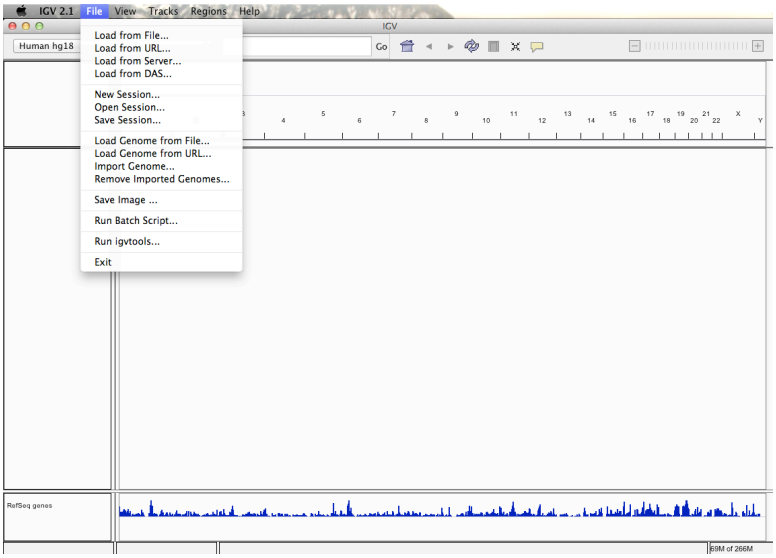
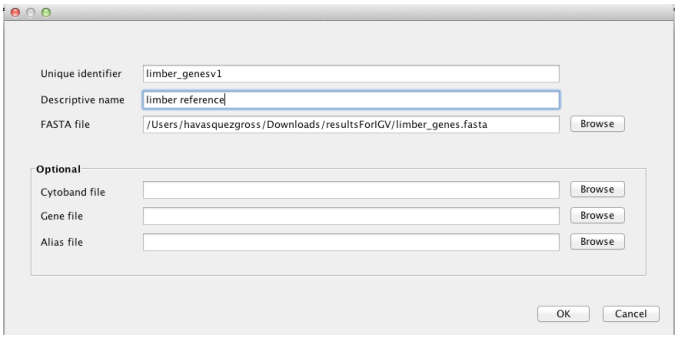
Introduction to IGV Tutorial:
Using IGV and setting it up to view data

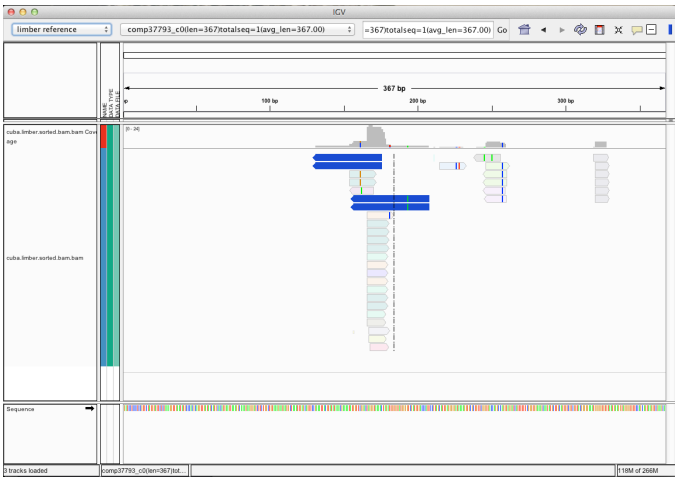
The **Integrative Genomics Viewer (IGV)** is a high-performance visualization tool for interactive exploration of large, integrated genomic datasets. It supports a wide variety of data types, including array-based and next-generation sequence data, and genomic annotations.

1. To use IGV, get the JAVA web launch from their website: http://www.broadinstitute.org/software/igv/download .
    a. The download section requires you to register your email address.
2. Once you can view the webpage, use the 2GB Launch (third option) unless you know you will need more memory.
3. Once you have the program running, use the *Import Genome* tool in the *File* menu to load the **reference fasta** file as a genome. You will have to pick a location to save this when you are done.



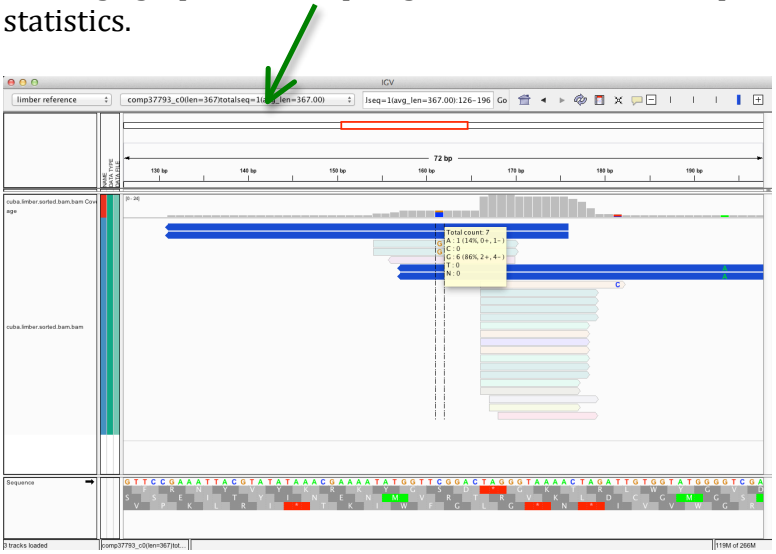


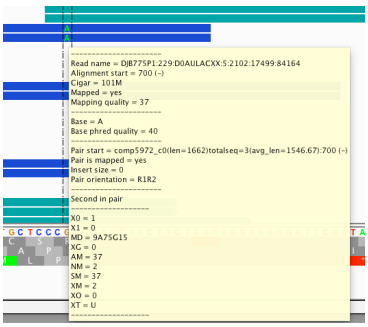
4. Then, click on the *Load from File* in the *File* menu and select ***.bam** files containing the aligned reads. You will need to transfer the associated ***.bam.bai** file (the index), so that IGV will load the bam file.



