

# DuckDB powering cancer genomics research

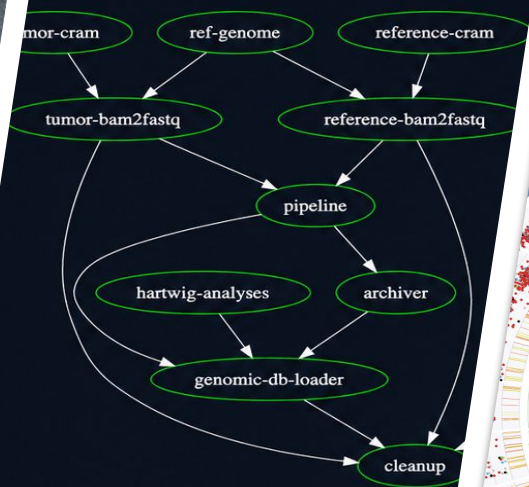
*Thomas Visser, Software Developer  
DuckCon #7, 2026-06-24*





h-dna-6-0-pilot-1/from-fastq/test110926690001t

### Flow Graph



Hartwig Medical OncoAct

### Stage States

Stage	State	Info
ref-genome	SUCCESS	
pipeline	SUCCESS	gcloud storage fastq/test110926690001t
tumor-bam2fastq	SUCCESS	gcloud storage fastq/test110926690001t



the chromosomes. present large gaps in the genome, i.e. regions of missing short

The third circle shows all observed tumor purity adjusted copy number changes, including both focal and chromosomal events. Copy number losses are indicated in red, green shows regions of copy number gain. The scale ranges from 0 (complete loss) to 6 (high level gains). If the absolute copy number is > 6 it is shown as 6 with green dot on the diagram.

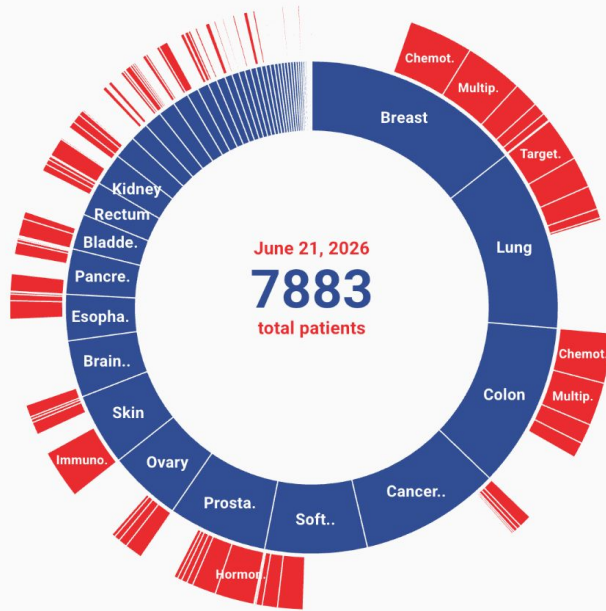
all tumor observed and intergenic regions)

**Filters**

Select filter...

+ Add new filter

Apply



Developed with support from **KWF**

Start by hovering over the sunburst chart.  
The results will be shown on this panel.

Request Access

Export Data

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Dimensions:

Primary tumor location

Treatment Type





# GenOnco



Explore - GenOnco

Not Secure middle-layer-poc.pilot-1/explore/session-1776334982930-1

GenOnco

Explore

Session 1

Data

Sources 1

Tables

```

WITH gene_totals AS (
  SELECT
    dc.gene,
    COUNT(DISTINCT dc.sampleId) AS n_samples_gene
  FROM driver_catalog dc
  WHERE dc.gene IS NOT NULL AND dc.gene <> ''
  GROUP BY 1
), top_genes AS (
  SELECT gene

