

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

The screenshot shows the cBioPortal interface for cancer genomics. It includes a top navigation bar with links like 'Data Sets', 'Web API', 'R/MATLAB', 'Tutorials', 'FAQ', 'News', 'Visualize Your Data', and 'About'. A 'Login' button is in the top right. The main content area is titled 'Query' and features a 'Quick Search Beta!' button and a 'Download' link. A search bar is located at the top right of the main content area. Below the search bar, there's a section for 'Select Studies for Visualization & Analysis:' which displays a list of studies organized by organ system. This list includes categories like 'PanCancer Studies', 'Cell lines', 'Adrenal Gland', 'Ampulla of Vater', 'Biliary Tract', 'Bladder/Urinary Tract', 'Bone', 'Bowel', 'Breast', 'CNS/Brain', 'Cervix', 'Esophagus/Stomach', 'Eye', and 'Head and Neck'. Each category shows the number of studies and samples. To the right of the list, there's a 'List of all studies, organized by organ system' section. At the bottom, there are buttons for 'Query By Gene' and 'Explore Selected Studies'. On the right side of the page, there's a 'What's New' section with a tweet from cBioPortal and a 'Cancer Studies' section with a bar chart titled 'Cases by Top 20 Primary Sites'.

Browse available datasets and select studies to explore or query

Search studies

Number of studies for each tissue of origin (click to filter)

List of all studies, organized by organ system

What's New

Cancer Studies

Cases by Top 20 Primary Sites

Single study query

1. Filter the list of studies (optional)

2. Check the box for study of interest.

3. Select "Query By Gene"

The screenshot displays the cBioPortal interface for a single study query. The top navigation bar includes links for Data Sets, Web API, R/MATLAB, Tutorials, FAQ, News, Visualize Your Data, and About. A search bar at the top right contains the text 'glioma'. Below the search bar, the 'Select Studies for Visualization & Analysis' section shows a list of studies. The 'CNS/Brain' category is selected, and the 'Brain Lower Grade Glioma (TCGA, Provisional)' study is checked. The 'Query By Gene' button is highlighted at the bottom.

Search Results:

Study	Samples
Brain Lower Grade Glioma (TCGA, PanCancer Atlas)	514 samples
<input checked="" type="checkbox"/> Brain Lower Grade Glioma (TCGA, Provisional)	530 samples
Glioma (MSK, 2018)	91 samples
Low-Grade Gliomas (UCSF, Science 2014)	61 samples
Merged Cohort of LGG and GBM (TCGA, Cell 2016)	1102 samples
GLIOBLASTOMA	
Brain Tumor PDXs (Mayo Clinic, 2019)	95 samples
Glioblastoma (TCGA, Cell 2013)	585 samples
Glioma (TCGA, Nature 2008)	206 samples
Glioma Multiforme (TCGA, PanCancer Atlas)	592 samples
Glioma Multiforme (TCGA, Provisional)	604 samples
OLIGODENDROGLIOMA	
Oligodendroglioma and Anaplastic Oligoastrocytoma (MSK...)	22 samples
ENCAPSULATED GLIOMA	
PILOCYTIC ASTROCYTOMA	
Pilocytic Astrocytoma (ICGC, Nature Genetics 2013)	96 samples
Miscellaneous Neuroepithelial Tumor	

Query By Gene OR **Explore Selected Studies**

Single study query

4. This section lists include all data types available for the selected study. Select data types to query.

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

The screenshot shows the 'Query' tab of the cBioPortal interface. At the top, there are tabs for 'Query', 'Quick Search Beta!', and 'Download', along with a citation: 'Please cite: Cerami et al., 2012 & Gao et al., 2013'. The 'Selected Studies' section shows 'Brain Lower Grade Glioma (TCGA, Provisional)' with '(530 total samples)'. The 'Select Genomic Profiles' section has checkboxes for 'Mutations', 'Putative copy-number alterations from GISTIC', 'mRNA Expression' (with sub-options for z-scores), and 'Protein expression Z-scores (RPPA)'. The 'Select Patient/Case Set' dropdown is set to 'Samples with mutation and CNA data (283)'. The 'Enter Genes' section has a 'User-defined List' input with 'IDH1 EGFR' entered, and a green confirmation bar stating 'All gene symbols are valid.' A 'Submit Query' button is at the bottom.

Query Quick Search Beta! Download Please cite: Cerami et al., 2012 & Gao et al., 2013

Selected Studies: Brain Lower Grade Glioma (TCGA, Provisional) (530 total samples)

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.

Enter Genes:

[Hint: Learn Onco Query Language \(OQL\) to write more powerful queries](#)

☒ All gene symbols are valid.

6. Submit query

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

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

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 name of the study.
Click to view the queried
samples in Study View.

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

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

OncoPrint

Cancer Types Summary

Mutual Exclusivity

Plots

Mutations

Co-expression

Enrichments

Survival

CN Segments

Network

Download

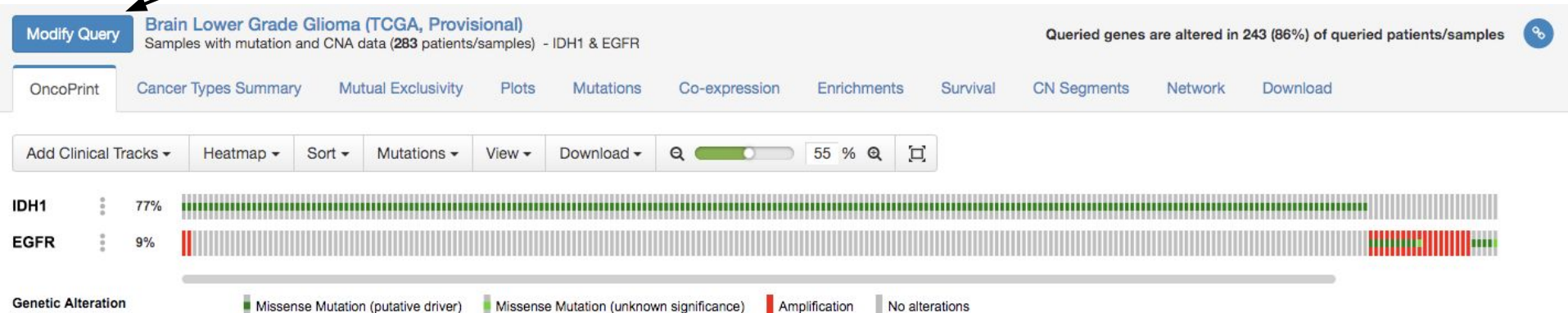
The number of samples and patients included
in the query. Note that these numbers can
differ from each other if some patients have
more than one tumor sample profiled.

