

COVID-19 subject UPHS-0676

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.

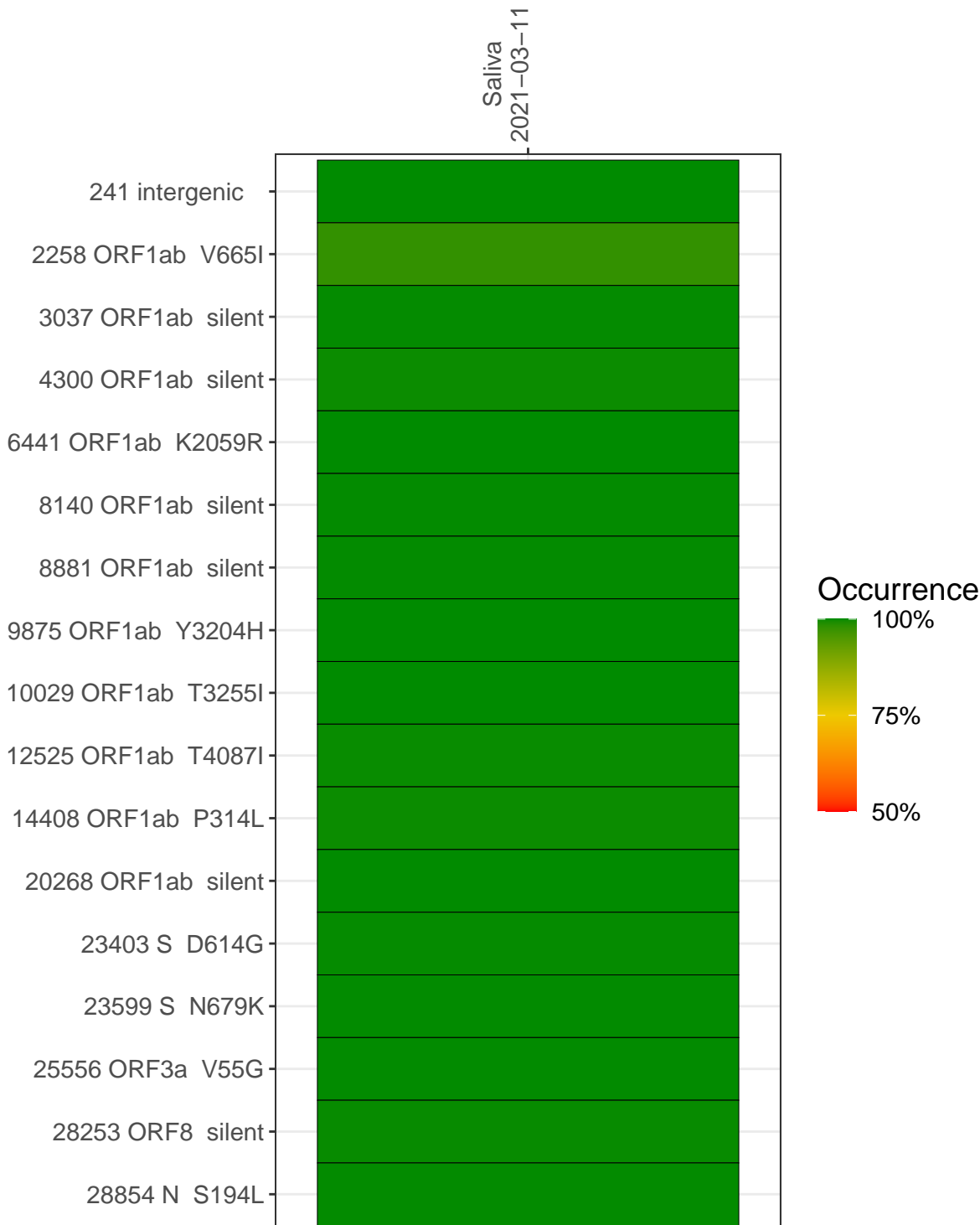
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with $> 90\%$ sequence coverage.

Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (≥ 5 reads)
VSP1894-1	single experiment	NA	Saliva	2021-03-11	29.89	B.1.234	99.9%	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
2021-03-11

241 intergenic	3052
2258 ORF1ab V665I	5707
3037 ORF1ab silent	6876
4300 ORF1ab silent	6515
6441 ORF1ab K2059R	9760
8140 ORF1ab silent	6767
8881 ORF1ab silent	2503
9875 ORF1ab Y3204H	2054
10029 ORF1ab T3255I	2553
12525 ORF1ab T4087I	9023
14408 ORF1ab P314L	11148
20268 ORF1ab silent	3718
23403 S D614G	10518
23599 S N679K	9316
25556 ORF3a V55G	9854
28253 ORF8 silent	7564
28854 N S194L	3098

