

**S1 Table. The summed number of C to U mutations and other mutations (non-C to U) that were observed at each viral region when the reference SARS-CoV-2 strain Wuhan-Hu-1 (accession MN908947) was compared to 98 SARS-CoV-2 genomes collected worldwide with unique collection dates.**

<b>Viral region</b>	<b>Sequence length</b>	<b>Synonymous (C to U)</b>	<b>Non-Synonymous (C to U)</b>	<b>Non-coding (C to U)</b>	<b>Synonymous (non C to U)</b>	<b>Non-synonymous (non C to U)</b>	<b>Non-coding (non-C to U)</b>
<b>5' UTR</b>	265	-	-	35	-	-	0
<b>ORF1</b>	21291	124	66	-	26	75	-
<b>S</b>	3819	3	3	-	5	44	-
<b>ORF3a</b>	828	2	2	-	0	34	-
<b>E</b>	225	2	0	-	0	0	-
<b>M</b>	666	5	0	-	0	1	-
<b>ORF6</b>	186	1	0	-	2	0	-
<b>ORF7a</b>	363	0	0	-	0	1	-
<b>ORF8</b>	363	0	6	-	0	0	-
<b>N</b>	1257	4	5	-	3	20	-
<b>ORF10</b>	114	3	0	-	0	0	-
<b>3' UTR</b>	229	-	-	1	-	-	4
<b>Total</b>	29112	144	82	36	36	175	4