

COVID-19 subject UPHS-0717

2021-06-23

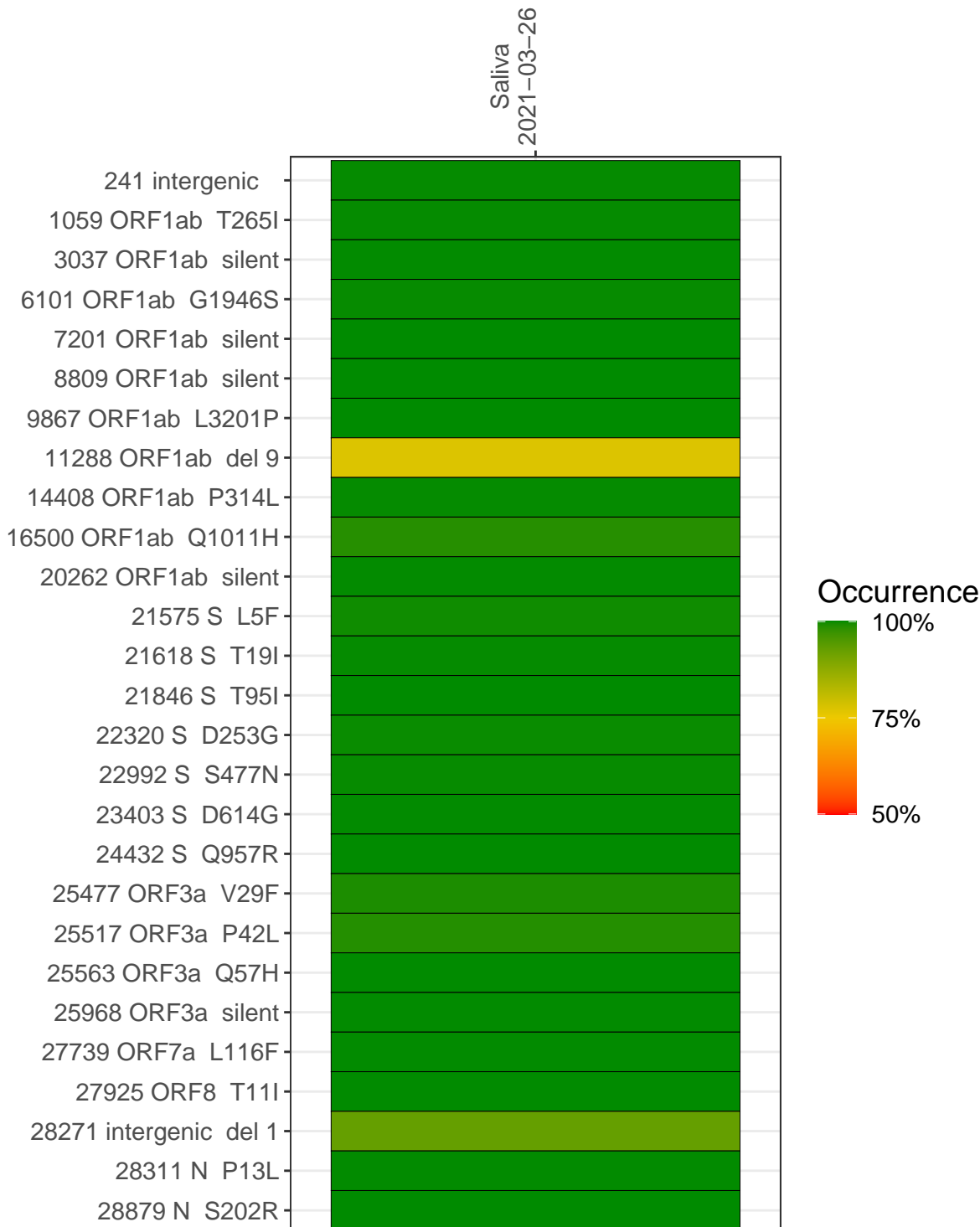
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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 (≥ 5 reads)
VSP1935-1	single experiment	NA	Saliva	2021-03-26	29.79	B.1.526	99.8%	99.8%

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 2021-03-26	
241 intergenic	2652	
1059 ORF1ab T265I	3557	
3037 ORF1ab silent	3446	
6101 ORF1ab G1946S	3970	
7201 ORF1ab silent	1031	
8809 ORF1ab silent	1844	
9867 ORF1ab L3201P	886	
11288 ORF1ab del 9	3461	
14408 ORF1ab P314L	7265	
16500 ORF1ab Q1011H	7846	
20262 ORF1ab silent	4453	
21575 S L5F	1933	
21618 S T19I	1712	
21846 S T95I	4746	
22320 S D253G	972	
22992 S S477N	699	
23403 S D614G	7127	
24432 S Q957R	4198	
25477 ORF3a V29F	5926	
25517 ORF3a P42L	5393	
25563 ORF3a Q57H	6722	
25968 ORF3a silent	6364	
27739 ORF7a L116F	4341	
27925 ORF8 T11I	9331	
28271 intergenic del 1	6740	
28311 N P13L	6760	
28879 N S202R	2075	
	VSP1935-1	

