

# cBioPortal Tutorial #2: Single Study Query

Query one or multiple genes in a single dataset

# Tutorial Objectives

- Show how to run a single-study query from the main page
- Walk through each of the data/analysis tabs in a single-study query
  - OncoPrint
  - Cancer Types Summary
  - Mutual Exclusivity
  - Plots
  - Mutations
  - Co-Expression
  - Enrichments
  - Survival
  - Network
  - CN Segments
  - Download
  - Bookmark
- Show how to modify and re-run a query

In this tutorial, blue boxes provide an overview of each tab on cBioPortal ...

... while green boxes ask a biological question that we can answer using cBioPortal.

# Overview of Tabs in a Single Study Query

Note that depending on the data available for a particular study, not all of these will be present (e.g. a study without outcome data will not have a Survival tab)

- **OncoPrint:** Overview of genetic alterations per sample in each query gene
- **Cancer Types Summary:** Frequency of alteration in each query gene in the detailed cancer types included in this study
- **Mutual Exclusivity:** Statistical analysis to determine if query genes are mutually exclusively altered
- **Plots:** explore the relationships among genetic alterations, gene expression, protein levels, DNA methylation and available clinical features
- **Mutations:** Details about mutations called in each query gene
- **Co-Expression:** Explore which genes have mRNA/protein levels correlated with query genes
- **Enrichments:** Explore which genes are altered in the set of samples with query gene alterations or in the set of samples without query gene alterations
- **Survival:** Compare survival of patients with alterations in query genes to the rest of the cohort
- **CN Segments:** Explore copy number changes with the Integrated Genomics Viewer (IGV)
- **Network:** Explore gene networks centered on the query genes
- **Download:** Download data or copy sample lists
- **Bookmark:** Link to save the query

We're going to run a query in the TCGA Lower-Grade Glioma study. The next few slides will show how to run this query from the Query page. You can also run the same query from a Single Study Exploration, as we did in Tutorial #1.

# Query overview

Browse available  
datasets and  
initiate queries

Number of  
studies for each  
organ system  
(click to filter)

Search  
studies

List of all studies,  
organized by  
organ system

The screenshot displays the cBioPortal website interface. At the top, the cBioPortal logo is on the left, and navigation links (Data Sets, Web API, R/MATLAB, Tutorials, FAQ, News, Visualize Your Data, About) and a Login button are on the right. Below the header, a paragraph describes the portal's purpose: providing visualization, analysis, and download of large-scale cancer genomics data sets, with a link to TCGA publication guidelines. A citation notice follows: "Please cite Gao et al. *Sci. Signal.* 2013 & Cerami et al. *Cancer Discov.* 2012 when publishing results based on cBioPortal."

The main content area is divided into sections. On the left, under the "Query" tab, is a "Select Studies:" section. It features a list of organ systems with the number of studies for each: PanCancer Studies (3), Cell lines (2), Adrenal Gland (2), Ampulla of Vater (1), Biliary Tract (8), Bladder/Urinary Tract (13), Bone (2), Bowel (7), Breast (14), and CNS/Brain (17). To the right of this list are "Quick select:" buttons for "TCGA PanCancer Atlas Studies" and "Curated set of non-redundant studies". Below these are three expandable sections: "PanCancer Studies" (listing MSK-IMPACT Clinical Sequencing Cohort, Pan-Lung Cancer, and Pediatric Pan-cancer), "Cell lines" (listing Cancer Cell Line Encyclopedia and NCI-60 Cell Lines), and "Adrenal Gland" (listing Adrenocortical Carcinoma). Each section shows the number of samples and icons for data visualization. At the bottom of the "Select Studies" section is an "Enter Genes:" field with a "User-defined List" dropdown and a text area for "Enter HUGO Gene Symbols, Gene Aliases, or OQL". A "Submit Query" button is at the bottom left of the main content area.

On the right side of the main content area, there is a "What's New" section with a cBioPortal logo and a tweet about a new feature: "Group Comparison". Below this is a "Sign up for low-volume email news alerts" section with a "Subscribe" button. Further down is a "Cancer Studies" section with a link to "The portal contains 250 cancer studies (details)". At the bottom right is a "Cases by Top 20 Primary Sites" section, which is a horizontal bar chart showing the number of cases for various cancer types: Breast, Lung, Lymphoid, CNS/Brain, Prostate, Kidney, Bowel, Stomach, Bladder, Head/Neck, Uterus, Ovary, Myeloid, Thyroid, Skin, Liver, PNS, Pancreas, and Soft Tissue.

Annotations with arrows point to specific parts of the interface: "Browse available datasets and initiate queries" points to the "Query" tab; "Number of studies for each organ system (click to filter)" points to the organ system list; "Search studies" points to the search bar; and "List of all studies, organized by organ system" points to the "PanCancer Studies" section.

# Single study query

1. Start typing tumor type of interest to filter the list of studies.

2. Check the box for study of interest.

3. This section will update to include all data types available for the selected study. Select data types to query.

4. Select sample set. For most studies, an appropriate sample set will be automatically selected given the data types selected in Step 3.

5. Type gene(s) or select from pre-defined gene lists. cBioPortal will confirm that all entries are valid gene symbols.

6. Submit query

Refine your query: You can use Onco Query Language (OQL) to define which specific alterations to include. See [specifications](#) or [OQL tutorial](#).

The screenshot shows the cBioPortal Single Study Query interface. At the top, there are tabs for 'Query', 'Quick Search Beta!', and 'Download'. Below this, the 'Select Studies' section shows '1 studies selected (530 samples)' and a 'View summary' button. A search bar on the right contains the text 'glioma'. The main list of studies is under the heading 'CNS/Brain'. The first study, 'Brain Lower Grade Glioma (TCGA, Provisional)', is selected with a blue checkbox. To its right, sample counts are listed: 514 samples, 530 samples, 91 samples, 61 samples, and 1122 samples. Below the study list is the 'Select Genomic Profiles' section, which has checkboxes for 'Mutations', 'Putative copy-number alterations from GISTIC', 'mRNA Expression', 'mRNA Expression z-Scores (microarray)', 'mRNA Expression z-Scores (RNA Seq V2 RSEM)', and 'Protein expression Z-scores (RPPA)'. The 'mRNA Expression' checkbox is checked. Below this is the 'Select Patient/Case Set' section, which has a dropdown menu showing 'Samples with mutation and CNA data (263)'. Below that is the 'Enter Genes' section, which has a dropdown menu showing 'User-defined List' and a text input field containing 'IDH1 EGFR'. A green message box below the input field says 'All gene symbols are valid.' At the bottom left, there is a 'Submit Query' button. Arrows from the numbered text boxes point to these specific elements: Box 1 points to the search bar, Box 2 points to the checkbox for the selected study, Box 3 points to the 'Select Genomic Profiles' section, Box 4 points to the 'Select Patient/Case Set' dropdown, Box 5 points to the 'Enter Genes' input field, and Box 6 points to the 'Submit Query' button.

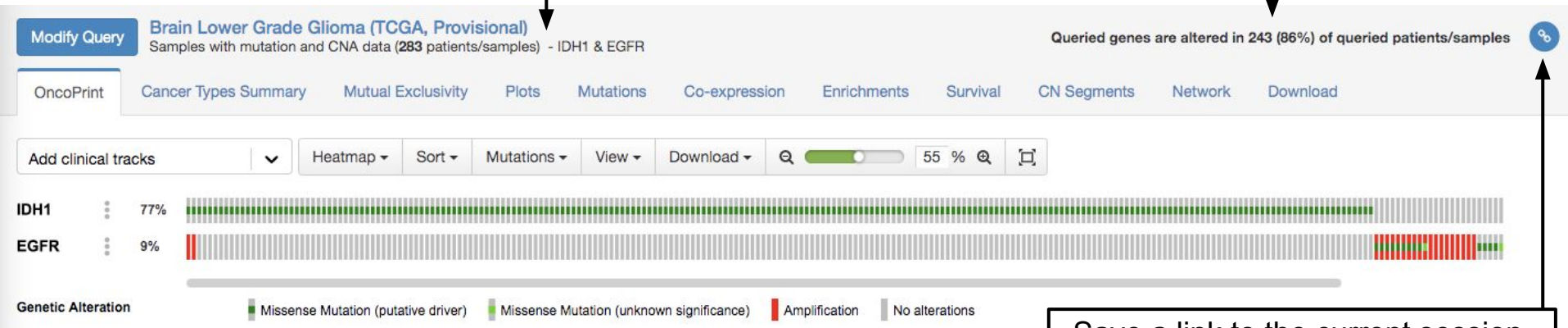
Performing a query as shown in the previous slides or as shown in Tutorial #1 will both bring you to Results View, shown on the next slide.

Results View is made up of multiple tabs, each with specific functionality, which all share a header.

# Results View Header

The number of samples and patients included in the query. Note that these numbers can differ from each other if some patients have more than one tumor sample profiled.

