



Medical and genomic tools and databases

Precision Oncology Course

Summary

Gene & Protein DBs

Functional Enrichment

Cancer Collections & Browsers

Therapy response

Cancer dependencies

Survival, Clinical & other useful info

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Genes

NCBI Gene

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

Ensembl

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

GeneCards

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

Expression Atlas

<https://www.ebi.ac.uk/gxa/home>

Network of Cancer Genes

<http://ncg.kcl.ac.uk/index.php>

GTEx

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

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Protein

Tumor Protein Atlas

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

The Human Protein Atlas

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

Exercise

Gene & Protein DBs

Exercise 1: Using NCBI gene.

- Go to NCBI's Gene database
- Do an Advanced search for
 - Organism: **homo sapiens**
 - Gene/Protein Name: **EGFR**

On which chromosome is the gene located?

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

EGFR: epidermal growth factor receptor [Homo sapiens (human)]
Gene ID: 1956, updated on 29-Nov-2015

SUMMARY

Official Symbol:	EGFR provided by HGNC
Official Full Name:	epidermal growth factor receptor provided by HGNC
Primary source:	U08QUGHC0026
Date last revised:	January 09, 2008; previous version(s)
Cause type:	protein coding
MIMFastaFile:	NB-VT-0013
Organism:	Homo sapiens
Tissue:	Blood; Brain; Colon; Esophagus; Kidney; Liver; Muscle; Pancreas; Skin; Stomach; Testis; Uterus; Vagina; Whole Blood
Amino Acids:	1041; H-D-E-T-Y-S-A-L-N-H-R-I-K-G-Q-M-S-P-W

Description: 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 self-protein activation. Mutations in this gene are associated with lung cancer. Multiple alternatively spliced transcripts variants that encode different protein isoforms have been found for this gene. [provided by RefSeq, Jul 2013]

Orthologs: NCBI all

Exercise

Gene & Protein DBs

Exercise 1: Using NCBI gene.

Look at the **GeneRIFs** of this gene. GeneRIFs are short sentences that describe the function of a gene product that are extracted from scientific publications. NCBI encourages scientists to submit these GeneRIFs together with the Pubmed ID of the publication to the Gene database and curates the submissions. In this way you don't have to go through the scientific literature yourself to get idea about the function of a gene product.

What is the function of the protein encoded by this gene ?

Check out al other info that you find here for EGFR and try to do a search on your favourite gene to see if you can find any new info on it.

Exercise

Gene & Protein DBs

Exercise 2: Using Ensembl

Search the human EGFR gene.

- Select the Human genome to search in
- Search for EGFR
- Click Go
- Click the EGFR (Human gene) link to go to the gene page of EGFR.



The screenshot displays the Ensembl genome browser interface. At the top, the Ensembl logo is visible alongside navigation links for BLAST/BLAT, Search, Tools, Downloads, Help & Documentation, Blog, and Mirrors. A search bar on the right contains the text 'EGFR'. Below the header, the 'Gene-based display' sidebar on the left lists various genomic data tracks, including Summary, Transcript comparison, Supporting evidence, Gene models, Sequence, Secondary structure, Protein structure, Regulation, Comparative Genomics, Genomic alignments, Annotations, Disease, Gene expression, Ontologies, Paralogs, Functional protein families, Phenotype, Genetic Variation, Variant table, Variant image, Structural variants, External data, Data representation, and Personal annotation. The main content area is titled 'Gene: EGFR' and provides detailed information about the gene, including its description as 'epidermal growth factor receptor (EGFR)', its location on 'Chromosome 7: 25,019,021-25,053,320 forward strand', and a summary of its function. A 'Show transcript table' button is also present.

Ensembl

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


Exercise


Gene & Protein DBs

Exercise 2: Using Ensembl

- On which chromosome and which strand of the genome is this gene located?
- How many transcripts (splice variants) does this gene have?
- How many CCDS are annotated for this gene?
- What's the name of the longest transcript?
- How long is the protein it encodes?
- Compare the sequence of the two longest protein-coding transcripts.

GeneCards <http://www.genecards.org/>







**GeneCards®**
HUMAN GENE DATABASE

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: G007P055019 ⓘ
GIFs: 74 ⓘ

[Jump to section](#)

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[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 ^{2 4}

Erb-B2 Receptor Tyrosine Kinase ^{2 3}

Proto-Oncogene C-ErbB-1 ^{3 4}

EC 2.7.10.1 ^{4 63}

ERBB1 ^{3 4}

ERBB ^{2 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



Tumor protein atlas <http://www.proteinatlas.org/>

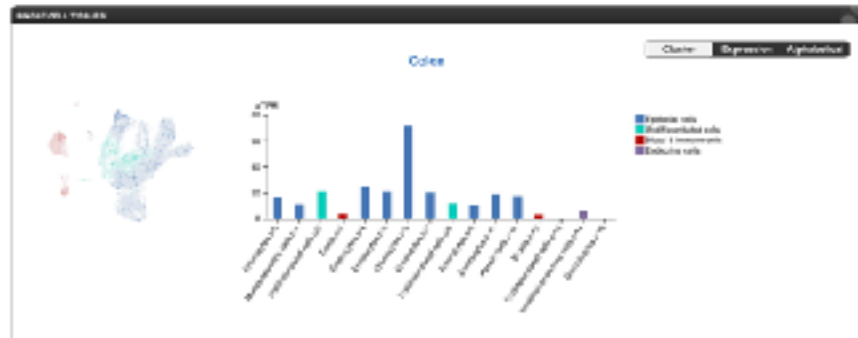
EGFR



GENERAL INFORMATION	
Gene name ¹	ECFP1
Gene description ²	EDENTIN-1 GROWTH FACTOR RECEPTOR
Protein class ³	Cancer-related genes Disease related genes Enzymes FDA approved drug targets Plasma proteins RAS pathway related proteins
Predicted location ⁴	Intracellular, Membrane span, Secretion
Number of transcripts ⁵	5

SUBCELLULAR PROTEIN ATLAS: LOCALIZATION	
RNAi screen reproducibility ¹	Tissues enhanced (glial cells)
RNAi screen distribution ²	DETECTED initially
Protein evidence ³	Evidence of protein level
Protein expression ⁴	Membranous and cytoplasmic expression in several tissues, most abundant in glial cells.