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 bring up the query interface from the homepage (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

Please cite: Cerami et al., 2012 & Gao et al., 2013

Query

Visualization & Analysis: 1 study selected (530 samples) Deselect all

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

- ☐ Adenoid Cystic Carcinoma Project (2019) 1049 samples
- ☐ Adrenocortical Carcinoma (TCGA, PanCancer Atlas) 92 samples

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

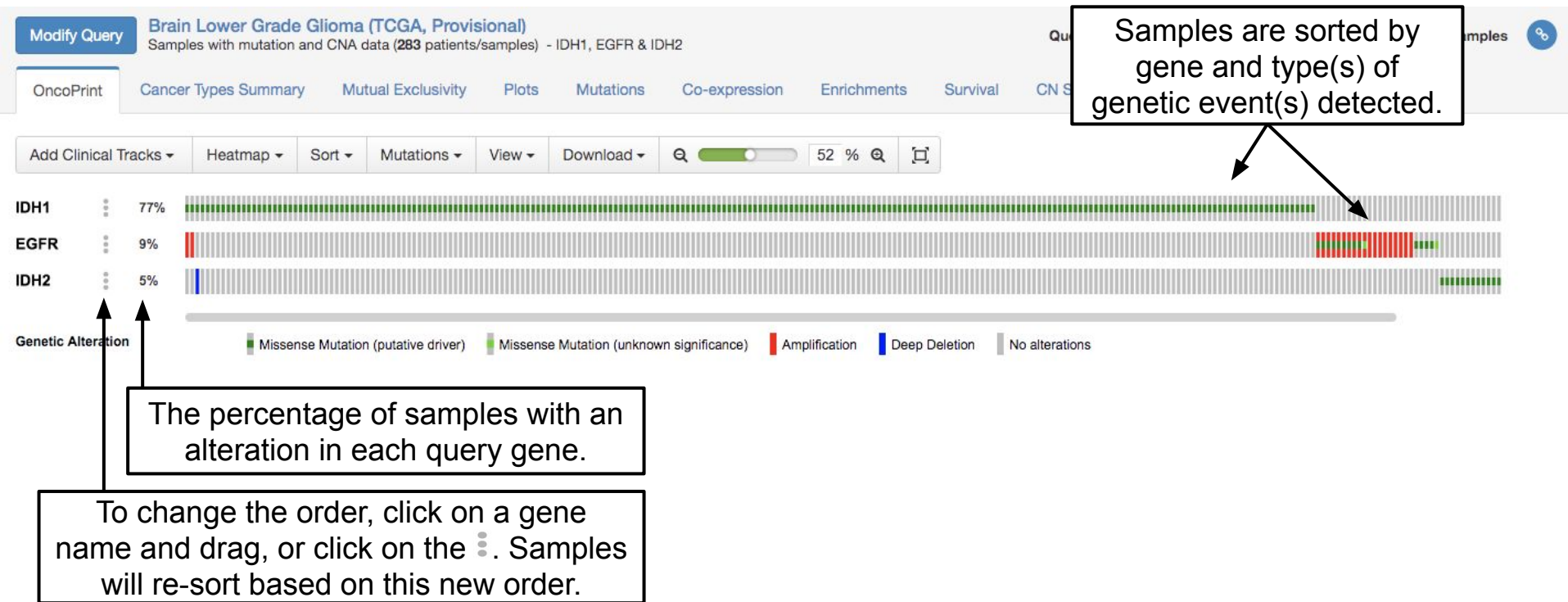
All gene symbols are valid.

Submit Query

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

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

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.

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

Add Clinical Tracks ▾

Heatmap ▾

Sort ▾

Mutations ▾

View ▾

Download ▾

🔍 52 % 🔍

🖨

Select all (3) Deselect all

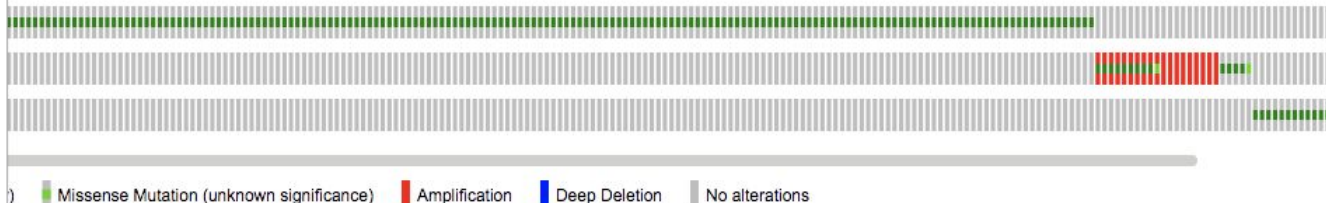
age

Name

Freq

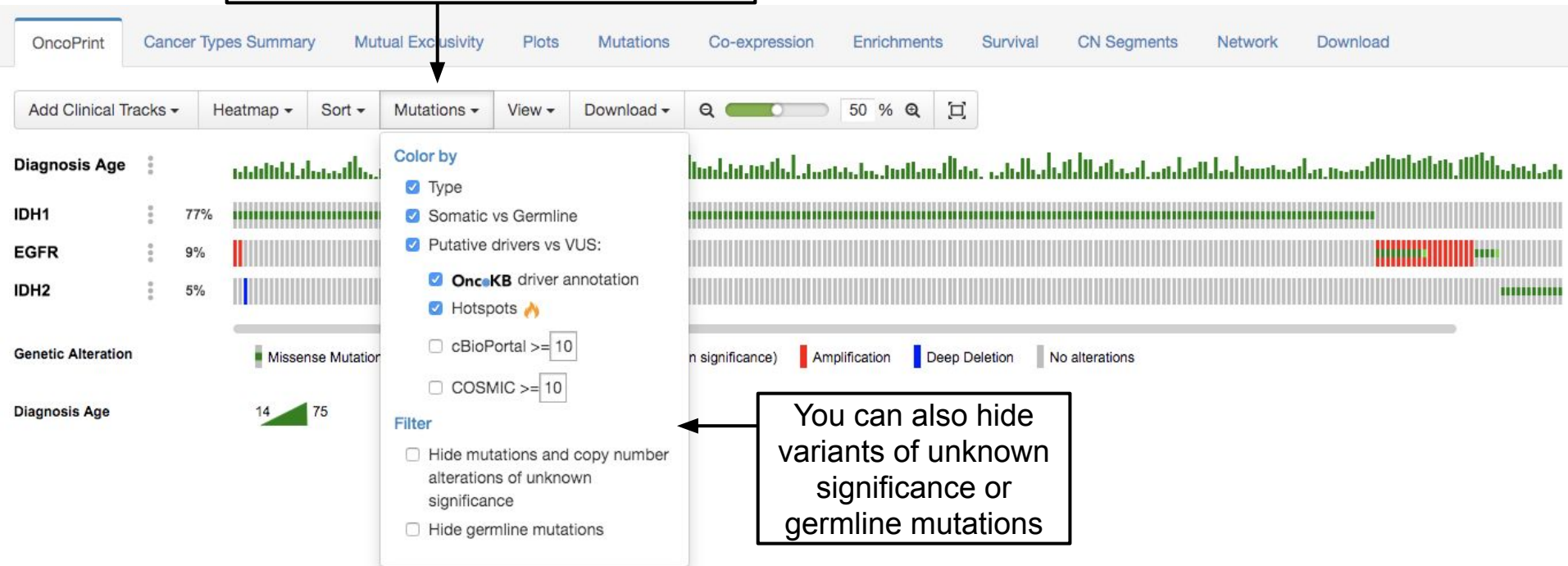
- ☒ Diagnosis Age
- ☐ Animal Insect Allergy Age
- ☐ Age of Food Allergy