The number (percentage) of samples/patients with an alteration in any of the query genes



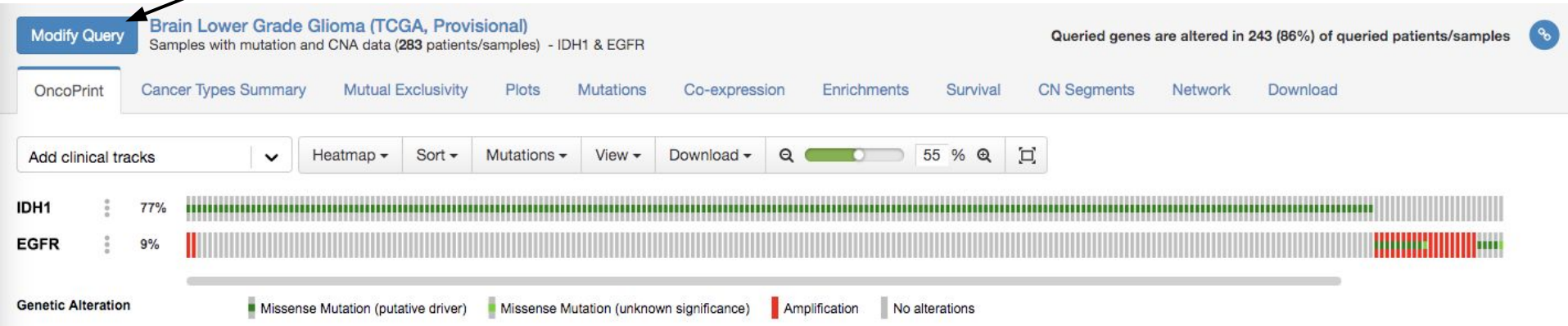
Save a link to the current session.  
Useful for sharing with others or  
returning to a query at a later date.



But wait! What if I changed my mind?  
Can we modify a query?

# Modify Query

Click on “Modify Query”. This button is available on all tabs and can be used at any time. This will populate the top of the page with a section that looks just like the original query page; the current page will be visible beneath the query section (see next slide for a screenshot).



# Modify Query

The existing query is pre-populated for your convenience. You can change the study, the genomic profiles, the patient/case set or the gene set. Simply hit “Submit” when you are happy with the modified query.

Cancel Modify Query

Brain Lower Grade Glioma (TCGA, Provisional)  
Samples with mutation and CNA data (283 patients/samples) - IDH1 & EGFR

Queried genes are altered in 243 (86%) of queried patients/samples

Query

1 studies selected (530 samples) Deselect all View summary

Search...

3

2

2

1

8

13

2

7

Bowel

Breast

CNS/Brain

Quick select:

TCGA PanCancer Atlas Studies

Curated set of non-redundant studies

PanCancer Studies

☐ MSK-IMPACT Clinical Sequencing Cohort (MSKCC, Nat Med 2017) 10945 samples

☐ Pan-Lung Cancer (TCGA, Nat Genet 2016) 1144 samples

☐ Pediatric Pan-cancer (Columbia U, Genome Med 2016) 103 samples

Cell lines

☐ Cancer Cell Line Encyclopedia (Novartis/Broad, Nature 2012) 1020 samples

☐ NCI-60 Cell Lines (NCI, Cancer Res 2012) 67 samples

Adrenal Gland

Adrenocortical Carcinoma

☐ Adrenocortical Carcinoma (TCGA, PanCancer Atlas) 92 samples

☐ Adrenocortical Carcinoma (TCGA, Provisional) 92 samples

Ampulla of Vater

Select Genomic Profiles:

☒ Mutations

☒ Putative copy-number alterations from GISTIC

☐ mRNA Expression. Select one of the profiles below:

☐ mRNA Expression z-scores (microarray)

☐ mRNA Expression z-scores (RNA Seq V2 RSEM)

☐ Protein expression Z-scores (RPPA)

Select Patient/Case Set:

To build your own case set, try out our enhanced Study View.

Samples with mutation and CNA data (283)

Enter Genes:

Hint: Learn Onco Query Language (OQL) to write more powerful queries

User-defined List

IDH1 EGFR IDH2

All gene symbols are valid.

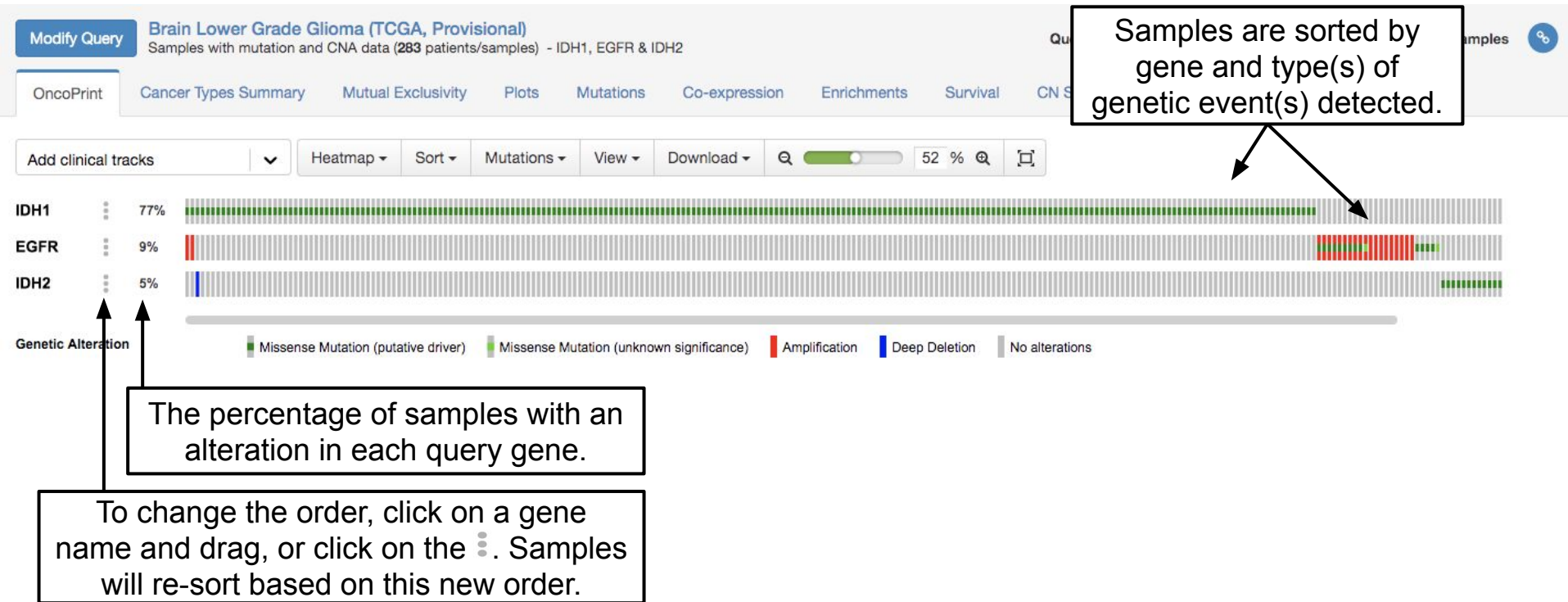
Submit Query

In this case, I've added a third gene (IDH2) to the query.

Link to this page

# OncoPrint

Summary of alterations per sample. Each sample is a column. Each gene is a row. Different kinds of genetic alterations are highlighted with different colors.



# OncoPrint: Features

Diagram illustrating the features of OncoPrint, showing the workflow from data selection to visualization and download options.

Key features highlighted by callouts:

- Add clinical tracks (options will vary depending on the data available for each study)
- Add a heatmap with RNA or protein levels
- Change the sample sorting order
- Customize visualization
- Download figure as PNG, PDF or SVG. Download patient/sample IDs in same order as OncoPrint.

The interface shows a navigation bar with tabs: OncoPrint, Cancer Types Summary, Mutual Exclusivity, Plots, Mutations, Co-expression, Enrichments, Survival, CN Segments, Network, and Download.

The main panel displays a heatmap visualization. The top row is labeled 'age'. The legend indicates the following categories:

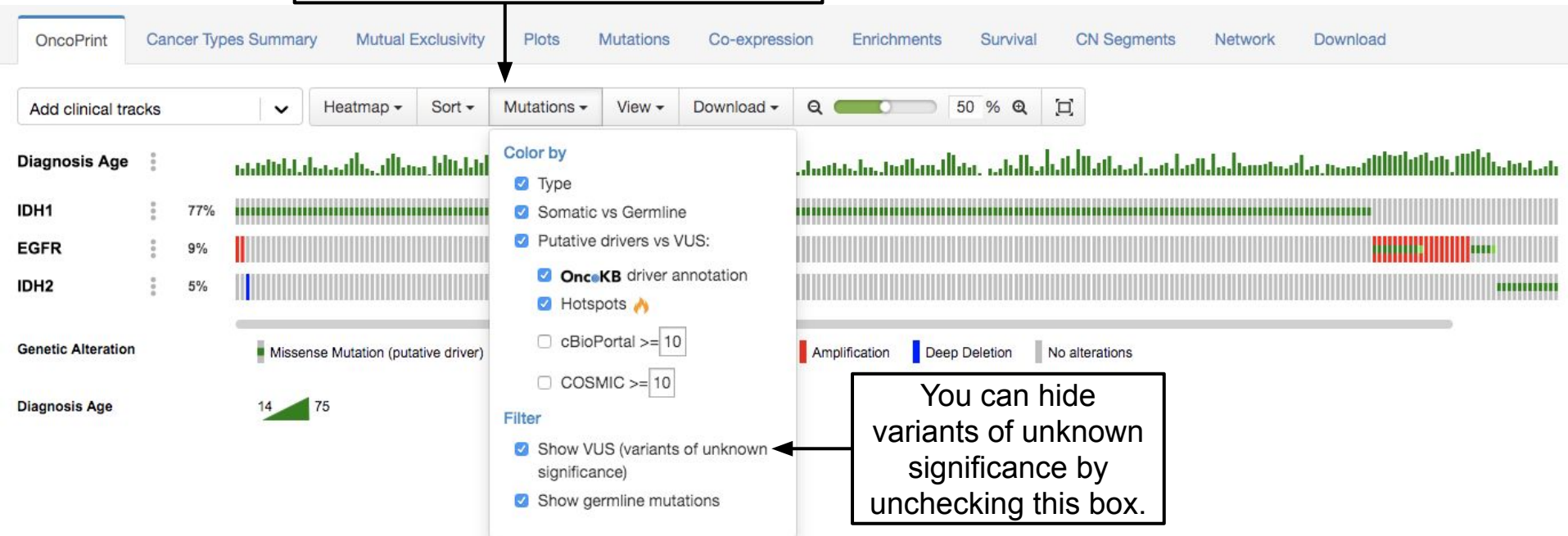
- Diagnosis Age (100%)
- Animal Insect Allergy Age (3%)
- Age of Food Allergy (1%)

The legend also includes a color key for genomic alterations:

- Missense Mutation (putative driver)
- Missense Mutation (unknown significance)
- Amplification
- Deep Deletion
- No alterations

# OncoPrint: Mutation Color Rules

Change the rules by which mutations are colored. This includes the rules to classify a mutation as a putative driver or passenger.



