Open Targets: integrating genetics, omics and chemistry for drug discovery

Cancer Research UK
Therapeutic Discovery Laboratories

31st January 2019

Denise Carvalho-Silva

Open Targets / EMBL-EBI
United Kingdom

Notes

This booklet is based on the December 2018 release (18.12) of the Open Targets Platform. These are some useful links:

1) Open Targets - Scientific overview
https://www.opentargets.org/science/

2) Open Targets Platform documentation
https://docs.targetvalidation.org/

3) Platform frequently asked questions
https://docs.targetvalidation.org/faq/frequently-asked-questions

4) Videos and animations
https://tinyurl.com/opentargets-youtube

5) Cite us
http://bit.ly/cite-us

Questions or suggestions?
support@targetvalidation.org

TABLE OF CONTENTS

OVERVIEW

Open Targets is a partnership to transform drug discovery through the systematic identification and prioritisation of targets.

We work to create a research and development (R&D) framework that can be applied to a wide range of human diseases. We share our results openly with the scientific community.

The consortium was launched in March 2014 under the name of Centre for Therapeutic Open Targets (CTTV) and started with GlaxoSmithKline (http://www.gsk.com/), the Wellcome Sanger Institute (http://www.sanger.ac.uk/) and the EMBL-EBI (European Bioinformatics Institute) (http://www.ebi.ac.uk/). In February 2016, Biogen (https://www.biogen.com/) joined the initiative. The consortium was rebranded to Open Targets in April 2016, and has welcome two three new partners since, namely Takeda in 2017), and Celgene and Sanofi, both in 2018.

In drug discovery, the *validation* of a target refers to the creation of a specific entity that modulates the activity of a target to provide therapeutic benefit to individuals with a disease.

The ultimate validation of a target is the creation of an effective therapeutic molecule. This is a long and costly endeavour with more high failure rates.

The goal of Open Targets is to transform this process by predicting if the modulation of a target is likely to provide therapeutic benefit. This would be done much earlier in the drug discovery process than is currently possible and far in advance of having a final, approved medicine.

Points covered in this workshop:
- The science carried out in Open Targets
- The Open Targets Platform
- How to browse the web interface of the Platform
- Alternative ways to access the Open Targets Platform data

INTRODUCTION TO OPEN TARGETS

Open Targets employs large-scale human genetics and genomics data to change the way drug targets are identified and prioritise. We have established a set of scientific projects to both **integrate** and **generate** data and analytical processes that implicate a target as valid.

Our experimental projects use CRISPR gene editing, induced pluripotent stem cells, single cell genomics, organoids to generate new data and provide insights in the validation of targets relevant to key therapeutic areas namely:

- Oncology

- Immunology

- Neurodegeneration

Our core bioinformatics and data pipelines team has developed the Open Targets Platform to provide easy access to data relevant to drug target identification and selection by a diverse audience of users.

More details on our projects can be found on our [Scientific Overview](#) page. The first set of results from our experimental work in Oncology is currently available on bioRxiv. Our paper is entitled "[Prioritisation of oncology therapeutic targets using CRISPR-Cas9 screening](#)".

The Open Targets Platform

The Open Targets Platform is a web application that integrates and displays publicly available data to facilitate the identification and selection of targets for new therapies.
We use genetics, omics and chemical data from different [data sources](#) to associate genes and diseases. Similar data sources are combined into the following data types:

> Genetic associations
> Somatic mutations
> Drugs

Pathways & systems biology
RNA expression
Text mining
Animal models.

The evidence (e.g. SNPs, scientific literature) is used to compute an association score, which depends on the frequency of evidence, the confidence and severity (e.g does the SNP change the amino acid of the target protein?). We then aggregate the evidence score using the sum of the harmonic progression to obtain the score at the data source and data type levels, as well as the overall score. The association score can be used to rank target and disease associations in the Platform. The latest release of the Platform (December 2018) contains:

- 28,386 targets

- 10,053 diseases

- 3,050,013 associations between targets and diseases

- 6,491,946 evidence

The Open Targets Platform is an open source and open access tool that can be applied in a variety of use cases in academia (e.g. understand disease biology) and pharma industry (e.g. target identification and prioritisation).

What can you do with the Open Targets Platform?

- Find which targets are associated with a disease
- Find which diseases are associated with a target
- Find the evidence supporting target-disease associations
- Find annotations for targets e.g. tractability data
- Find annotations for diseases
- Use the batch search tool to search for a list of targets
- Carry out more complex queries using the REST-API
- Download all evidence and association objects for downstream analyses

Connect with us
❖ Open Targets Blog

❖ Follow us on Twitter, Facebook, LinkedIn, and YouTube

We will guide you through the website using multiple sclerosis (MS), as an example of a disease, then we will explore the evidence associating CD86 with MS.

The following points will be addressed during the walkthrough:

- o How to find targets associated with multiple sclerosis
- o How to filter down the number of targets based on specific type of evidence
- o How to find out how strong the association between CD86 and MS is
- o How to view the evidence that supports this association
- o How to find other diseases (than MS) associated with CD86
- o How to visualise CD86 in the context of the human genome
- o How to find drugs currently in clinical trials for CD86
- o How to filter the Open Targets associations by a list of genes already known to be linked to MS

Demo 1: Disease centric workflow

Go to www.targetvalidation.org:

Search for ovarian carcinoma and select the first hit to be directed to a page like this:

The current release of the Open Targets Platform (December 2018) lists 5500 targets associated with ovarian carcinoma.

The above table is sorted by default with the best hit at the top of the table i.e. BRCA1. This first target is the gene that contains the most compelling set of supporting evidence. This is summarised by the overall association score. The association score can vary from 0 to 1; the closer to 1 the more evidence we have for an association. This score is computed for each piece of evidence that is used to support the association. Then individual evidence scores within a data source are aggregated into one data source score followed by the aggregation of data source scores into a common data type score. The Overall association score column in the above table is the aggregation of all data source scores.

Note 1: whenever we aggregate scores (e.g. evidence and data source), we apply a harmonic sum.

Note 2: The ranking in the image above (e.g. BRCA1 > BRCA2 > RAD51C) relies on the number of evidence available for the individual associations. Although the overall association score is 1 for all of those three targets, we have more evidence available for BRCA1, hence it comes before BRCA2.

We also give different weight to different data types whilst computing our score. RNA expression, animal models and text mining data are all down weighted by a factor of 0.2. Sysbio is also down weighted by a factor of 0.5.

You can sort the table by alphabetical order of the list of targets, or by the association score values (either overall or per data type e.g. Genetic associations, Drugs, Text mining, etc).

