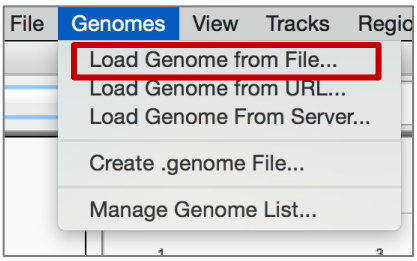
IGV Hands-on Exercise | Load genome from file

1. Clear out the data from the previous exercise: Select *File* > *New Session*

2. Select ***Genomes*** > *Load Genome from File*



Note this is the **Genome** menu, not the File menu

and browse to the **igvData** workshop folder, and then to the **genome** subfolder and open ***chr1.fasta***

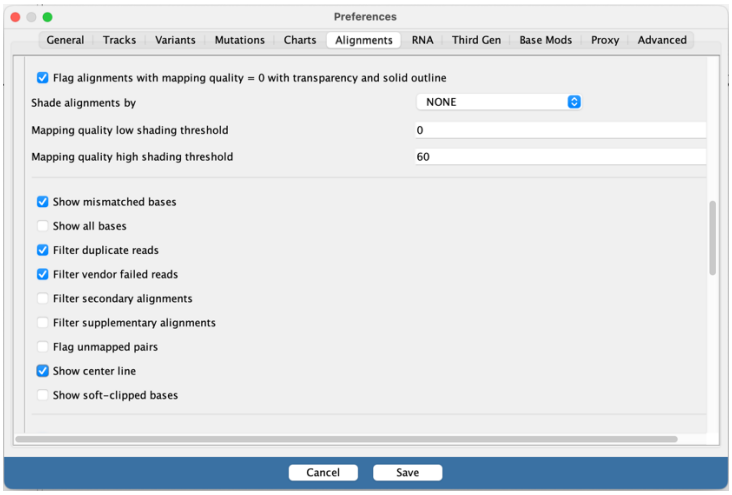
The *chr1.fasta* file contains chromosome 1 from Human hg18.

3. Note in the IGV window: there is no gene track, and no cytoband ideogram in the genome ruler.

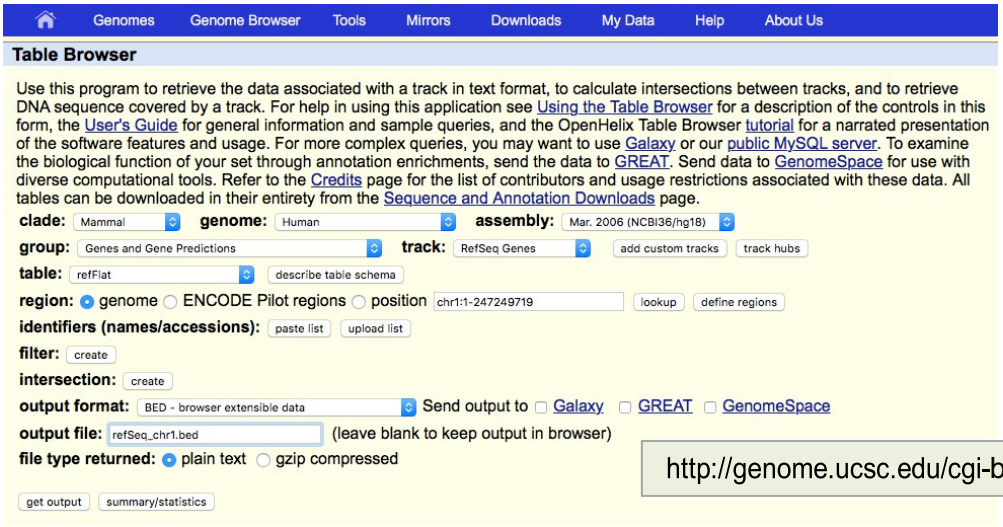
IGV hosted genomes package everything together, but you loaded only the FASTA file with the sequence. You can zoom in and out as before, and enter the numeric value of a locus, but you cannot find a gene locus by entering the name in the search box.

4. Ensure show centerline setting is set

Select "View > Preferences > Alignments tab". About 1/2 way down is an option "Show center line", check that.



[Not part of this exercise, but you can use the **UCSC Table Browser** to get a file of gene annotations]



http://genome.ucsc.edu/cgi-bin/hgTables

5. The cytoband cannot be loaded separately into the genome ruler.

END OF EXERCISE