Table S1. Summary of analysis tools for SARS-CoV-2 whole genome reconstruction.

Program consensus reconstruction	**Type of data**	**Clade/lineage identrification**	**Note:**
IRMA [96]	Illumina / Ion Torrent	Pangolin; nextclade	open source program, included in ion suite
Dragen [97]	Illumina	Pangolin; nextclade	included in illumina program analysis
ASPICov [99]; poreCov [98]; ESCA [23]	Illumina/ Ion Torrent/ Nanopore	Pangolin; nextclade	open sorce program
RECoVERY [102]	Illumina/ Ion Torrent	Pangolin; nextclade	Italy analysis program
EDGE COVID-19 [100]	illumina/ Nanopore	Pangolin; nextclade	web platform