Check our help page to find out more about our data sources: https://docs.targetvalidation.org/data-sources/data-sources

The association table (heatmap) listing all > 5,000 targets associated with ovarian carcinoma can be filtered by six categories:

1) Data types

2) Pathway types

3) Target class

4) RNA tissue specificity

5) Target tractability

6) Your target list

Let's have a look at the individual options for each of these filters below:

1) Data types: we collect data from various sources and combine them into categories called Data types. Examples of data sources are GWAS catalog and UniProt, both combined into the Genetic associations data types. Note that data from an individual source can contribute to different data types, e.g. data from EVA is observed in two data types, Genetic associations and Somatic mutations.

These are the data types where evidence was used for the associations with ovarian carcinoma:
Genetic associations
Somatic mutations
Drugs

Pathways & systems biology
RNA expression
Text mining
Animal models

Note: as our data types above can be made up of different data sources, click on the grey arrows to expand the options and filter the table to focus on specific data sources, such as Cancer Gene Census (data source) within Somatic mutations (data type):

2) Pathway types: Reactome is the resource that provides us with pathway classification e.g. immune system (and its subtypes e.g. neutrophil degranulation), hemostasis (platelet degranulation), etc.

These are some of the pathway types currently available:
    Immune System
    Signal Transduction
    Metabolism
    …

3) Target class: ChEMBL provides us targets into grouped into different classes such as Enzyme, Ion channel, Membrane receptor, etc.

4) RNA tissue specificity: RNA tissue specificity: the tissue specificity of a target is computed as the number of standard deviations from the mean of the log RNA expression of the target across the available tissues. This is a standard z-score calculation. A target is considered to be tissue specific if the z-score is greater than 0.674 (or the 75th percentile of a perfect normal distribution). We remove data for under-expressed targets before the z-score calculation. This RNA expression data comes from Expression Atlas.

This filter allows users to select the organs (or anatomical system) where the target is significantly more expressed in the selected tissues than the mean of the other tissues.

5) Target tractability: tractability of a target is the confidence that we can identify a modulator that interacts with the target to elicit a desired biological effect. Currently we assess whether the targets can be modulated by a Small molecule or Antibody.

6) Your target list: in the associations page for a given disease, you can also filter the targets based on your own targets of interest. You can upload a list of targets (as .csv or .txt) and restrict the table to show only the targets in your list. This can help you to see the evidence Open Targets has integrated for your targets. Your own list of genes should be noted in official gene symbols from HGNC or Ensembl Gene IDs.

Note that in this associations page, there are two views, the Associations view and the Prioritisation view. The latter shows whether the available targets can be modulated by either small molecule, antibody, both modalities or neither:
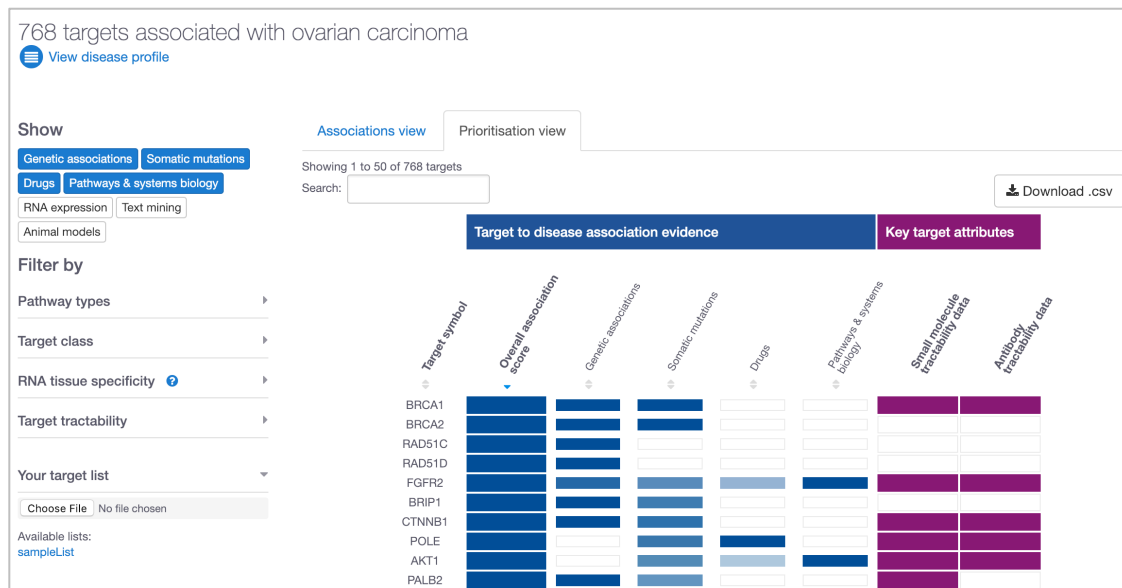
Now that we have looked at the different filters and explored the Prioritisation view, let's now restrict our data based on evidence coming from Cancer Gene Census only. The number of targets goes down from 5500 to 343. Let's focus on ERBB2 by searching for this gene symbol:
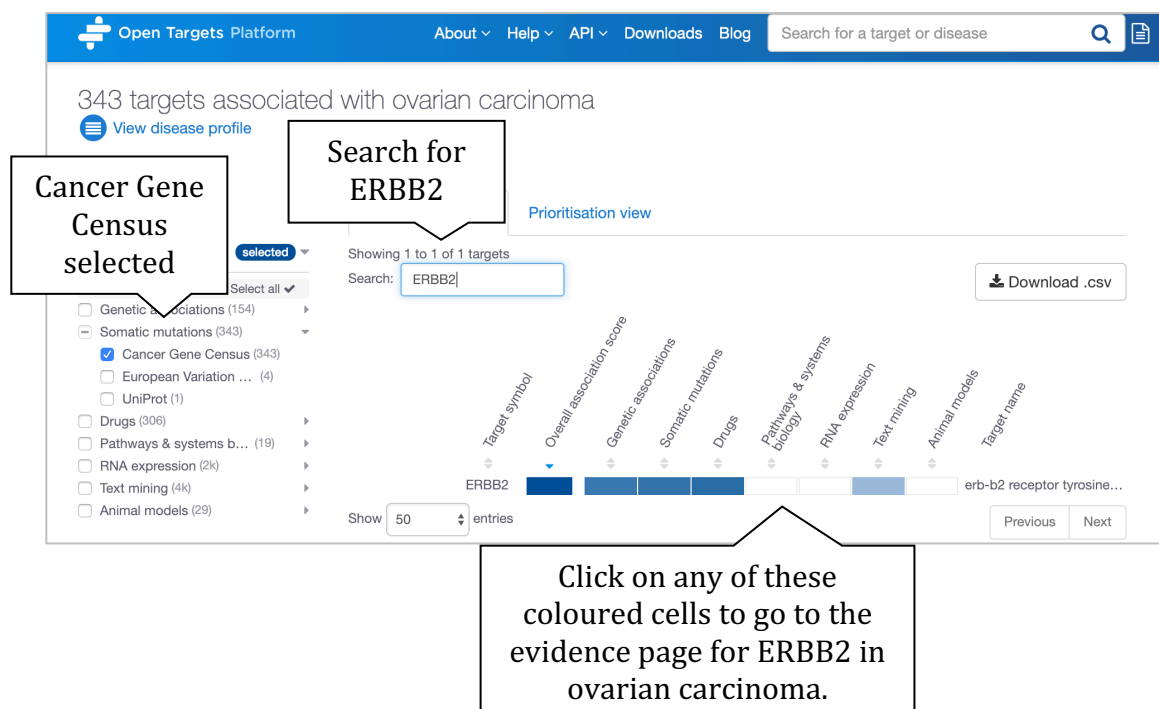
Click on any of the blue cells in the table to go to the evidence page:
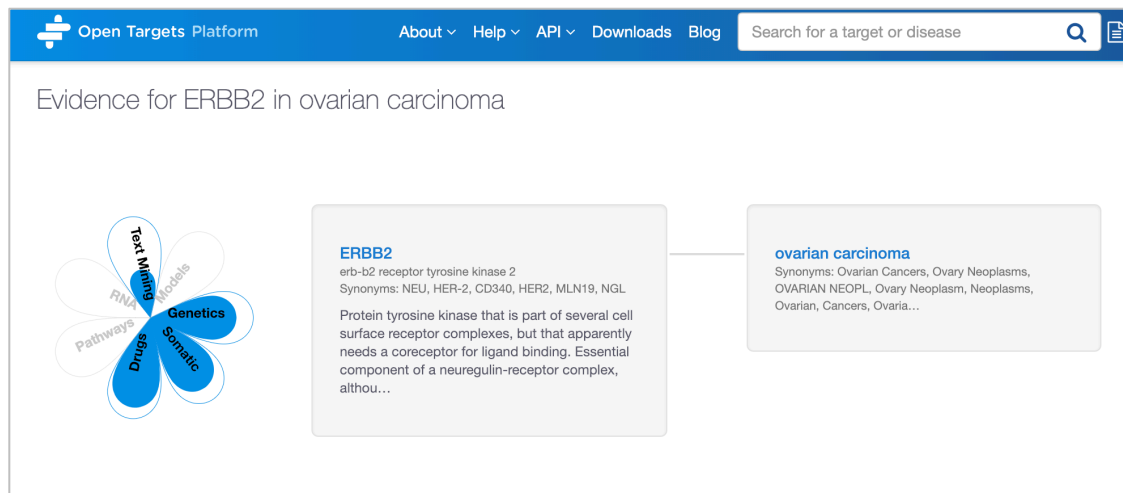
In the evidence page, you can explore the evidence used for the association between ERBB2 and ovarian carcinoma.

