

At Medical Genomics Visualization group (MGviz) we recently have developed fully integrated QC and data análisis procedures that creates automatic NGS clinical reports for clinicians to review. We provide integrated and summarized quality control measures with threshold based in all the previous runs that allow detecting any kind of bias or sample performance problems and any kind of sample swap. Also we provide very intuitive interactive tools that help prioritize and select the variants of interest related to the patient's phenotype from our NGS gene panels and other common products like TruSightOne from Illumina or whole exome capture from Agilent.

Available components

gviz-table

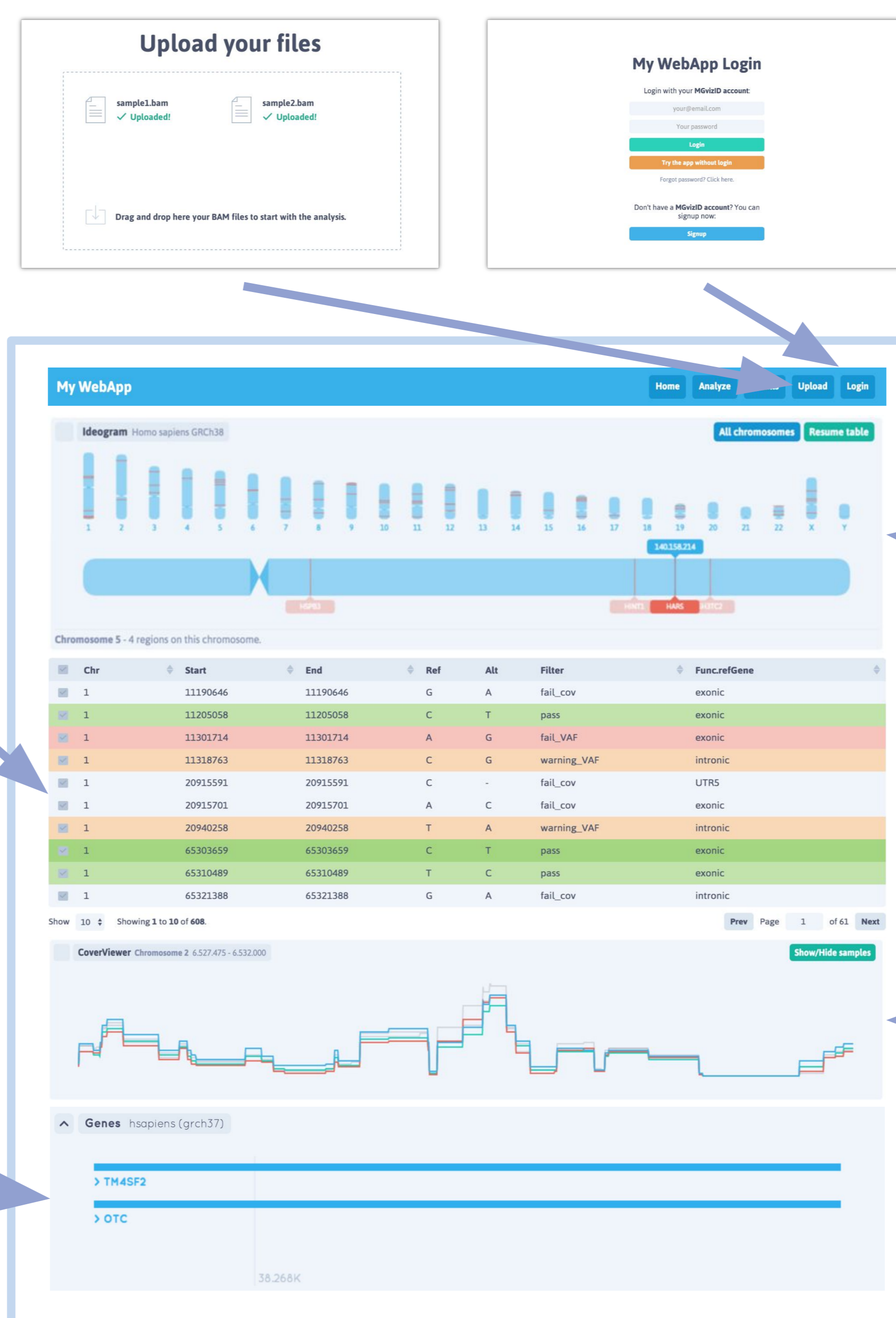
A flexible element to display, sort, filter and highlight large data in a table format.

