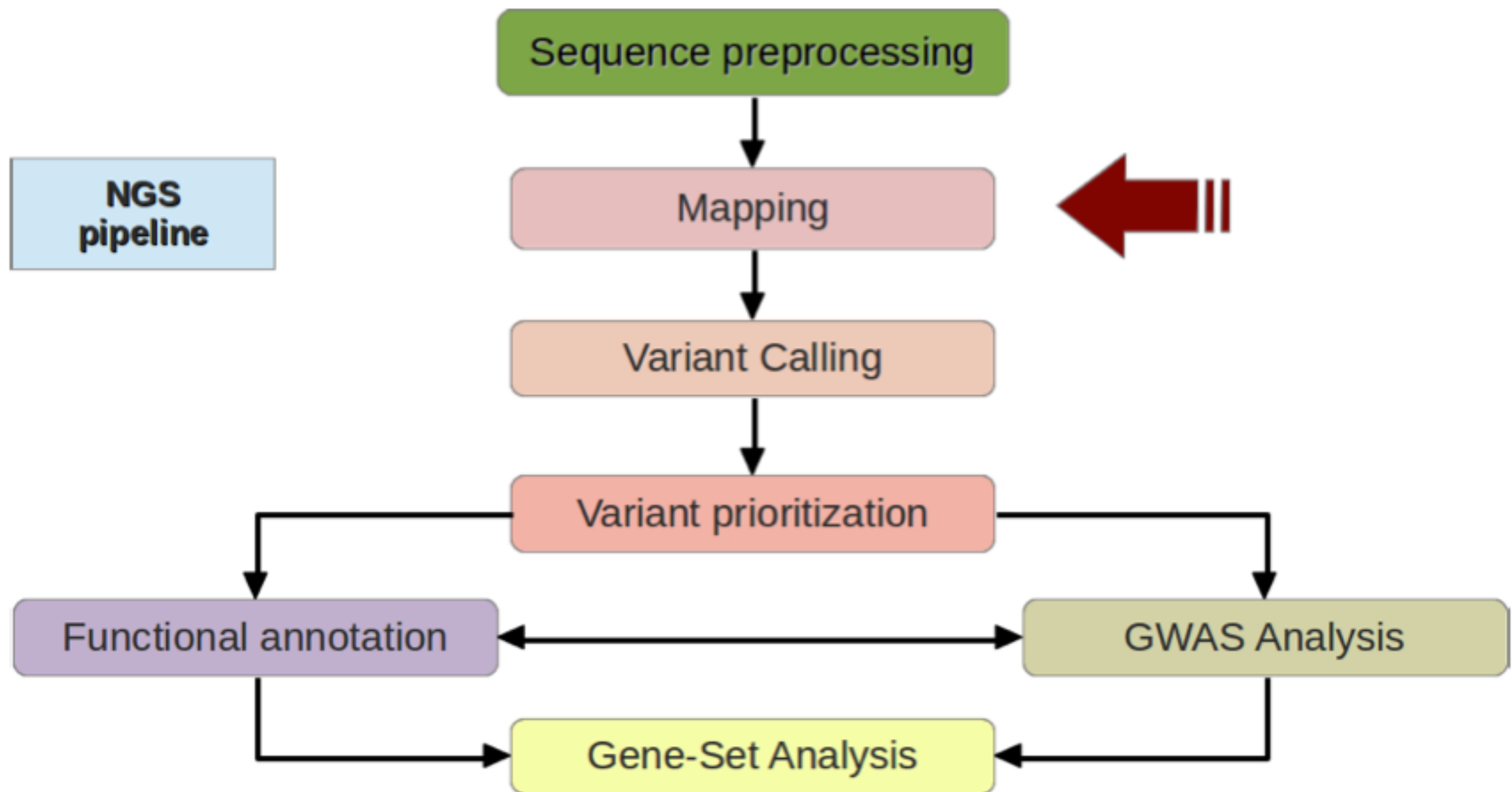




# **Visualização dos Dados NGS**

Marcel Caraciolo  
[marcel@genomika.com.br](mailto:marcel@genomika.com.br)