The coloured petals on the flower plot represent the data types that support this association namely:

Genetic associations
Somatic mutaions
Drugs
Text mining

Note: If you wish to suggest data types or resources we could/should incorporate into our Platform, please get in touch: support@targetvalidation.org

Grey areas in the flower plot above indicate there is no information for those data types.

Let's now scroll down on the page and expand the tabs available, for example, Somatic mutations (with links to COSMIC) and Drugs, to find out if there are drugs currently in clinical trials targeting ERBB2 in patients with ovarian carcinoma (or children terms of this disease). There are currently four drugs currently listed in different phases of different clinical trials. Do you know why there are seven entries, although only four unique drugs? Are there any drugs in late phases of clinical trials i.e. phase III?

Have a look at the results from our text mining approach as well and see which papers have been used as evidence for the associations between ERRB2 and ovarian carcinoma.

Once we explore the evidence and go through the different data listed in there, we can move on to look at the annotations for the target (ERBB2) and disease (ovarian carcinoma).

Demo 2: Target and disease annotations

Let's now scroll back up to the top of this page and click on the "ERBB2" link:

When clicking on ERRB2 in the above image you will be redirected to the Target profile page of this gene:

https://www.targetvalidation.org/target/ENSG00000141736

This is the target profile page where you can find gene specific information for ERRB2, e.g. RNA and protein baseline expression levels, protein structure, gene ontology terms, information on tractability of ERRB2, cancer biomarkers, and cancer hallmarks:

Let's now expand the RNA and protein baseline expression to find out in which organs or anatomical systems ERRB2 is highly expressed.

You will find three tabs in there: Summary, Expression Atlas (data from several projects including the Illumina Body Map) and GTEx variability.

In the Summary tab, you can compare the mRNA and protein expression side by side and learn that the expression in the reproductive system is higher at the protein than RNA level. You can click on the tissue names to get further granularity such as different different tissues in the digestive system such as Esophagus, small intestine, etc:
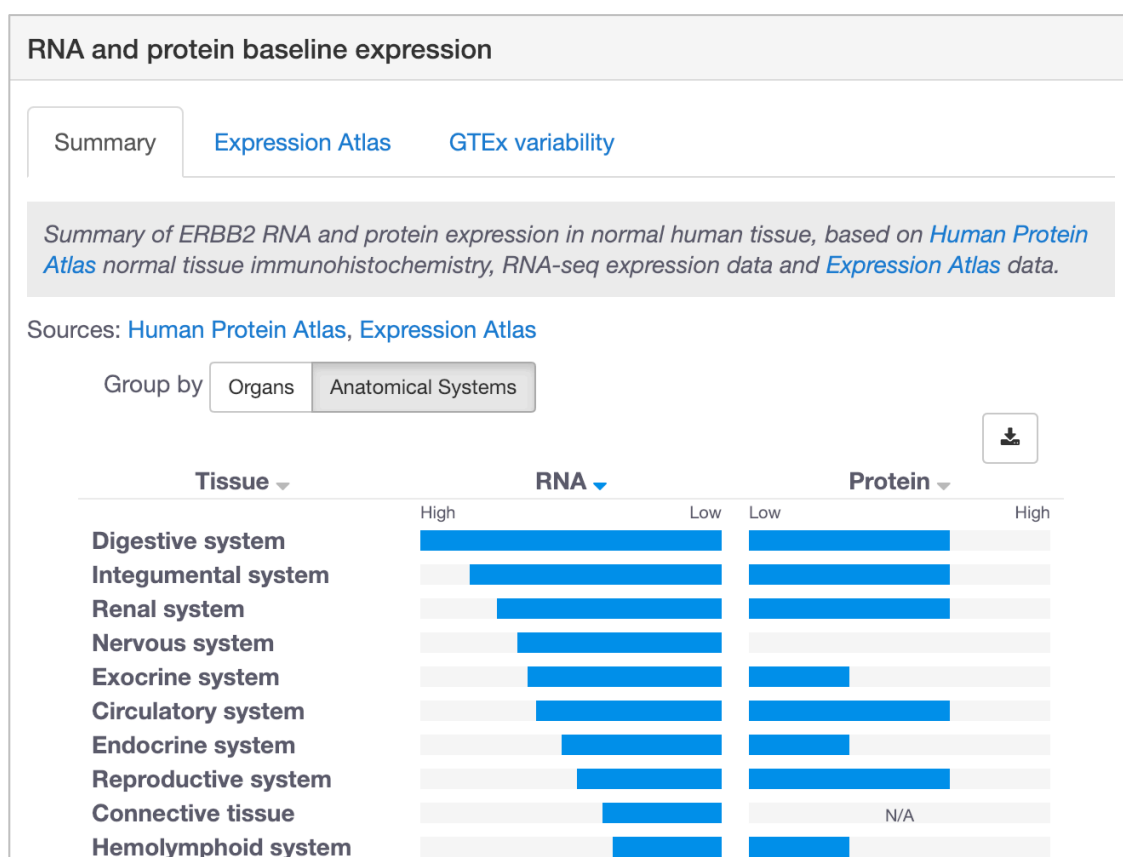
Note that from the target profile page you can also explore other diseases associated with ERBB2, apart from ovarian carcinoma, if you click on View associated diseases:

But let's now go back to the previous evidence page (the flower page):

You can click on the disease name and explore the annotations for ovarian carcinoma:

https://www.targetvalidation.org/disease/EFO_0001075

Scroll down to view the disease ontology (disease concepts and relationships) under the Classification tab. This comes from the EFO (Experimental Factor Ontology), an ontology developed and maintained by EMBL-EBI.
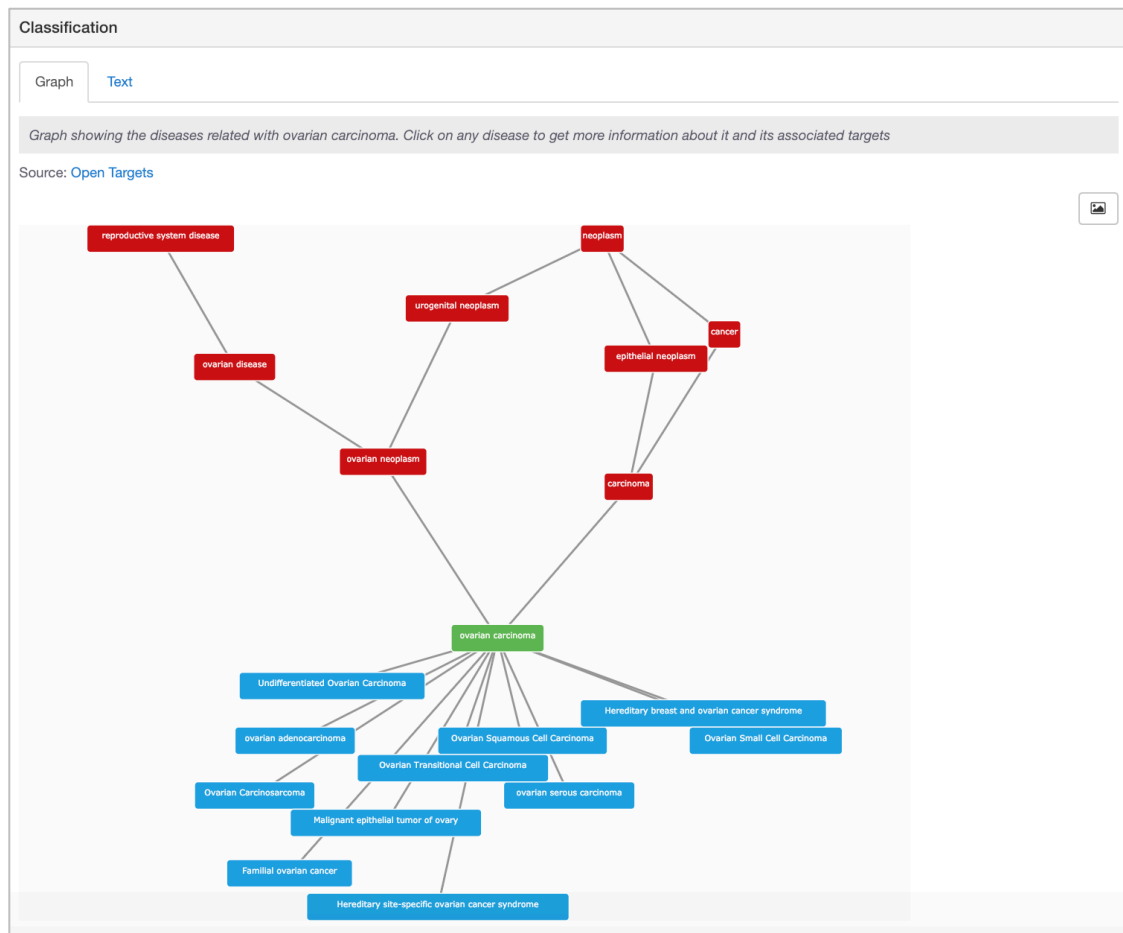
Ovarian carcinoma is represented in green. Red nodes correspond to parental terms, whereas the children terms of ovarian carcinoma are shown in blue (e.g. ovarian small cell carcinoma). Click on any of the disease names to get a pop-up box with the (first) 10 targets associated with any disease:

By relying on the disease ontology and its subtype relationships, we can derive new associations that do not have direct evidence. For instance, IBD is an autoimmune disease that will have direct evidence for its association with its targets. We can propagate this direct evidence up to higher terms in the ontology of IBD and use this evidence (now indirect) to associate target X with autoimmune disease (a parent term of IBD). This procedure can allow us to find common targets across groups of related diseases (e.g. Ulcerative Colitis, Crohn's disease and IBD) even when direct evidence is not available.

