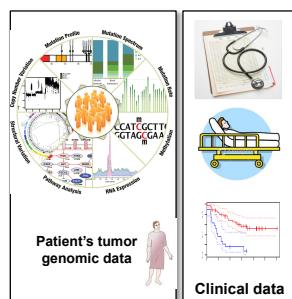
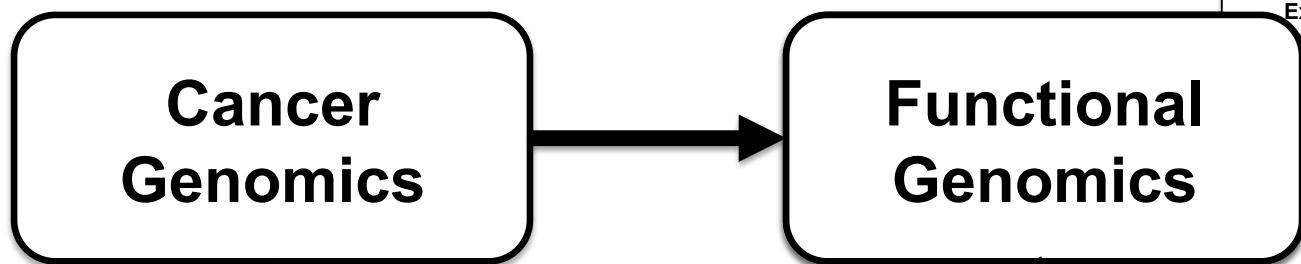
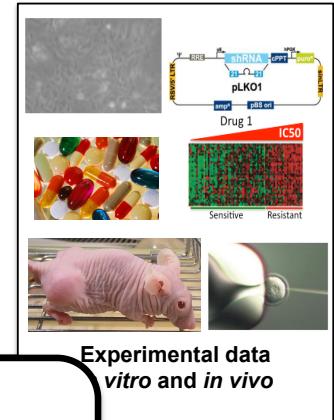
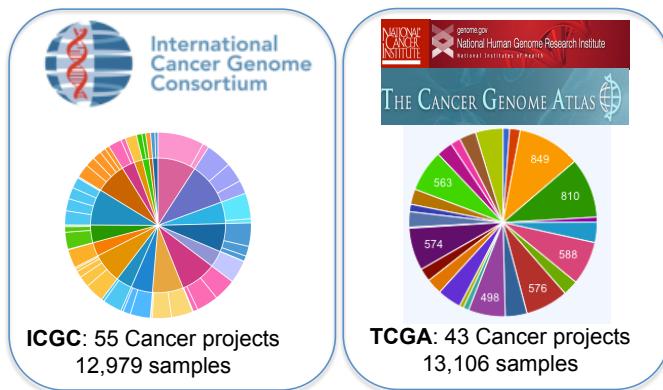


Cancer Genomics Resources

Databases

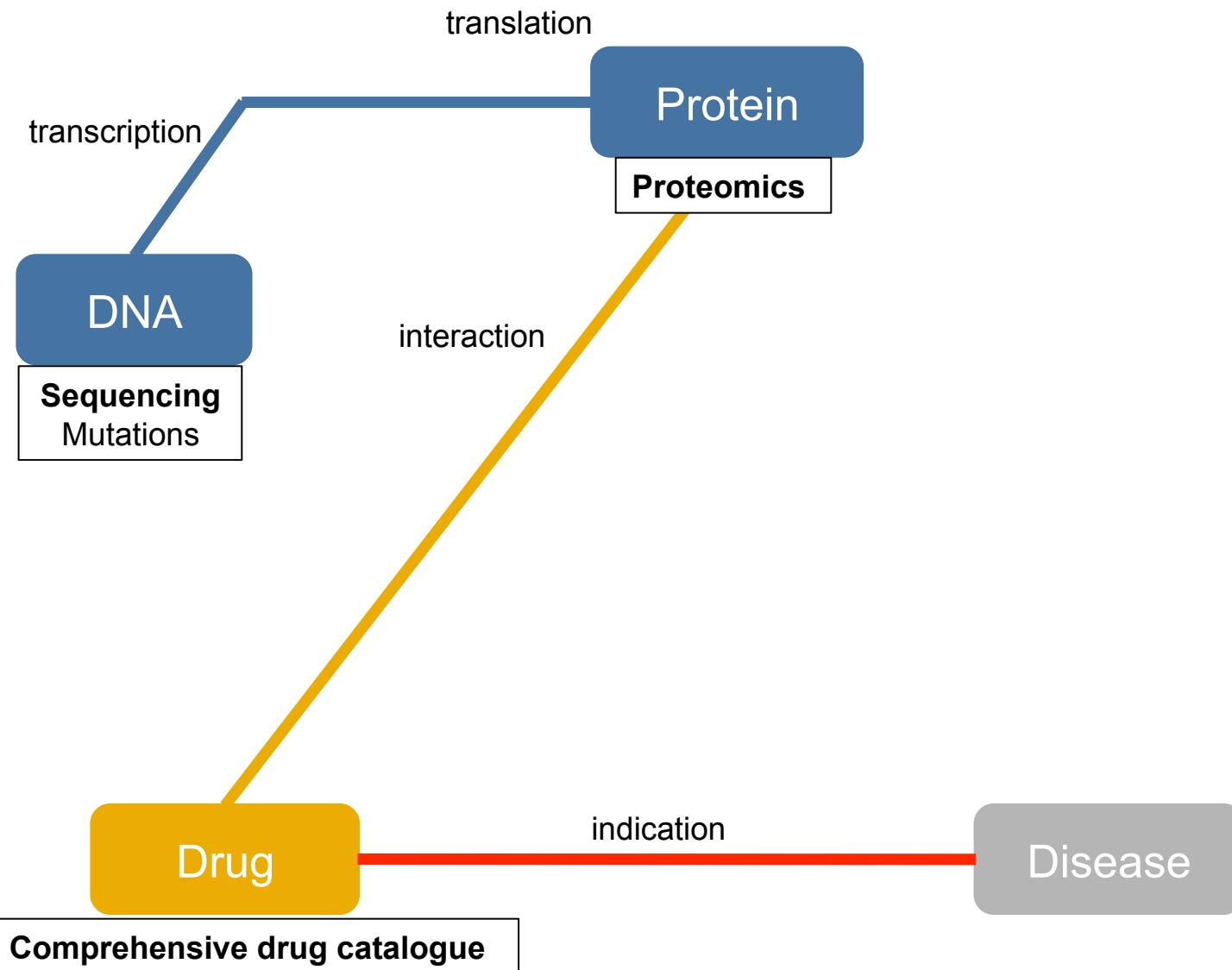
Tools

Translational Cancer Genomics



Discovery of new biomarkers

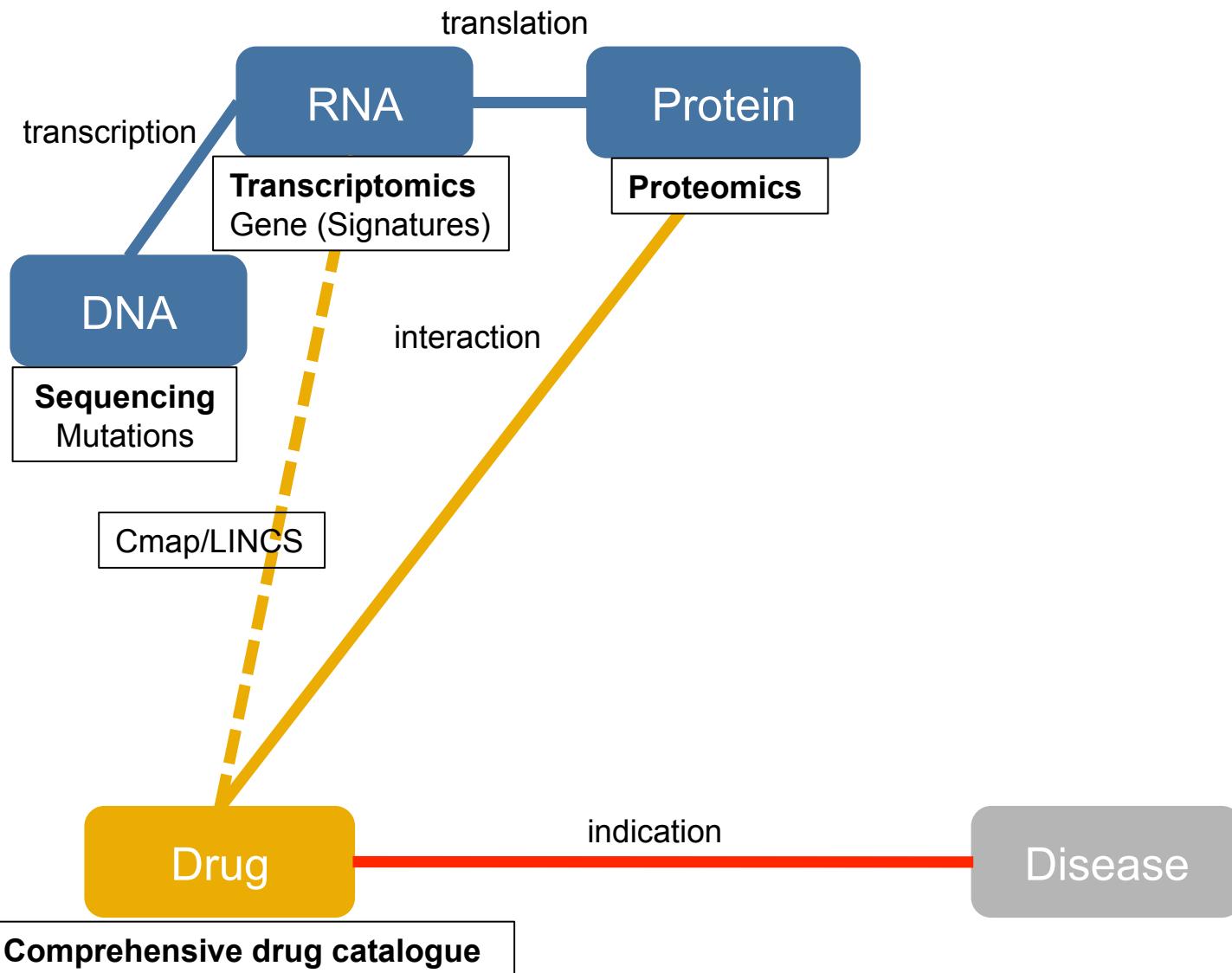
To identify new Drug-Gene/Protein associations



Adapted from Closet et al

Discovery of new biomarkers

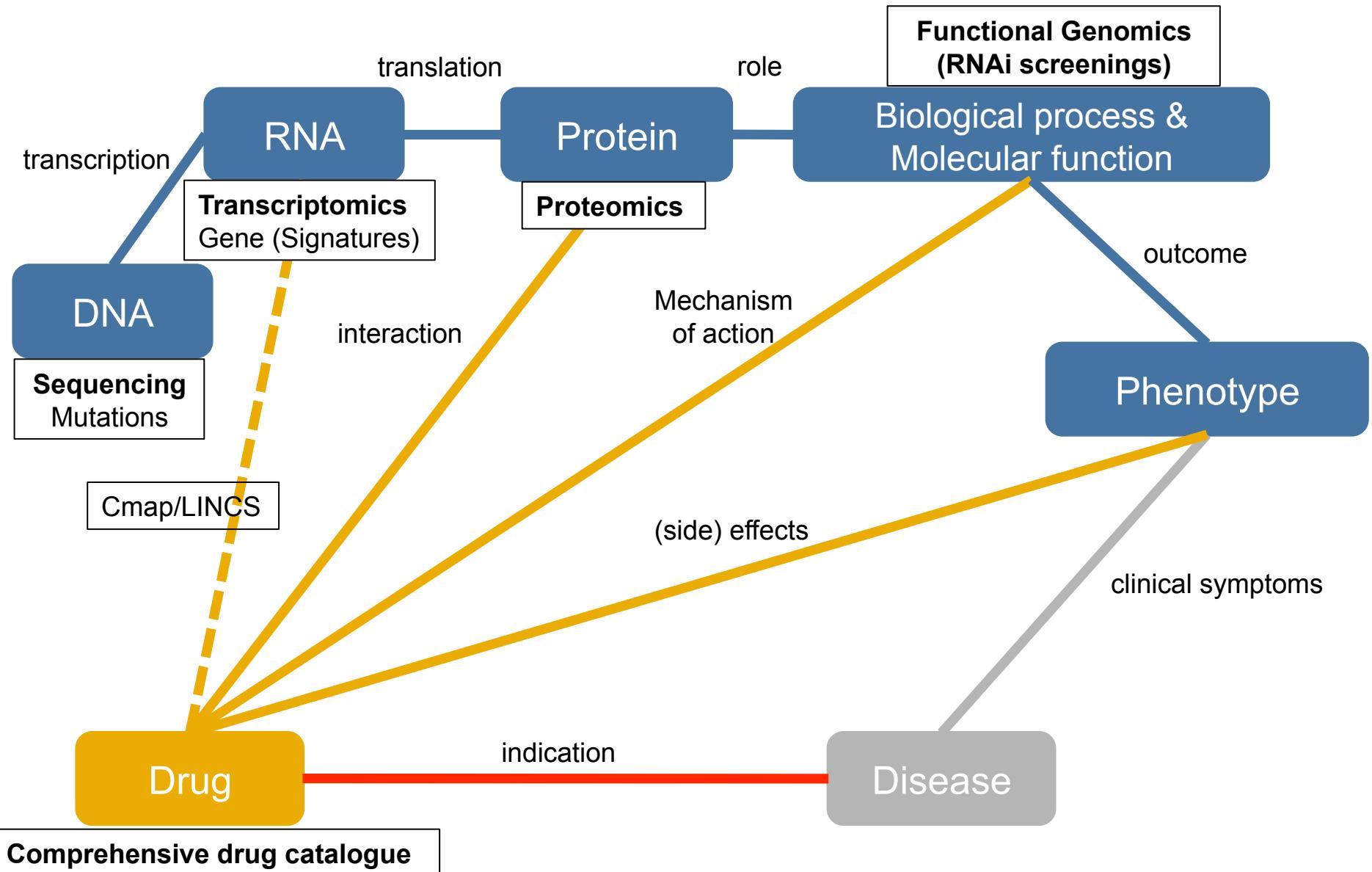
To identify new Drug-Gene/Protein/Signature/Module/Network associations



Adapted from Closet et al

Discovery of new biomarkers

To identify new Drug-Gene/Protein/Signature/Module/Network associations



Adapted from Closet et al

NCBI Gene

<http://www.ncbi.nlm.nih.gov/gene/>

The screenshot shows the NCBI Gene search interface. At the top, there's a blue header bar with the NCBI logo, 'Resources' (with a dropdown arrow), and 'How To' (with a dropdown arrow). Below the header, the word 'Gene' is selected in a dropdown menu next to a search input field. Below the search field is a link 'Advanced'. At the bottom of the search area, there are links for 'Full Report' and 'Send to:' followed by a dropdown arrow.

EGFR epidermal growth factor receptor [*Homo sapiens* (human)]

Gene ID: 1956, updated on 29-Nov-2015

The screenshot shows the detailed summary page for the EGFR gene. At the top, there's a 'Summary' tab and some icons. Below the tabs, there are several data entries:

- Official Symbol**: EGFR provided by HGNC
- Official Full Name**: epidermal growth factor receptor provided by HGNC
- Primary source**: HGNC:HGNC:3236
- See related**: Ensembl:ENSG00000146648; HPRD:00579; MIM:131550; Vega:OTTHUMG00000023661
- Gene type**: protein coding
- RefSeq status**: REVIEWED
- Organism**: *Homo sapiens*
- Lineage**: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo
- Also known as**: ERBB; HER1; mENA; ERBB1; PIG61; NISBD2
- Summary**: 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 factor family. EGFR is a cell surface protein that binds to epidermal growth factor. Binding of the protein to a ligand induces receptor dimerization and tyrosine autophosphorylation and leads to cell proliferation. Mutations in this gene are associated with lung cancer. Multiple alternatively spliced transcript variants that encode different protein isoforms have been found for this gene. [provided by RefSeq, Jul 2010]
- Orthologs**: mouse [all](#)

Ensembl

http://www.ensembl.org/

Human (GRCh38.p3) ▾ Location: 7:55,019,021-55,256,620 Gene: EGFR

Login/Register

Gene-based displays

- [-] **Summary**
- [-] Splice variants
- [-] Transcript comparison
- [-] Supporting evidence
- [-] Gene alleles
- [-] **Sequence**
 - [+] Secondary Structure
- [-] External references
- [-] Regulation
- [-] Comparative Genomics
 - [-] Genomic alignments
 - [-] Gene tree
 - [-] Gene gain/loss tree
 - [-] Orthologues
 - [-] Paralogues
 - [-] Ensembl protein families
- [-] Phenotype
- [-] Genetic Variation
 - [+] Variant table
 - [-] Variant image
 - [-] Structural variants
- [-] External data
 - [+] Gene expression
 - [-] Personal annotation

Gene: EGFR ENSG00000146648

Description epidermal growth factor receptor [Source:HGNC Symbol;Acc:[HGNC:3236](#)]

Synonyms ERBB, ERBB1

Location [Chromosome 7: 55,019,021-55,256,620](#) forward strand.
GRCh38:CM000669.2

About this gene This gene has 11 transcripts ([splice variants](#)), [77 orthologues](#), [13 paralogues](#), is a member of [1 Ensembl protein family](#) and is associated with [14 phenotypes](#).

