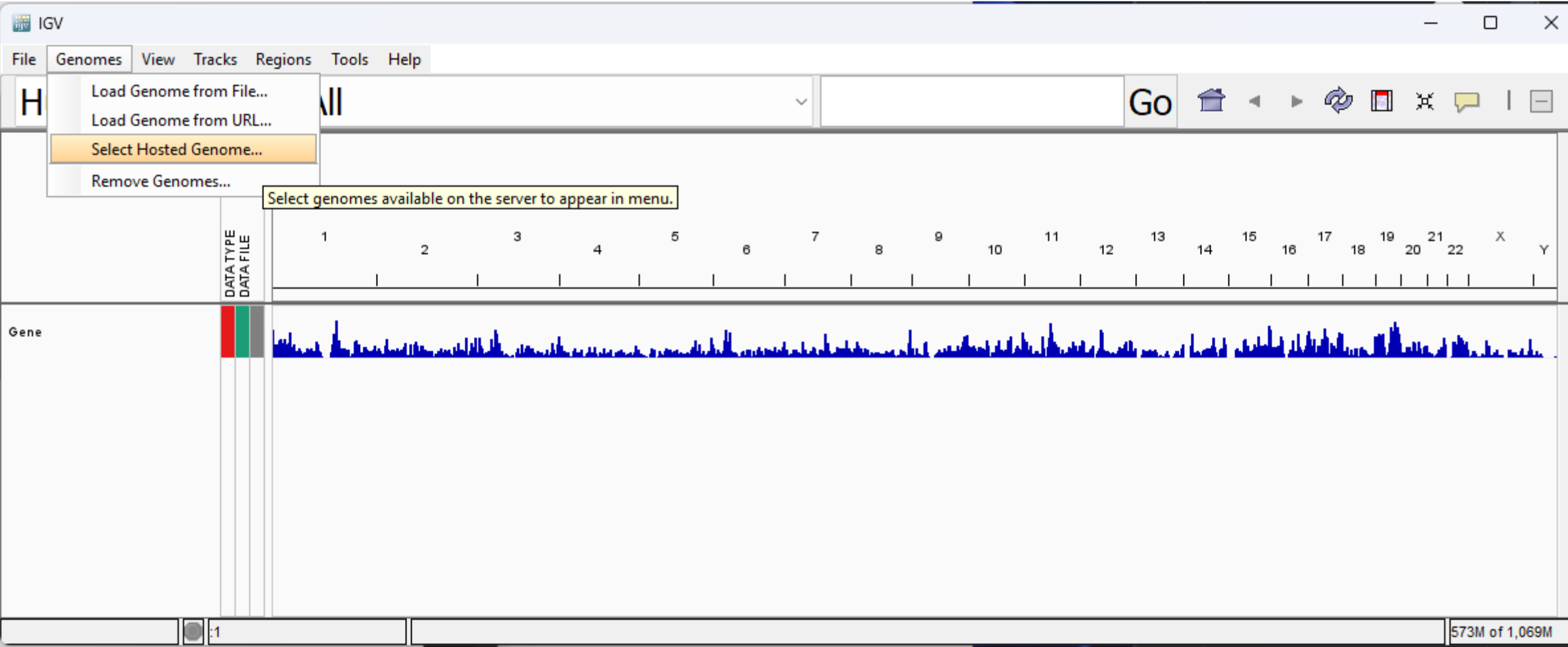


To load a popular reference genome:



Selected genomes will be downloaded and added to the genome dropdown list.

Filter:

