# COVID-19 subject UPHS-0731

2021-06-23

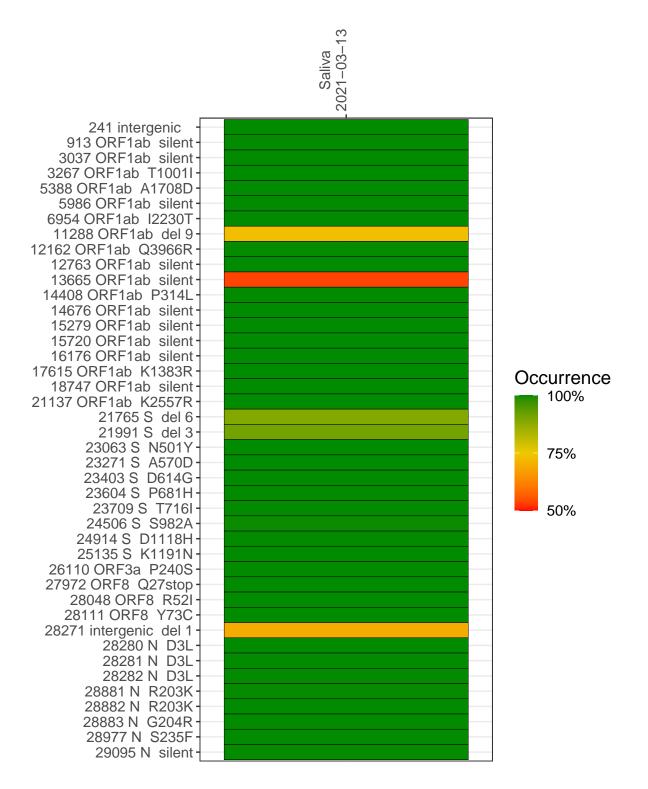
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1949-1	single experiment	NA	Saliva	2021-03-13	29.67	B.1.1.7	99.2%	99.1%

#### 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 2021-03-13

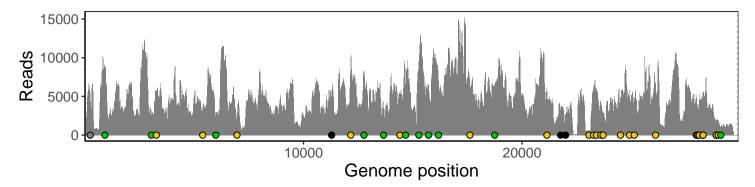
	2021-03-13
241 intergenic	4616
913 ORF1ab silent	7887
3037 ORF1ab silent	2584
3267 ORF1ab T1001I	5831
5388 ORF1ab A1708D	3152
5986 ORF1ab silent	2348
6954 ORF1ab I2230T	1870
11288 ORF1ab del 9	3194
12162 ORF1ab Q3966R	8359
12763 ORF1ab silent	8092
13665 ORF1ab silent	3381
14408 ORF1ab P314L	5031
14676 ORF1ab silent	6023
15279 ORF1ab silent	8316
15720 ORF1ab silent	6354
16176 ORF1ab silent	6760
17615 ORF1ab K1383R	6192
18747 ORF1ab silent	5789
21137 ORF1ab K2557R	5478
21765 S del 6	2714
21991 S del 3	2290
23063 S N501Y	567
23271 S A570D	5558
23403 S D614G	5715
23604 S P681H	4064
23709 S T716I	2822
24506 S S982A	4836
24914 S D1118H	5406
25135 S K1191N	4542
26110 ORF3a P240S	6391
27972 ORF8 Q27stop	4861
28048 ORF8 R52I	3015
28111 ORF8 Y73C	4519
28271 intergenic del 1	4297
28280 N D3L	2871
28280 N D3L	2871
28282 N D3L	3073
28881 N R203K	1339
28882 N R203K	1334
28883 N G204R	1338
28977 N S235F	1883
29095 N silent	1056
	949-1
	946
	_



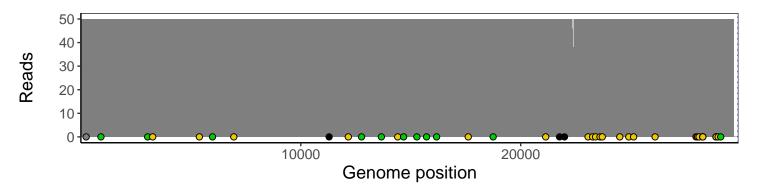
## Analyses of individual experiments and composite results

## VSP1949-1 | 2021-03-13 | Saliva | UPHS-0731 | genomes | single experiment

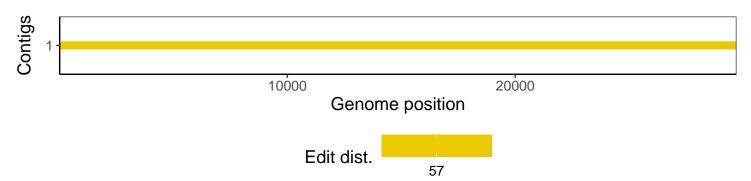
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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