Transcripts [Show transcript table](#)

Summary [?](#)

Name [EGFR](#) (HGNC Symbol)

This gene is a member of the Human CCDS set: [CCDS47587.1](#), [CCDS5514.1](#), [CCDS5515.1](#), [CCDS5516.1](#)

UniProtKB This gene has proteins that correspond to the following Uniprot identifiers: [P00533](#)

RefSeq Overlapping RefSeq Gene ID [1956](#) matches and has similar biotype of protein_coding

LRG [LRG_304](#) provides a stable genomic reference framework for describing sequence variants for this gene

Ensembl version ENSG00000146648 15

GeneCards

http://www.genecards.org/

FREE for academic non-profit institutions. Other users need a Commercial license

INSTITUTE OF SCIENCE  LifeMap SCIENCES 

Keywords ▾ Search Term  Advanced

Home User Guide Analysis Tools ▾ News And Views About ▾ My Genes Log In / Sign Up

EGFR Gene (Protein Coding)

Epidermal Growth Factor Receptor

GCID: GC07P055019  GIFTs: 74 

Jump to section [Aliases](#) [Disorders](#) [Domains](#) [Drugs](#) [Expression](#) [Function](#) [Genomics](#) [Localization](#) [Orthologs](#) [Paralogs](#) [Pathways](#) [Products](#) [Proteins](#) [Publications](#) [Sources](#) [Summaries](#) [Transcripts](#) [Variants](#)

 Proteins & Enzymes
Antibodies Assays & Kits

 Proteins Antibodies Assays
Genes shRNA Primers
CRISPR

 Genes Peptides Proteins
CRISPR

Aliases for EGFR Gene

Aliases for EGFR Gene

Epidermal Growth Factor Receptor ^{2 3}
Receptor Tyrosine-Protein Kinase ErbB-1 ^{3 4}
Erb-B2 Receptor Tyrosine Kinase 1 ^{2 3}
Proto-Oncogene C-ErbB-1 ^{3 4}
EC 2.7.10.1 ^{4 63}
ERBB1 ^{3 4}
ERBB ^{3 4}

Erythroblastic Leukemia Viral (V-Erb-B) Oncogene Homolog (Avian) ²
Avian Erythroblastic Leukemia Viral (V-Erb-B) Oncogene Homolog ³
Cell Proliferation-Inducing Protein 61 ³
Cell Growth Inhibiting Protein 40 ³
EC 2.7.10 ⁶³



GenScript
CRISPR gRNA
constructs

Tumor Protein Atlas

<https://www.proteinatlas.org/>

The image displays two side-by-side screenshots of the Tumor Protein Atlas interface, comparing the original version on the left with a modified version on the right.

Left Screenshot (Original Version):

- Header:** THE HUMAN PROTEIN ATLAS ABOUT HELP BLOG
- Search Bar:** AMBRA1
- Gene Summary:** AMBRA1 (Autophagy/becn1 regulator 1)
- General Information:**
 - Gene name: AMBRA1
 - Gene description: Autophagy/becn1 regulator 1
 - Protein class: Predicted intracellular proteins
 - Predicted localization: Intracellular
 - Number of transcripts: 7
- HPA Pathology:** Antibody validation, Dictionary, Tissue proteome
- HPA Pathology Summary:** RNA expression (TPM) and Protein expression (score) across various tissues.
- Prognostic Summary:** Kaplan-Meier survival plot for Renal cancer.
- RNA Expression Overview:** Box plot showing RNA expression levels across various cancer datasets.
- Protein Expression:** Representative IHC images for Colorectal cancer, Breast cancer, Prostate cancer, Lung cancer, and Liver cancer.
- Protein Expression Overview:** Bar chart showing protein expression scores across various cancers.

Right Screenshot (Modified Version):

- Header:** THE HUMAN PROTEIN ATLAS ABOUT HELP BLOG
- Search Bar:** AMBRA1
- Gene Summary:** AMBRA1 (Autophagy/becn1 regulator 1)
- General Information:**
 - Gene name: AMBRA1
 - Gene description: Autophagy/becn1 regulator 1
 - Protein class: Predicted intracellular proteins
 - Predicted localization: Intracellular
 - Number of transcripts: 7
- HPA Pathology:** Antibody validation, Dictionary, Tissue proteome
- HPA Pathology Summary:** RNA expression (TPM) and Protein expression (score) across various tissues.
- Prognostic Summary:** Kaplan-Meier survival plot for Renal cancer.
- RNA Expression Overview:** Box plot showing RNA expression levels across various cancer datasets.
- Protein Expression:** Representative IHC images for various tissues including Cervical, Lung, Liver, Kidney, and Testis.
- Protein Expression Overview:** Bar chart showing protein expression scores across various cancers.

GTEx

<http://www.gtexportal.org/>

Correlations between genotype and tissue-specific gene expression levels will help identify regions of the genome that influence whether and how much a gene is expressed

CANCER BROWSERS

cBio Portal for Cancer genomics

<http://www.cbiportal.org/>

cBioPortal
for Cancer Genomics

Visualize, analyze, discover.

Memorial Sloan Kettering Cancer Center.

HOME DATA SETS WEB API R/MATLAB TUTORIALS FAQ NEWS TOOLS ABOUT VISUALIZE YOUR DATA

The cBioPortal for Cancer Genomics provides **visualization**, **analysis** and **download** of large-scale **cancer genomics** data sets. [Pin it](#)

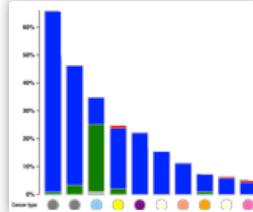
Please adhere to [the TCGA publication guidelines](#) when using TCGA data in your publications.

Please cite [Gao et al. Sci. Signal. 2013](#) & [Cerami et al. Cancer Discov. 2012](#) when publishing results based on cBioPortal.

Query Download Data

Select Cancer Study:

Search... No studies selected.

- All (105)
 - Adrenal Gland (1)
 - Adrenocortical Carcinoma (1)
 - Adrenocortical Carcinoma (TCGA, Provisional) 92 samples
 - Biliary Tract (4)
 - Cholangiocarcinoma (3)
 - Intrahepatic Cholangiocarcinoma (Johns Hopkins University, Nature Genetics 2013) 40 samples

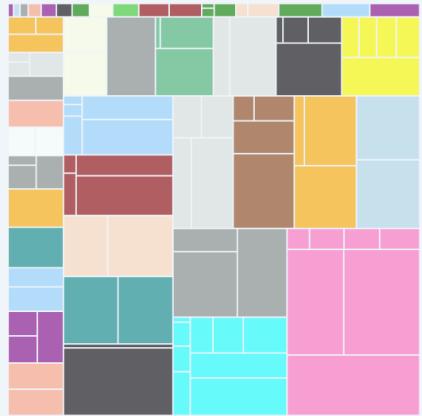
What's New

New Jobs available at Dana-Farber to work on cBioPortal
Sign up for low-volume email news alerts:
 [Subscribe](#)

Or follow us @cbiportal on Twitter

Data Sets

The Portal contains **105 cancer studies**. [\[Details\]](#)



Example Queries

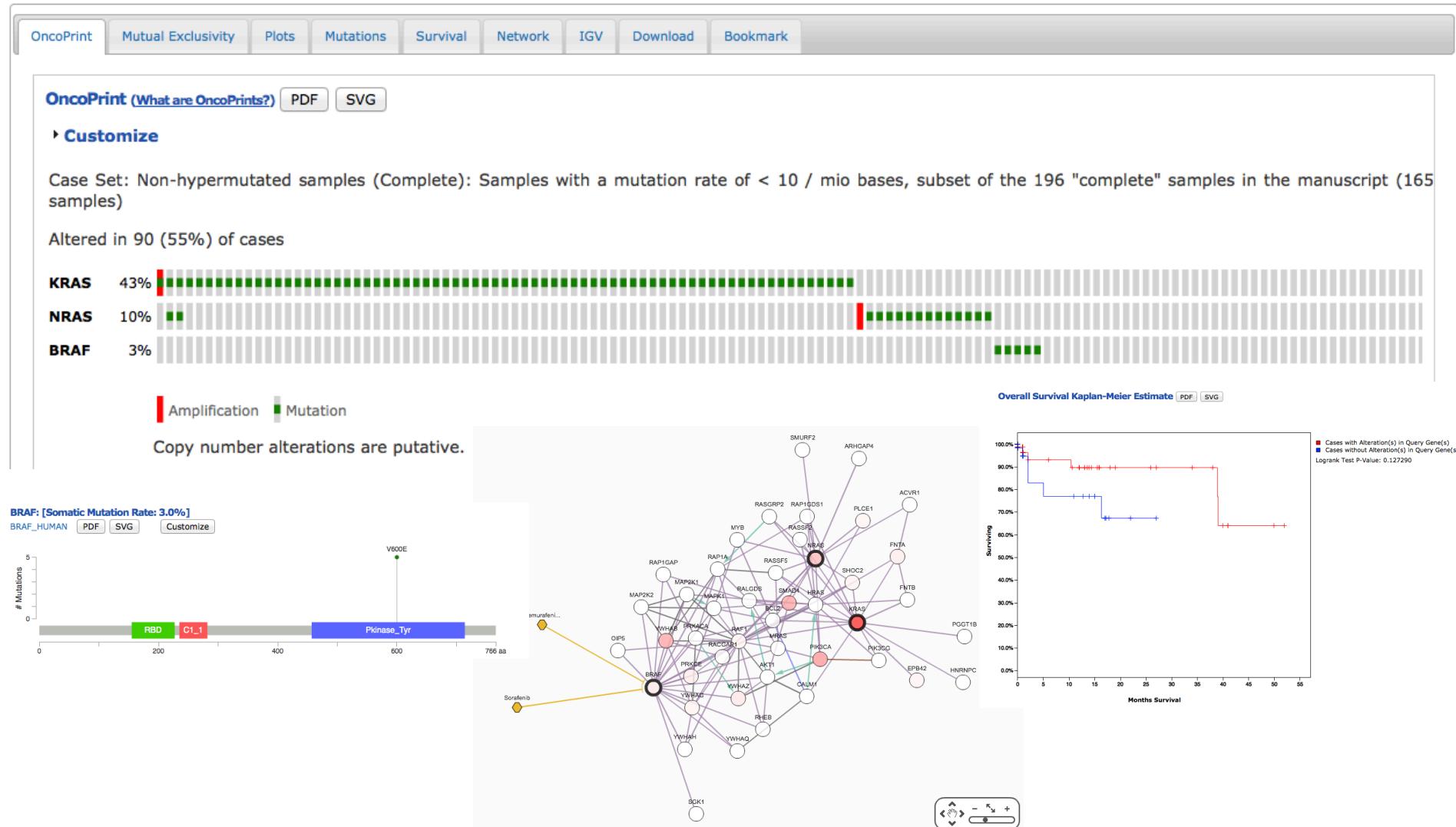
RAS/RAF alterations in colorectal cancer

RAS/RAF alterations in colorectal cancer

Gene Set / Pathway is altered in 54.5% of all cases.

Colon and Rectum Adenocarcinoma (TCGA, Nature 2012)/Non-hypermutated samples (Complete): (165)/User-defined List/3genes

► Modify Query



International Cancer Genome Consortium

<http://dcc.icgc.org/>



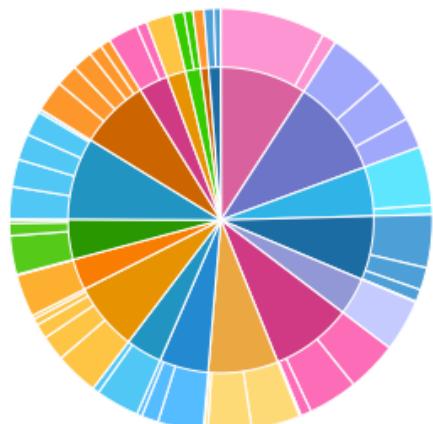
ICGC Data Portal

[Cancer Projects](#)[Advanced Search](#)[Data Analysis](#)[Data Repository](#)

eg. BRAF, KRAS G12D, DO35100, MU7870, apoptosis, Cancer Gene Census, GO:0016049

Data Release 19
June 16th, 2015

Donor Distribution by Primary Site



Cancer projects	55
Cancer primary sites	21
Donors	12,979
Simple somatic mutations	16,459,160
Mutated genes	57,543

COSMIC

<http://cancer.sanger.ac.uk/cosmic/>



Catalogue of somatic mutations in cancer

Home ▾ About ▾ Licensing ▾ Data Download ▾ News ▾ Help ▾ Enter search here... Login ▾

COSMIC v75

eg: Braf, COLO-829, Carcinoma, V600E, BRCA-UK, Campbell **SEARCH**

R Resources

Key COSMIC resources

- Cell Lines Project
- COSMIC Whole Genomes
- Cancer Gene Census
- Drug Sensitivity
- Mutational Signatures
- GRCh37 Cancer Archive

T Tools

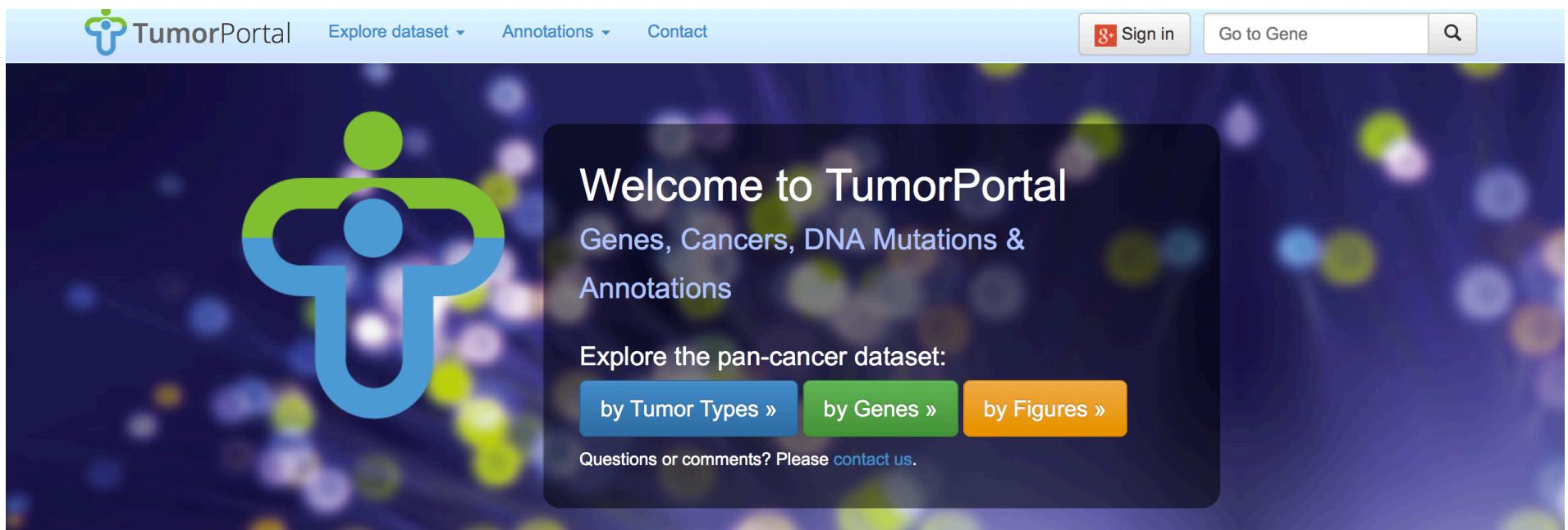
Additional tools to explore COSMIC

- Cancer Browser
- Genome Browser
- CONAN
- Beacon
- COSMIC Mart

Genomic Landscape of Cancer

TumorPortal

<http://www.tumorportal.org/>



The screenshot shows the TumorPortal homepage. At the top left is the TumorPortal logo. To its right are navigation links: "Explore dataset ▾", "Annotations ▾", and "Contact". On the far right are "Sign in" (with a Google+ icon), "Go to Gene", and a search icon. The main content area has a dark background with a blue and green abstract graphic on the left. A central box contains the text "Welcome to TumorPortal" and "Genes, Cancers, DNA Mutations & Annotations". Below this is the heading "Explore the pan-cancer dataset:" followed by three buttons: "by Tumor Types ▾", "by Genes ▾", and "by Figures ▾". At the bottom of the central box is the text "Questions or comments? Please contact us.".

