

# COVID-19 subject UPHS-0696

*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.

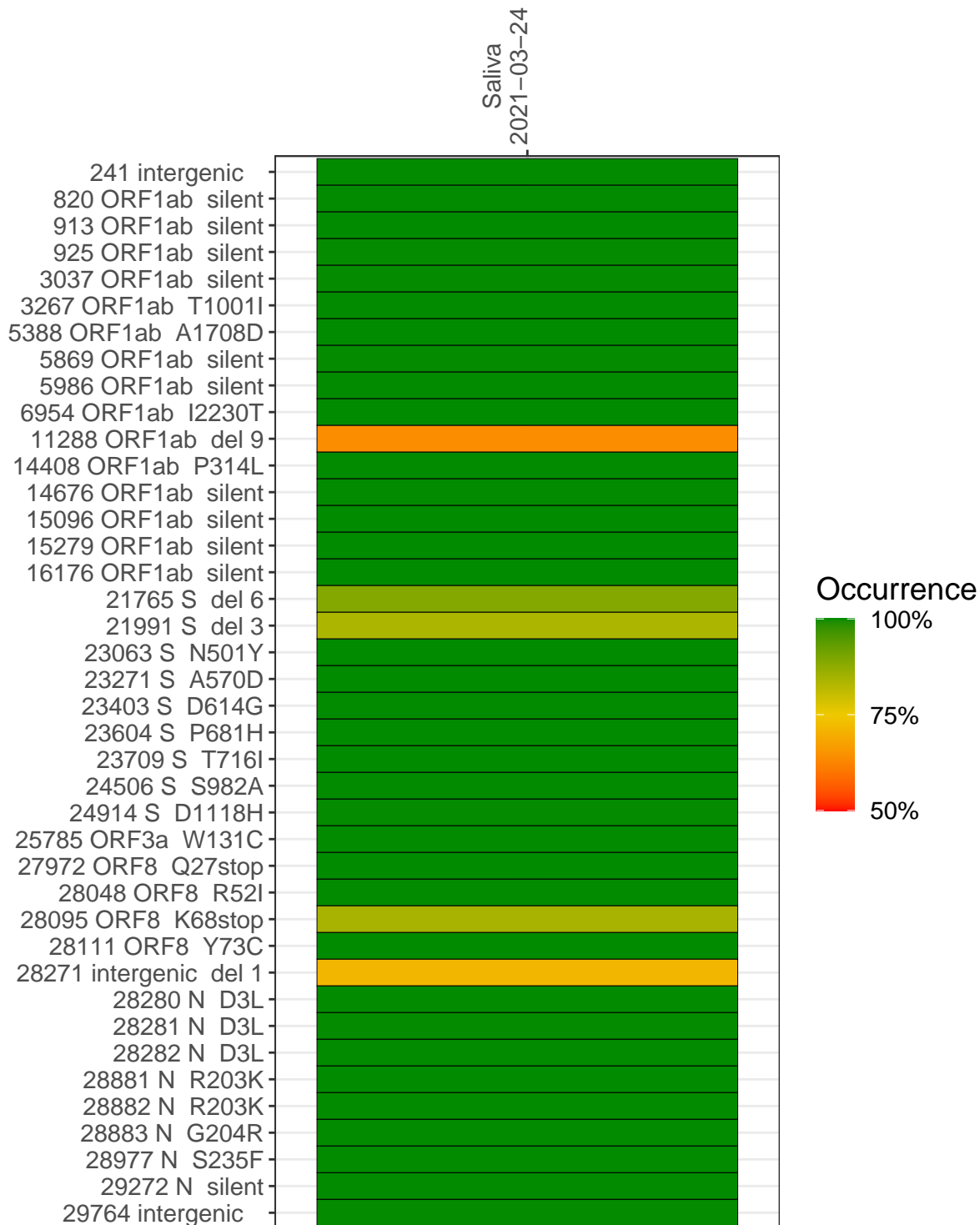
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with  $> 90\%$  sequence coverage.

Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage ( $\geq 5$ reads)
VSP1914-1	single experiment	NA	Saliva	2021-03-24	29.83	B.1.1.7	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 2021-03-24	
241 intergenic	6913	
820 ORF1ab silent	13402	
913 ORF1ab silent	10900	
925 ORF1ab silent	11695	
3037 ORF1ab silent	5243	
3267 ORF1ab T1001I	9872	
5388 ORF1ab A1708D	7965	
5869 ORF1ab silent	4529	
5986 ORF1ab silent	3863	
6954 ORF1ab I2230T	1741	
11288 ORF1ab del 9	3687	
14408 ORF1ab P314L	7357	
14676 ORF1ab silent	8911	
15096 ORF1ab silent	8183	
15279 ORF1ab silent	15502	
16176 ORF1ab silent	17888	
21765 S del 6	4270	
21991 S del 3	1818	
23063 S N501Y	2297	
23271 S A570D	8096	
23403 S D614G	8759	
23604 S P681H	8370	
23709 S T716I	5652	
24506 S S982A	6895	
24914 S D1118H	9395	
25785 ORF3a W131C	9870	
27972 ORF8 Q27stop	18995	
28048 ORF8 R52I	13156	
28095 ORF8 K68stop	15761	
28111 ORF8 Y73C	16171	
28271 intergenic del 1	16365	
28280 N D3L	11381	
28281 N D3L	11381	
28282 N D3L	12152	
28881 N R203K	4777	
28882 N R203K	4763	
28883 N G204R	4783	
28977 N S235F	6395	
29272 N silent	14166	
29764 intergenic	2196	
	VSP1914-1	