# OncoPrint: Zoom

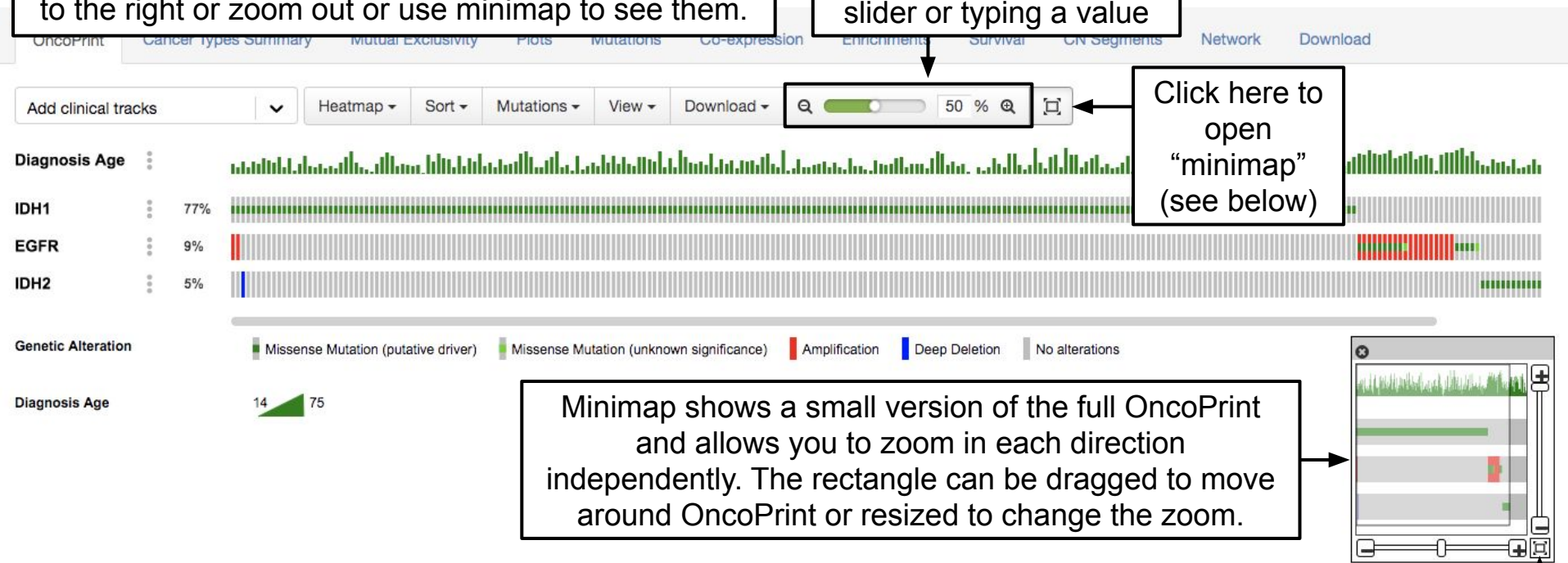
There may be more samples hiding off-screen. Scroll to the right or zoom out or use minimap to see them.

Change the zoom by clicking the zoom in/out icons or moving the slider or typing a value

Click here to open "minimap" (see below)

Minimap shows a small version of the full OncoPrint and allows you to zoom in each direction independently. The rectangle can be dragged to move around OncoPrint or resized to change the zoom.

This button zooms OncoPrint to show all samples with alterations





# OncoPrint: What can we learn?



**Q:** Are genetic alterations in these genes mutually exclusive?

**A:** We can see that samples with alterations in one gene tend to not have alterations in the other genes.

**Q:** Is there an association between alterations in a particular query gene and age?

**A:** We can see that patients with mutations or amplifications in EGFR tend to be older than those with mutations in IDH1/IDH2



Now we're going to go through all the other tabs and ask some questions about alterations in *IDH1*, *IDH2* and *EGFR* in the TCGA Lower-Grade Glioma study.

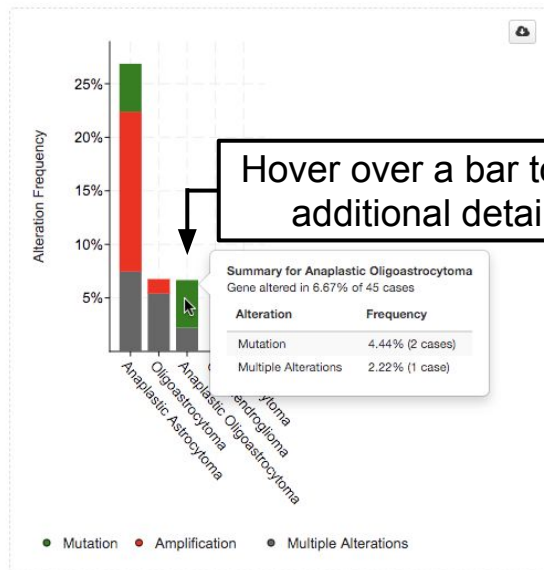
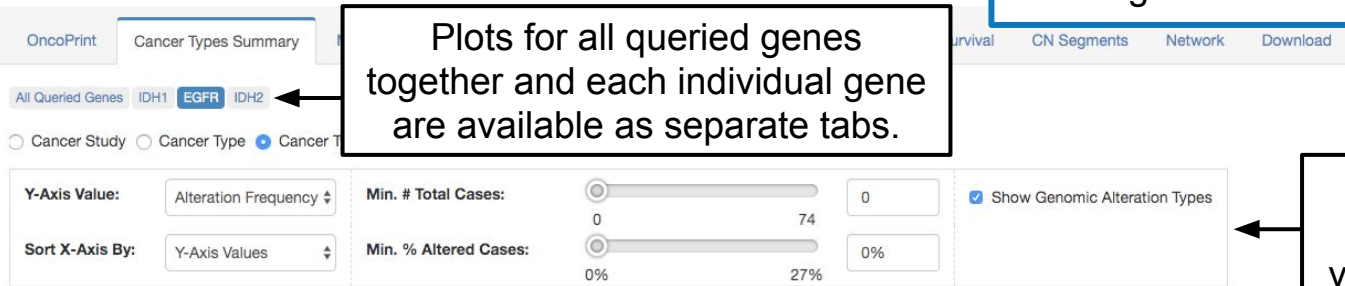
Note: Depending on the data available for a particular study, not all of the following tabs will be present (e.g. a study without outcome data will not have a Survival tab)

# Cancer Types Summary

Histogram of the frequency of alterations in each gene for each detailed cancer type.

Plots for all queried genes together and each individual gene are available as separate tabs.

Options to customize visualization



Hover over a bar to see additional details.

**Q:** Are alterations in EGFR more frequent in a particular subtype of glioma?

**A:** Yes, anaplastic astrocytoma appears to have a much higher frequency of EGFR alteration than oligoastrocytoma or anaplastic oligoastrocytoma.

# Mutual Exclusivity

All pairwise combinations of query genes analyzed for mutual exclusivity or co-occurrence in the queried samples.

On the OncoPrint tab we could see visually that alterations in these three query genes tended to be mutually exclusive. Here we can address that same question with a statistical analysis.

OncoPrint Cancer Types Summary Mutual Exclusivity Plots Mutations Co Segments

The analysis tested 3 pairs between the 3 tracks in the OncoPrint.

☒ Mutual exclusivity ☒ Co-occurrence ☐ Significant only

Columns

A	B	Neither	A Not B	B Not A	Both	Log2 Odds Ratio	p-Value	q-Value ▲	Tendency
IDH1	EGFR	40	217	24	2	<-3	<0.001	<0.001	Mutual exclusivity
IDH1	IDH2	52	218	12	1	<-3	<0.001	<0.001	Mutual exclusivity
EGFR	IDH2	244	26	13	0	<-3	0.278	0.278	Mutual exclusivity

Showing 1-3 of 3

A positive value here suggests that alterations in these genes co-occur in the same samples, while a negative value suggests that alterations in these genes are mutually exclusive and occur in different samples.

$$\log_2 \left( \frac{\text{odds of alteration in B given alteration in A}}{\text{odds of alteration in B given lack of alteration in A}} \right)$$

Click on any column header to sort. Hover over the column names for more details about how values are calculated.

# Plots

Depending on available data types for a given study, this tab allows for plots comparing mutations, copy number, mRNA expression, protein levels and DNA methylation of query genes, along with any available clinical attributes.

Choose type of data

Select a query gene

Swap horizontal  
& vertical axis

OncoPrint Cancer Types Summary Mutual Exclusivity **Plots**

**Horizontal Axis**

Data Type  
Copy Number

Copy Number Profile  
Putative copy-number alteration..

