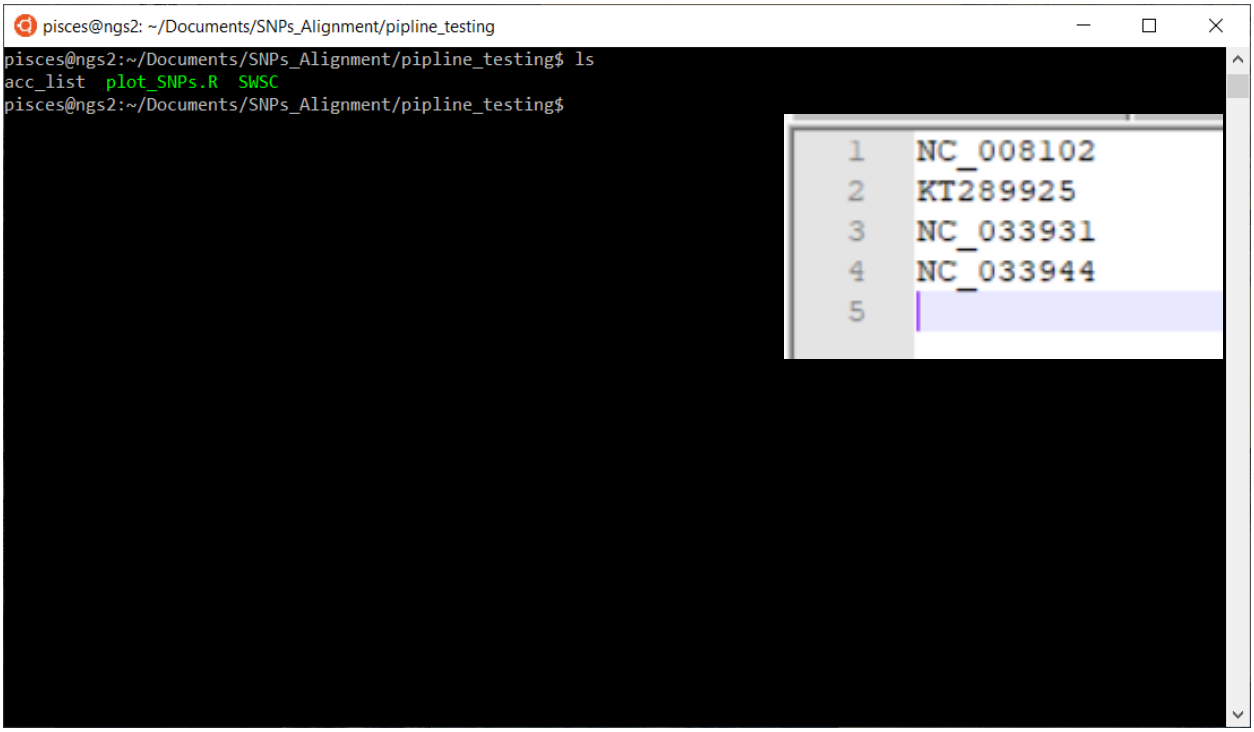
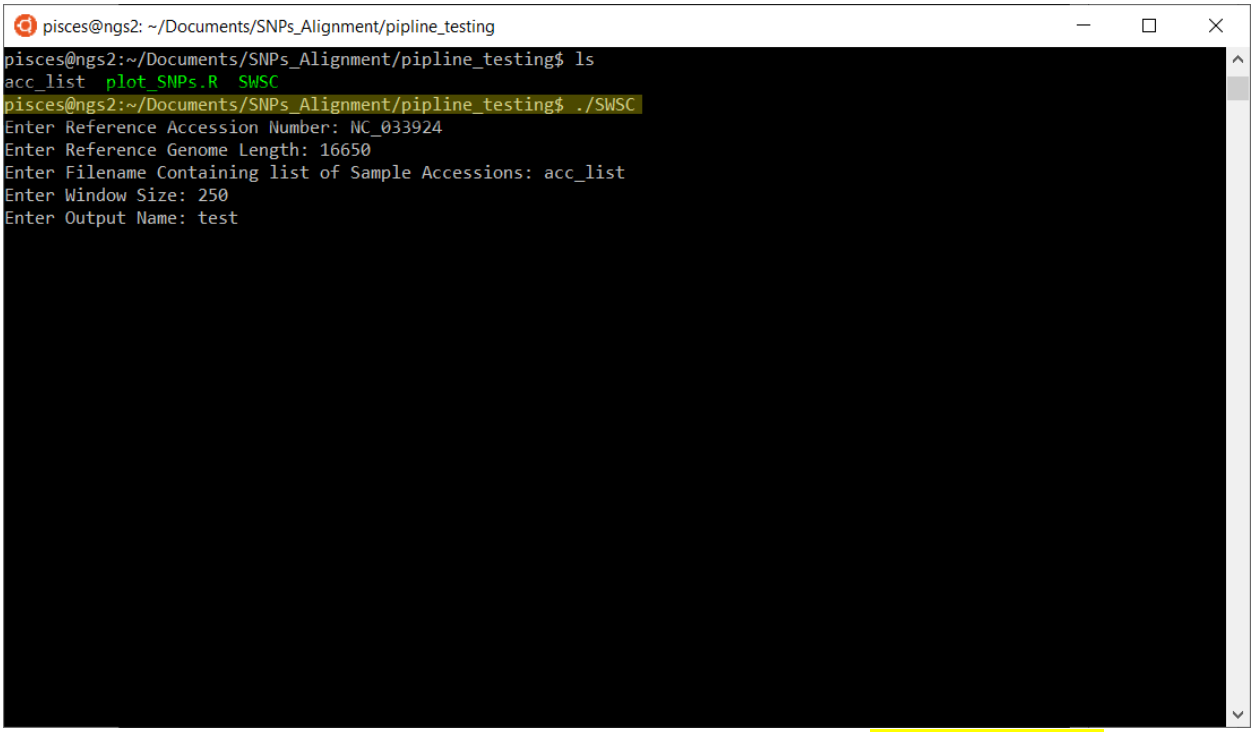
Running the Script

