Given the dramatic increase in available genomic information pertaining to SARS-CoV-2 in publicly available databases, an inclusivity *In-Silico* analysis, aimed at determining the potential alignment capability of the CDC-defined primers relative to the numerous SARS-CoV-2 sequences publicly available. Accession numbers pertaining to 2532 SARS-CoV-2 *complete* sequence entries were obtained from the Severe acute respiratory syndrome coronavirus 2 data hub. Assay primer sequences were aligned to the 2532 sequences using BLASTN suite available from NCBI with the default parameters for aligning a short input sequence. Alignments were reduced to the highest scoring alignment for each sequence queried.

*Results*

Table 1. Results of the *In-Silico* inclusivity analysis which aligned

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| *Primer/Probe* | *Minimum % identity* | *Maximum mismatches* | *Total alignments* | *Number of alignments with mismatches* | *% alignments with 100% identity* | *Mismatch*  *Accession*  *Numbers* |
| N1 Forward | 95 | 1 | 2532 | 1 | 99.96 | MT350243.1 |
| N1 Reverse | 95.833 | 1 | 2532 | 2 | 99.92 | MT293178.1, MT451217.1 |
| N1 Probe | 95.833 | 1 | 2532 | 2 | 99.92 | MT450956.1, MT304491.1 |
| N2 Forward | 100 | 0 | 2532 | 0 | 100 | N/A |
| N2 Reverse | 94.444 | 1 | 2532 | 1 | 99.96 | MT385471.1 |
| N2 Probe | 95.652 | 1 | 2532 | 2 | 99.92 | MT412284.1, MT451410.1 |

|  |  |  |  |
| --- | --- | --- | --- |
| *Primer/Probe* | *Mean Alignment Length* | *% Sequences with Alignment Length Equal to full length of primer* | *Minimum Alignment Length* |
| N1 Forward | 19.99881517 | 99.96 | 17 |
| N1 Reverse | 23.98538705 | 99.61 | 20 |
| N1 Probe | 23.94510269 | 98.14 | 21 |
| N2 Forward | 19.99486572 | 99.92 | 11 |
| N2 Reverse | 17.99881517 | 99.92 | 16 |
| N2 Probe | 22.99210111 | 99.72 | 10 |