Gene  
EGFR

**Vertical Axis**

Data Type  
mRNA

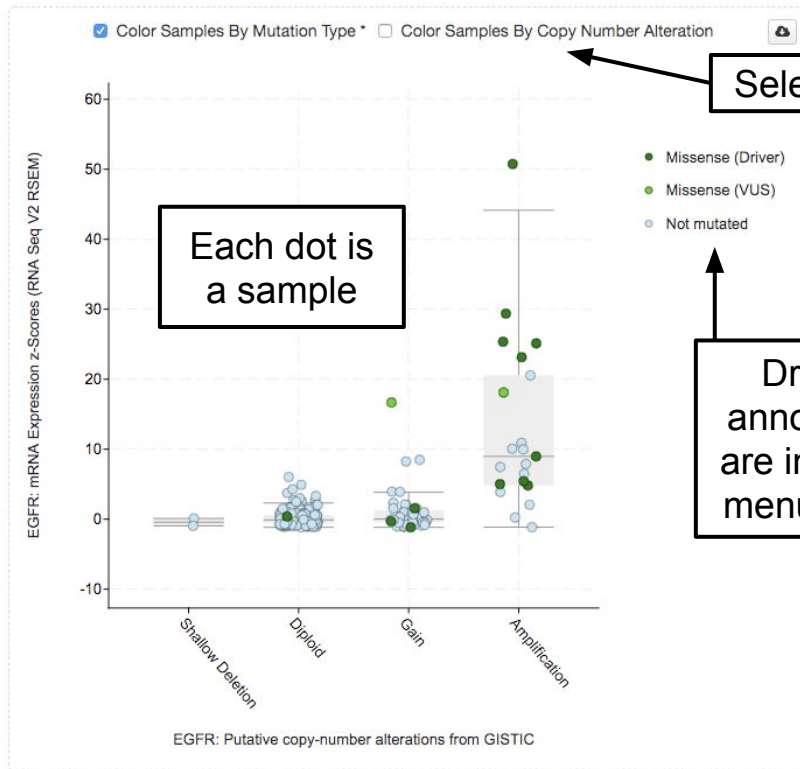
mRNA Profile  
mRNA Expression z-Scores (RN..

Gene  
Same gene (EGFR)

Search Case(s)  
Case ID..

Search Mutation(s)  
Protein Change..

↑ Swap Axes ↓



Select color scheme

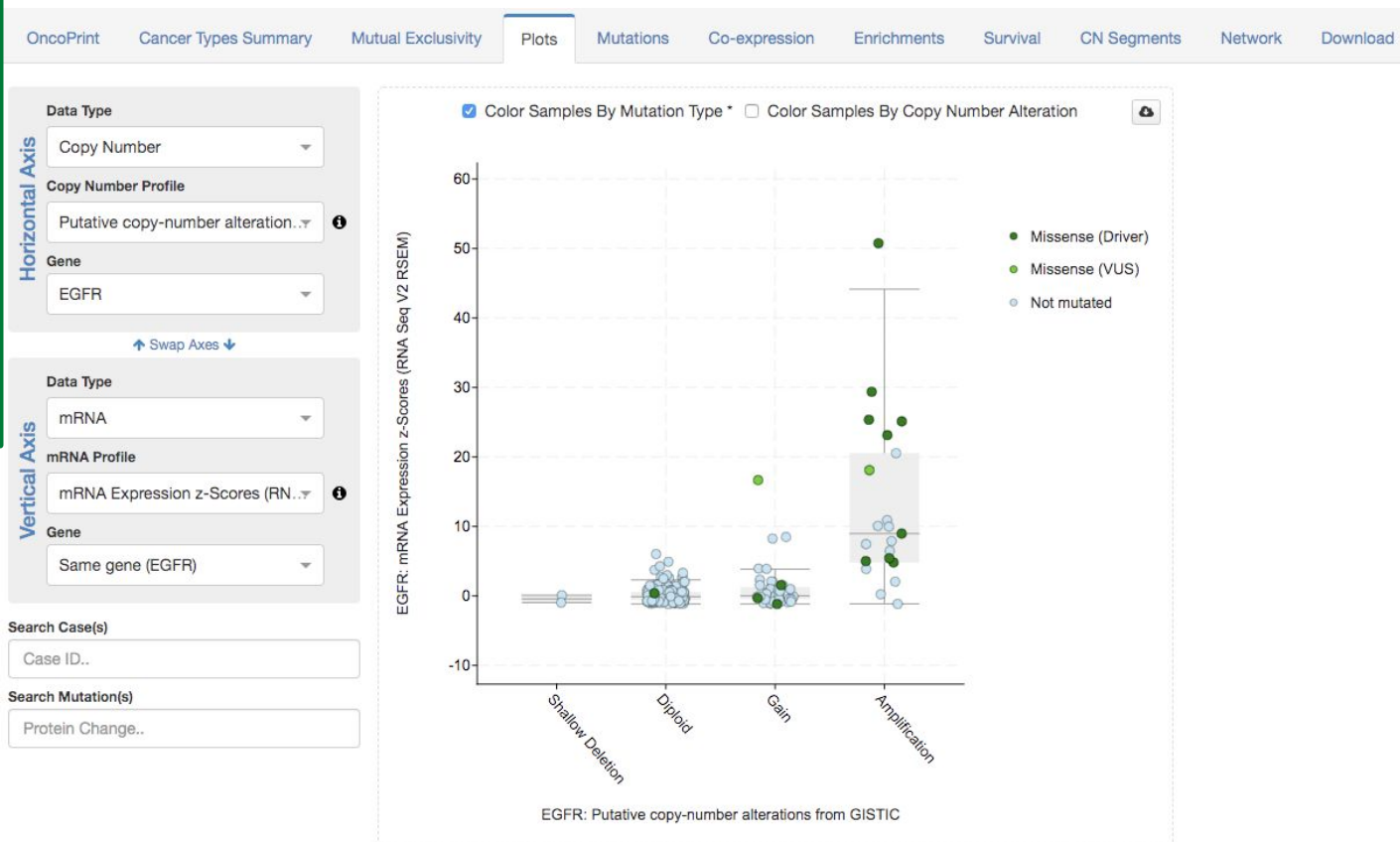
Driver vs. VUS  
annotation settings  
are in the Mutations  
menu of OncoPrint.

\* Driver annotation settings are located in the Mutation Color menu of the OncoPrint.

# Plots

**Q:** Does amplification of EGFR alter gene expression?

**A:** Yes, we can see that higher copy number of EGFR (x-axis) is associated with increased expression (y-axis).



\* Driver annotation settings are located in the Mutation Color menu of the OncoPrint.

# Mutations

This tab shows details about all mutations called in a particular gene.































Each gene appears on a separate tab

Table of all mutations with annotations

Statistics about mutation frequency



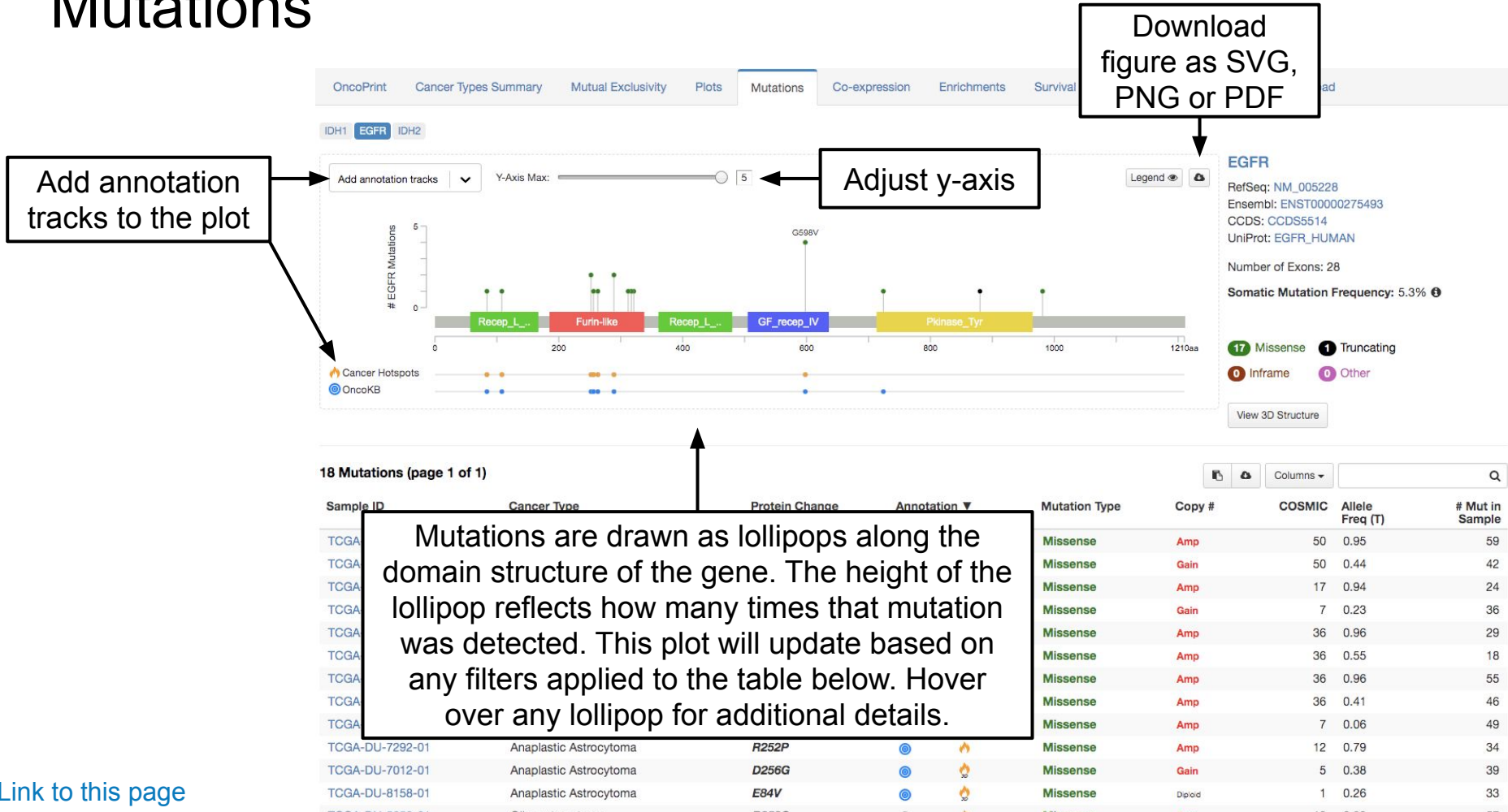
18 Mutations (page 1 of 1)