Explore dataset by tumor types

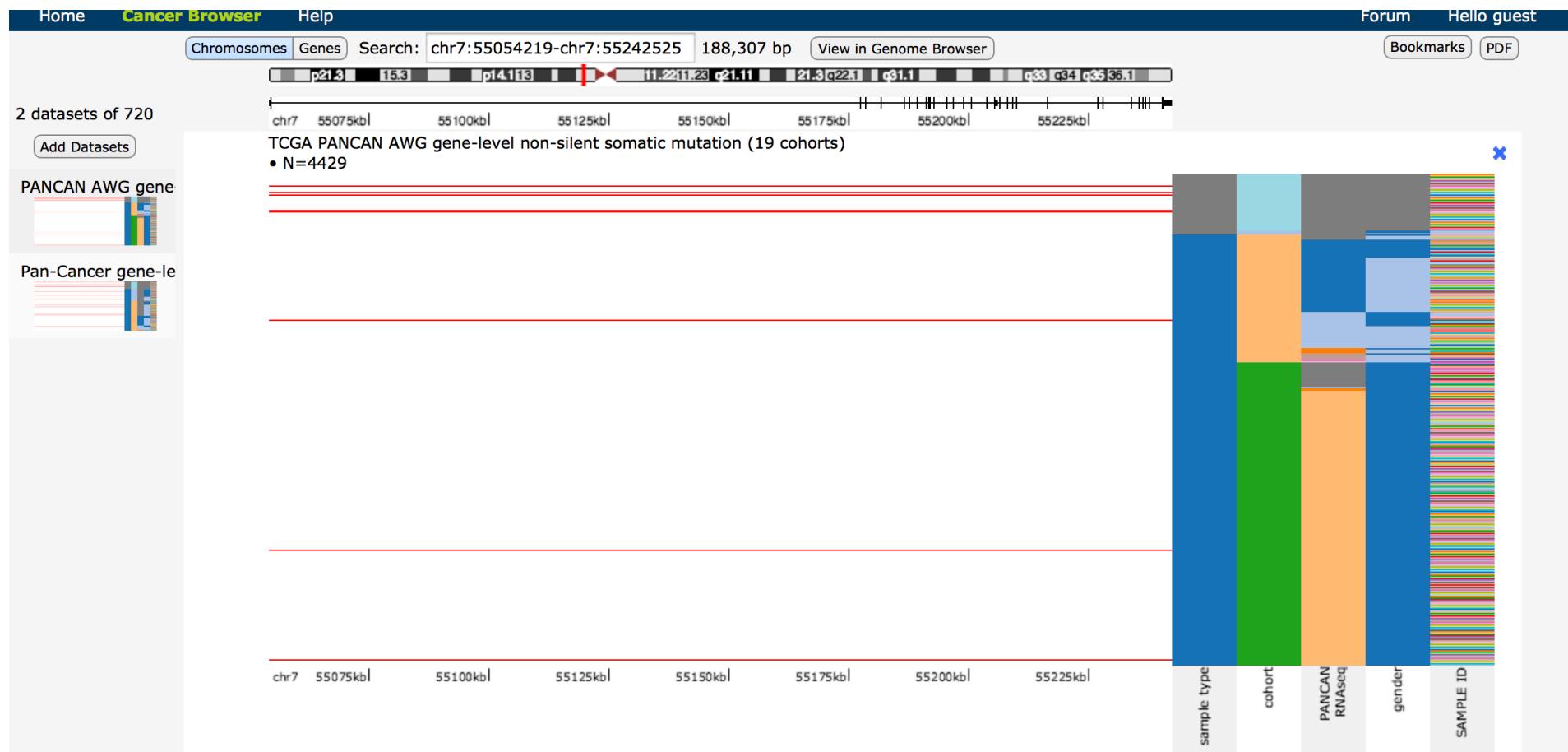
Click on a tumor type to see what genes are significantly mutated in it (and other details).

[Show Annotation Activity](#)

Acute myeloid leukemia AML 196 patients	Bladder BLCA 99 patients	Breast BRCA 892 patients	Carcinoid CARC 54 patients	Chronic lymphocytic leukemia CLL 159 patients	Colorectal CRC 233 patients	Diffuse large B-cell lymphoma DLBCL 58 patients	Esophageal adenocarcinoma ESO 141 patients	Glioblastoma multiforme GBM 291 patients
--	---------------------------------------	---------------------------------------	---	--	--	--	---	---

Cancer Genome Browser UCSC

<https://genome-cancer.ucsc.edu/>



Integrative Onco Genomics

<https://www.intogen.org/>



intOGen Integrative Onco Genomics

e.g. Recurrence of TP53 mutations

Search example | Show more examples

Release 2014.12

Plot Table

IntOGen Mutations 2014.12

Cancer types and projects chart

Cancer Types 28
Projects 48
Samples 6792
Somatic mutations 1341752

Coding sequence mutations (CSMs) 21648
in driver genes 1341706
in all genes

Protein affecting mutations (PAMs) 18649
in driver genes 603770
in all genes

Cloud Plot Table

Mutational cancer driver genes: 459

This driver cloud represents the most recurrently mutated cancer driver genes. The size of the gene symbol is relative to the count of samples with PAMs.

Harmonizome

http://amp.pharm.mssm.edu/Harmonizome//



Harmonizome

Search for genes or proteins and their functional terms extracted and organized from over a hundred publicly available resources. [Learn more.](#)

Example searches

achilles STAT3 breast cancer

Enrichr

<http://amp.pharm.mssm.edu/Enrichr/>



Analyze

What's New?

Libraries

Find a Gene

About

Help

[Login](#) | [Register](#)

8,068,311 lists analyzed

232,994 terms

125 libraries

Input data

Choose an input file to upload. Either in BED format or a list of genes. For a quantitative set, add a comma and the level of membership of that gene. The membership level is a number between 0.0 and 1.0 to represent a weight for each gene, where the weight of 0.0 will completely discard the gene from the enrichment analysis and the weight of 1.0 is the maximum.

Try an example [BED file](#).

No file selected.

Or paste in a list of gene symbols optionally followed by a comma and levels of membership. Try two examples:
[crisp set example](#), [fuzzy set example](#)

0 gene(s) entered

Enter a brief description for the list in case you want to share it. (Optional)

[Contribute](#)

NETWORKS

Networks: STRING

<http://string-db.org/>

[Home](#) • [Download](#) • [Help](#) • [My Data](#)

 STRING 10

STRING - Known and Predicted Protein-Protein Interactions

search by name search by protein sequence multiple names multiple sequences

protein name: (examples: #1 #2 #3)
|

(STRING understands a variety of protein names and accessions; you can also try a random entry)

organism:
auto-detect ▼

interactors wanted:

COGS Proteins Reset GO !

What it does ...

STRING is a database of known and predicted protein interactions. The interactions include direct (physical) and indirect (functional) associations; they are derived from four sources:

Genomic Context



High-throughput Experiments



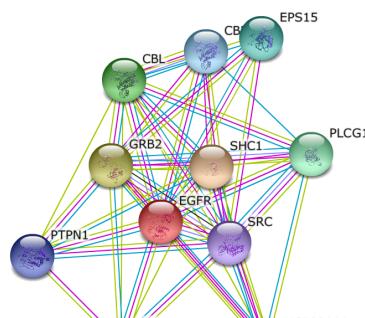
(Conserved) Coexpression



Previous Knowledge



STRING quantitatively integrates interaction data from these sources for a large number of organisms, and transfers information between these organisms where applicable. The database currently covers 9'643'763 proteins from 2'031 organisms.



This is the **evidence view**. Different line colors represent the types of evidence for the association.



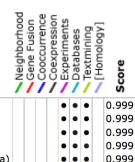
(requires Flash player 10 or better)

Your Input:

- EGFR epidermal growth factor receptor (1210 aa)
(*Homo sapiens*)

Predicted Functional Partners:

SHC1	SHC (Src homology 2 domain containing) transforming protein 1 (584 aa) growth factor receptor-binding protein 2; Adapter protein that provides a critical link between c [...] (217 aa)
GRB2	signal transducer and activator of transcription 3 (acute-phase response factor); Signal trans [...] (770 aa)
STAT3	Cbl proto-oncogene, E3 ubiquitin protein ligase; Adapter protein that functions as a negative [...] (906 aa)
CBL	phosphatidylinositol-3-OH kinase, gamma 1; Mediates the production of the second messenger molecules diacylglycerol [...] (1291 aa)
PLCG1	



PATHiVAR

<http://pathivar.babelomics.org/>



PATHiVAR



PATHiVAR

Try it now

Overview

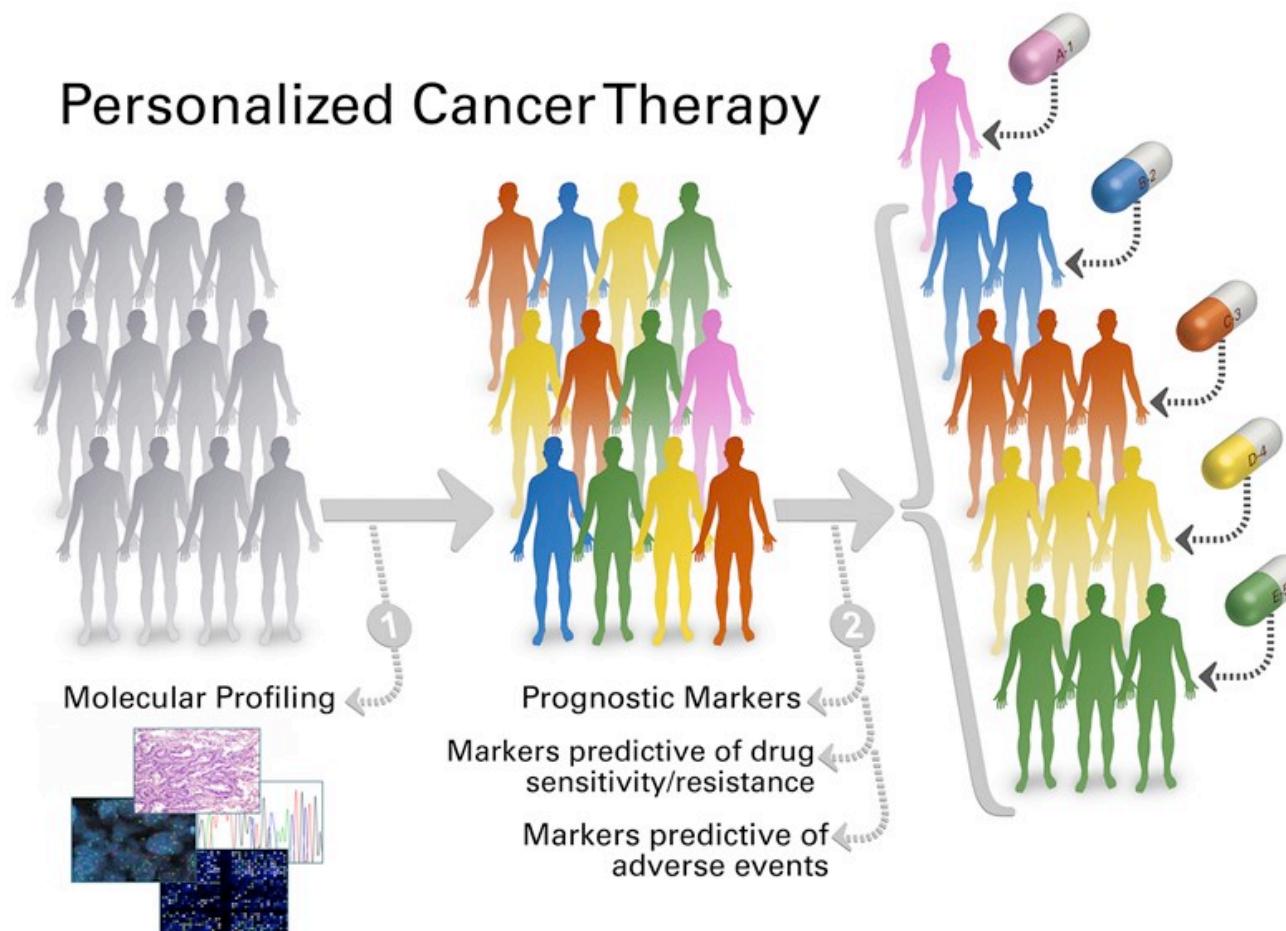
PATHiVAR estimates the functional impact that mutations have over the human signalling network.

PATHiVAR analyses VCF files, extract the deleterious mutations, locate them over the signalling pathways in the selected tissue (with the appropriate expression pattern) and provides a comprehensive, graphic and interactive view of the predicted signal transduction probabilities across the different signalling pathways.

DRUGS/THERAPIES

Personalized Cancer Therapy

<https://pct.mdanderson.org/>



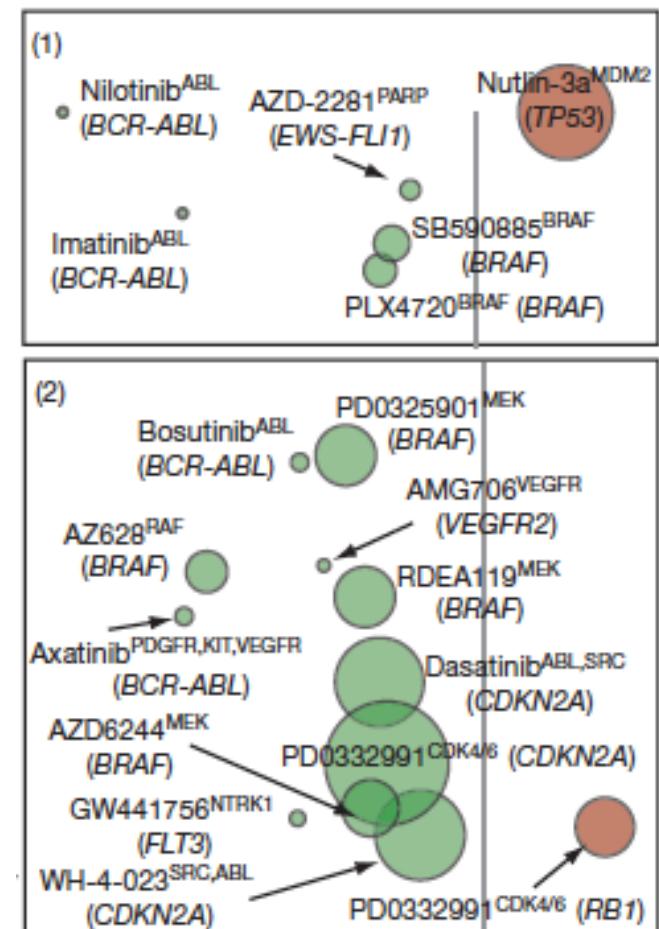
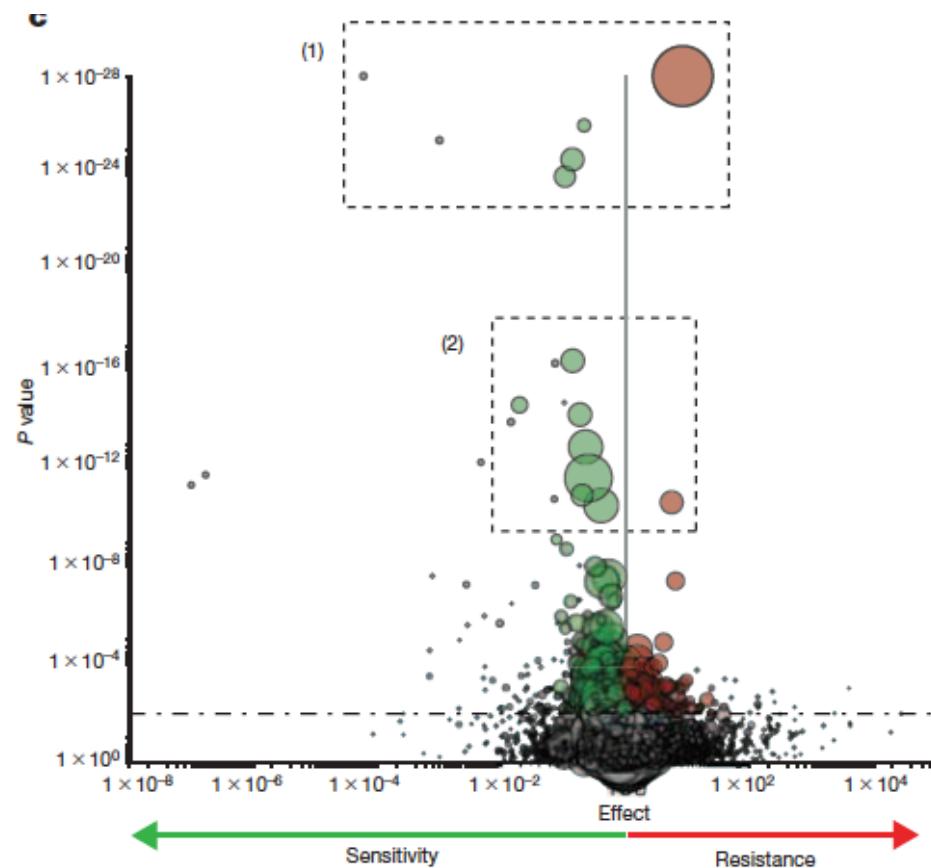
Genomics of Drug Sensitivity in Cancer

