COVID-19 subject UPHS-0719

2021-06-23

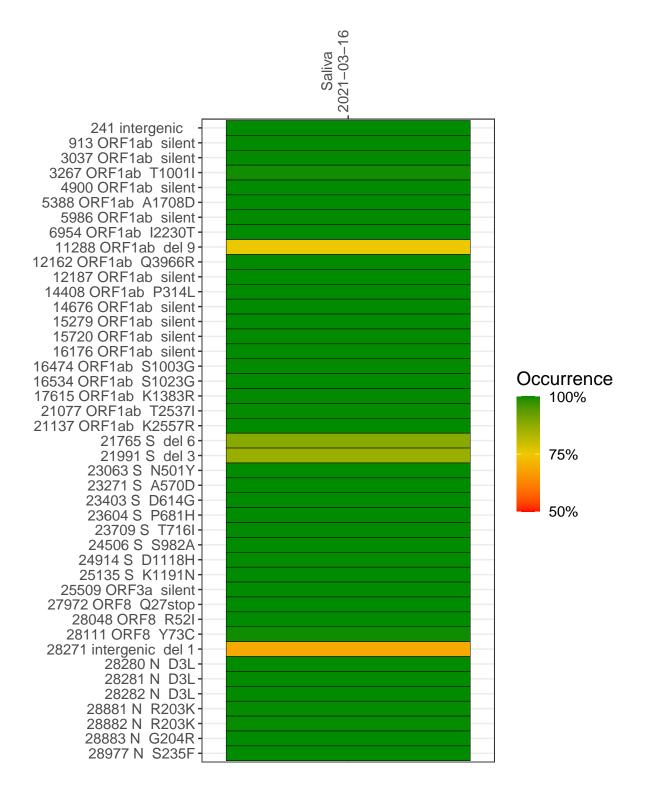
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1937-1	single experiment	NA	Saliva	2021-03-16	29.80	B.1.1.7	99.7%	99.7%

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.



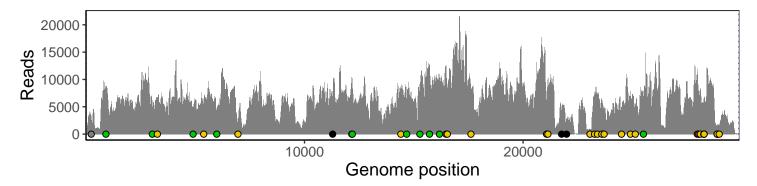
Saliva 2021–03–16

	2021-03-16
241 intergenic	2872
913 ORF1ab silent	7607
3037 ORF1ab silent	5054
3267 ORF1ab T1001I	6727
4900 ORF1ab silent	4362
5388 ORF1ab A1708D	5480
5986 ORF1ab silent	4055
6954 ORF1ab I2230T	2123
11288 ORF1ab del 9	4480
12162 ORF1ab Q3966R	9124
12187 ORF1ab silent	10120
14408 ORF1ab P314L	7772
14676 ORF1ab silent	5841
15279 ORF1ab silent	7452
15720 ORF1ab silent	12371
16176 ORF1ab silent	10119
16474 ORF1ab S1003G	11917
16534 ORF1ab S1023G	7720
17615 ORF1ab K1383R	8040
21077 ORF1ab T2537I	3962
21137 ORF1ab K2557R	9528
21765 S del 6	3559
21991 S del 3	2414
23063 S N501Y	916
23271 S A570D	6805
23403 S D614G	7168
23604 S P681H	6019
23709 S T716I	4773
24506 S S982A	4980
24914 S D1118H	7462
25135 S K1191N	5239
25509 ORF3a silent	6731
27972 ORF8 Q27stop	11380
28048 ORF8 R52I	6489
28111 ORF8 Y73C	7883
28271 intergenic del 1	5282
28280 N D3L	3549
28281 N D3L	3549
28282 N D3L	3778
28881 N R203K	1146
28882 N R203K	1140
28883 N G204R	1142
28977 N S235F	1560
	937–1
	137
	<u>0</u>

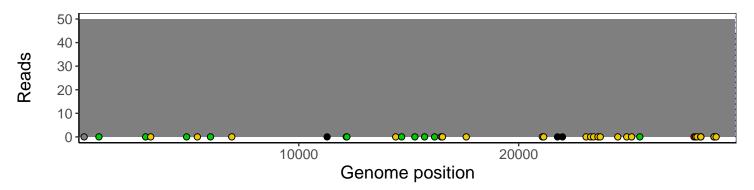
Analyses of individual experiments and composite results

VSP1937-1 | 2021-03-16 | Saliva | UPHS-0719 | genomes | single experiment

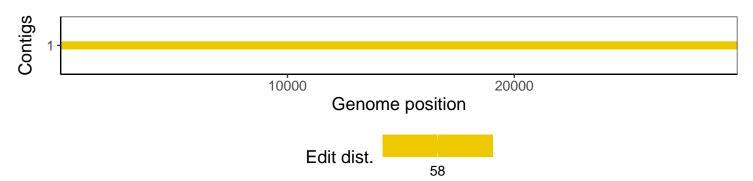
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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