In order to run the script to count SNPs in a sliding window you must have the script 'SWSC' in the same working directory as a text file with the list of the accession numbers for your non-target species.

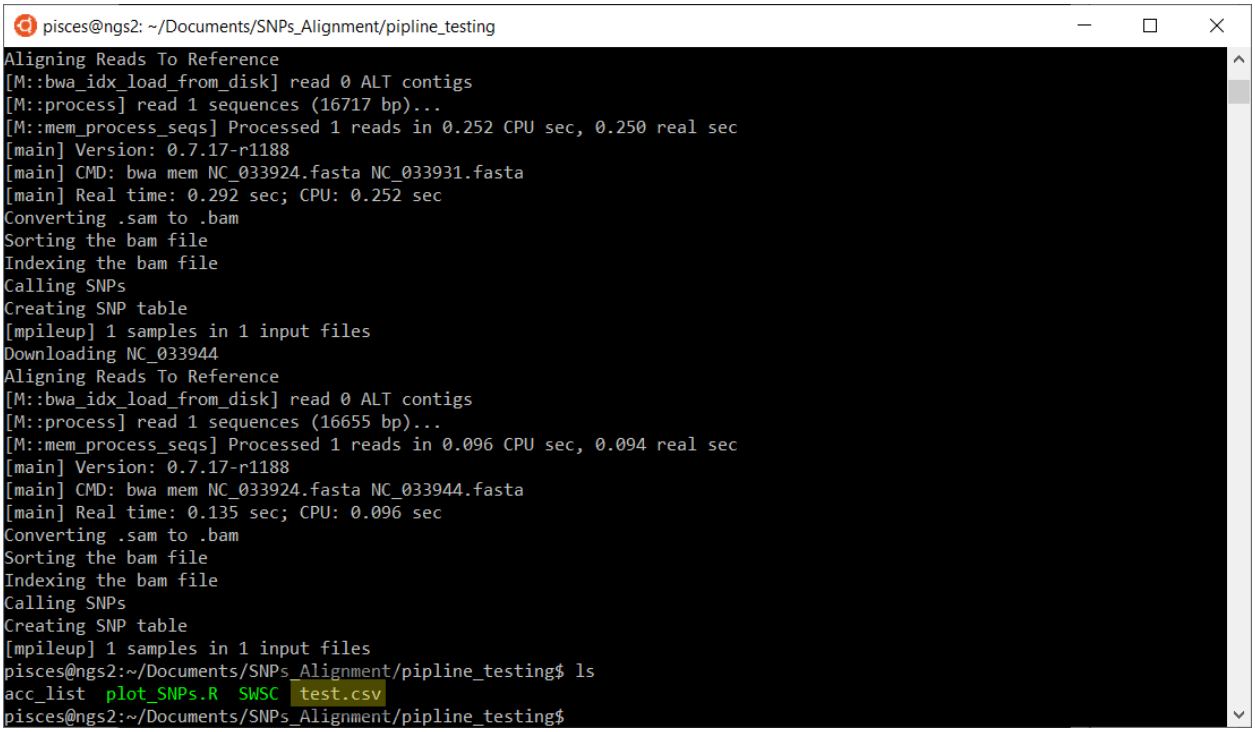


To run the script, just type './SWSC' and it will prompt you for the inputs it will need to run.

