

Visualization of mapped reads

Integrative Genomics Viewer (IGV)

University of Cambridge

Cambridge, UK

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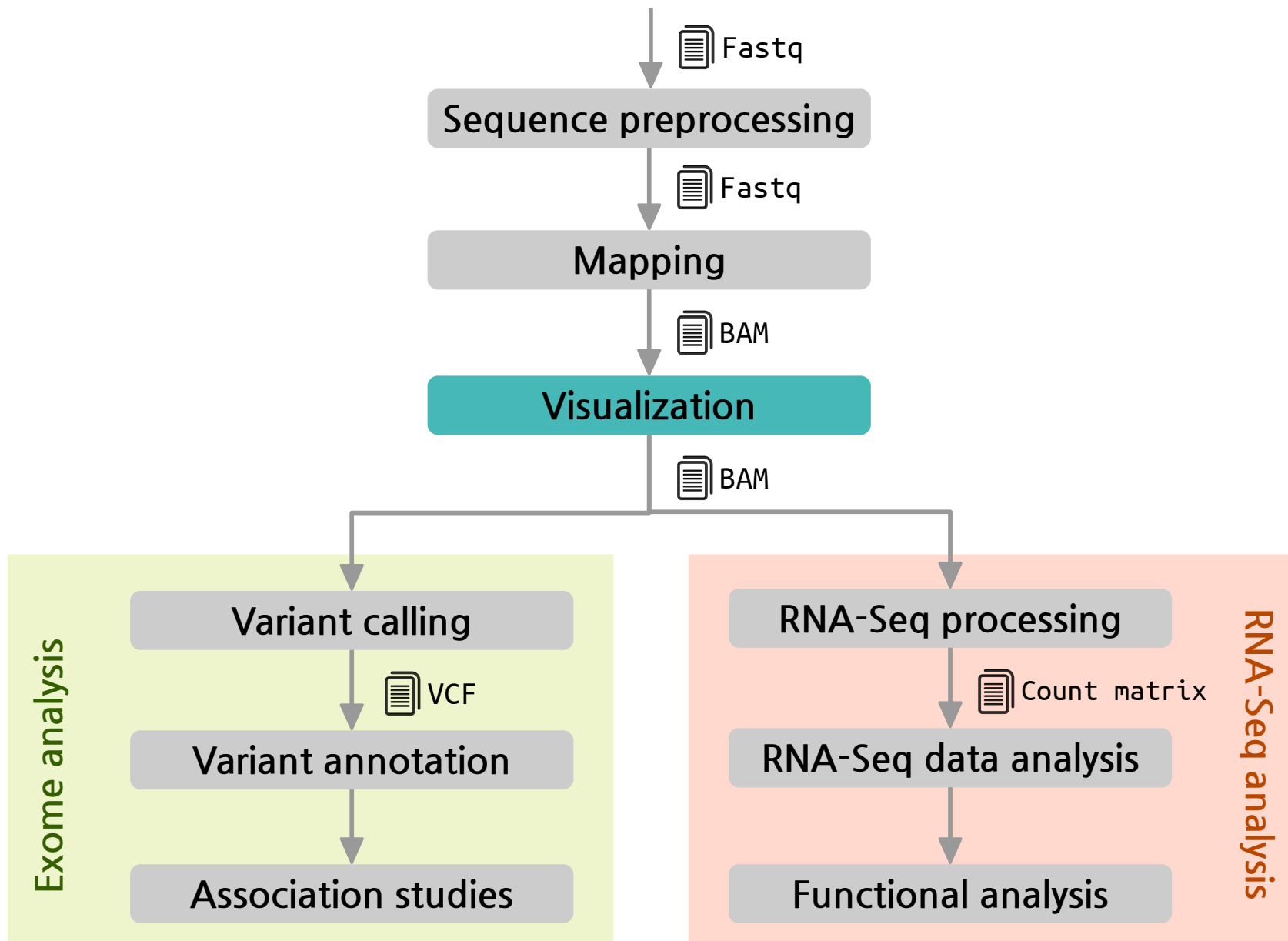
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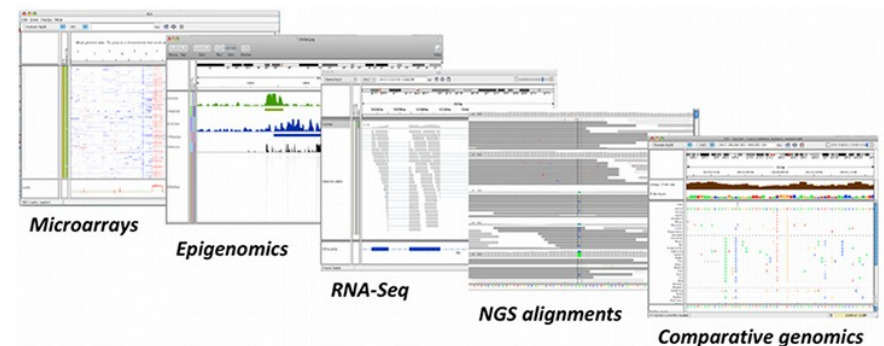
Cambridge, UK

