Visualization of mapped reads

Integrative Genomics Viewer (IGV)

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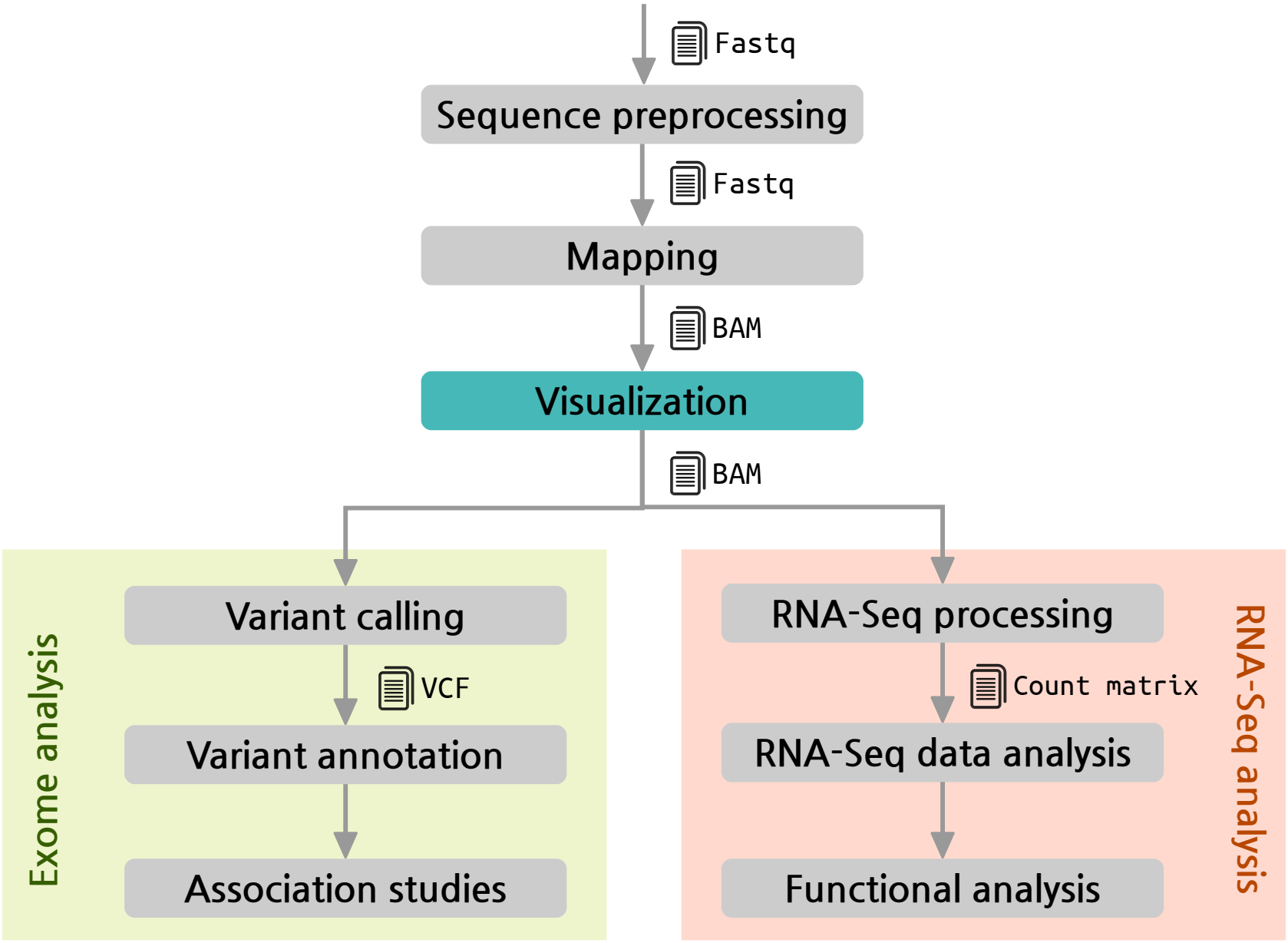
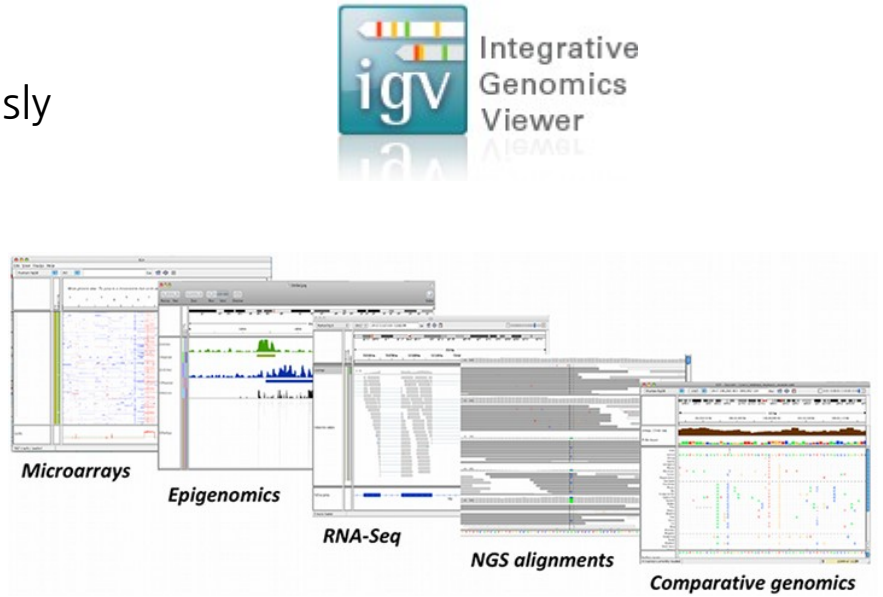
The pipeline