This element is available at:
github.com/jviz/jviz-table

gviz-featureviewer

A simple and light genome browser that can display genomic features like genes, transcripts, exons...

This element will be available at:
github.com/jviz/jviz-featureviewer



gviz-ideogram

An interactive element for display genomic features of interest in chromosomes.

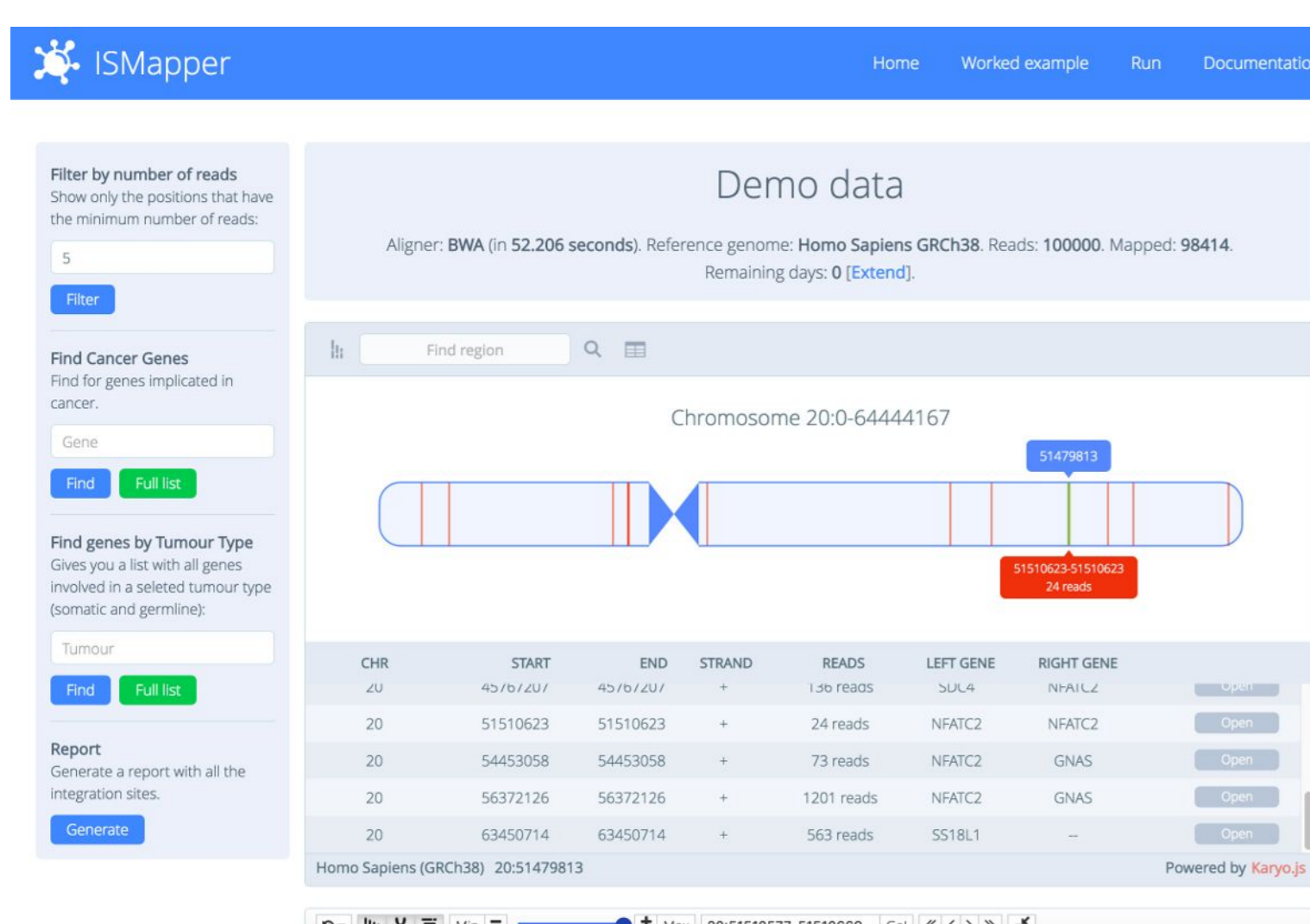
This element is available at:
github.com/jviz/jviz-ideogram

gviz-coverviewer

An Interactive element for visualizing sequence coverage in delimited regions.

