The Progenetix oncogenicomics resource provides sample-specific cancer genome profiling data and biomedical annotations as well as provenance data for cancer studies. Especially through more than 100k genomic copy number number (CNV) profiles from over 500 cancer types, Progenetix is the most comprehensive reference resources for copy number aberration in cancer, empowers comparative analyses vastly exceeding individual studies and diagnostic concepts as well as supports development of data standards and exchange protocols through Global Alliance for Genomics and Health (GA4GH).

Database URL: progenetix.org

### Data standards

**CURIE, GA4GH, Phenopackets schema**

**FAIR**

- Compact URI (CURIE) syntax, e.g. `pgx:pgxbs-kftvkg8h`
- GA4GH specification for variation data, i.e. individual -> biosample -> callset -> variant
- Phenopackets for phenotype data, i.e. id, phenotypes, EHR, provenance, biosample, biosample...

### New meta-data

**Domain-specific mapping**

- ICD-O system vs. NCI thesaurus

### New data sources

**Sample expansion**

- Gene Expression Omnibus (GEO)
- Array Express
- The Cancer Genome Atlas (TCGA)
- cbioPortal

### Beacon protocol

**Features and prospects**

- A Beacon answers a query for a specific variant against an individual or aggregated collection
- Support single or range query
- Filter by disease, phenotype, ...
- Authentication (to come...)