: None

Data-Type: COPY_NUMBER

Dataset: Chromosome-level Chrom

[Submit Analysis](#)

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.

The screenshot shows the G-DQC Plus web application interface. The top navigation bar includes links for Home, Studies, Lists, Analyses, Groups, Notifications, Study Options, and Help. The main content area is titled "Notifications" and lists various analyses with their completion status. Below this, the "Analysis Results" section is displayed, showing a table of results for a specific analysis.

Notifications

Below are your latest running analyses. Once completed, click on the Analysis name to see detailed results.

Analysis Name	Status
GROUP_COMPARISON (456 1/30/2017)	Complete
GROUP_COMPARISON (349 1/30/2017)	Complete
GROUP_COMPARISON (334 1/30/2017)	Complete
GROUP_COMPARISON (331 1/30/2017)	Complete
GROUP_COMPARISON (314 1/30/2017)	Complete
PCA (255 1/30/2017)	Complete
GROUP_COMPARISON (253 1/30/2017)	Complete
GROUP_COMPARISON (252 1/30/2017)	Complete
HEATMAP (244 1/30/2017)	Complete
PCA (242 1/30/2017)	Complete
GROUP_COMPARISON (241 1/30/2017)	Complete
PCA (236 1/30/2017)	Complete
PCA (235 1/30/2017)	Complete
GROUP_COMPARISON (230 1/30/2017)	Complete
PCA (219 1/30/2017)	Complete
PCA (217 1/30/2017)	Complete
PCA (215 1/30/2017)	Complete
PCA (214 1/30/2017)	Complete
GROUP_COMPARISON (213 1/30/2017)	Complete
PCA (212 1/30/2017)	Complete
PCA (210 1/30/2017)	Complete
GROUP_COMPARISON (209 1/30/2017)	Complete
CIN (157 1/30/2017)	Complete
CIN (150 1/30/2017)	Complete

Analysis Results

Statistical Method: TTest

Adjustment: NONE

Fold Change: 1.5

Pvalue: .05

Study: REMBRANDT

Data File: REMBRANDT_CIN_CYTOBANDS_XBA.Rda

Baseline Group: Rem_oligo

Groups: Rem_astro

List Name: Save Selected

[View HeatMap for selected reporters](#)

Analysis Results Table

Reporter ID	Cytoband	p-value	Fold Change	Mean Baseline (ic)	Mean Group (log)	Std Baseline	Std Group
1p22.1	1p22.1	6.636 x 10 ⁻⁸	-2.034	1.118	0.094	0.926	0.378
1p13.3	1p13.3	2.664 x 10 ⁻⁷	-2.264	1.374	0.193	1.096	0.516
1p34.3	1p34.3	3.126 x 10 ⁻⁷	-2.345	1.463	0.233	1.161	0.528
19q13.32	19q13.32	3.344 x 10 ⁻⁷	-1.895	1.123	0.201	0.886	0.378
1p13.1	1p13.1	6.658 x 10 ⁻⁷	-1.602	0.760	0.080	0.700	0.243
19q13.11	19q13.11	7.798 x 10 ⁻⁷	-1.732	0.881	0.088	0.831	0.268
1p36.12	1p36.12	1.148 x 10 ⁻⁶	-1.778	0.934	0.103	0.831	0.382
19q13.2	19q13.2	2.473 x 10 ⁻⁶	-1.625	0.858	0.157	0.715	0.356
1p36.21	1p36.21	2.873 x 10 ⁻⁶	-2.012	1.272	0.263	0.908	0.660
1p22.2	1p22.2	2.982 x 10 ⁻⁶	-2.022	1.191	0.173	1.053	0.512
19q12	19q12	3.340 x 10 ⁻⁶	-1.824	0.962	0.094	0.989	0.291
1p13.2	1p13.2	6.851 x 10 ⁻⁶	-2.042	1.247	0.217	1.147	0.498
19q13.42	19q13.42	7.383 x 10 ⁻⁶	-1.523	0.797	0.191	0.650	0.334
1p36.22	1p36.22	7.778 x 10 ⁻⁶	-1.691	0.964	0.206	0.787	0.454

Export results Page 1 of 1 10 View 1 - 32 of 32

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](#)?

Format: Abstract

Send to

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 YK¹, Park K, Park CK, Paek SH, Jung HW, Park SH.

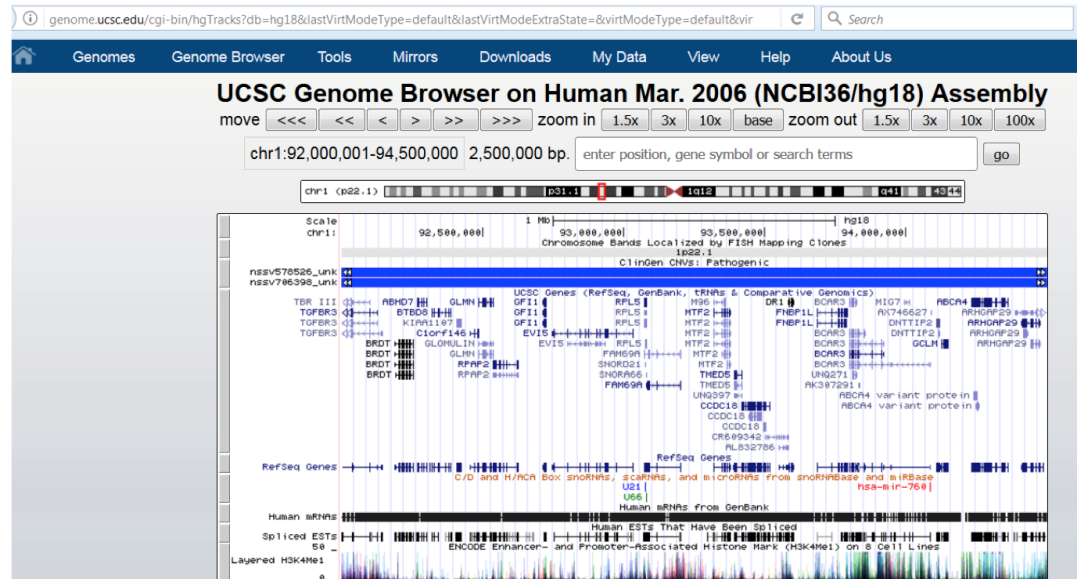
Author information

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]



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.