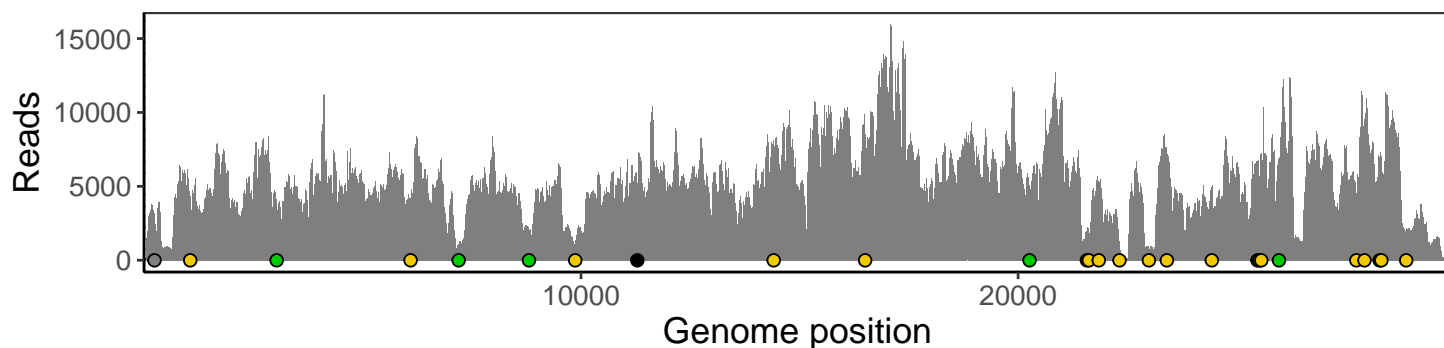
Base change

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

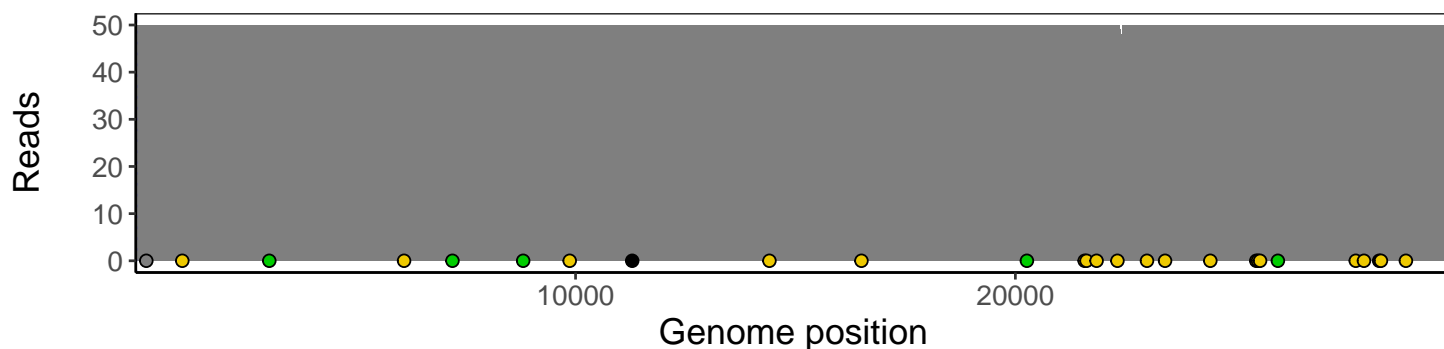
Analyses of individual experiments and composite results

VSP1935-1 | 2021-03-26 | Saliva | UPHS-0717 | genomes | single experiment

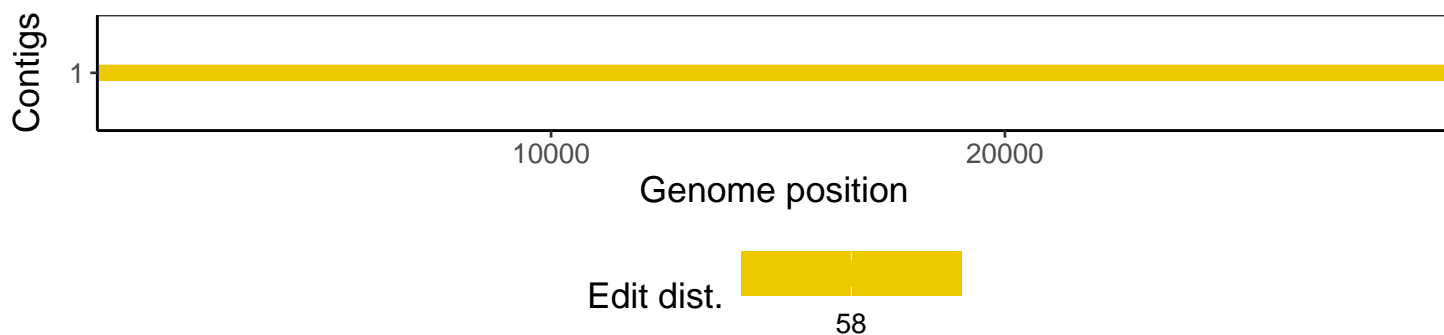
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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