COVID-19 subject H2103160769

2021-06-23

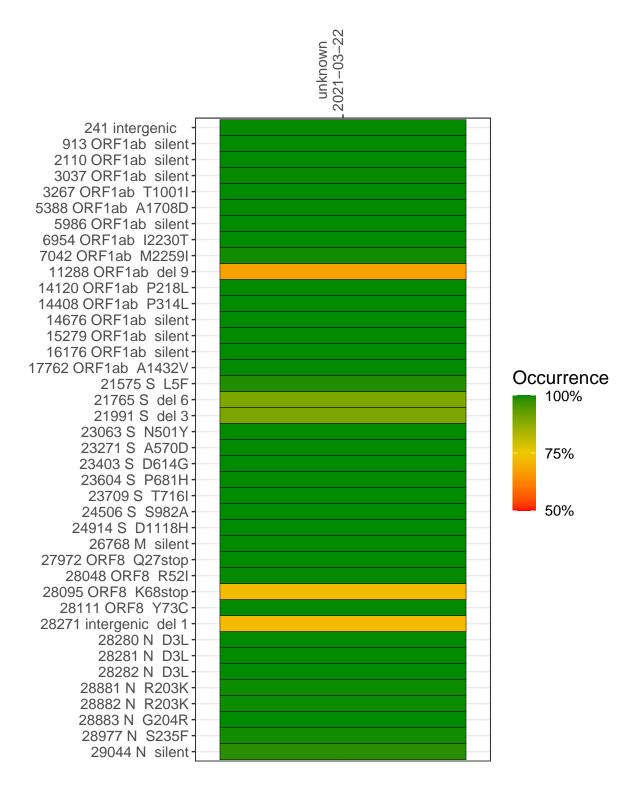
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

Table 1. Sample summary.

Experiment	Туре	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0711-1	single experiment	NA	unknown	2021-03-22	29.80	B.1.1.7	99.8%	99.8%

Variants shared across samples

The heat map below shows how variants (reference genome /home/common/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) are shared across subject samples where the percent variance is colored. Variants are called if a variant position is covered by 5 or more reads, the alternative base is found in > 50% of read pairs and the variant yields a PHRED score > 20. Gray tiles denote positions where the variant was not the major variant or no variants were found. The relative base compositions of each experiment used to calculate tiles are shown in the following plot where the total number of position reads are shown atop of each plot.



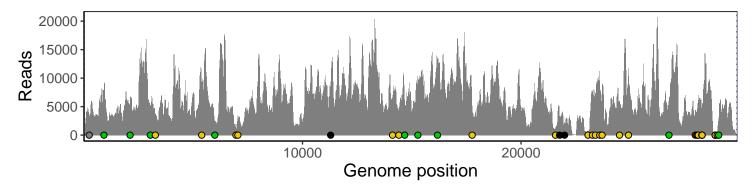
unknown 2021-03-22

	2021-03-22
241 intergenic	3233
913 ORF1ab silent	7519
2110 ORF1ab silent	5228
3037 ORF1ab silent	4384
3267 ORF1ab T1001I	3777
5388 ORF1ab A1708D	8866
5986 ORF1ab silent	2479
6954 ORF1ab I2230T	909
7042 ORF1ab M2259I	2869
11288 ORF1ab del 9	5385
14120 ORF1ab P218L	6100
14408 ORF1ab P314L	3659
14676 ORF1ab silent	5152
15279 ORF1ab silent	8535
16176 ORF1ab silent	12681
17762 ORF1ab A1432V	4639
21575 S L5F	1008
21765 S del 6	3007
21991 S del 3	1873
23063 S N501Y	736
23271 S A570D	7008
23403 S D614G	7227
23604 S P681H	9153
23709 S T716I	7221
24506 S S982A	5949
24914 S D1118H	11186
26768 M silent	5945
27972 ORF8 Q27stop	4336
28048 ORF8 R52I	3714
28095 ORF8 K68stop	5591
28111 ORF8 Y73C	5937
28271 intergenic del 1	4208
28280 N D3L	2884
28281 N D3L	2884
28282 N D3L	3126
28881 N R203K	330
28882 N R203K	330
28883 N G204R	331
28977 N S235F	612
29044 N silent	2645
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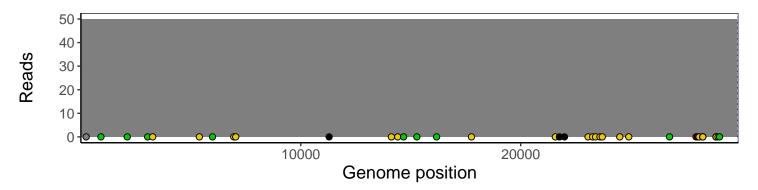
Analyses of individual experiments and composite results

VSP0711-1 | 2021-03-22 | unknown | H2103160769 | genomes | single experiment

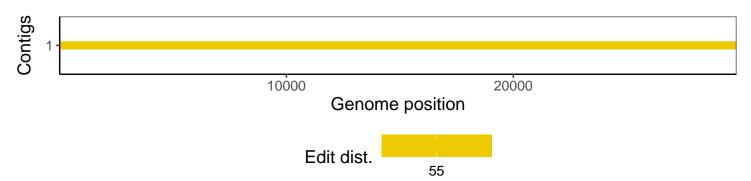
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



Software environment

Software/R package	Version
R	3.4.0
bwa	0.7.17-r1198-dirty
samtools	1.10 Using htslib 1.10
bcftools	1.10.2-34-g1a12af0-dirty Using htslib $1.10.2-57-gf58a6f3$
pangolin	3.1.3
genbankr	1.4.0
optparse	1.6.0
forcats	0.3.0
stringr	1.4.0
dplyr	0.8.1
purrr	0.2.5
readr	1.1.1
tidyr	0.8.1
tibble	2.1.2
ggplot2	3.3.3
tidyverse	1.2.1
ShortRead	1.34.2
GenomicAlignments	1.12.2
${\bf Summarized Experiment}$	1.6.5
DelayedArray	0.2.7
matrixStats	0.54.0
Biobase	2.36.2
Rsamtools	1.28.0
GenomicRanges	1.28.6
GenomeInfoDb	1.12.3
Biostrings	2.44.2
XVector	0.16.0
IRanges	2.10.5
S4Vectors	0.14.7
BiocParallel	1.10.1
BiocGenerics	0.22.1