**Name: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

**Part II – Online Databases, Alignments and Mutation Rates**

**Section A – Primer/Probe Sequences from the Original TaqMan Assay**

Step 3: Copy this sequence, and paste into your answer sheet. For each one, make a header line starting with a > followed by the name of the region (i.e. N1). Identify the probe sequence in bold (you can just compare by eye to identify the probe sequence)

Step 5: Are these matches near the beginning or end of the virus?

Step 7: What is the name and function of this gene?

**Section B – Comparing the Viruses that Cause SARS and COVID-19**

Step 7: What are two regions that would be good targets for a test that would detect ONLY SARS-CoV-2, but not SARS-CoV?

What are two regions that would be good targets for a test that would detect BOTH SARS-CoV and SARS-CoV-2 (provide screenshots).

**Section C – Mutation of SARS-CoV-2 Over Time**

Why are transmission events not the same as cell infections? Which number is expected to be higher, transmission events or cell infections? Will this lead to an over-or underestimation of mutation rate in our calculations?

Steps 2-5. Complete the table.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Accession Number | Collection Date | Country | Genome Size | # of Mutations compared to RefSeq | Days from RefSeq | # of Transmissions since RefSeq  | s/n/c |
| [NC\_045512](https://www.ncbi.nlm.nih.gov/nuccore/NC_045512) | 12/23/19 | China | 29903 | NA | NA | NA | NA |
| [MT093631](https://www.ncbi.nlm.nih.gov/nuccore/MT093631) |   |   |   |   |   |   |   |
| [MN997409](https://www.ncbi.nlm.nih.gov/nuccore/MN994467.1) |   |   |   |   |   |   |   |
| [MT093571.1](https://www.ncbi.nlm.nih.gov/nuccore/MT093571.1) |   |   |   |   |   |   |   |
| [MT152824](https://www.ncbi.nlm.nih.gov/nuccore/MT152824) |   |   |   |   |   |   |   |
| [MT263074](https://www.ncbi.nlm.nih.gov/nuccore/MT263074) |   |   |   |   |   |   |   |
| [MT263430](https://www.ncbi.nlm.nih.gov/nuccore/MT263430) |   |   |   |   |   |   |   |
| Average |   |   |   |   |   |   |   |
| Std. Dev. |   |   |   |   |   |   |   |

How does this number compare to the known mutation rates for coronaviruses?

In addition to assumptions about transmission time and equating transmissions to cell infections, what other factors could contribute to differences between the mutation rate you calculated and the actual mutation rate?

**Section D – Effect of Mutation Rate on Genetic Tests**

Step 1: Have any of the viruses obtained a mutation in the N1 region that would potentially prevent the test from working? If so, show evidence using a screen grab.

Step 2: Have any of the viruses obtained a mutation in the any of the test regions that would potentially prevent the test from working? If so, show evidence using a screen grab.

What are the implications of the viral mutation rate for the ability of the original test to positively identify new strains of the virus as the pandemic continues? What are the chances that a virus would accumulate a mutation in both the N1 and N2 regions, according to your calculations?