

Additional file 1: Isolate-wise variation information of the four SARS-CoV-2 isolates used in this study.

Isolate S2								
Start position	End position	Base	Ref base	Ref annotation position	Annotation Type	Protein.Position.Amino acids change	Gene.Position.Codons	Impact
29742	29742	A	REF:G	START:3'UTR	downstream gene variant	QHI42199.1	gene-ORF10	MODIFIER; DISTANCE=68
7	7	C	REF:G	START:5'UTR	intergenic variant	-	-	MODIFIER
12	12	T	REF:A	START:5'UTR	intergenic variant	-	-	MODIFIER
29893	29893	G	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
29895	29895	T	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
29896	29896	C	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
29897	29897	G	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
29898	29898	G	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
29901	29901	G	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
2	2	TA	REF:T	START:5'UTR	intergenic variant	-	-	MODIFIER
9	9	TTTTCGC	REF:T	START:5'UTR	intergenic variant	-	-	MODIFIER
29864	29891	G	REF:GAATG ACAAAAAA AAAAAAA AAAAAAA	START:3'UTR	intergenic variant	-	-	MODIFIER
29903	29903	GCCGTCGT	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
10329	10329	G	REF:A	START:gene- orf1ab	missense variant	QHD43415. 1:p.3355D> G	gene- orf1ab:c.100 64gAt>gGt	MODERATE
28144	28144	C	REF:T	START:gene- ORF8	missense variant	QHD43422. 1:p.84L>S	gene- ORF8:c.251t Ta>tCa	MODERATE
28878	28878	A	REF:G	START:gene- N	missense variant	QHD43423. 2:p.202S>N	gene- N:c.605aGt> aAt	MODERATE
29392	29392	T	REF:G	START:gene- N	missense variant	QHD43423. 2:p.373K>N	gene- N:c.1119aaG >aaT	MODERATE

601	601	T	REF:C	START:gene- orf1ab	synonymous variant	QHD43415. 1:p.112G	gene- orf1ab:c.336 ggC>ggT	LOW
8782	8782	T	REF:C	START:gene- orf1ab	synonymous variant	QHD43415. 1:p.2839S	gene- orf1ab:c.851 7agC>agT	LOW
15324	15324	T	REF:C	START:gene- orf1ab	synonymous variant	QHD43415. 1:p.5020N	gene- orf1ab:c.150 60aaC>aaT	LOW
22468	22468	T	REF:G	START:gene- S	synonymous variant	QHD43416. 1:p.302T	gene- S:c.906acG> acT	LOW

### Isolate S3

Start position	End position	Base	Ref base	Ref annotation position	Annotation Type	Protein.Position. Amino acids change	Gene.Position. Codons	Impact
29742	29742	A	REF:G	START:3'UTR	downstream gene variant	QHI42199.1	gene-ORF10	MODIFIER; DISTANCE=68
1	12	-	REF:ATTAA AGGTTTA	START:5'UTR	intergenic variant	-	-	MODIFIER
29870	29903	C	REF:CAAAA AAAAAAAA AAAAAAAA AAAAAA	START:3'UTR	intergenic variant	-	-	MODIFIER
10329	10329	G	REF:A	START:gene- orf1ab	missense variant	QHD43415. 1:p.3355D> G	gene- orf1ab:c.100 64gAt>gGt	MODERATE
28144	28144	C	REF:T	START:gene- ORF8	missense variant	QHD43422. 1:p.84L>S	gene- ORF8:c.251t Ta>tCa	MODERATE
28878	28878	A	REF:G	START:gene- N	missense variant	QHD43423. 2:p.202S>N	gene- N:c.605aGt> aAt	MODERATE
29392	29392	T	REF:G	START:gene- N	missense variant	QHD43423. 2:p.373K>N	gene- N:c.1119aaG >aaT	MODERATE
601	601	T	REF:C	START:gene- orf1ab	synonymous variant	QHD43415. 1:p.112G	gene- orf1ab:c.336 ggC>ggT	LOW
8782	8782	T	REF:C	START:gene- orf1ab	synonymous variant	QHD43415. 1:p.2839S	gene- orf1ab:c.851 7agC>agT	LOW

15324	15324	T	REF:C	START:gene- orf1ab	synonymous variant	QHD43415. 1:p.5020N	gene- orf1ab:c.150 60aaC>aaT	LOW
22468	22468	T	REF:G	START:gene- S	synonymous variant	QHD43416. 1:p.302T	gene- S:c.906acG> acT	LOW

