

Visualization of mapped reads

Integrative Genomics Viewer (IGV)

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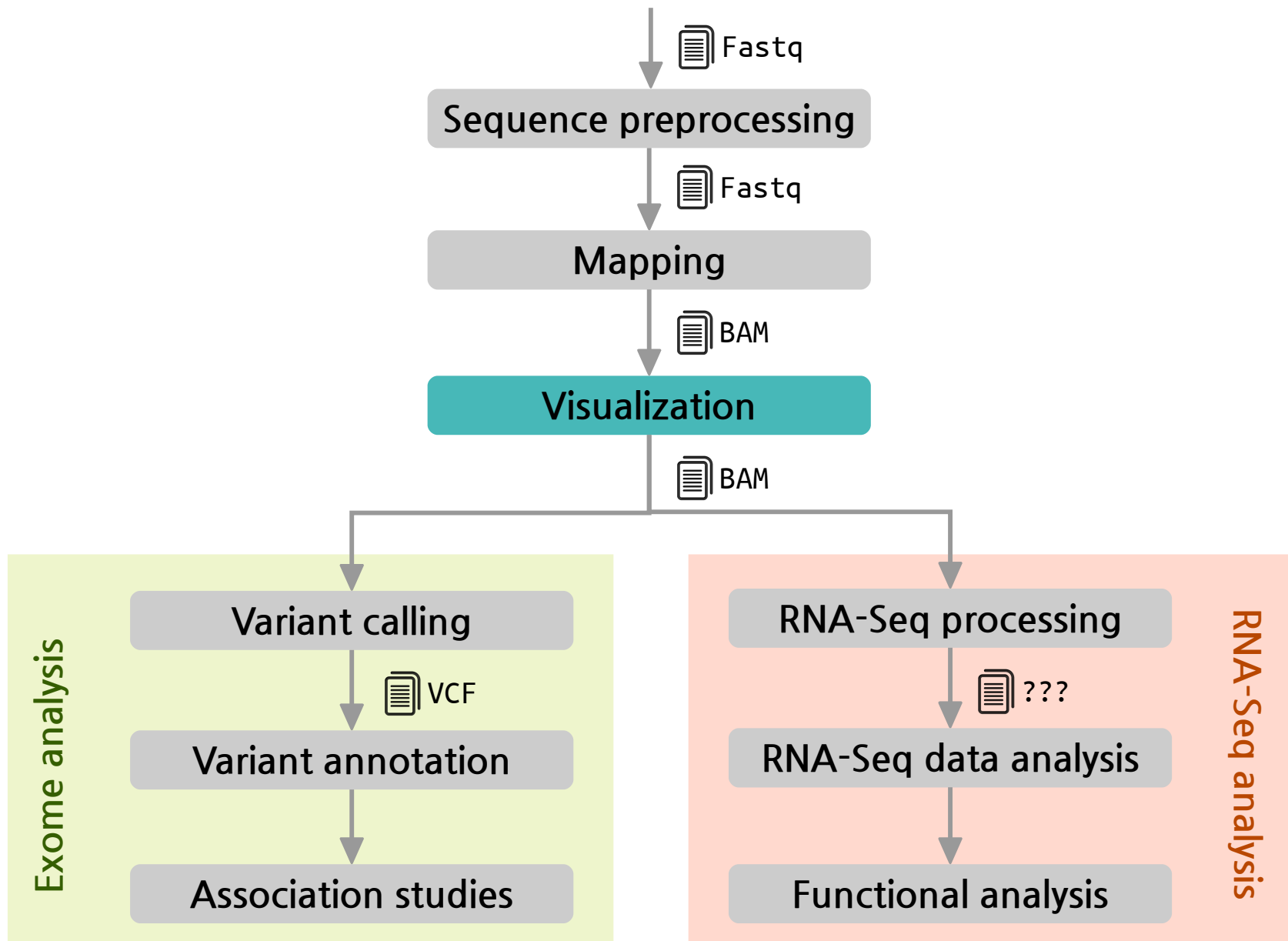
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Centro de Investigación Príncipe Felipe (CIPF)

