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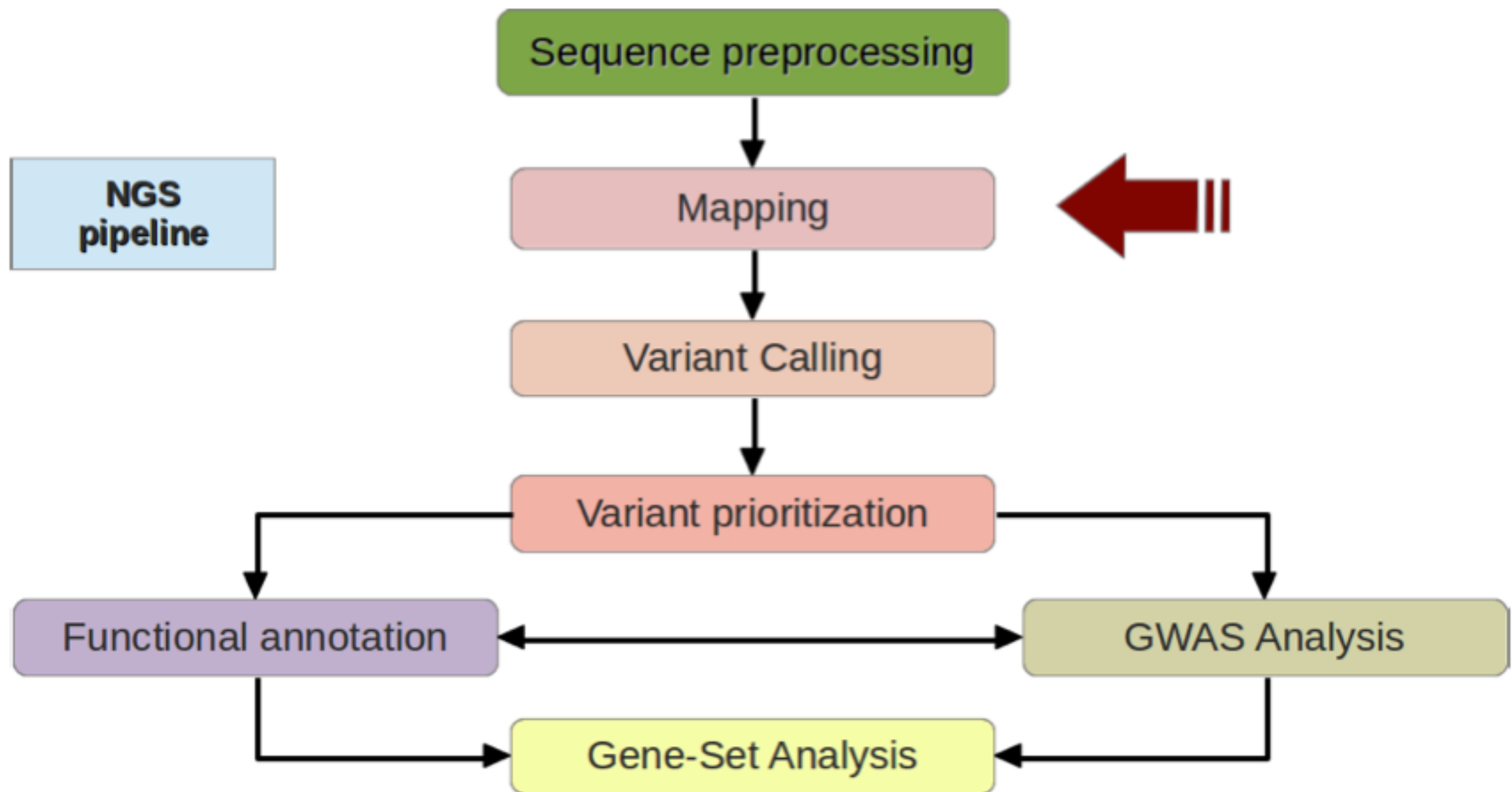
Visualização dos Dados NGS

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Where are we ?

What will we see ?

1. IGV: The Basics

2. Viewing NGS Data

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igv Integrative Genomics Viewer

What is IGV ?

IGV is an integrate visualization tool of large data types and annotations in the context of the genome.