Sample ID	Cancer Type	Protein Change	Annotation ▼	Mutation Type	Copy #	COSSMIC	Allele Freq (T)	# Mut in Sample
TCGA-FG-6692-01	Anaplastic Oligoastrocytoma	A289V	  	Missense	Amp	50	0.95	59
TCGA-DU-A5TT-01	Anaplastic Oligoastrocytoma	A289V	  	Missense	Gain	50	0.44	42
TCGA-HT-8110-01	Anaplastic Astrocytoma	R108K	  	Missense	Gain	50	0.94	42
TCGA-HT-A61C-01	Anaplastic Oligoastrocytoma	T263P	  	Missense	Gain	50	0.23	42
TCGA-DU-7013-01	Anaplastic Astrocytoma	G598V	  	Missense	Gain	50	0.96	42
TCGA-DU-8162-01	Oligoastrocytoma	G598V	  	Missense	Gain	50	0.96	42
TCGA-FG-A4MU-01	Oligoastrocytoma	G598V	  	Missense	Amp	36	0.96	42
TCGA-HT-A5RC-01	Anaplastic Astrocytoma	G598V	  	Missense	Amp	36	0.41	42
TCGA-HT-8104-01	Anaplastic Astrocytoma	G724S	 	Missense	Amp	7	0.06	49
TCGA-DU-7292-01	Anaplastic Astrocytoma	R252P	 	Missense	Amp	12	0.79	34
TCGA-DU-7012-01	Anaplastic Astrocytoma	D256G	 	Missense	Gain	5	0.38	39
TCGA-DU-8158-01	Anaplastic Astrocytoma	F84V		Missense	Gain	1	0.26	33

Show additional columns

Filter based on any visible text column

# Mutations

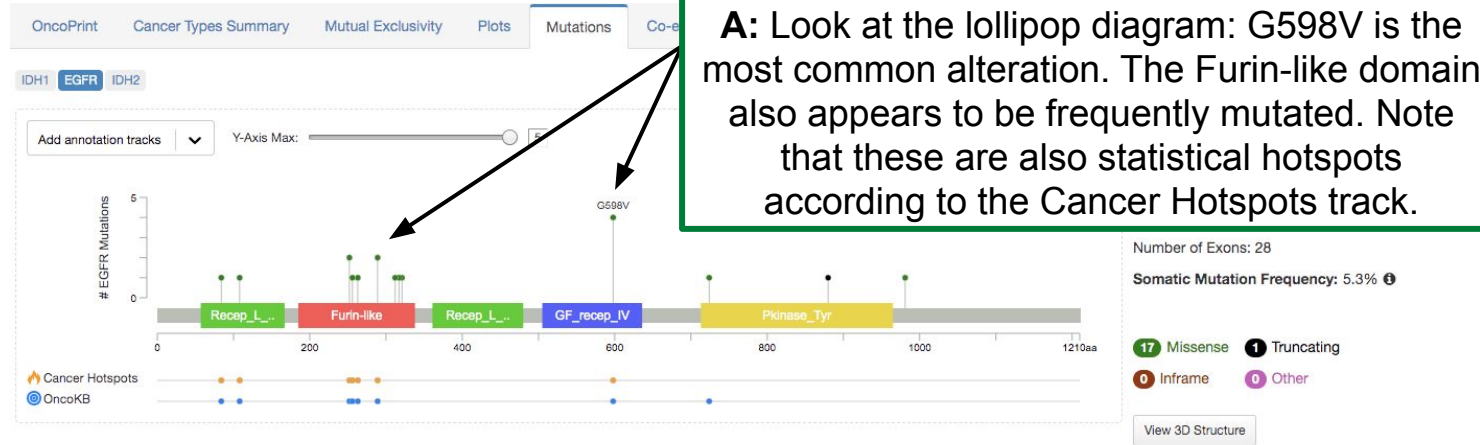




# Mutations

**Q:** What are the hotspots for EGFR mutation in glioma?

**A:** Look at the lollipop diagram: G598V is the most common alteration. The Furin-like domain also appears to be frequently mutated. Note that these are also statistical hotspots according to the Cancer Hotspots track.



## 18 Mutations (page 1 of 1)

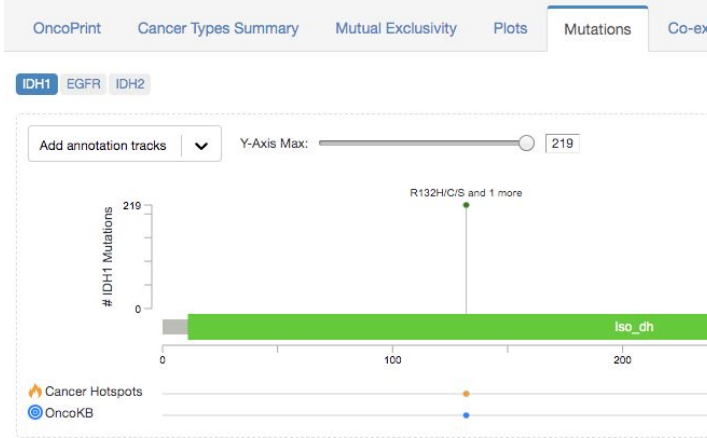
Sample ID	Cancer Type	Protein Change	Annotation ▼	Mutation Type	Copy #	COSMIC	Allele Freq (T)	# Mut in Sample
TCGA-FG-6692-01	Anaplastic Oligoastrocytoma	A289V	Ⓢ Ⓜ 🔥	Missense	Amp	50	0.95	59
TCGA-DU-A5TT-01	Anaplastic Oligoastrocytoma	A289V	Ⓢ Ⓜ 🔥	Missense	Gain	50	0.44	42
TCGA-HT-8110-01	Anaplastic Astrocytoma	R108K	Ⓢ Ⓜ 🔥	Missense	Amp	17	0.94	24
TCGA-HT-A61C-01	Anaplastic Oligoastrocytoma	T263P	Ⓢ Ⓜ 🔥	Missense	Gain	7	0.23	36
TCGA-DU-7013-01	Anaplastic Astrocytoma	G598V	Ⓢ Ⓜ 🔥	Missense	Amp	36	0.96	29
TCGA-DU-8162-01	Oligoastrocytoma	G598V	Ⓢ Ⓜ 🔥	Missense	Amp	36	0.55	18
TCGA-FG-A4MU-01	Oligoastrocytoma	G598V	Ⓢ Ⓜ 🔥	Missense	Amp	36	0.96	55
TCGA-HT-A5RC-01	Anaplastic Astrocytoma	G598V	Ⓢ Ⓜ 🔥	Missense	Amp	36	0.41	46
TCGA-HT-8104-01	Anaplastic Astrocytoma	G724S	Ⓢ Ⓜ 🔥	Missense	Amp	7	0.06	49
TCGA-DU-7292-01	Anaplastic Astrocytoma	R252P	Ⓢ 🔥	Missense	Amp	12	0.79	34
TCGA-DU-7012-01	Anaplastic Astrocytoma	D256G	Ⓢ 🔥	Missense	Gain	5	0.38	39
TCGA-DU-8158-01	Anaplastic Astrocytoma	E84V	Ⓢ 🔥	Missense	Diploid	1	0.26	33




# Mutations


**Q:** The mutations in IDH1 appear to be highly recurrent. Are these mutations known hotspots? Known oncogenic drivers? Biomarkers for any drugs?


**A:** Look at the annotation tracks below the lollipop plot and the Annotation column in the table. Each mutation is annotated against 4 different databases with information about recurrence, oncogenicity and drugability.



 This mutation is in [OncoKB](#) as a Level 2 variant. Hover over this symbol to see additional information, including that this is a known oncogenic mutation.

 This mutation is a [recurrent hotspot](#) based on a [statistical analysis of mutation frequency](#).

You may also see this symbol  which means the mutation is a [recurrent hotspot](#) based on a [statistical analysis of 3D protein conformation](#).

 This mutation is annotated in [CIViC](#). Hover over this symbol for additional information.

 This mutation is in [My Cancer Genome](#).