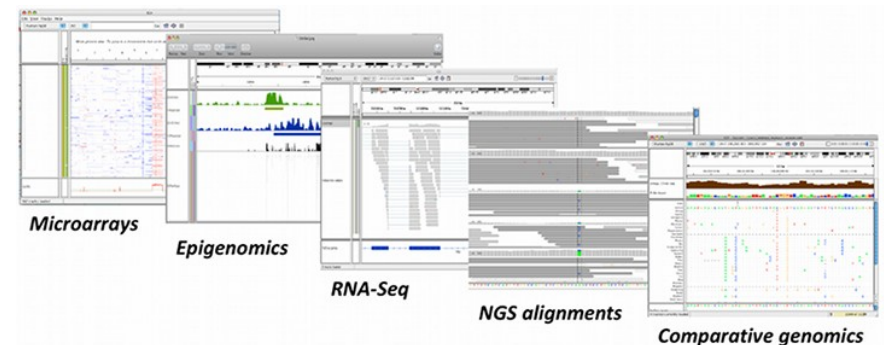
Valencia, Spain

The pipeline



Introduction

- **Large** quantities of genomic **data** (NGS, array based methods, etc)
- **Human interpretation** and judgment using visualization can help complex biological relationships
- Integrative Genomics Viewer (**IGV**)
 - **Integrate** different data types simultaneously
 - View **large datasets** easily
 - Faster navigation or browsing
 - Runs **locally** on your desktop
 - Used by large-scale projects
 - Open source and **freely available**



Helga Thorvaldsdóttir, James T. Robinson, and Jill P. Mesirov
Integrative Genomics Viewer (IGV): high-performance genomics data visualization and exploration
Brief Bioinform (2013) 14 (2): 178-192

Data types

- Any data related to genome coordinates
- Sample annotations or attributes
- Genome annotations

Recommended file formats

Source data	Recommended File Formats
Sequence alignment data	SAM (must be sorted/indexed) BAM (must be indexed)
Genome annotations	GFF or GFF3 format BED format
ChIP-Seq, RNA-Seq	TDF format (can be generated using igvtools)
Any numeric data	IGV format, TAB format WIG format
Gene expression data	GCT format RES format

Indexing a BAM file

- BAM format: Binary **SAM** file → Reduces disk space and time
 - For each read, provides the position(s) where it maps and information about the alignment
 - BAM files need to be **indexed** (using **samtools**) → SAM files will be sorted by start position and indexed

Index an example BAM file

```
samtools index NA12878_child.bam  
samtools index NA12891_dad.bam  
samtools index NA12892_mom.bam
```

Take a look at the file size

```
ls -lh
```

Registration and download

1. Be sure that **Java 6 or later** is installed on your machine
2. Go to the IGV website:

<http://www.broadinstitute.org/igv/home>

3. Click **Downloads** at the left panel
4. Click to register and fill the form

Log In

To use IGV, registration is required.
[Click here](#) to register.

If you have already registered for IGV please enter your registration email address below.

email address:

Login

5. Download the most suitable file for your system

Downloads

Mac users: Download the following archive. should unzip automatically, then double-click the IGV application to run. The application can be moved to the "Applications" folder, or anywhere else.

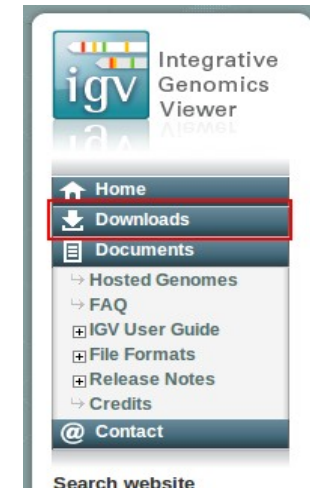
- [IGV 2.3.30.app.zip](#)

Windows and Linux users: Download and unzip the archive in a folder of your choosing. IGV is launched from a command prompt, follow instructions in the "readme" file. Windows users, use the "igv.bat". On Linux, use "igv.sh".