Data reliability description	Medium consistency between antibody staining and RNA expression data. At least one protein variant sequenced, tissue location of RNA and protein might differ and nomenclature is complex.
Reliability score ²	Enhanced
Antibodies ³	HPA0123X, HPA01533, CAB00695, CAS80885, CAB07254



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Gene Expression Signatures

MSigDB

<http://software.broadinstitute.org/gsea/msigdb/annotate.jsp>

Enrichr

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

Harmonizome


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

GeneMania

<http://genemania.org/>

Functional Enrichment

- Go to <https://maayanlab.cloud/Enrichr/>
- Expand into a gene set the term:
triple negative breast cancer
- Submit the query
- Go to the Diseases/Drugs section
- Check the COVID-19 related gene sets 2021 collection



[login / register](#)
[10,124,345 genes analyzed](#)
[572,345 terms](#)
[140 databases](#)

[Analyze](#)
[What's new?](#)
[Uploads](#)
[Gene search](#)
[Term search](#)
[About](#)
[Help](#)

Input data

Expand a gene, a term, or a variable into a gene set

Try an example [Lipid A biosynthesis](#) [muscle cell](#)
 Include the top 100 most relevant genes

Expanded [Lipid A biosynthesis](#) into a gene set
 expression matrix by identifying the top 100 genes that
 are co-expressed with [ESR1](#)

Expand gene sets
[Lipid A biosynthesis](#) [muscle cell](#) [muscle cell](#)

Alternatively, try the [Gene Search](#) or the [Term Search](#)
 features to find an already Enrichr gene set.

☐
 Combine your sets or sets be selected by others

Please acknowledge Enrichr in your publications by citing the following references:

Chen H, Tanaka K, Wu S, Buatois D, McInnes J, Shi D, McInnes K
 Enrichr: interactive and collaborative HPD data enrichment analysis tool. BMC Bioinformatics. 2016;17:171

Enrichr: An integrative and collaborative HPD data enrichment analysis tool. BMC Bioinformatics. 2016;17:171

Enrichr: An integrative and collaborative HPD data enrichment analysis tool. BMC Bioinformatics. 2016;17:171

Chen H, Tanaka K, Wu S, Buatois D, McInnes J, Shi D, McInnes K
 Enrichr: An integrative and collaborative HPD data enrichment analysis tool. BMC Bioinformatics. 2016;17:171

Chen H, Tanaka K, Wu S, Buatois D, McInnes J, Shi D, McInnes K
 Enrichr: An integrative and collaborative HPD data enrichment analysis tool. BMC Bioinformatics. 2016;17:171

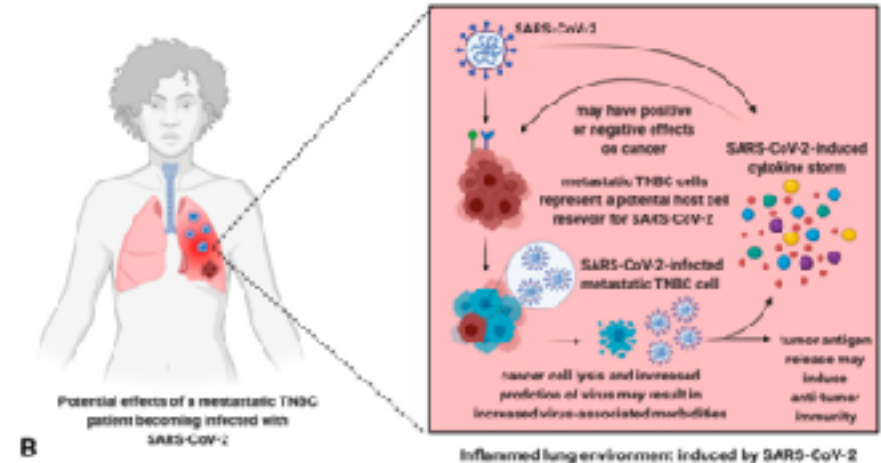
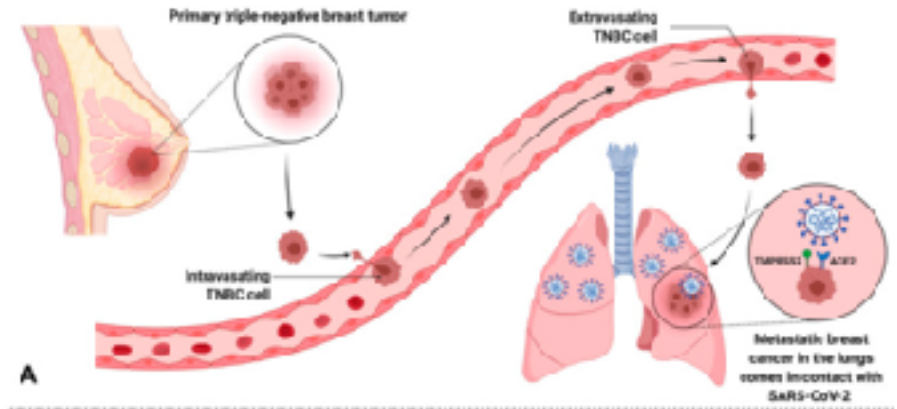
Exercise

Functional Enrichment


Metastatic breast cancer cells may represent an additional host cell SARS-CoV-2 reservoir, leading to increased viral load and virus-associated morbidities, and unknown consequences on the progression of the cancer.

Source:

Brown JM, Wasson MD, Marcato P. Triple-Negative Breast Cancer and the COVID-19 Pandemic: Clinical Management Perspectives and Potential Consequences of Infection. *Cancers*. 2021 Jan;13(2). DOI: 10.3390/cancers13020296. PMID: 33467411; PMCID: PMC7830590.



MSigDB <http://www.software.broadinstitute.org/gsea/msigdb>



Gene Set Enrichment Analysis

[logi](#)
[register](#)

[GSEA Home](#) [Downloads](#) [Molecular Signatures Database](#) [Documentation](#) [Contact](#)

- MSigDB Home
- About Collections
- Browse Gene Sets
- Search Gene Sets
- Investigate Gene Sets
- View Gene Families
- Help



MSigDB
Molecular Signatures
Database

Molecular Signatures Database v6.2

Overview

The Molecular Signatures Database (MSigDB) is a collection of annotated gene sets for use with GSEA software. From this web site, you can

- **Search** for gene sets by keyword.
- **Browse** gene sets by name or collection.

