Unfortunately, I did not notice until this evening when I went to finalize my Assignment 5 work, tarball it, and submit it that I had not used the correct fasta file, and as a result my present work presented is the SNPs of SARS-CoV-1, accession number NC\_004718.3. The results of SARS-CoV-2 SNPs will be uploaded briefly, once the results are in hand. There are 7361 SNPs identified in the file SC\_covid\_SNPs.csv across the 194 sequences.