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
Variant data	VCF
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
- BAM/SAM files need to be **indexed** (using **samtools**) → SAM files will be sorted by start position and indexed
- Index files must reside in the **same directory** as the BAM or SAM file

Index the example BAM file

```
samtools index igv1.bam
```

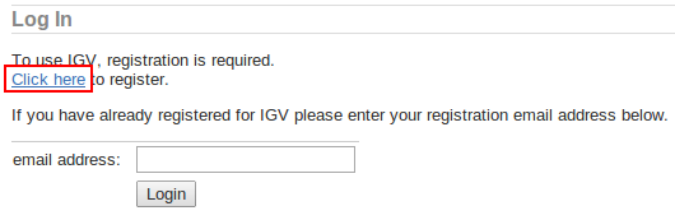
Take a look at the file size

```
ls -lh
```

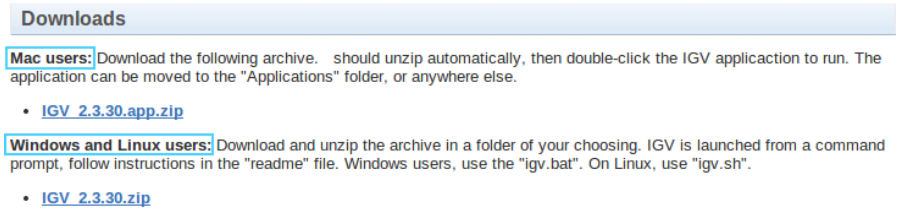
Registration and download

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



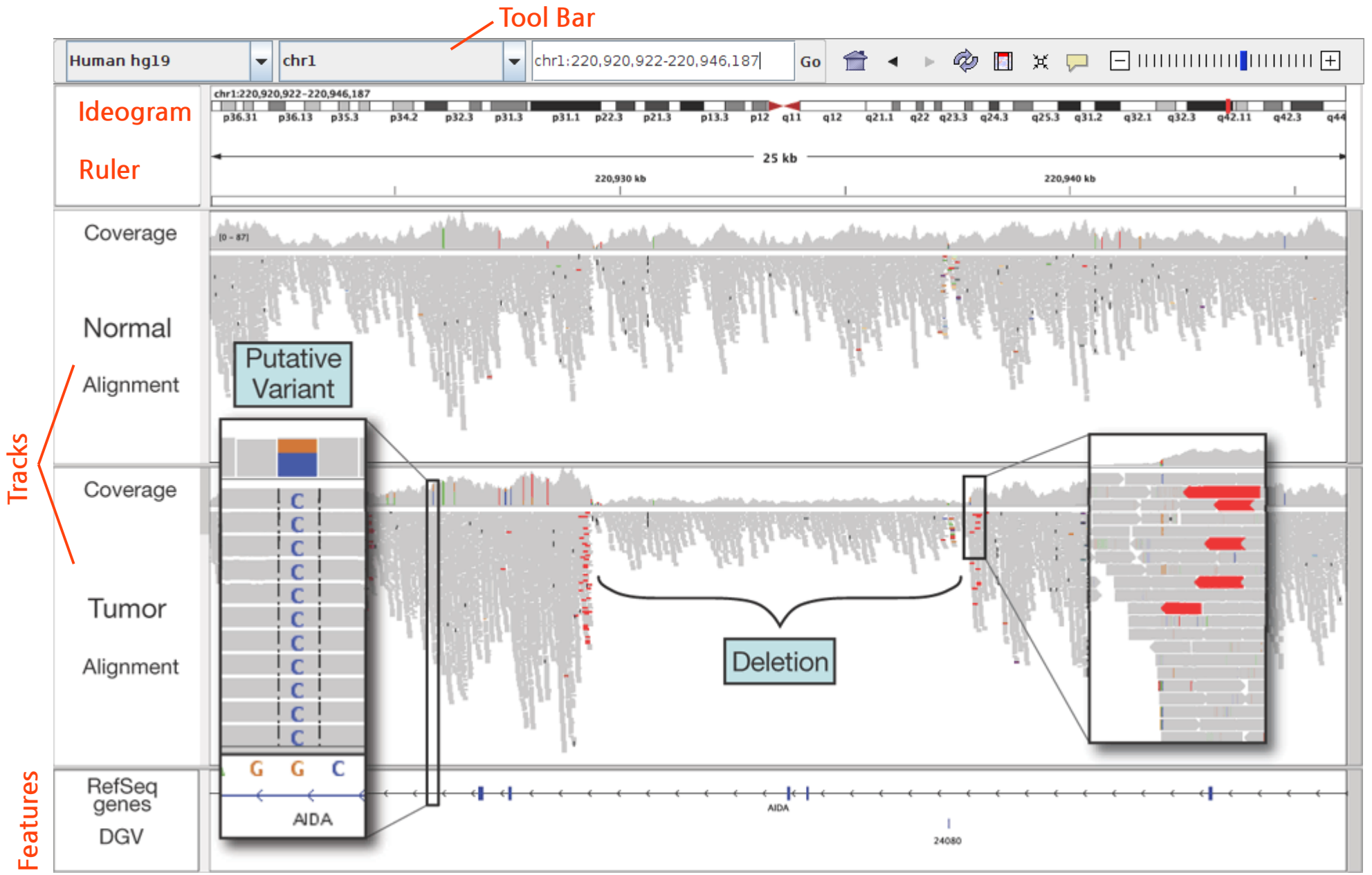
5. Download the most suitable file for your system