For more on this, check our blog post:
https://blog.opentargets.org/direct-versus-indirect-evidence-should-you-care/

Still on the disease profile page, check the Similar diseases (based on targets in common) tab:
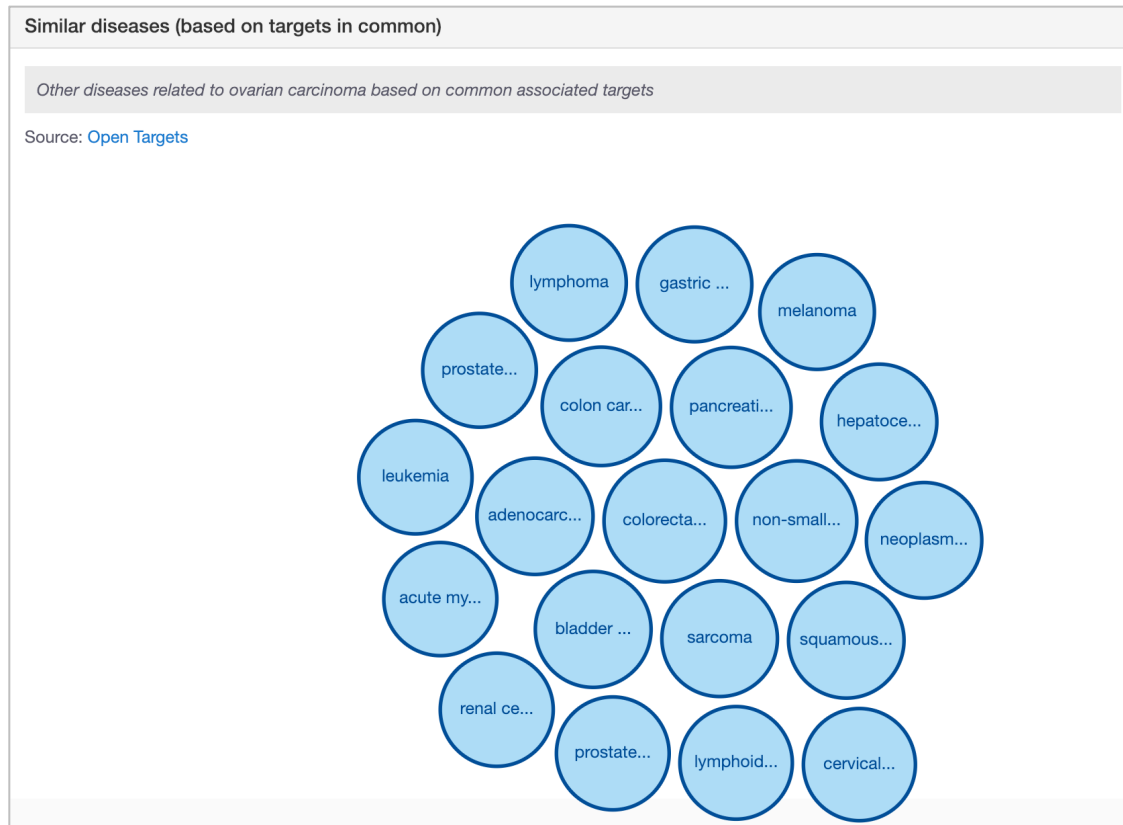
For each pair of diseases, we compute the overlap of shared targets against the total number of connections to both targets, correcting each pair by the significance and the specificity of these connections.

This procedure will consider targets that are specifically linked to fewer diseases more relevant than targets that are commonly linked to many types of diseases.

You will see that the target profile page has a similar visualisation under the tab Similar targets (based on diseases in common). There we will compute a closer distance between two targets sharing a rare disease than two targets sharing diseases that are highly connected to many genes, such as cancer.

You can click on any of the bubbles to get details on the targets in common between any two diseases and the evidence used for the

associations (conversely for the diseases in common among any two targets that you can see in the target profile page):
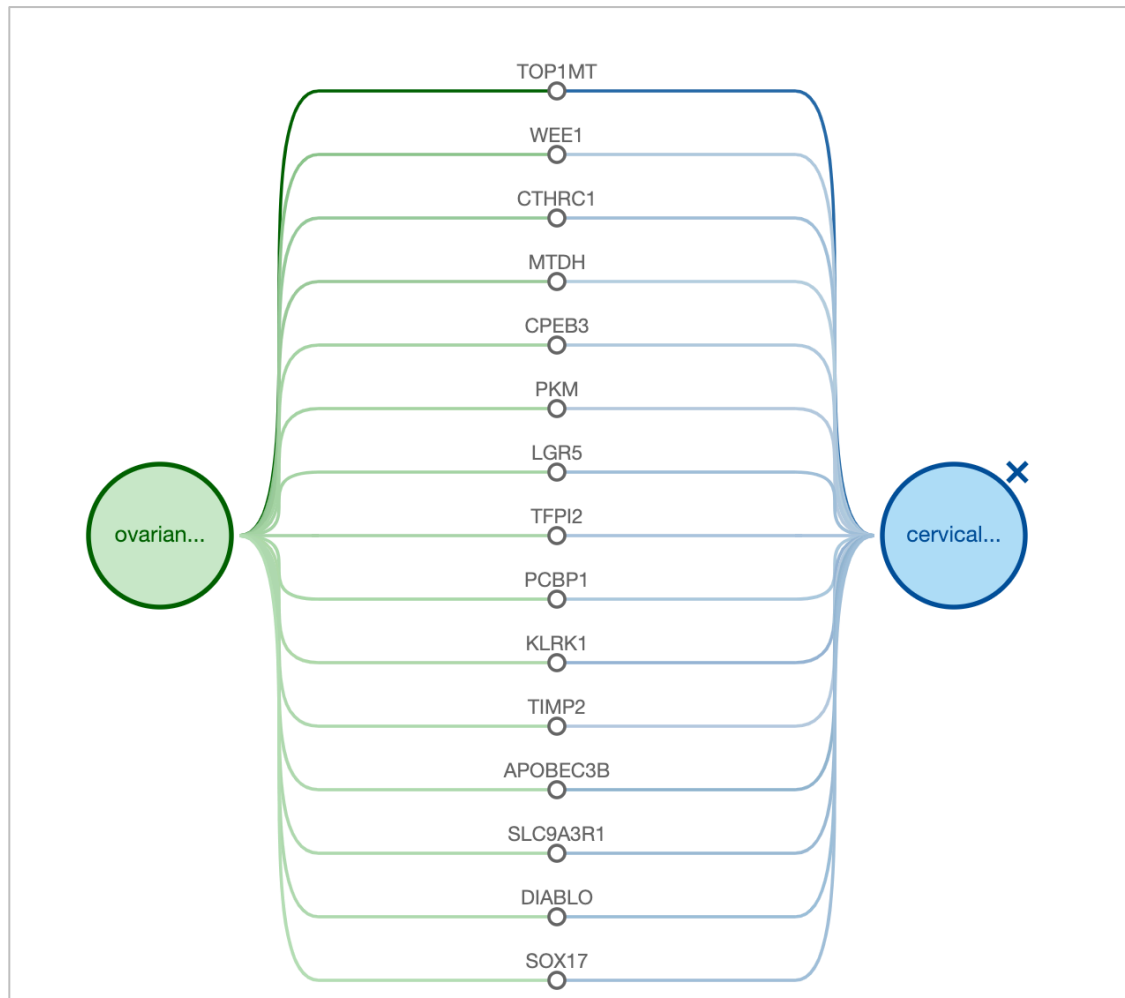
Demo 3: Target centric workflow

You can also use the Open Targets Platform from a target standpoint. Let's have a search for TP53 and explore visualisations and some the functionalities available in our user interface.

