

# cBioPortal Tutorial #6: Group Comparison

Compare clinical and genomic features of  
user-defined groups of samples/patients

# Tutorial Objectives

- Explain what the new group comparison functionality enables
- Delineate the different ways to define groups and enter the group comparison view
- Highlight potential use cases for group comparison functionality

# Group Comparison Overview

Group Comparison is a new suite of analysis features which allow you to compare the clinical and genomic features of user-defined groups of samples.

Groups can be defined in Study View based on any clinical or genomic features.

Groups can also be defined within the Group Comparison page based on the union/intersection of the compared groups.

In this tutorial, we will demonstrate two different ways to enter the group comparison view.

We begin by selecting a study of interest and viewing it in the Study Summary page.

# Select a study

Query      Quick Search Beta!      Download

CNS/Brain      14       Select all listed studies matching filter (15)

Soft Tissue      1       Select all listed studies matching filter (1)

Select Studies for Visualization & Analysis:      1 study selected (1102 samples)      Deselect all

glioma      X      Cerami et al., 2012 & Gao et al., 2013

Diffuse Glioma

- Brain Lower Grade Glioma (TCGA, PanCancer Atlas)
- Brain Lower Grade Glioma (TCGA, Provisional)
- Glioma (MSK, 2018)
- Low-Grade Gliomas (UCSF, Science 2014)
- Merged Cohort of LGG and GBM (TCGA, Cell 2016)

GLIOBLASTOMA

- Brain Tumor PDXs (Mayo Clinic, 2019)

1. Start typing tumor type of interest...

2. Select the checkbox next to the study of interest and click "Explore Selected Studies"

3. Or click on "View study summary" button

514 samples      530 samples      91 samples      61 samples      1102 samples

95 samples      585 samples      206 samples      592 samples      604 samples

22 samples      96 samples

Query By Gene      OR      Explore Selected Studies

[Link to this page](#)

# Study View

Notice this new “Groups” button. We’ll use this in the second example.

Merged Cohort of LGG and GBM (TCGA, Cell 2016) [Download](#)  
Whole-exome sequencing from 1,122 TCGA LGG and GBM cases. [PubMed](#)

Summary Clinical Data Heatmaps Selected: 1,122 patients | 1,122 samples Custom Selection Charts Groups ▾

Quick Filters:  812 samples with mutation data  1,084 samples with CNA data

Overall Survival

Mutated Genes (812 profiled samples)

Gene	# Mut	#	Freq ▾
IDH1	411	411	50.6%
TP53	398	322	39.7%
ATRX	216	208	25.6%
PTEN	109	108	13.3%
EGFR	93	87	10.7%
CIC	85	79	9.7%
PIK3CA	67	63	7.8%
NF1	65	53	6.5%
PIK3R1	47	45	5.5%
FUBP1	44	44	5.4%
PCLO	34	33	4.1%

CNA Genes (1084 profiled samples)

Gene	Cytoband	CNA	#	Freq ▾
CDKN2A	9p21.3	DEL	382	35.3%
CDKN2B	9p21.3	DEL	382	35.3%
MTAP	9p21.3	DEL	382	35.3%
EGFR	7p11.2	AMP	382	35.3%
CDK4	12q14.1	AMP	382	35.3%
FIP1L1	4q12	AMP	382	35.3%
PDGFRA	4q12	AMP	382	35.3%
CHIC2	4q12	AMP	382	35.3%
MLLT3	9p21.3	DEL	382	35.3%
KIT	4q12	AMP	382	35.3%
MDM4	1q32.1	AMP	382	35.3%

Sex

For this first example, I want to use a chart that isn't visible by default, so on the next slide we'll use the “Charts” button to add it.

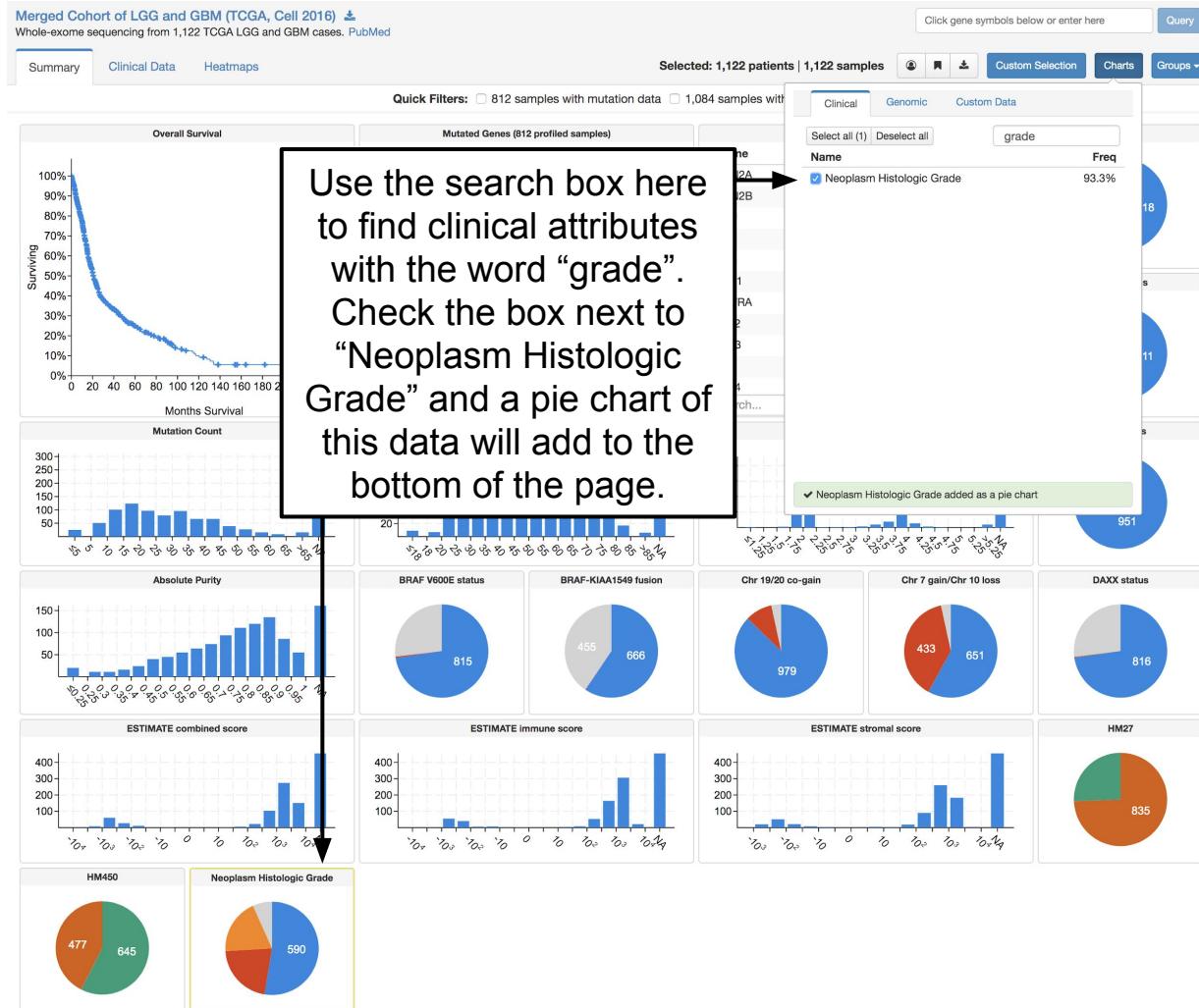
Mutation Count

Diagnosis Age

Absolute Extract Ploidy

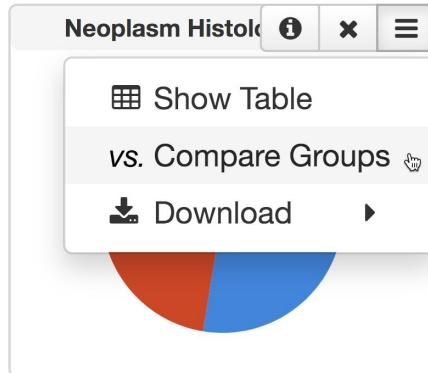
BCR Status

# Study View



# Study View

Let's compare samples of different histologic grades. Hover over the "Neoplasm Histologic Grade" pie chart menu icon (≡) and notice the vs. Compare Groups option. We're going to click on this, and it will bring us to the new group comparison page where we can compare the clinical & genomic features of samples/patients by grade.