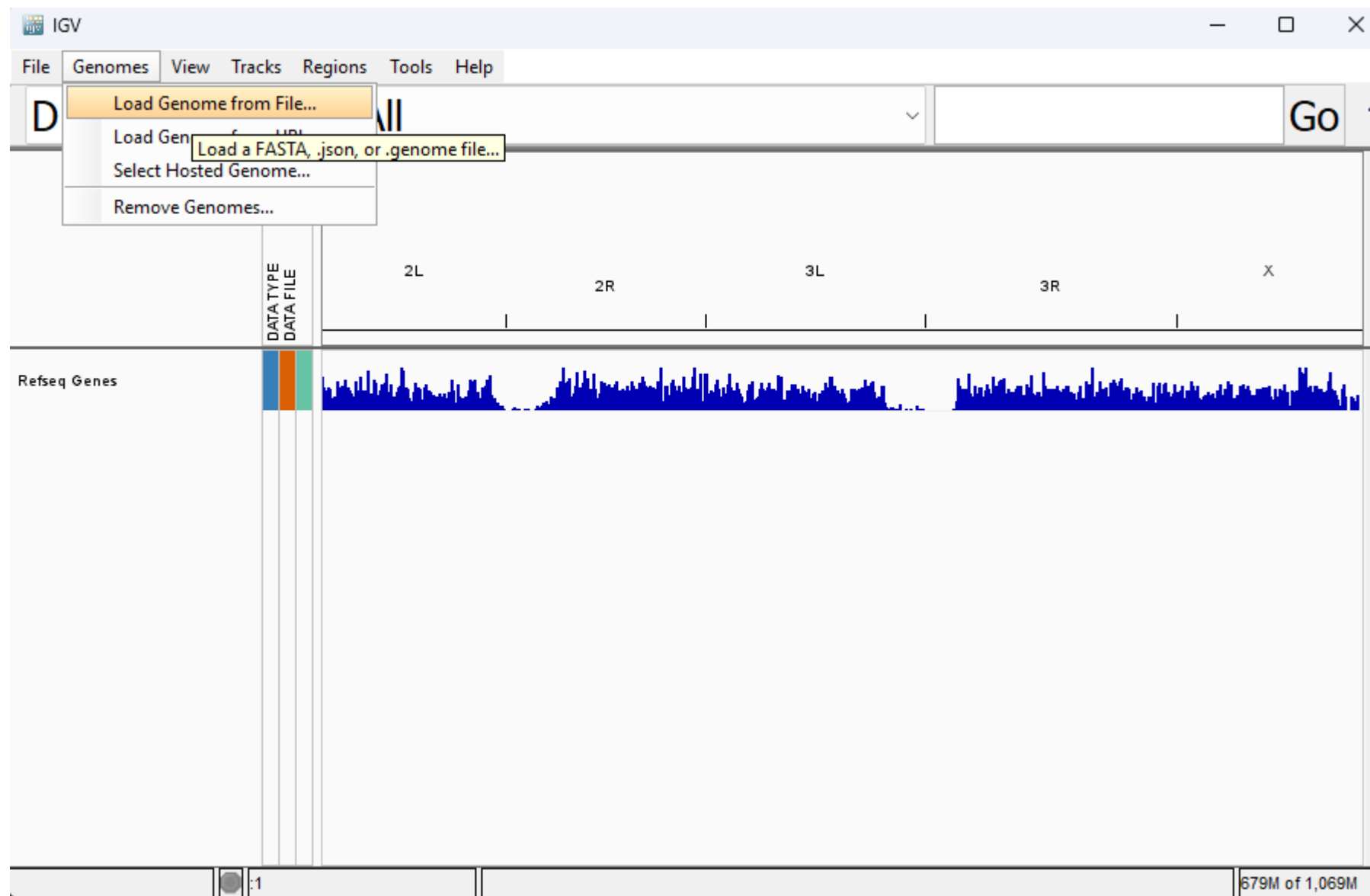
Chimp (panTro4)  
Chimp (panTro5)  
Chimp (panTro6)  
Cow (bosTau7)  
Cow (bosTau8)  
Cow (bosTau9)  
D. melanogaster (dm3)  
D. melanogaster (dm6)  
D. melanogaster (r5.9)  
Dog (canFam3)  
Dog (canFam5)  
E. coli K-12 (NC\_000913.3)  
E. coli K-12 MG1655 (NC\_000913.2)  
Ferret (MusPutFur1.0)  
Francisella tularensis (NC\_008601)  
Glycine max (v8.0)

☐ Download Sequence

OK

Cancel

If genome is custom:



I suggest you create a json file with the path to the fasta and index files, like the example below, and then load that file onto igv [Note, you can also add bed files if you have annotations for that specific genome, etc]:

```
{
  "id": "CHM1",
  "name": "Human (CHM1)",
  "fastaURL": "https://s3-us-west-2.amazonaws.com/stergachis-internal/CHM1/hub/chm1_cens_v18.fa?AWSAccessKeyId=[REDACTED]3D",
  "indexURL": "https://s3-us-west-2.amazonaws.com/stergachis-internal/CHM1/hub/chm1_cens_v18.fa.fai?AWSAccessKeyId=[REDACTED]3D",
  "tracks": [
    {
      "name": "Annotation_orig",
      "url": "https://s3-us-west-2.amazonaws.com/stergachis-internal/CHM1/hub/AS-HORs-vs-chm1_cens_v18.clean.bed?AWSAccessKeyId=AI[REDACTED]%3D"
    }
  ]
}
```



