

# G-DOC *Plus*

## Introduction and Help

Innovation Center for Biomedical Informatics

Georgetown University

# Overview

- Register
- Login
- Navigation
- How to create patient groups
- Group comparison
- Gene expression KM plot
- Clinical KM plot

# Register as a First time user



The Innovation Center for Biomedical Informatics (ICBI)  
Lombardi Comprehensive Cancer Center

Thu Jan 22, 2015

email or net-id

[register now](#) | [forgot password](#)



Welcome to GDOC Plus Beta!

Precision Medicine

Registration with Georgetown Net ID (or any other email). You will get an email with a link that you need to click to confirm registration

## Understanding Data in G-DOC Plus

It all begins with a study...

All data in G-DOC Plus derives from studies on topics such as breast cancer, wound healing, or even 1,000 Genomes. Each study may contain clinical and/or biospecimen data. Below is an overview of studies by topic.

\* private studies, ones which are uploaded and marked private, are not counted here

### News

October 02, 2014: ICBI Symposium 2014

[\[read\]](#)

May 02, 2014: Featured in Frontiers' Top 10  
2013 Most viewed Genetics Research articles

[\[read\]](#)

March 12, 2014: AAAS Big Data Blog [\[read\]](#)

# Login



The Innovation Center for Biomedical Informatics (ICBI)  
Lombardi Comprehensive Cancer Center

Thu Jan 22, 2015

kb472

\*\*\*\*\*

Log In

[register now](#) | [forgot password](#)



## Welcome to GDOC Plus Beta!

The Georgetown Database of Cancer Plus other diseases (G-DOC Plus) is a precision medicine platform containing molecular and clinical data from thousands of patients and cell lines, along with tools for analysis and data visualization. The platform enables the integrative analysis of multiple data types to understand disease

**Precision Medicine**

**Translational research**

**Population genetics**

## News

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## Understanding Data in G-DOC Plus

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# Launch Pad

## G-DOC Plus Launch Pad!

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



**It All Starts Here!**



G-DOC has over seventy studies, We know this can be overwhelming! Let us guide you to choose the study that is relevant for your research.

Let's Go! >



Groups



Notifications 0

# Transitional Research

[Home](#)[Studies](#)[Lists](#)[Analyses](#)[Groups](#)[Notifications](#)[Study Options ▾](#)[Help](#)[kb472 ▾](#)

## What's your area of interest?

G-DOC Plus has three overlapping entry points for the user based on their interests. Choose your area of interest to launch the workflow.



### Precision Medicine

Patients' molecular diagnostics and clinical data.



### Translational Research

Analytic tools and workflows to enable discovery.



### Population Genetics

Race-based, genomic reporting and comparison.



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[SYSTEM REQUIREMENTS](#) | [CITATION POLICY](#) | [PUBLICATIONS USING G-DOC](#) | [DATA ACCESS POLICY](#) | [LICENSE INFO](#) | [CONTACT US](#) | [G-DOC Plus ® TEAM](#)