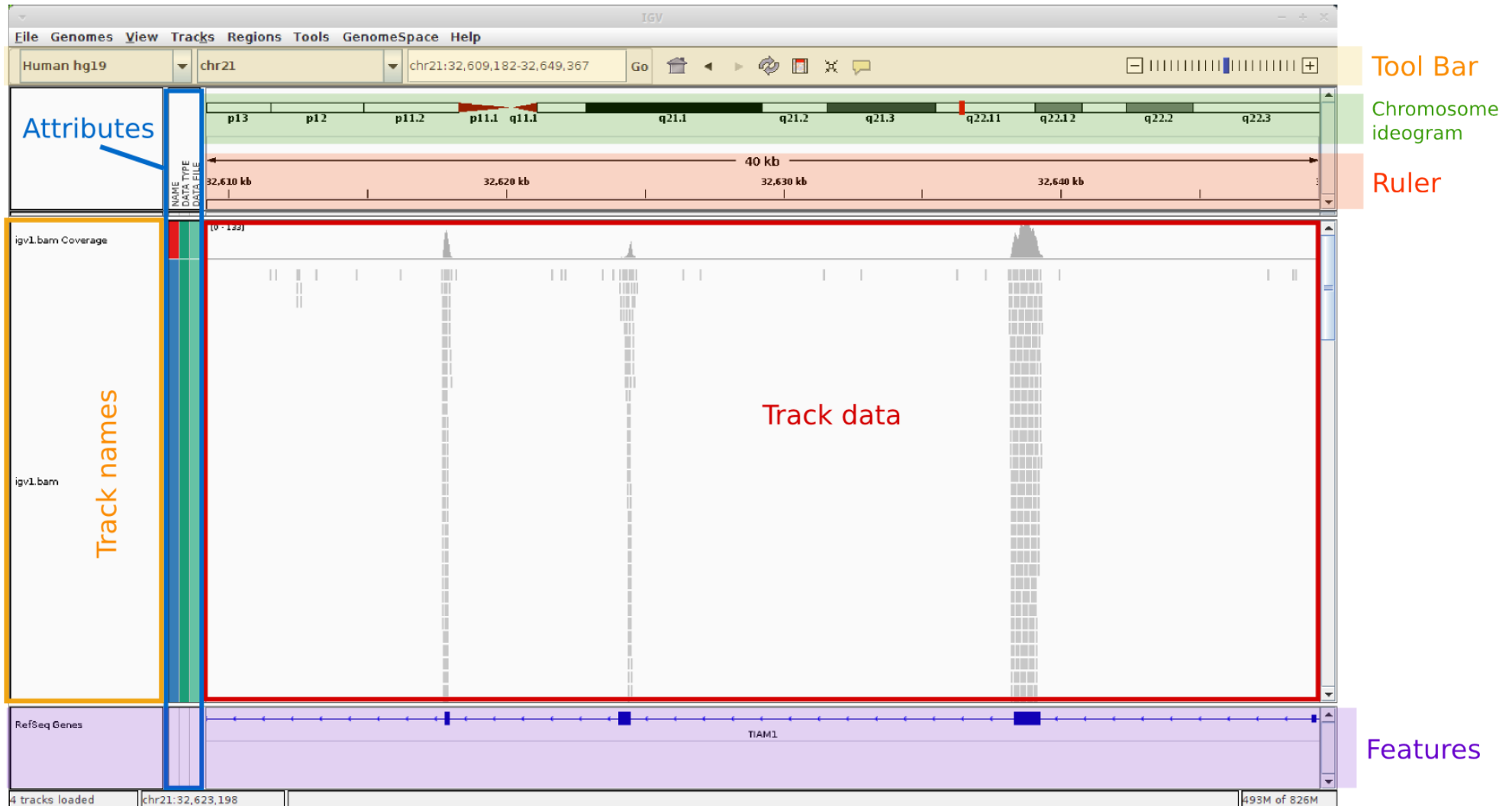
- [IGV 2.3.30.zip](#)

