COVID-19 subject UPHS-0739

2021-06-23

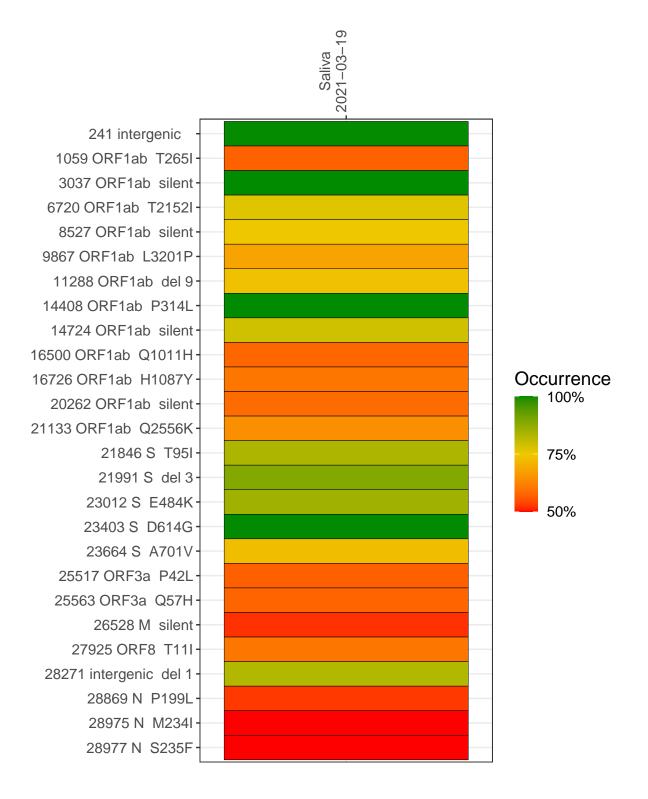
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1957-1	single experiment	NA	Saliva	2021-03-19	29.69	B.1.526	99.3%	99.3%

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.



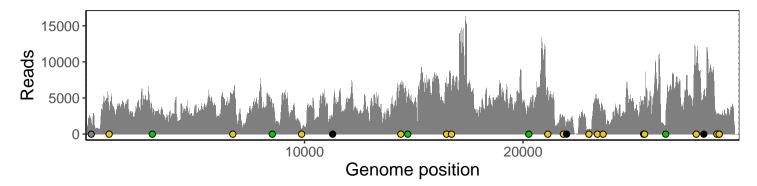
Saliva 2021–03–19

	2021-03-19
241 intergenic	1619
1059 ORF1ab T265I	3316
3037 ORF1ab silent	3016
6720 ORF1ab T2152I	5449
8527 ORF1ab silent	3607
9867 ORF1ab L3201P	453
11288 ORF1ab del 9	1506
14408 ORF1ab P314L	6435
14724 ORF1ab silent	4157
16500 ORF1ab Q1011H	6430
16726 ORF1ab H1087Y	6006
20262 ORF1ab silent	3165
21133 ORF1ab Q2556K	5728
21846 S T95I	2223
21991 S del 3	1455
23012 S E484K	510
23403 S D614G	4705
23664 S A701V	3105
25517 ORF3a P42L	3937
25563 ORF3a Q57H	4994
26528 M silent	1163
27925 ORF8 T11I	9471
28271 intergenic del 1	5269
28869 N P199L	2529
28975 N M234I	2780
28977 N S235F	2716
	1957–1
	195

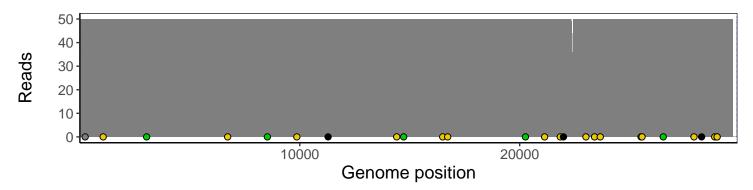
Analyses of individual experiments and composite results

VSP1957-1 | 2021-03-19 | Saliva | UPHS-0739 | genomes | single experiment

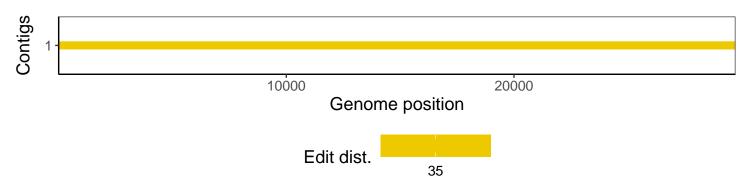
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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