# Select disease/data of interest

## DEMENTIA

**1**  
*study*

**30**  
*samples*

**30**  
*biospecimen*

## PEDIATRIC CANCERS

**5**  
*studies*

**256**  
*samples*

**256**  
*biospecimen*

## BREAST CANCER

**25**  
*studies*

**3952**  
*samples*

**4532**  
*biospecimen*

## COLON CANCER

**10**  
*studies*

**1226**  
*samples*

**1262**  
*biospecimen*

## LUNG CANCER

**1**  
*study*

**478**  
*samples*

**443**  
*biospecimen*

## MUSCULAR DYSTROPHY

**1**  
*study*

**36**  
*samples*

**36**  
*biospecimen*

## LIVER CANCER

**3**  
*studies*

**298**  
*samples*

**468**  
*biospecimen*

## CELL\_LINE\_COLLECTIONS

**1**  
*study*

**60**  
*samples*

**59**  
*biospecimen*

## OVARIAN CANCER

**1**  
*study*

**1711**  
*samples*

**564**  
*biospecimen*

## PROSTATE CANCER

**1**  
*study*

**465**  
*samples*

**538**  
*biospecimen*

## PANCREATIC CANCER

**1**  
*study*

**52**  
*samples*

**51**  
*biospecimen*

## BRAIN CANCER

**1**  
*study*

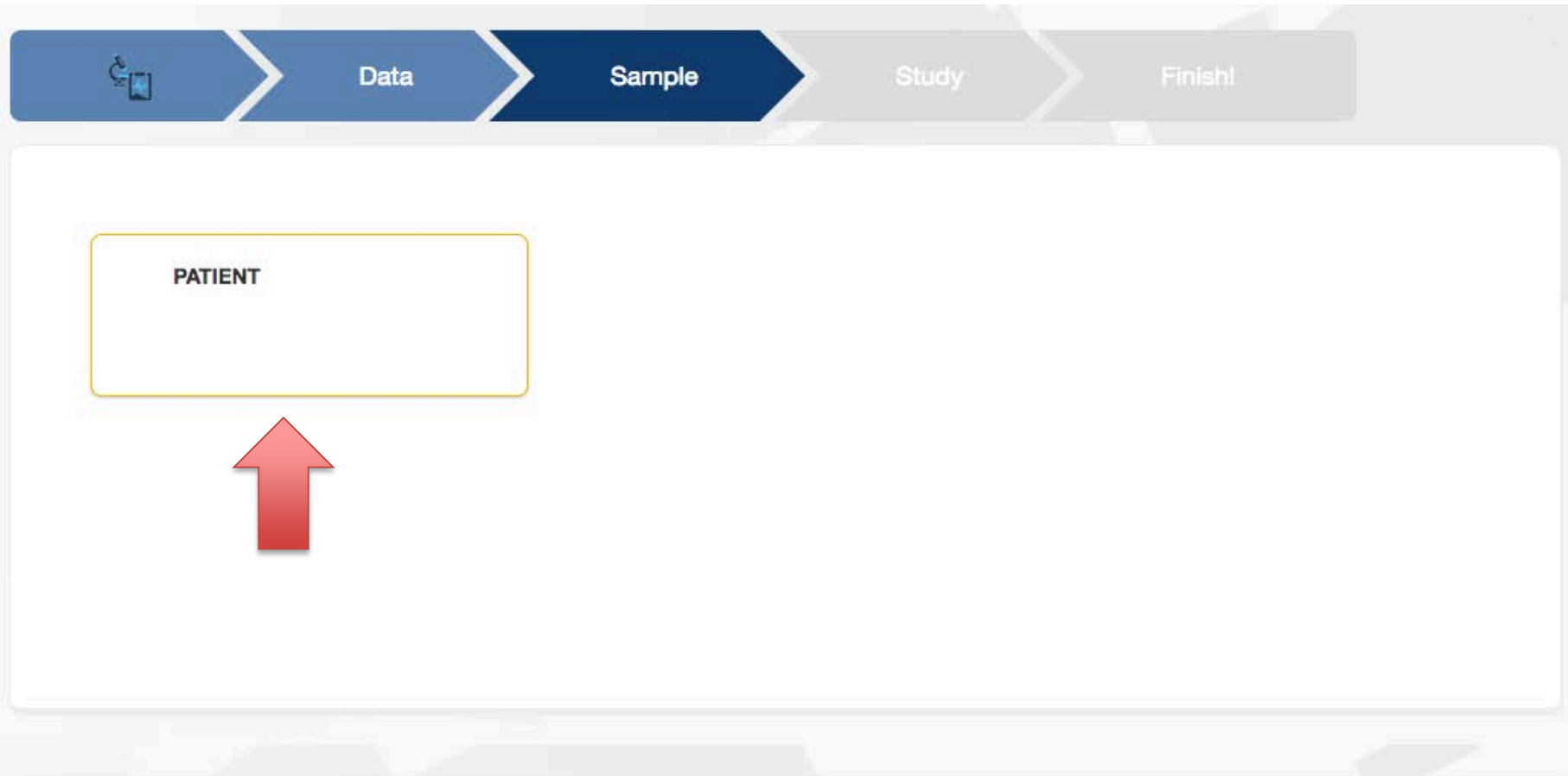
**671**  
*samples*

**804**  
*biospecimen*



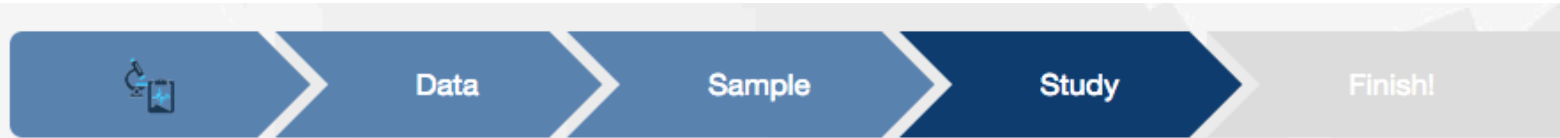


# Choose between patient and cell line data





# Select study



## REMBRANDT

**Title:** NCI Rembrandt Study: Molecular Analysis of Brain Neoplasia

**Data Type Details:**  
CLINIC,MICROARRAY,COPY\_NUMBER

**Abstract:** This is the NCI Rembrandt Study: Molecular Analysis of Brain Neoplasia. 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

**671**  
*samples*

**804**  
*biospecimen*

[More>>](#)



Note: If you click on “More,” you will see a complete description of the dataset.

# Study selected. Let's now create some groups

The screenshot shows the G-DOC Plus web application interface. At the top is a dark blue navigation bar with the G-DOC Plus logo on the left and a series of menu items: Home, Studies, Lists, Analyses, Groups, Notifications, Study Options (with a dropdown arrow), and Help. To the right of the menu items is a search bar with a magnifying glass icon and the text 'kb472' followed by a dropdown arrow. Below the navigation bar is a workflow bar with five steps: a first step with a microscope icon, 'Data', 'Sample', 'Study', and 'Finish!'