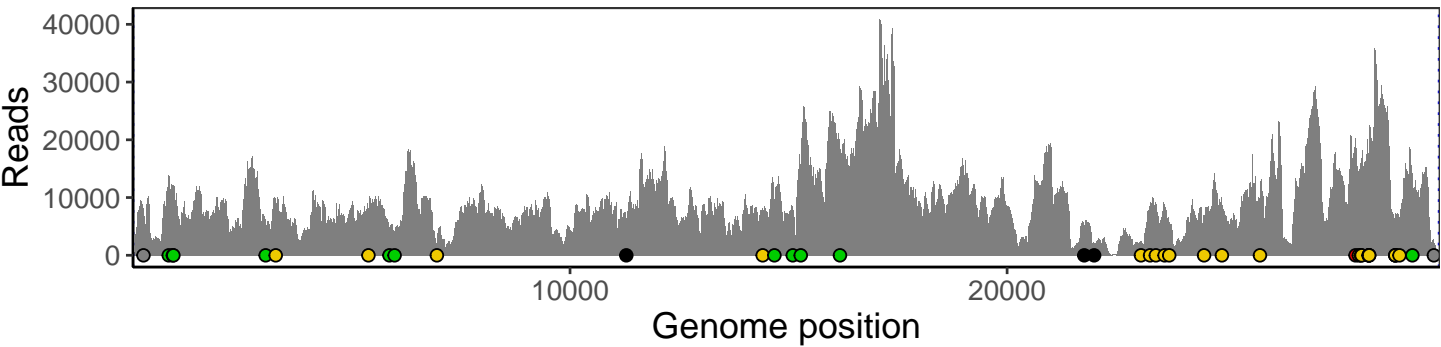
Base change

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

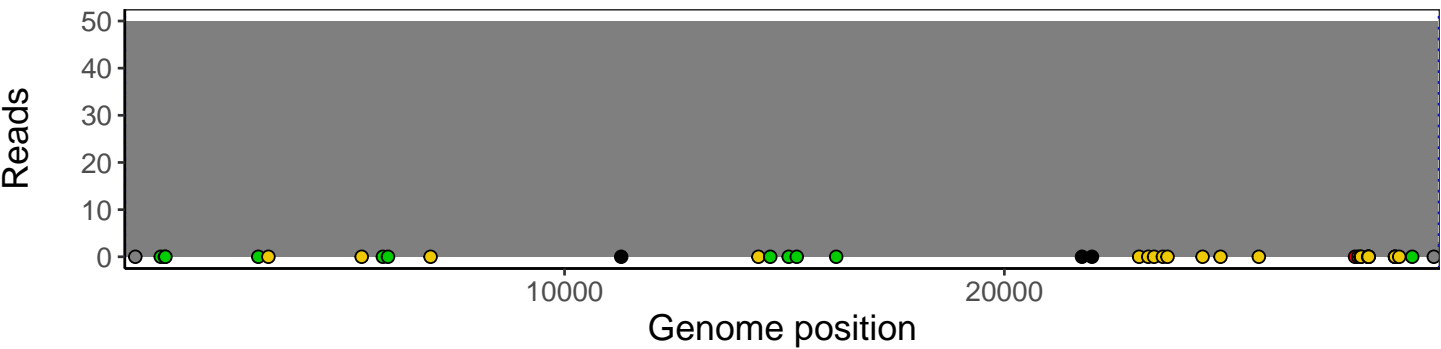
# Analyses of individual experiments and composite results

VSP1914-1 | 2021-03-24 | Saliva | UPHS-0696 | genomes | single experiment

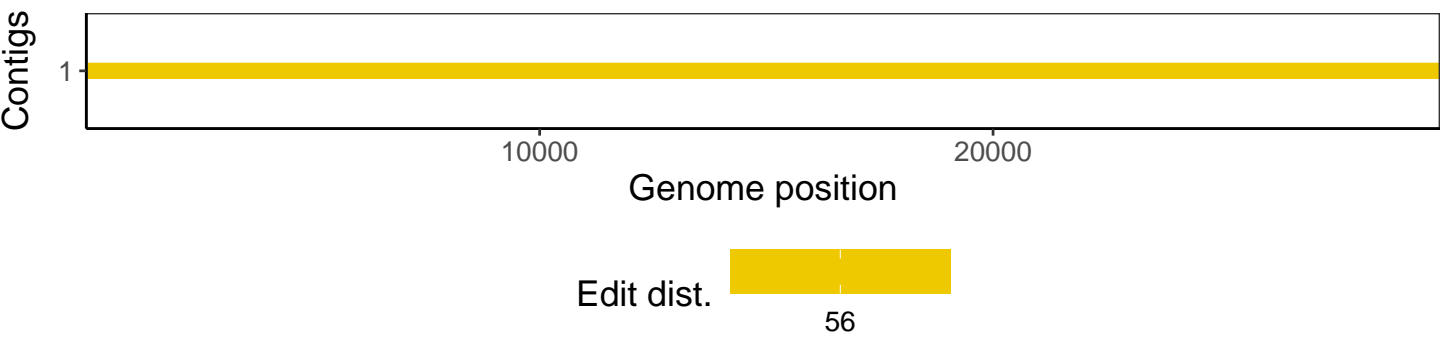
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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 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