Collections

The MSigDB gene sets are divided into 8 major collections:

H **hallmark gene sets** are coherently expressed signatures derived by aggregating many MSigDB gene sets to represent well-defined biological states or processes.

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Pathways and Networks

Networks: STRING

<http://string-db.org>

PATHiVAR

<http://pathivar.babelomics.org>

WikiPathways

<https://www.wikipathways.org/index.php/WikiPathways>

KEGG

<https://www.genome.jp/kegg/>

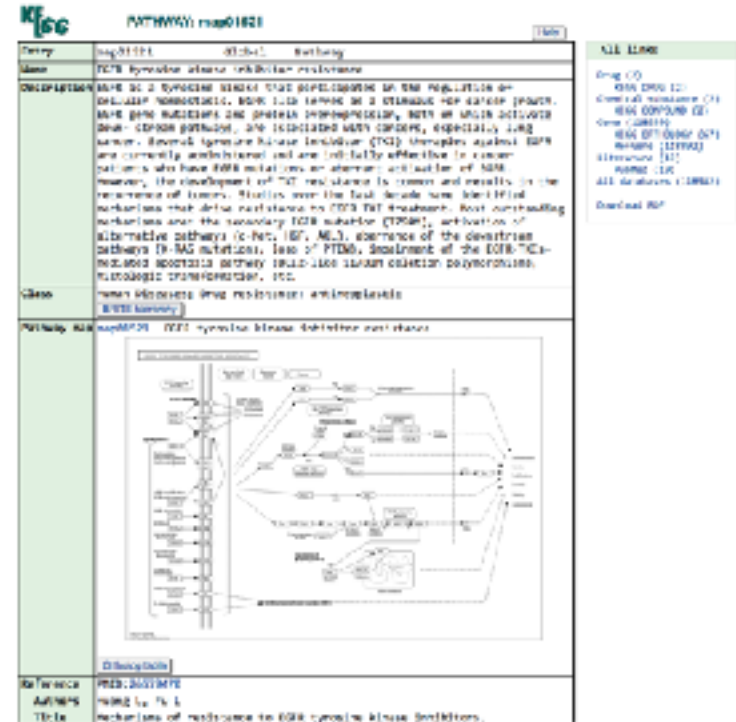
Exercise

Functional Enrichment

Exercise: Using KEGG

- Go to <https://www.genome.jp/kegg/>
- Load a map of the EGFR tyrosine kinase inhibitor resistance pathway

What are the names of the chemical compounds that are related to the EGFR pathway according to KEGG ?



Exercise

Functional Enrichment

Exercise: Using STRING

Go to the STRING [website](http://string-db.org) <http://string-db.org>

How to find the interaction network of a protein ?

On the top of the results page, the interaction network is visualized.

- The network nodes are proteins.
- The edges represent the predicted functional associations.
- The color of the edges reflects the evidence:

- Red line - indicates the presence of fusion evidence
- Green line - neighborhood evidence
- Blue line - cooccurrence evidence
- Purple line - experimental evidence
- Yellow line - textmining evidence
- Light blue line - database evidence
- Black line - coexpression evidence.



Wikipathways <https://www.wikipathways.org/index.php/WikiPathways>

BETA
WIKIPATHWAYS
Pathways for All

Search

Find Pathways

How to use:

- Home
- About Us
- Contact Us
- Help & Support
- How to use

Download:

- Download files
- WEGO service API
- WikiPathways API
- Download data

Activity:

- Browser pathways
- Recent changes
- New pathways
- WikiPathways
- Create pathway
- Statistics

Welcome to WikiPathways BETA

WikiPathways is a database of biological pathways maintained by and for the scientific community.

Find Pathways

Search

Search

You can search by:

- Pathway name (topology)
- Gene or protein name (PDB)
- Gene name or function (function)

Get Pathways

Download

Download by species

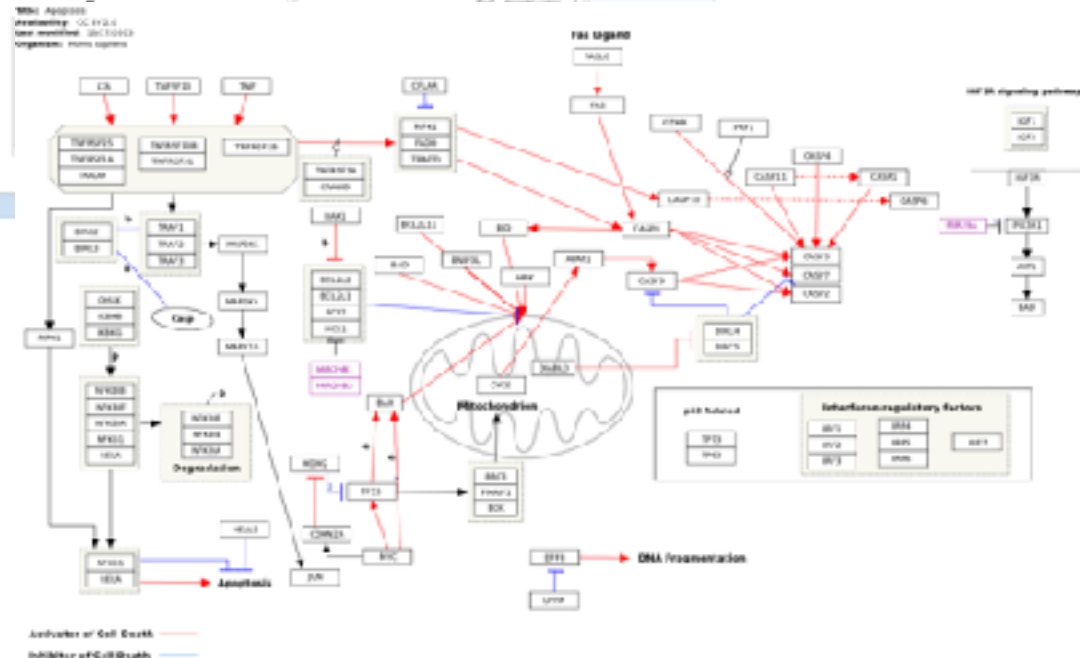
Download by species

Download by species

Today's Featured Pathway

Ascorbic Acid Biosynthesis (Ascidicola thalassae)

Ascorbic Acid Biosynthesis (Ascidicola thalassae)