. The 'Study' step is currently selected. Below the workflow bar is a white box containing the text 'Based upon the study you picked, here is a list of tools you can use:'. This box is divided into two columns. The left column is titled 'Analyze' and contains a bulleted list of tools: Classification, KM Clinical Plot, HeatMap Viewer, KM Gene Expression Plots, Group Comparison, and Chromosomal Instability Index. The right column is titled 'Search' and contains a bulleted list: Gene Expression Data and Explore Clinical Data and Create Groups. A red arrow points upwards to the underlined link. A tooltip box next to the link contains the text 'Explore clinical data and create groups'.

G-DOC<sup>®</sup> Plus

Home Studies Lists Analyses Groups Notifications Study Options ▾ Help

Search kb472 ▾


Workflow: [Icon] → Data → Sample → Study → Finish!

Based upon the study you picked, here is a list of tools you can use:

Analyze	Search
<ul style="list-style-type: none"><li>• Classification</li><li>• KM Clinical Plot</li><li>• HeatMap Viewer</li><li>• KM Gene Expression Plots</li><li>• Group Comparison</li><li>• Chromosomal Instability Index</li></ul>	<ul style="list-style-type: none"><li>• Gene Expression Data</li><li>• <u>Explore Clinical Data and Create Groups</u></li></ul>

Explore clinical data and create groups

# Explore clinical data or create groups



HomeStudiesListsAnalysesGroupsNotificationsStudy Options ▾Help

kb472 ▾

Filter [reset] tips | advanced search ]

Demographics

☐ Age range ⓘ  
☐ Gender ⓘ  
☐ Race ⓘ

Sample details

☐ Anti convulsant status ⓘ  
☐ Copy number data ⓘ  
☐ Gene expression data ⓘ  
view all (4 more ...)  
☐ Steroid dose status ⓘ  
☐ Institution name ⓘ  
☐ Prior therapy surgery done at first follow up ⓘ  
☐ Prior therapy surgery done at second follow up ⓘ

Disease details

☒ Disease ⓘ

Subject Search

WHO\_GRADE(All) > DISEASE\_TYPE(All) >  
Current Split Attribute ⓘ  
WHO grade ▾

Disease	WHO_GRADE_I	WHO_GRADE_II	WHO_GRADE_III	WHO_GRADE_IV
OLIGODENDROGLIOMA	0	40	25	0
ASTROCYTOMA	0	66	63	0
UNKNOWN	0	0	1	0
UNCLASSIFIED	0	0	0	0