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
```

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

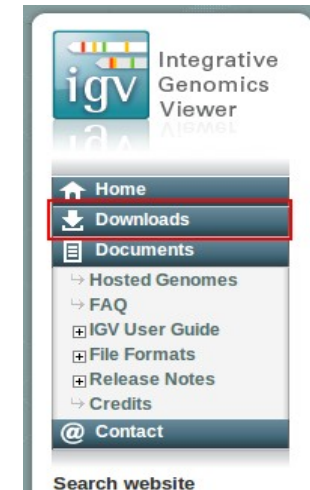
Log In

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



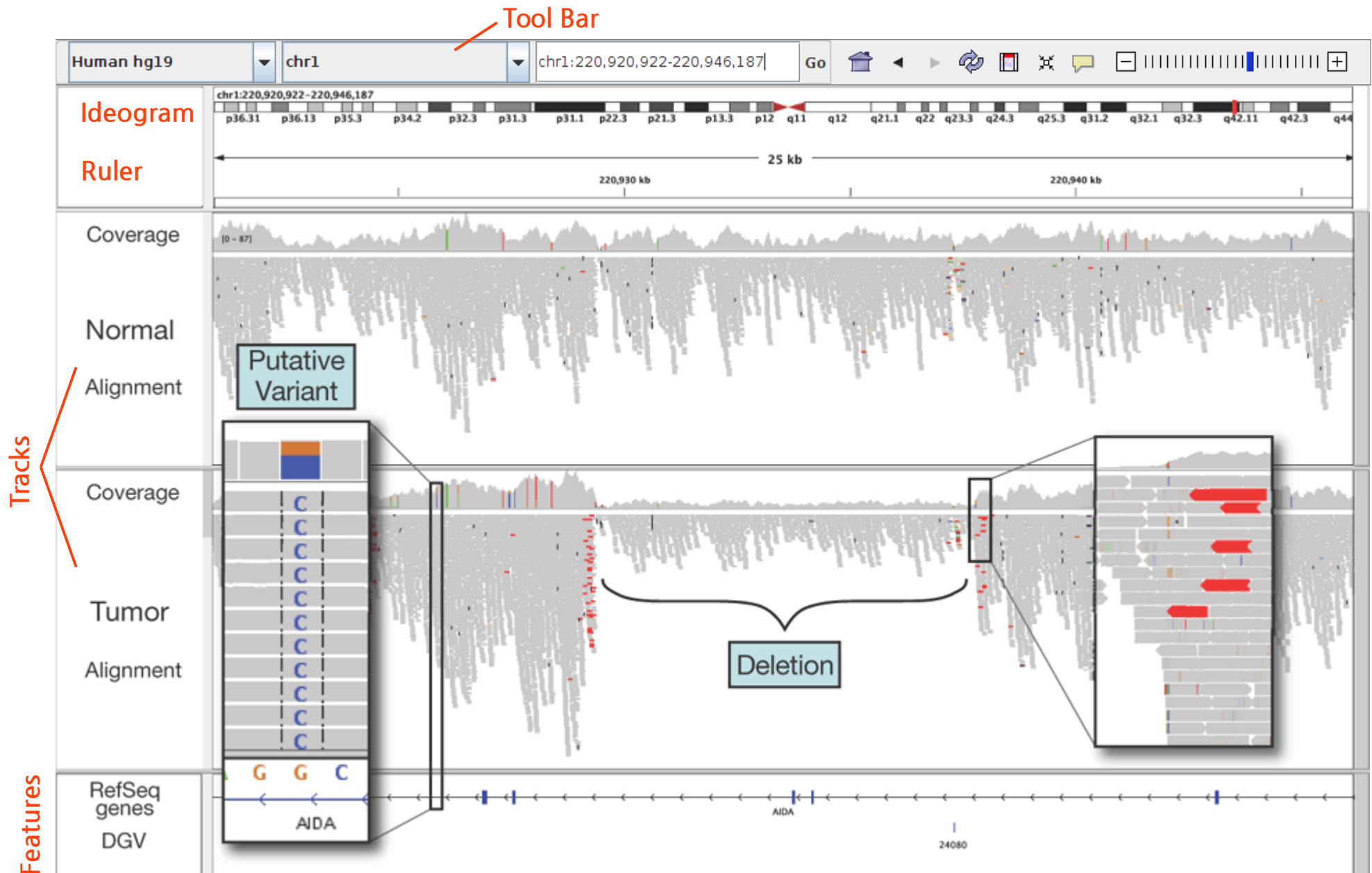
* Requires Java 7



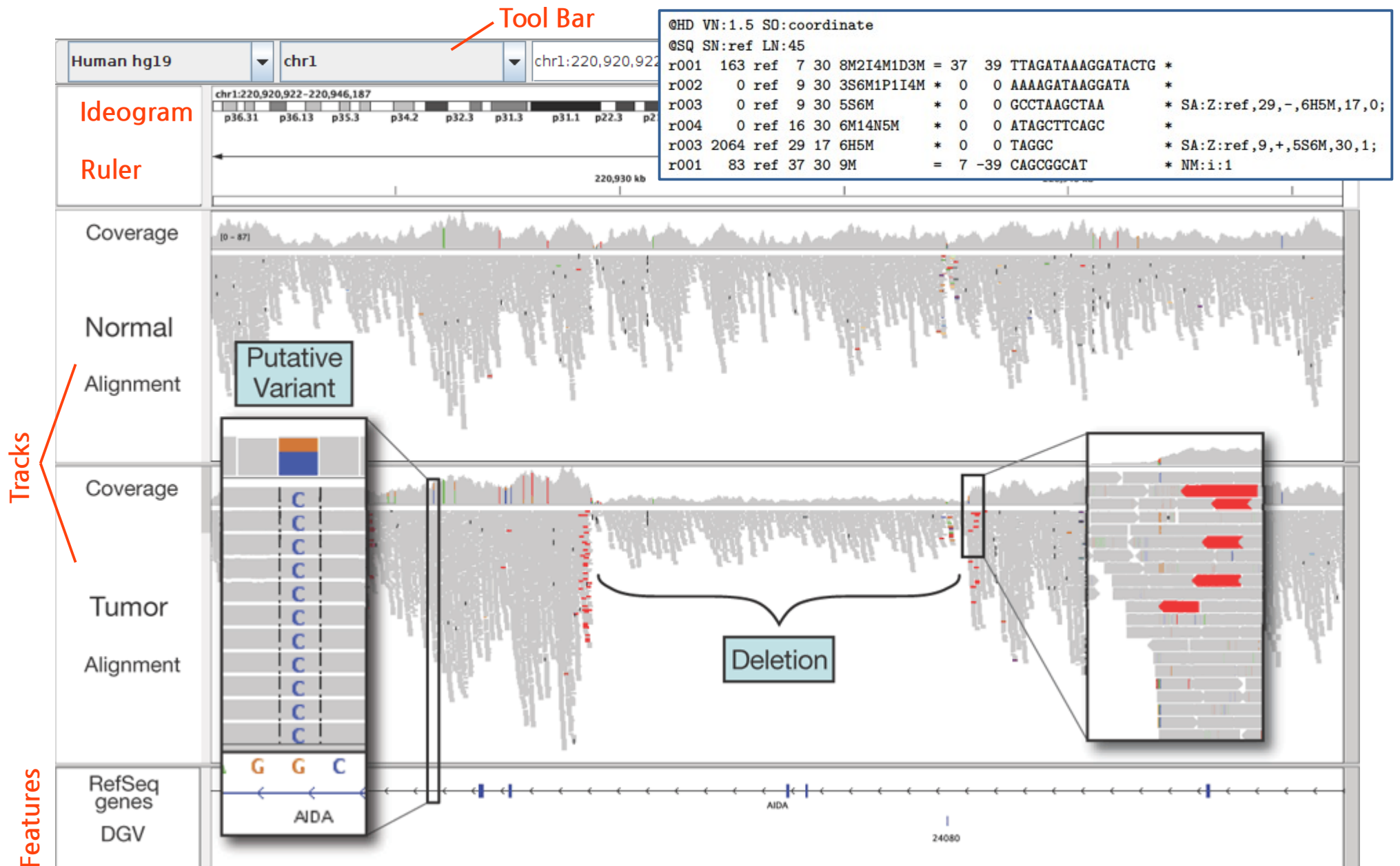
6. Run IGV from the terminal

