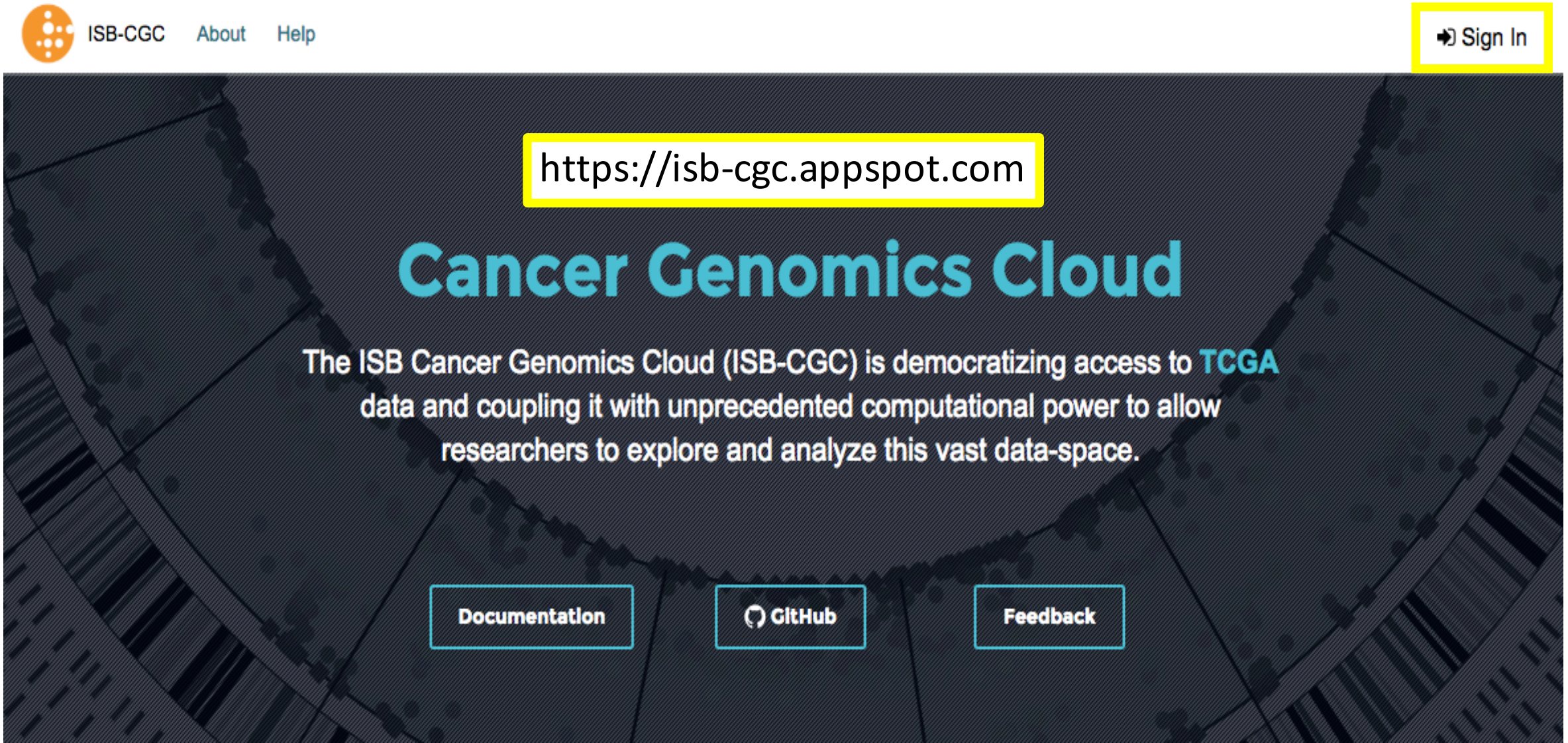
An Introduction to the ISB-CGC Web App IGV

brought to you by

The ISB Cancer Genomics Cloud

Main Landing Page

- Handy place to access documentation, code, and send feedback
- You may only log in using a Google Managed identity by clicking the signin button



CCLE

New Workbook | Edit | Comments | Duplicate | Delete | View Files | Download IDs | Share | Shared With (0)