<http://www.cancerrxgene.org>

Systematic identification of genomic markers of drug sensitivity in cancer cells

Garnett et al. Nature 2012

Mathew J. Garnett^{1*}, Elena J. Edelman^{2*}, Sonja J. Heidorn^{1*}, Chris D. Greenman^{1†}, Anahita Dastur², King Wai Lau¹, Patricia Greninger², I. Richard Thompson¹, Xi Luo², Jorge Soares¹, Qingsong Liu^{3,4}, Francesco Iorio^{1,5}, Didier Surdez⁶, Li Chen², Randy J. Milano², Graham R. Bignell¹, Ah T. Tam², Helen Davies¹, Jesse A. Stevenson², Syd Barthorpe¹, Stephen R. Lutz², Fiona Kogera¹, Karl Lawrence¹, Anne McLaren-Douglas¹, Xeni Mitropoulos², Tatiana Mironenko¹, Helen Thi², Laura Richardson¹, Wenjun Zhou^{3,4}, Frances Jewitt¹, Tinghu Zhang^{3,4}, Patrick O'Brien¹, Jessica L. Boisvert², Stacey Price¹, Wooyoung Hur^{3,4}, Wanjuan Yang¹, Xianming Deng^{3,4}, Adam Butler¹, Hwan Geun Choi^{3,4}, Jae Won Chang^{3,4}, Jose Baselga², Ivan Stamenkovic⁷, Jeffrey A. Engelman², Sreenath V. Sharma^{2†}, Olivier Delattre⁶, Julio Saez-Rodriguez⁵, Nathanael S. Gray^{3,4}, Jeffrey Settleman², P. Andrew Futreal¹, Daniel A. Haber^{2,8}, Michael R. Stratton¹, Sridhar Ramaswamy², Ultan McDermott¹ & Cyril H. Benes²



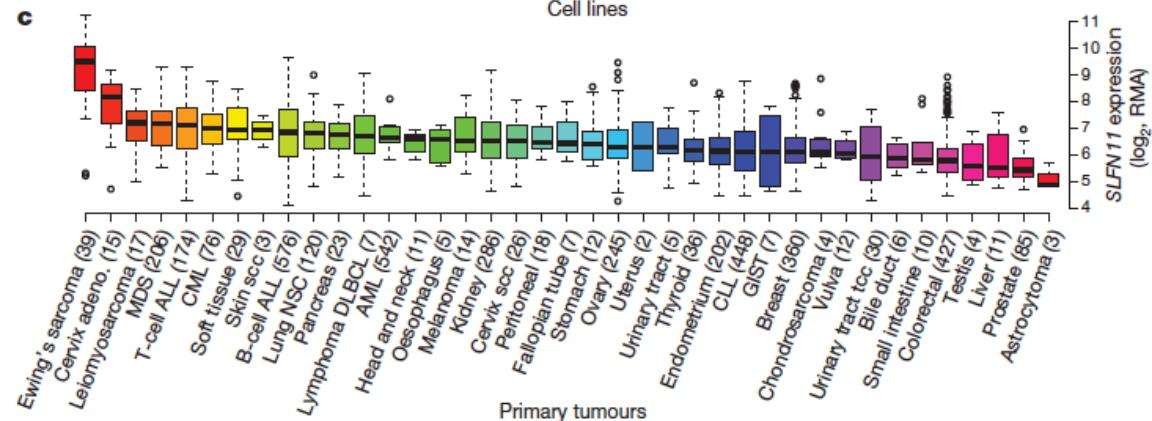
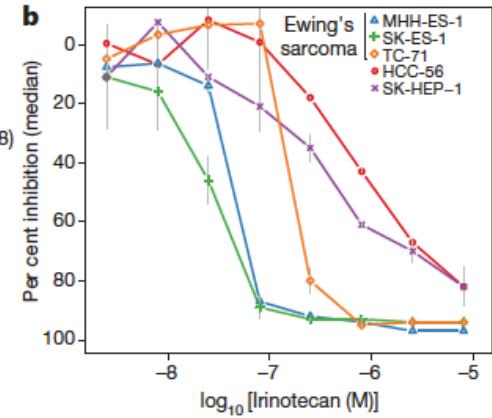
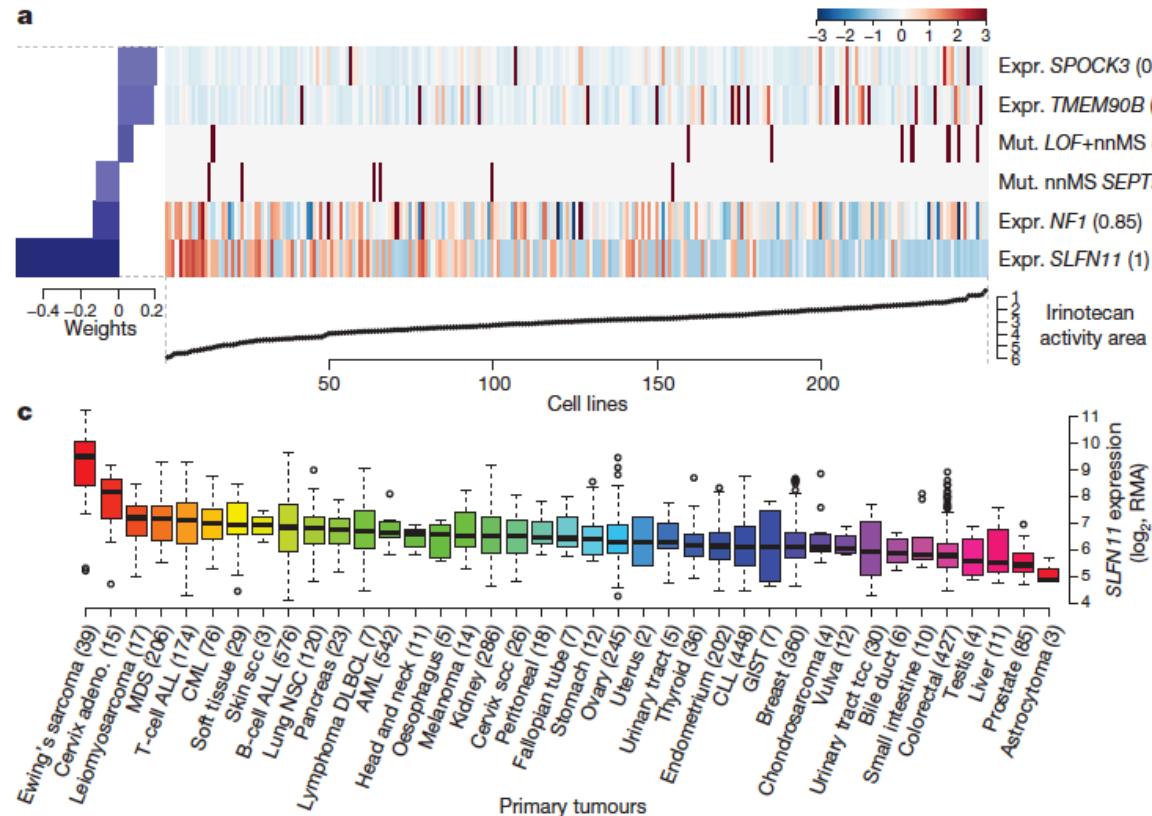
Cancer Cell Line Encyclopedia

<http://www.broadinstitute.org/ccle/>

The Cancer Cell Line Encyclopedia enables predictive modelling of anticancer drug sensitivity

Barretina et al. Nature 2012

Jordi Barretina^{1,2,3†*}, Giordano Caponigro^{4*}, Nicolas Stransky^{1*}, Kavitha Venkatesan^{4*}, Adam A. Margolin^{1†*}, Sungjoon Kim⁵, Christopher J. Wilson⁴, Joseph Lehar⁴, Gregory V. Kryukov¹, Dmitry Sonkin⁴, Anupama Reddy⁴, Manway Liu⁴, Lauren Murray¹, Michael F. Berger[†], John E. Monahan⁴, Paula Morais¹, Jodi Meltzer⁴, Adam Korejwa⁴, Judit Jane-Valbuena^{1,2}, Felipa A. Mapa⁴, Joseph Thibault⁵, Eva Bric-Furlong⁴, Pichai Raman⁴, Aaron Shipway⁵, Ingo H. Engels⁵, Jill Cheng⁵, Guoying K. Yu⁶, Jianjun Yu⁶, Peter Aspasia Jr⁴, Melanie de Silva⁴, Kalpana Jagtap⁴, Michael D. Jones⁴, Li Wang⁴, Charles Hatton¹, Emanuele Palascandolo³, Supriya Gupta², Scott Mahan¹, Carrie Sougnez⁴, Robert C. Onofrio¹, Ted Liefeld¹, Laura MacConaill^{1,3}, Wendy Winckler¹, Michael Reich¹, Nanxin Li⁵, Jill P. Mesinov¹, Stacey B. Gabriel¹, Gad Getz¹, Kristin Ardlie¹, Vivien Chan⁶, Vic E. Myer⁴, Barbara L. Weber⁴, Jeff Porter⁴, Markus Warmuth⁴, Peter Finan⁴, Jennifer L. Harris⁵, Matthew Meyerson^{1,2,3}, Todd R. Golub^{1,3,7,8}, Michael P. Morrissey^{4*}, William R. Sellers^{4*}, Robert Schlegel^{4*} & Levi A. Garraway^{1,2,3*}



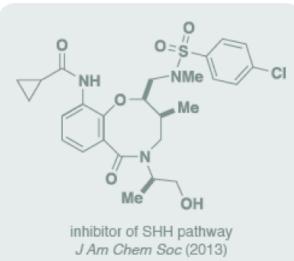
Cancer Therapeutics Response Portal

<http://www.broadinstitute.org/ctrp/>

Cancer Therapeutics Response Portal v2

COMPOUNDS FEATURES TARGETS CLUSTER

Identifying and targeting cancer dependencies with small molecules



The Cancer Therapeutics Response Portal (CTRP) links genetic, lineage, and other cellular features of cancer cell lines to small-molecule sensitivity with the goal of accelerating discovery of patient-matched cancer therapeutics.

We generated an 'Informer Set' of 481 small-molecule probes and drugs that selectively target distinct nodes in cell circuitry and that collectively modulate a broad array of cell processes. We quantitatively measured the sensitivity of 860 deeply characterized cancer-cell lines to Informer Set compounds, and have undertaken analyses connecting sensitivity to cancer features, including mutations, gene expression, copy-number variation, and lineage. These analyses, and links to the underlying data, are provided openly on the CTRP.

The CTRP is a living resource for the biomedical research community that can be mined to develop insights into small-molecule mechanisms of action and novel therapeutic hypotheses, and to support future discovery of drugs matched to patients based on predictive biomarkers.

Publications

Please cite our cancer cell-line profiling Resource by referencing:
"Harnessing Connectivity in a Large-Scale Small-Molecule Sensitivity Dataset" Seashore-Ludlow *et al.*, *Cancer Discovery*, **5**, 1210-1223 (2015), and
"An Interactive Resource to Identify Cancer Genetic and Lineage Dependencies Targeted by Small Molecules" Basu, Bodycombe, Cheah, *et al.*, *Cell*, **154**, 1151-1161 (2013).

Acknowledgements

Complementary Resources

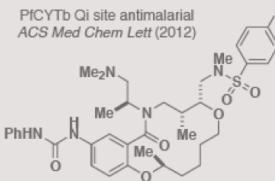
The National Cancer Institute's CTD2 Network maintains an [Open-Access Data Portal](#) that makes available raw data downloads from member Centers, including all raw sensitivity and enrichment data and other supporting information from the Broad related to this portal.

The [Cancer Cell Line Encyclopedia](#) provides public access to genomic data, analysis and visualization for about 1000 cell lines.

CTRP v2

- 481 compounds X 860 CCLs
- interactive interface to explore clustering by small molecule and CCL
- cluster enrichments for small molecule and CCL annotations
- annotations for small molecules by protein target
- annotations for CCLs by mutation and lineage

<< You are here



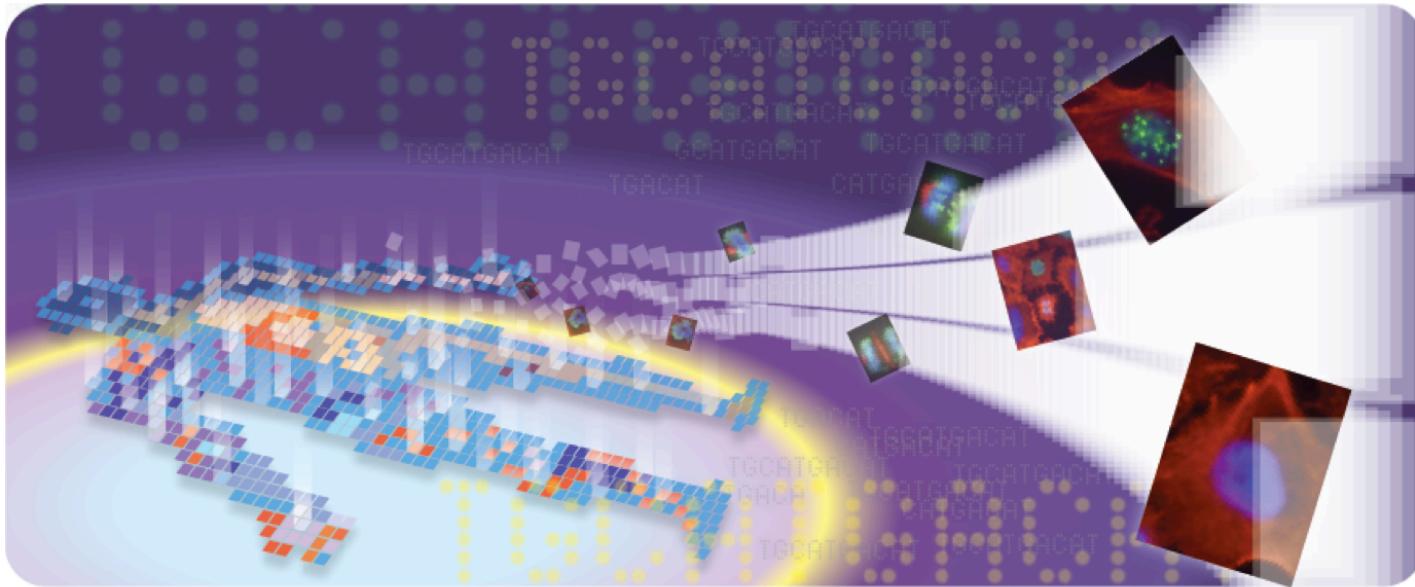
CTRP v1

- 185 compounds X 242 CCLs
- pre-computed enrichment analysis and visualizations
- filter by lineage, CCLE mutation source, confounding factors
- 76,703 significant connections ($q < 0.01$)

[Visit CTRPv1 >>](#)

Project Achilles

<http://www.broadinstitute.org/achilles>



The Project Achilles website features a purple header bar with the project name and the Broad Institute logo. A navigation menu includes links for Data, Resources, About, and Contact, along with a Login button. Below the header is a large, stylized graphic of a DNA double helix composed of colored squares (blue, red, yellow) against a purple background with floating microscopy images of cells.

Project Achilles is a systematic effort aimed at identifying and cataloging genetic vulnerabilities across hundreds of genetically characterized cancer cell lines. The project uses genome-wide genetic perturbation reagents (shRNAs or Cas9/sgRNAs) to silence or knock-out individual genes and identify those genes that affect cell survival. Large-scale functional screening of cancer cell lines provides a complementary approach to those studies that aim to characterize the molecular alterations (e.g. mutations, copy number alterations) of primary tumors, such as The Cancer Genome Atlas (TCGA). The overall goal of the project is to identify cancer genetic dependencies and link them to molecular characteristics in order to prioritize targets for therapeutic development and identify the patient population that might benefit from such targets.

CancerGD: Genomic dependencies

http://www.cancergd.org/

Home/Search About Tutorial Drivers Studies FAQ Contact

CancerGD: analysis of genetic dependencies in cancer

Search filter: Driver gene: ERBB2 Tissue type: Pan cancer Study: All studies Search

Driver gene: ERBB2 Synonyms: HER-2 | HER2 | NEU | CD340 | NGL

Gene alteration considered: Amplifications

Gene Description: erb-b2 receptor tyrosine kinase 2

External links: GeneCards | Entrez | Ensembl | OMIM | CancerRxGene | cBioPortal | COSMIC | CanSAR | UniProtKB | GenomeRNAi | Open Targets

For driver gene **ERBB2**, a total of **1990 dependencies** were found in tissue type **Pan cancer** in **All studies**

(Use scrollbar at right of this table to scroll down. Click column header to sort by that column. Click on the gene name in the dependency column to view the box-plot. Enter text into the search box at top of column to optionally filter these results. In the 'Effect size' column search box you can enter eg: ">75" to filter results.)