# Group Comparison: Header

All group comparison pages share the same header:

The screenshot shows the header of a Group Comparison page. At the top, it says "Merged Cohort of LGG and GBM (TCGA, Cell 2016)". Below that, it says "Groups from **Neoplasm Histologic Grade**". Underneath, there's a section titled "Groups: (drag to reorder)" with three items: (A) G2 (216), (B) G3 (241), and (C) G4 (590). To the right of these are "Select all" and "Deselect all" buttons. Below this, there are five tabs: Overlap (selected), Survival, Clinical, Mutations, and Copy-number.

**The attribute used to create the groups.**

**Each tab has specific functionality. We'll go through these one-by-one over the next few slides.**

**The original study. Click to return to study view.**

**The available groups. Click on a group name to include or exclude it from analysis. Click the “x” to remove the group from the comparison session. Groups can also be reordered by dragging the group name.**

# Group Comparison: Overlap

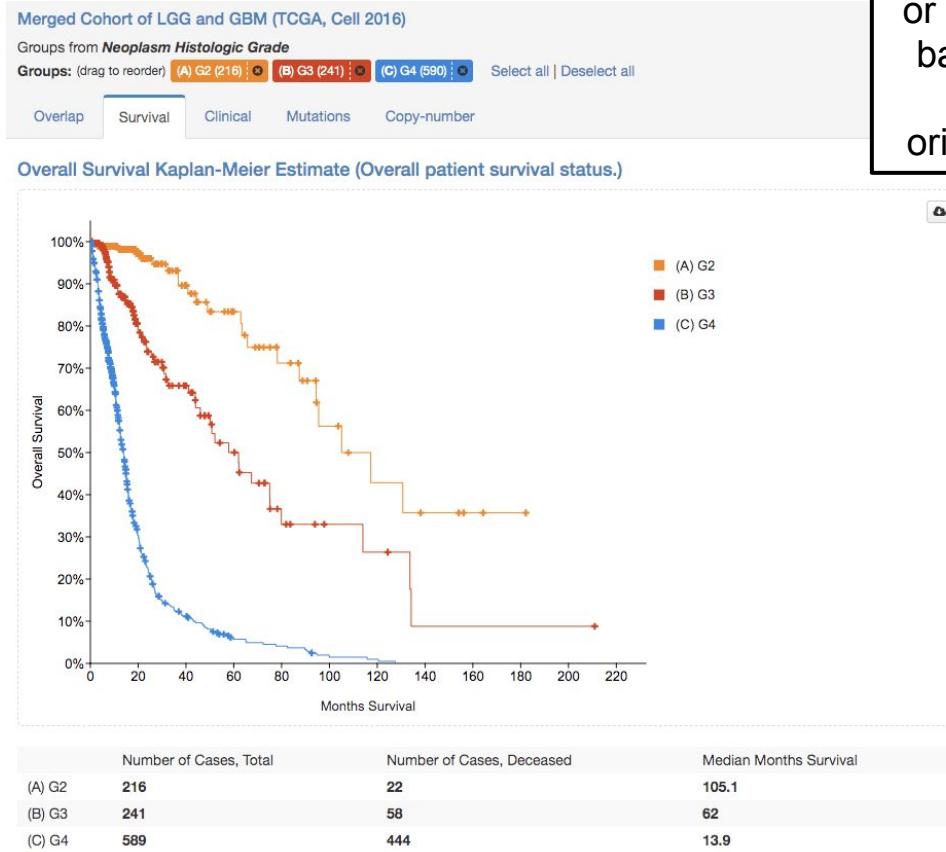


The Overlap tab shows which samples or patients may overlap among the selected groups. In this example, we can see that there is no overlap in samples or patients.

In the next example, we'll look at how overlapping samples/patients are managed.

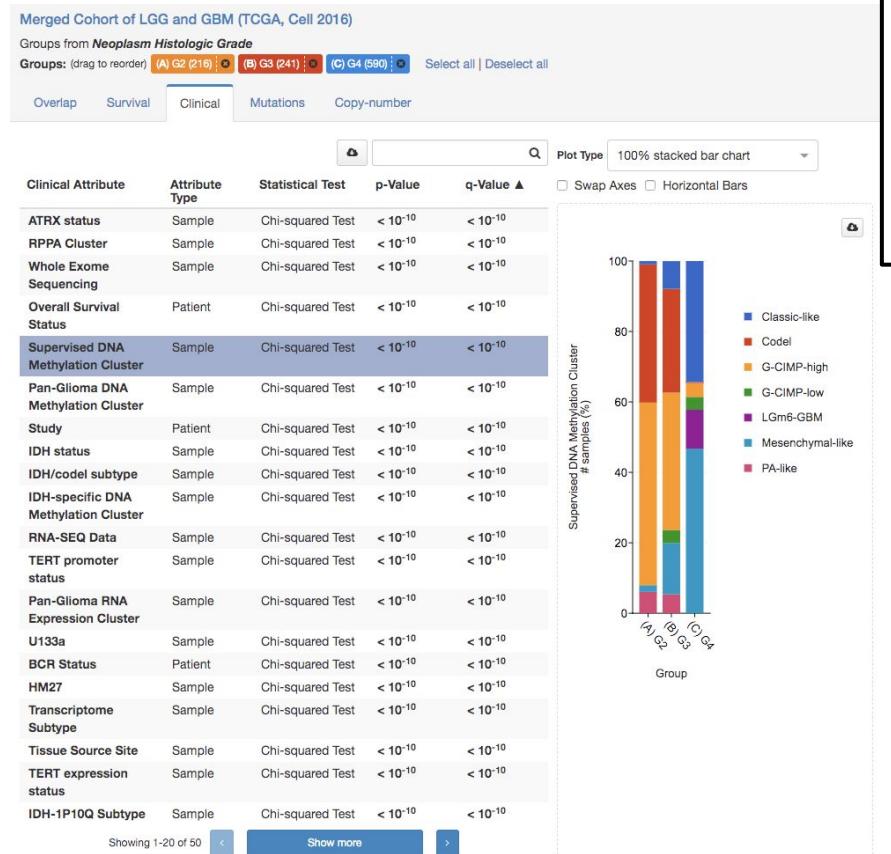
This view can also be used to create additional groups. We'll do this later.

# Group Comparison: Survival



The Survival tab shows a Kaplan-Meier plot of Overall Survival or Disease/Progression-free Survival based on the selected groups. This tab will only be visible when the original study contains survival data.

# Group Comparison: Clinical



The Clinical tab shows all the same clinical attributes that are present in Study View. Select a clinical attribute in the table (Supervised DNA Methylation Cluster is selected here) and a plot will appear to the right with the distribution of that clinical attribute across the selected groups.

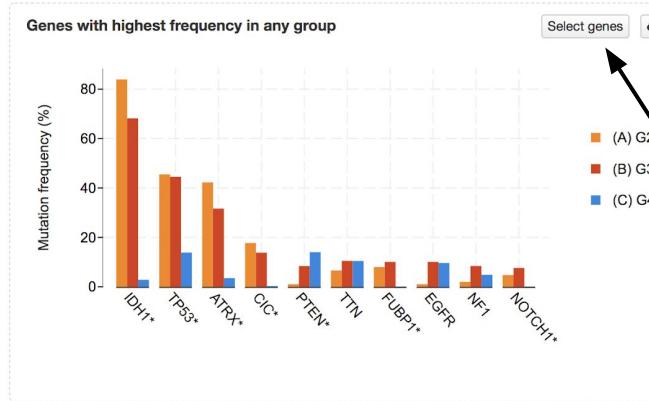
# Group Comparison: Mutations

Merged Cohort of LGG and GBM (TCGA, Cell 2016)

Groups from *Neoplasm Histologic Grade*

Groups: (drag to reorder) (A) G2 (216) (B) G3 (241) (C) G4 (690) Select all | Deselect all

Overlap Survival Clinical Mutations Copy-number



The Mutations tab compares the frequency of mutations in genes across the selected groups. The visible plots change depending on how many groups are selected. This screenshot shows the view with 3 or more groups selected.