This page allows you to explore the clinical data. This is an online shopping type of experience. Feel free to check and uncheck the boxes on the left – this will update the patient numbers in the table.

e.g. In this example you can see that among Oligodendroglioma patients, 40 patients have WHO tumor grade II and 25 patients have grade III tumor

# Let's save the Oligodendroglioma patients with tumor grade II and grade III

Filter [reset | tips | advanced search]

## Demographics

- ☐ Age range
- ☐ Gender
- ☐ Race

## Sample details

- ☐ Anti convulsant status
- ☐ Copy number data
- ☐ Gene expression data
- view all (4 more ...)
- ☐ Steroid dose status
- ☐ Institution name
- ☐ Prior therapy surgery done at first follow up
- ☐ Prior therapy surgery done at second follow up

## Disease details

- ☒ Disease

## Clinical evaluation

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

## Subject Search

WHO\_GRADE(All) > DISEASE\_TYPE(All) >

Current Split Attribute

WHO grade

Disease	WHO_GRADE_I	WHO_GRADE_II	WHO_GRADE_III	WHO_GRADE_IV
OLIGODENDROGLIOMA	0	<a href="#">40</a>	<a href="#">25</a>	0
ASTROCYTOMA	0	<a href="#">66</a>		0
UNKNOWN	0	0	0	0
UNCLASSIFIED	0	0	0	0
NON TUMOR	0	0	0	0
GBM	<a href="#">2</a>	0	0	<a href="#">140</a>
MIXED	0	<a href="#">4</a>	<a href="#">4</a>	0
Total	<a href="#">2</a>	<a href="#">110</a>	<a href="#">93</a>	<a href="#">140</a>

View Detailed Report

Save ids as list

To save a list of patients, click on the hyperlinked number, and select "Save ids as list."

Repeat this procedure to create as many number of patient groups as needed.

Note: "View detailed report" shows a detailed clinical report of those selected patients.

# Enter a name for the list, and click “Save”

- On the Save your list dialog box, enter a name, for example, `rem_olig_grade2`, and click Save.

Save your list

List Type:	clinical, patient
List Name:	<input type="text" value="Rem_olig_grade2"/>
<input type="button" value="Cancel"/> <input type="button" value="Save"/> <a href="#">close</a>	

# Now, we want to compare the Oligodendroglioma tumor grade II patients with Oligo grade III patients

**G-DOC<sup>plus</sup>** Home Studies Lists Analyses Groups Notifications Study Options ▾ Help

Filter [ reset | tips | advanced search ]

**Demographics**

- ☐ Age range
- ☐ Gender
- ☐ Race

**Sample details**

- ☐ Anti convulsant status
- ☐ Copy number data
- ☐ Gene expression data
- view all (4 more ...)
- ☐ Steroid dose status
- ☐ Institution name
- ☐ Prior therapy surgery done at first follow up
- ☐ Prior therapy surgery done at second follow up

**Disease details**

- ☒ Disease

**Clinical evaluation**

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

**Subject Search**

WHO\_GRADE(All) > DISEASE\_TYPE

Current Split Attribute

WHO grade

Disease	WHO
OLIGODENDROGLIOMA	0
ASTROCYTOMA	0
UNKNOWN	0
UNCLASSIFIED	0
NON TUMOR	0
GBM	2
MIXED	0
Total	2

**Study Selected**

REMBRANDT

**SEARCH**

- Genome Browser
- Compound/Drug Targets
- Findings
- Explore Clinical Data and Create Groups
- Gene Expression Data

**ANALYZE**

- Group Comparison**
- Chromosomal Instability Index
- KM Clinical Plot
- KM Gene Expression Plots
- Classification
- HeatMap Viewer

GRADE_III	WHO_GRADE_IV
	0
	0
	0
	0
	140
	0
	140

# Performing a group comparison

**G-DOC<sup>®</sup> Plus** Home Studies Lists Analyses Groups Notifications Study Options Help   kb472 ▾

## Perform Group Comparison Analysis

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

Select a baseline group and a comparison group(s)

Select baseline group	p-value	Multiple Comparison Adjustment
Rem_olig_grade2 ▾	.05	False Discovery Rate(FDR): B ▾
Select comparison group	Fold Change	Data-Type
Rem_olig_grade3 ▾	1.5	GENE EXPRESSION ▾
	Statistical Method	Dataset
	T-Test: Two Sample Test ▾	mas5 normalization ▾

Select a baseline group (control group), a comparison group, and settings for the comparison analysis.