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Collections

NCI60

<https://discover.nci.nih.gov/cellminer/>

Cancer Cell Line Encyclopedia

<https://portals.broadinstitute.org/ccle>

International Cancer Genome Consortium

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

The Cancer Genome Atlas

<https://cancergenome.nih.gov/>

COSMIC

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

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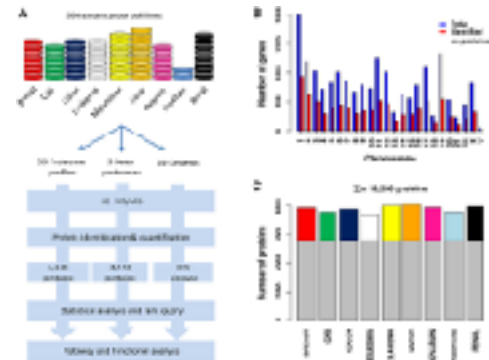
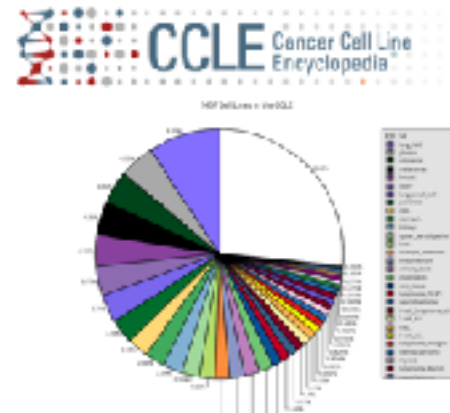
Cell lines

NCI60

<https://discover.nci.nih.gov/cellminer/>

Cancer Cell Line Encyclopedia

<https://portals.broadinstitute.org/ccle>



Amin Moghaddas Gholami, Hannes Hahne, Zhixiang Wu, Florian Johann Auer, Chen Meng, Mathias Wilhelm, Bernhard Kuster, Global Proteome Analysis of the NCI-60 Cell Line Panel, Cell Reports, Volume 4, Issue 3, 2013, Pages 609-620, ISSN 2211-1247 <https://doi.org/10.1016/j.celrep.2013.07.018>.

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Cancer Cell Line Encyclopedia

<https://portals.broadinstitute.org/ccle>

The Cancer Genome Atlas

<https://cancergenome.nih.gov/>

International Cancer Genome Consortium

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

Tumor samples

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Collections

NCI60

<https://discover.nci.nih.gov/cellr>

Cancer Cell Line Encyclopedia

<https://portals.broadinstitute.org>

The Cancer Genome Atlas

<https://cancergenome.nih.gov/>



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NCI60

<https://discover.nci.nih.gov/cellminer/>

Cancer Cell Line Encyclopedia

<https://portals.broadinstitute.org/ccle>

Tumor samples

 **ICGC Data Portal**

International Cancer Genome Consortium

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



Cancer projects	55
Cancer primary sites	41
Donors	12,979
Simple somatic mutations	16,159,160
Mutated genes	67,643

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<https://discover.nci.nih.gov/cellminer/>

Cancer Cell Line Encyclopedia

<https://portals.broadinstitute.org/ccle>

Tumor samples

 **ICGC Data Portal**

International Cancer Genome Consortium

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



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Cancer Cell Line Encyclopedia

<https://portals.broadinstitute.org/ccle>

International Cancer Genome Consortium

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

The Cancer Genome Atlas

<https://cancergenome.nih.gov/>

Both

COSMIC

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

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Browsers

**cBio Portal for Cancer
genomics**

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

Integrative Onco Genomics

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

Oncomine

<https://www.oncomine.org/resource/login.html>

TumorPortal

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

XenaBrowser

<https://xena.ucsc.edu/>

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GDSC

<http://www.cancerrxgene.org>

Cancer Cell Line Encyclopedia

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

Cancer Therapeutics Response Portal

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

Open Targets

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

Connectivity Map

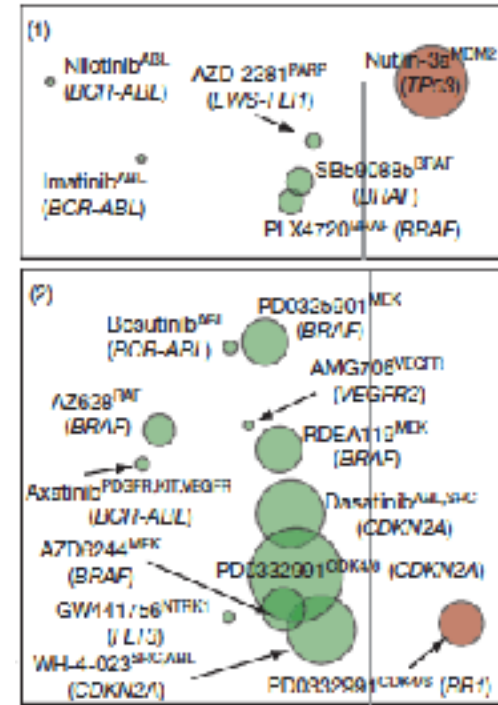
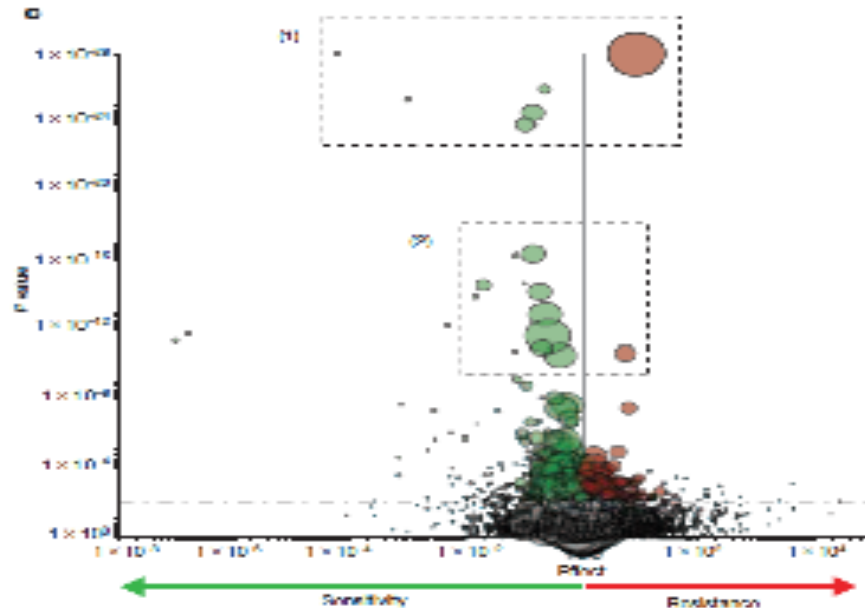
<https://clue.io/>