Use this button to customize the plot to show different sets or numbers of genes, or a user-defined gene list

## Mutations

Sample-level enrichments  Select enriched groups   Significant only   Columns 

Gene	Cytoband	(A) G2	(B) G3	(C) G4	p-Value	q-Value ▲	Most enriched in
ATRX	Xq21.1	91 (42.13%)	76 (31.54%)	20 (3.39%)	0.00	0.00	(A) G2
CIC	19q13.2	38 (17.59%)	33 (13.69%)	1 (0.17%)	0.00	0.00	(A) G2
IDH1	2q34	181 (83.80%)	164 (68.05%)	16 (2.71%)	0.00	0.00	(A) G2
TP53	17p13.1	98 (45.37%)	107 (44.40%)	81 (13.73%)	0.00	0.00	(A) G2
FUBP1	1p31.1	17 (7.87%)	24 (9.96%)	0 (0.00%)	5.63e-13	1.04e-9	(B) G3
NOTCH1	9q34.3	10 (4.63%)	18 (7.47%)	0 (0.00%)	1.47e-9	2.277e-6	(B) G3
PTEN	10q23.31	2 (0.93%)	20 (8.30%)	82 (13.90%)	2.18e-7	2.889e-4	(C) G4

[Link to this page](#)

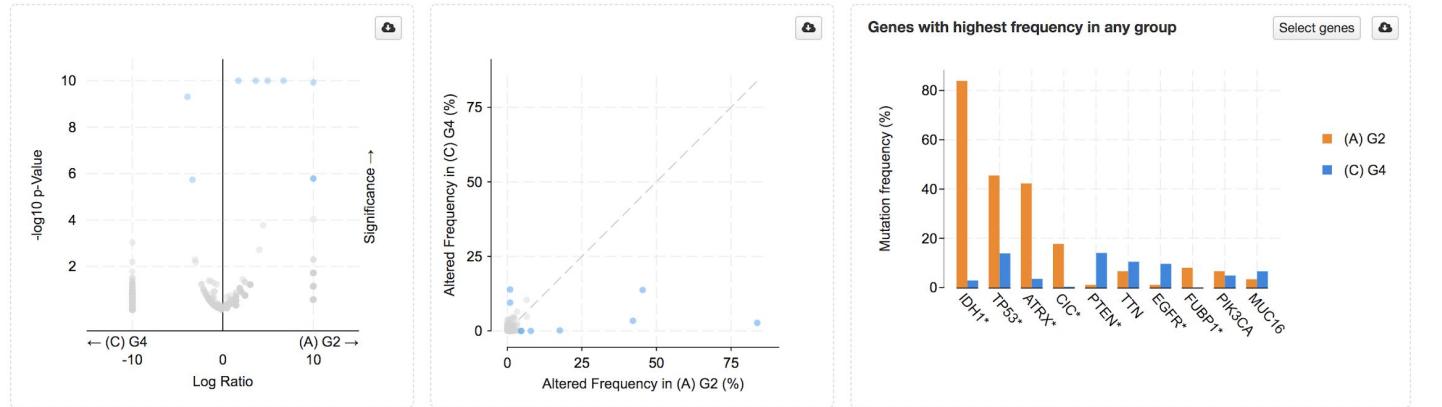
# Group Comparison: Mutations

Merged Cohort of LGG and GBM (TCGA, Cell 2016)

Groups from *Neoplasm Histologic Grade*

Groups: (drag to reorder) (A) G2 (216) (B) G3 (241) (C) G4 (690) Select all | Deselect all

Overlap Survival Clinical Mutations Copy-number



## Mutations

Sample-level enrichments		Select enriched groups	<input type="checkbox"/> Significant only				Columns ▾	Q
Gene	Cytoband	(A) G2	(C) G4	Co-occurrence Pattern	Log Ratio	p-Value	q-Value ▲	Enriched in
IDH1	2q34	181 (83.80%)	16 (2.71%)		4.95	1.49e-122	1.13e-118	(A) G2
ATRX	Xq21.1	91 (42.13%)	20 (3.39%)		3.64	3.98e-40	1.51e-36	(A) G2
CIC	19q13.2	38 (17.59%)	1 (0.17%)		6.70	4.27e-22	1.08e-18	(A) G2
TP53	17p13.1	98 (45.37%)	81 (13.73%)		1.72	5.41e-20	1.03e-16	(A) G2
FUBP1	1p31.1	17 (7.87%)	0 (0.00%)		>10	1.18e-10	1.79e-7	(A) G2
PTEN	10q23.31	2 (0.93%)	82 (13.90%)		-3.91	4.93e-10	6.24e-7	(C) G4

This screenshot shows the view with 2 groups selected (notice that I deselected group "(B) G3" by clicking on it). Two additional plots are shown when exactly 2 groups are compared.

[Link to this page](#)

# Group Comparison: Copy-Number

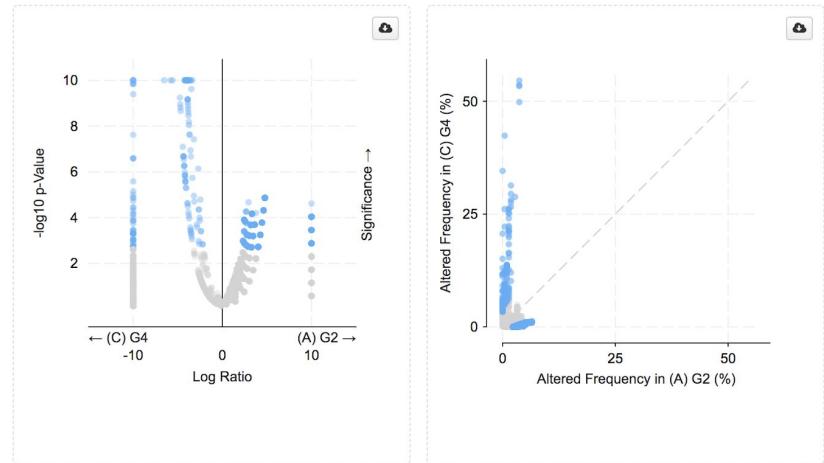
Merged Cohort of LGG and GBM (TCGA, Cell 2016)

Groups from *Neoplasm Histologic Grade*

Groups: (drag to reorder) (A) G2 (216) (B) G3 (241) (C) G4 (590) Select all | Deselect all

Overlap Survival Clinical Mutations

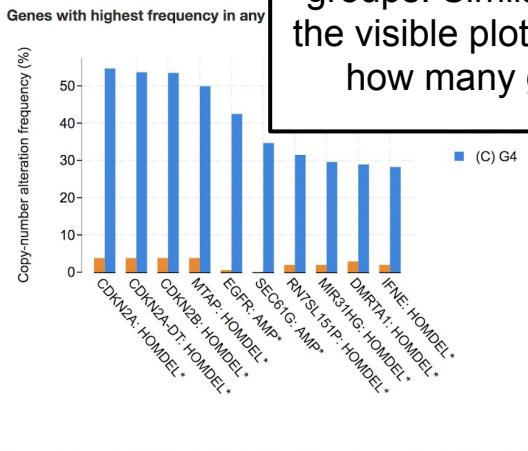
Copy-number



## Putative copy-number alterations from GISTIC

Sample-level enrichments		Select enriched groups	<input type="checkbox"/> Significant only			Columns ▾	<input type="text"/>		
Gene	Cytoband	Alteration	(A) G2	(C) G4	Co-occurrence Pattern	Log Ratio	p-Value	q-Value ▲	Enriched in
CDKN2A	9p21.3	DeepDel	8 (3.70%)	322 (54.58%)		-3.88	5.85e-47	1.75e-42	(C) G4
CDKN2A-DT	9p21.3	DeepDel	8 (3.70%)	316 (53.56%)		-3.85	1.53e-45	2.30e-41	(C) G4
CDKN2B	9p21.3	DeepDel	8 (3.70%)	315 (53.39%)		-3.85	2.62e-45	2.62e-41	(C) G4
EGFR	7p11.2	Amp	1 (0.46%)	250 (42.37%)		-6.52	7.69e-41	5.77e-37	(C) G4

The Copy-number tab compares the frequency of amplifications and deep deletions in genes across the selected groups. Similar to the Mutations tab, the visible plots change depending on how many groups are selected.



[Link to this page](#)

For the second approach to group comparison, we will define our own groups.

To do this, you must be logged in.

# Logging in



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Login

This button is in the header on all pages.  
Click on it. It will bring you to a page  
where you can sign in (or register) using  
any Google or Microsoft account.



Welcome to cBioPortal - sign in with your Google or Microsoft account to store your [virtual studies](#) and [groups](#). This will allow you to access your studies and groups from any computer, and cBioPortal will also remember your study view charts preferences for each study (i.e. order of the charts, type of charts and visibility). Login is optional and not required to access any of the other features of cBioPortal.