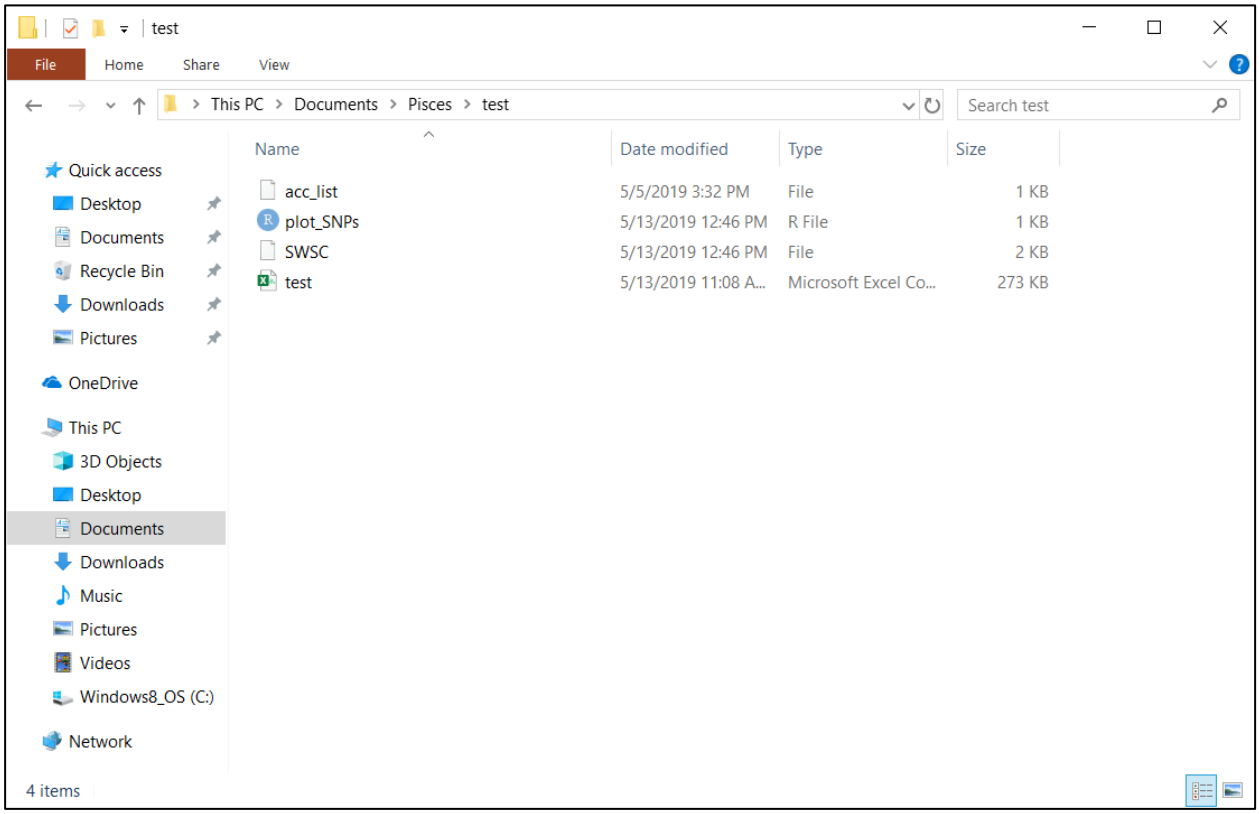


*If the script won't run due to a permissions problem, run this command: 'chmod 700 SWSC'

When finished, the script will output a CSV file named however you chose in the input.



In order to plot the data, you will need to open and run the R script ‘plot_SNPs.R’ in R studio.



Plotting the Data

In R Studio, all you need to change is the reference genome length on line 2 so that the X axis is labeled properly. Then you can highlight everything, and press Ctrl-Enter to create the plot. If you click on zoom, a new window will open and you can resize it however you would like and save it by right clicking. If you uncomment line 14 by deleting the '#' the plot will output directly to a PDF, but the plot won't be sized very well.