Note: If after loading the genome and the bam file you still can not see any data, use the zoom tool in the top right corner to zoom in. Also, right clicking on the nucleotides in the bottom sequence window will toggle a 3 frameshift translation. This could then be flipped by right clicking in this same window to get the other 3 frameshift translation.

5. Polymorphic nucleotides are displayed in the sequence as letters. You can hover the coverage graph on the top to get counts or on the sequence read for more quality statistics.



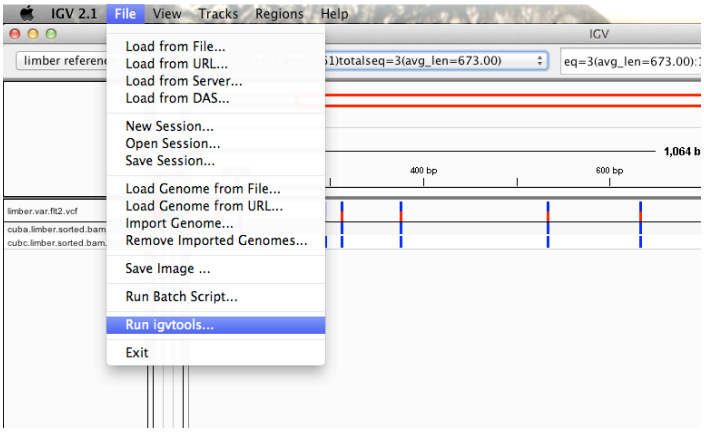


6. Lastly, different contigs can be chosen for further exploration in the second drop down menu on the top indicated with the green arrow. This concludes the brief tutorial.

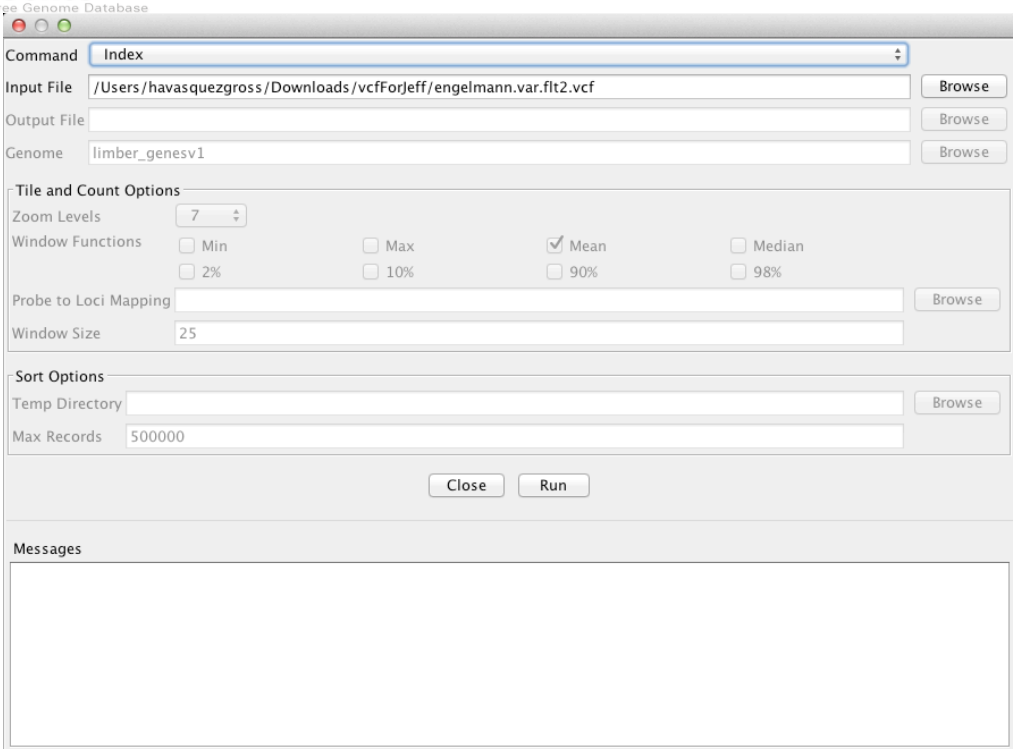
Introduction to IGV Tutorial:
Using IGV to view VCF files (variant calls)

1. After setting up your genome in the pervious tutorial, you may want to load VCF files to be viewed in IGV.

2. First, we must make an index of the VCF file. To do this, click on *Run igvtools…* from the *File* menu.



3. In the Command dropdown menu, choose *Index* while browsing to your *Input File*. Click on the *Run* button at the bottom of the screen which will start the indexing job. This may take a few minutes to run.



4. Now, click on the *File* menu at the top and choose *Load from file …* In the next screen, navigate to where your VCF file is located and select it. IGV should now load it into the viewer.

5. Below is an example of two VCF files that are loaded in IGV with a custom reference genome.