PanDrugs

<http://pandrugs.biinfo.cnio.es/>

Systematic identification of genomic markers of drug sensitivity in cancer cells

Matthew J. Garnett^{1*}, Elena J. Heston^{1*}, Sonja J. Heston^{1*}, Chris D. Greenman¹, Anahita Dastar¹, King Wai Lau¹, Patricia Grenier¹, David Thomson¹, Xi Li^{1,2}, Sarah Green¹, Christopher Lee^{1,4}, Emmanuel Leke^{1,5}, Fabrice Gaudin¹, Li Chen², Randy J. Milne¹, Rona Kogut¹, Wenjun Zou^{1,6}, Wanjuan Yang¹, Jeffrey A. Engel¹, Andrew P. Futcher¹



Exercise

Therapy response

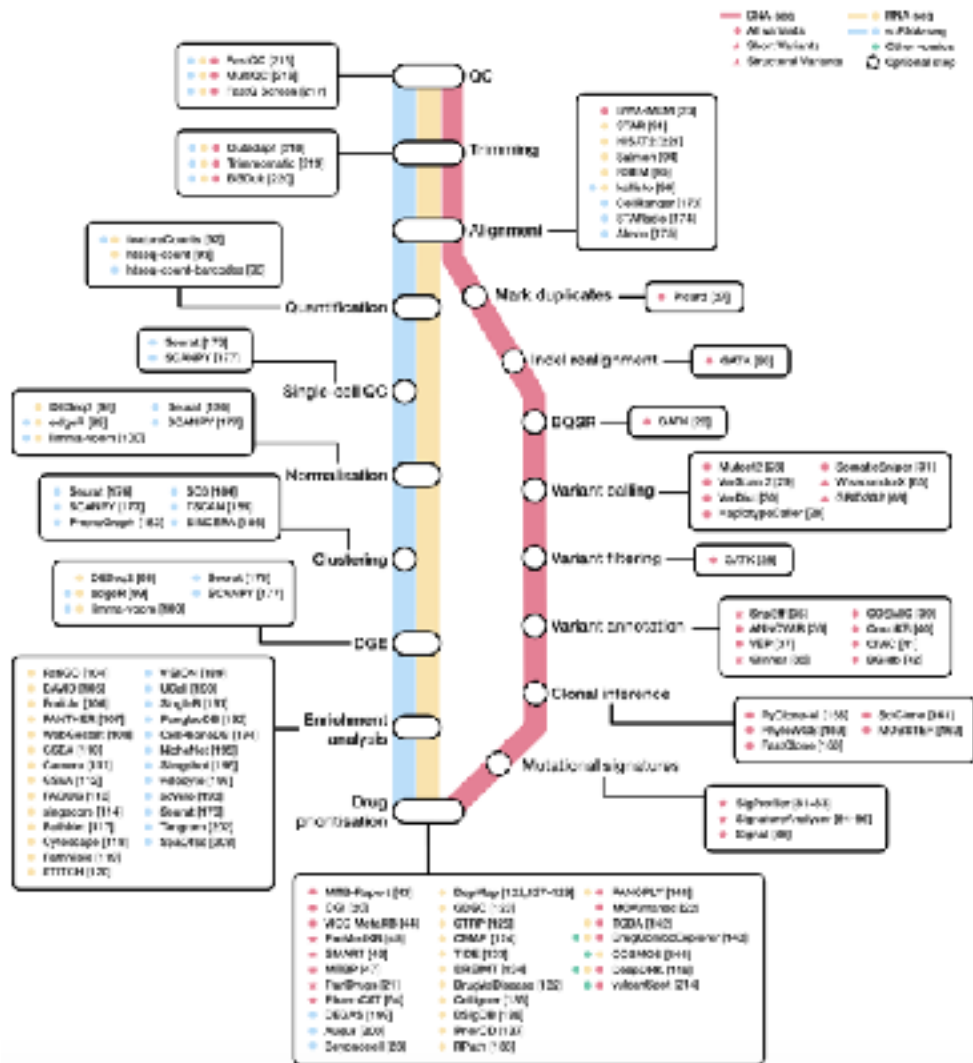
Exercise: Using GDSC

- Go to the GDSC [website](#)
- Look for the EGFR gene

To which drugs are sensitive the EGFR mutated cell lines?

- Choose a compound of interest
- Look for other sensitivity/resistance associations related to that same compound

Name	Description	Input	Output	URL
MTB-Report [43]	R script that filters and classifies cancer variants into levels of evidence using gene-drug databases.	Tables with SNVs, CNVs and/or gene fusions (somatic).	Molecular Tumour Board (MTB) report with actionable variants in PDF. Downloadable tables of a) Annotated variants, including information about the oncogenicity and biological consequence, and b) drug-variant associations with evidence level and response prediction.	https://github.com/jperera-be/MTB-Report
Cancer Genome Interpreter (CGI) [20]	Web tool that annotates cancer variants and identifies potential oncogenic alterations and genomic biomarkers of drug response.	List of SNVs, indels, CNVs and/or gene fusions (somatic).		https://www.cancergenomeinterpreter.org/home
ICCC MetaKB [44]	Web tool for cancer variant interpretation that harmonises 6 different variant annotation knowledgebases with information about variant, gene, disease and drug associations and their corresponding evidence levels.	List of variants (somatic), including gene fusions, genes, diseases and/or drugs.	Interactive report with variant-gene-disease-drug associations, each one with its evidence label and supporting links.	https://search.cancervariants.org/#/
PreMedKB [45]	Web tool for integrating information on diseases, genes, variants, drugs, and the relationships between any two or more of these four components.	List of short variants (somatic), genes, drugs and/or diseases.	Interactive semantic network displaying components as nodes and their relationships as edges. Results can be downloaded in either JSON or PNG format.	http://www.fudan-pgx.org/premedkb/index.html#/home
SMART Cancer Navigator [46]	Web application for variant interpretation that associates the corresponding genes to diseases, known drugs and relevant clinical trials.	List of short variants (somatic and germline).	Interactive report with variant, gene, disease and drug information.	https://smart-cancer-navigator.github.io/home
PanDrugs [21]	Web tool to prioritise anticancer drug treatments according to individual genomics data. PanDrugs computes two scores, the Gene Score (GScore) and the Drug Score (DScore). The GScore ranges from 0 to 1 and is estimated according to gene essentiality and tumoural vulnerability, gene relevance in cancer, the biological impact of mutations, the frequency of gene alterations and their clinical implications. The DScore ranges from -1 to 1, considers drug indication and status, gene-drug associations and number of hits and estimates resistance (negative values) or sensitivity (positive values).	VCF, a list or a ranking of genes or a drug query (somatic).	Report with a prioritised list of anticancer therapies. PanDrugs resolves the Best Therapeutic Candidates based on the accumulated and weighted scoring of the GScore and the DScore.	https://www.pandrugs.org/#/
MTBP [47]	Web tool that annotates somatic and germline short variants (SNVs and indels) functionally and clinically, categorising the cancer biomarkers (diagnosis, prognosis and drug response) found in the tumour.	VCF or a list of short variants (somatic and germline).	HTML report with annotated variants, the evidence supporting the variants' functional classification and their associated actionability.	https://mtbp.org/
PharmCAT [54]	A tool for identifying germinal variants, inferring patients' haplotypes and genotypes and suggesting treatments following the Clinical Pharmacogenetics Implementation Consortium (CPIC)	VCF (germline).	HTML/JSON report with drug suggestions based on germinal variants.	https://pharmacat.org/