Click “Submit analysis.”



# Notifications page

## Notifications

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

GROUP\_COMPARISON (2:05 1/22/2015 )

Complete



Once you click “submit analysis,” you will be re-directed to the “Notifications” page. Once the status is “Complete,” click on “Group comparison.”

# Results of group comparison

## Analysis Results

Current Study: REMBRANDT

Analysis Results	
Statistical Method	TTest
Adjustment	FDR
Fold Change	1.5
Pvalue	.05
Study	REMBRANDT
Data File	REMBRANDT.Rda
Baseline Group	Rem_olig_grade2
Groups	Rem_olig_grade3

List Name:

Save Selected ↓

View HeatMap for selected reporters

These are the results of the group comparison.

You can sort this table based on any of the columns.

In this example, they are sorted based on fold change.

Analysis Results									
<input type="checkbox"/>	Reporter ID	Gene Symbol	p-value	Fold Change ↕	Mean Baseline (log)	Mean Group (log2)	Std Baseline	Std Group	Target Data
<input type="checkbox"/>	209937_at	TM4SF4	$1.073 \times 10^{-3}$	12.039	5.403	8.993	2.563	1.988	
<input type="checkbox"/>	1553467_at	FLJ32742	$1.295 \times 10^{-3}$	9.743	6.182	9.466	2.384	1.901	
<input type="checkbox"/>	1557053_s_at	UBE2G2	$1.371 \times 10^{-3}$	7.776	5.409	8.368	1.787	2.266	
<input type="checkbox"/>	201981_at	PAPPA	$1.776 \times 10^{-3}$	7.771	7.376	10.334	2.265	1.779	
<input type="checkbox"/>	1555409_a_at	BAGE2	$1.378 \times 10^{-2}$	7.102	8.637	11.465	2.428	2.642	
<input type="checkbox"/>	208672_s_at	SFRS3	$9.744 \times 10^{-4}$	6.746	5.102	7.856	1.918	1.573	

# Going from Group Comparison to Gene expression KM

Analysis Results	
Statistical Method	TTest
Adjustment	FDR
Fold Change	1.5
Pvalue	.05
Study	REMBRANDT
Data File	REMBRANDT.Rda
Baseline Group	Rem_olig_grade2
Groups	Rem_olig_grade3

List Name:

Analysis Results	
<input type="checkbox"/>	Reporter ID
<input type="checkbox"/>	209937_at
<input type="checkbox"/>	1553467_at
<input type="checkbox"/>	1557053_s_at
<input type="checkbox"/>	201981_at
<input type="checkbox"/>	1555409_a_at
<input type="checkbox"/>	208672_s_at
<input type="checkbox"/>	1554593_s_at
<input type="checkbox"/>	208765_s_at
<input type="checkbox"/>	1555238_at
<input type="checkbox"/>	209997_x_at
<input type="checkbox"/>	215234_at

- Perform Gene Expression KM ▶
- Perform Gene Expression Search
- Search in Entrez
- View in UCSC Genome Browser
- Search in iHOP
- Search in PIR
- Search in Ensembl Gene View
- Search in Reactome
- View at KEGG
- View at QuickGO
- View at GeneCards
- View at String DB