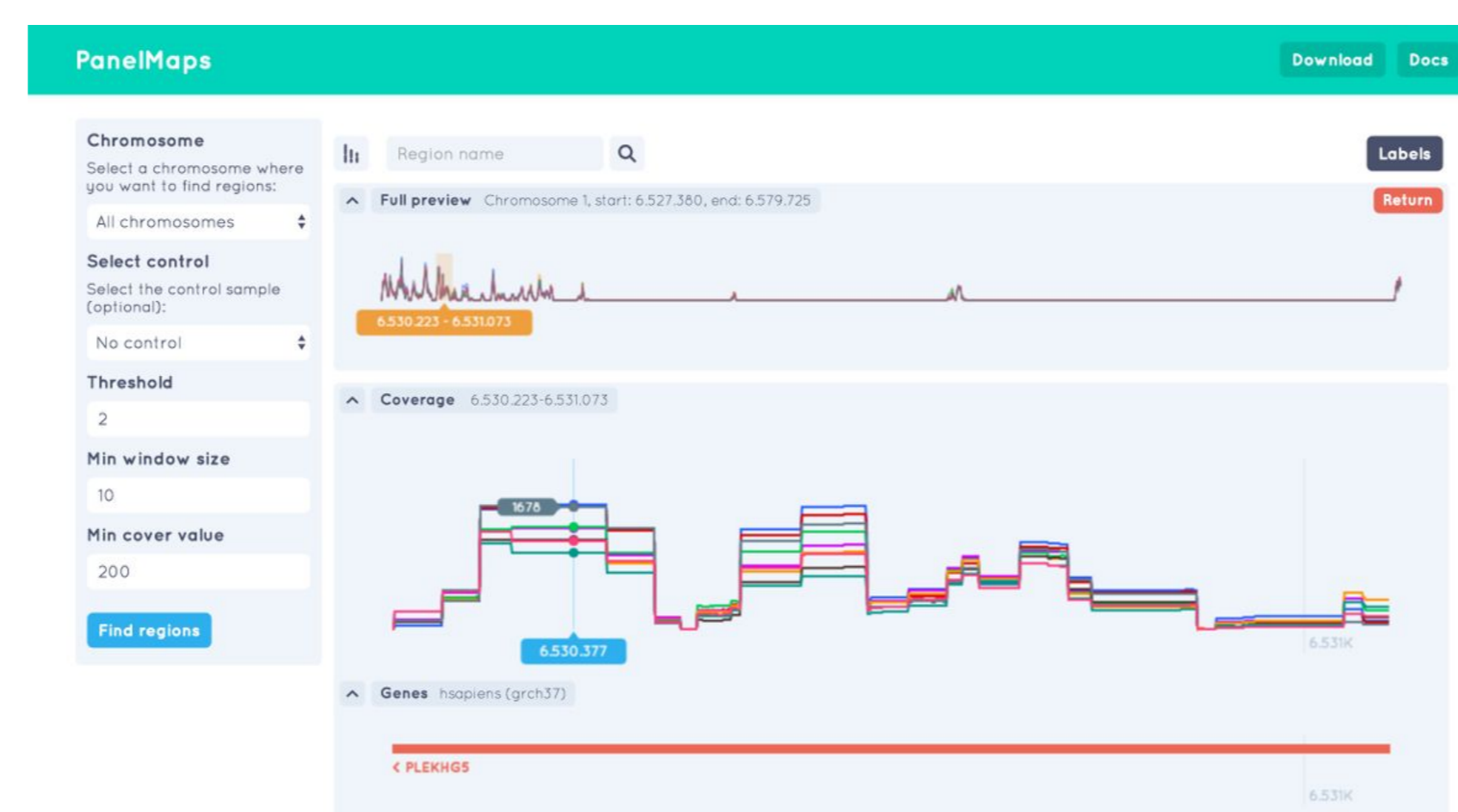
This element is available at:
github.com/jviz/jviz-coverviewer