There are three different displays that can be used to view the diseases associated with any given target:

- Table view

In this view, we list all diseases associated with a target, ordered by the association score, which is colour coded. When there is no evidence to support the association, the cells in this table are coloured

in white (score of zero). You can show the 10 first entries and get the pagination for the remaining entries.

This table can be exported in CSV format (look for the download .csv button).

Tip: The different shades of blue in the table convey the strength of the association based on the available evidence (strongest association is represented in dark blue). The score varies from 0 to 1. Hover over the cells in the table to view the numbers. Alternatively, you can select the cells in the table so that you can view the numerical values.

- Bubble view

In this view, we group diseases into bubbles based on the disease ontology. Large bubbles correspond to a therapeutic area and consist of smaller bubbles representing diseases within this area. A disease can belong to several therapeutic areas and therefore can appear within more than one large bubble. The strength of the association between the target and a disease is represented by the size of the bubble and the shade of its blue colour; the larger the bubble and the darker the blue, the stronger the association.

- Tree view

In the Tree view, you can visualise the evidence across the therapeutic areas in a tree format that represents the classification of diseases by subtypes. Therapeutic areas have a square symbol (e.g. Genetic disorders), while the diseases (e.g. multiple sclerosis) are represented as circles. The squares and circles are colour coded in blue, and the darker the blue, the stronger the association:
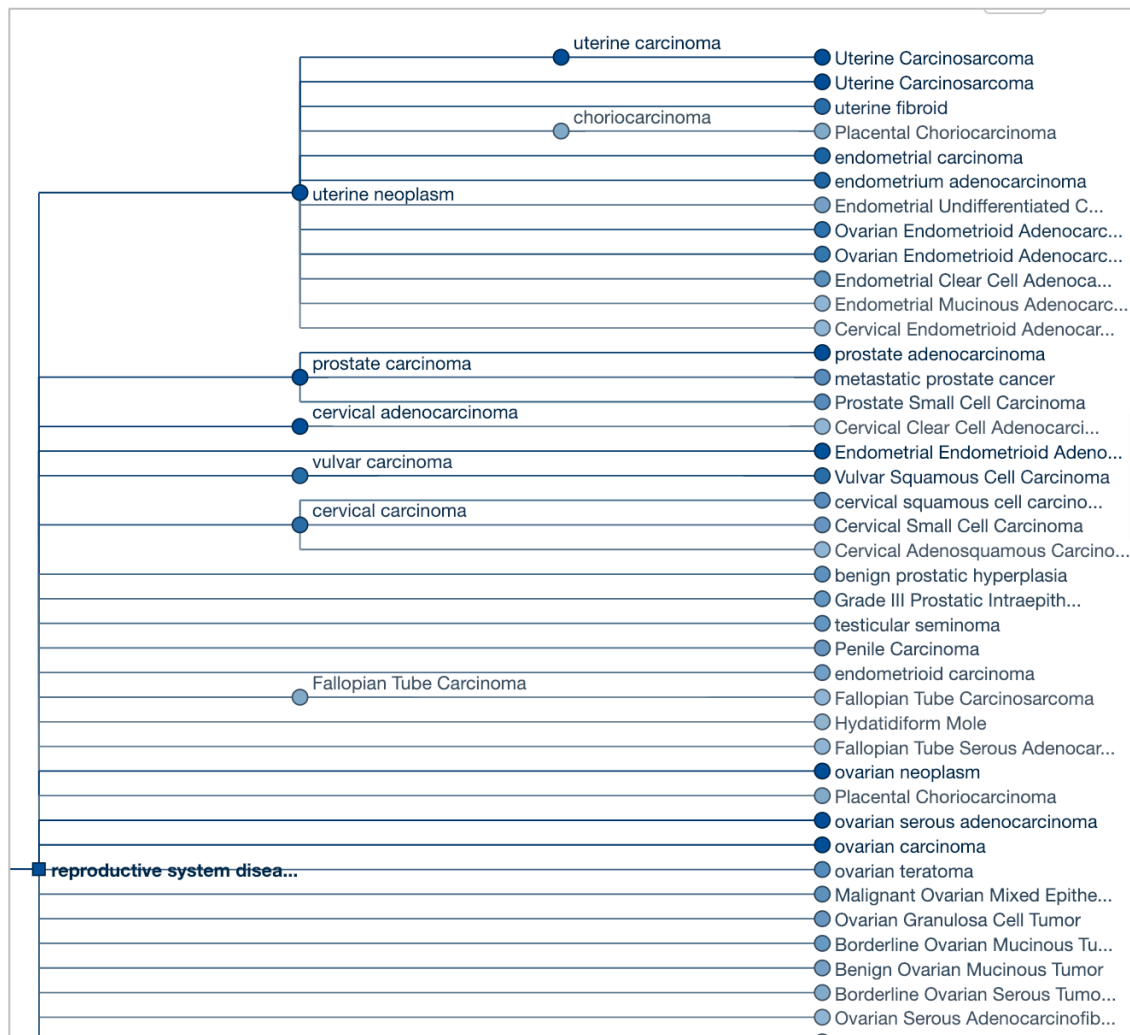
For all these three different views, you have the option to filter the data according to Data type or Therapeutic area. You can, for example, explore all diseases of the Reproductive system associated with this target.

In the December 2018 release of the Platform, there are 110 of them. These are some examples: 'Cervical adenocarcinoma' and 'prostate adenocarcinoma'.