Microarrays

Epigenomics

RNA-Seq

NGS alignments

Comparative genomics

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igv Integrative Genomics Viewer
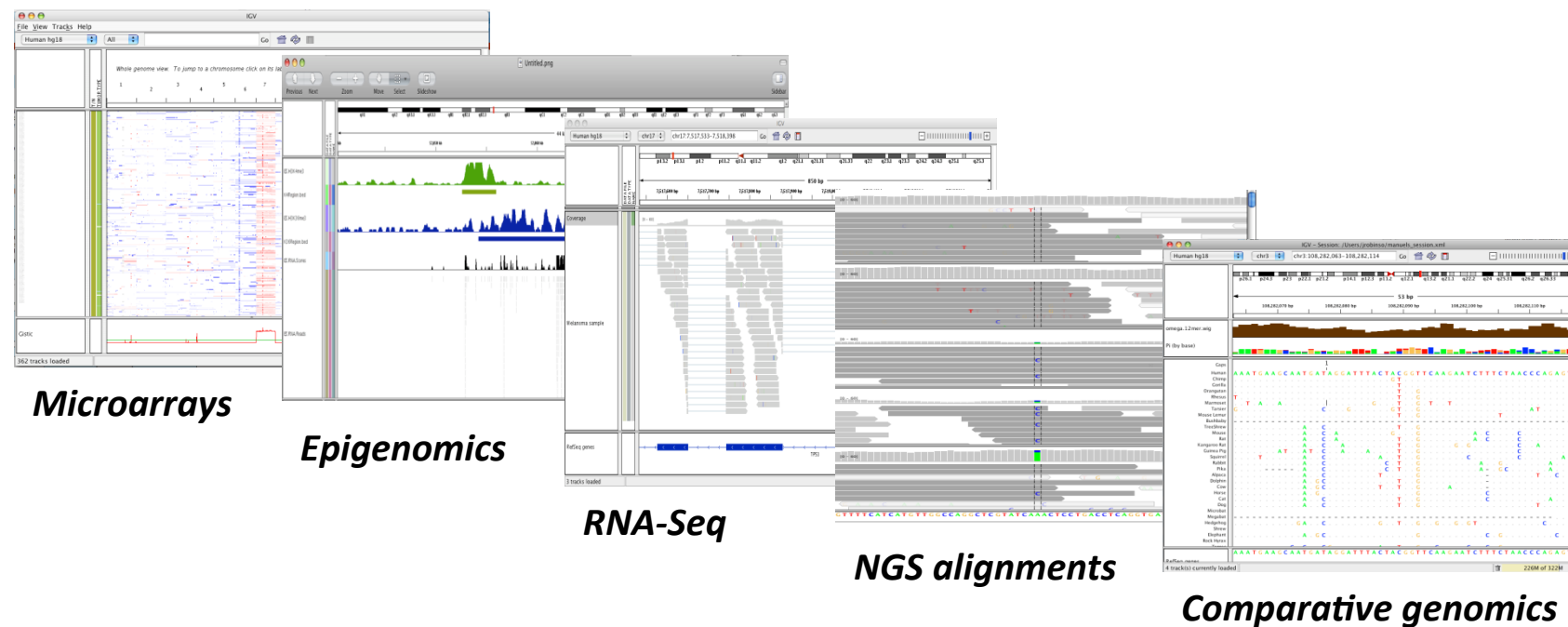
Why IGV ?

- Integrate different data types simultaneously
- View large datasets easily
- Fast navigation
- Run it locally on desktop
- Easy to use interface

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igv Integrative Genomics Viewer

