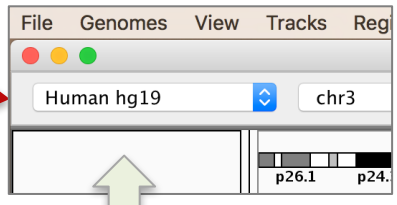
IGV Hands-on Exercise | IGV Basics

1. Launch IGV

2. Select reference genome.

- Click on *Human hg19* in the genome drop-down menu in the upper left corner.

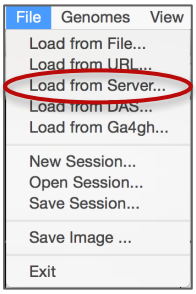
If you only see *Human hg18* in the menu, it's ok to select that instead



If this is the first time you run IGV, there may be **only one** entry in the menu. More about that later…

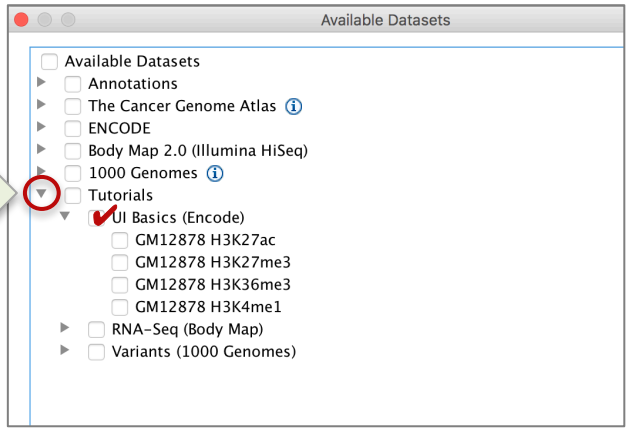
3. Load data from the IGV hosted server.

- Select *File > Load from Server…*

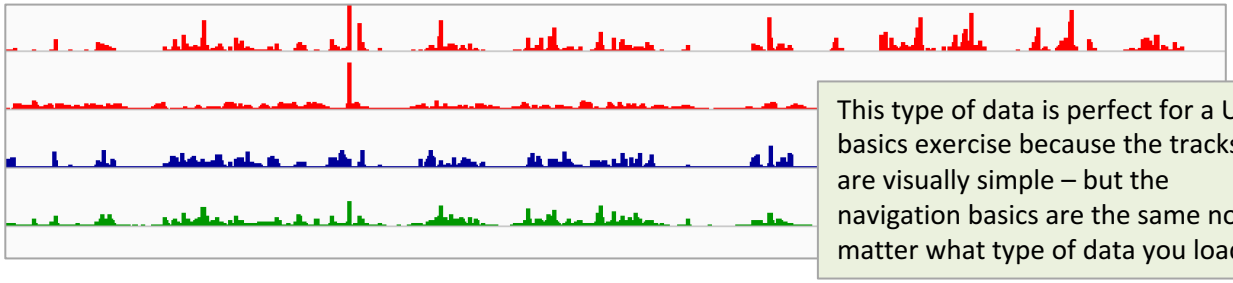


- Open the *Tutorials* menu (Use ▶ on Mac, and + on Windows) and click on the *UI Basics* checkbox.

Make sure you only **open** the *Tutorials* menu. Do **not** check the box next to *Tutorials.* That will select everything under *Tutorials,* but we only want *UI Basics* for this exercise.



Four tracks are loaded: ENCODE project ChIP-seq data representing histone modifications. Each track is displayed as a bar chart of signal intensities.

