IGV Hands-on Exercise | Pre-compute coverage track

This exercise assumes the following have already been loaded in the previous exercises:

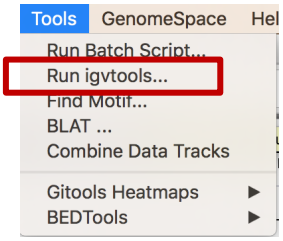
a) Reference genome chr1.fasta
(from exercise "Load genome from file")

b) BAM file from workshop folder: igvData / snps / *NA12878.SLX.sample.bam*
(from exercise "Viewing SNPs")

1. First, zoom all the way out by clicking on the leftmost tick on the railroad track in the zoom tool.

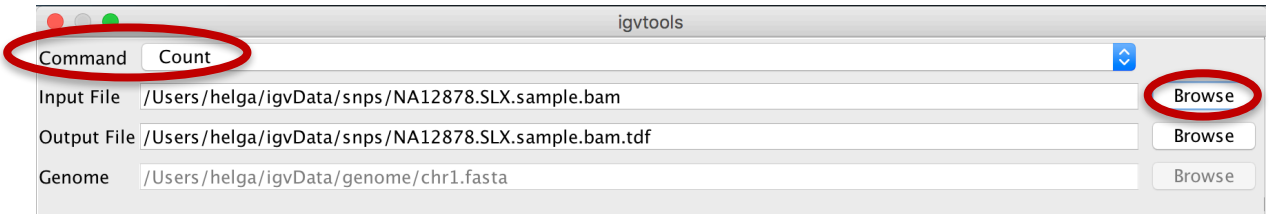
Observe there is no coverage track

2. Launch igvtools: click ***Tools > Run igvtools***



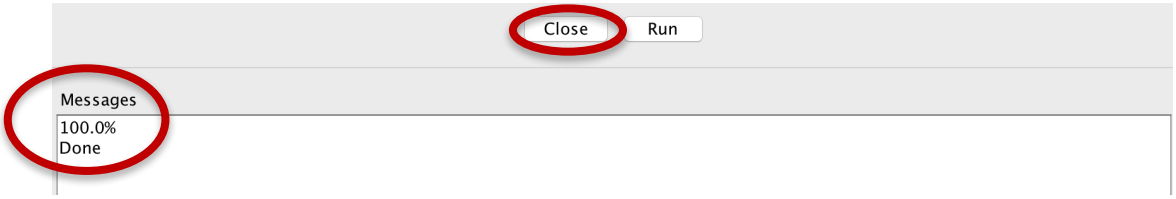
3. Run the Count tool

> Select ***Count*** from the *Command* dropdown menu
> Set the *Input File* to the ***NA12878.SLX.sample.bam*** file in the workshop folder *igvData / snps.*
The *Output File* will automatically be set to the same folder, and same name + *.tdf* suffix



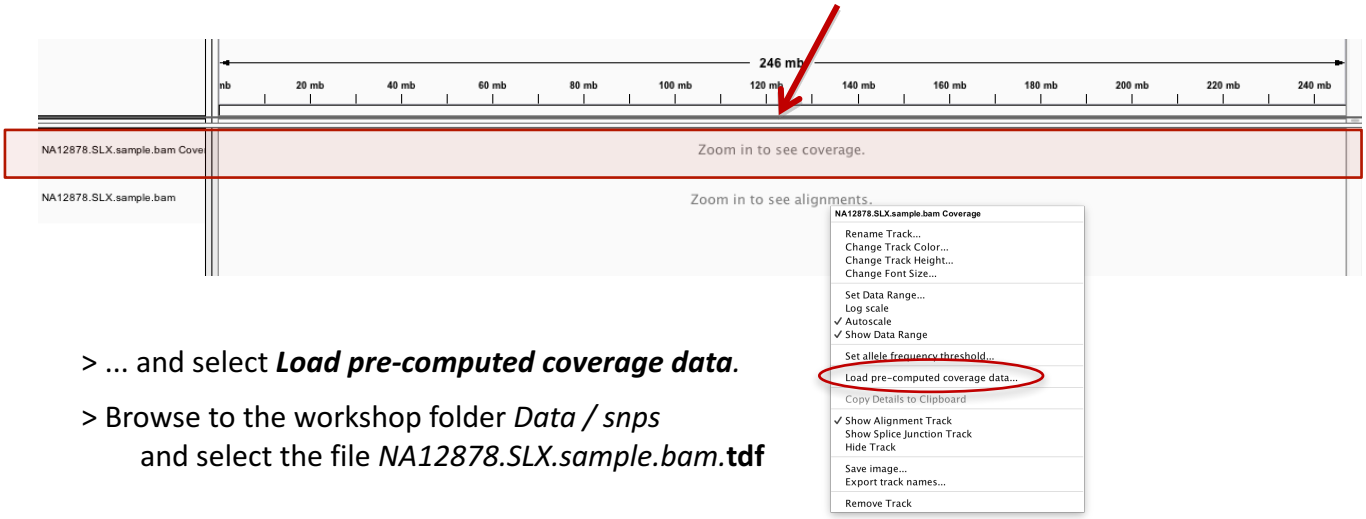
> Keep the defaults for all other values.
> Click ***Run***

Wait until you see "Done" in the *Messages* area, and click ***Close***.



4. Associate the new .tdf file with the coverage track

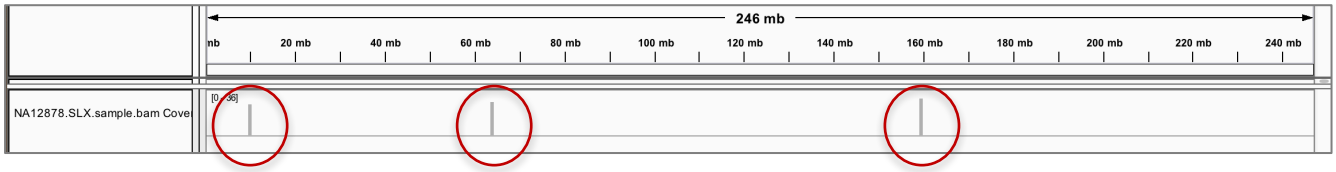
> Right-click (command-click on Mac) anywhere on the **coverage track** in the IGV window ...



> ... and select ***Load pre-computed coverage data***.

> Browse to the workshop folder *Data / snps*
and select the file *NA12878.SLX.sample.bam.***tdf**

2. Observe the 3 spikes in the coverage track.



The .bam file for the exercise was stripped down and only has data in these 3 regions.

If you zoom in on the leftmost spike, you will see the *snp1* locus from the *Viewing SNPs* exercise.

END OF EXERCISE