6. Run IGV

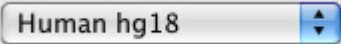

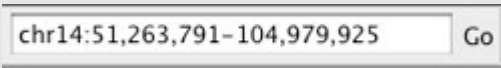







igv



IGV interface



IGV Tool Bar

	Genome drop-down box
	Chromosome drop-down box
	Search box
	Whole genome view
	Moves backward and forward through views of the genome
	Refreshes the display
	Defines a region of interest on the chromosome
	Reduces the row height on all tracks to fit all data
	Toggles the pop-up information windows in IGV on or off
	Zooms in and out on a chromosome

Download genome

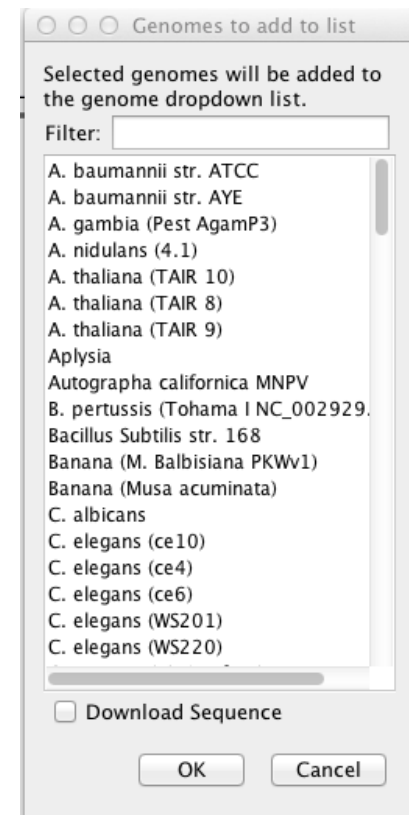
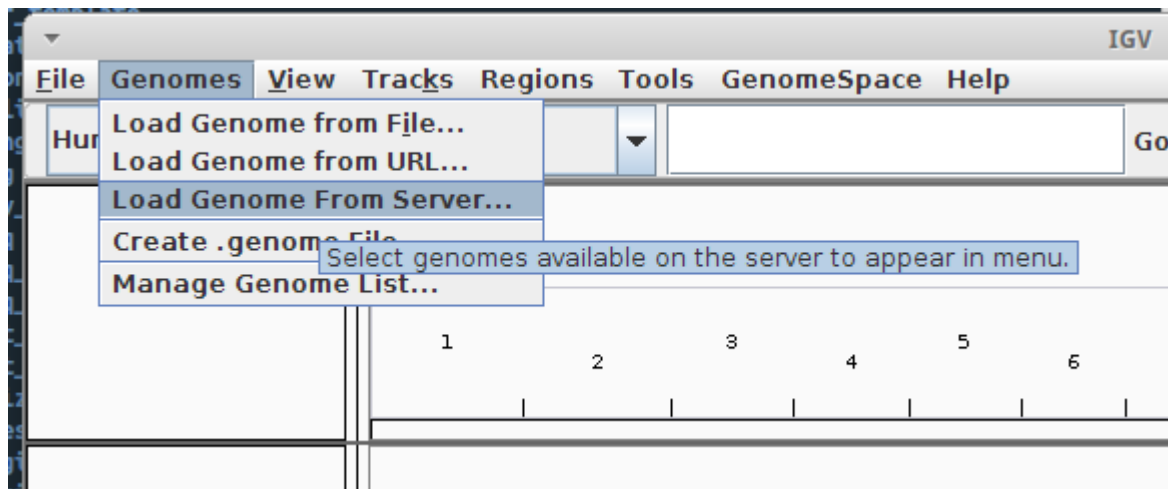
Initially, the genome drop-down list contains a single item, "Human hg18"

IGV provides a number of genomes that are hosted on a server at the Broad Institute

List of genomes hosted: <http://www.broadinstitute.org/software/igv/Genomes>

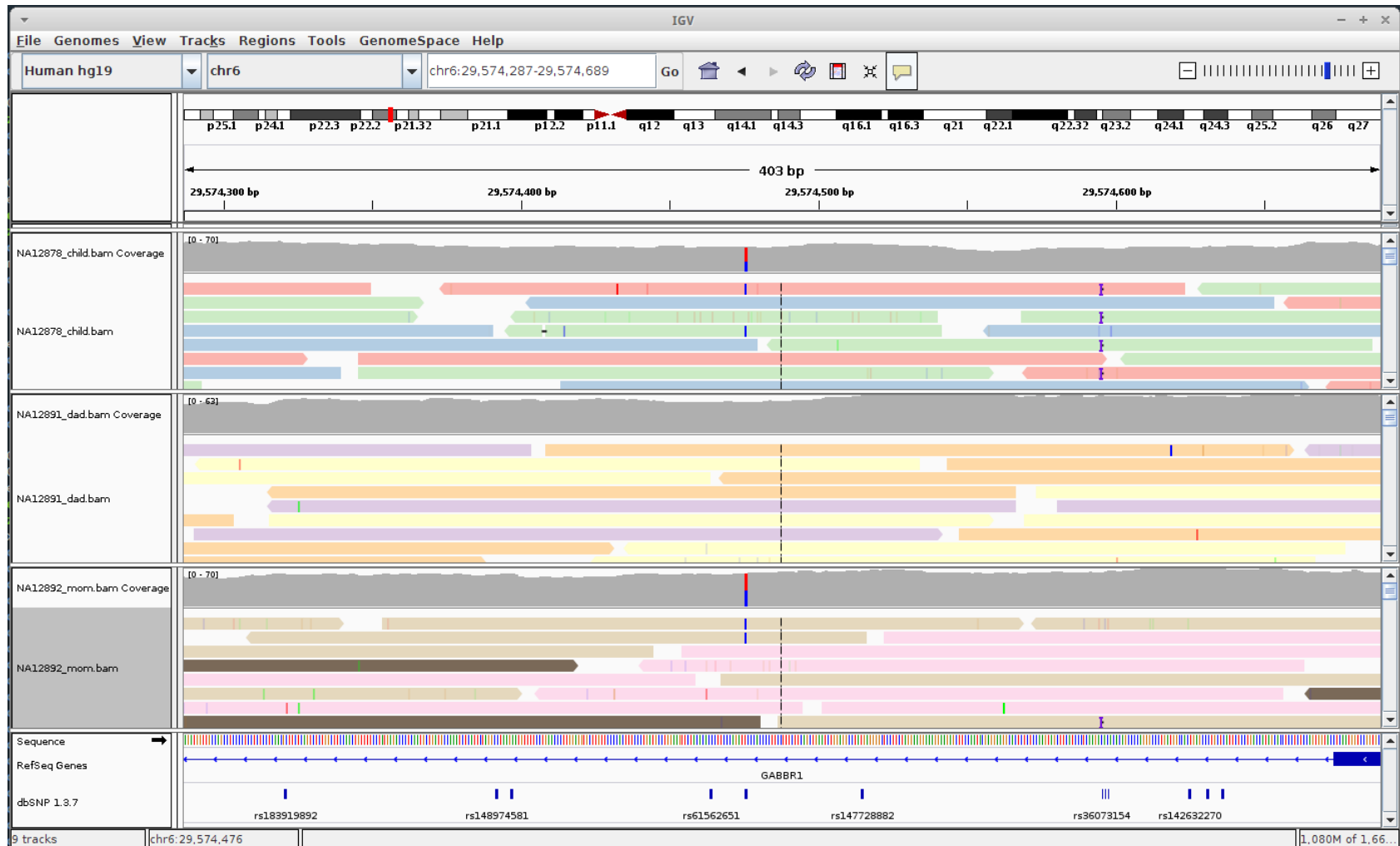
- Genomes → Load genome from server...

Select Human hg19



Loading and browsing files

- File → Load from file...
Select `NA12878_child.bam`, `NA12891_dad.bam` and `NA12892_mom.bam`



THANK YOU.