You can view the same information in a bubble view. Click on any of the smaller bubbles, which represent a specific disease. This will bring a pop-up window with the flower plot (an overview on the evidence used for the association) and the following options:
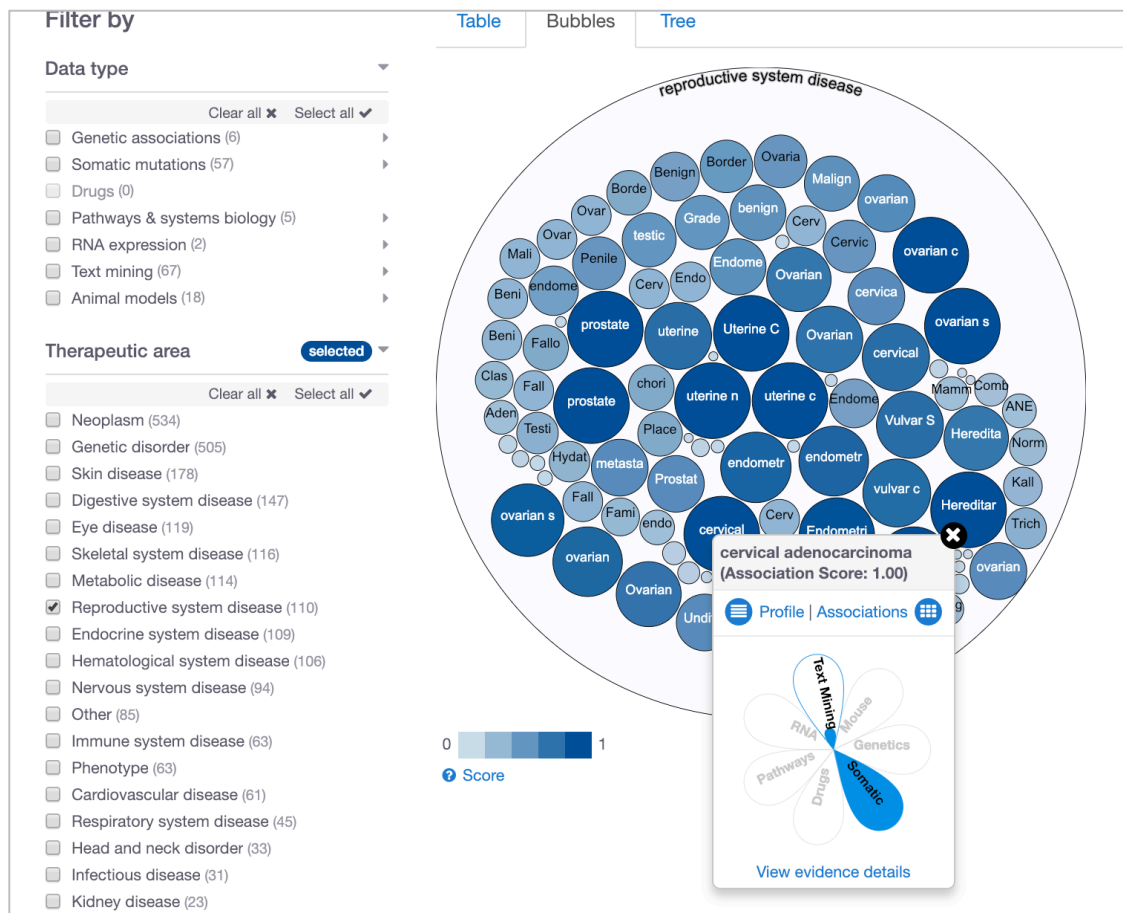
- "Profile" to get to the profile page of the disease

- "Associations" to get all the target associations for the disease

- "View evidence details" to see the underlying evidence for the associations

On the other hand, if you are in the tree view, click on any of the square or circles for a similar pop-up menu.

End of the walkthrough

HANDS-ON EXERCISES

Exercise 1: Osimertinib and non-small cell lung carcinoma

BACKGROUND
AstraZeneca and MedImmune have recently announced the final overall survival (OS) results for the Phase III MYSTIC trial, a randomised, open-label, multi-centre, global trial of durvalumab, a human monoclonal antibody that binds to PD-L1 and blocks the interaction of PD-L1 with PD-1 and CD80, countering the tumour's immune-evading tactics and releasing the inhibition of immune responses.

QUESTIONS
a) You can search for durvalumab (and any other drug) using the Open Targets Platform and find out how many targets have associations involving this drug. Which targets do you find in the Platform when searching for that antibody? Note the extent of the match between the returned hits and the search term on the search results page.

b) Let's now focus on the target, returned in the result of the previous question. Which data sources support the association of this target with non-small cell lung carcinoma (NSCLC)? In addition to durvalumab, are there other drugs currently in phase III of clinical trials with recruitment of patients still ongoing?

c) Is there any evidence for the association between this disease and CD274 showing differential expression at the RNA level when comparing this tumour with an adjacent normal tissue in the lung?

d) Now click on the durvalumab link in the Drug information table. What is the mechanism of action of this drug? Have any adverse effects been reported for this drug? When was this drug first approved? In non-small cell lung carcinoma, can you name other diseases where this drug is associated with?

Exercise 2: Advancing research in the field of pancreatic carcinoma

BACKGROUND
Pancreatic acinar cell carcinoma (PACC) is a rare neoplasm and has been considered a cancer with poor prognosis. Patients who present with PACCs usually have non-specific symptoms. Their complaints consist of abdominal pain or discomfort, nausea, vomiting, weight loss, and diarrhea.

QUESTIONS
a) How many targets that are membrane receptors are associated with pancreatic acinar cell carcinoma? Are there any of these tractable either by small molecule or antibody?

b) Let's focus on LIFR and explore its profile page to answer the following:

- Which amino acids corresponds to an antibody binding sequence in the protein encoded by this gene?
- Which pathways is this protein involved at?
- Which tissue has the highest level of RNA baseline expression? Does this correspond to the highest expression at the protein level as well?

c) Can you list some of the diseases that are similar to Pancreatic acinar cell carcinoma based on the set of targets in common? Which targets are in common between pancreatic acinar cell carcinoma and familial pancreatic cancer?

EXTRA HANDS-ON EXERCISES

Exercise E1: The EGFR gene, a receptor tyrosine kinase

BACKGROUND
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.

QUESTIONS
a) How long is the protein encoded by this gene/target?

b) Which amino acids correspond to the kinase domain? Are there other domains and/or sites mapped to this protein?

c) Can you list a few examples of molecular functions the EGFR protein may be involved with according to the Gene Ontology consortium?

e) Is there any mouse phenotype associated with neoplasm for the knockout version of this gene in mice?

f) Can you find out if the activation of the EGFR pathway is involved in the promotion of tumour associated angiogenesis? (tip: look for the cancer hallmarks).

g) Can you list some of the cancer biomarkers of drug response available for this gene?