Endpoint: Overall survival in months

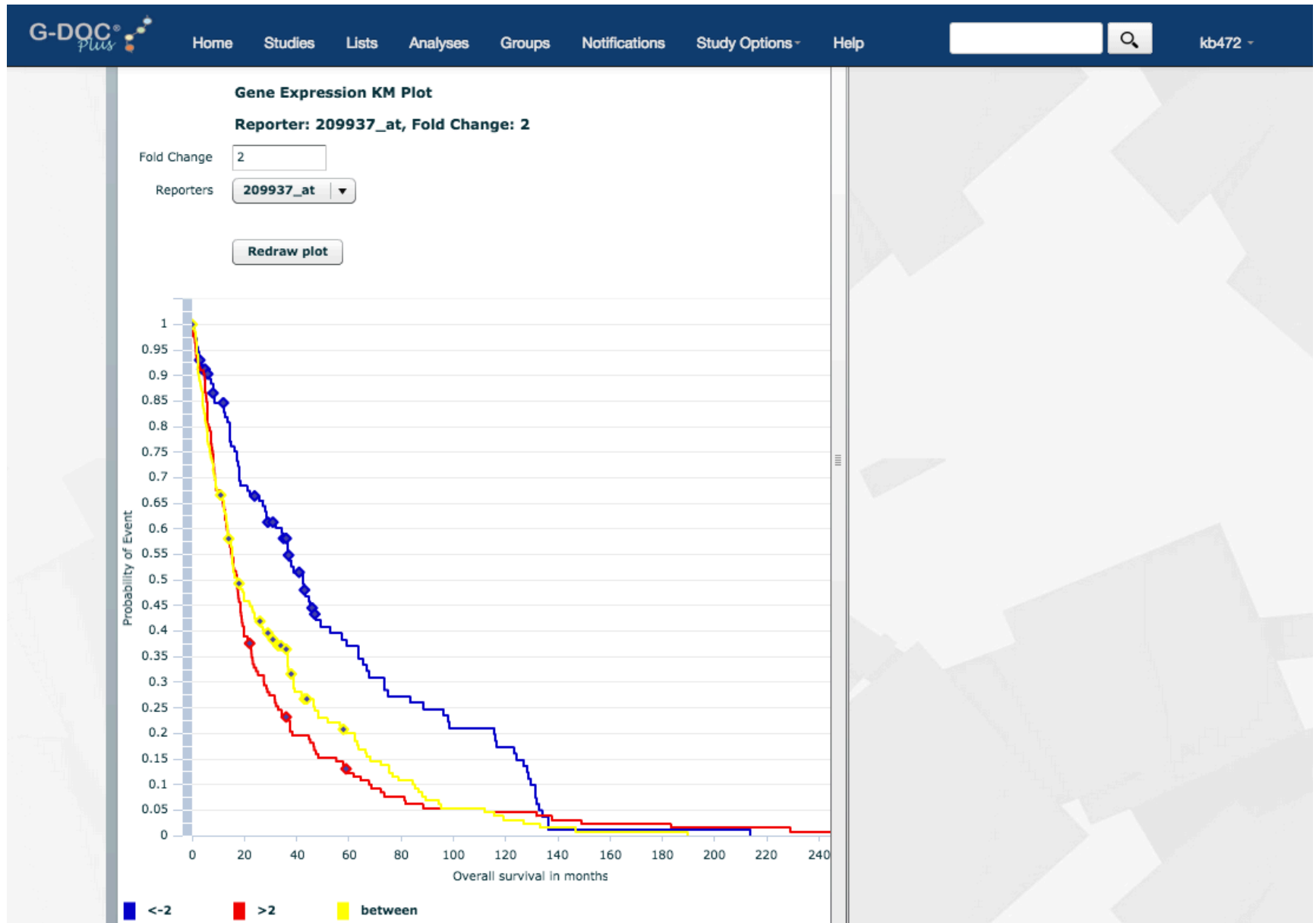
Fold Change	Mean Baseline (log)	Mean Group (log2)	Std Baseline	Std Group	Target Data
2.039	5.403	8.993	2.563	1.988	
743	6.182	9.466	2.384	1.901	
776	5.409	8.368	1.787	2.266	
771	7.376	10.334	2.265	1.779	
102	8.637	11.465	2.428	2.642	
746	5.102	7.856	1.918	1.573	
469	6.001	8.695	1.764	1.884	
434	5.398	8.084	1.843	1.989	
404	5.562	8.241	1.629	1.810	
328	6.215	8.877	1.709	1.521	
1.011 × 10 <sup>-2</sup>	5.660	8.205	1.137	2.165	

Going from Group Comparison to Gene expression KM:

- Click on gene of interest – Select “Perform Gene expression KM” – Select endpoint.

G-DOC allows users to perform Gene expression KM on either all samples or a group of samples.

# Gene expression KM plot



# How to do a clinical KM plot

## G-DOC Plus Launch Pad

Welcome! The G-DOC Plus Launch Pad is your one-stop re started on the platform.