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Now that we're logged in,  
let's go back to study view.

# Study View: Defining Groups

Merged Cohort of LGG and GBM (TCGA, Cell 2016)

Whole-exome sequencing from 1,122 TCGA LGG and GBM cases. [PubMed](#)

Summary Clinical Data Heatmaps Selected: 1,122 patients | 1,122 samples

Quick Filters:  812 samples with mutation data  1,084 samples with CNA data

**Overall Survival**

**Mutated Genes (812 profiled samples)**

Gene	# Mut	#	Freq ▾
IDH1	411	411	50.6%
TP53	398	322	39.7%
ATRX	216	208	25.6%
PTEN	109	108	13.3%
EGFR	93	87	10.7%
CIC	85	79	9.7%
PIK3CA	67	63	7.8%
NF1	65	53	6.5%
PIK3R1	47	45	5.5%
FUBP1	44	44	5.4%
PCLO	34	33	4.1%

**CNA Genes (1084 profiled samples)**

Gene	Cytoband	CNA	#	Freq ▾
CDKN2A	9p21.3	DEL	383	35.3%
CDKN2B	9p21.3	DEL	377	34.8%
MTAP	9p21.3	DEL	348	32.1%
EGFR	7p11.2	AMP	289	26.7%
CDK4	12q14.1	AMP	101	9.3%
FIP1L1	4q12	AMP	92	8.5%
PDGFRA	4q12	AMP	90	8.3%
CHIC2	4q12	AMP	87	8.0%
MLLT3	9p21.3	DEL	84	7.7%
KIT	4q12	AMP	67	6.2%
MDM4	1q32.1	AMP	67	6.2%

**Sex**

**ATRX status**

**BCR Status**

**Mutation Count**

**Diagnosis Age**

**Absolute Extract Ploidy**

Let's use this "Groups" button to define groups for comparison.

# Define Groups by Filtering

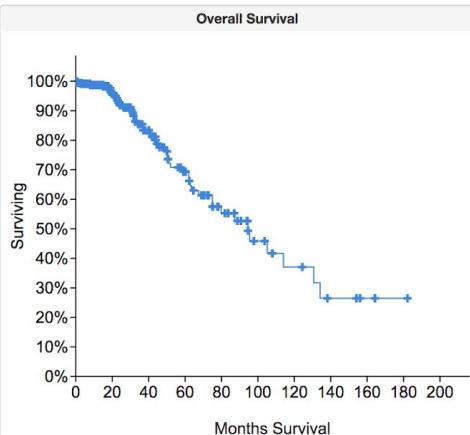
Merged Cohort of LGG and GBM (TCGA, C  
Whole-exome sequencing from 1,122 TCGA LGG and

IDH1  Clear All Filters

Summary Clinical Data Heatmaps

1. Use this table to select samples with IDH1 mutations

(Click the check box in the "#" column, then "Select Samples" at the bottom of the table)



Mutated Genes (411 profiled samples)			
Gene	# Mut	#	Freq ▾
IDH1	411	<input checked="" type="checkbox"/> 411	100.0%
TP53	290	<input type="checkbox"/> 237	57.7%
ATRX	198	<input type="checkbox"/> 190	46.2%
CIC	78	<input type="checkbox"/> 72	17.5%
FUBP1	42	<input type="checkbox"/> 42	10.2%
NOTCH1	31	<input type="checkbox"/> 27	6.6%
PIK3CA	26	<input type="checkbox"/> 25	6.1%
SMARCA4	21	<input type="checkbox"/> 21	5.1%
PIK3R1	19	<input type="checkbox"/> 18	4.4%
TCF12	11	<input type="checkbox"/> 11	2.7%
BCOR	9	<input type="checkbox"/> 9	2.2%

We define groups by applying filters in study view.  
Here, I select samples with IDH1 mutations:

Selected:  411 samples with mutation data  408 samples with CNA data

Custom Selection Charts Groups ▾

Select all (0) Deselect all Search..

Group comparison allows you to create custom groups and compare their clinical and genomic features. Use the button below to create groups based on selections.

Create new group from selected samples (411)

Select all (0) Deselect all Search..

Group comparison allows you to create custom groups and compare their clinical and genomic features. Use the button below to create groups based on selections.

IDH1 mutant Create

Select all (1) Deselect all Search..

IDH1 mutant (411 samples/patients)

Compare View

Create new group from selected samples (411)

# Define Groups by Filtering

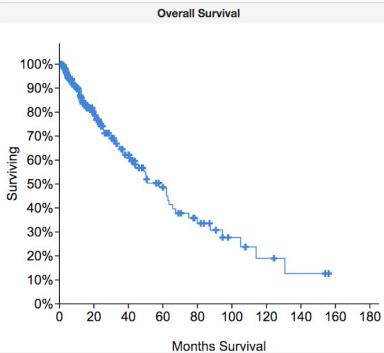
Merged Cohort of LGG and GBM (TCGA, Cell 2016) [Download](#)  
Whole-exome sequencing from 1,122 TCGA LGG and GBM cases. PubMed

TP53 Clear All Filters

Summary Clinical Data Heatmaps

Selected: 322 patients | 322 samples

Clinical  
Data



Quick Filters:  322 samples with mutation data  319 samples with CNA data

Mutated Genes (322 profiled samples)

Gene	# Mut	#	Freq
TP53	398	322	100.0%
IDH1	237	237	73.6%
ATRX	193	185	57.5%
PTEN	32	31	9.6%
PIK3CA	17	16	5.0%

Merged Cohort of LGG and GBM (TCGA, Cell 2016) [Download](#)  
Whole-exome sequencing from 1,122 TCGA LGG and GBM cases. PubMed

EGFR Clear All Filters

Summary Clinical Data Heatmaps

Clear that filter, and continue to apply new filters to define as many groups as you like. Here, I create groups for TP53 mutant samples and EGFR amplified samples.

Custom Selection Charts Groups

Select all (1) Deselect all Search..

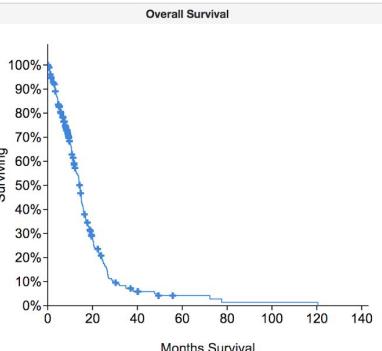
IDH1 mutant (411 samples/patients)

Compare View

Create new group from selected samples (322)

Click gene symbols below or enter here

Query



Quick Filters:  178 samples with mutation data  289 samples with CNA data

Mutated Genes (178 profiled samples)

Gene	# Mut	#	Freq
EGFR	68	64	36.0%
PTEN	39	39	21.9%
TP53	23	21	11.8%
PIK3CA	17	16	9.0%
PIK3R1	13	12	6.7%
PCLO	13	12	6.7%
KEL	10	10	5.6%
NF1	11	10	5.6%
RELN	11	10	5.6%
RB1	7	7	3.9%
LRP1B	9	7	3.9%

CNA Genes (289 profiled samples)

Gene	Cytoband	CNA
EGFR	7p11.2	AMP
CDKN2A	9p21.3	DEL
CDKN2B	9p21.3	DEL
MTAP	9p21.3	DEL
MLLT3	9p21.3	DEL
CDK4	12q14.1	AMP
MDM4	1q32.1	AMP
PIK3C2B	1q32.1	AMP
FIP1L1	4q12	AMP
PDGFRA	4q12	AMP
PTEN	10q23.31	DEL

Select all (2) Deselect all Search..

IDH1 mutant (411 samples/patients)

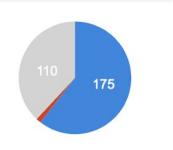
TP53 mutant (322 samples/patients)

Compare View

Create new group from selected samples (289)

Search...