# Where are we ?



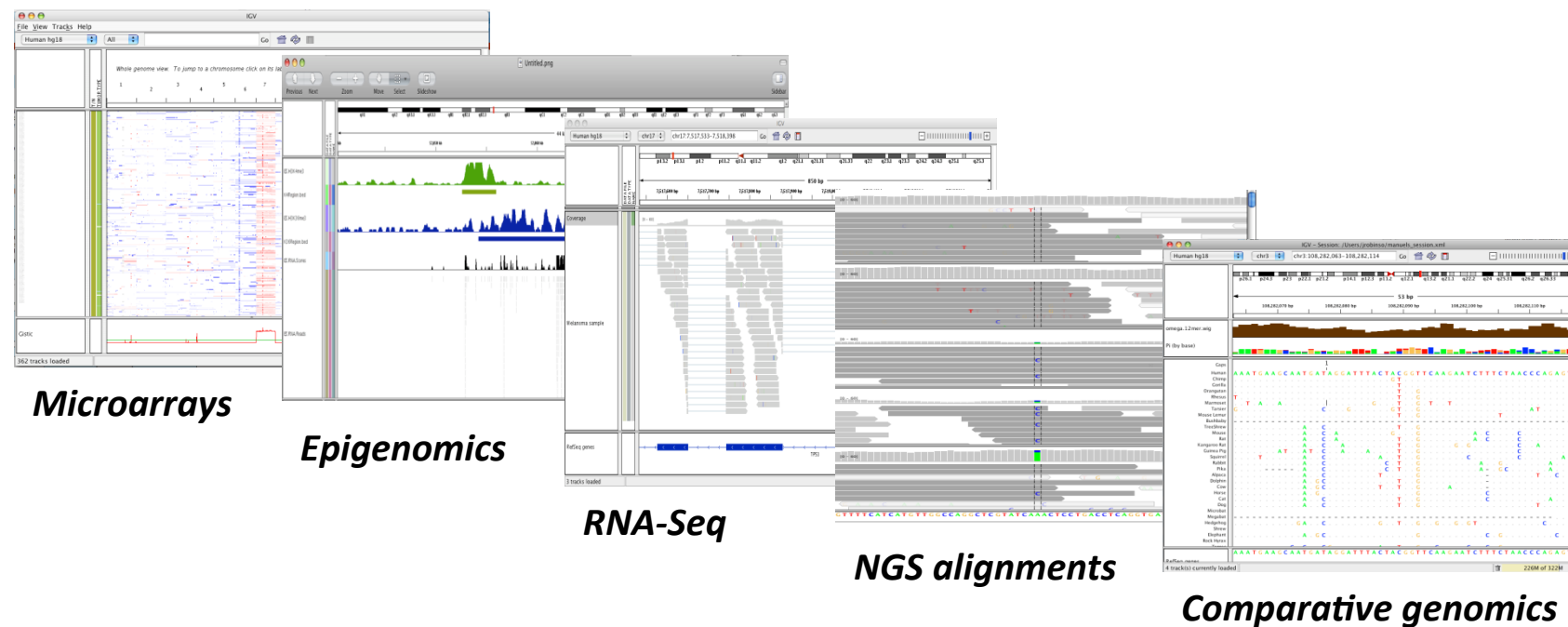
# What will we see ?

## 1. IGV: The Basics

## 2. Viewing NGS Data

# What is IGV ?

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



# Why IGV ?

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

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

The screenshot shows the homepage of the Integrative Genomics Viewer (IGV) website. On the left is a sidebar with the IGV logo and a navigation menu including Home, Downloads, Documents, Hosted Genomes, FAQ, IGV User Guide, File Formats, Release Notes, Credits, and Contact. Below the menu is a search bar and the Broad Institute logo. The main content area has a 'Home' header and a large banner image of the IGV interface. Below the banner are sections for 'What's New' (listing hiring and workshop announcements), 'Citing IGV' (providing citation information), 'Overview' (describing the tool's capabilities), 'Funding' (listing funding sources), and 'Downloads' (providing registration and license information). Logos for funding partners like the National Cancer Institute and GENOMESPACE are shown at the bottom right.

**Home**

# Integrative Genomics Viewer

**What's New**

**June 2014.** We're hiring! See the [job description](#) on the Broad Institute careers website.

**October 2013.** We're presenting an IGV workshop at the [ASHG annual meeting](#) in Boston on October 25, 2013.

**April 2013.** IGV 2.3 has been released. See the [release notes](#) for more details.

**Citing IGV**

To cite your use of IGV in your publication:

Helga Thorvaldsdóttir, James T. Robinson, Jill P. Mesirov. [Integrative Genomics Viewer \(IGV\): high-performance genomics data visualization and exploration](#). *Briefings in Bioinformatics* 2012.

James T. Robinson, Helga Thorvaldsdóttir, Wendy Winckler, Mitchell Guttman, Eric S. Lander, Gad Getz, Jill P. Mesirov. [Integrative Genomics Viewer](#). *Nature Biotechnology* 29, 24–26 (2011)

**Overview**

The Integrative Genomics Viewer (IGV) is a high-performance visualization tool for interactive exploration of large, integrated genomic datasets. It supports a wide variety of data types, including array-based and next-generation sequence data, and genomic annotations.

**Funding**

Development of IGV is made possible by funding from the [National Cancer Institute](#), the [National Institute of General Medical Sciences](#) of the [National Institutes of Health](#), and the [Starr Cancer Consortium](#).