Jiménez-Santos et al. 2022 coming soon

Connectivity Map <https://clue.io>



ConnectivityMap



Unravel biology with the world's largest
perturbation-driven gene expression dataset.

> TYPE COMPOUND, GENE, MoA, OR PERTURBAGEN CLASS TO SEE OVERVIEW
> TYPE A SLASH CHARACTER "/" TO SEE LIST OF COMMANDS

DATA VERSION: 1.1.1.2 / SOFTWARE VERSION: 1.1.1.36

CONNECTIVITY MAP LAUNCHES THIRD CROWDSOURCED CONTEST

The Connectivity Map team at the Broad Institute is happy to announce its latest crowdsourced contest, launched in collaboration with the Laboratory for Innovation challenge is focused on enhancing the CMap 1,000 in total prizes available. [Register today](#)

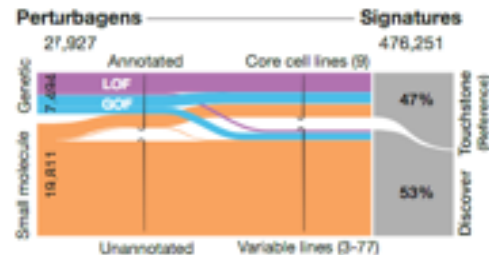
The aim is to generate perturbational profiles across multiple cell and perturbation types

- Small Molecules
 - 1300 FDA approved drugs
 - 5500 bioactive compounds
- Gene Knock-Outs and Over Expression

Data and Tools

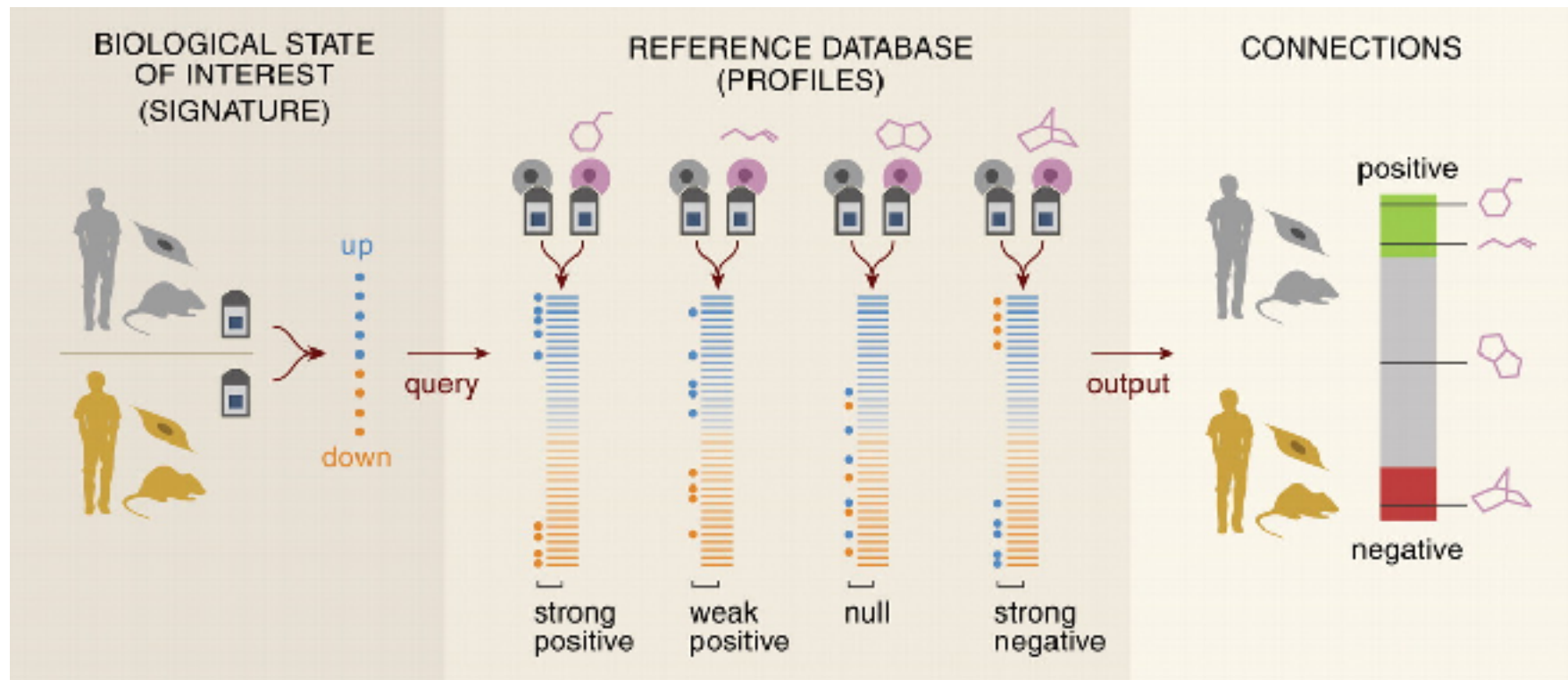
The CMap dataset of cellular signatures catalogs transcriptional responses of human cells to chemical and genetic perturbation. Here you can find the 1.3M L1000 profiles and the tools for their analysis.