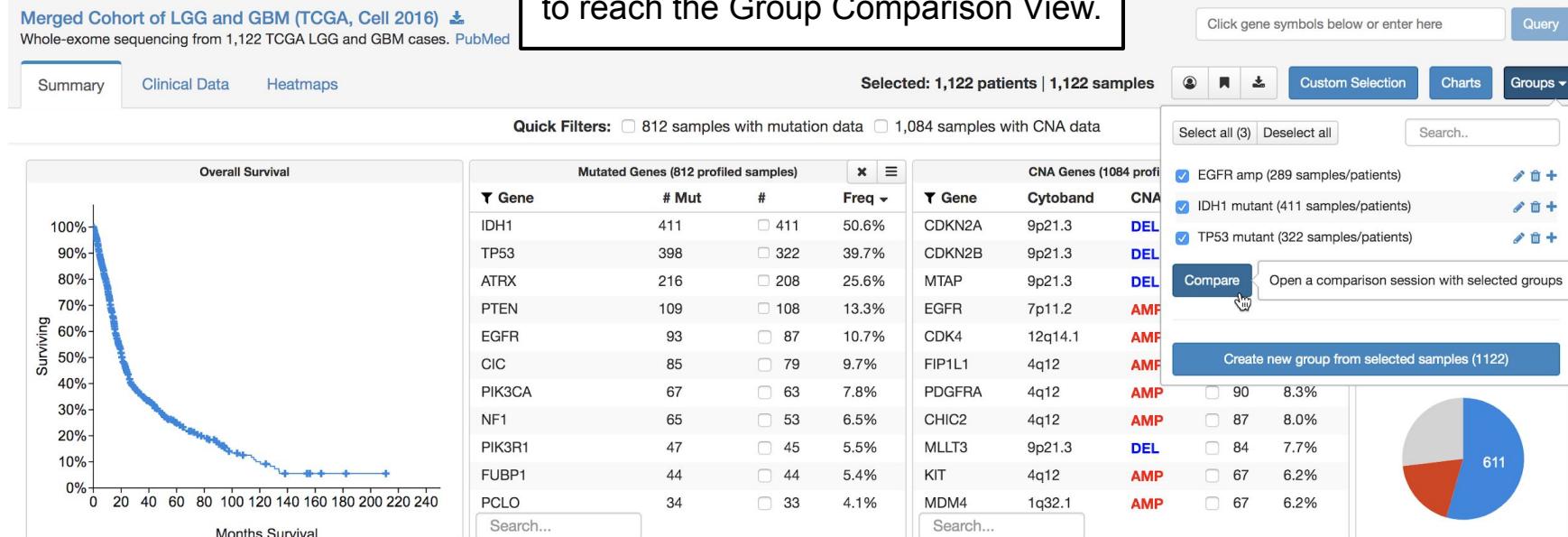
ATRX status



[Link to this page](#)

# Compare User-Defined Groups

Once all groups are defined, select them and click the “Compare” button to reach the Group Comparison View.



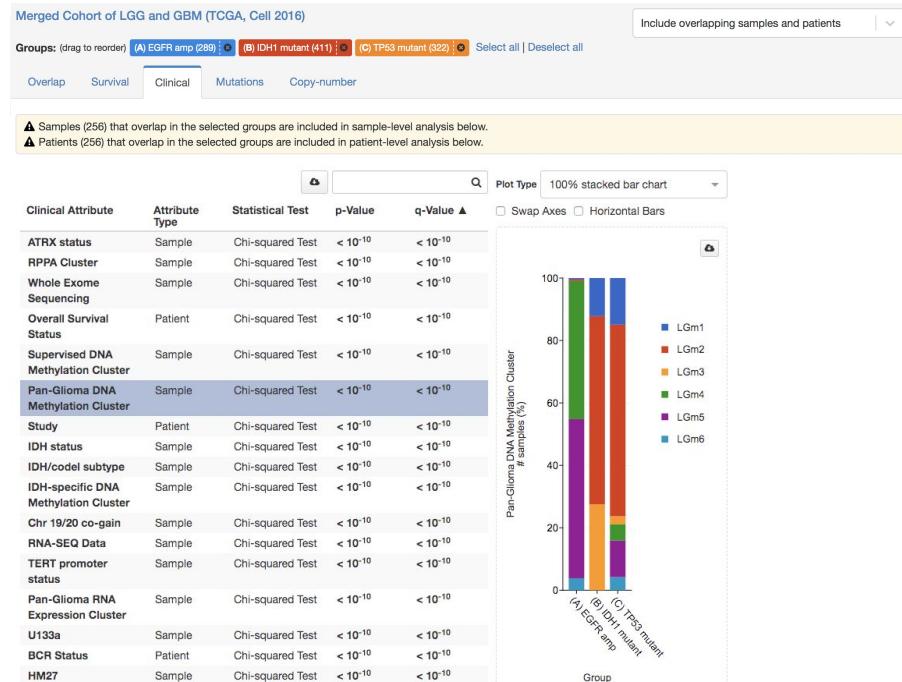
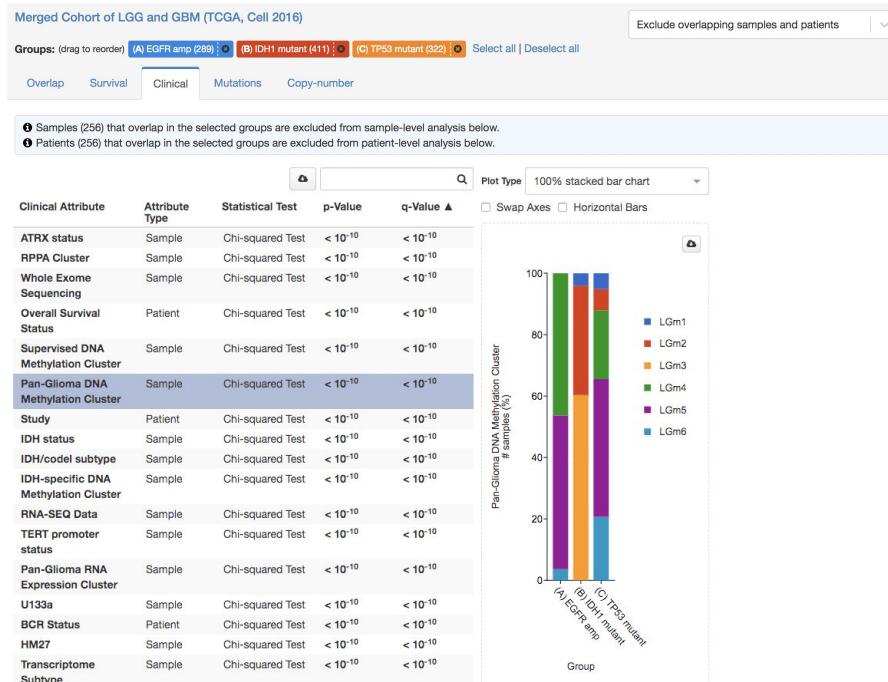
# Group Comparison: Overlapping Samples/Patients



When samples/patients overlap among groups, a drop-down appears in the header which allows you to decide to exclude (default) or include those overlapping samples/patients in the analysis.

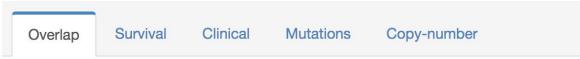
# Group Comparison: Overlapping Samples/Patients

When samples/patients overlap among groups, each tab will include a warning message to make clear how those samples/patients are handled. This can be changed at any time by using the drop-down menu in the header of the page.

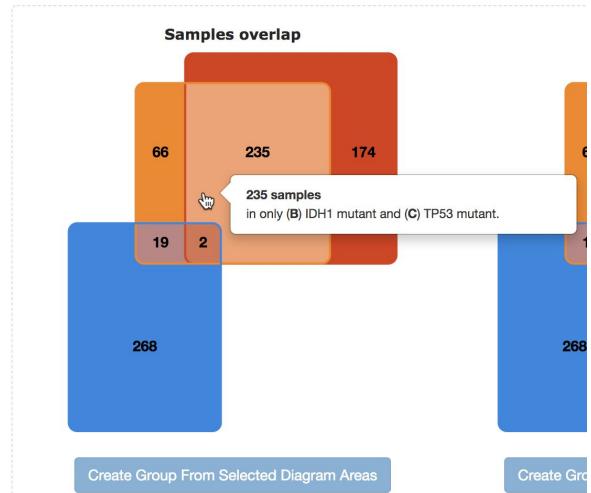


The Overlap tab can also be used to create new groups. For example, let's say I want to create a group of samples with mutations in both IDH1 and TP53, and without amplification of EGFR.