TCGA-HT-7693-01	Oligodendroglioma	R132C	Annotation	Missense	ShallowDel	4964	0.48	24
TCGA-HT-7855-01	Anaplastic Astrocytoma	R132C	Annotation	Missense	ShallowDel	4964	0.46	30
TCGA-DB-A4XD-01			Annotation	Missense	ShallowDel	4964	0.39	28
TCGA-DB-A4XF-01			Annotation	Missense	ShallowDel	4964	0.40	17
TCGA-P5-A5EZ-01			Annotation	Missense	ShallowDel	4964	0.24	25
TCGA-P5-A5F4-01			Annotation	Missense	ShallowDel	4964	0.31	24
TCGA-DB-A64S-01			Annotation	Missense	ShallowDel	4964	0.31	10

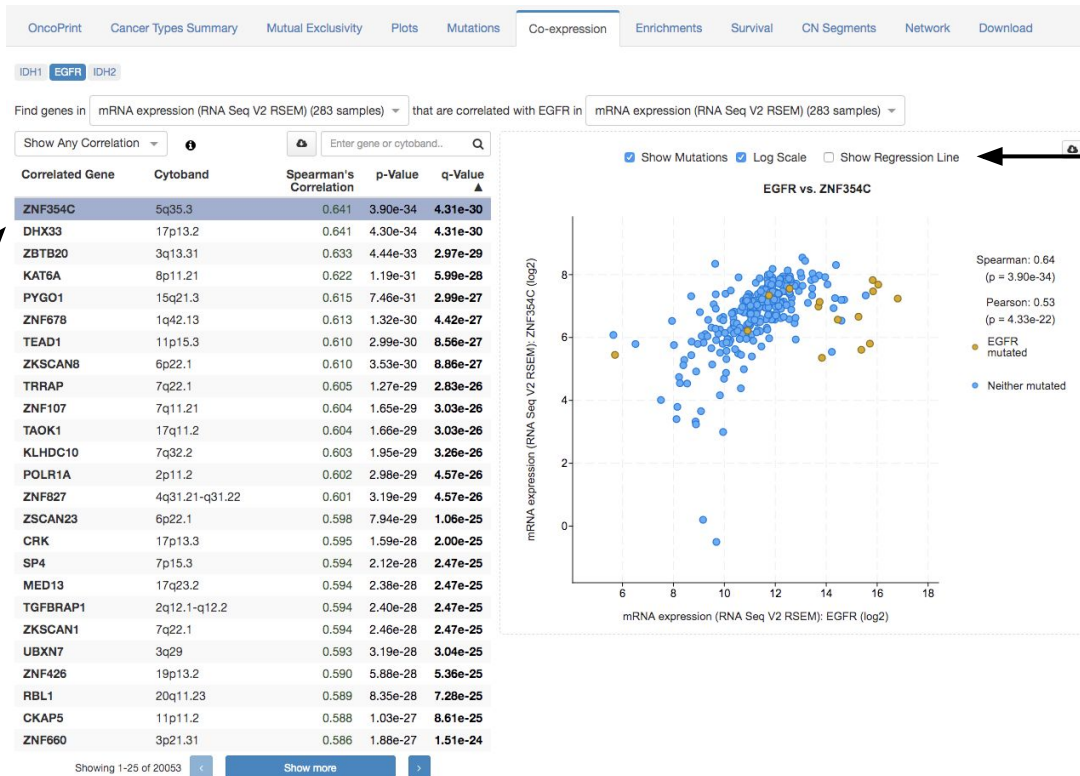
# Co-Expression

Compares mRNA/protein level expression of your query genes against all other genes.

Each gene appears on a separate tab

Select from available data types

Click on a gene name to see correlation plot



Check boxes to color-code sample dots by mutation status or change x- or y-axis to log scale

# Co-Expression

**Q:** Which genes have expression that correlates with EGFR expression across the cohort?

**A:** EGFR is on chr7 and many other genes located on chr7 have expression levels correlated with EGFR expression (see table on the left). Chr7 is frequently gained in some subtypes of glioma which could explain these correlated increases in expression.

OncoPrint Cancer Types Summary Mutual Exclusivity

IDH1 EGFR IDH2

Find genes in mRNA expression (RNA Seq V2 RSEM) (283 samples)

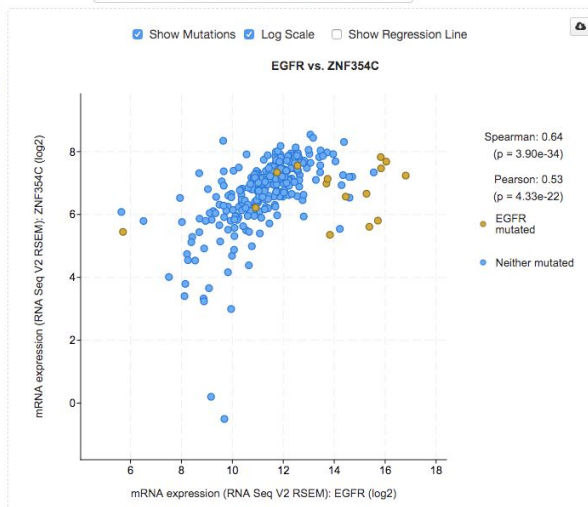
Show Any Correlation

Enter gene or cytoband...

Correlated Gene	Cytoband	Spearman's Correlation	p-Value	q-Value
ZNF354C	5q35.3	0.641	3.90e-34	4.31e-30
DHX33	17p13.2	0.641	4.30e-34	4.31e-30
ZBTB20	3q13.31	0.633	4.44e-33	2.97e-29
KAT6A	8p11.21	0.622	1.19e-31	5.99e-28
PYGO1	15q21.3	0.615	7.46e-31	2.99e-27
ZNF678	1q42.13	0.613	1.32e-30	4.42e-27
TEAD1	11p15.3	0.610	2.99e-30	8.56e-27
ZKSCAN8	6p22.1	0.610	3.53e-30	8.86e-27
TRRAP	7q22.1	0.605	1.27e-29	2.83e-26
ZNF107	7q11.21	0.604	1.65e-29	3.03e-26
TAOK1	17q11.2	0.604	1.66e-29	3.03e-26
KLHDC10	7q32.2	0.603	1.95e-29	3.26e-26
POLR1A	2p11.2	0.602	2.98e-29	4.57e-26
ZNF827	4q31.21-q31.22	0.601	3.19e-29	4.57e-26
ZSCAN23	6p22.1	0.598	7.94e-29	1.06e-25
CRK	17p13.3	0.595	1.59e-28	2.00e-25
SP4	7p15.3	0.594	2.12e-28	2.47e-25
MED13	17q23.2	0.594	2.38e-28	2.47e-25
TGFBRAP1	2q12.1-q12.2	0.594	2.40e-28	2.47e-25
ZKSCAN1	7q22.1	0.594	2.46e-28	2.47e-25
UBXN7	3q29	0.593	3.19e-28	3.04e-25
ZNF426	19p13.2	0.590	5.88e-28	5.36e-25
RBL1	20q11.23	0.589	8.35e-28	7.28e-25
CKAP5	11p11.2	0.588	1.03e-27	8.61e-25
ZNF660	3p21.31	0.586	1.88e-27	1.51e-24