IGV participates in the [GenomeSpace](#) initiative, which is funded by the [National Human Genome Research Institute](#).

**Downloads**

Please [register](#) to download IGV. After registering, you can log in at any time using your email address. Permission to use IGV is granted under the GNU [LGPL license](#).

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**GENOMESPACE**

# 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>

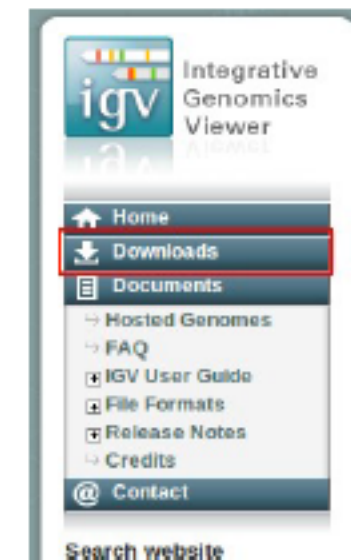
3. Click **Downloads** at the left panel
4. Click to register and fill the form

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:



5. Download the most suitable file for your system

**Downloads**

**Mac users:** Download the following archive. It 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](#)

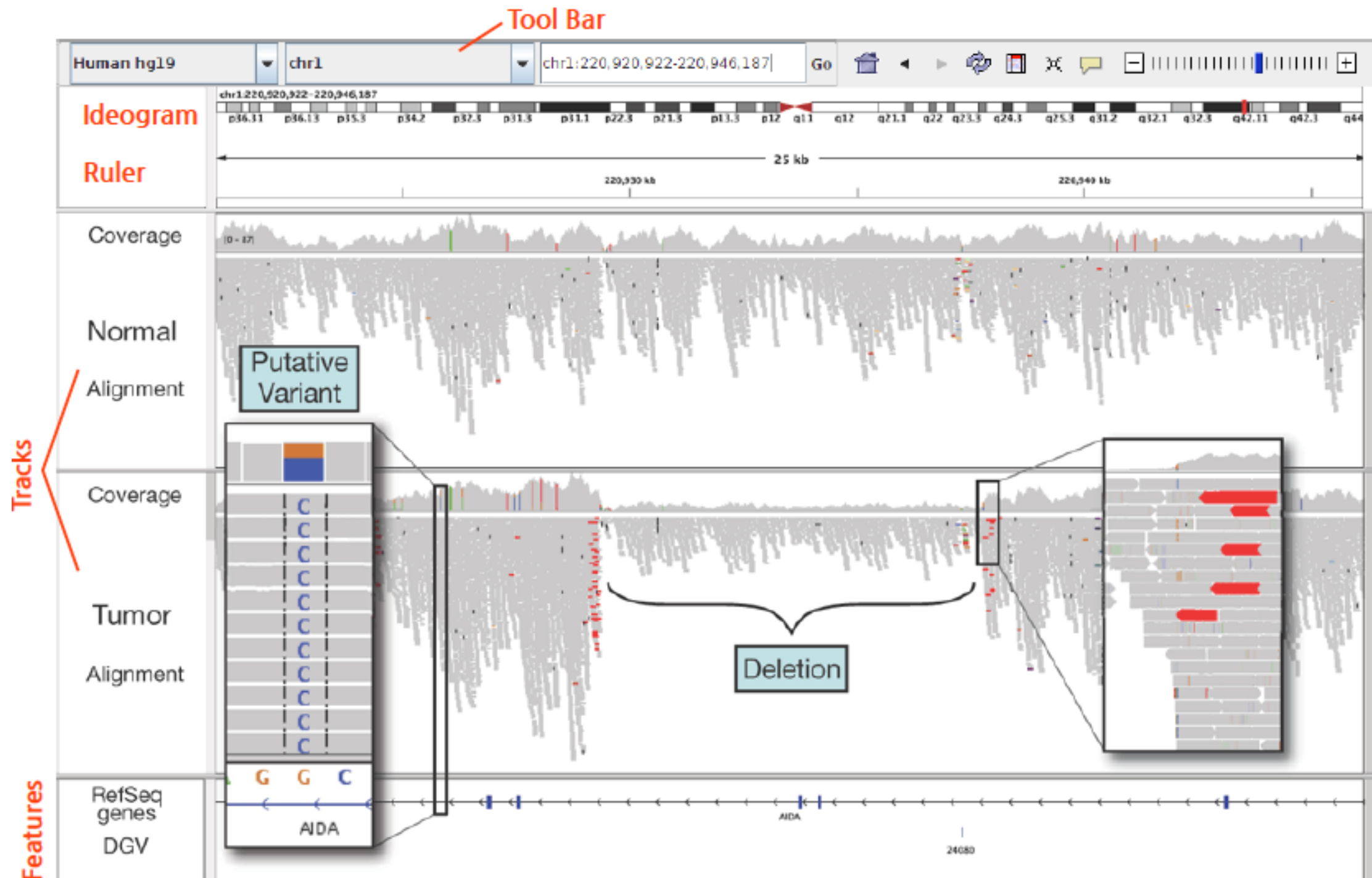
**Windows and Linux users:** Download and unzip the archive in a folder of your choosing. IGV is launched from a command prompt, follow instructions in the "readme" file. Windows users, use the "igv.bat". On Linux, use "igv.sh".

