COVID-19 subject 196

2021-03-01

The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with > 90% sequence coverage.

Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0008	composite	NA	ETA	2020-04-08	1.04	NA	58.9%	33.7%
VSP0008-1m	single experiment	NA	ETA	2020-04-08	1.04	NA	28.8%	22.6%
VSP0008-2	single experiment	4410	ETA	2020-04-08	0.70	NA	44.8%	16.7%