100.0%
2.8%
1.4%



OncoPrint: Mutation Classification Rules

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



You can also hide variants of unknown significance or germline mutations

OncoPrint: Zoom

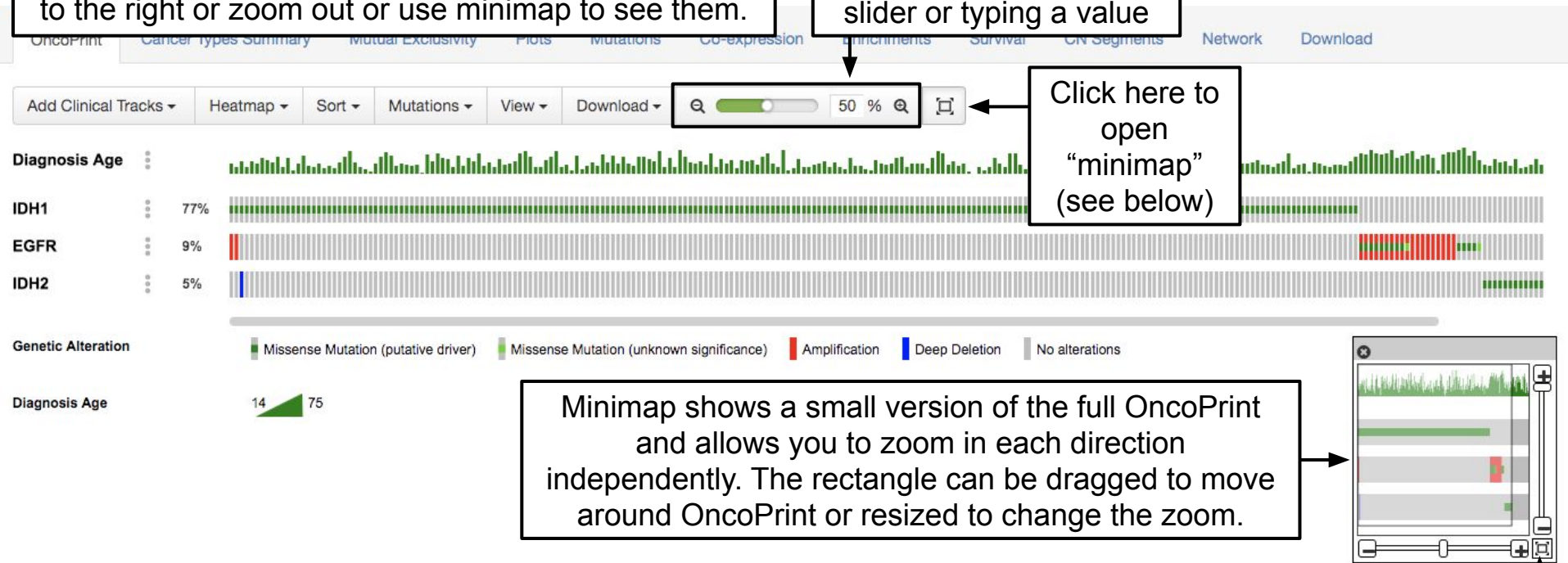
There may be more samples hiding off-screen. Scroll to the right or zoom out or use minimap to see them.

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

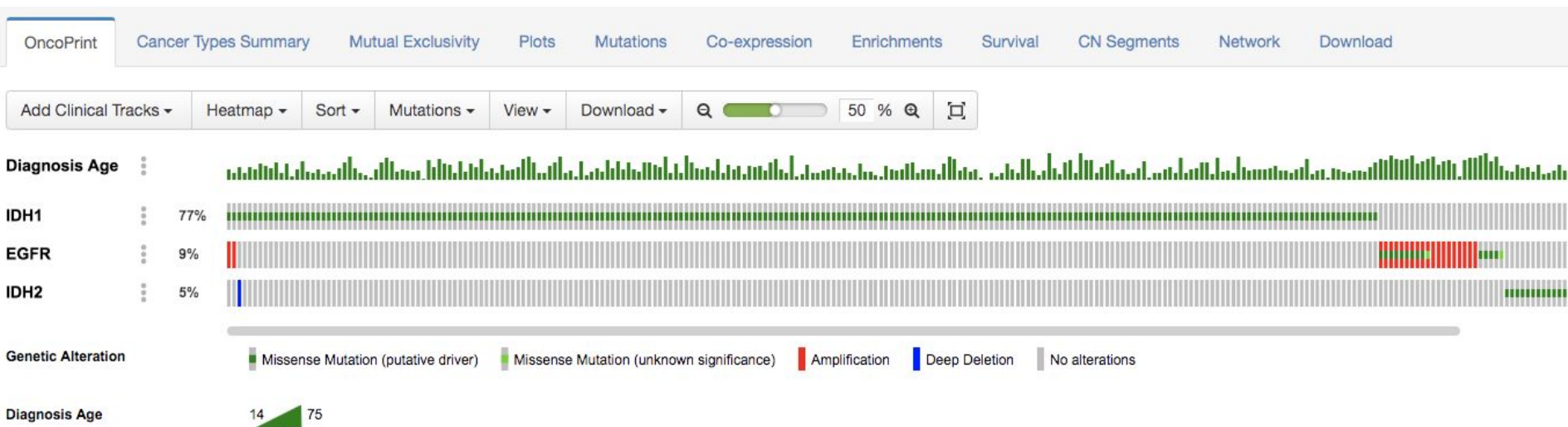
Click here to open "minimap" (see below)

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

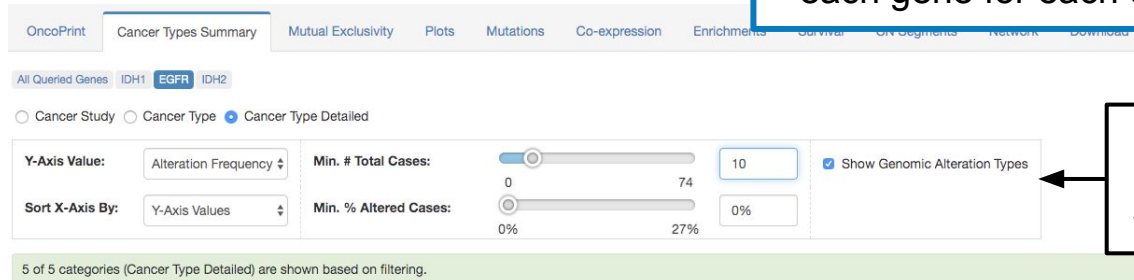
Now we're going to go through all the other tabs and ask some questions about alterations in *IDH1*, *IDH2* and *EGFR* in the TCGA Lower-Grade Glioma study.

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)

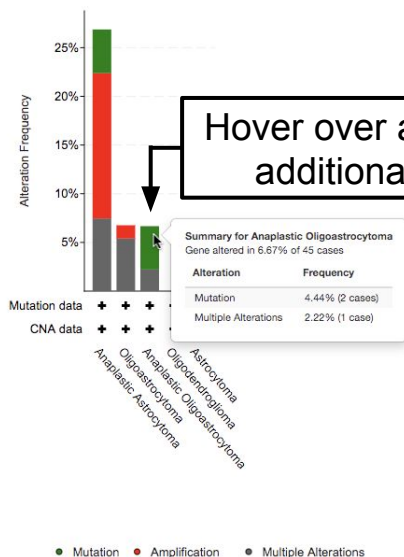
Cancer Types Summary

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 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

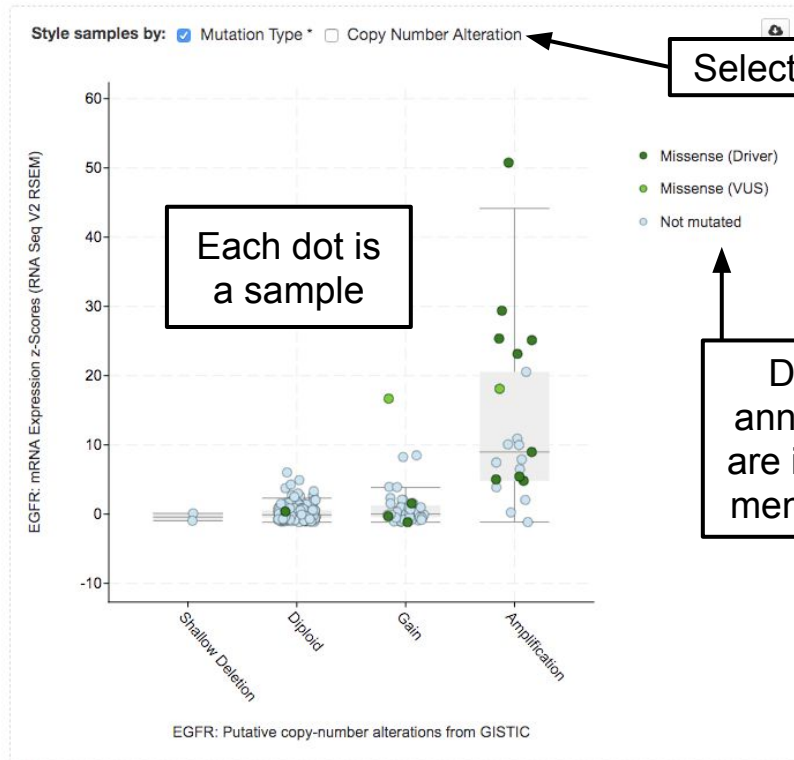
mRNA Profile
mRNA Expression z-Scores (RN..