A total of 27,927 perturbagens have been profiled to produce 476,251 expression signatures. About half of those signatures make up the Touchstone (reference) dataset generated from testing well-annotated genetic and small-molecular perturbagens in a core panel of cell lines. The remainder make up the Discover dataset, generated from profiling uncharacterized small molecules in a variable number of cell lines.



Start exploring the data by using the text-box on this page to look up perturbagens of interest in Touchstone. To see the suite of tools, including apps to query your gene expression signatures and analyze resulting connections, click on Tools in the menu bar.

Connectivity Map <https://clue.io>



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Cancer Dependencies

DepMap

<https://depmap.org/portal/>

CancerGD

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

vulcanSpot

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

Cancer dependency map <https://www.depmap.org/portal/>



CancerGD: analysis of genetic dependencies in cancer

Search filter: Driver gene: Tissue type: Study:

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](#) | [dBioPortal](#) | [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.)

for 1990 rows (max: 300)

Dependency	P-value	Effect size (%)	ΔScore	Study	Experiment Type	Multiple Hit	String Interaction	Inhibitors
<input type="text" value="Search"/>	<0.05	>= 66.0	< 0.0	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>
MTOR	1×10^{-6}	92.5	-1.89	Cowley(2014)	shRNA	Yes	High	GDC-0680..[new]
PSMC2	1×10^{-6}	93.7	-2.45	Marocotte(2012)	shRNA			BORTEZO..[new]
ERBB2	4×10^{-6}	87.6	-1.78	Campbell(2015)	siRNA	Yes	Highest	AEE 788..[new]
HIST1H2AK	4×10^{-6}	89.3	-0.73	Cowley(2014)	shRNA			

vulcanspot https://www.vulcanspot.org

[illegible]

Summary

Gene & Protein DBs

Functional Enrichment

Cancer Collections & Browsers

Therapy response

Cancer dependencies

Survival, Clinical & other useful info

VCF annotators

Variant Effect Predictor

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

SnpEff

<http://snpeff.sourceforge.net/>

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Clinical Variants Annotators

ClinVAR

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

ExAC

<http://exac.broadinstitute.org>

gnomAD

<http://gnomAD.broadinstitute.org>

Kaplan-Meier Plotter Lung Cancer

Study ID/Name: M2009_001 [View analysis details](#)

Survival: OS (0-1000)

Split patients by: sex [Auto select best cutoff](#) [?](#)

Follow up threshold: at [Censor at threshold](#) [?](#)

Complete median event time selected: [?](#)

Protein test options

- ☒ Use selected protein set
- ☐ Use all protein sets per gene [?](#)
- ☐ Only test test protein set [?](#)

Plot downstream graph of protein distributions: [?](#)

Using the selected parameters, the analysis will run on **1000** patients [?](#)

Restrict analysis to subtypes...

Histology: all [?](#)

Stage: all [?](#)

AJCC stage I: all [?](#)

AJCC stage II: all [?](#)

AJCC stage III: all [?](#)

AJCC stage IV: all [?](#)

Gender: all [?](#)

Smoking history: all [?](#)

Restrict analysis to treatment groups...

Surgery success: all [?](#)

Chemotherapy: all [?](#)

Radiotherapy: all [?](#)

Use selected cohorts

Cohort: all [?](#)

Cox regression

- ☒ univariate [?](#)
- ☐ multivariate [?](#)

Use online release of the database:

Apply quality controls: [Full release](#) [?](#)

[Restrict release to selected IDs](#) [?](#)

[View Kaplan-Meier plot](#)

n = number of patients with available data: 4029

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

How to cite: Györfi D, Szekely T, Buzsaki J, Lencsik A. Online survival analysis software to assess the prognostic value of biomarkers using transcriptomic data in non-small-cell lung cancer. *PLoS One*. 2013 Oct 28;8(10):e82213. doi: 10.1371/journal.pone.0082213. [?](#)

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Survival Analysis

<https://www.tcga-survival.com/> **Cell Reports 2022**

[https://bbisr.shinyapps.winship.emory.edu/
SurvivalGenie/](https://bbisr.shinyapps.winship.emory.edu/SurvivalGenie/)