# Custom Groups from Overlap Tab



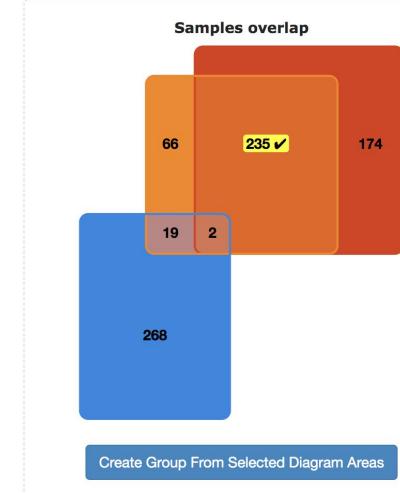
- Samples (256) that overlap in the selected groups are excluded from sample-level analysis
- Patients (256) that overlap in the selected groups are excluded from patient-level analysis



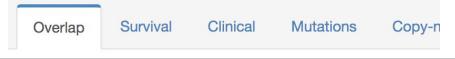
Hover over the venn diagram to find the segment of interest.  
Click on it.



- Samples (256) that overlap in the selected groups are excluded from sample-level analysis
- Patients (256) that overlap in the selected groups are excluded from patient-level analysis



The “Create Group...” button is now enabled.  
Click on it.



Note this option to “Save group to user account”. If selected (default), this new group will appear in the groups menu in study view.

Save group to user account

IDH1 and TP53

Submit

Create Group From Selected Diagram Areas

Samples only in (B) IDH1 mutant and (C) TP53 mutant.

Enter a name for this new group and click “Submit”.

# Custom Groups from Overlap Tab

Merged Cohort of LGG and GBM (TCGA, Cell 2016)

Exclude overlapping samples and patients

Groups: (drag to reorder) (A) EGFR amp (289) (B) IDH1 and TP53 (226) (C) IDH1 mutant (411) (D) TP53 mutant (322) Select all | Deselect all

Overlap

Survival

Clinical

Mutations

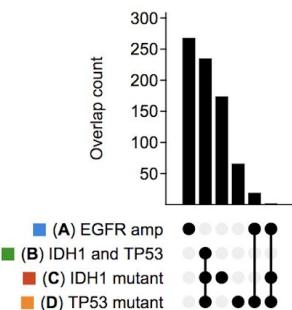
Copy-number

• (B) IDH1 and TP53 is completely overlapping with other selected groups, so is excluded from analysis in other tabs.

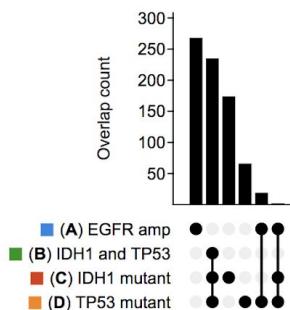
• Samples (256) that overlap between (A) EGFR amp, (C) IDH1 mutant, and (D) TP53 mutant are excluded from sample-level analysis in other tabs.

• Patients (256) that overlap between (A) EGFR amp, (C) IDH1 mutant, and (D) TP53 mutant are excluded from patient-level analysis in other tabs.

Samples overlap



Patients overlap

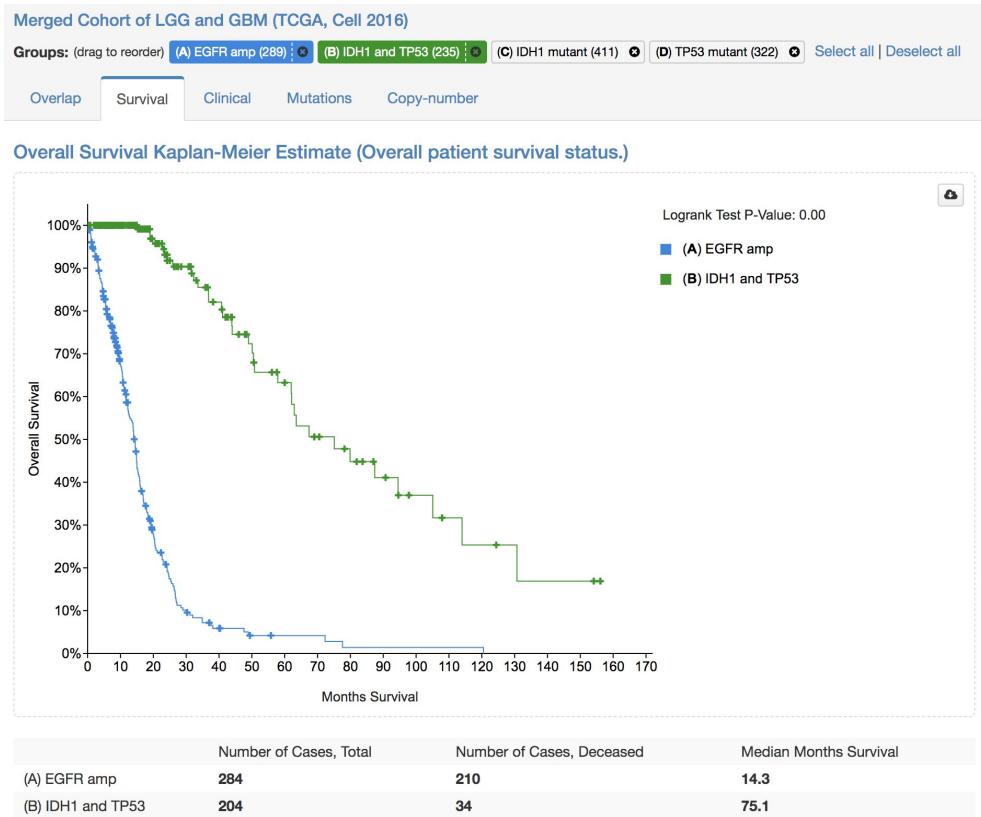


Create Group From Selected Diagram Areas

Create Group From Selected Diagram Areas

The Overlap tab looks different when 4+ groups are selected. Rather than a venn diagram, comparisons among 4+ groups are visualized with an [UpSet diagram](#).

# Custom Groups from Overlap Tab



Now I can select and de-select groups in the header to compare, for example, overall survival for patients with EGFR amplification vs IDH1 and TP53 mutations.

There are many powerful ways to take advantage of this new functionality.

What follows are a few possibilities...

# Identify/Compare Samples Without a Specific Alteration

How can we compare samples with or without specific genomic features? As an example, let's take samples with IDH1 or IDH2 mutations and compare to samples without mutations in either gene.

Merged Cohort of LGG and GBM (TCGA, Cell 2016) Whole-exome sequencing from 1,122 TCGA LGG and GBM cases. PubMed

Summary Clinical Data Heatmaps

Quick Filters:  812 samples with mutation data  1,084 samples with CNA data

Selected: 812 patients | 812 samples

Overall Survival

Surviving (%) vs Months Survival (0 to 240)

Gene: idh

Filter: Selected Samples

Mutated Genes (812 profiled samples)

Gene	# Mut	#	Freq
IDH1	411	411	50.6%
IDH2	19	19	2.3%

MTAP 8p21.3 DEL 348 32.1%

Merged Cohort of LGG and GBM (TCGA, Cell 2016) Whole-exome sequencing from 1,122 TCGA LGG and GBM cases. PubMed

With Mutation Data: YES |  NO | Clear All Filters

Summary Clinical Data Heatmaps

Selected: 812 patients | 812 samples

Quick Filters:  812 samples with mutation data  794 samples with CNA data

Overall Survival

Surviving (%) vs Months Survival (0 to 240)

Gene: IDH1

Filter: Selected Samples

Mutated Genes (812 profiled samples)

Gene	# Mut	#	Freq						
IDH1	411	411	50.6%						
TP53	ATRX	PTEN	EGFR	CIC	PIK3CA	NF1	PIK3R1	FUBP1	PCLO

CNA Genes (794 profiled samples)

Gene	Cytoband	CNA	#	Freq
TP53	8p21.3	DEL	348	32.1%

Sex

1. Filter to samples with mutations in either gene. Create a group from these samples.

2. We can't directly identify samples without mutations in particular genes. But we can create a group of all samples with mutation data, and then use the overlap tab to find the samples with mutations data but without mutations in IDH1 or IDH2.

