# COVID-19 subject UPHS-0690

2021-05-05

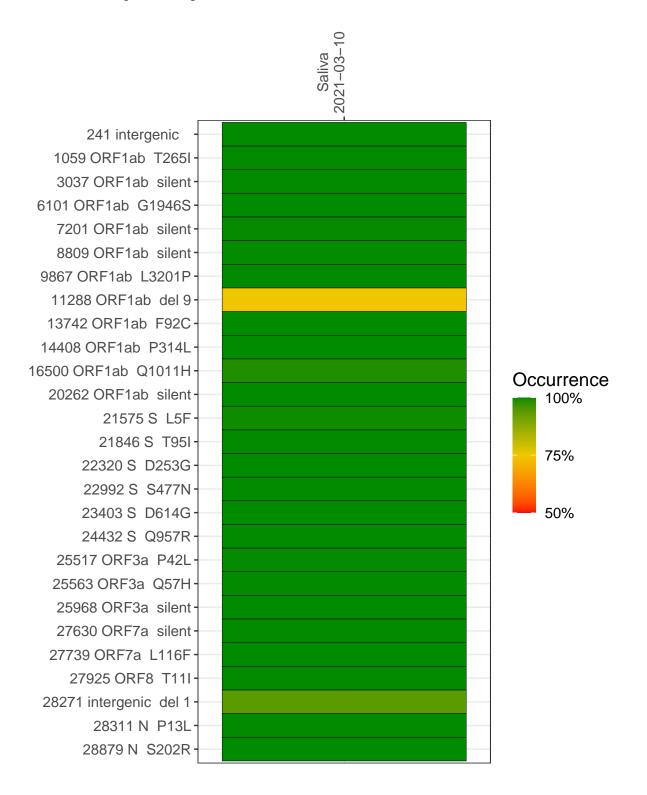
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1908-1	single experiment	NA	Saliva	2021-03-10	29.84	B.1.526.2	99.9%	99.7%

#### Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/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 2021-03-10

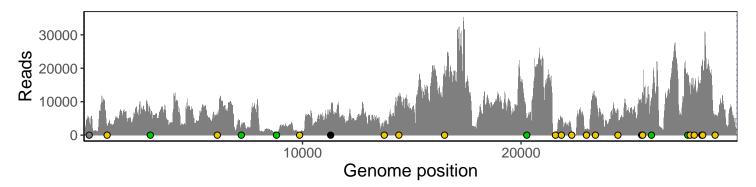
	2021-03-10
241 intergenic	4114
1059 ORF1ab T265I	2606
3037 ORF1ab silent	6305
6101 ORF1ab G1946S	5585
7201 ORF1ab silent	2936
8809 ORF1ab silent	857
9867 ORF1ab L3201P	502
11288 ORF1ab del 9	4344
13742 ORF1ab F92C	3597
14408 ORF1ab P314L	10863
16500 ORF1ab Q1011H	16948
20262 ORF1ab silent	4579
21575 S L5F	903
21846 S T95I	4884
22320 S D253G	1209
22992 S S477N	1506
23403 S D614G	11145
24432 S Q957R	6745
25517 ORF3a P42L	9152
25563 ORF3a Q57H	12003
25968 ORF3a silent	10287
27630 ORF7a silent	17056
27739 ORF7a L116F	11649
27925 ORF8 T11I	14115
28271 intergenic del 1	19712
28311 N P13L	21298
28879 N S202R	6048
	008-1
	Q



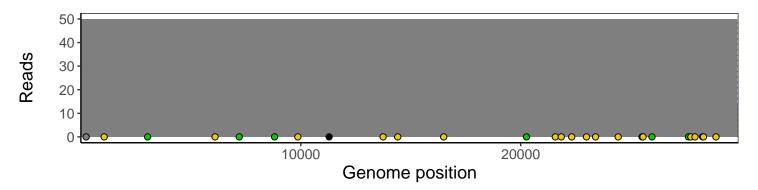
### Analyses of individual experiments and composite results

#### VSP1908-1 | 2021-03-10 | Saliva | UPHS-0690 | genomes | single experiment

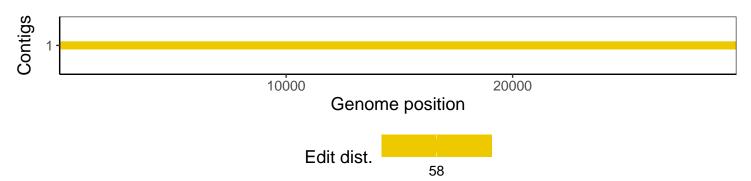
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.8
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	3.0.0
tidyverse	1.2.1
ShortRead	1.34.2
${\it Genomic Alignments}$	1.12.2
SummarizedExperiment	1.6.5
DelayedArray	0.2.7
matrixStats	0.54.0
Biobase	2.36.2
Rsamtools	1.28.0
GenomicRanges	1.28.6
$\operatorname{GenomeInfoDb}$	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