

# COVID-19 subject UPHS-0728

*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.

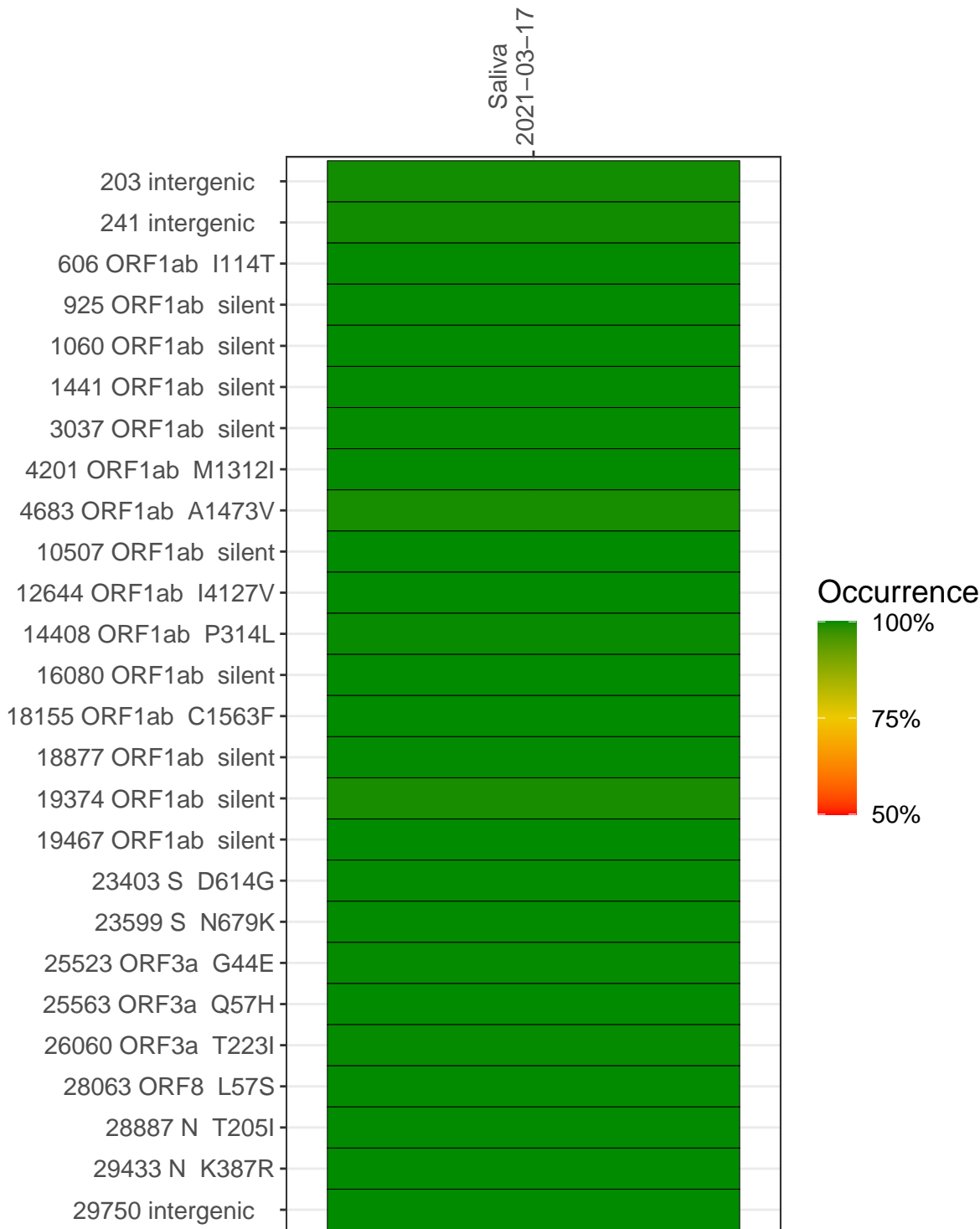
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with  $> 90\%$  sequence coverage.

Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage ( $\geq 5$ reads)
VSP1946-1	single experiment	NA	Saliva	2021-03-17	29.89	B.1.111	99.8%	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  
2021-03-17

203 intergenic	3638
241 intergenic	3095
606 ORF1ab I114T	1625
925 ORF1ab silent	6933
1060 ORF1ab silent	5266
1441 ORF1ab silent	5889
3037 ORF1ab silent	5010
4201 ORF1ab M1312I	7256
4683 ORF1ab A1473V	6810
10507 ORF1ab silent	3522
12644 ORF1ab I4127V	6898
14408 ORF1ab P314L	8485
16080 ORF1ab silent	11915
18155 ORF1ab C1563F	7202
18877 ORF1ab silent	9897
19374 ORF1ab silent	5041
19467 ORF1ab silent	6996
23403 S D614G	8904
23599 S N679K	5113
25523 ORF3a G44E	4845
25563 ORF3a Q57H	6891
26060 ORF3a T223I	13033
28063 ORF8 L57S	9286
28887 N T205I	1997
29433 N K387R	2151
29750 intergenic	1190