Selected Filters

SAMP:Project: CCLE

Details

Total Number of Samples: **3**

Total Number of Participants: **3**

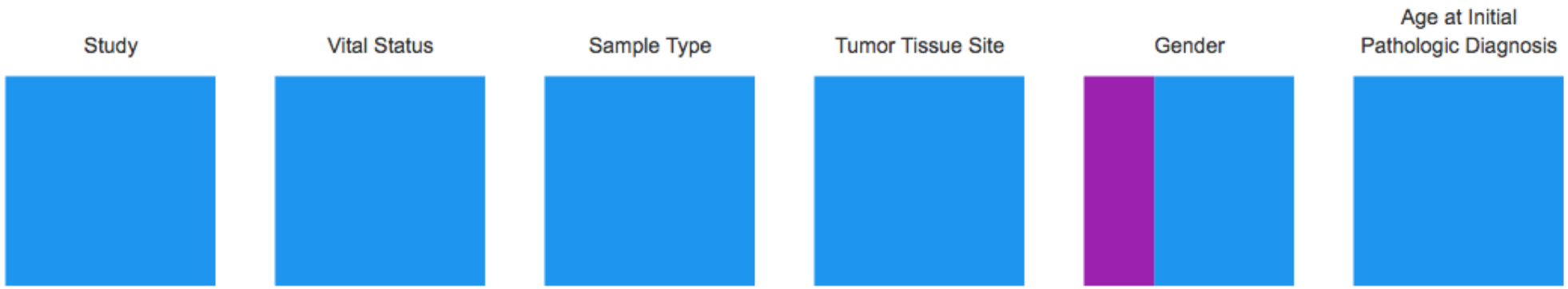
Your Permissions: OWNER

Revision History:

There is no revision history.

1. Log into the system
2. Create a cohort of only CCLE Samples

Clinical Features



CCLE

New Workbook | Edit | Comments | Duplicate | Delete | View Files | Download IDs | Share | Shared With (0)

Selected Filters

SAMP:Project: CCLE

Details

Total Number of Samples: **3**

Total Number of Participants: **3**

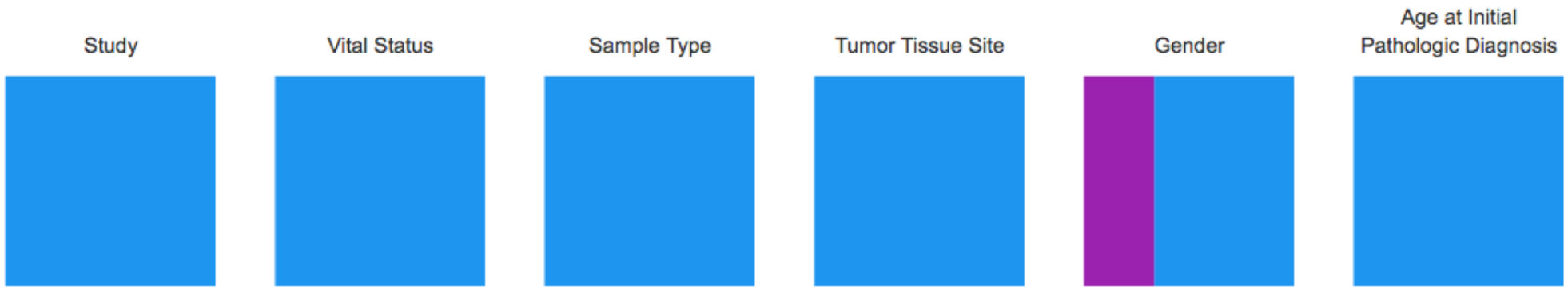
Your Permissions: OWNER

Revision History:

There is no revision history.

