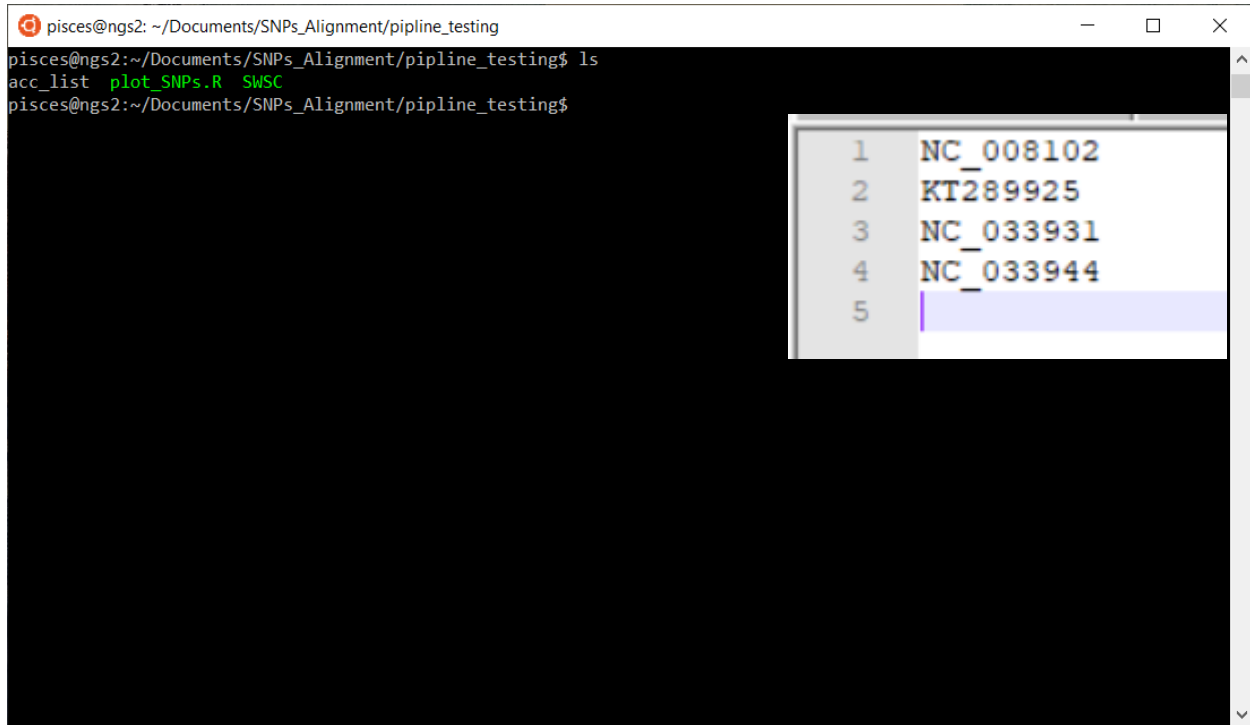


## Running the Script

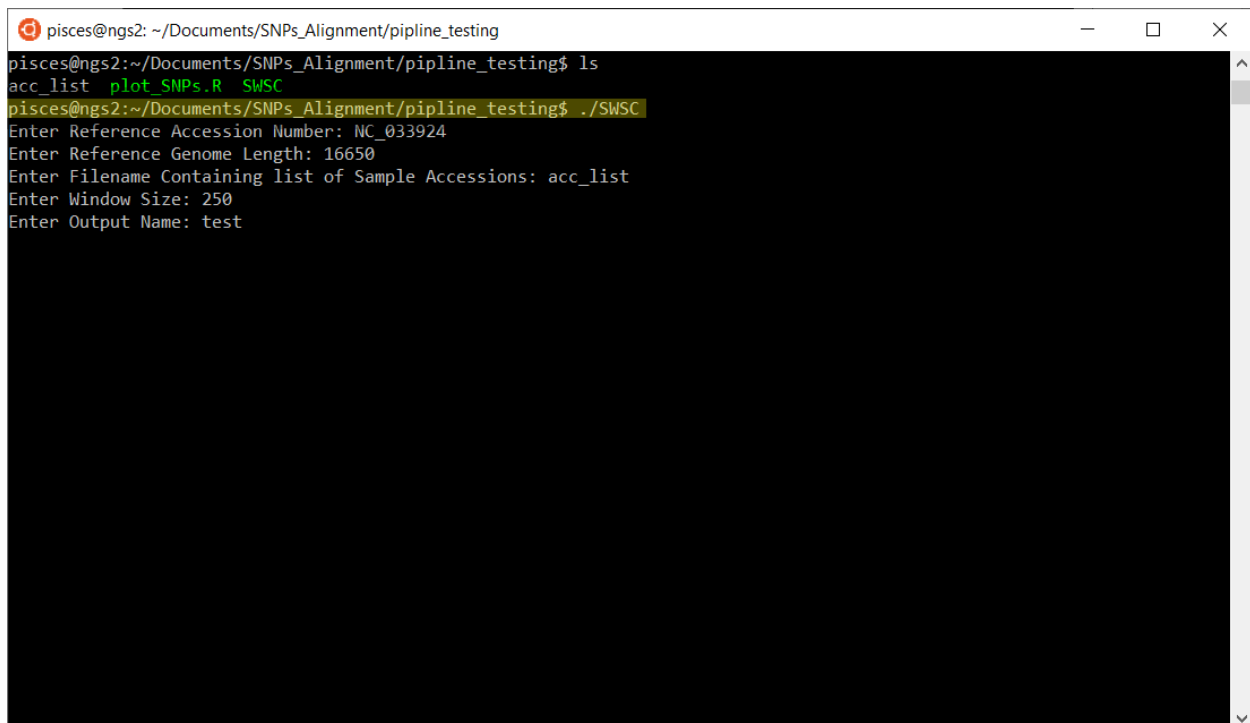
In order to run the script to count SNPs in a sliding window you must have the script 'SWSC' in the same working directory as a text file with the list of the accession numbers for your non-target species.



```
pisces@ngs2: ~/Documents/SNPs_Alignment/pipline_testing
pisces@ngs2:~/Documents/SNPs_Alignment/pipline_testing$ ls
acc_list  plot_SNPs.R  SWSC
pisces@ngs2:~/Documents/SNPs_Alignment/pipline_testing$
```

1	NC_008102
2	KT289925
3	NC_033931
4	NC_033944
5	

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



```
pisces@ngs2: ~/Documents/SNPs_Alignment/pipline_testing
pisces@ngs2:~/Documents/SNPs_Alignment/pipline_testing$ ls
acc_list  plot_SNPs.R  SWSC
pisces@ngs2:~/Documents/SNPs_Alignment/pipline_testing$ ./SWSC
Enter Reference Accession Number: NC_033924
Enter Reference Genome Length: 16650
Enter Filename Containing list of Sample Accessions: acc_list
Enter Window Size: 250
Enter Output Name: test
```