Applications developed / in development



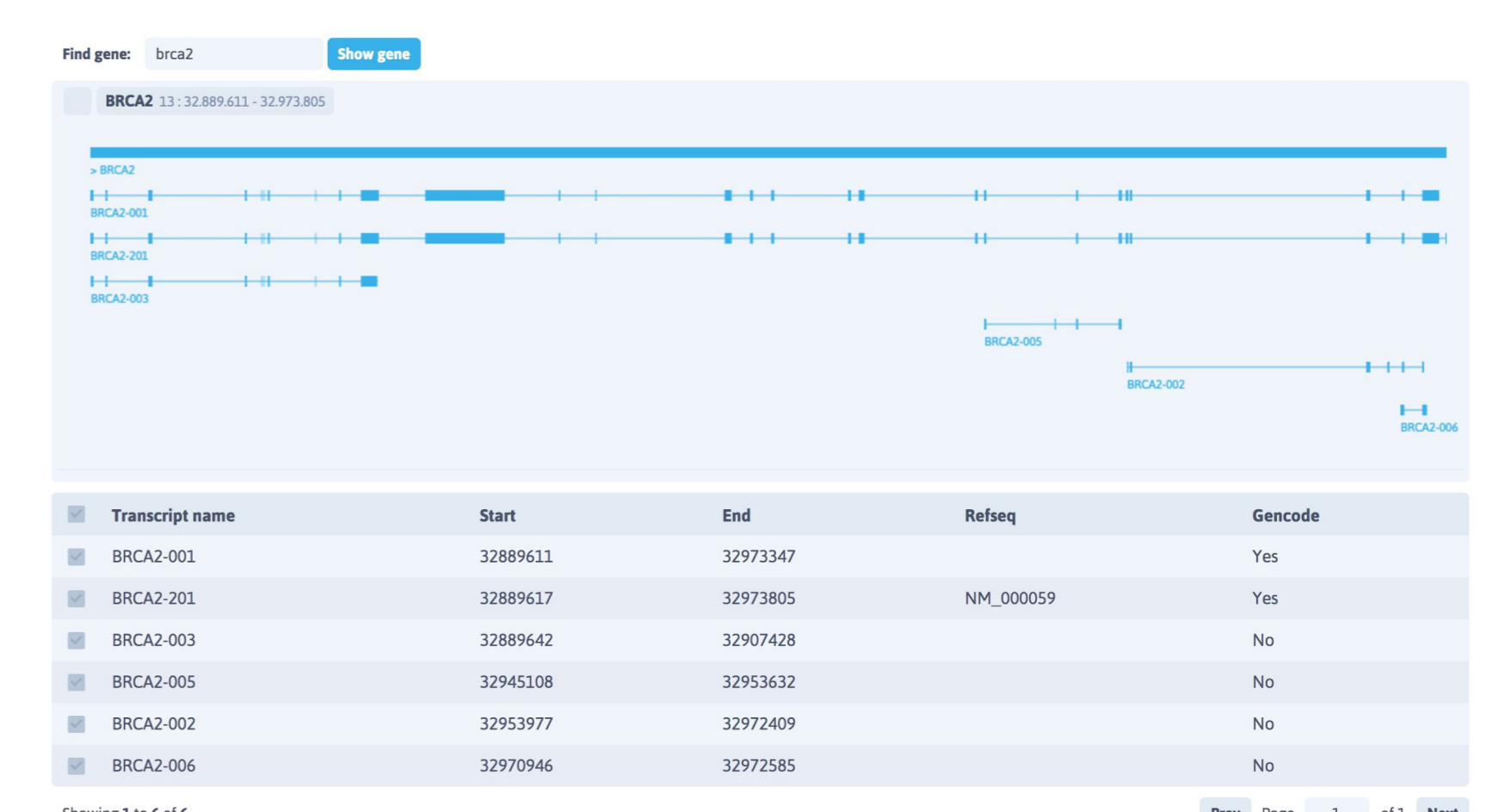
VISMMapper is an interactive web tool to manage sequencing data for the detection of viral insertion sites in gene therapy experiments.

<http://vismapper.bamelomics.org>



PanelMaps is a web tool for detection and visualization of altered regions for targeted sequencing.

Available on April 2017
<https://panelmaps.mgviz.org>



Transcripts Selector is an aid for selecting the wanted transcripts for your experiment based in different features (mainly clinical relevance)

Coming soon.
<https://tools.mgviz.org>