Gene
Same gene (EGFR)

Search Case(s)
Case ID..

Search Mutation(s)
Protein Change..

↑ Swap Axes ↓



Select color scheme

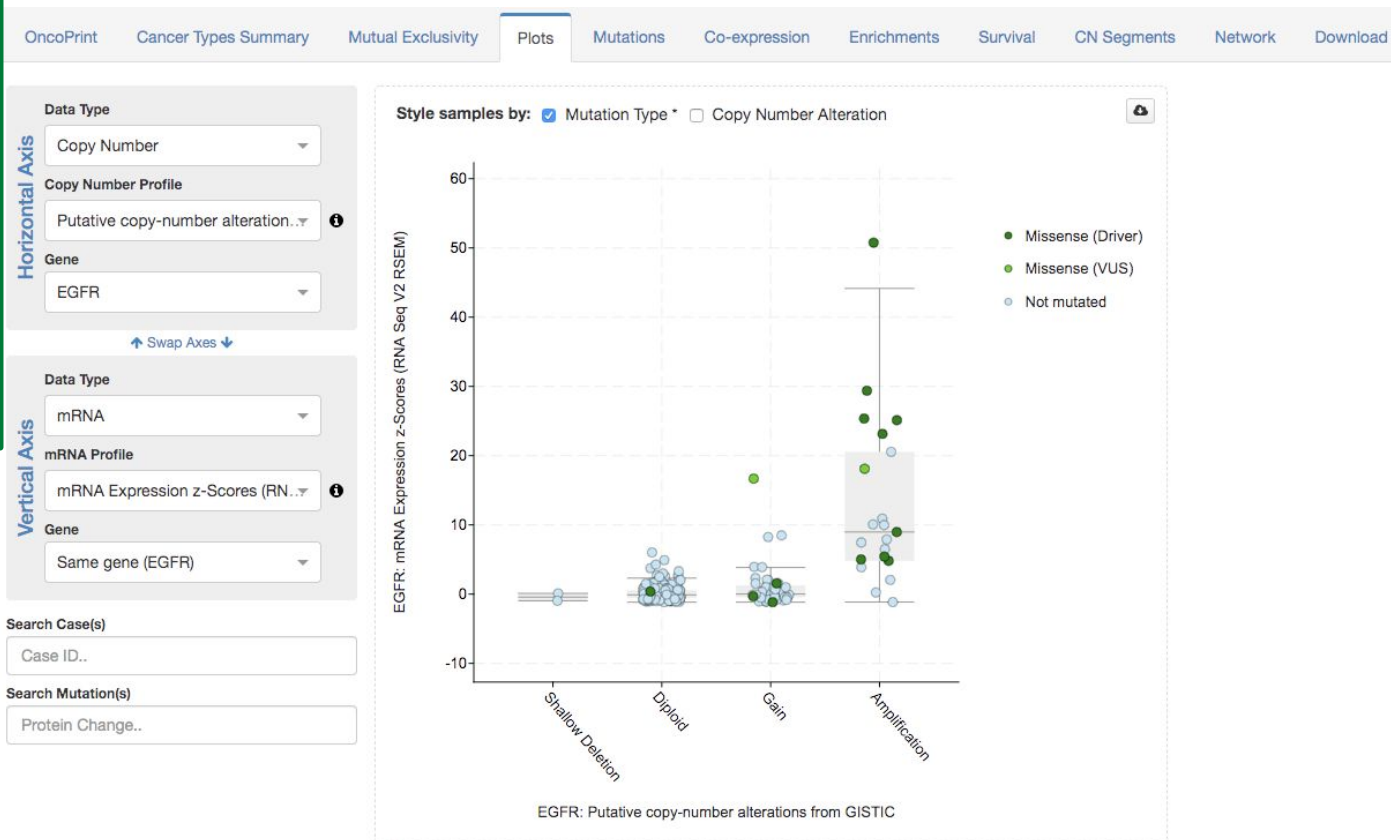
Driver vs. VUS
annotation settings
are in the Mutations
menu of OncoPrint.

* 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.