Showing 1-25 of 20053

Show more

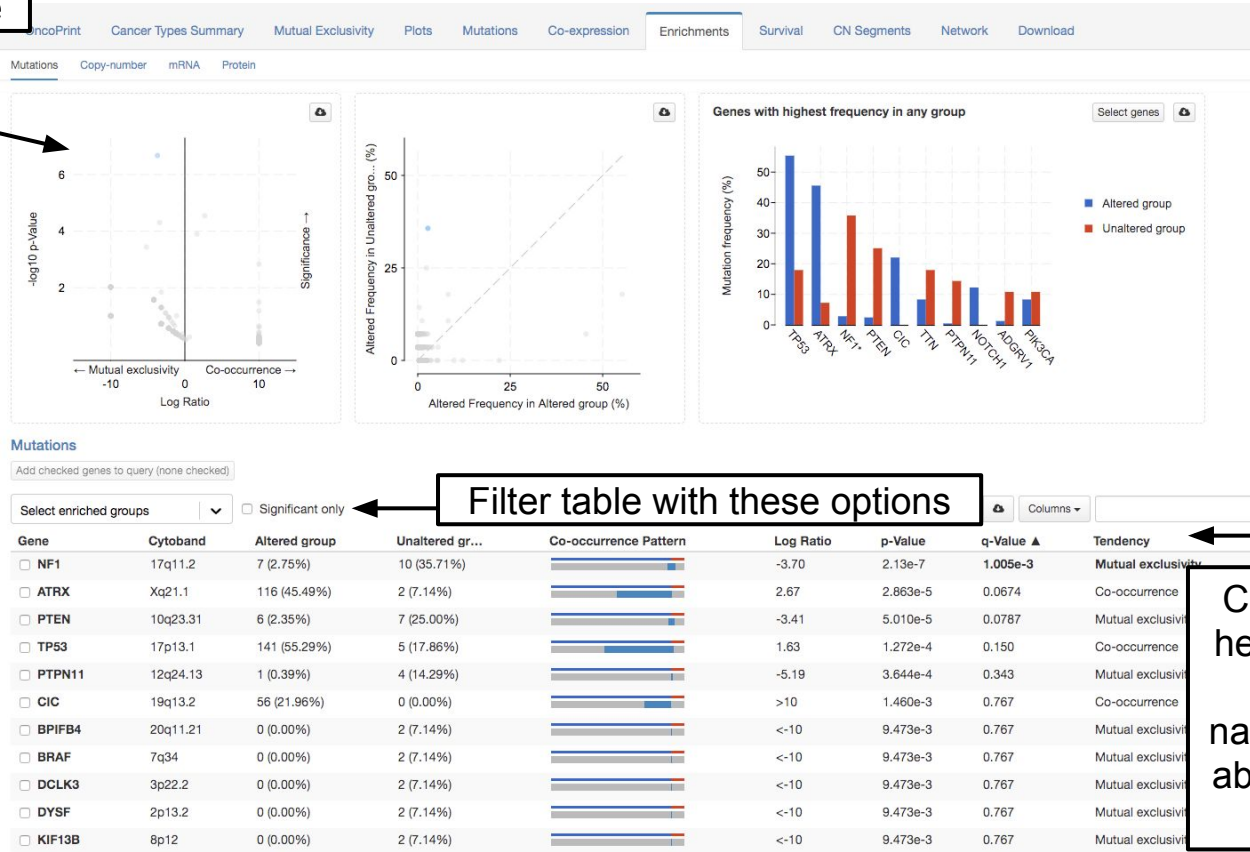


# Enrichments

Select type of data to examine

Hover over a dot to see the gene name

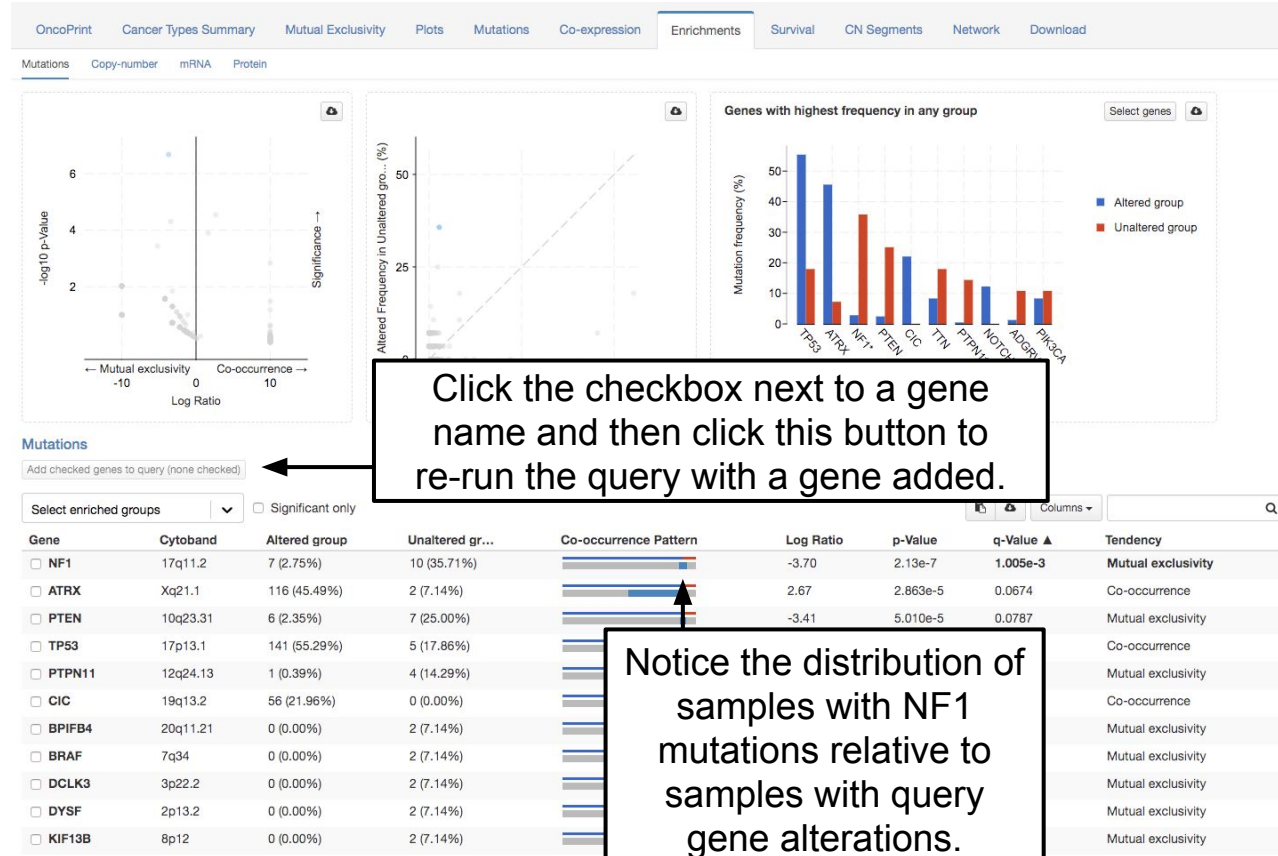
This tab takes samples with alterations in any query gene as a set and looks to see whether other genes are frequently altered in the same set of samples (co-occurring) or in the set of samples without query gene alterations (mutually exclusive).



# Enrichments

**Q:** Alterations in IDH1, IDH2 and EGFR are mutually exclusive but some samples have alterations in none of these genes. Do samples without IDH1, IDH2 or EGFR alterations commonly have mutations in one or more other genes?

**A:** Mutations in NF1 are significantly mutually exclusive with alterations in IDH1, IDH2 and EGFR (see table). Try adding NF1 to the query (check the box next to NF1 and then click “Add checked genes to query”) and examine the OncoPrint and the Mutual Exclusivity tabs.

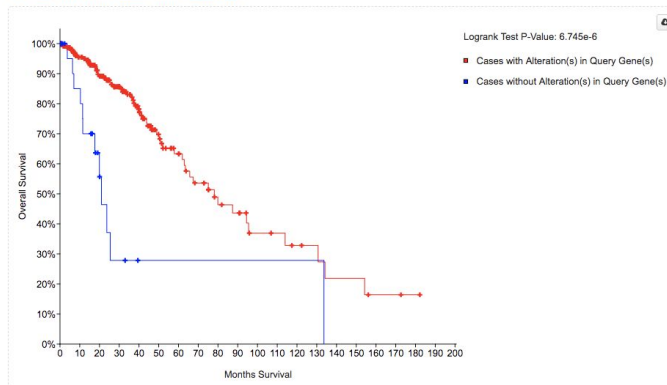


# Survival

For studies with outcome data, this tab has Overall Survival and Disease Free Survival Kaplan-Meier plots. In red are cases with one or more alterations in the query gene(s). In blue are all other cases in the study.

Note: These plots reflect data as provided by the study. We do not perform any additional processing.

Overall Survival Kaplan-Meier Estimate

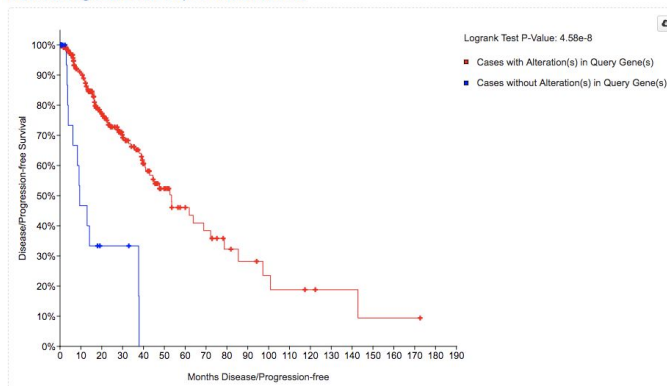


	Number of Cases, Total	Number of Cases, Deceased	Median Months Survival
Cases with Alteration(s) in Query Gene(s)	254	60	78.15
Cases without Alteration(s) in Query Gene(s)	28	12	20.99

Download plots or data

Number of cases in the plot

Disease/Progression-free Kaplan-Meier Estimate



	Number of Cases, Total	Number of Cases, Relapsed/Progressed	Median Months Disease-free
Cases with Alteration(s) in Query Gene(s)	237	78	53.45
Cases without Alteration(s) in Query Gene(s)	23	12	9.43

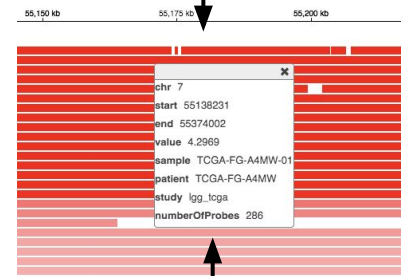
**Q:** Do patients with alterations in IDH1, IDH2 or EGFR have different outcomes compared to patients without alterations in any of those genes?

**A:** Patients with alterations in IDH1, IDH2 or EGFR have significantly better OS and DFS than patients without those alterations.

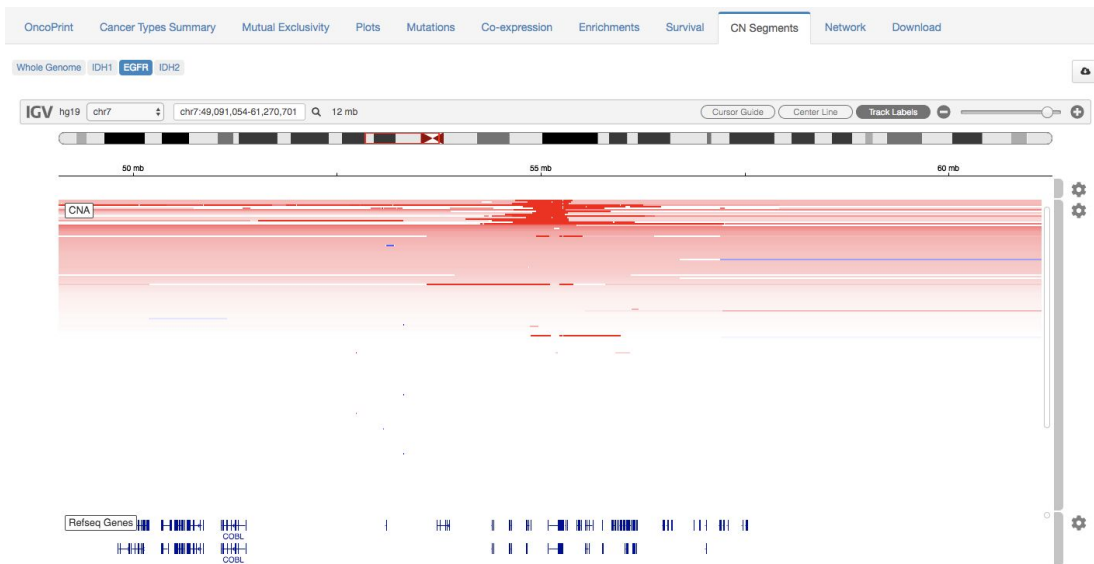


# CN Segments

View copy number for each sample at each query gene via the [Integrated Genomics Viewer](#) (IGV).



# CN Segments



**Q:** Are amplifications of EGFR focal or broad?

**A:** By zooming out, we can see that high-level amplifications (deeper red) are focal at the EGFR locus, while low-level gains (lighter red) are broad. If we continue to zoom out, we will see that the low-level gain encompasses the entire chromosome.