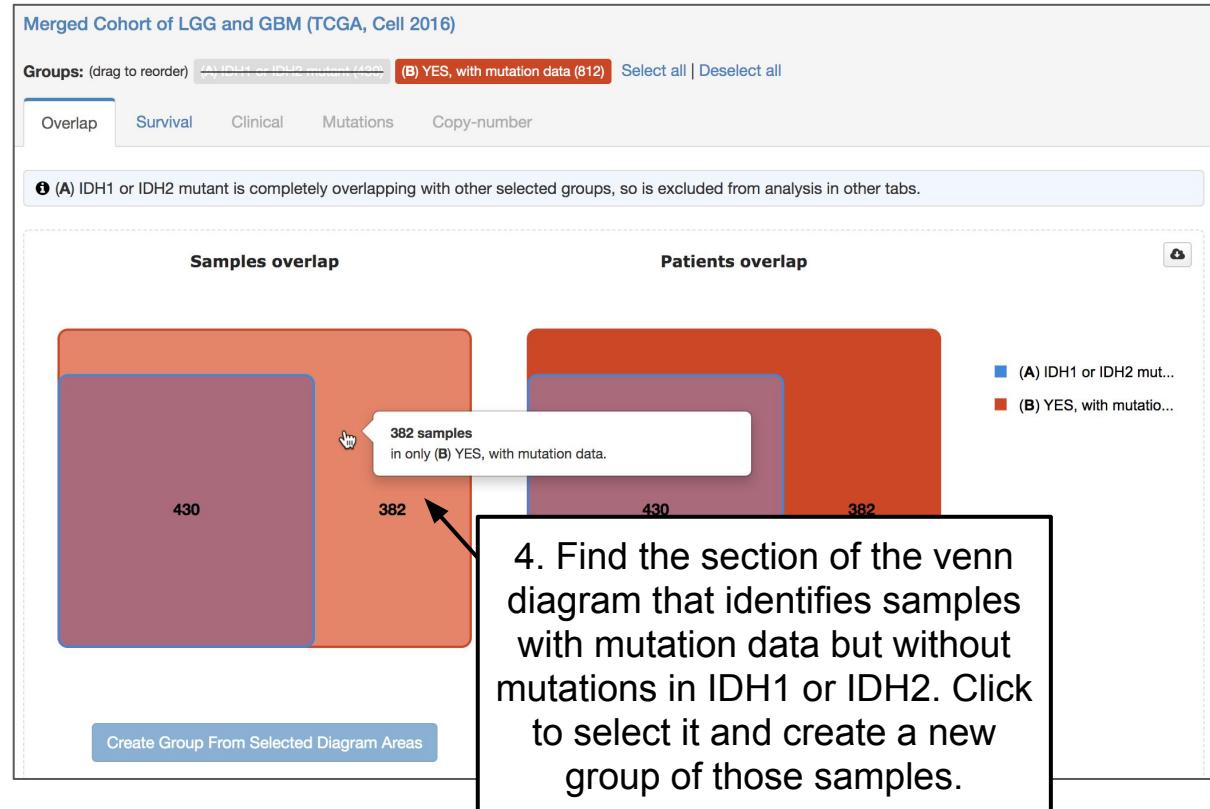
# Identify/Compare Samples Without a Specific Alteration

Select all (6) Deselect all Search..

- EGFR amp (289 samples/patients) [edit] [trash] [add]
- IDH1 and TP53 (235 samples/patients) [edit] [trash] [add]
- IDH1 mutant (411 samples/patients) [edit] [trash] [add]
- IDH1 or IDH2 mutant (430 samples/patients) [edit] [trash] [add]
- TP53 mutant (322 samples/patients) [edit] [trash] [add]
- YES, with mutation data (812 samples/patients) [edit] [trash] [add]

Compare View

3. Run a comparison between these two groups.



# Identify/Compare Samples Without a Specific Alteration

Merged Cohort of LGG and GBM (TCGA, Cell 2016)

Groups: (drag to reorder) (A) IDH1 or IDH2 mutant (430) (B) IDH1/2 no mutation (382) → (C) YES, with mutation data (812) Select all | Deselect all

Overlap Survival Clinical Mutations Copy-number

(C) YES, with mutation data is completely overlapping with other selected groups, so is excluded from analysis in other tabs.

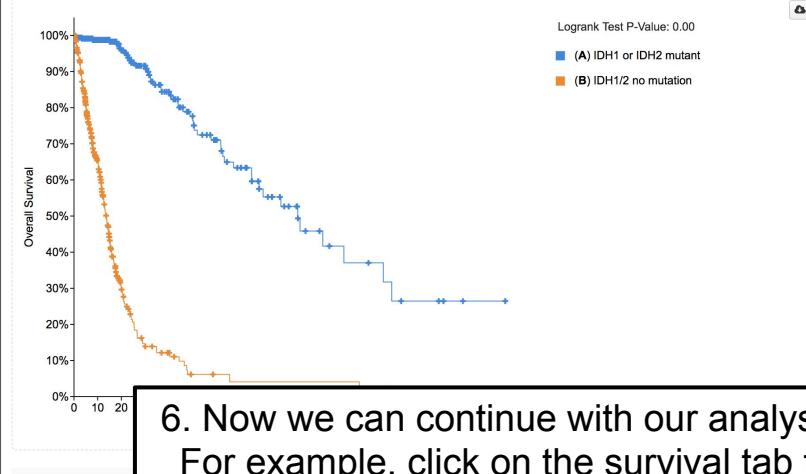
5. When the page reloads, we see the newly created group and a warning that some groups are excluded from analysis due to all samples overlapping with another group. Deselect the “(C) YES, with m...” group.

Merged Cohort of LGG and GBM (TCGA, Cell 2016)

Groups: (drag to reorder) (A) IDH1 or IDH2 mutant (430) (B) IDH1/2 no mutation (382) (C) YES, with mutation data (812) Select all | Deselect all

Overlap Survival Clinical Mutations Copy-number

Overall Survival Kaplan-Meier Estimate (Overall patient survival status.)



6. Now we can continue with our analysis. For example, click on the survival tab to see how IDH1/2 mutant patients compare to those without IDH1/2 mutations.

[Link to this page](#)

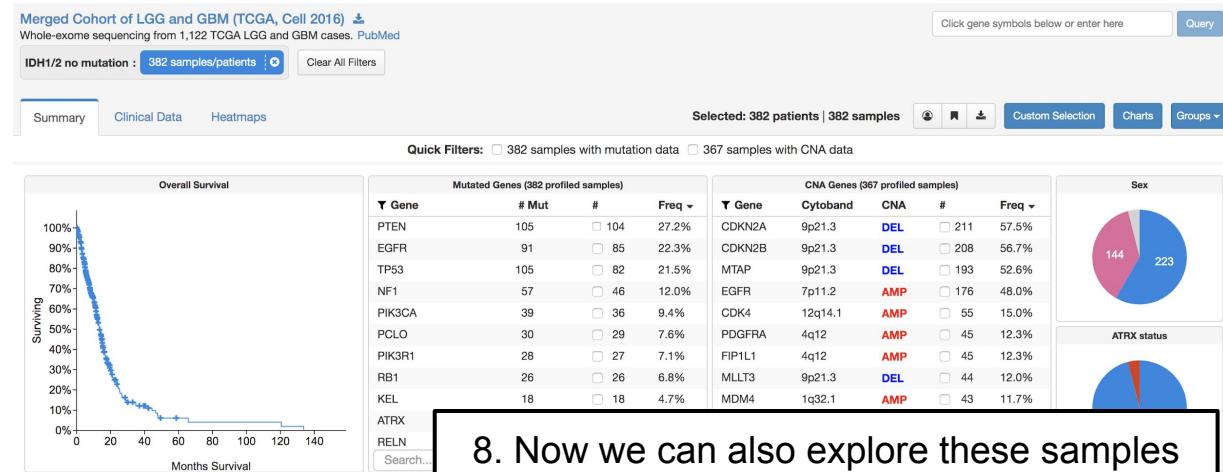
# Identify/Compare Samples Without a Specific Alteration

Select all (7) Deselect all Search..

- EGFR amp (289 samples/patients) + -
- IDH1 and TP53 (235 samples/patients) + -
- IDH1 mutant (411 samples/patients) + -
- IDH1 or IDH2 mutant (430 samples/patients) + -
- IDH1/2 no mutation (382 samples/patients) + -
- TP53 mutant (322 samples/patients) + -
- YES, with mutation data (512 samples/patients) + -

**Compare** **View** View

7. Remember that these new groups get saved back to Study View. You can use the Groups dropdown to filter study view to this newly defined group.



8. Now we can also explore these samples without IDH1/2 mutations in study view.

# Create a Group from a User-Defined List

What if you have identified a set of samples of interest based on your own analysis? You can create a group from that list in study view.

The screenshot displays two instances of the OncoPrint interface. The left instance shows a histogram for the IDH1 mutation status (MUT=R132C) across 794 samples, indicating 2.1% are mutated. The right instance shows a 'Downloadable Data Files' section with various options for download, including 'Copy'. A large callout box on the left provides instructions for defining samples of interest using OQL, while another on the right instructs how to use the 'Download' tab to copy a list of altered samples.