```

HMf Patients Dump 2026-02 Table

Gene x TumorType heatmap

Export < YAML Split Diagram

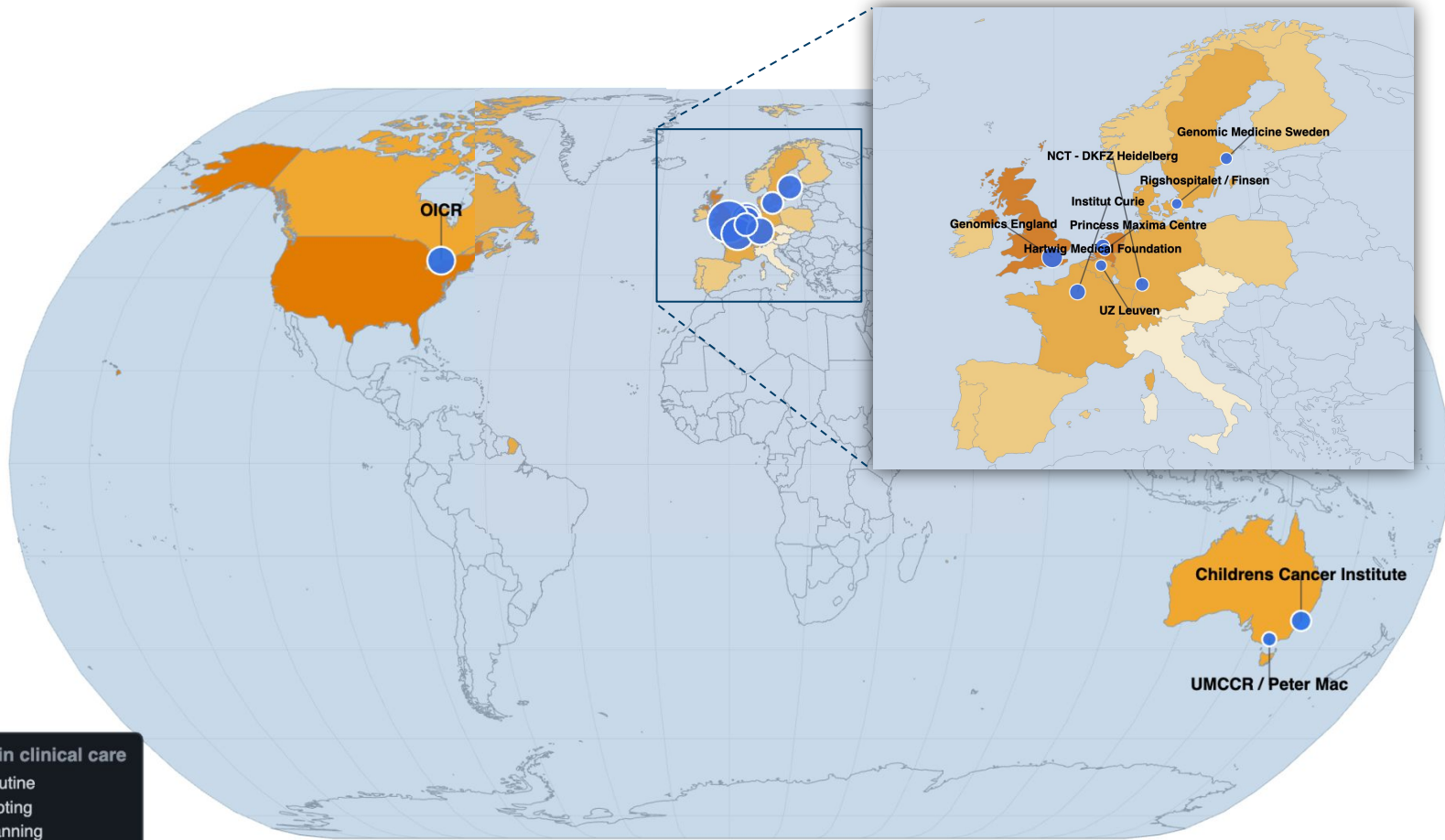
```

1 hconcat:
2   - vconcat:
3     - plot:
4       - mark: barY
5         data: { from: _query }
6         x: gene
7         y: { sum: n_samples }
8         z: mutationType
9         fill: mutationType
10        tip: true
11        width: 965
12        height: 180
13        marginLeft: 227
14        marginBottom: 10
15        marginTop: 20
16        marginRight: -6
17        xTickRotate: 60
18        xAxis: null
19      - plot:
20        - mark: cell
21          data: { from: _query }
22          x: gene
23          y: tumorType
24          fill: { sum: n_samples }
25          inset: 0.5

