The Beacon framework was created for global and federated queries. To facilitate variant sharing, we have built our novel cancer cell line resource on the Beacon framework.

cancercelllines.org is the daughter of progenetix (a cancer copy number variant (CNV) database), including over 5600 cell line CNVs.

We have mapped additional known cancer cell line variants from resources like CCLE and ClinVar to our database, resulting in 16178 cell lines total from 400 different NCIT disease classifications.

Known information about each cell line (from Cellosaurus) is displayed on the cell line page e.g. age at collection, genome ancestry and genotypic sex.

Each cell line is represented hierarchically and includes an NCIT diagnostic code. Both hierarchies can be accessed in the database.

Annotated Single Nucleotide Variants

We mapped known cancer cell line single nucleotide variants (SNVs), including parental SNVs annotated on Cellosaurus.

SNVs mapped from ClinVar show known severity of the variant and disease ontologies.

SNVs mapped from CCLE include data about variant effect.

As an example, some of the annotated SNVs for breast cancer cell line MDA-MB-453 are listed on the right.

Copy Number Profiles of Cancer Cell Lines

Over 5600 unique copy number profiles from more than 2000 cancer cell lines.

Copy number profiles from cancer cell lines and their origins (from Progenetix) can be used for comparison.

On the right are 4 CNV profiles for tumor and its cell line example.

Fun fact: cell line MDA-MB-435 has been found to be misidentified. It was thought to originate from breast carcinoma but has been shown to originate from amelanotic melanoma instead.