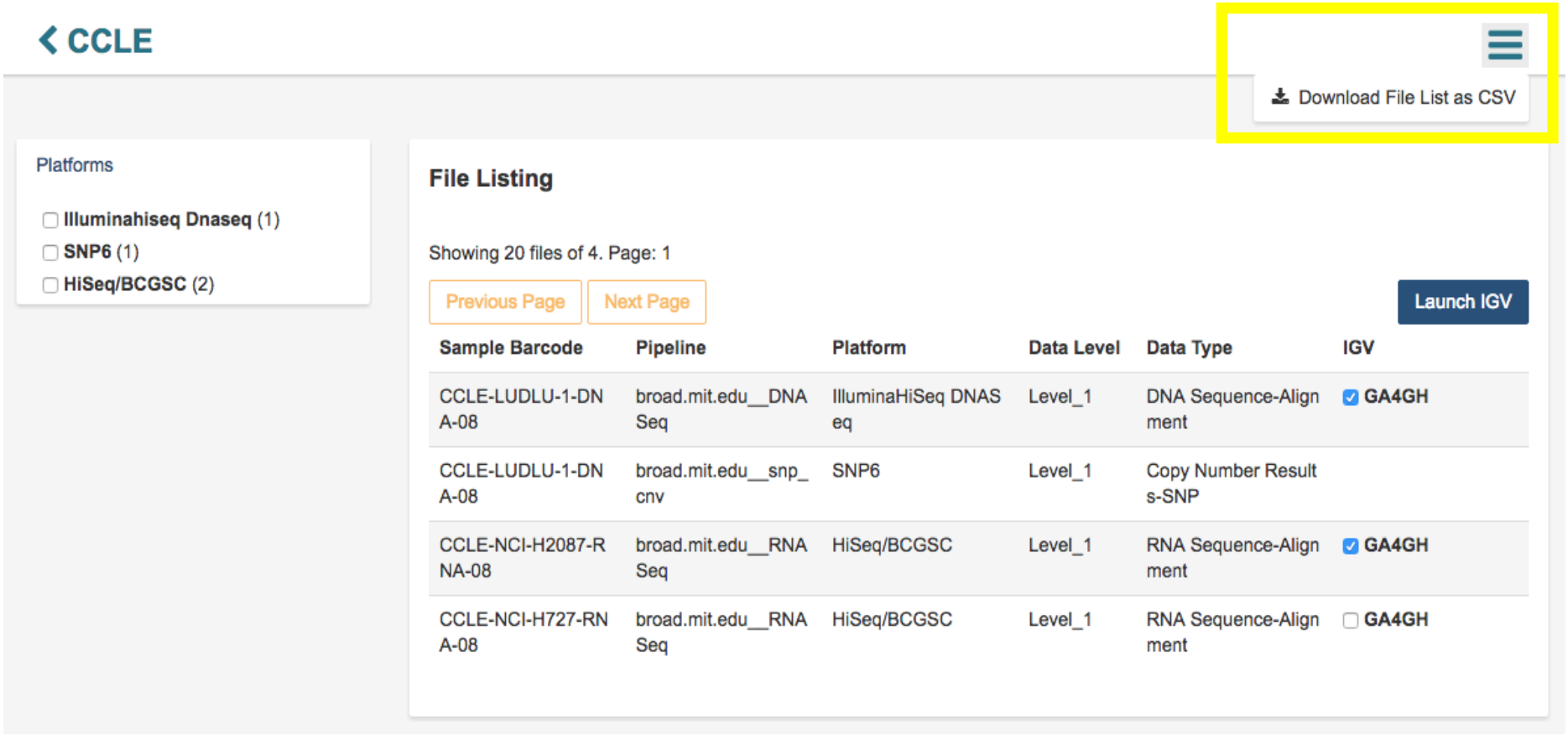
3. Click View Files Button

Clinical Features

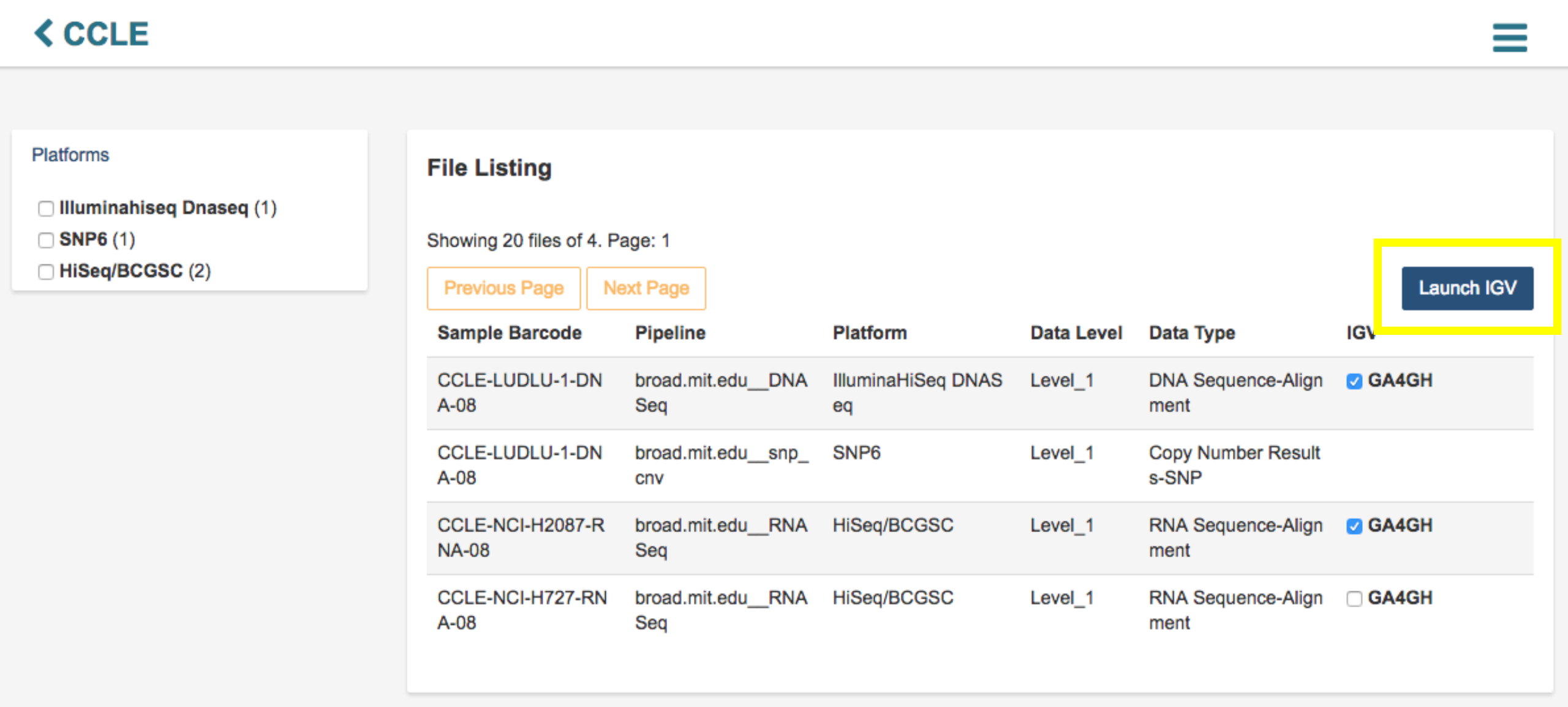


4. File Listing Page

- You can see what kind of files are available for the cohort you are looking at based on sample barcode.
- You can also download the file list as a CSV. **Note**: that if the list of files is too large, you will get an error. Try making the cohort smaller to trim down the file list size.
- If the file is available in Google Genomics, then the IGV column will be populated with a GA4GH checkbox.
- If the file is available in Google Cloud Storage as a .bam file, then the IGV column will also have that option available.
- The checkboxes will be disabled if you do not have the correct permissions to view the data.
- Selecting one or more will activate the Launch IGV button.



4. File Listing Page



5. IGV Browser

- You will be prompted to log in again to authorize access of the information required to display. Please be sure to allow pop-ups on this page for that, otherwise you may receive an access denied error.
- Here, we have the two samples that were previously selected displayed and the IGV browser is accessing the reads from Google Genomics using the GA4GH API.

All TCGA Data

Owner: | New Workbook | Comments | Duplicate | Remove | View Files | Download IDs | Shared With (13)

Selected Filters

There were no filters used to create this cohort.

Details

Total Number of Samples: **1378**

Total Number of Participants: **594**

Your Permissions: READER

Revision History:

There is no revision history.