```



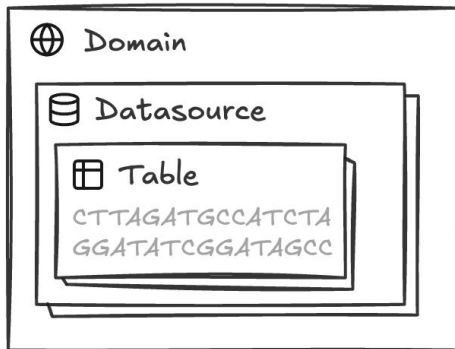
<https://idl.uw.edu/mosaic>



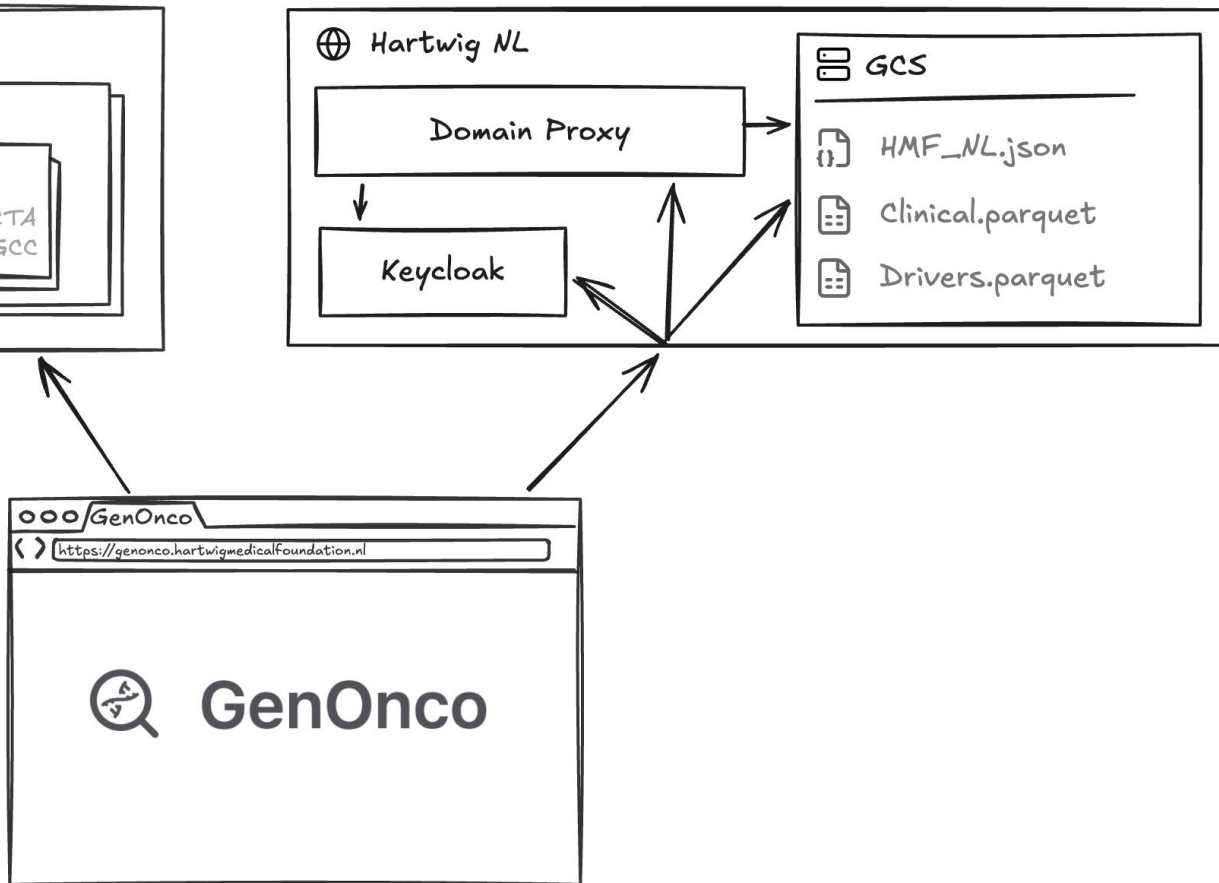
**WGS in clinical care**

- Routine
- Piloting
- Planning
- Research
- No data

## Concepts



## Example



GenOnco

Explore +

Session 1

Data

Sources 2




**Tables**

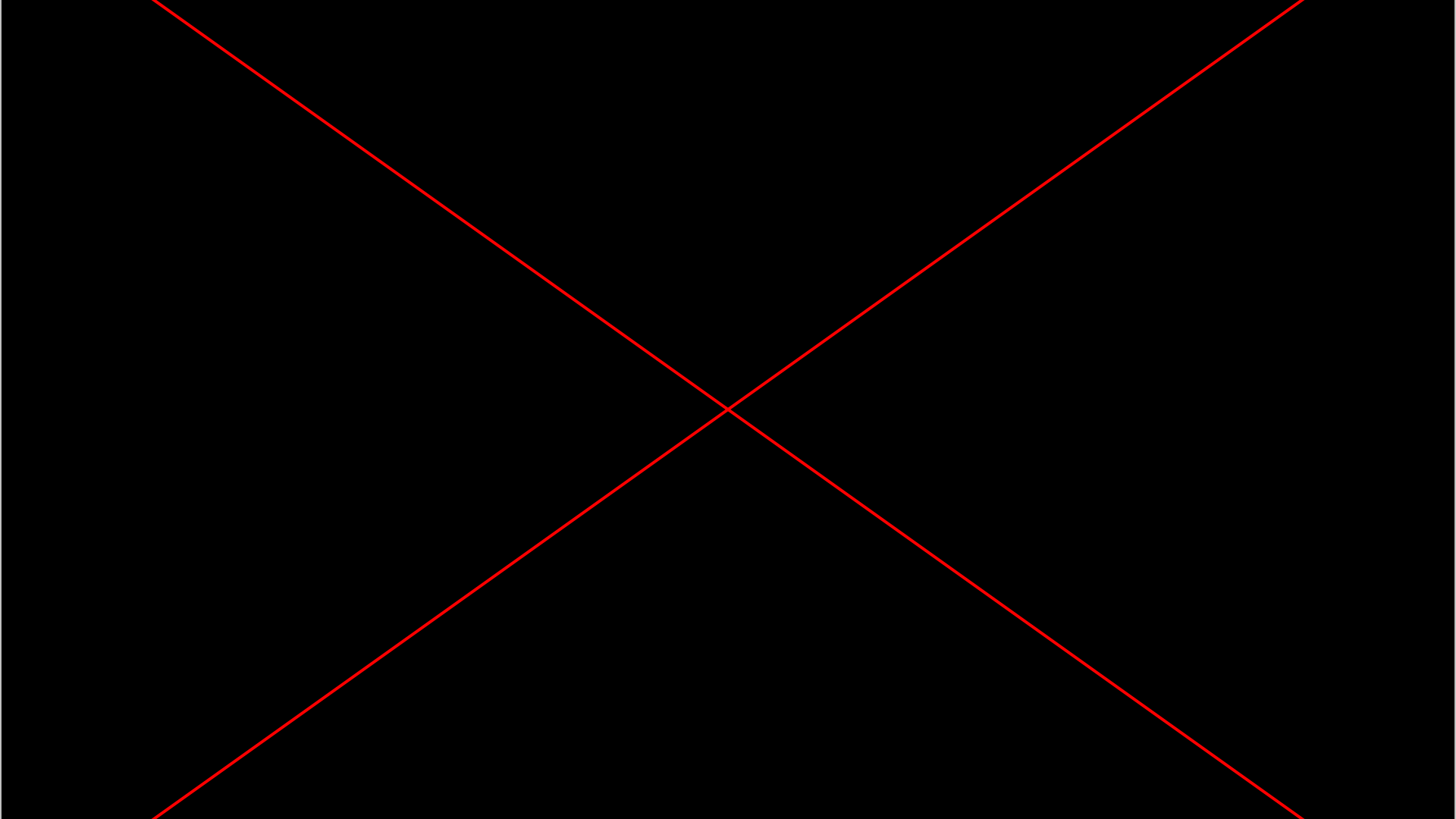
Feedback

Settings

### Tables Refresh

Merged Datasources All datasources ▾

Name	Type	Sources	Rows
 catalog_nl	View	Catalog NL 1/2, Catalog NL 2/2	8,165
 ds_self_catalog_nl_1_2_catalog_nl	View		4,083
 ds_self_catalog_nl_2_2_catalog_nl	View		4,082



# Thank you!

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hartwigmedical



hartwig-medical-foundation