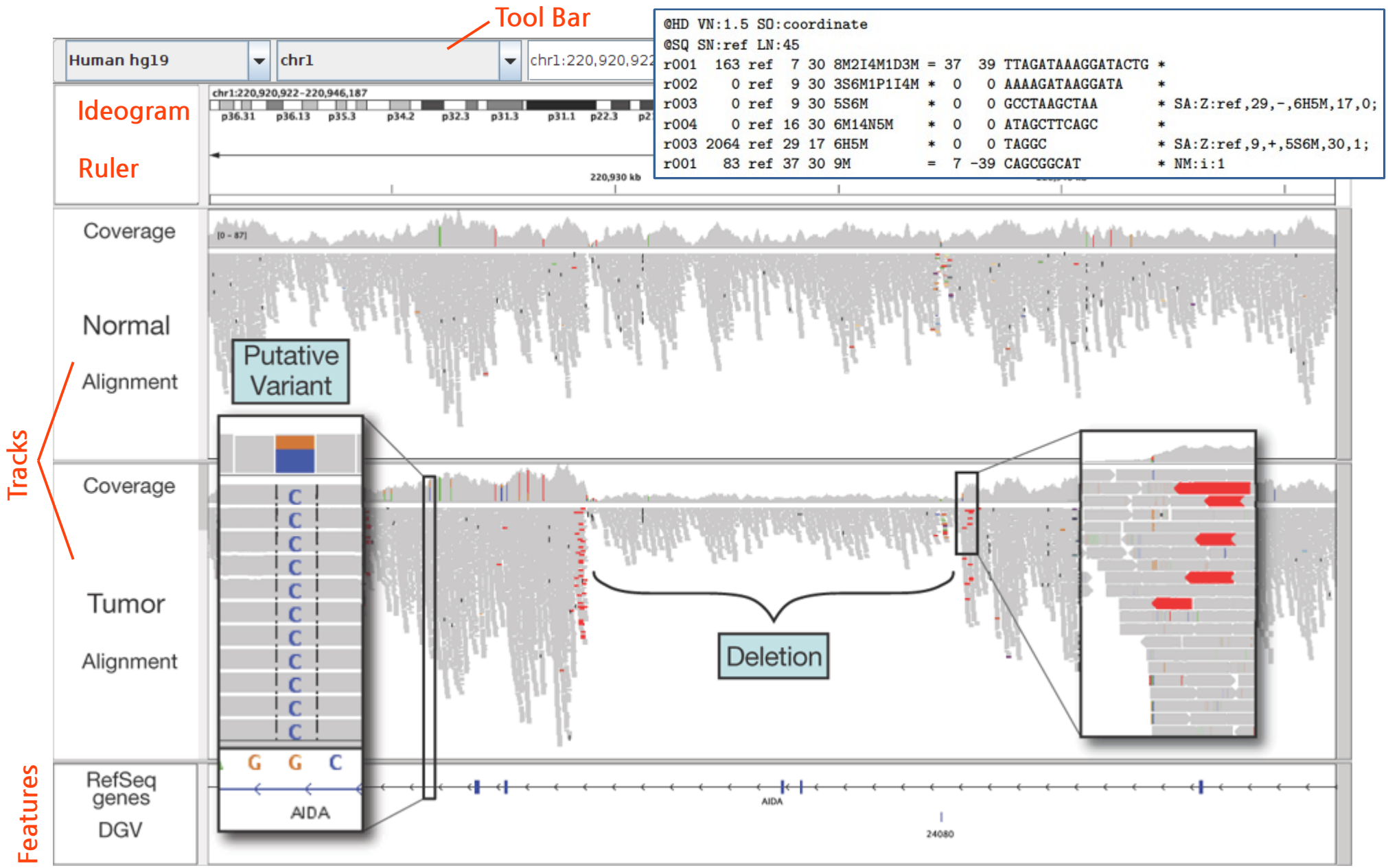
6. Run IGV

```
./igv.sh
```

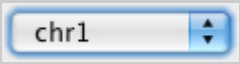
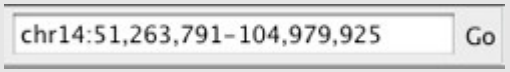
IGV interface



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

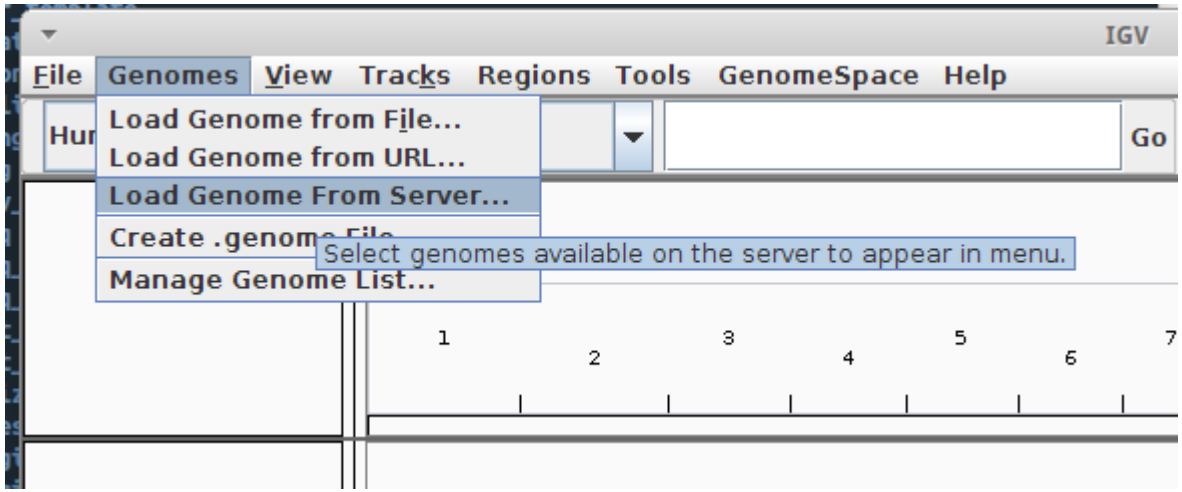