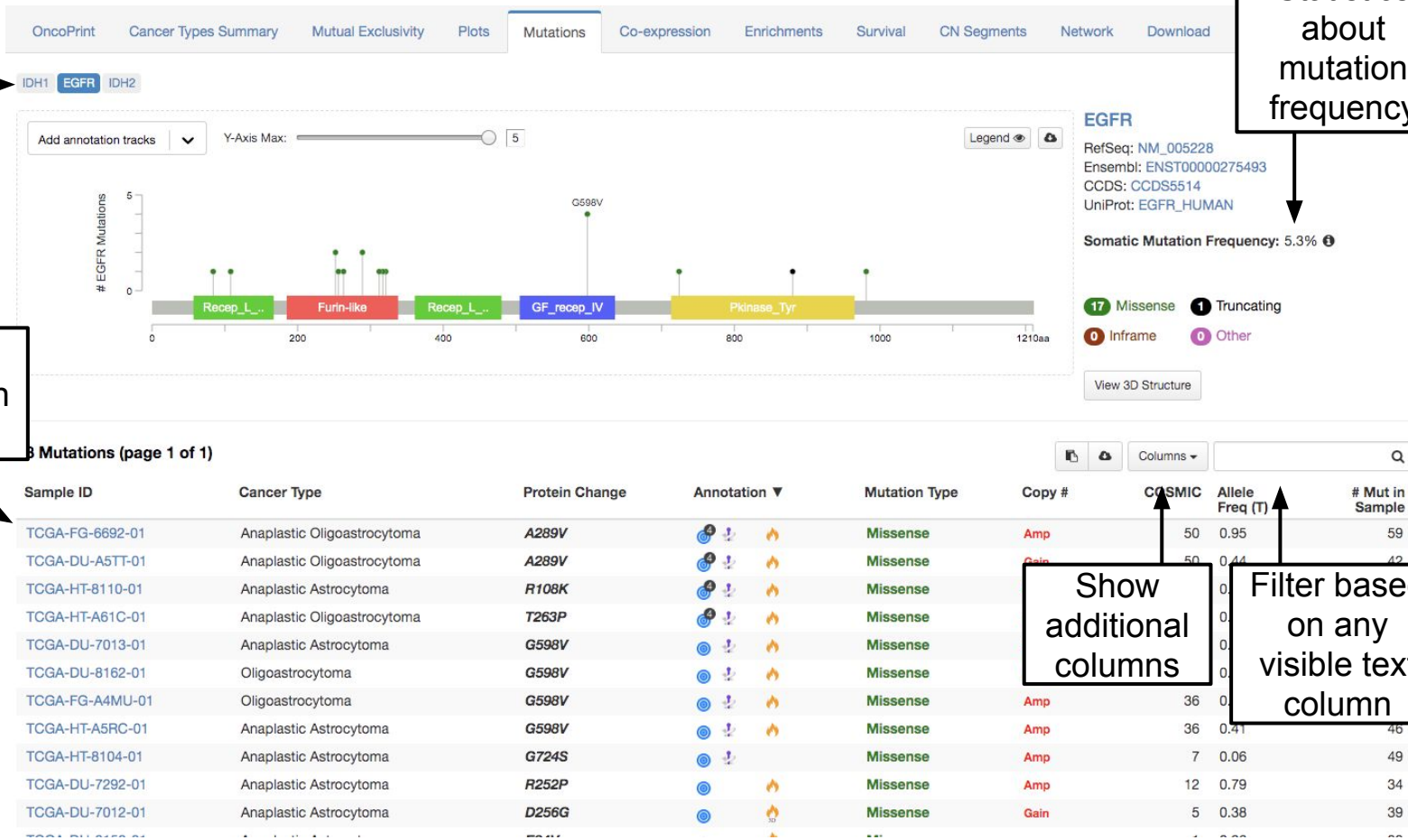
Mutations

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

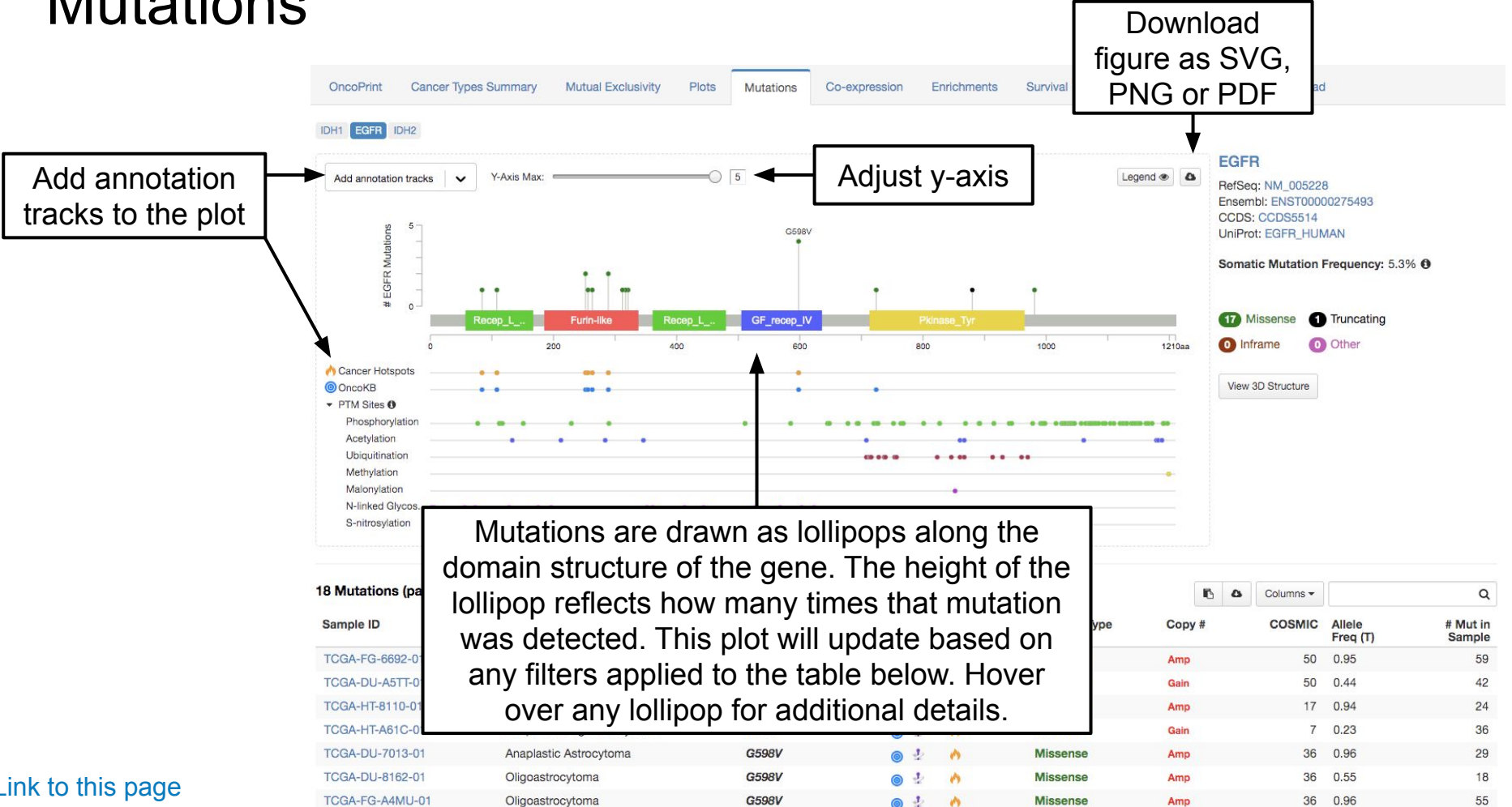
Statistics about mutation frequency



Show additional columns

Filter based on any visible text column

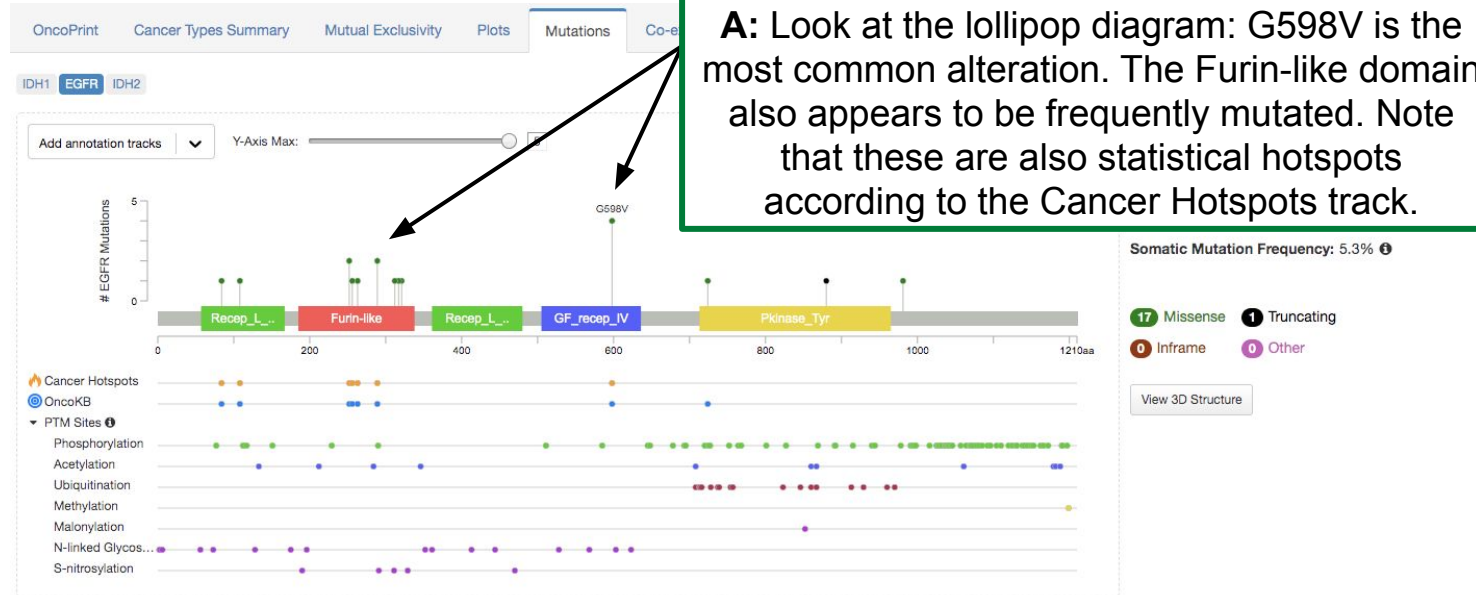
Mutations



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.



