

S1 Appendix. Primers and Analysis Workflow.

The Artic Network primer V3 were used for sequencing (https://github.com/artic-network/artic-ncov2019/tree/master/primer_schemes/nCoV-2019/V3). Gaps in the sequences were noted at four amplicon positions, additional primers were designed for these regions, a separate PCR reaction was set up to amplify these regions and sequencing was performed to fill these gaps. Details of primers are provided in the table below.

Sl.no	Primer Name	Primer Sequence (5'- 3')	No of bases
1	V20_15K_L	CACCGTAGCTGGTGTCTCTA	20
	V20_15K_R	GCATCTCCTGATGAGGTTCCA	21
2	V20_5K_L	CAACATTAACCTCCACACGCA	21
	V20_5K_R	CACCAGCCCTTGCTCTGTAA	20
3	V20_26K_L	ACGGTTCATCCGGAGTTGTT	20
	V20_26K_R	GTACCGTTGGAATCTGCCAT	20
4	V20_28K_L	CTTTTGGTTCTCACTTGAAGTGC	23
	V20_28K_R	CAACACGAACGTCATGATACTCT	23

A schematic of the analysis workflow from sequencing reads to consensus generation is provided below.