Initially, the genome drop-down list contains a single item, "**Human hg18**"

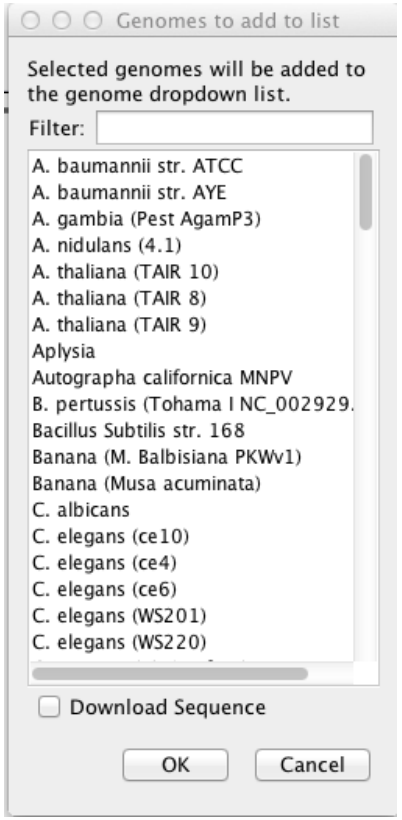
IGV provides **a number of genomes that are hosted** on a server at the Broad Institute

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

- Genomes → Load genome from server...

  Select **Human hg19**





Hands on!