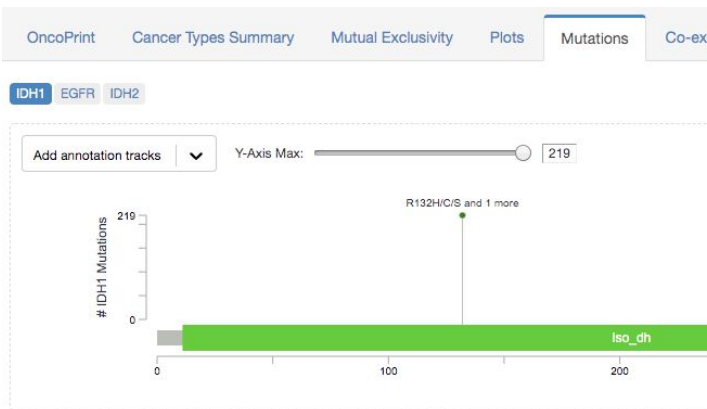
18 Mutations (page 1 of 1)


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


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				Missense	ShallowDel	4964	0.48	24
TCGA-HT-7855-01	Anaplastic Astrocytoma	R132C				Missense	DeepDel	4964	0.46	30
TCGA-DB-A4XD-01								4964	0.39	28
TCGA-DB-A4XF-01								4964	0.40	17
TCGA-P5-A5EZ-01								4964	0.24	25
TCGA-P5-A5F4-01								4964	0.31	24
TCGA-DB-A64S-01						Missense	Diploid	4964	0.31	10
TCGA-DB-5276-01	Oligoastrocytoma	R132C				Missense	Diploid	4964	0.20	13

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)

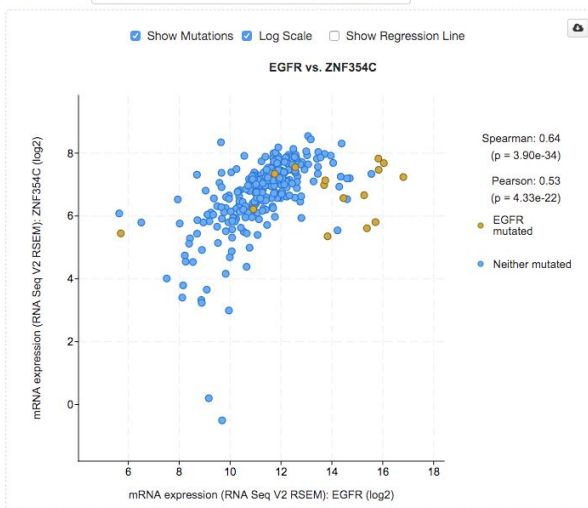
Show Any Correlation

Enter gene or cytoband...

Correlated Gene	Cytoband	Spearman's Correlation	p-Value	q-Value
ZNF354C	5q35.3	0.641	3.90e-34	4.32e-30
DHX33	17p13.2	0.641	4.30e-34	4.32e-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 20056

Show more

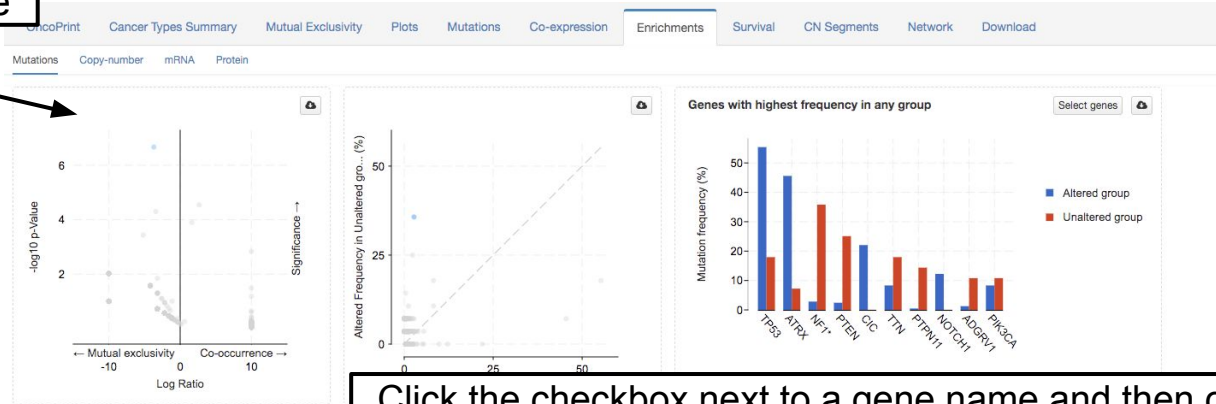


Enrichments

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).

Select type of data to examine

Hover over a dot to see the gene name



Click the checkbox next to a gene name and then click this button to re-run the query with a gene added.

Select sample-level or patient-level analysis

Mutations

Add checked genes to query (none checked)

this button to re-run the query with a gene added

Sample-level enrichments

▼

Select enriched groups

▼

☐ Significant only

Columns

▼

Gene

Cytoband

Altered group

Unaltered group

Co-occurrence Pattern

Log Ratio

p-Value

q-Value ▲

Tendency

☐ NF1

17q11.2

7 (2.75%)

10 (35.71%)

-3.70

2.13e-7

1.005e-3

Mutual exclusivity

☐ ATRX

Xq21.1

116 (45.49%)

2 (7.14%)

2.67

2.863e-5

0.0674

☐ PTEN

10q23.31

6 (2.35%)

7 (25.00%)

-3.41

5.010e-5

0.0787

☐ TP53

17p13.1

141 (55.29%)

5 (17.86%)

1.63

1.272e-4

0.150

☐ PTPN11

12q24.13

1 (0.39%)

4 (14.29%)

-5.19

3.644e-4

0.343

☐ CIC

19q13.2

56 (21.96%)

0 (0.00%)

>10

1.460e-3

0.767

☐ BPIFB4

20q11.21

0 (0.00%)

2 (7.14%)

<-10

9.473e-3

0.767

☐ BRAF

7q34

0 (0.00%)

2 (7.14%)

<-10

9.473e-3

0.767

☐ DCLK3

3p22.2

0 (0.00%)

2 (7.14%)

<-10

9.473e-3

0.767

☐ DYSF

2p13.2

0 (0.00%)

2 (7.14%)

<-10

9.473e-3

0.767

☐ KIF13B

8p12

0 (0.00%)

2 (7.14%)