- [IGV\\_2.3.30.zip](#)

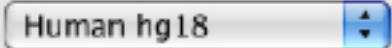

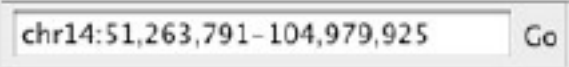







6. Run IGV

igv

# IGV Interface



# IGV Toolbar

	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 the genome

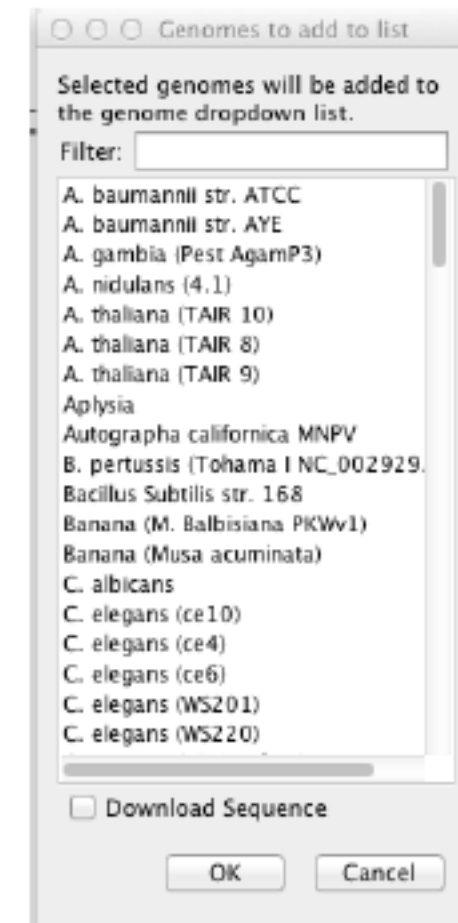
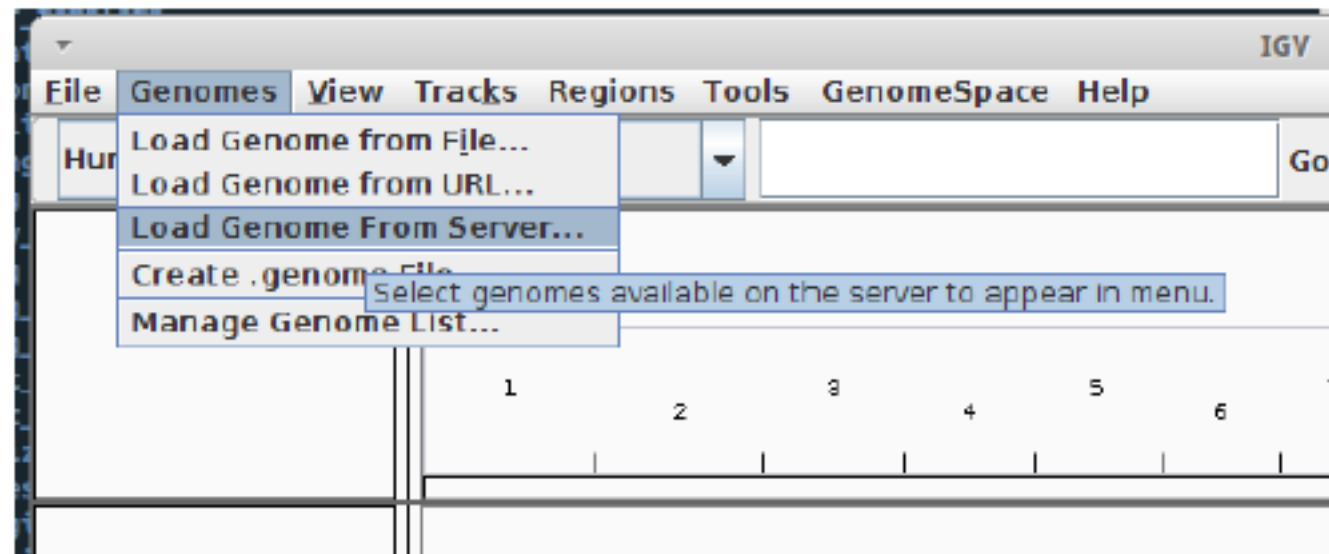
Current version of IGV has "Human hg18" and "Human hg19" already loaded

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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