IGV

File Genomes View Tracks Regions Tools Help

D. melanoga...

All

Go

DATA TYPE  
DATA FILE

Refseq Genes

Load Genome

Look in: CHM1



Home



Desktop



Libraries



This PC



Network

Name

Date modified

Type

CHM1\_genome.json

5/3/2022 5:07 PM

JSON

igv\_session.xml

5/4/2022 11:22 AM

Micro

File name:

CHM1\_genome.json

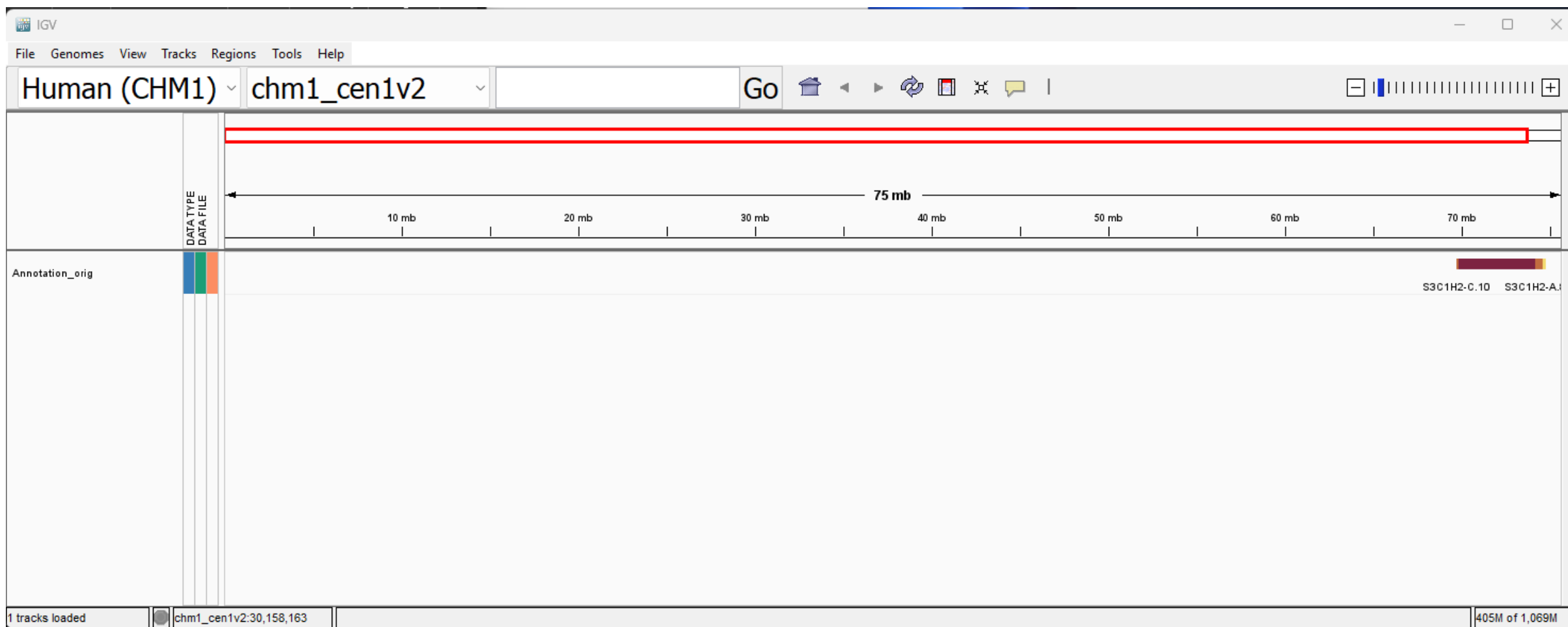
Files of type:

All Files (\*.\*)