# Network

Visualize biological interaction networks centered on your query genes, with color-coding and filter options based on the frequency of genomic alterations in each gene. Click on the “Help” tab for a more detailed explanation.

Change zoom and move around network

View or modify the nodes included in the network (e.g. add drugs, filter genes by alteration frequency)

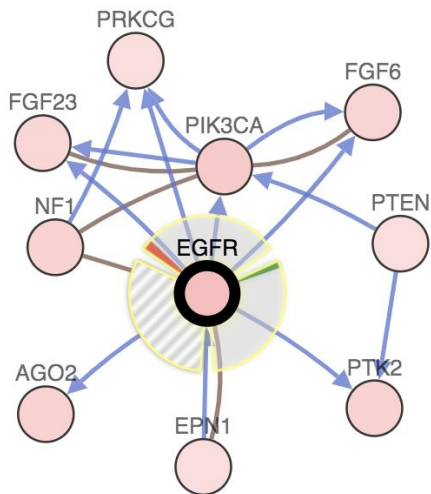
View or modify the types of interactions (edges) utilized in the plot

Click on any node to see detailed information about the gene here

GenoPrint Cancer Types Summary Mutual Exclusivity Plots Mutations Co-ex

The network below contains 53 nodes, including your 3 query genes and the 50 most frequently altered neighbor genes (out of a total of 430). Download the complete network in GraphML or SIF for import into Cytoscape (GraphMLReader plugin is required for importing GraphML).

Topo View Layout Legends Double-click nodes/edges for details.



Genes Interactions Details Help

Drugs of Specified Genes

Hide Drugs

Genes

Filter Neighbors by Alteration (%)

0 MAX 5

Submit New Query

AGO2  
EGFR  
EPN1  
FGF23  
FGF6  
IDH1  
IDH2  
NF1  
PIK3CA  
PRKCG  
PTEN  
PTK2

Genes Interactions Details Help

Type:

Controls State Change of 32.7%

In Complex With 7.6%

Targeted by Drug 3.9%

Modify...

Source:

pid  
Reactome  
PANTHER  
HumanCyc  
PhosphoSite  
DrugBank  
CancerRxGene  
KEGG Drugs  
Cancer Cell Line Encyclopedia  
PubMed:21804595  
CTRP  
Unknown

Modify...

Genes Interactions Details Help

Genomic Profile(s):

Total Alteration 9.2%

Amplification 7.4%

Mutation 5.3%

Gene Symbol: EGFR

Description: epidermal growth factor receptor

Aliases: ERBB, HER1, mENA, ERBB1, PIIG1, NISB2

Designations: avian erythroblastic leukemia viral (v-erb-b) oncogene homolog, cell growth inhibiting protein 40, cell proliferation-inducing protein 61, epidermal growth factor receptor tyrosine [...]

Chromosome Location: 7p11.2

MIM: 131550

Gene ID: 1956

Gene Function: The protein encoded by this gene is a transmembrane glycoprotein that is a member of the protein kinase superfamily. This protein is a receptor for members of the epidermal growth [...]

# Download

Download data or copy lists of samples.

OncoPrint Cancer Types Summary Mutual Exclusivity Plots Mutations Co-expression Enrichments Survival CN Segments Network **Download**

## Downloadable Data Files

Copy-number Alterations

[Tab Delimited Format](#) | [Transposed Matrix](#)

Mutations

[Tab Delimited Format](#) | [Transposed Matrix](#)

Samples affected: Only samples with an alteration are included

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Sample matrix: 1 = Sample harbors alteration in one of the input genes

[Copy](#) | [Download](#)

Download mutations and copy number

## Gene Alteration Frequency

Gene Symbol	Num Samples Altered	Percent Samples Altered ▼
IDH1	219	77.4%
EGFR	26	9.2%
IDH2	13	4.6%

Showing 1-3 of 3

Frequency of gene alteration for each gene in the query

## Type of Genetic Alterations Across All Samples

Study ID	Sample ID	Patient ID	Altered ▼	IDH1 CNA	IDH1 MUT	IDH1 FUSION	EGFR CNA	EGFR MUT	EGFR FUSION	IDH2 CNA	IDH2 MUT	IDH2 FUSION
lgg_tcga	TCGA-CS-6290-01	TCGA-CS-6290	1	no alteration	<b>R132H</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-5849-01	TCGA-DU-5849	1	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	<b>R172K</b>	no alteration
lgg_tcga	TCGA-DU-5852-01	TCGA-DU-5852	1	no alteration	no alteration	no alteration	<b>AMP</b>	<b>R252C,I961F</b>	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-5854-01	TCGA-DU-5854	1	no alteration	no alteration	no alteration	<b>AMP</b>	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-5855-01	TCGA-DU-5855	1	no alteration	<b>R132H</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-5870-01	TCGA-DU-5870	1	no alteration	<b>R132H</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-5871-01	TCGA-DU-5871	1	no alteration	<b>R132G</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-5872-01	TCGA-DU-5872	1	no alteration	<b>R132H</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-5874-01	TCGA-DU-5874	1	no alteration	<b>R132H</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-6393-01	TCGA-DU-6393	1	no alteration	<b>R132H</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-6394-01	TCGA-DU-6394	1	no alteration	<b>R132H</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-6395-01	TCGA-DU-6395	1	no alteration	<b>R132H</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-6396-01	TCGA-DU-6396	1	no alteration	<b>R132H</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-6397-01	TCGA-DU-6397	1	no alteration	<b>R132H</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-6399-01	TCGA-DU-6399	1	no alteration	<b>R132H</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-6400-01	TCGA-DU-6400	1	no alteration	<b>R132H</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-6401-01	TCGA-DU-6401	1	no alteration	<b>R132S</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-6403-01	TCGA-DU-6403	1	no alteration	no alteration	no alteration	<b>AMP</b>	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-6405-01	TCGA-DU-6405	1	no alteration	no alteration	no alteration	<b>AMP</b>	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-6407-01	TCGA-DU-6407	1	no alteration	<b>R132H</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration

Showing 1-20 of 283

Show more

Reset

List of all samples with status of each query gene for each type of alteration queried (see [OQL tutorial](#) for explanation of alteration types included in a query)

# Download

Download data or copy lists of samples.

OncoPrint Cancer Types Summary Mutual Exclusivity Plots Mutations Co-expression Enrichments Survival CN Segments Network **Download**

## Downloadable Data Files

Copy-number Alterations

[Tab Delimited Format](#) | [Transposed Matrix](#)

Mutations

[Tab Delimited Format](#) | [Transposed Matrix](#)

Samples affected: Only samples with an alteration are included

[Copy](#) | [Download](#)

Sample matrix: 1 = Sample harbors alteration in one of the input genes

[Copy](#) | [Download](#)

List of samples that have an alteration in one or more query genes

List of all samples with summary classification:  
0 = no alteration in any query gene  
1 = alteration in one or more query genes

## Gene Alteration Frequency

Gene Symbol	Num Samples Altered	Percent Samples Altered ▼
IDH1	219	77.4%
EGFR	26	9.2%
IDH2	13	4.6%

Showing 1-3 of 3

## Type of Genetic Alterations Across All Samples

Study ID	Sample ID	Patient ID	Altered ▼	IDH1 CNA	IDH1 MUT	IDH1 FUSION	EGFR CNA	EGFR MUT	EGFR FUSION	IDH2 CNA	IDH2 MUT	IDH2 FUSION
lgg_tcga	TCGA-CS-6290-01	TCGA-CS-6290	1	no alteration	<b>R132H</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-5849-01	TCGA-DU-5849	1	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	<b>R172K</b>	no alteration
lgg_tcga	TCGA-DU-5852-01	TCGA-DU-5852	1	no alteration	no alteration	no alteration	<b>AMP</b>	<b>R252C,I961F</b>	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-5854-01	TCGA-DU-5854	1	no alteration	no alteration	no alteration	<b>AMP</b>	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-5855-01	TCGA-DU-5855	1	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-5870-01	TCGA-DU-5870	1	no alteration	<b>R132H</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-5871-01	TCGA-DU-5871	1	no alteration	<b>R132G</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-5872-01	TCGA-DU-5872	1	no alteration	<b>R132H</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-5874-01	TCGA-DU-5874	1	no alteration	<b>R132H</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-6393-01	TCGA-DU-6393	1	no alteration	<b>R132H</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-6394-01	TCGA-DU-6394	1	no alteration	<b>R132H</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-6395-01	TCGA-DU-6395	1	no alteration	<b>R132H</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-6396-01	TCGA-DU-6396	1	no alteration	<b>R132H</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-6397-01	TCGA-DU-6397	1	no alteration	<b>R132H</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-6399-01	TCGA-DU-6399	1	no alteration	<b>R132H</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-6400-01	TCGA-DU-6400	1	no alteration	<b>R132H</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-6401-01	TCGA-DU-6401	1	no alteration	<b>R132S</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-6403-01	TCGA-DU-6403	1	no alteration	no alteration	no alteration	<b>AMP</b>	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-6405-01	TCGA-DU-6405	1	no alteration	no alteration	no alteration	<b>AMP</b>	no alteration	no alteration	no alteration	no alteration	no alteration
lgg_tcga	TCGA-DU-6407-01	TCGA-DU-6407	1	no alteration	<b>R132H</b>	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration	no alteration

Showing 1-20 of 283

[Show more](#)

[Reset](#)

Advanced feature: use these lists to build a custom sample list to run a new query or create a virtual study. Use the “Samples affected” list to select the subset of samples with a particular genetic alteration. Use the “Sample matrix” to select the subset of samples without alterations.

Questions?

Check out our other tutorials  
or email us at:

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