**Modify Query** Merged Cohort of LGG and GBM (TCGA, Cell 2016)  
Samples with mutation and CNA data (794 patients/samples) - IDH1

Oncoprint Cancer Types Summary Plots Mutations Enrichments Survival Network Download

✓ The results below reflect the OQL specification from your query.

Add Clinical Tracks Sort Mutations View Down

IDH1: MUT=R132C 2.1% (putative driver)

**1. Define your samples of interest. Here, I will identify samples with IDH1 R132C mutations by running a query with OQL...**

**Modify Query** Merged Cohort of LGG and GBM (TCGA, Cell 2016)  
Samples with mutation and CNA data (794 patients/samples) - IDH1

Oncoprint Cancer Types Summary Plots Mutations Enrichments Survival Network Download

✓ The results below reflect the OQL specification from your query.

**Downloadable Data Files**

- Copy-number Alterations (OQL is not in effect)
- Mutations (OQL is not in effect)
- Altered samples: List of samples with alterations
- Unaltered samples: List of samples without any alteration
- Sample matrix: List of all samples where 1=altered and 0=unaltered

Tab Delimited Format | Transposed Matrix  
Tab Delimited Format | Transposed Matrix  
**Copy** | Download | Query | Virtual Study  
**Copy** | Download | Query | Virtual Study  
**Copy** | Download

**2. ...and then use the Download tab to copy a list of the altered samples.**

# Create a Group from a User-Defined List

Merged Cohort of LGG and GBM (TCGA, Cell 2016) [Download](#)  
Whole-exome sequencing from 1,122 TCGA LGG and GBM cases. [PubMed](#)

Summary Clinical Data Heatmaps

Selected: 1,122 patients | 1,122 samples [Custom Selection](#) [Charts](#) [Groups](#)

Quick Filters:  812 samples with mutation data  1,084 samples with CNA

By sample ID  By patient ID  
Use currently selected samples/patients [Data Format](#)

Overall Survival

Surviving (%) vs. Months (0-40)

FUBP1 44 44 5.4% KIT

3. Go to study view, click the “Custom Selection” button, and paste in that copied list of samples. Click “Select” to filter to that sample list.

CNA Gene Cytoband ID

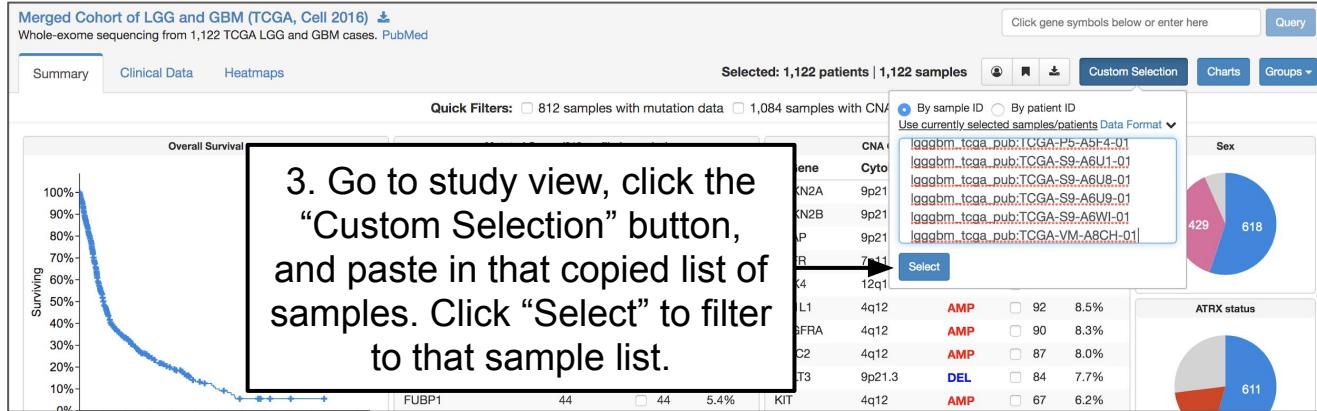
KN2A	9p21	7q11	12q1
KN2B	9p21	7q11	12q1
ATR	9p21	7q11	12q1
L1	4q12	AMP	92 8.5%
SFRP1	4q12	AMP	90 8.3%
C2	4q12	AMP	87 8.0%
T3	9p21.3	DEL	84 7.7%
	4q12	AMP	67 6.2%

Sex

429 618

ATRX status

611



Merged Cohort of LGG and GBM (TCGA, Cell 2016) [Download](#)  
Whole-exome sequencing from 1,122 TCGA LGG and GBM cases. [PubMed](#)

Custom Selection : 17 samples [Clear All Filters](#)

Selected: 17 patients | 17 samples [Custom Selection](#) [Charts](#) [Groups](#)

Quick Filters:  17 samples with mutation data  17 samples with CNA data

Overall Survival

Surviving (%) vs. Months (0-40)

Mutated Genes (17 profiled samples)

Gene	# Mut	#	Freq
IDH1	17	17	100.0%
ATRX	14	12	70.6%
TP53	14	12	70.6%
RHOH	1	1	5.9%
EPHA3	1	1	5.9%

CNA Genes (17 profiled samples)

Gene	Cytoband	CNA
INPP5D	2q37.1	DEL
PDCD1	2q37.3	DEL
HDAC4	2q37.3	DEL
PASK	2q37.3	DEL
ACKR3	2q37.3	DEL

Select all (7) Deselect all Search..

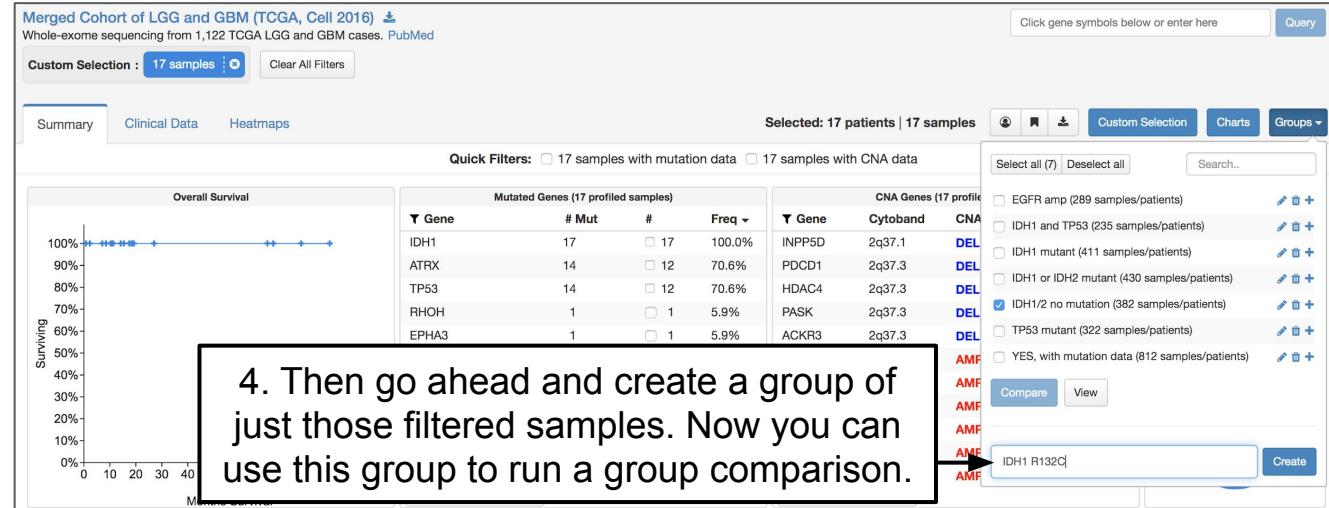
- EGFR amp (289 samples/patients)
- IDH1 and TP53 (235 samples/patients)
- IDH1 mutant (411 samples/patients)
- IDH1 or IDH2 mutant (430 samples/patients)
- IDH1/2 no mutation (382 samples/patients)
- TP53 mutant (322 samples/patients)
- YES, with mutation data (612 samples/patients)

Compare View

4. Then go ahead and create a group of just those filtered samples. Now you can use this group to run a group comparison.

IDH1 R132C

Create



[Link to this page](#)

Questions?

Check out our other tutorials  
or email us at:

[cboportal@googlegroups.com](mailto:cboportal@googlegroups.com)