## Isolate S4

Start position	End position	Base	Ref base	Ref annotation position	Annotation Type	Protein.Position.Amino acids change	Gene.Position.Codons	Impact
29742	29742	A	REF:G	START:3'UTR	downstream gene variant	QHI42199.1	gene-ORF10	MODIFIER; DISTANCE=68
4	4	T	REF:A	START:5'UTR	intergenic variant	-	-	MODIFIER
13	13	C	REF:T	START:5'UTR	intergenic variant	-	-	MODIFIER
29870	29870	G	REF:C	START:3'UTR	intergenic variant	-	-	MODIFIER
29872	29872	T	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
29873	29873	C	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
29874	29874	G	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
29875	29875	G	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
29878	29878	T	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
29880	29880	G	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
29882	29882	G	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
29883	29883	T	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
29884	29884	C	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
29885	29885	G	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
29886	29886	T	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
29887	29887	G	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
29888	29888	T	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
29890	29890	G	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
29891	29891	G	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER

29892	29892	G	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
29896	29896	G	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
29898	29898	G	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
29900	29900	G	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
2	2	TTTCAAAG ATCAAGTC A	REF:T	START:5'UTR	intergenic variant	-	-	MODIFIER
29901	29903	A	REF:AAA	START:3'UTR	intergenic variant	-	-	MODIFIER
10329	10329	G	REF:A	START:gene- orf1ab	missense variant	QHD43415. 1:p.3355D> G	gene- orf1ab:c.100 64gAt>gGt	MODERATE
12119	12119	T	REF:C	START:gene- orf1ab	missense variant	QHD43415. 1:p.3952P>S	gene- orf1ab:c.118 54Cca>Tca	MODERATE
19414	19414	A	REF:G	START:gene- orf1ab	missense variant	QHD43415. 1:p.6384V>I	gene- orf1ab:c.191 50Gta>Ata	MODERATE
28144	28144	C	REF:T	START:gene- ORF8	missense variant	QHD43422. 1:p.84L>S	gene- ORF8:c.251t Ta>tCa	MODERATE
28878	28878	A	REF:G	START:gene- N	missense variant	QHD43423. 2:p.202S>N	gene- N:c.605aGt> aAt	MODERATE
280	280	T	REF:C	START:gene- orf1ab	synonymous variant	QHD43415. 1:p.5V	gene- orf1ab:c.15g tC>gtT	LOW
8782	8782	T	REF:C	START:gene- orf1ab	synonymous variant	QHD43415. 1:p.2839S	gene- orf1ab:c.851 7agC>agT	LOW
10870	10870	T	REF:G	START:gene- orf1ab	synonymous variant	QHD43415. 1:p.3535L	gene- orf1ab:c.106 05ctG>ctT	LOW
15324	15324	T	REF:C	START:gene- orf1ab	synonymous variant	QHD43415. 1:p.5020N	gene- orf1ab:c.150 60aaC>aaT	LOW
22468	22468	T	REF:G	START:gene- S	synonymous variant	QHD43416. 1:p.302T	gene- S:c.906acG> acT	LOW

## Isolate S9

Start position	End position	Base	Ref base	Ref annotation position	Annotation Type	Protein.Position.Amino acids change	Gene.Position.Codons	Impact
29742	29742	A	REF:G	START:3'UTR	downstream gene variant	QHI42199.1	gene-ORF10	MODIFIER; DISTANCE=68
29856	29856	A	REF:T	START:3'UTR	intergenic variant	-	-	MODIFIER
29858	29858	A	REF:T	START:3'UTR	intergenic variant	-	-	MODIFIER
29895	29895	T	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
29897	29897	G	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
29898	29898	T	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
29901	29901	G	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
1	14	-	REF:ATTAA AGGTTTAT A	START:5'UTR	intergenic variant	-	-	MODIFIER
29864	29893	T	REF:GAATG ACAAAAAA AAAAAAA AAAAAAA A	START:3'UTR	intergenic variant	-	-	MODIFIER
29903	29903	GCGTCGTG T	REF:A	START:3'UTR	intergenic variant	-	-	MODIFIER
10323	10323	G	REF:A	START:gene- orf1ab	missense variant	QHD43415. 1:p.3353K>R	gene- orf1ab:c.100 58aAg>aGg	MODERATE
25505	25505	T	REF:A	START:gene- ORF3a	missense variant	QHD43417. 1:p.38Q>L	gene- ORF3a:c.113 cAa>cTa	MODERATE
28087	28087	T	REF:C	START:gene- ORF8	missense variant	QHD43422. 1:p.65A>V	gene- ORF8:c.194g Ct>gTt	MODERATE
28144	28144	C	REF:T	START:gene- ORF8	missense variant	QHD43422. 1:p.84L>S	gene- ORF8:c.251t Ta>tCa	MODERATE
28878	28878	A	REF:G	START:gene- N	missense variant	QHD43423. 2:p.202S>N	gene- N:c.605aGt> aAt	MODERATE
8782	8782	T	REF:C	START:gene- orf1ab	synonymous variant	QHD43415. 1:p.2839S	gene- orf1ab:c.851 7agC>agT	LOW
22468	22468	T	REF:G	START:gene- S	synonymous variant	QHD43416. 1:p.302T	gene- S:c.906acG> acT	LOW

23320	23320	T	REF:C	START:gene- S	synonymous variant	QHD43416. 1:p.586D	gene- S:c.1758gaC >gaT	LOW
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