http://www.broadinstitute.org/igv/

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

Before opening the BAM

- 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
```

Before opening the 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]
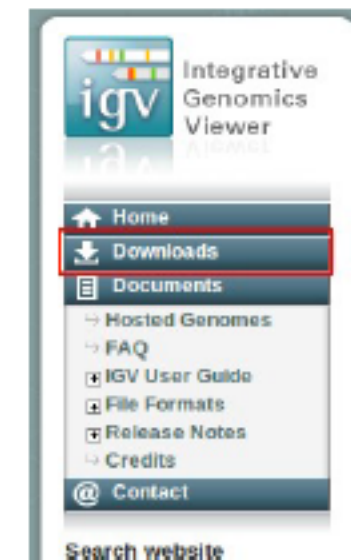
5. Download the most suitable file for your system

   Downloads

   Mac users: Download the following archive. should unzip automatically, then double-click the IGV applicaction to run. The application can be moved to the "Applications" folder, or anywhere else.
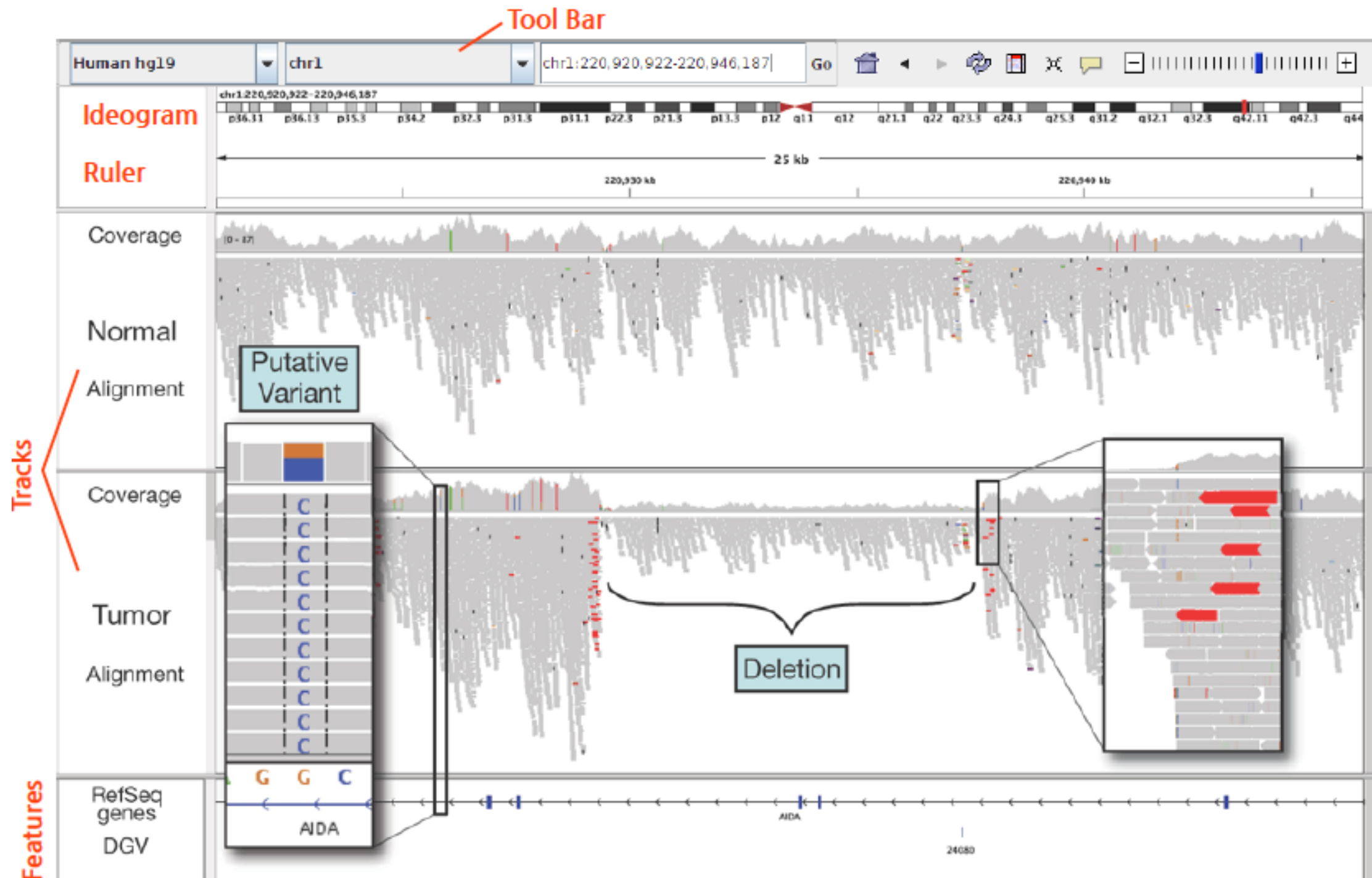
   - IGV_2.3.30.app.zip

   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".
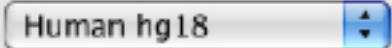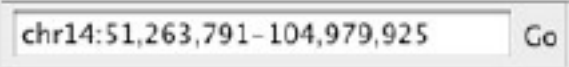
   - IGV_2.3.30.zip

6. Run IGV

   ```
   igv
   ```