Exercise E2: Filtering prostate cancer associations based on my own list of targets

BACKGROUND

A drug discovery scientist at CRUK Therapeutic Discovery Laboratories in London has a list of eight targets that seem to be associated with prostate carcinoma based on literature reviews. These are CHEK2, AR, CDKN1A, CDK12, PTEN, TSC2, KLF6, and MXI. Copy and paste these targets, one per line, and save this in plain text file (.txt).

Then go to the Open Targets Platform and search for prostate carcinoma. In the association page listing the targets for this disease, scroll down the page till you see the filter option Your target list. Click on the Choose file button, find your file (saved above) and upload this to the Open Targets Platform. You will be able to answer the following:

QUESTIONS

a) Which of those eight targets have higher levels of mRNA expression in the brain than in any other tissue? Note: this is known in the Open Targets Platform as 'RNA tissue specificity'.

b) Are any of these classified as enzymes? Note: you can filter targets based on the Target class filter.

c) Let's now explore this enzyme in more detail and answer the following:

- Which amino acids correspond to the transmembrane domain of this protein?
- Which pathway is this enzyme involved with?
- Are there mutations in this gene that have been associated with AD?

QUICK GUIDE TO DATABASES

Here is a list of databases and projects that may be useful for you. Some of them are used as data sources for gene-disease associations available through our Open Targets Platform.

PROTEINS

UniProtKB – The "Protein knowledgebase" is a comprehensive set of protein sequences. It is divided into two parts: TrEMBL and Swiss-Prot. The later is manually annotated and reviewed, therefore provides a set of protein sequences of high quality.
http://www.uniprot.org/

GENE NOMENCLATURE COMMITTEES

HGNC – The HUGO Gene Nomenclature Committee assigns unique names and symbols to every single human gene, whether they are coding or not. These gene names and symbols are the official ones for human genes.
http://www.genenames.org/

MGI – The HGNC counterpart for naming mouse genes and symbols.
http://www.informatics.jax.org/

GENETIC VARIANTS and SOMATIC MUTATIONS

GWAS Catalog– The catalog of Genome Wide Association Studies (GWAS) provides genetic variants (e.g. SNPs) that are associated with a disease.
https://www.ebi.ac.uk/gwas/

EVA – The European Variation Archive (EVA) provides genetic variants and somatic mutations (associated with cancer).
https://www.ebi.ac.uk/eva/

Cancer Gene Census – A catalogue of genes for which mutations have been causally implicated in cancer. The Catalogue of Somatic Mutations in Cancer (COSMIC) at the Wellcome Sanger Institute provides us with the set of genes associated with specific cancers in the Cancer Gene Census, in addition to other cancers associated with that gene in the COSMIC database.
www.cancer.sanger.ac.uk/census/

COSMIC is also the database that provides us with the cancer hallmarks:

https://cosmic-blog.sanger.ac.uk/hallmarks-cancer/

IntOgen - It provides evidence of somatic mutations (driver mutations), genes and pathways involved in cancer biology from 6,792 samples across 28 cancer types.
https://www.intogen.org/search

Gene2Phenotype - The data in Gene2Phenotype (G2P) provides evidence of genetic variants that are manually curated from the literature by consultant clinical geneticists in the UK. This is provided by DECIPHER, a database of genomic variants and phenotypes in patients with developmental disorders.
https://www.ebi.ac.uk/gene2phenotype

Genomics England PanelApp - The Genomics England PanelApp is a knowledgebase that combines crowdsourcing of expertise with curation to provide gene-disease relationships to aid the clinical interpretation of genomes within the 100,000 Genomes Project.
https://panelapp.extge.co.uk/crowdsourcing/PanelApp/

PheWAS Catalog
The PheWAS (phenome-wide association studies) resources provide associations between a genetic variant and multiple phenotypes. It contains clinical phenotypes derived from the electronic medical record (EMR)-linked DNA biobank BioVU by the Center for Precision Medicine at the Vanderbilt University Medical Center.
https://phewascatalog.org/

DRUGS

ChEMBL - The ChEMBL database at the EMBL-EBI provides evidence from known drugs that can be linked to a disease and a known target.
https://www.ebi.ac.uk/chembl/

RNA EXPRESSION

Expression Atlas – The Expression Atlas at EMBL-EBI provides information on genes that are differentially expressed between normal and disease samples, or among disease samples from different studies. In addition to differential expression, they provide baseline expression information for each gene.
https://www.ebi.ac.uk/gxa/home

PATHWAYS & SYSTEMS BIOLOGY

Reactome – The Reactome database at the EMBL-EBI contains pathway information on biochemical reactions sourced from manual curation. It identifies reaction pathways that are affected by pathogenic mutations.
http://www.reactome.org/

SLAPenrich – It's a statistical framework for the identification of significantly mutated pathways, at the sample population level. We include in the Open Targets Platform the data obtained using SLAPenrich on somatic mutations from the The Cancer Genome Atlas across 25 different cancer types and a collection of pathway gene sets from Reactome.
https://saezlab.github.io/SLAPenrich/

PROGENy – PROGENy (Pathway RespOnsive GENes) is a linear regression model that calculates pathway activity based on consensus gene signatures obtained from perturbation experiments. We use PROGENy (Schubert et al) for the systematic comparison of pathway activities between normal and primary samples from The Cancer Genome Atlas (TCGA). We include in our Open Targets Platform sample-level pathway activities inferred from RNA-seq for 9,250 tumour and 741 normal TCGA samples from 14 tumour types, and compute differential pathway activities between matched normal and tumour samples. We cover the following pathways: EGFR, hypoxia, JAK.STAT, MAPK, NFkB, PI3K, TGFb, TNFa, Trail, VEGF, and p53. See Schubert et al (2018) for more details.

SYSBIO - Sysbio includes six gene lists curated from four systems biology analysis papers. These publications integrate different types of data to identify key drivers (or regulators) in the following diseases (or phenotypes):

- Inflammatory bowel disease (PMID:28892060)
- Coronary heart disease (PMID:23539213)
- Late-onset Alzheimer's disease (PMID:23622250)
- Cognitive decline of Alzheimer's disease (PMID:29802388)

In the Platform, we have 406 evidence strings used to associate targets to any of the diseases or phenotype above.

TEXT MINING

Europe PMC - The Europe PubMed Central at the EMBL-EBI mines the titles, abstracts and full text research articles from both PubMed and PubMed Central to provide evidence of links between targets and diseases.
http://europepmc.org/

ANIMAL MODELS

Phenodigm - Phenodigm is an algorithm developed by Damian Smedley at the Wellcome Trust Sanger Institute that use a semantic approach to map between clinical features observed in humans and mouse phenotype annotations. The results are made available on the IMPC portal:
https://www.mousephenotype.org