Open

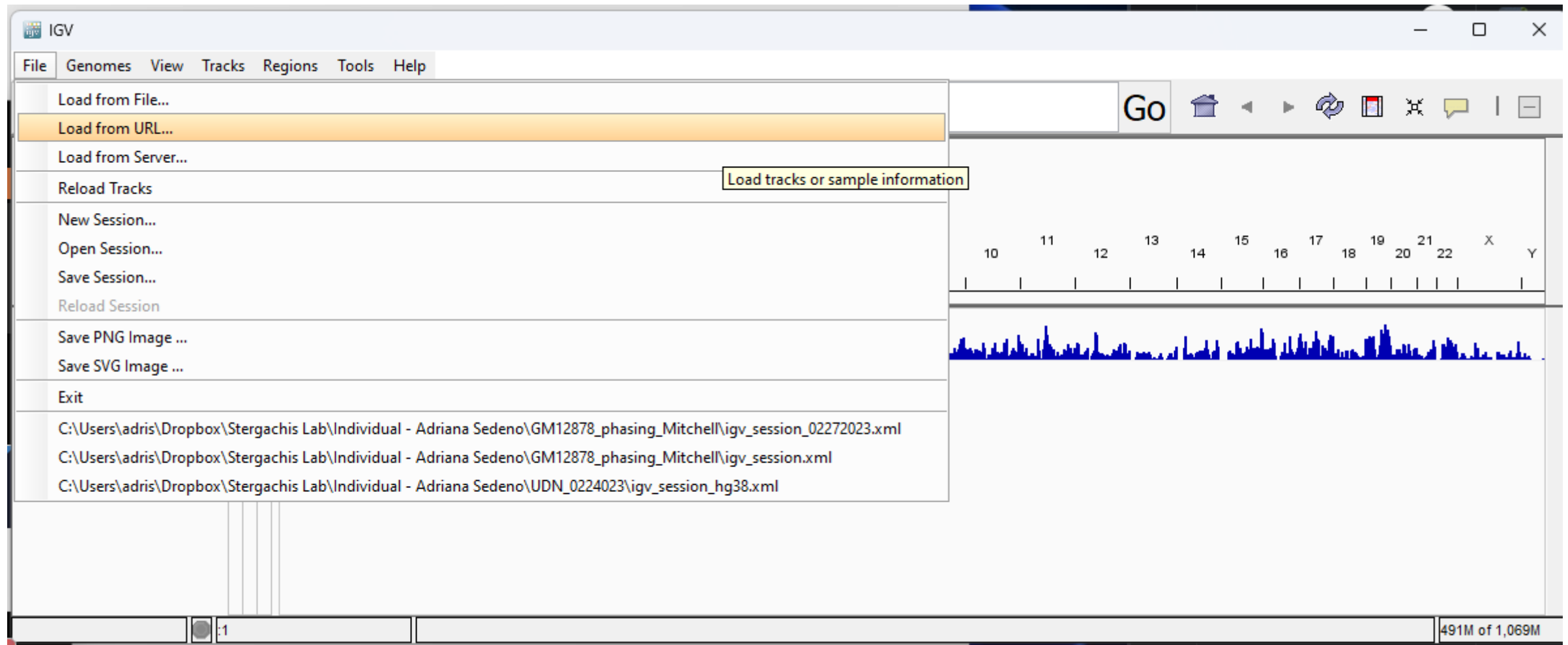
Cancel

IGV will now show the custom genome and if you incorporated annotations to the json file, those will be loaded too:

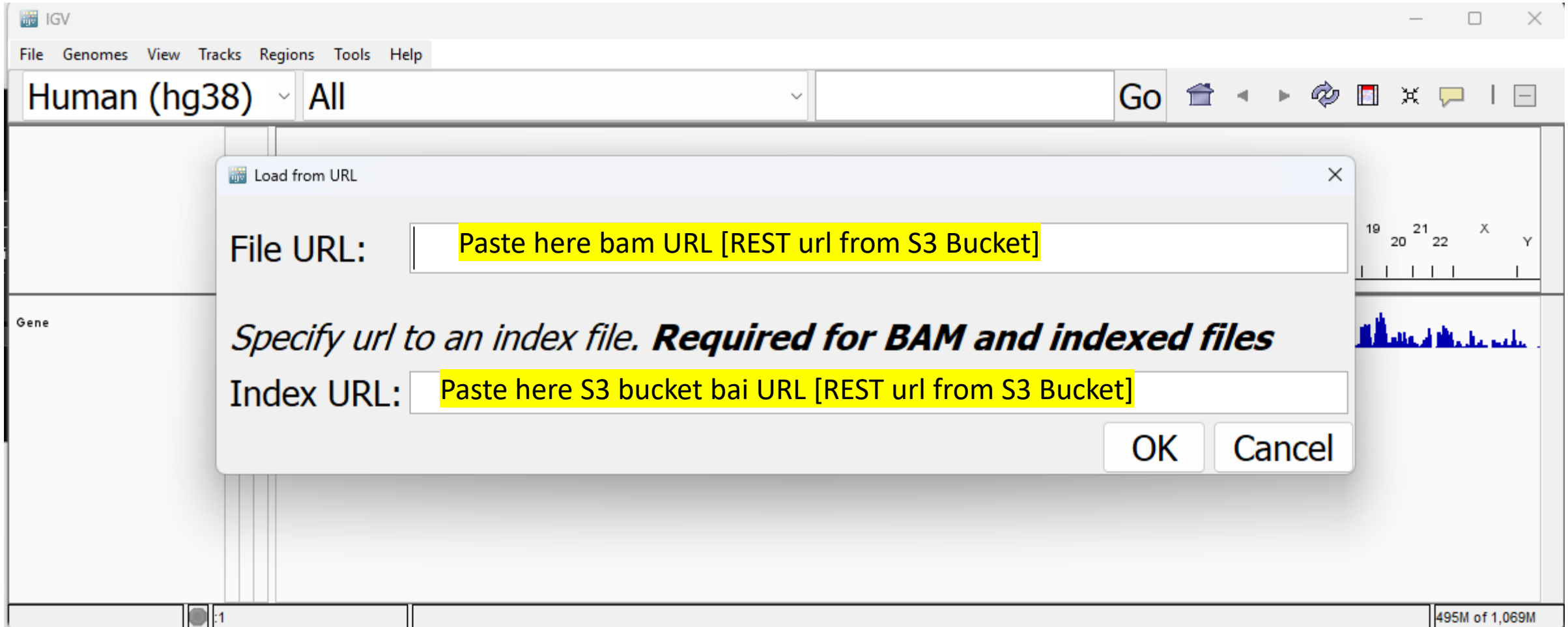


Genome is now loaded. Now, we can start adding data tracks onto the session:

To load a bam file onto IGV:



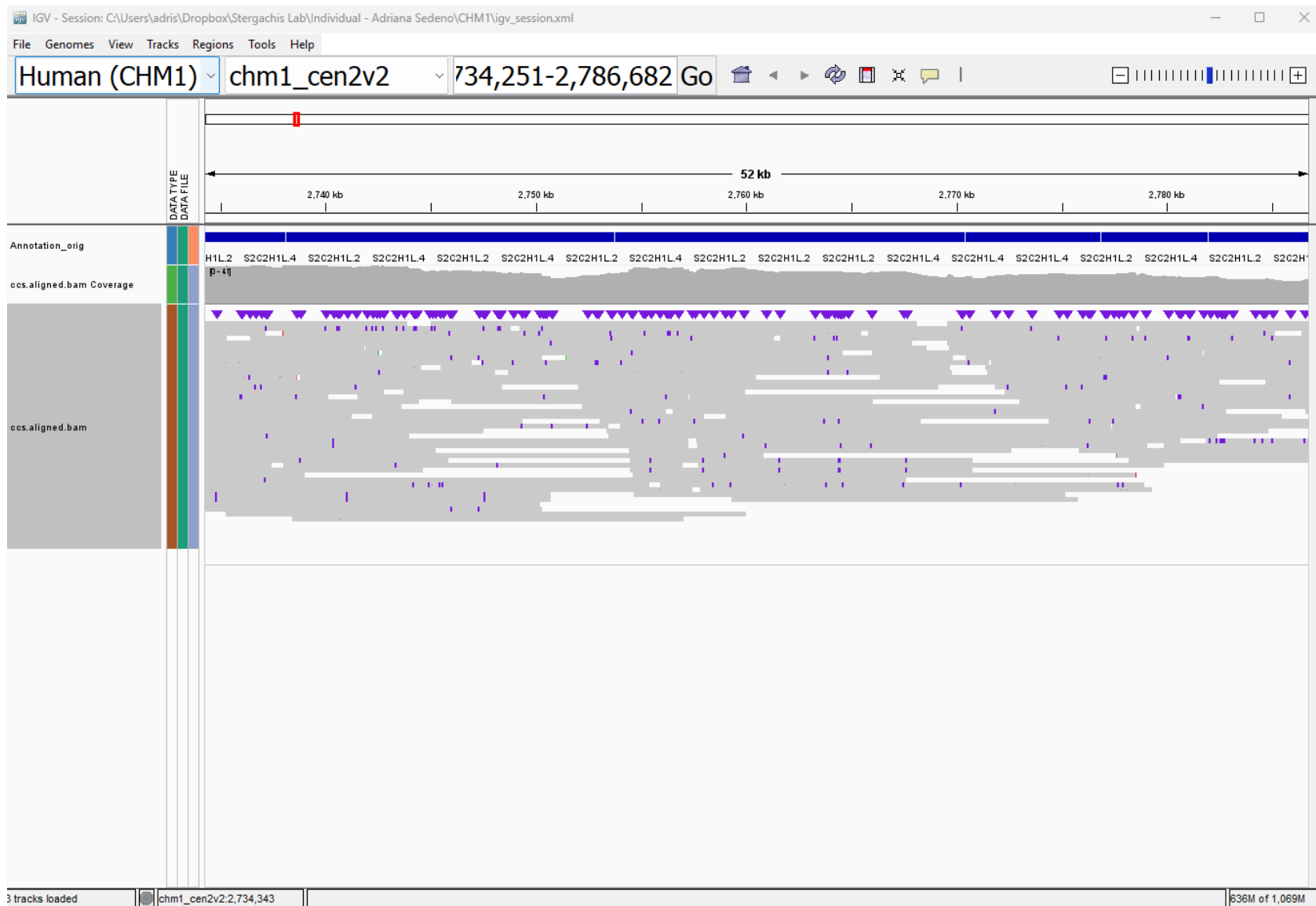
Note: This same tab also works for other data types (bed, bedgraph, etc)