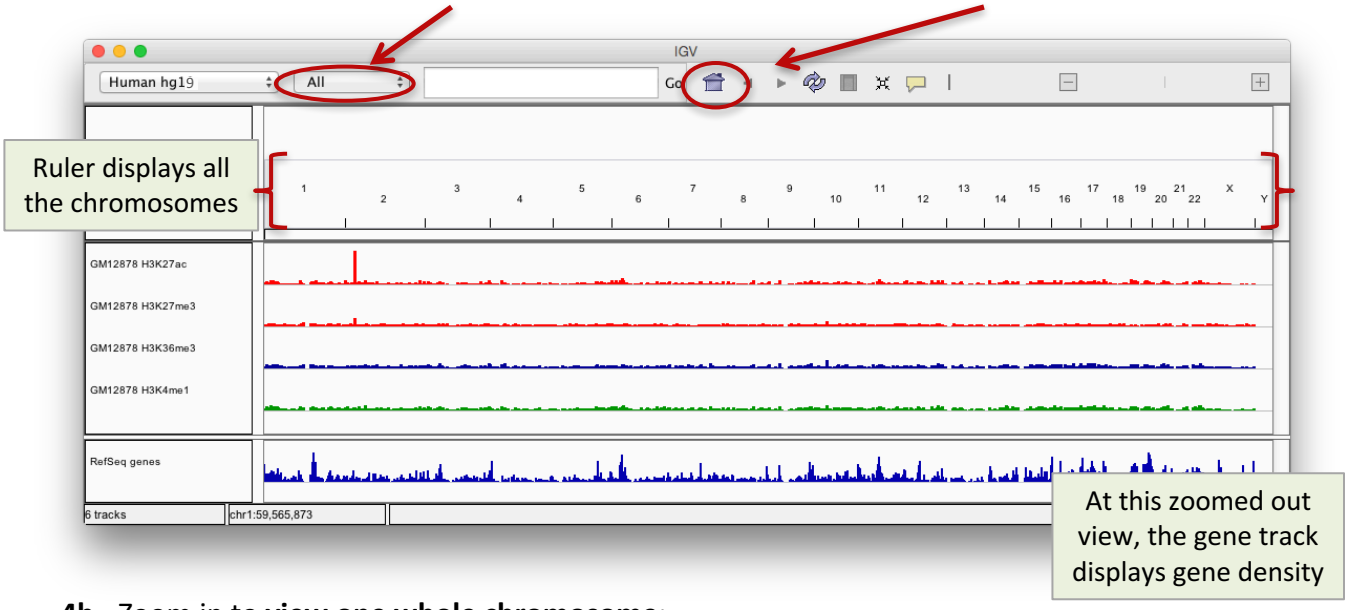


This type of data is perfect for a UI basics exercise because the tracks are visually simple – but the navigation basics are the same no matter what type of data you load.

4. **Navigate** across different genomic loci and at different zoom levels, from whole genome view and down to base-pair resolution.

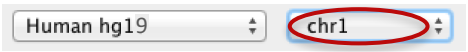
4a. Start at **whole genome view**:

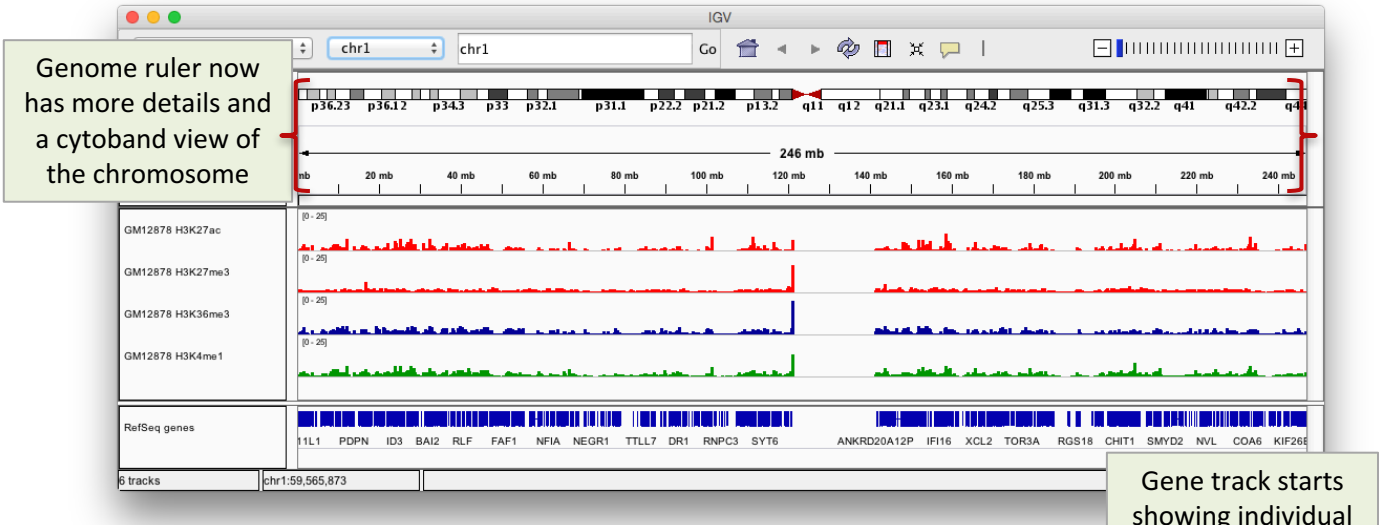
- Select *All* from the chromosome drop-down menu –OR– Click the *Home* button.



4b. Zoom in to **view one whole chromosome**:

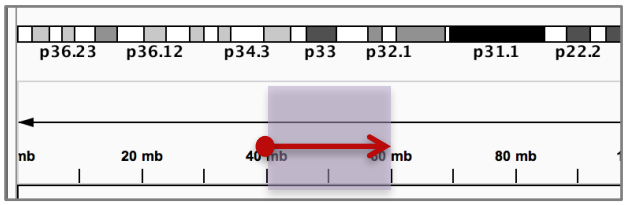
- Select *Chr1* from the chromosome drop-down menu –OR– Click the *1* in the genome ruler.



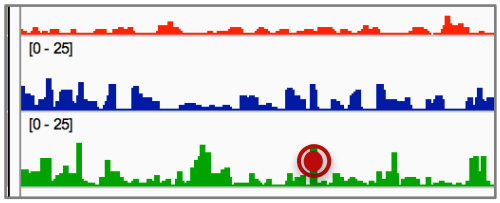


4c. Zoom in further:

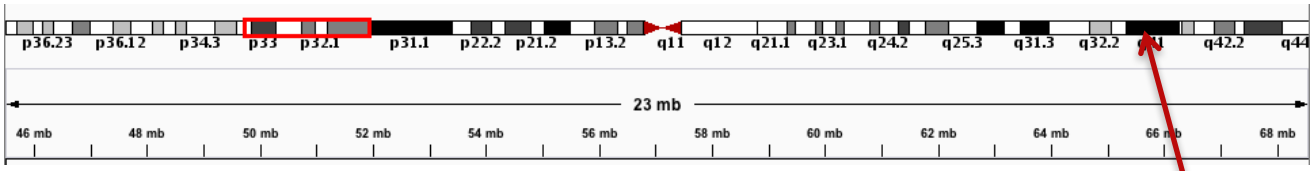
- Click and drag to zoom in on a region swept out in the ruler



- Double-click in the data track to zoom in on a point of interest. [Alt-click to zoom out]

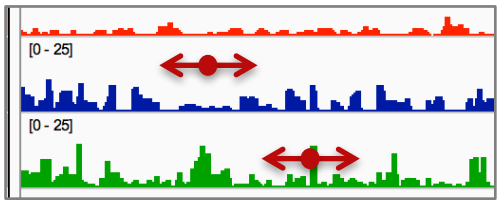


Ruler measurements and a red box on the cytoband diagram show where you are in the chromosome



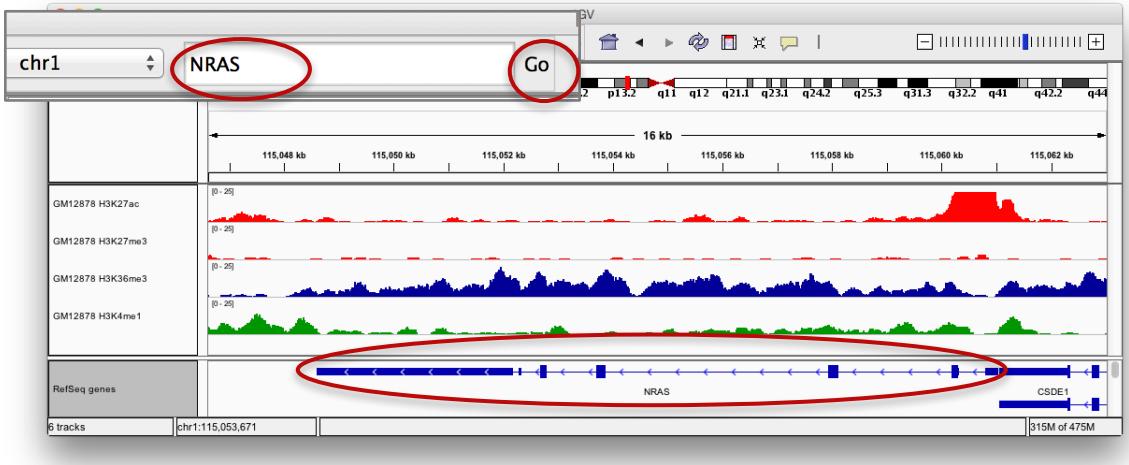
4d. Move around within the chromosome:

- **Jump** to another region in the same chromosome (no change in zoom level): Click anywhere in the cytoband diagram.
- **Scroll** across genome coordinates: Click anywhere in the data panel and drag left & right.



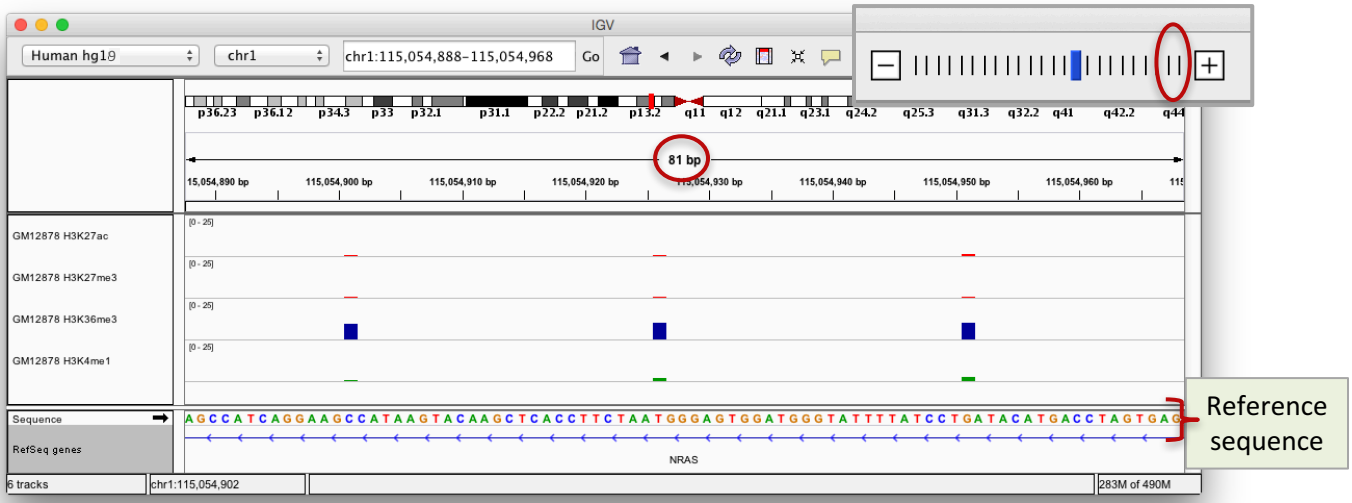
4e. Navigate to specific locus or gene on any chromosome

- Type into the search box in the IGV toolbar and click *Go:*
  either a locus in **genomic coordinates** (e.g. chr1:144,874-969,268) or a **gene name** (e.g. NRAS)



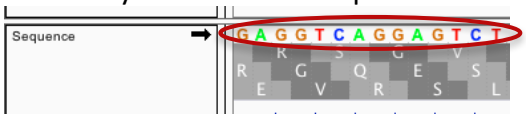
4f. Zoom in to base-pair resolution:

- Keep zooming in as before, or click on one of the rightmost ticks on the "railroad track" zoom widget in the upper right corner.

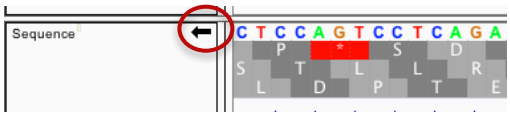


5. Options for viewing the reference sequence track

- Click anywhere on the sequence to show/hide a 3-frame translation

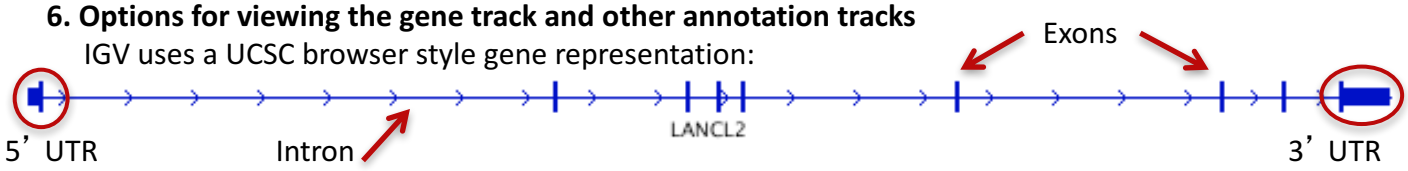


- By default, the sequence for the forward strand is shown. Click on the arrow to reverse the strand.

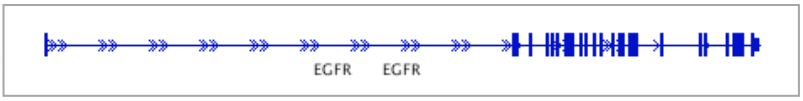


6. Options for viewing the gene track and other annotation tracks

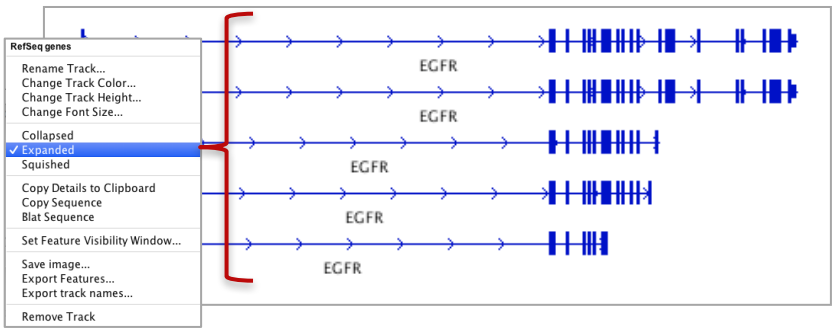
IGV uses a UCSC browser style gene representation:



Features are drawn in a single line, by default



- *Expand* the track using the right-click popup menu



Use *Squished* for an even more compact view

END OF EXERCISE