Base change

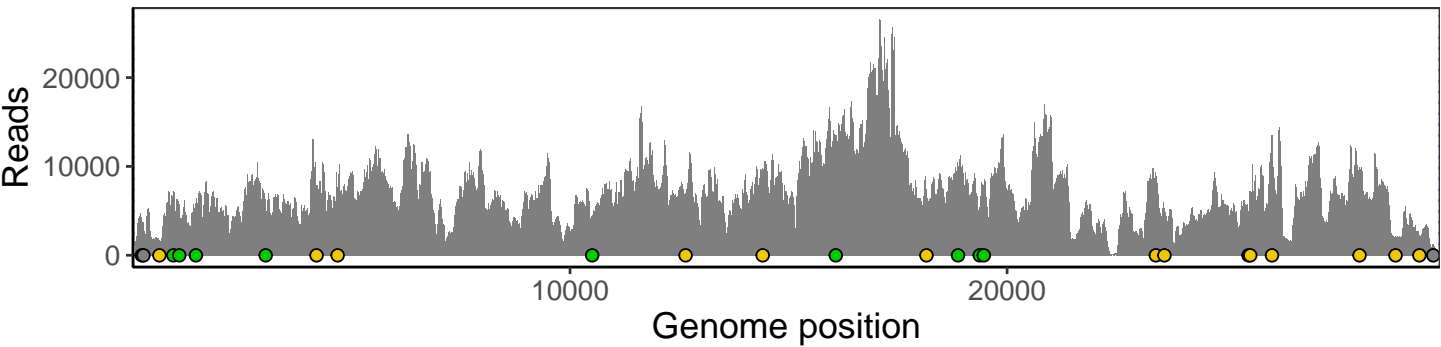
- Expected
- A
- T
- C
- G
- N
- Ins/Del
- No data

VSP1946-1

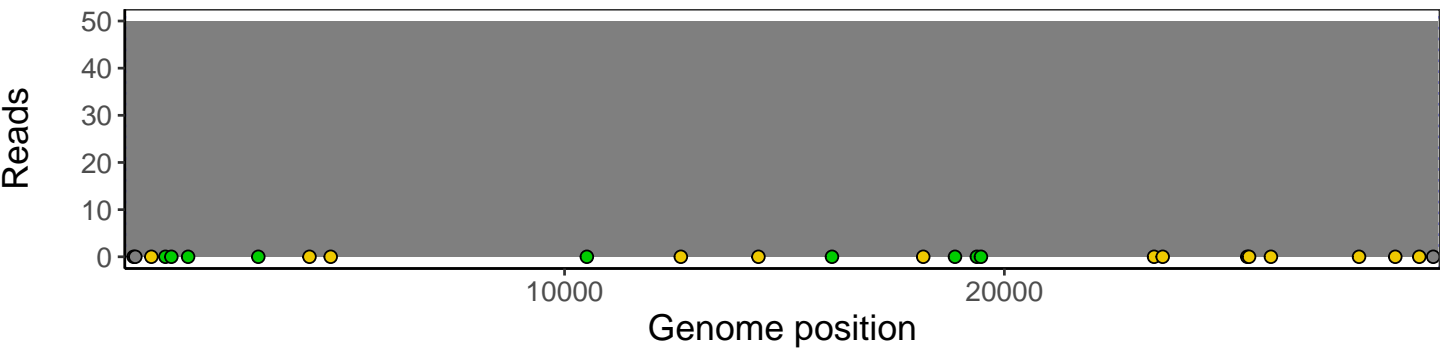
# Analyses of individual experiments and composite results

VSP1946-1 | 2021-03-17 | Saliva | UPHS-0728 | genomes | single experiment

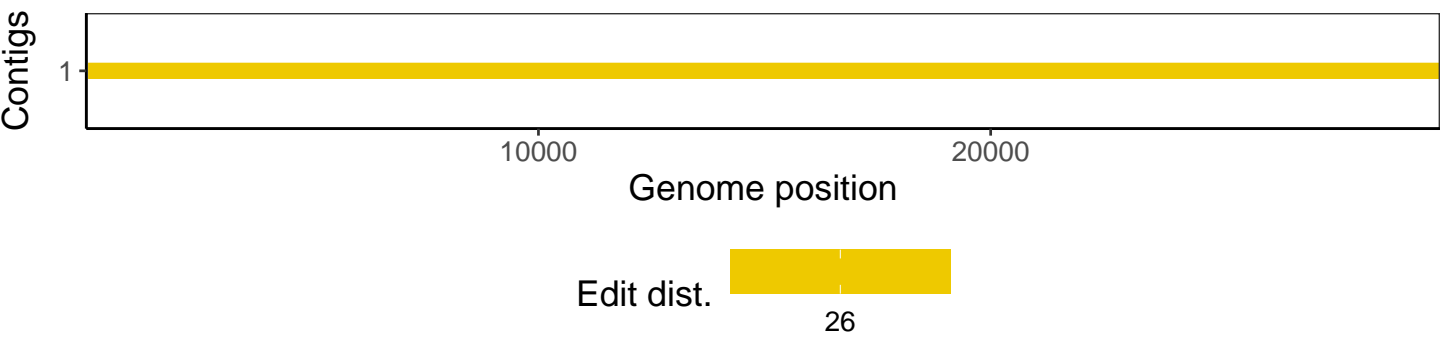
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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 htlib 1.10
bcftools	1.10.2-34-g1a12af0-dirty Using htlib 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
SummarizedExperiment	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