6. All TCGA Cohort

Clinical Features

Study

Vital Status

Sample Type

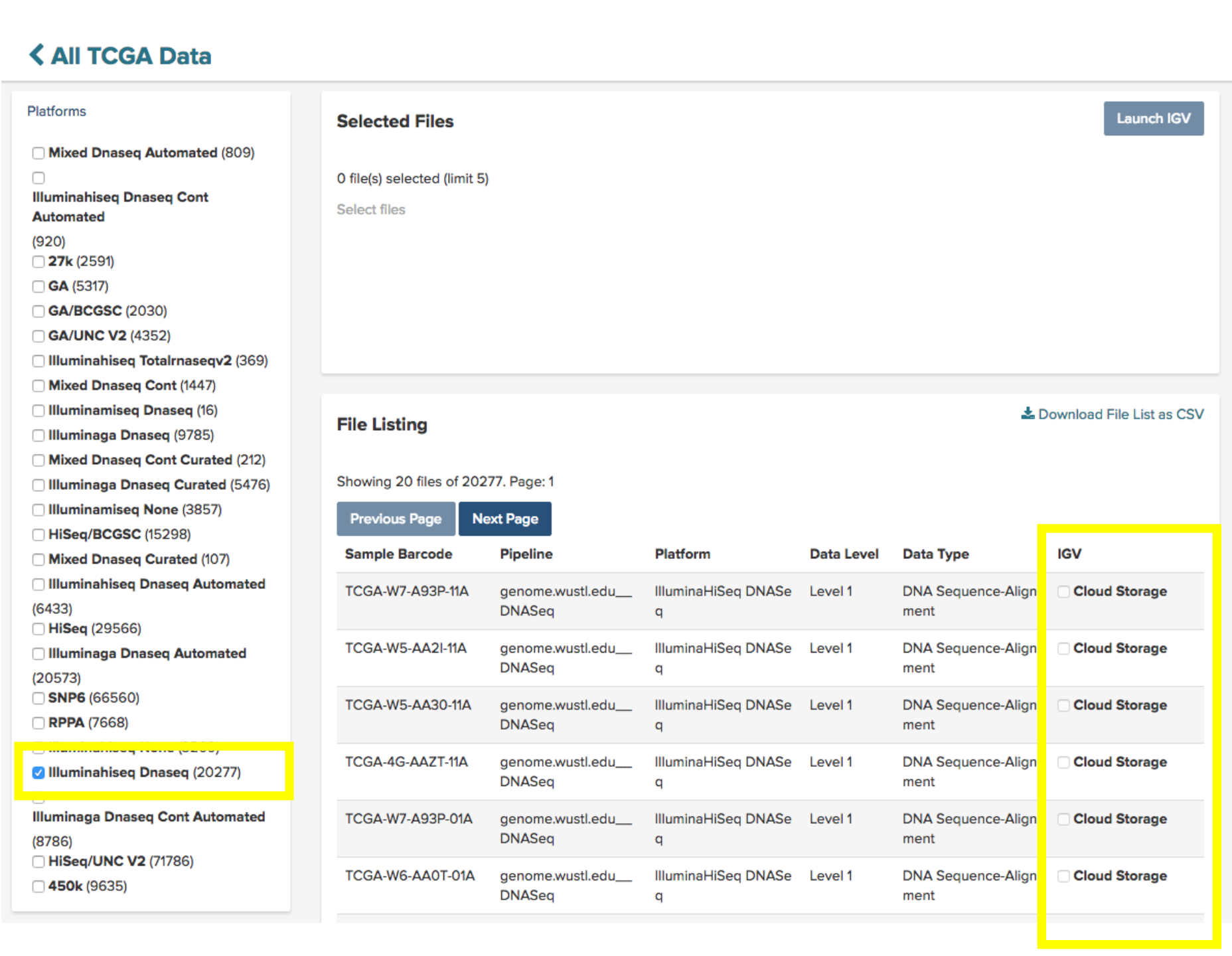
Tumor Tissue Site

Gender

Age at Initial Pathologic Diagnosis

7. All TCGA Cohort File Listing

- Selected are all files that were produced using the Illumina HiSeq
- Note that the entire IGV column has Cloud Storage data available. However, the checkboxes are disabled because this user has not authenticated and authorized their ERA Commons ID.
- After authenticating, these checkboxes will be active.