Download as CSV file Download as Excel file Stringdb Image Stringdb Interactive for 1990 rows (max: 300)

Dependency	P-value	Effect size (%)	ΔScore	Study	Experiment Type	Multiple Hit	String Interaction	Inhibitors
Search	<0.05	>= 65.0	< 0.0					
MTOR	1 x 10 ⁻⁵	92.5	-1.60	Cowley(2014)	shRNA	Yes	High	GDC-098..[more]
PSMC2	1 x 10 ⁻⁵	95.7	-2.45	Marcotte(2012)	shRNA			BORTEZO..[more]
ERBB2	4 x 10 ⁻⁵	87.6	-1.78	Campbell(2016)	siRNA	Yes	Highest	AEE 788..[more]
HIST1H2AK	4 x 10 ⁻⁵	89.3	-0.73	Cowley(2014)	shRNA			

Networks: STITCH

<http://stitch.embl.de/>

 **STITCH 4.0**

[Input Page](#) | [Downloads](#) | [Help/Info](#) | [My Data](#)

[search by name](#) [chemical structure\(s\)](#) [protein sequence\(s\)](#) [multiple names](#) [batch import](#)

name: (examples: #1 #2 #3)

(STITCH understands a variety of chemical/protein names, accessions and InChIKeys; you can also try a [random entry](#))

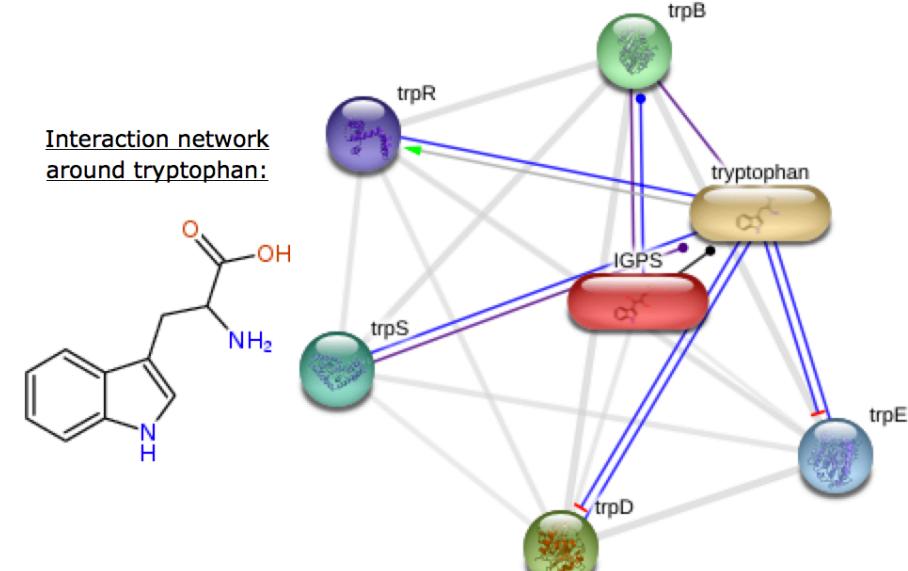
organism:
auto-detect ▼
(in case of chemicals, the organism with the most likely interaction is chosen)

[Reset](#) [GO !](#)

please enter your protein or chemical of interest...

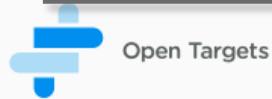
STITCH: Chemical-Protein Interactions

Interaction network around tryptophan:



The diagram illustrates the interaction network around tryptophan. Tryptophan is represented by a yellow oval. It is connected to several proteins: trpR (purple), trpB (green), trpS (teal), IGPS (red), trpD (orange), and trpE (blue). The connections are shown as lines. A chemical structure of tryptophan is also shown, featuring a tryptamine core with a side chain containing a carboxylic acid group (-NH₂-CH₂-COOH).

Open Targets <https://www.opentargets.org/>



About Us People Projects News Contact [Target Validation Platform](#)

Welcome to **Open Targets**

For biomedical researchers who need to identify a biological target for a new therapy, Open Targets is a public-private initiative to generate evidence on the validity of therapeutic targets based on genome-scale experiments and analysis. Open Targets is working to create an R&D framework that applies to a wide range of human diseases, and is committed to sharing its data openly with the scientific community.

[View the platform ➤](#)



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Site maintained by the Web Development team at EMBL-EBI | [Terms of Use](#) | [Privacy](#) | [Cookies](#)

Target Validation Platform <https://www.targetvalidation.org/>



Open Targets

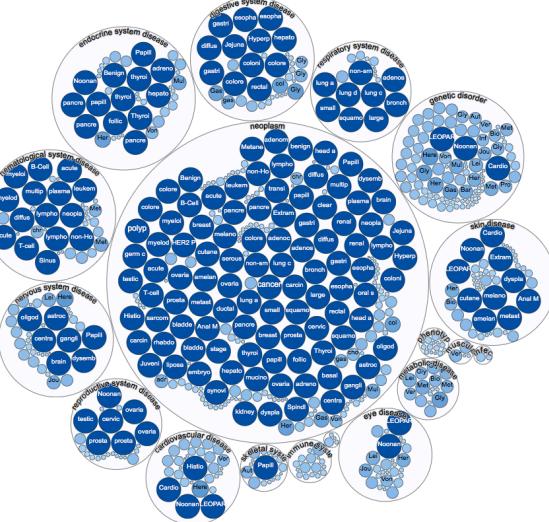
Search for a target or disease (e.g. BRAF or asthma) 

I am interested in target T:
Which diseases can be treated by modulating target T?

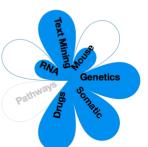
384 diseases associated with BRAF 

Filter by
Data types Genetic associations (118) Somatic mutations (108) Drugs (55) Affected pathways (0) RNA expression (36) Text mining (201) Animal models (61)

Therapeutic area Neoplasm (222) Genetic disorder (88) Skin disease (47) Endocrine system disease (38) Hematological system disease (37) Nervous system disease (37) Digestive system disease (34) Cardiovascular disease (28) Eye disease (26) Reproductive system disease (23) Phenotype (22) Respiratory system disease (18) Immune system disease (16) Skeletal system disease (16) Metabolic disease (15) Infectious disease (8) Muscular disease (4) Other (4)



Disease	Association score	Genetic associations	Somatic mutations	Drugs	Affected pathways	mRNA expression	Text mining	Animal models	Therapeutic area
neoplasm									neoplasm
cancer									neoplasm
carcinoma									neoplasm
skin disease									neoplasm
lung disease									respiratory system disease
lung carcinoma									neoplasm, respiratory system di
adenocarcinoma									neoplasm
non-small cell lung carcinoma									neoplasm, respiratory system di
melanoma									skin disease, neoplasm
colonic neoplasm									neoplasm, digestive system dise
thyroid disease									endocrine system disease
lymphoid neoplasm									hematological system disease, r
thyroid carcinoma									endocrine system disease, neop
colorectal adenocarcinoma									digestive system disease, neop
genetic disorder									
papillary thyroid carcinoma									endocrine system disease, neop
kidney neoplasm									neoplasm
lung adenocarcinoma									neoplasm, respiratory system di
sarcoma									neoplasm
cutaneous melanoma									skin disease, neoplasm
squamous cell carcinoma									neoplasm



BRAF
B-Raf proto-oncogene, serine/threonine kinase
 Synonyms: BRAF1, RAFB1
 Protein kinase involved in the transduction of mitogenic signals from the cell membrane to the nucleus. May play a role in the postsynaptic responses of hippocampal neuron. Phosphorylates MAP2K1, and ...

Genetic associations

Somatic mutations

Drugs

Affected pathways

mRNA expression

Text mining

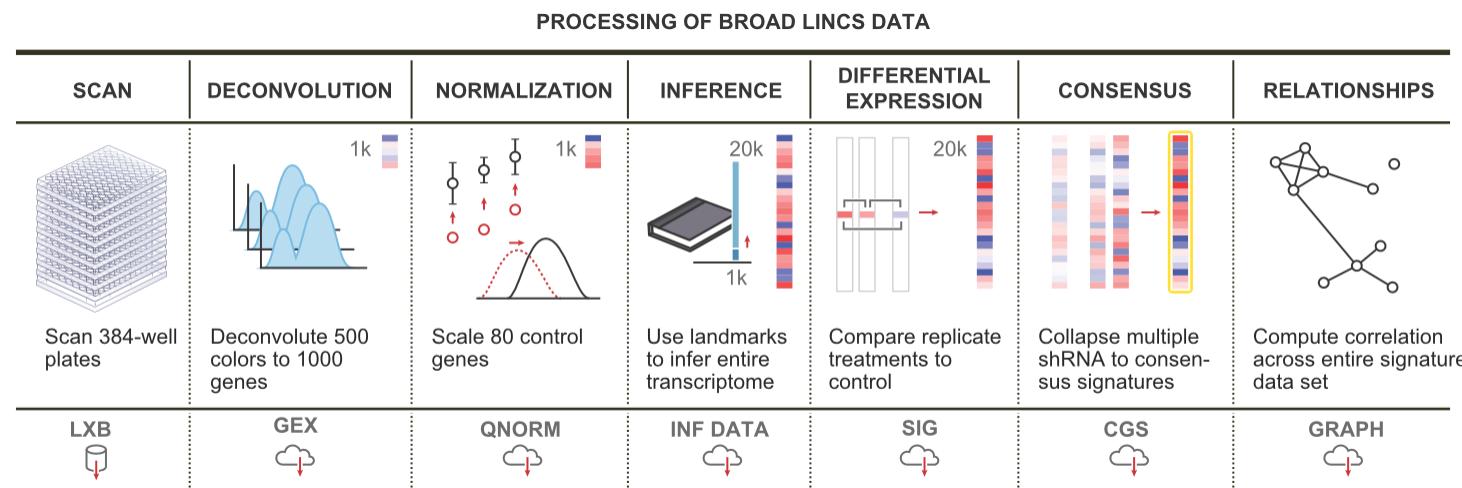
Animal models

LINCS Cloud

<https://clue.io/>



- Library of Integrated Cellular Signatures
- The aim is to generate perturbational profiles across multiple cell and perturbation types
 - Small Molecules
 - 1300 FDA approved drugs
 - 5500 bioactive compounds
 - Gene Knock-Outs and Over Expression



VCF ANNOTATORS

Variant Effect Predictor

<http://www.ensembl.org/info/docs/tools/vep/index.html/>

The screenshot shows the Ensembl homepage with the VEP tool selected. The main content area is titled "Variant Effect Predictor" and includes a "New VEP job:" section. This section contains a note about VEP for Human GRCh37 and a "Input" section where the species is set to "Human (Homo sapiens)" and the assembly to "GRCh38.p3". There is also a field for "Name for this data (optional)". Below this is a text area for pasting data.

Ensembl

BLAST/BLAT | BioMart | Tools | Downloads | Help & Documentation | Blog | Mirrors

Login/Register

Species ▾ VEP ▾

Web Tools

- Web Tools
 - BLAST/BLAT
 - Variant Effect Predictor**
 - Assembly Converter

Configure this page

Add your data

Export data

Share this page

Bookmark this page

Variant Effect Predictor ⓘ

New VEP job:

ⓘ **VEP for Human GRCh37**

If you are looking for VEP for Human GRCh37, please go to [GRCh37 website](#).

Input

Species: Human (Homo sapiens)

Assembly: GRCh38.p3

Name for this data (optional):

Either paste data:

SnpEff

http://snpeff.sourceforge.net/

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SNPEFF

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[Who uses SnpEff?](#)

[Integration](#)

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SnpEff

Genetic variant annotation and effect prediction toolbox.

[Download SnpEff](#)

Important: This version implements the [new VCF annotation standard 'ANN' field](#).

Latest version 4.2 (2015-12-05)

Requires Java 1.7

StructurePPI

http://structureppi.bioinfo.cnio.es/

Structure PPI

Structure – Annotate

Annotates genomic mutations based on the protein features that are overlapping amino-acid changes

database (default: UniProt)

UniProt

principal (default: true)

mutations

Browse... No file selected. or use the text area below

Structure PPI

organism (default: Hsa/feb2014)

Hsa/feb2014

Tasks

annotate
Annotates genomic mutations based on the protein features that are overlapping amino-acid changes

annotate_mi
Annotates mutated isoforms based on the protein features that are overlapping amino-acid changes

annotate_mi_neighbours
Annotates mutated isoforms based on the protein features that are in close physical proximity to amino-acid changes

annotate_neighbours
Annotates genomic mutations based on the protein features that are in close physical proximity to amino-acid changes

interfaces

This workflow offers several functionalities to explore the consequence of protein mutations. It reports features that overlap the mutations, or that are in close physical proximity.

The features reported include protein domains, variants, helices, ligand binding residues, catalytic sites, transmembrane domains, InterPro domains, and known somatic mutations in different types of cancer. This information is extracted from resources such as UniProt, COSMIC, InterPro and Appris. It can also identify mutations affecting the interfaces of protein complexes.

This workflow makes use of PDB files to calculate residues in close proximity. This information is used to find features close to the mutations, at a distance of 5 angstroms, or mutations in residues close to residues in a complex partner, at a distance of up to 8 angstroms.

Wizard

Use the following textbox to input your mutations and retrieve all annotations, including neighbours and interfaces. This method is limited to 1000 variants, use the other (more granular) tasks if your mutation set is larger. Mutations can be specified as genomic mutation 18:6237978:g, a mutated isoform ENSP0000382976:L257R, or using any identifier instead of the Ensembl Protein ID such as

PDBs are extracted from Interactome3d, which organizes thousands of PDBs, for both experimental structures and structure models, of individual proteins and protein complexes.

Pairwise (Smith-Waterman) alignment is used to fix all inconsistencies between protein sequences in PDBs, Uniprot and Ensembl Protein ID.

Reference:

Vazquez M, Valencia A, Pons T. (2015) Structure-PPI: a module for the annotation of cancer-related single-nucleotide variants at protein-protein interfaces. *Bioinformatics* (2015); 31(14):2397-2399 (doi: 10.1093/bioinformatics/btv142)

contributes has been selected based on expert opinion and guided by empirical results on the COSMIC and 1000 Genomes data. The scoring scheme is as follows:

- Appris features: we add 2 if at least one ligand binding or catalytic site annotated in firestar is affected; if none of the affected features meets this condition we add only 1
- COSMIC mutations: 3 if more than ten COSMIC samples have

PanDrugs

http://pandrugs.bioinfo.cnio.es/

Welcome to **PANDRUGS**

A resource to study drug-gene interactions in a cancer disease context

Query database! ✓

Query Pandrugs: Genes

Genes

Enter HUGO Gene symbols

Advanced Options

Drug status level

Cancer

- FDA approved
- Clinical trials

Other pathologies

- FDA approved
- Clinical trials Experimental

Interaction evidence level

- Target
- Marker

Select Cancer Types

Select all Clear all

SURVIVAL, CLINICAL INFORMATION

Survival: Prognoscan

<http://www.abren.net/Prognoscan/>

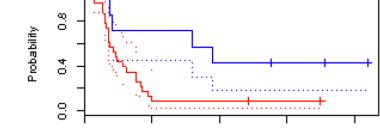
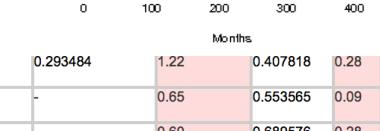
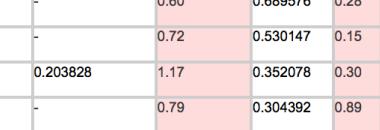
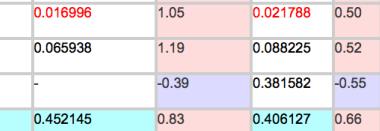
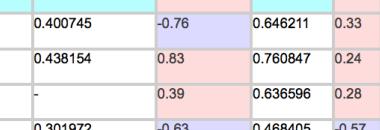
Prognoscan: A new database for meta-analysis of the prognostic value of genes.