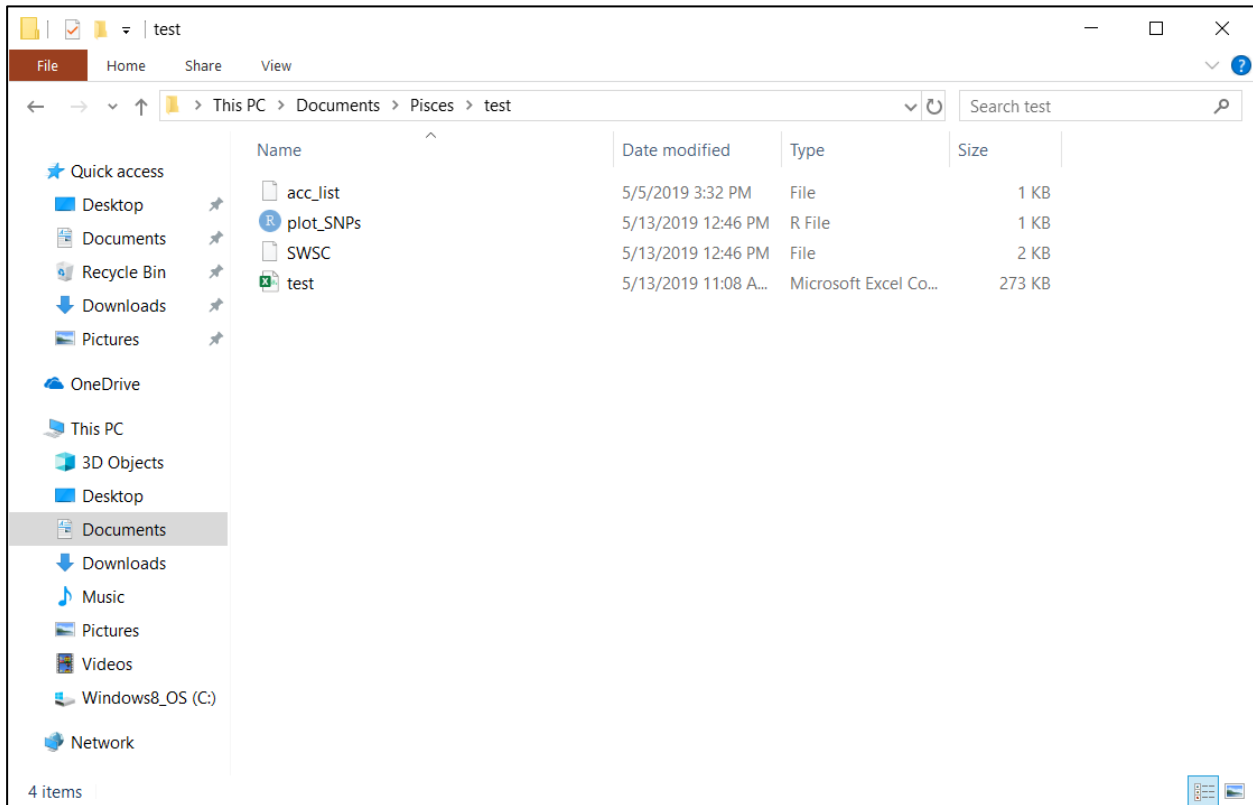
\*If the script won't run due to a permissions problem, run this command: 'chmod 700 SWSC'

## Plotting the Data

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

```
piscis@ngs2: ~/Documents/SNPs_Alignment/pipline_testing
Aligning Reads To Reference
[M::bwa_idx_load_from_disk] read 0 ALT contigs
[M::process] read 1 sequences (16717 bp)...
[M::mem_process_seqs] Processed 1 reads in 0.252 CPU sec, 0.250 real sec
[main] Version: 0.7.17-r1188
[main] CMD: bwa mem NC_033924.fasta NC_033931.fasta
[main] Real time: 0.292 sec; CPU: 0.252 sec
Converting .sam to .bam
Sorting the bam file
Indexing the bam file
Calling SNPs
Creating SNP table
[mpileup] 1 samples in 1 input files
Downloading NC_033944
Aligning Reads To Reference
[M::bwa_idx_load_from_disk] read 0 ALT contigs
[M::process] read 1 sequences (16655 bp)...
[M::mem_process_seqs] Processed 1 reads in 0.096 CPU sec, 0.094 real sec
[main] Version: 0.7.17-r1188
[main] CMD: bwa mem NC_033924.fasta NC_033944.fasta
[main] Real time: 0.135 sec; CPU: 0.096 sec
Converting .sam to .bam
Sorting the bam file
Indexing the bam file
Calling SNPs
Creating SNP table
[mpileup] 1 samples in 1 input files
piscis@ngs2:~/Documents/SNPs_Alignment/pipline_testing$ ls
acc_list  plot_SNPs.R  SWSC  test.csv
piscis@ngs2:~/Documents/SNPs_Alignment/pipline_testing$
```

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.