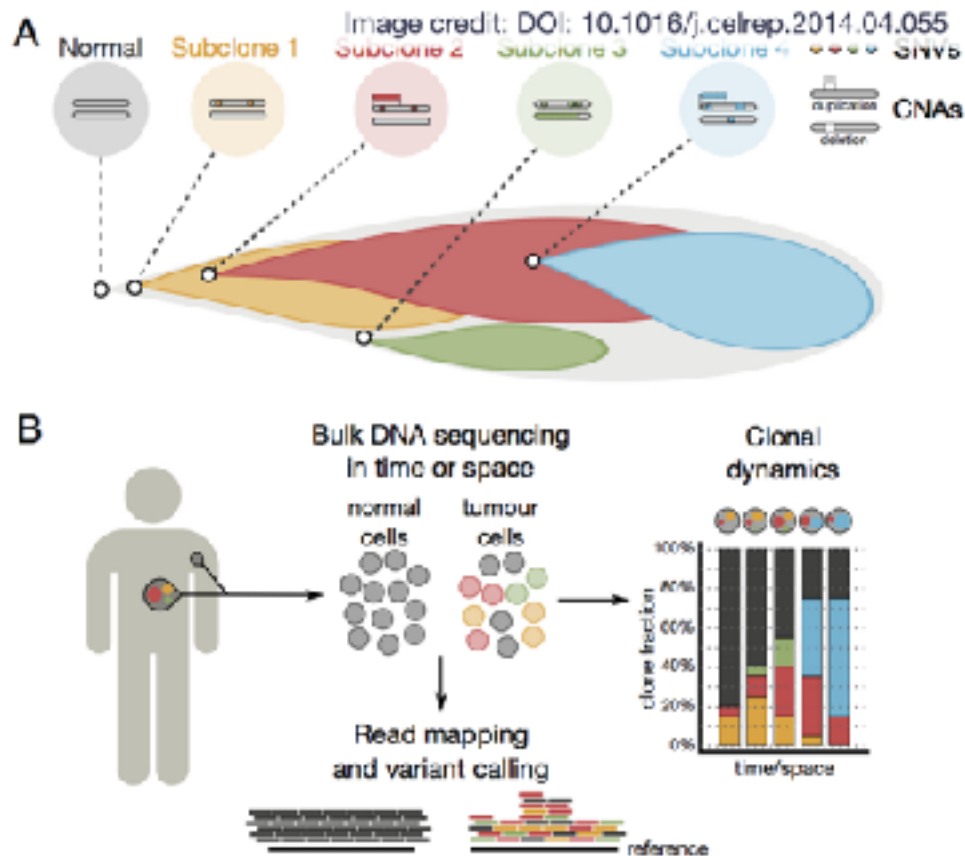
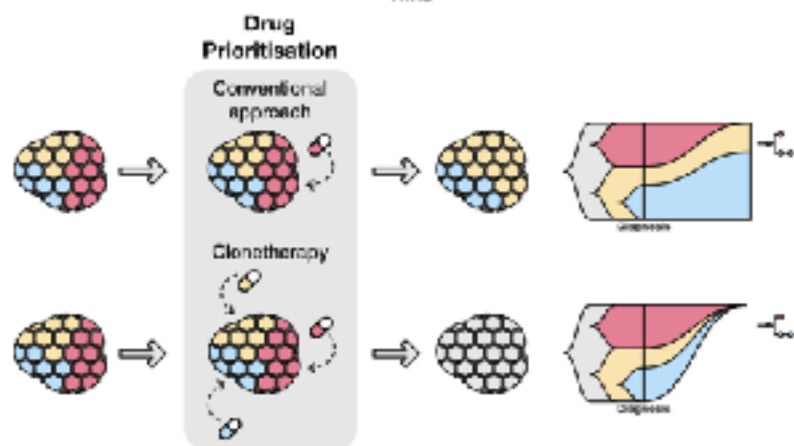
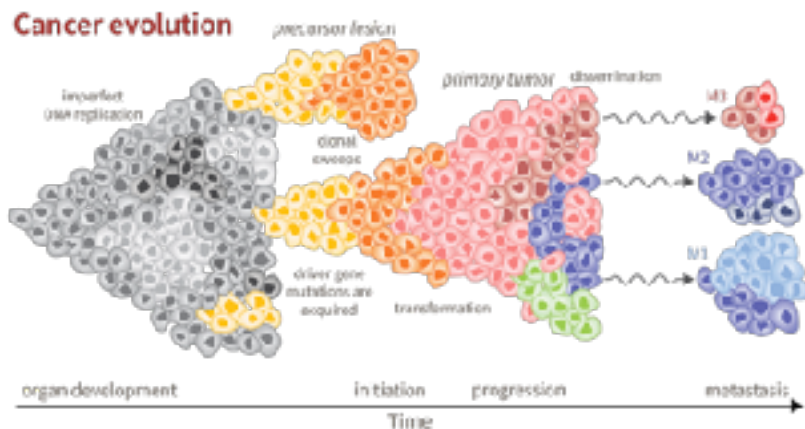
Survival: Kaplan Meier Plotter
<http://kmplot.com/analysis/index.php>

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


Other

Tumour clonality

<http://tracex.co.uk/>




PyClone2, FastClone, Subclone, etc

DREIMT

Drug prioritizationSignature comparisonDatabaseHelpREST APIQuery history

Welcome to



A tool for immune modulation drug prioritization

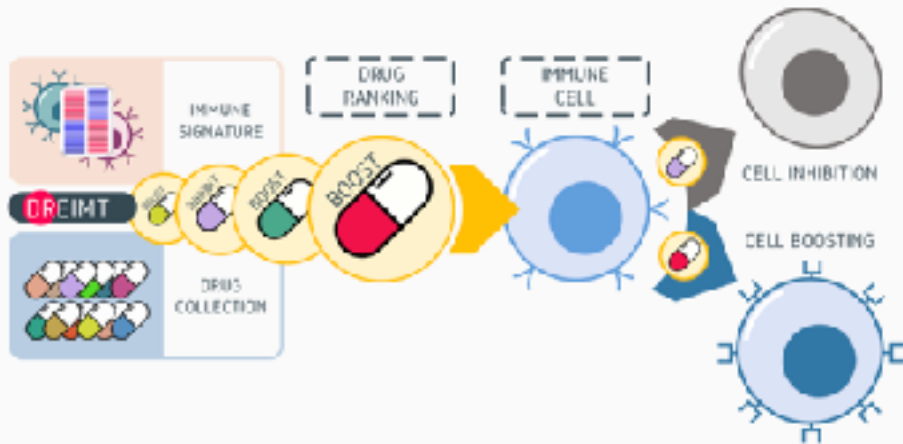
Drug prioritizationSignature comparisonDatabase

What is DREIMT?

DREIMT is a bioinformatics tool for hypothesis generation and prioritization of drugs capable of modulating immune cell activity from transcriptomics data.

DREIMT integrates 4,694 drug profiles from The Library of Network-Based Cellular Signatures (LINCS) L1000 data set and 2,687 manually curated immune gene expression signatures from multiple resources to generate a drug-immune signature association database.

DREIMT can also prioritize drug associations from user-provided immune signatures.



The diagram illustrates the DREIMT workflow. It starts with 'IMMUNE SIGNATURE' (represented by a virus icon) and 'DRUG COLLECTION' (represented by a grid of colored circles). These inputs feed into the 'DREIMT' tool (represented by a yellow circle with a red 'DREIMT' label). The output of DREIMT is 'DRUG RANKING' (represented by a yellow circle with a red 'DREIMT' label) and 'IMMUNE CELL' (represented by a blue circle with a red 'DREIMT' label). The 'IMMUNE CELL' then leads to 'CELL INHIBITION' (represented by a grey circle) and 'CELL BOOSTING' (represented by a blue circle). The 'CELL INHIBITION' and 'CELL BOOSTING' outcomes are further detailed by 'CELL INHIBITION' and 'CELL BOOSTING' icons (represented by a virus and a cell respectively).

Extra

Downloading the reference genome

- **Gencode:** <https://www.gencodegenes.org/>
- **UCSC:** <https://hgdownload.soe.ucsc.edu/downloads.html>

Downloading published experiments

- **GEO:** <https://www.ncbi.nlm.nih.gov/geo/>
- **SRA:** <https://www.ncbi.nlm.nih.gov/sra>
- **Single Cell Portal:** https://portals.broadinstitute.org/single_cell