```
igv
```

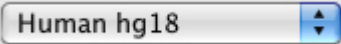

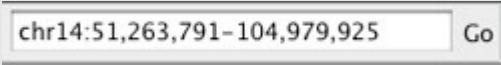







IGV interface



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

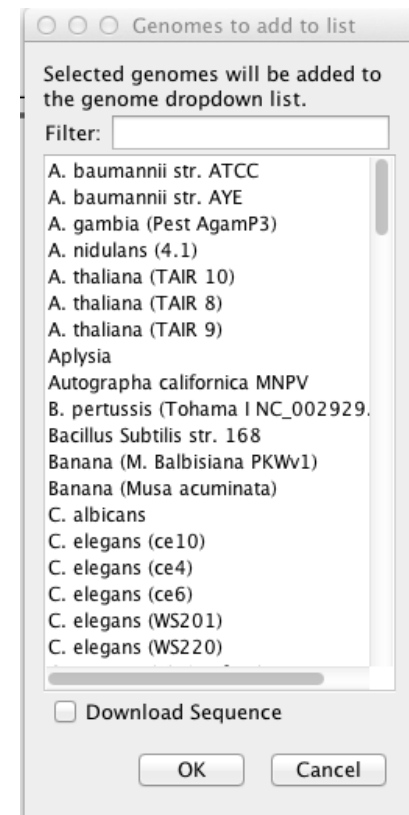
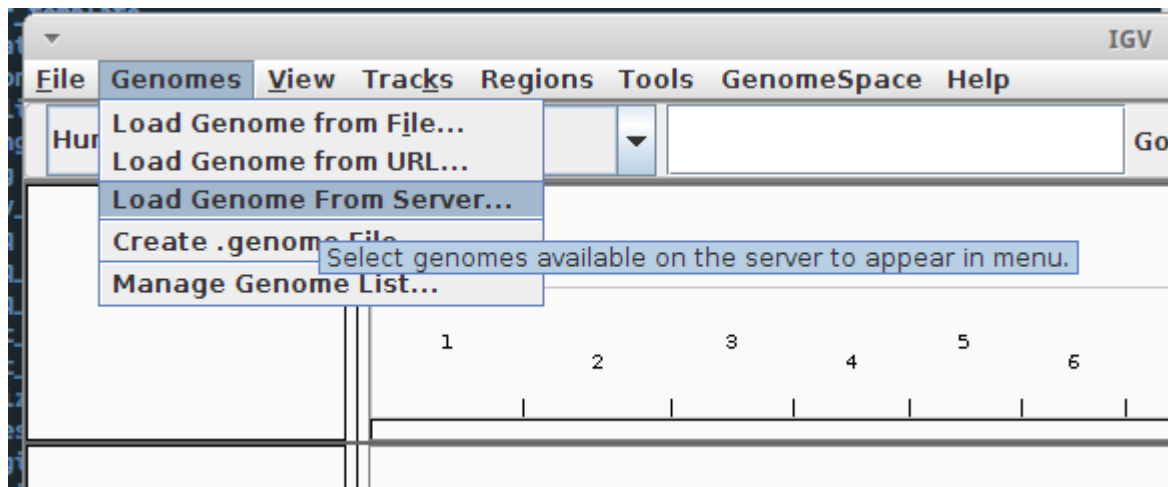
Current version of IGV has "Human hg18" and "Human hg19" already loaded

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!