Enter gene identifier(s) [[Find gene at Entrez](#)]

+

submit

GENE_SYMBOL EGFR
GENE_DESCRIPTION epidermal growth factor receptor

Dataset	Cancer Type	Subtype	Endpoint	Cohort	Contributor	Array Type	Probe	# of patients	P-value	Kaplan-Meier plot
GSE5287	Bladder cancer		Overall Survival	Aarhus (1995-2004)	Als	HG-U133A	210984_x_at	30	0.23	
GSE5287	Bladder cancer		Overall Survival	Aarhus (1995-2004)	Als	HG-U133A	201983_s_at	30	0.43	
GSE5287	Bladder cancer		Overall Survival	Aarhus (1995-2004)	Als	HG-U133A	211551_at	30	0.43	
GSE5287	Bladder cancer		Overall Survival	Aarhus (1995-2004)	Als	HG-U133A	201984_s_at	30	0.87	
GSE5287	Bladder cancer		Overall Survival	Aarhus (1995-2004)	Als	HG-U133A	211607_x_at	30	0.33	
GSE5287	Bladder cancer		Overall Survival	Aarhus (1995-2004)	Als	HG-U133A	211550_at	30	0.73	
GSE13507	Bladder cancer		Overall Survival	CNUH	Kim	Human-6 v2	ILMN_1696521	165	0.90	
GSE13507	Bladder cancer	Transitional cell carcinoma	Disease Specific Survival	CNUH	Kim	Human-6 v2	ILMN_1696521	165	0.90	
GSE12417-GPL96	Blood cancer	AML	Overall Survival	AMLCG (1999-2003)	Metzeler	HG-U133A	201984_s_at	163	0.15	
GSE12417-GPL96	Blood cancer	AML	Overall Survival	AMLCG (1999-2003)	Metzeler	HG-U133A	211550_at	163	0.10	
GSE12417-GPL96	Blood cancer	AML	Overall Survival	AMLCG (1999-2003)	Metzeler	HG-U133A	211607_x_at	163	0.89	
GSE12417-GPL96	Blood cancer	AML	Overall Survival	AMLCG (1999-2003)	Metzeler	HG-U133A	210984_x_at	163	0.11	
GSE12417-GPL96	Blood cancer	AML	Overall Survival	AMLCG (1999-2003)	Metzeler	HG-U133A	201983_s_at	163	0.29	
GSE12417-GPL96	Blood cancer	AML	Overall Survival	AMLCG (1999-2003)	Metzeler	HG-U133A	211551_at	163	0.11	
GSE12417-GPL96	Blood cancer	AML	Overall Survival	AMLCG (2004)	Metzeler	HG-U133_Plus_2	210984_x_at	79	0.11	

Survival: Kaplan Meier Plotter

<http://kmplot.com/analysis/index.php>

Kaplan-Meier Plotter

Breast Cancer

Lung

KM plotter Home Download Updates Contact

What is the KM plotter?

The Kaplan Meier plotter is capable to assess the effect of **54,675 / 22,277 genes** on survival using **10,188 cancer samples**. These include **4,142 breast, 1,648 ovarian, 2,437 lung and 1,065 gastric cancer patients** with a mean follow-up of 69 / 40 / 49 / 33 months. Primary purpose of the tool is a meta-analysis based **biomarker assessment**.

Start KM Plotter for breast cancer

Start KM Plotter for ovarian cancer

Start KM Plotter for lung cancer

Start KM Plotter for gastric cancer

Kaplan-Meier Plotter

Affy id/Gene symbol: 204009_s_at Use multigene classifier
Survival: OS (n=1928) Split patients by: median Auto select best cutoff: Follow up threshold: all Censor at threshold: Compute median over entire dataset:

Probe set options: user selected probe set Use all probe sets per gene only JetSet best probe set Plot beeswarm graph of probe distribution:

Restrict analysis to subtypes... Histology: all Grade: all Stage: all AJCC stage T: all AJCC stage N: all AJCC stage M: all Gender: all Smoking history: all

Include in multivariate: Surgery success: all Chemotherapy: all Radiotherapy: all

Use selected cohort: Dataset: all

Cox regression: univariate multivariate
Use earlier release of the database: 2015 version (n= 2435)
Array quality control: exclude biased arrays (n=2435)

Draw Kaplan-Meier plot

n = number of patients with available clinical data

Please note: the generated p value does **not** include correction for [multiple hypothesis testing](#) by default.

How to cite: Györfi B, Surovská P, Budczies J, Lanczky A. Online survival analysis software to assess the prognostic value of biomarkers using transcriptomic data in non-small-cell lung cancer. *PLoS One*, 2013 Dec 18;8(12):e82241. doi: 10.1371/journal.pone.0082241.

P value: 0.0389

HR = 0.88 (0.77 - 0.99)
logrank P = 0.039

Probability

Time (months)

Number at risk

Expression low high

Time (months)	Number at risk (low)	Number at risk (high)
0	963	963
50	369	459
100	69	134
150	18	39
200	2	5

ClinVAR

<http://www.ncbi.nlm.nih.gov/clinvar/>

ClinVar ClinVar EGFR[gene] [Create alert](#) [Advanced](#) Help

Home About Access Using the website How to submit Statistics FTP site

Gene Tabular 100 per page Sort by Location Download:

Clinical significance Uncertain significance (6) Likely pathogenic (1) Pathogenic (6)

Review status Single submitter (50) At least one star (50)

Allele origin Germline (22) Somatic (149)

Method type Literature only (17) Clinical testing (156)

Molecular consequence Frameshift (6)

Showing for results for variants in the **EGFR** gene. [Search instead for all ClinVar records that mention EGFR](#)

Search results

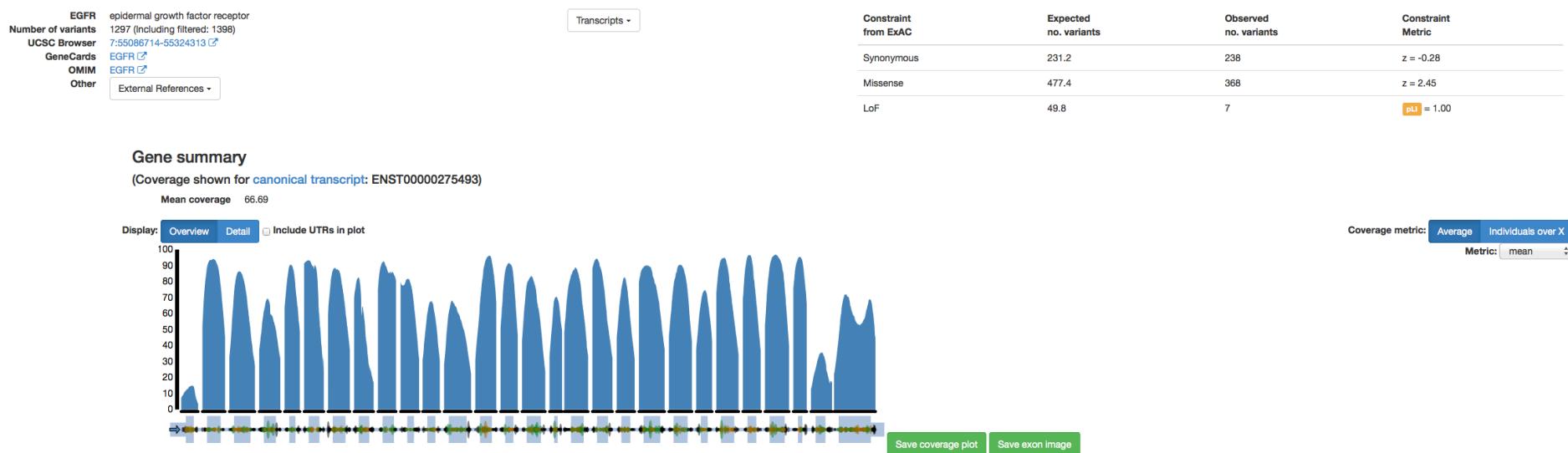
Items: 1 to 100 of 185 << First < Prev Page of 2 Next > Last >>

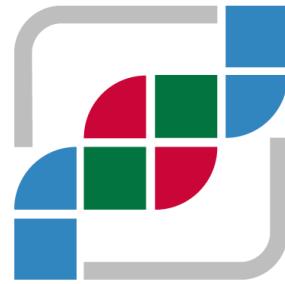
	Variation Location	Gene(s)	Condition(s)	Frequency	Clinical significance (Last reviewed)	Review status
1.	NM_005228.3(EGFR):c.493C>T (p.Ar g165Trp) <i>GRCh37: Chr7:55214367 GRCh38: Chr7:55146674</i>	EGFR	not specified		not provided (Sep 19, 2013)	no assertion provided
2.	NM_005228.3(EGFR):c.1177G>C (p. Asp393His) <i>GRCh37: Chr7:55224495 GRCh38: Chr7:55156802</i>	EGFR	not specified		not provided (Sep 19, 2013)	no assertion provided

ExAC

<http://exac.broadinstitute.org>

Gene: EGFR



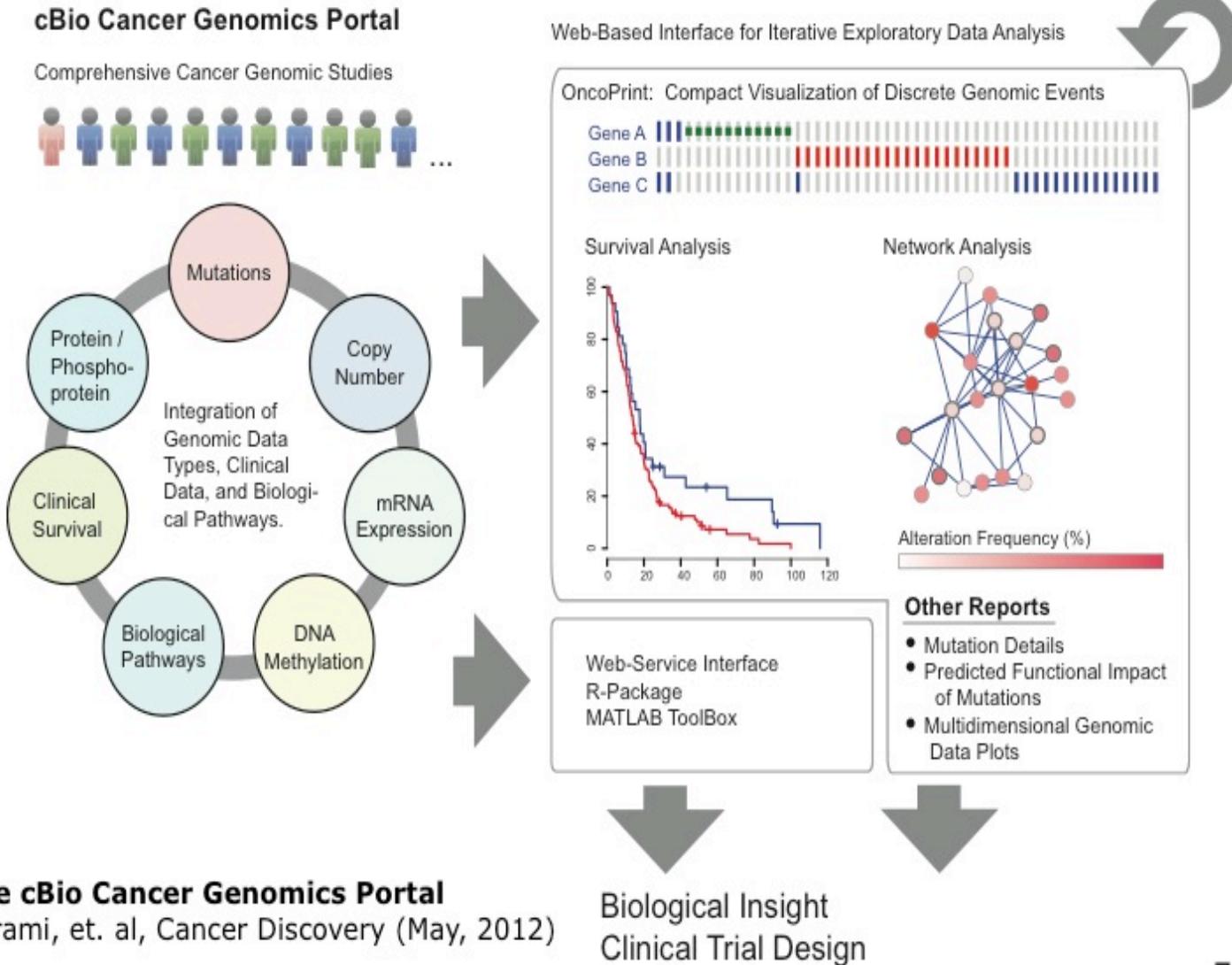


cbiportal.org



Memorial Sloan Kettering
Cancer Center™

Overview of data integration in cBioPortal

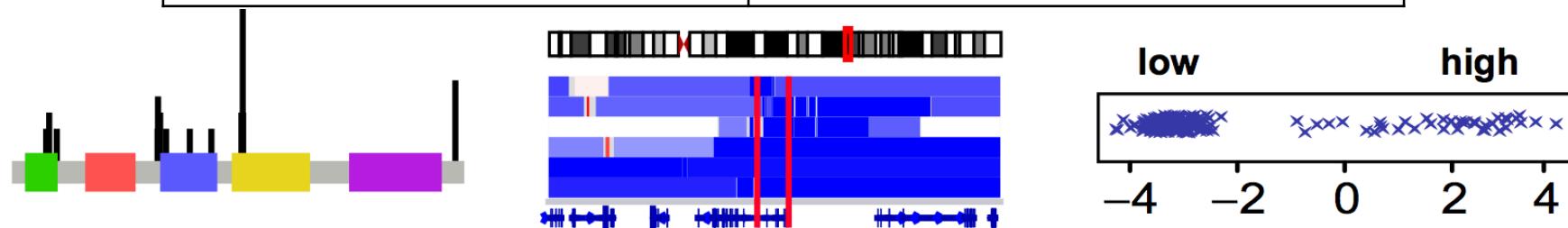


Key abstraction: gene alteration events per sample

Which genes are **altered** in each individual tumor sample?

Event calls

Data type	Alteration event calls
Mutations	Non-synonymous somatic mutations
Copy number changes	Homozygous deletion or amplification
Methylation	Epigenetic silencing
mRNA and/or DNA	Gene fusions
mRNA expression changes	Over- or under-expression



Alteration types and thresholds can be customized for each gene

4-Step Web Interface

4-step web interface for querying a single cancer study

Query Download Data

Select Cancer Study: 1 Select a Cancer Study or “All Cancer Studies”
The Cancer Genome Atlas (TCGA) Glioblastoma project. 206 primary glioblastoma samples.
Nature 2008. Raw data via the TCGA Data Portal.

Select Genomic Profiles:
 Mutation
 Copy Number Data. Select one of the profiles below:
 Putative copy-number alterations (OBM Pathways)
 Putative copy-number alterations (RAE)
 mRNA Expression z-Scores 2 Select one or more genomic profiles
For example: Mutation and Copy Number Data

Select Patient/Case Set: 3 Select a Patient Set

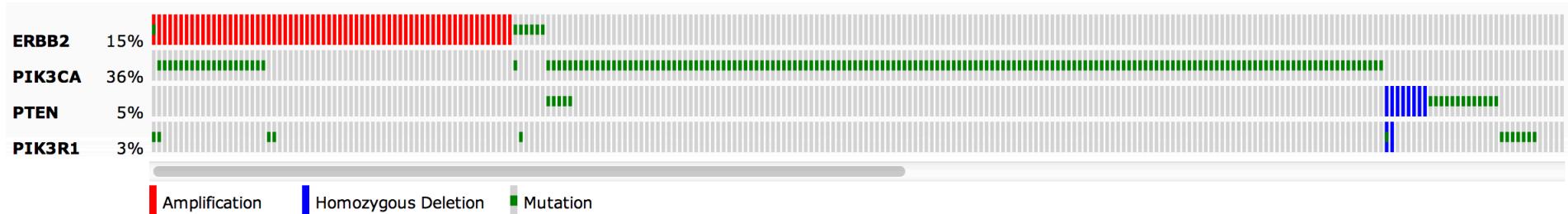
Enter Gene Set: Advanced: Onco Query Language (OQL)
 4 Enter a Gene or Gene Set

Or Select from Example Gene Sets:
 5

Optional Arguments:
 Compute Mutual Exclusivity / Co-occurrence between all pairs of genes.
(Not recommended for more than 10 genes.) 6 Optional argument to compute mutual exclusivity / co-occurrence between all pairs of genes.