<-10

9.473e-3

0.767

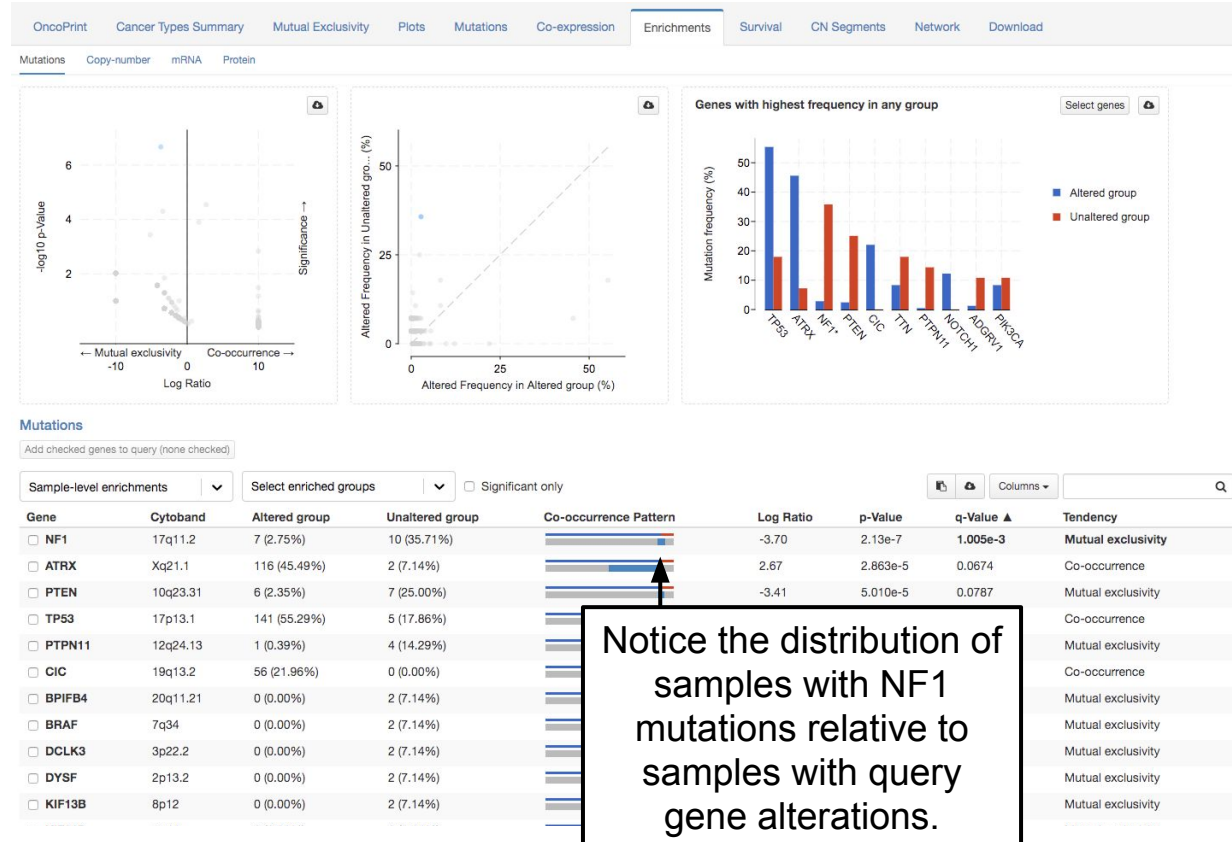
Click on header to filter over the gene name for about how many calls

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

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.

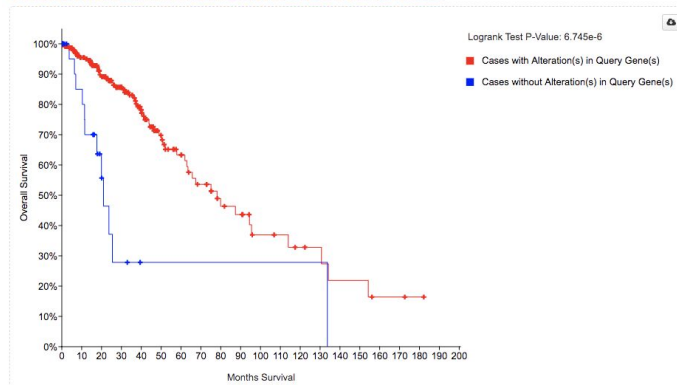


Survival

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 (Overall patient survival status.)

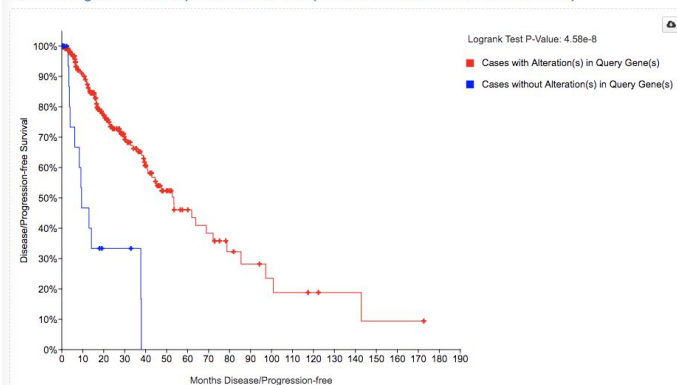


	Number of Cases, Total	Number of Cases, Deceased	Median Months Survival
Cases with Alteration(s) in Query Gene(s)	254	60	78.15
Cases without Alteration(s) in Query Gene(s)	28	12	20.99

Download plots or data

Number of cases in the plot

Disease/Progression-free Kaplan-Meier Estimate (Disease free status since initial treatment.)



	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).



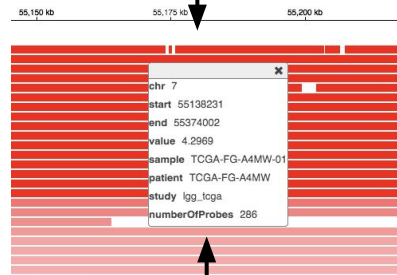
Plots for each gene appear on a separate tab.

Toggle track labels, a vertical line marking the center of the viewing screen, and a vertical line that moves with your cursor. Use to zoom in or out.

Click for track settings, including expanding the height of each sample (see below)