Base change

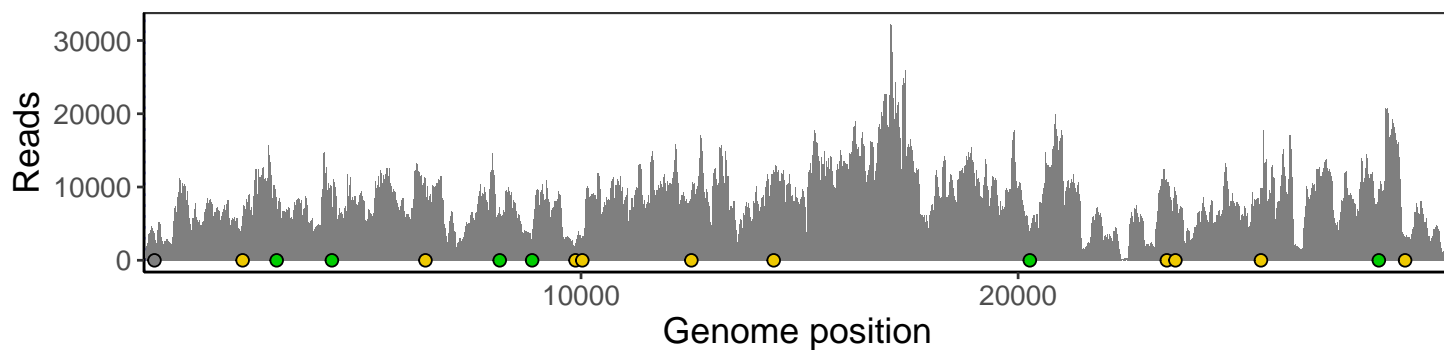
- Expected
- A
- T
- C
- G
- N
- Ins/Del
- No data

VSP1894-1

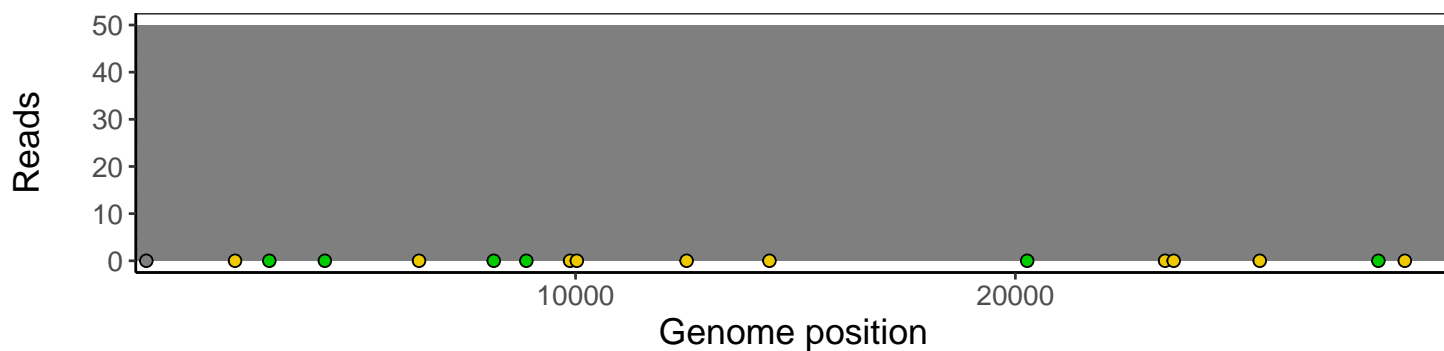
Analyses of individual experiments and composite results

VSP1894-1 | 2021-03-11 | Saliva | UPHS-0676 | genomes | single experiment

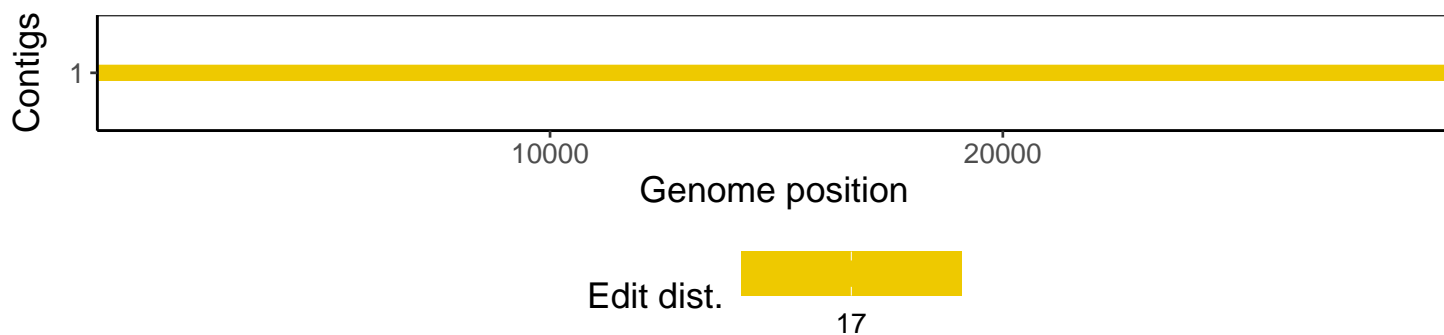
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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