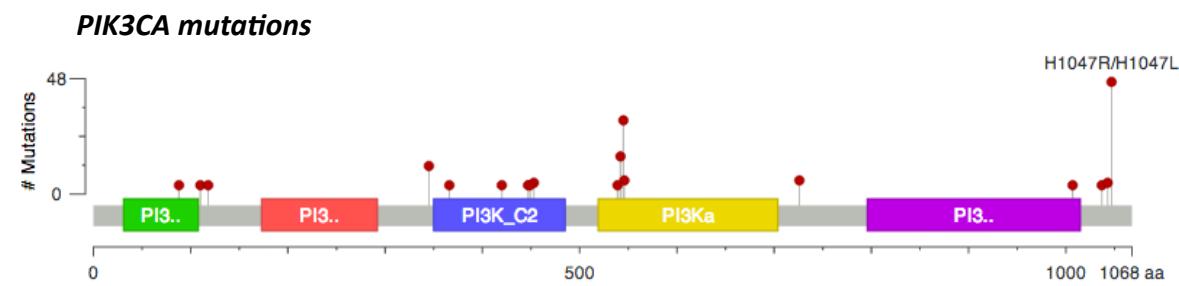
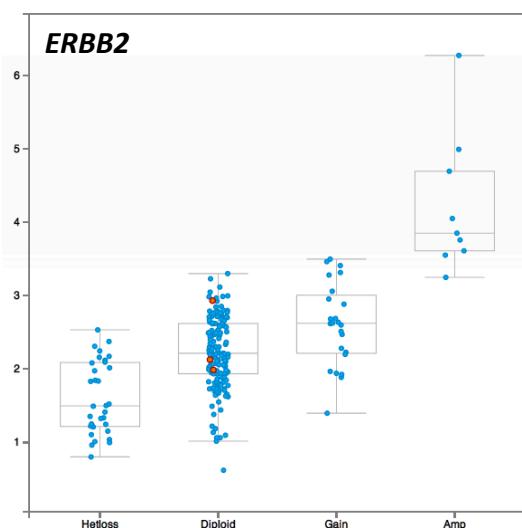
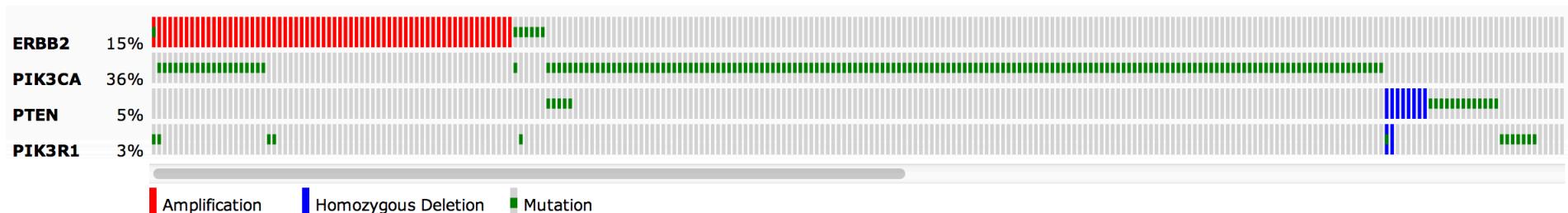
cBioPortal for Cancer Genomics: Three modes of access

1. Queries across a cohort: Example Breast Cancer



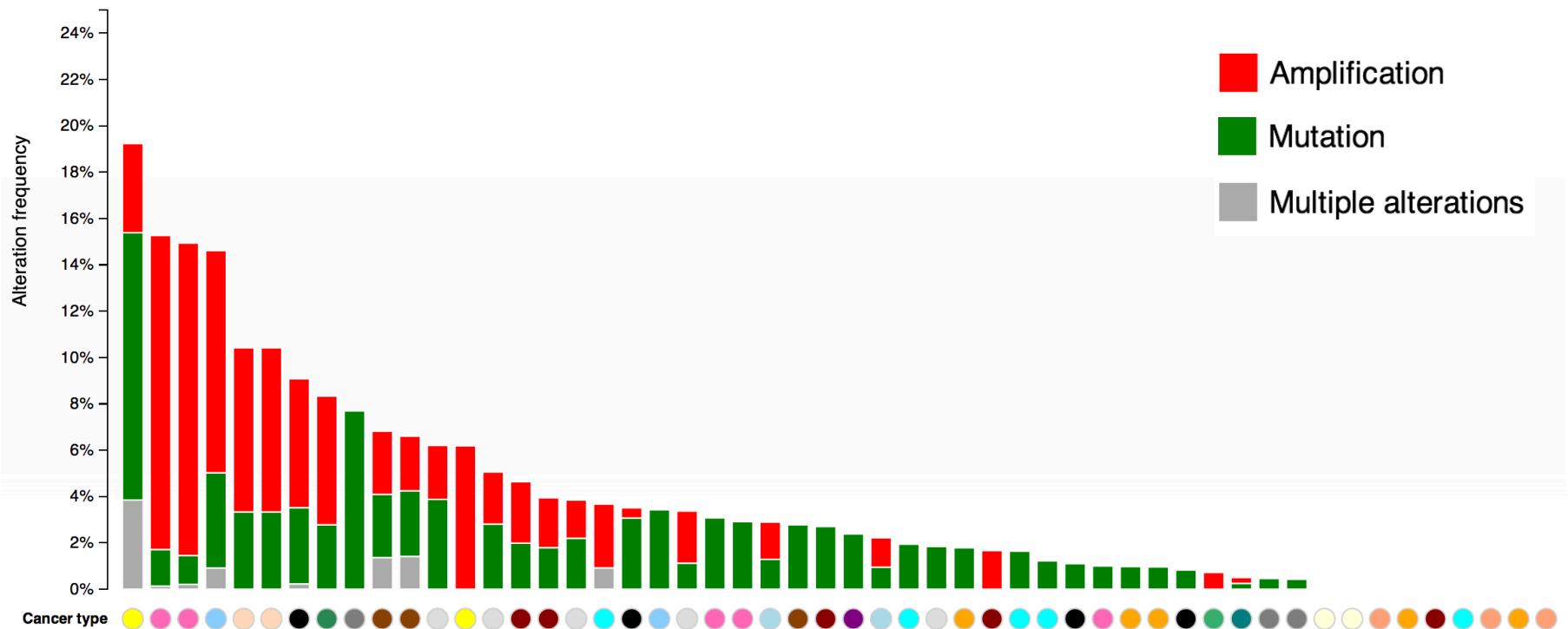
cBioPortal for Cancer Genomics: Three modes of access

1. Queries across a cohort: Example Breast Cancer



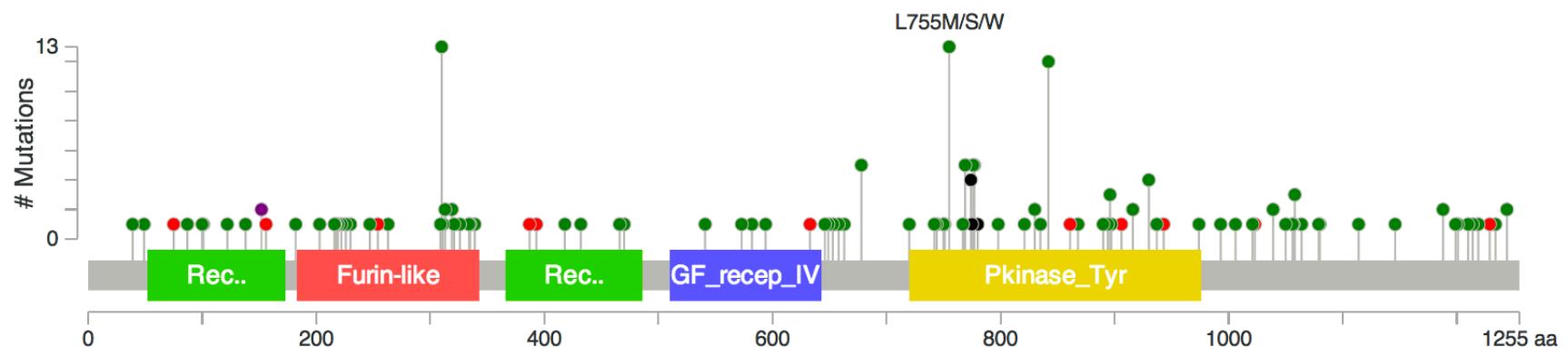
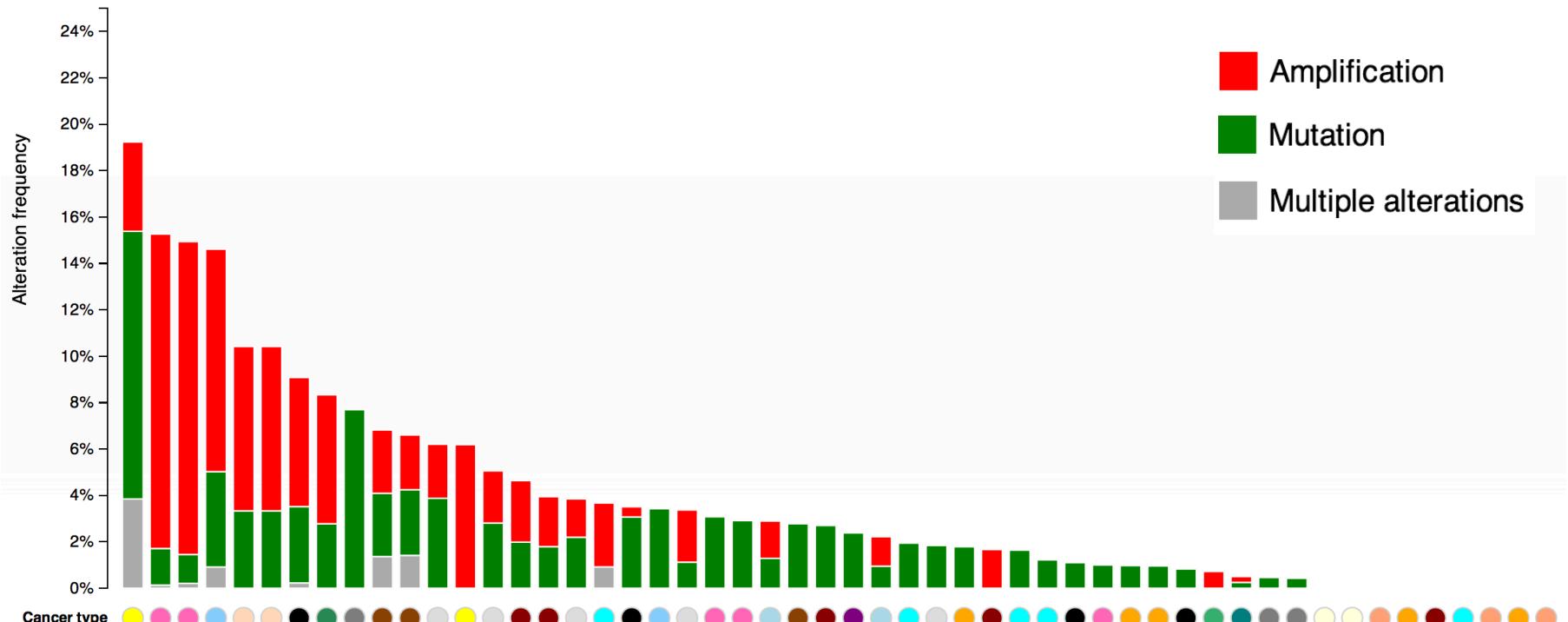
cBioPortal for Cancer Genomics: Three modes of access

2. Cross-cancer queries: Example ERBB2



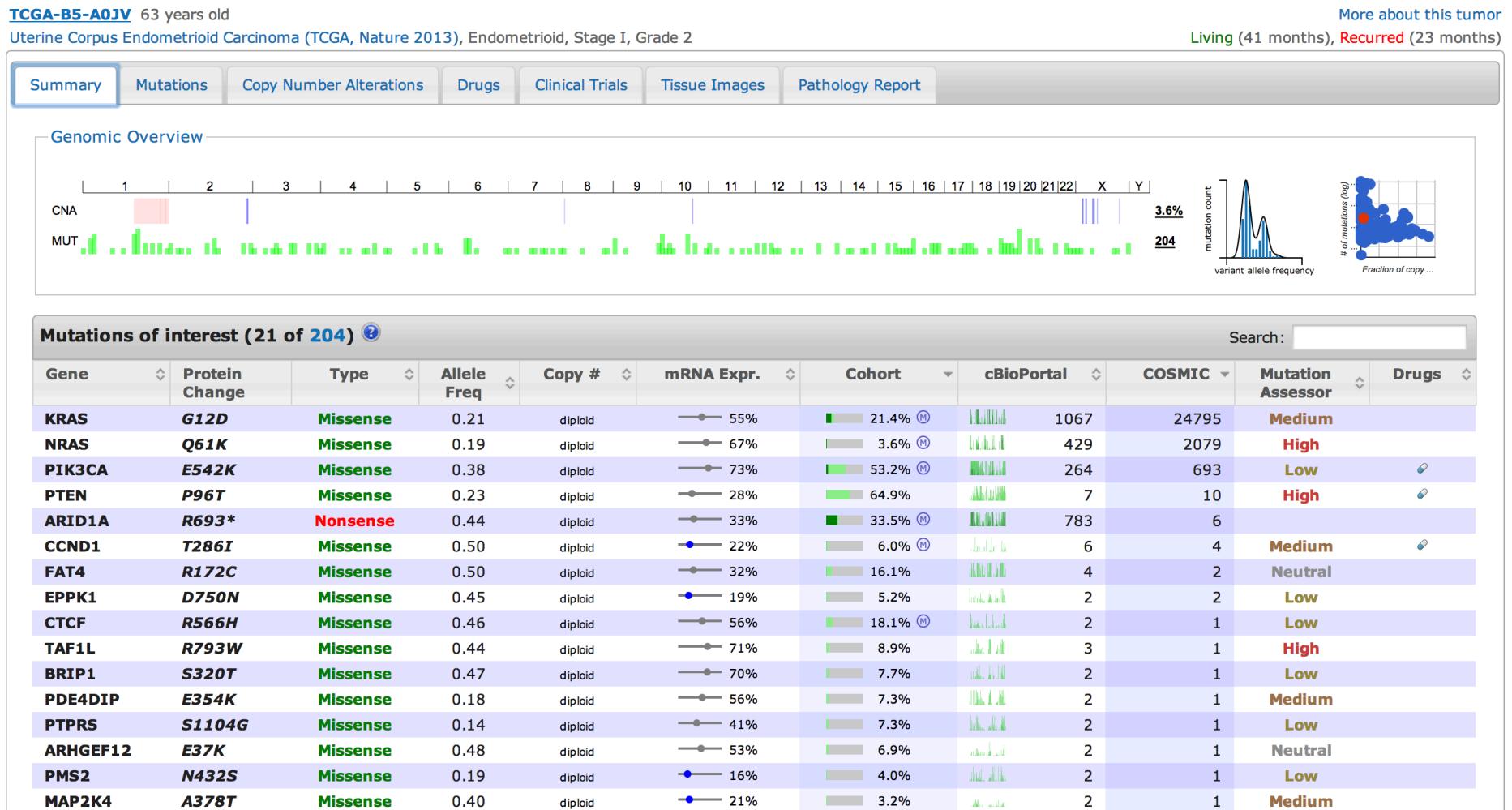
cBioPortal for Cancer Genomics: Three modes of access

2. Cross-cancer queries: Example ERBB2



cBioPortal for Cancer Genomics: Three modes of access

3. Visualization / interpretation of individual tumor samples



Hands-on exercise with cBioPortal

- **Select Cancer Study:**
 - Glioblastoma -> Glioblastoma (TCGA, Cell 2013)
- **Select Genomic Profiles:**
 - Mutations
 - Putative copy-number alterations from GISTIC
 - mRNA Expression z-Scores (threshold: 2.0)
- **Select Patient/Case Set:**
 - All Complete Tumors (291)

Enter Gene Set:

IDH1 CDK4 TP53 CDKN2A EGFR RB1

Questions:

- 1) What gene is the most frequently deleted?
- 2) Can you identify significant mutual exclusivity or co-occurrent alterations with CDK4?
- 3) Which is the most frequent point mutation in EGFR?
- 4) Is this group of genes a molecular marker of overall survival?
- 5) For the patient TCGA-06-0650-01 and based on her molecular alterations which treatment might receive?

Thank You !

Results



Results



Data Sets Web API R/MATLAB Tutorials FAQ News Tools About Visualize Your Data

Modify Query

Glioblastoma (TCGA, Cell 2013)

All Complete Tumors (291 samples) / 6 Genes

Gene Set / Pathway is altered in 271 (93.1%) of queried samples

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

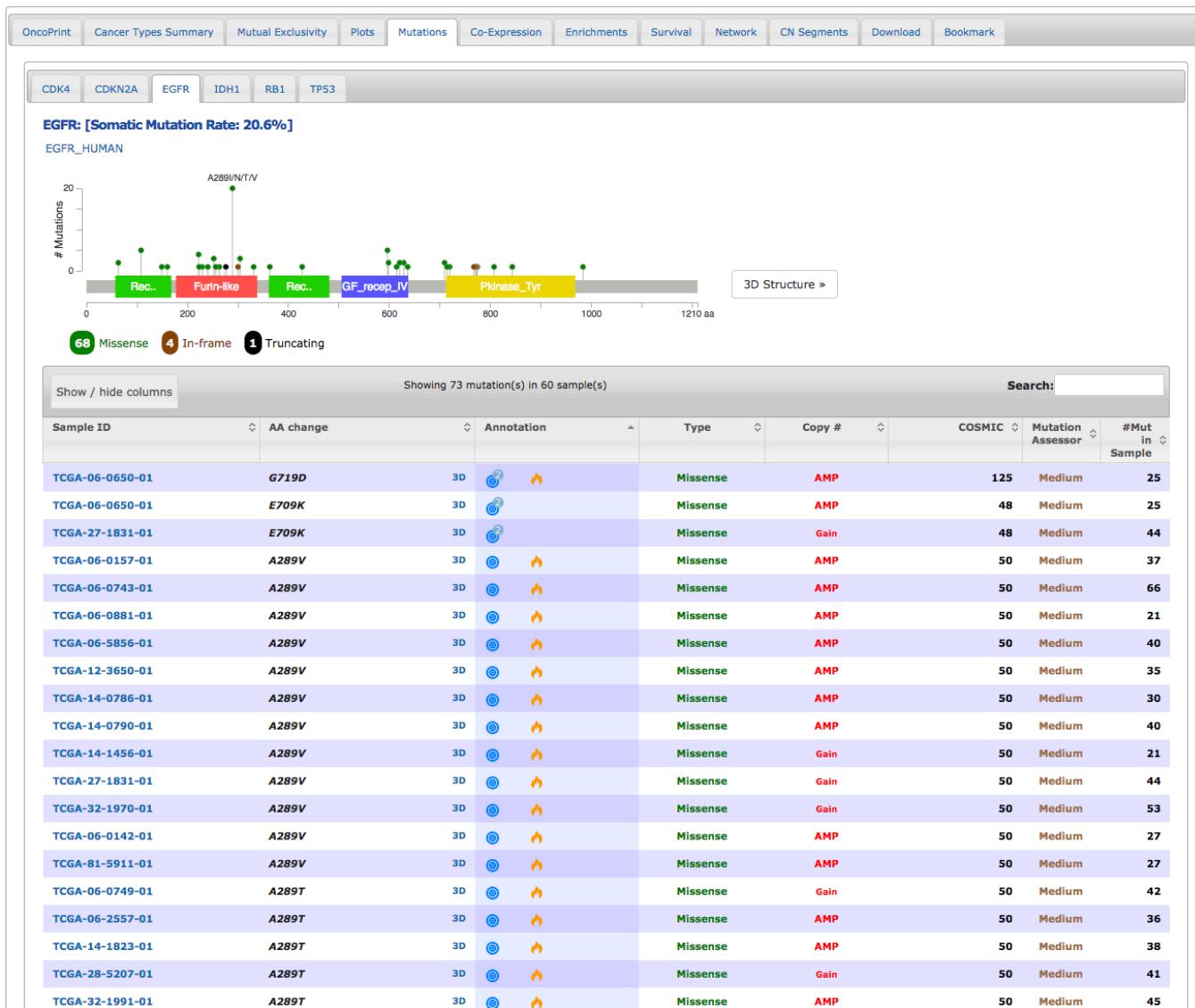
The query contains **10** gene pairs with mutually exclusive alterations (**6** significant), and **5** gene pairs with co-occurrent alterations (**4** significant).