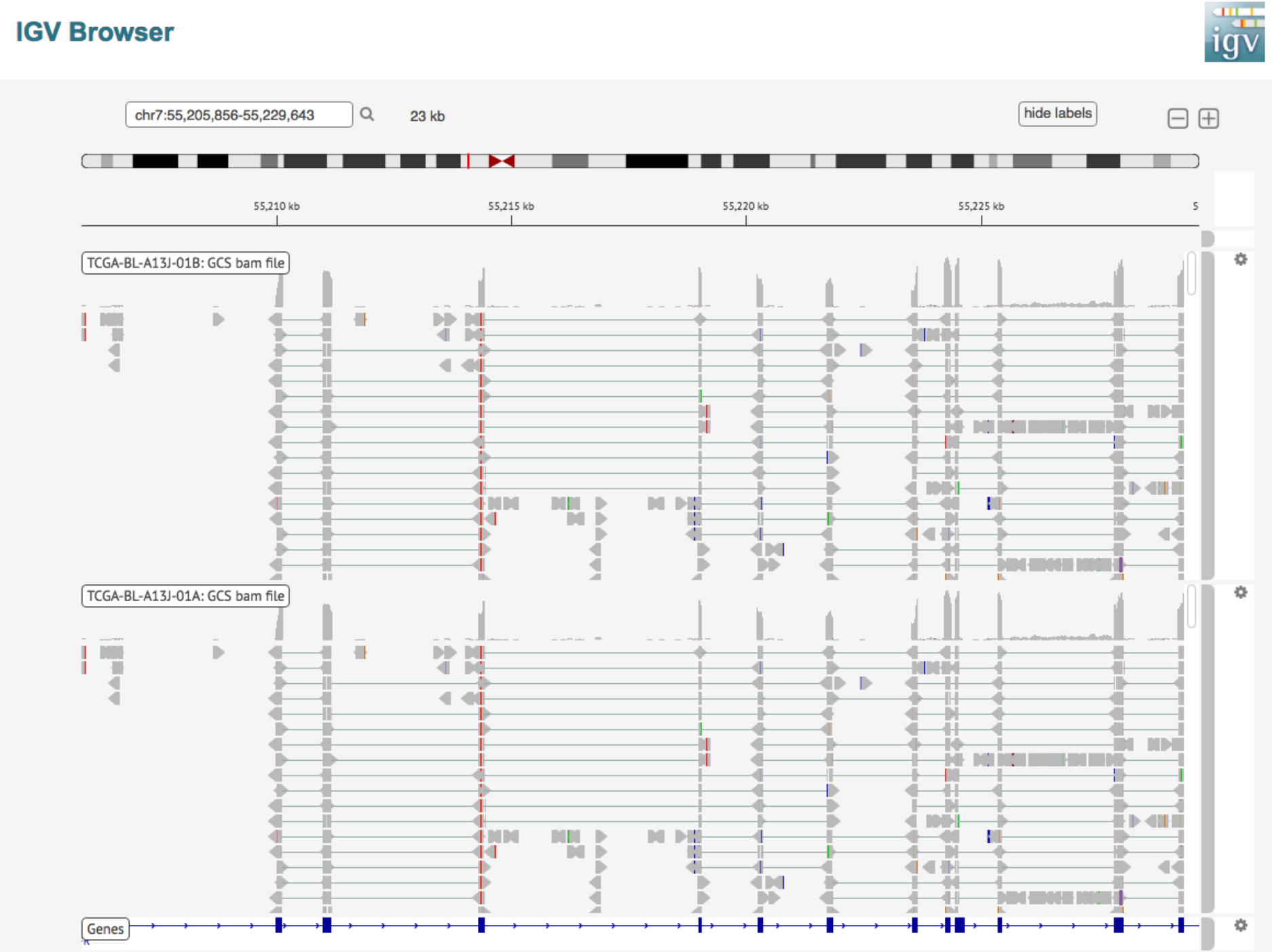


8. Associating your Google Identity with a valid NIH login.

- Documentation can be found here:
  - Short Version: http://bit.ly/1TJErfN
  - Long Version: http://isb-cancer-genomics-cloud.readthedocs.io/en/latest/sections/webapp/Gaining-Access-To-TCGA-Contolled-Access-Data.html
- Note: To access TCGA controlled-access data, you must also be authorized by dbGaP.

9. IGV Browser

- You will be prompted to log in again to authorize access of the information required to display. Please be sure to allow pop-ups on this page for that, otherwise you may receive an access denied error.
- Here, we have two samples and we are looking at. The labels on the two tracks show that they are TCGA samples and GCS bam files.
- Note: this is a mock bam file that has been associated with a real TCGA sample identifier.



Acknowledgements

We are grateful to the IGV team for their assistance in integrating the IGV into the ISB-CGC web application.