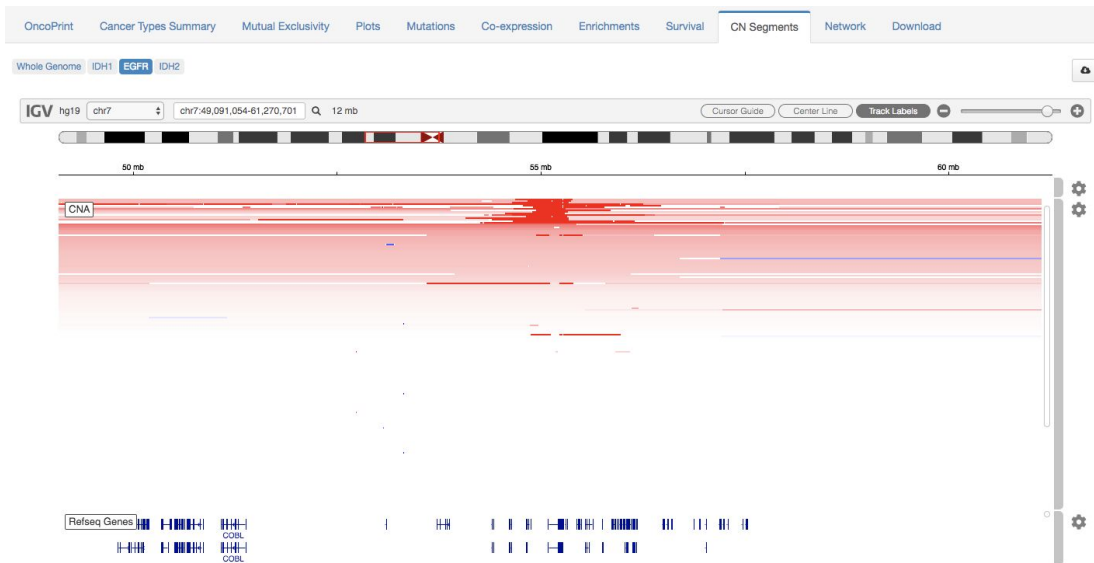
Each row is a single sample

Gene structures



Click on a read for details

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

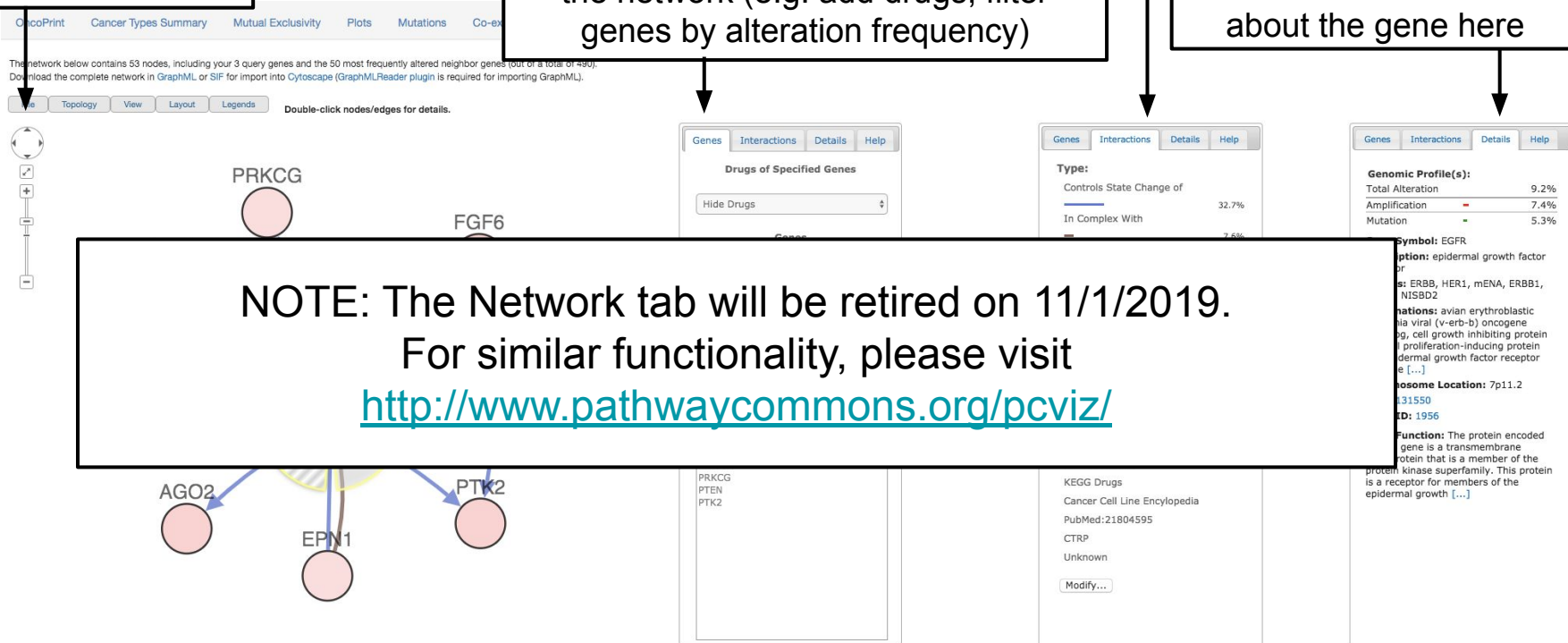
Visualize biological interaction networks centered on your query genes, with color-coding and filter options based on the frequency of genomic alterations in each gene. Click on the “Help” tab for a more detailed explanation.

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

Change zoom and move around network

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

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



Download

Download data or copy lists of samples.

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

Copy-number Alterations (OQL is not in effect)	Tab Delimited Format	Transposed Matrix
Mutations (OQL is not in effect)	Tab Delimited Format	Transposed Matrix
Altered samples: List of samples with alterations	Copy Download	Query Virtual Study
Unaltered samples: List of samples without any alteration	Copy Download	Query Virtual Study
Sample matrix: List of all samples where 1=altered and 0=unaltered	Copy Download	
Relative linear copy-number values 🔗	Tab Delimited Format	Transposed Matrix
mRNA expression (microarray) 🔗	Tab Delimited Format	Transposed Matrix
mRNA Expression z-Scores (microarray) 🔗	Tab Delimited Format	Transposed Matrix
mRNA expression (RNA Seq V2 RSEM) 🔗	Tab Delimited Format	Transposed Matrix
mRNA Expression z-Scores (RNA Seq V2 RSEM) 🔗	Tab Delimited Format	Transposed Matrix
Methylation (HM450) 🔗	Tab Delimited Format	Transposed Matrix
Protein expression (RPPA) 🔗	Tab Delimited Format	Transposed Matrix
Protein expression Z-scores (RPPA) 🔗	Tab Delimited Format	Transposed Matrix

Download queried data types for the queried genes.

Download all other data types for the queried 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

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	EGFR	IDH2
lgg_tcga	TCGA-CS-6290-01	TCGA-CS-6290	1	R132H	no alteration	no alteration
lgg_tcga	TCGA-DU-5849-01	TCGA-DU-5849	1	no alteration	no alteration	R172K
lgg_tcga	TCGA-DU-5852-01	TCGA-DU-5852	1	no alteration	AMP, R252C, 1981F	no alteration
lgg_tcga	TCGA-DU-5854-01	TCGA-DU-5854	1	no alteration	AMP	no alteration
lgg_tcga	TCGA-DU-5855-01	TCGA-DU-5855	1	R132H	no alteration	no alteration
lgg_tcga	TCGA-DU-5870-01	TCGA-DU-5870	1	R132H	no alteration	no alteration
lgg_tcga	TCGA-DU-5871-01	TCGA-DU-5871	1	R132G	no alteration	no alteration
lgg_tcga	TCGA-DU-5872-01	TCGA-DU-5872	1	R132H	no alteration	no alteration

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 (OQL is not in effect)	Tab Delimited Format	Transposed Matrix		
Mutations (OQL is not in effect)	Tab Delimited Format	Transposed Matrix		
Altered samples: List of samples with alterations	Copy	Download	Query	Virtual Study
Unaltered samples: List of samples without any alteration	Copy	Download	Query	Virtual Study
Sample matrix: List of all samples where 1=altered and 0=unaltered	Copy	Download		
Relative linear copy-number values	Tab Delimited Format	Transposed Matrix		
mRNA expression (microarray)	Tab Delimited Format	Transposed Matrix		
mRNA Expression z-Scores (microarray)	Tab Delimited Format	Transposed Matrix		
mRNA expression (RNA Seq V2 RSEM)	Tab Delimited Format	Transposed Matrix		
mRNA Expression z-Scores (RNA Seq V2 RSEM)	Tab Delimited Format	Transposed Matrix		
Methylation (HM450)	Tab Delimited Format	Transposed Matrix		
Protein expression (RPPA)	Tab Delimited Format	Transposed Matrix		
Protein expression Z-scores (RPPA)	Tab Delimited Format	Transposed Matrix		

Gene Alteration Frequency

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Showing 1-3 of 3

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lgg_tcga	TCGA-DU-5849-01	TCGA-DU-5849	1	no alteration	no alteration	R172K
lgg_tcga	TCGA-DU-5852-01	TCGA-DU-5852	1	no alteration	AMP, R252C, 1981F	no alteration
lgg_tcga	TCGA-DU-5854-01	TCGA-DU-5854	1	no alteration	AMP	no alteration
lgg_tcga	TCGA-DU-5855-01	TCGA-DU-5855	1	R132H	no alteration	no alteration
lgg_tcga	TCGA-DU-5870-01	TCGA-DU-5870	1	R132H	no alteration	no alteration
lgg_tcga	TCGA-DU-5871-01	TCGA-DU-5871	1	R132G	no alteration	no alteration
lgg_tcga	TCGA-DU-5872-01	TCGA-DU-5872	1	R132H	no alteration	no alteration

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

List of samples that have no alterations in any query genes

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

Advanced feature: use these lists to build a custom sample list to run a new query, to create [virtual studies](#) or to build [custom groups](#).

Questions?

Check out our other tutorials
or email us at:

cbioportal@googlegroups.com