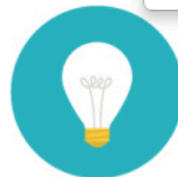
Studies



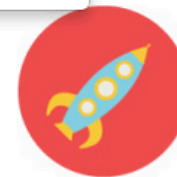
Lists



Groups



Notifications 1



Help me pick a study

Study Selected

REMBRANDT

SEARCH

Genome Browser

Compound/Drug Targets

Findings

Explore Clinical Data and Create Groups

Gene Expression Data

ANALYZE

Group Comparison

Chromosomal Instability Index

**KM Clinical Plot**


KM Gene Expression Plots

Classification

HeatMap Viewer

From either the home page, or the current page you are in, go to Study options - > KM Clinical plot.

# A Clinical KM Plot



HomeStudiesListsAnalysesGroupsNotificationsStudy Options▼Help

kb472▼

## Create Clinical KM Plot

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

Select Patient Groups:

Rem\_GBM  
Rem\_Oligo  
Rem\_Astro  
Rem\_NonTumor

Add  
Remove

Rem\_olig\_grade2  
Rem\_olig\_grade3

Select Endpoint:

Overall survival in months ▼

Plot

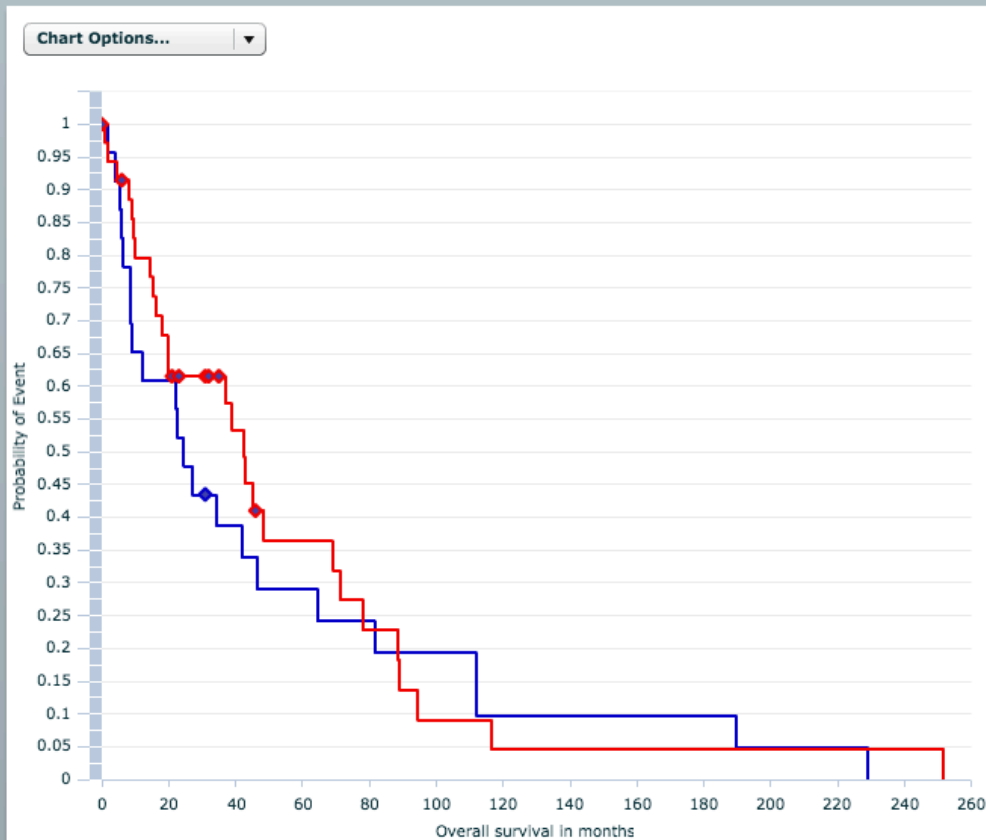
- Select patient group(s) of interest using the “Add” button.
- Select endpoint.
- Click “Plot.”

# Clinical KM plot results

## KM Plot Results

Current Study: REMBRANDT

KM Plot



Log-rank p-value: 0.5210015465230854



Rem\_olig\_grade3



Rem\_olig\_grade2