Supplementary Table 1. Sample Cohort demographics.

Age	**Total**	**Vaccination Status**				
		Unvaccinated	One Dose	One or Two Doses	Two Doses	Unknown
All	203,065	106,501	15,451	1,050	5,844	74,255
<35	72,148	54,960	3,485	274	1,870	11,559
35-50	38,967	28,160	4,133	242	1,215	5,217
50-65	27,532	16,769	5,517	355	1,527	3,364
65+	9,718	5,307	2,058	170	1,147	1,036
Unknown	54,700	1,305	222	9	85	53,079

Supplementary Table 2. Quality Control Metrics for SARS-CoV-2 Sequencing Runs

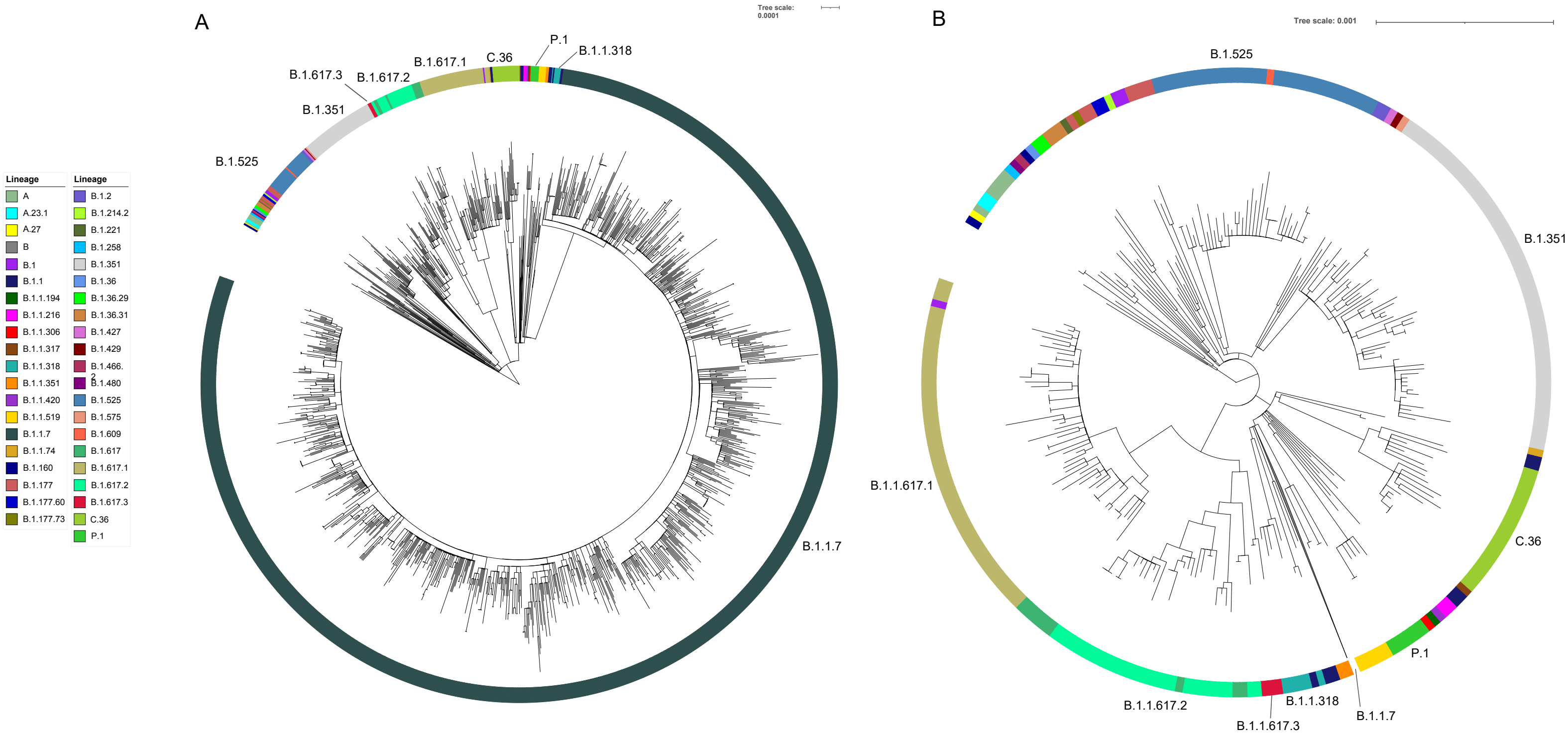
Quality Metric	**Criteria**
Chip Loading	> 60%
Total Reads	> 45 million
Enrichment	>95%
Polyclonal Ratio	< 55%[a]
Low Quality	< 26%
Usable Reads	> 30%
Aligned Bases	> 80%[b]
Mean Raw Accuracy	~100%
Chip Test Fragment Alignment	> 80%

[a] Slightly higher polyclonals acceptable if low quality < 10%

[b] Can be less if base coverage and % reads on target is high

Supplementary Table 3. Quality Control Metrics for SARS-CoV-2 Sequencing Samples

Quality Metric	**Criteria**
Number of Mapped Reads	> 500,000
Percent Reads on Target	>90%
Average Base Coverage Depth	> 1,200
Uniformity of Base Coverage	> 85%
Assigned Amplicon Reads	> 90%
Amplicons with No Strand Bias	> 90%
Amplicons Reading End to End	> 80%
Bases in Target Regions	30,253
Base Reads on Target	> 85%
Target Base Coverage (100x)	> 90%



Supplementary Figure 1: **A)** Phylogenetic analysis of 1,361 SARS-CoV-2 sequences using IQ-TREE2 and visualised in iTOL. **B)** Phylogenetic tree excluding B.1.1.7.