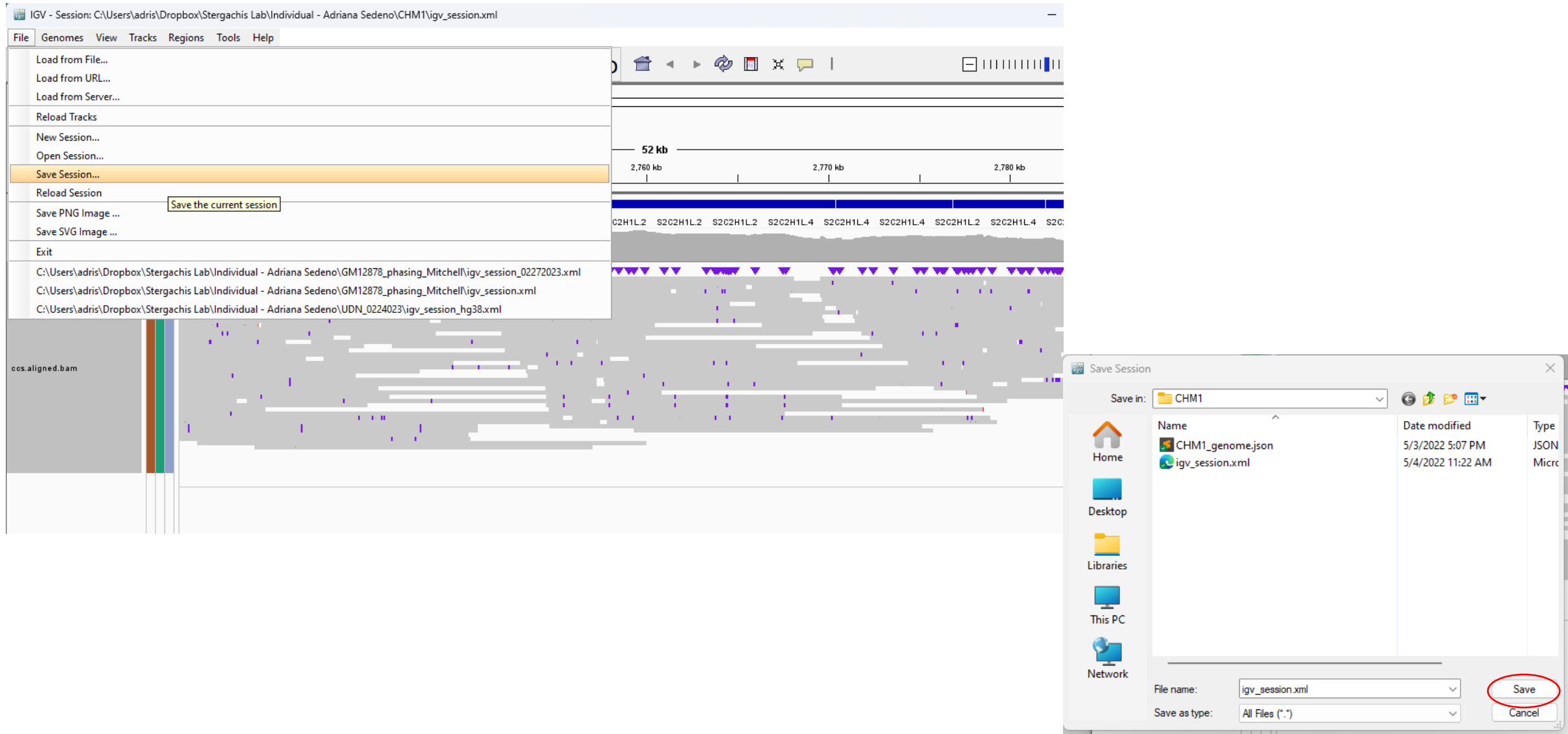
Other data types might not need an index