Mutual exclusivity					Co-occurrence		Significant pairs		Search Gene
Gene A	Gene B	p-Value	Log Odds Ratio	Association					
CDK4	CDKN2A	<0.001	-2.067	Tendency towards mutual exclusivity	Significant				
TP53	CDKN2A	<0.001	-1.202	Tendency towards mutual exclusivity	Significant				
TP53	EGFR	<0.001	-0.908	Tendency towards mutual exclusivity	Significant				
TP53	RB1	<0.001	1.520	Tendency towards co-occurrence	Significant				
CDKN2A	RB1	<0.001	-1.620	Tendency towards mutual exclusivity	Significant				
EGFR	RB1	<0.001	-1.661	Tendency towards mutual exclusivity	Significant				
CDK4	RB1	0.004	<-3	Tendency towards mutual exclusivity	Significant				
CDKN2A	EGFR	0.007	0.625	Tendency towards co-occurrence	Significant				
IDH1	TP53	0.015	1.109	Tendency towards co-occurrence	Significant				
CDK4	TP53	0.034	0.688	Tendency towards co-occurrence	Significant				
IDH1	EGFR	0.051	-0.836	Tendency towards mutual exclusivity					
IDH1	CDKN2A	0.247	-0.399	Tendency towards mutual exclusivity					
IDH1	CDK4	0.304	0.408	Tendency towards co-occurrence					
CDK4	EGFR	0.422	-0.110	Tendency towards mutual exclusivity					
IDH1	RB1	0.644	-0.068	Tendency towards mutual exclusivity					

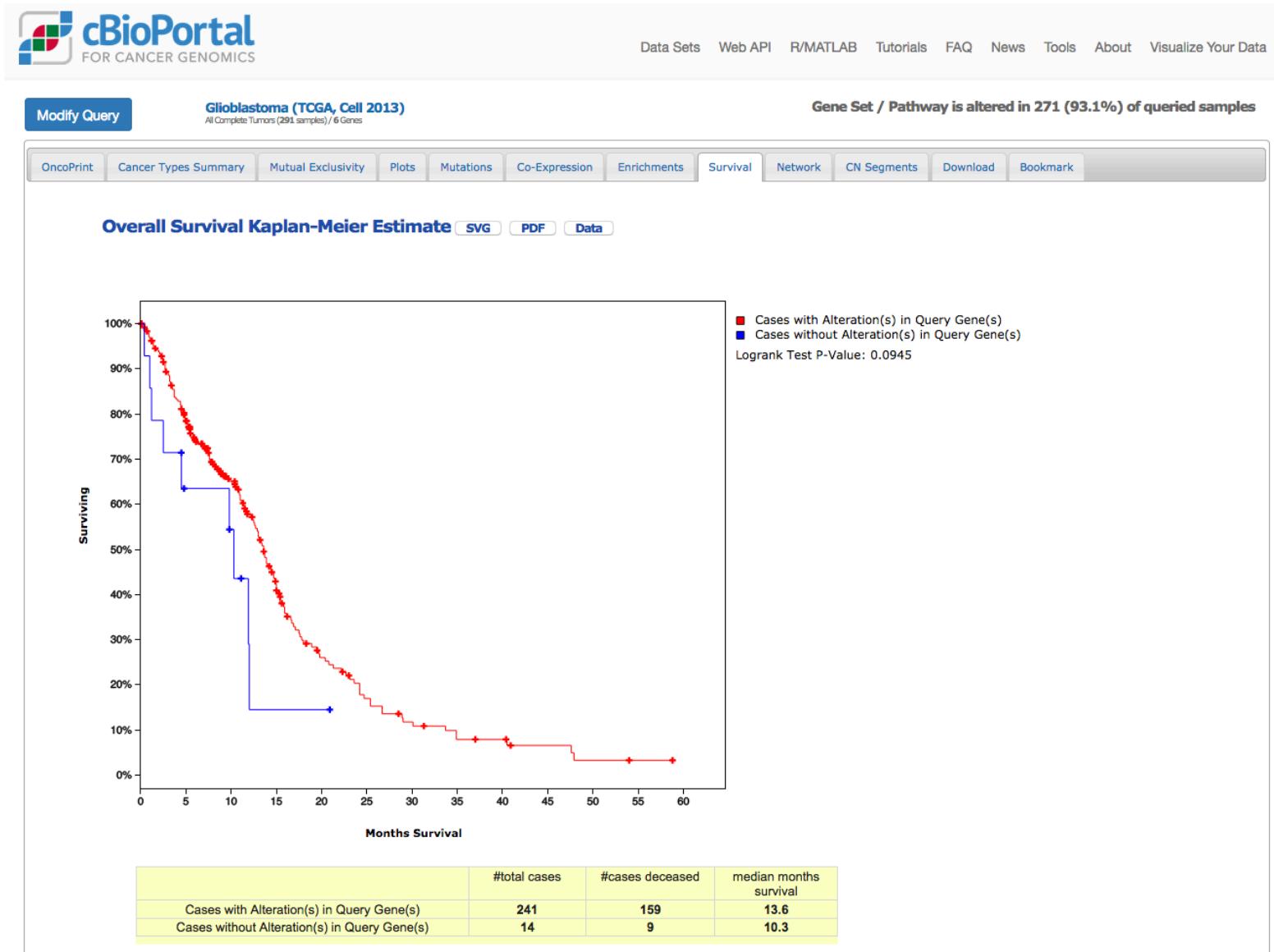
Showing 1 to 15 of 15 entries

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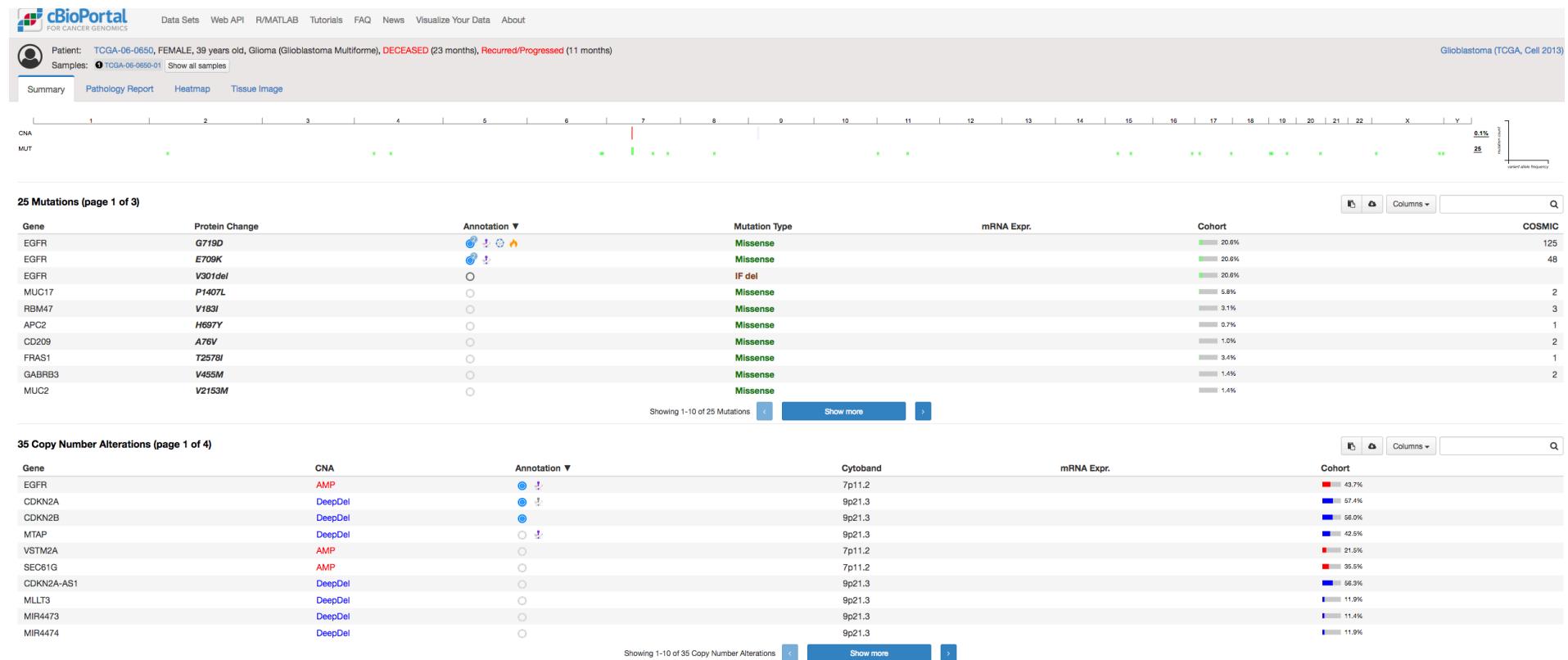
Results



Results



Results: TCGA-06-0650



Results

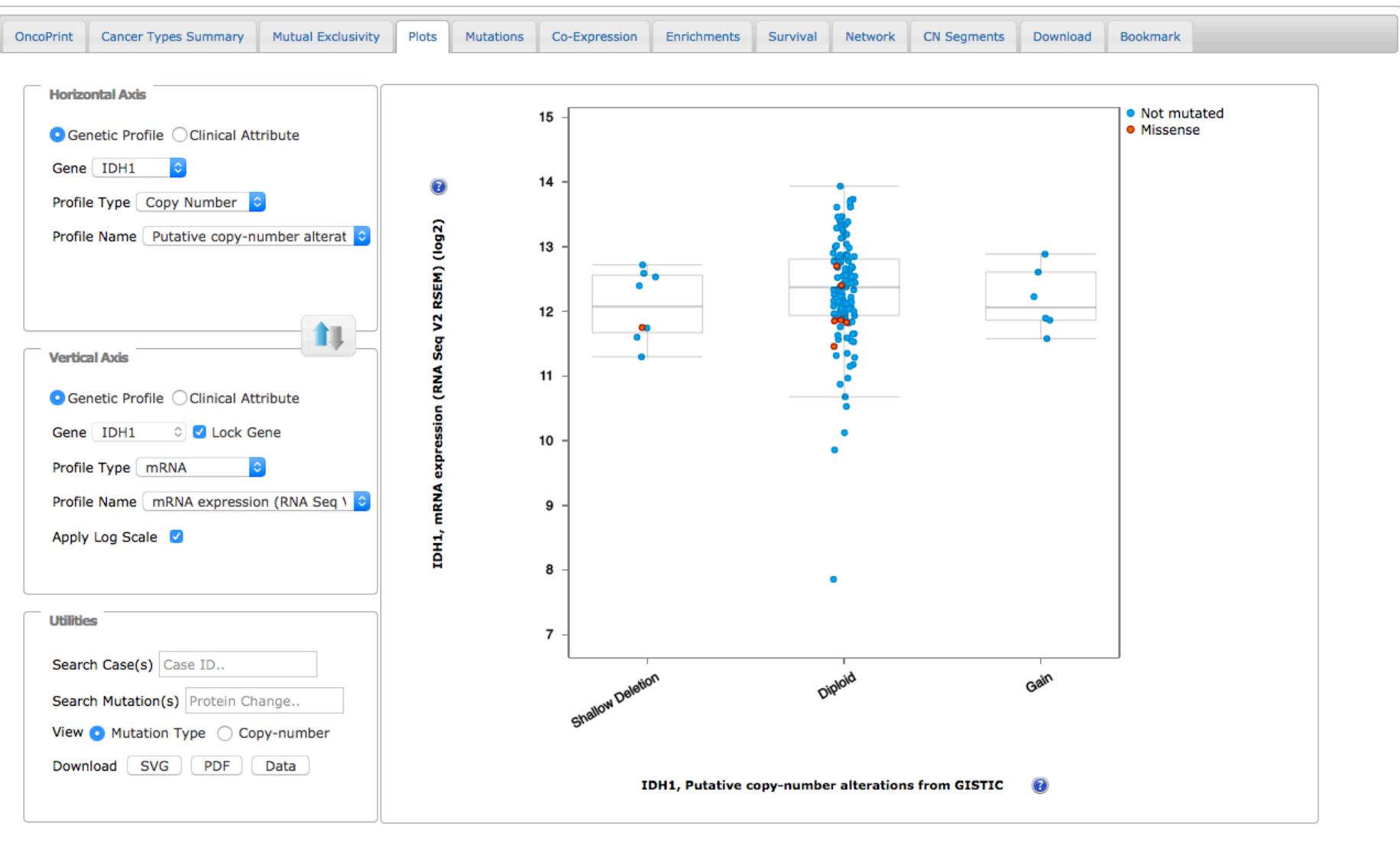


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Modify Query

Glioblastoma (TCGA, Cell 2013)
All Complete Tumors (291 samples) / 6 Genes

Gene Set / Pathway is altered in 271 (93.1%) of queried samples



Results

Modify Query **Glioblastoma (TCGA, Cell 2013)** All Complete Tumors (291 samples) / 6 Genes Gene Set / Pathway is altered in 271 (93.1%) of queried samples

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Data Set mRNA expression (RNA Seq V2 RSEM) This table lists the genes with the highest expression correlation with the query genes. Click on a row to see the corresponding correlation plot. ?

Correlated Gene	Cytoband	Pearson's Correlation	Spearman's Correlation
IDH1	Xq28	0.30	0.33
CDK4	Xq28	0.35	0.39
TP53	Xq28	0.37	0.39
CDKN2A	Xq28	0.32	0.34
EGFR	Xq28	0.35	0.45
RB1	Xq28	0.34	0.44
ATP6AP1	Xq28	0.30	0.33
DKC1	Xq28	0.35	0.39
HMGB3	Xq28	0.37	0.39
IDH3G	Xq28	0.32	0.34
MAGEA12	Xq28	0.35	0.45
VBP1	Xq28	0.34	0.44
NAA10	Xq28	0.39	0.43
UBL4A	Xq28	0.40	0.48
BCAP31	Xq28	0.39	0.42
BRCC3	Xq28	0.35	0.37
CXORF40B	Xq28	0.38	0.42
NSDHL	Xq28	0.39	0.42
TMLHE	Xq28	0.43	0.42
HAUS7	Xq28	0.32	0.38
CXORF40A	Xq28	0.33	0.36
UBE2NL	Xq27.3	0.40	0.35
PHF6	Xq26.3	0.34	0.36
RBMX	Xq26.3	0.42	0.44
MMGT1	Xq26.3	0.35	0.35
AIFM1	Xq26.1	0.38	0.39
UTP14A	Xq26.1	0.41	0.42
RBMX2	Xq26.1	0.47	0.49
XIAP	Xq25	0.43	0.38
STAG2	Xq25	0.38	0.40
SLC25A5	Xq24	0.47	0.57
UBE2A	Xq24	0.41	0.45
RNF113A	Xq24	0.40	0.41

1 to 30 of 4782 Download Full Results

mRNA co-expression: IDH1 vs. ATP6AP1

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ATP6AP1, mRNA expression (RNA Seq V2 RSEM)

IDH1, mRNA expression (RNA Seq V2 RSEM)

Results