Integrative Genomics Viewer

- Home
- Downloads
- Documents
  - Hosted Genomes
  - FAQ
  - IGV User Guide
  - File Formats
  - Release Notes
  - Credits
- Contact

Search website

IGV Interface

IGV Toolbar

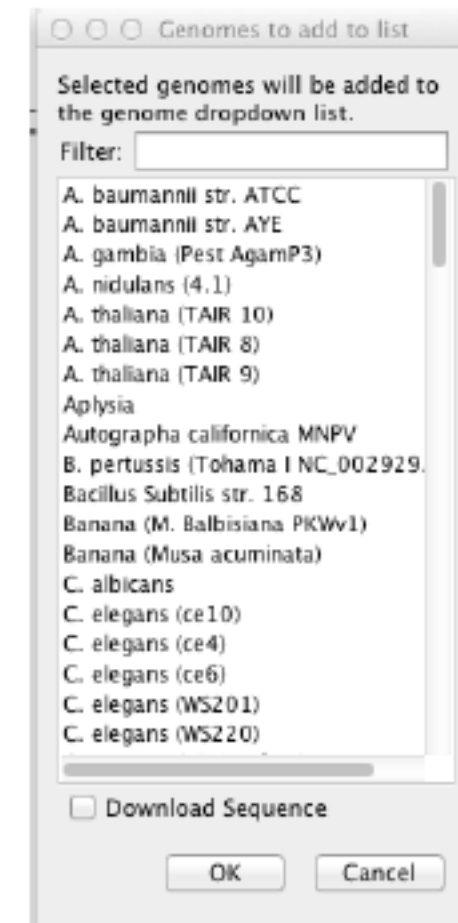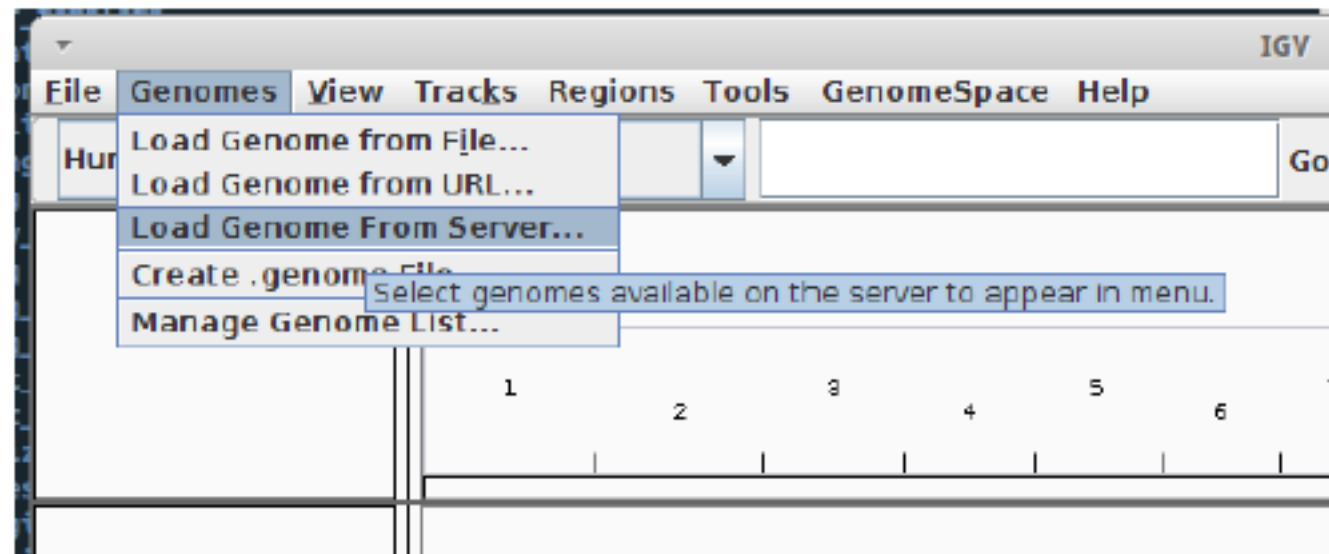|	
Human hg18 ▲▼	Genome drop-down box
chr1 ▲▼	Chromosome drop-down box
chr14:51,263,791–104,979,925　Go	Search box
🗑	Whole genome view
◄ ►	Moves backward and forward through views of the genome
↻	Refreshes the display
▯	Defines a region of interest on the chromosome
✕	Reduces the row height on all tracks to fit all data
💬	Toggles the pop-up information windows in IGV on or off
⊟ ‖‖‖‖‖‖‖‖‖‖‖‖‖‖‖ ⊞	Zooms in and out on a chromosome

Download the 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**

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