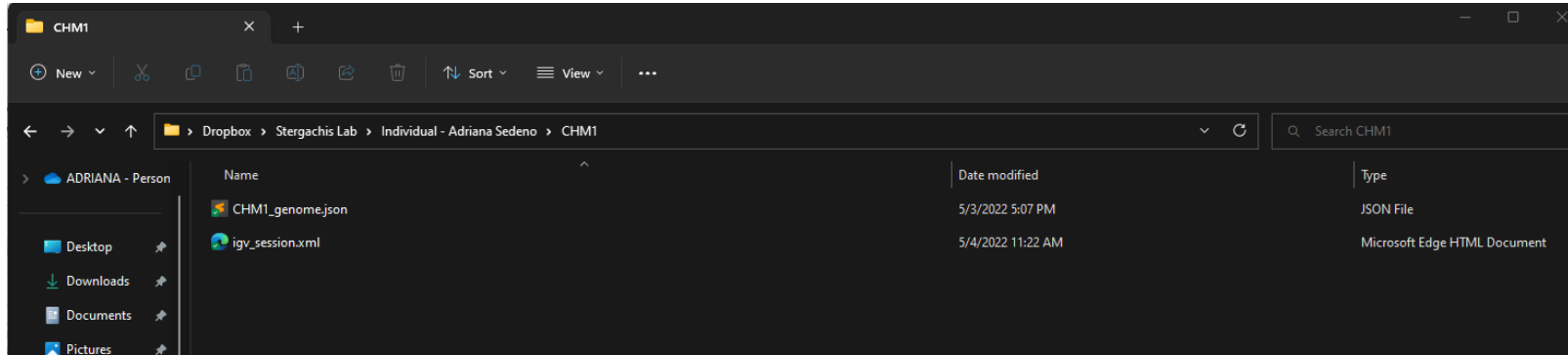
Session now has the loaded bam file and it also shows coverage as a separate track at the top:



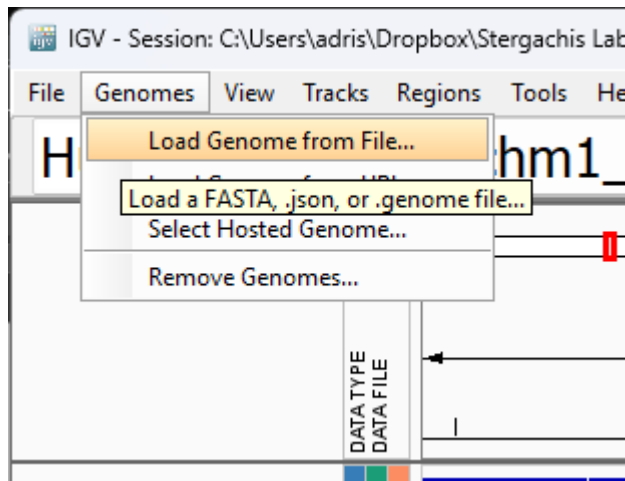
When you're done loading all the data, just save the session next to the folder where you keep your reference genome Json file. I keep mine on dropbox:



Share with Andrew (or any other user) those two files:



Ask them to load first the genome json file:



And then the xml session:

