COVID-19 subject UPHS-0661

2021-06-23

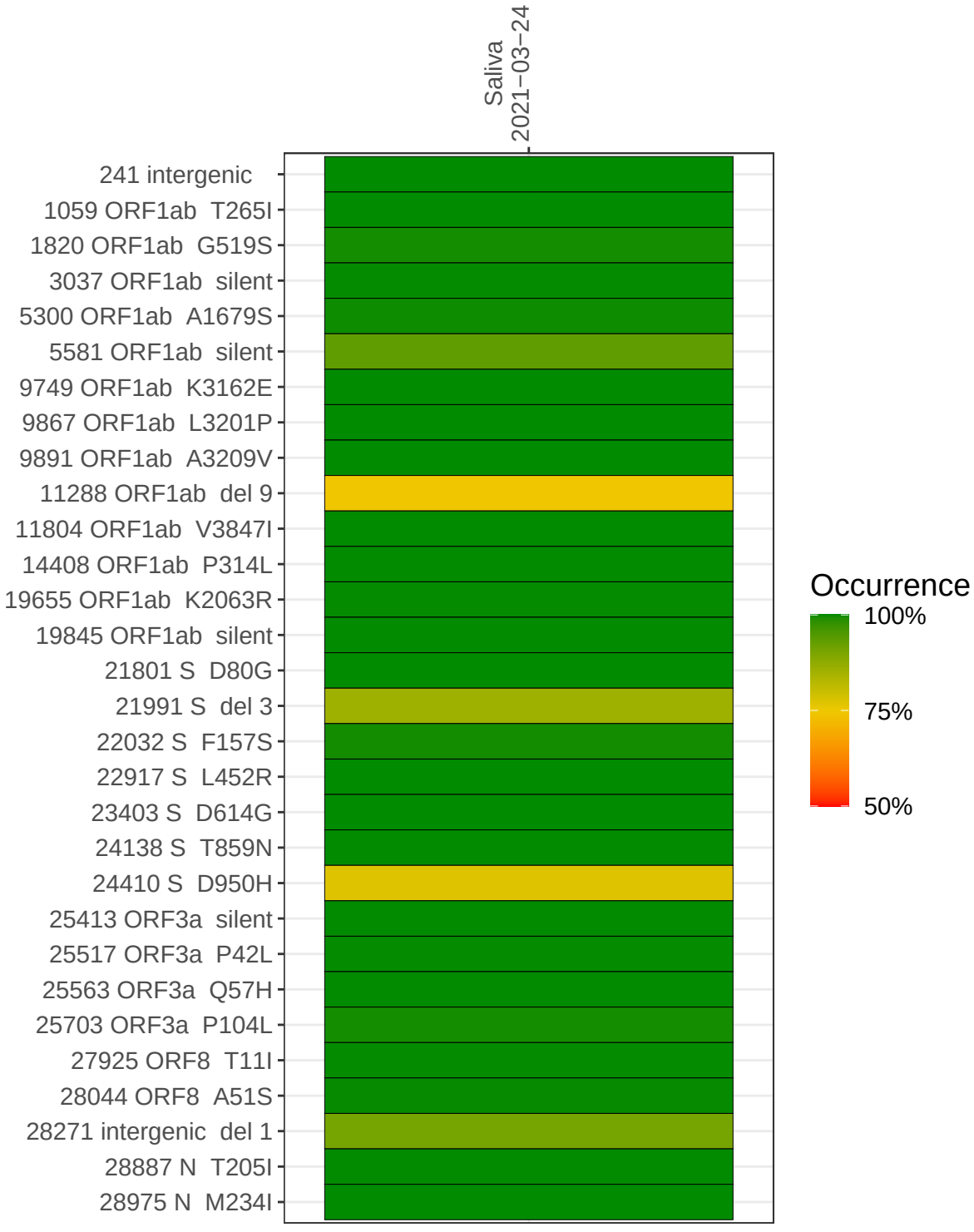
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

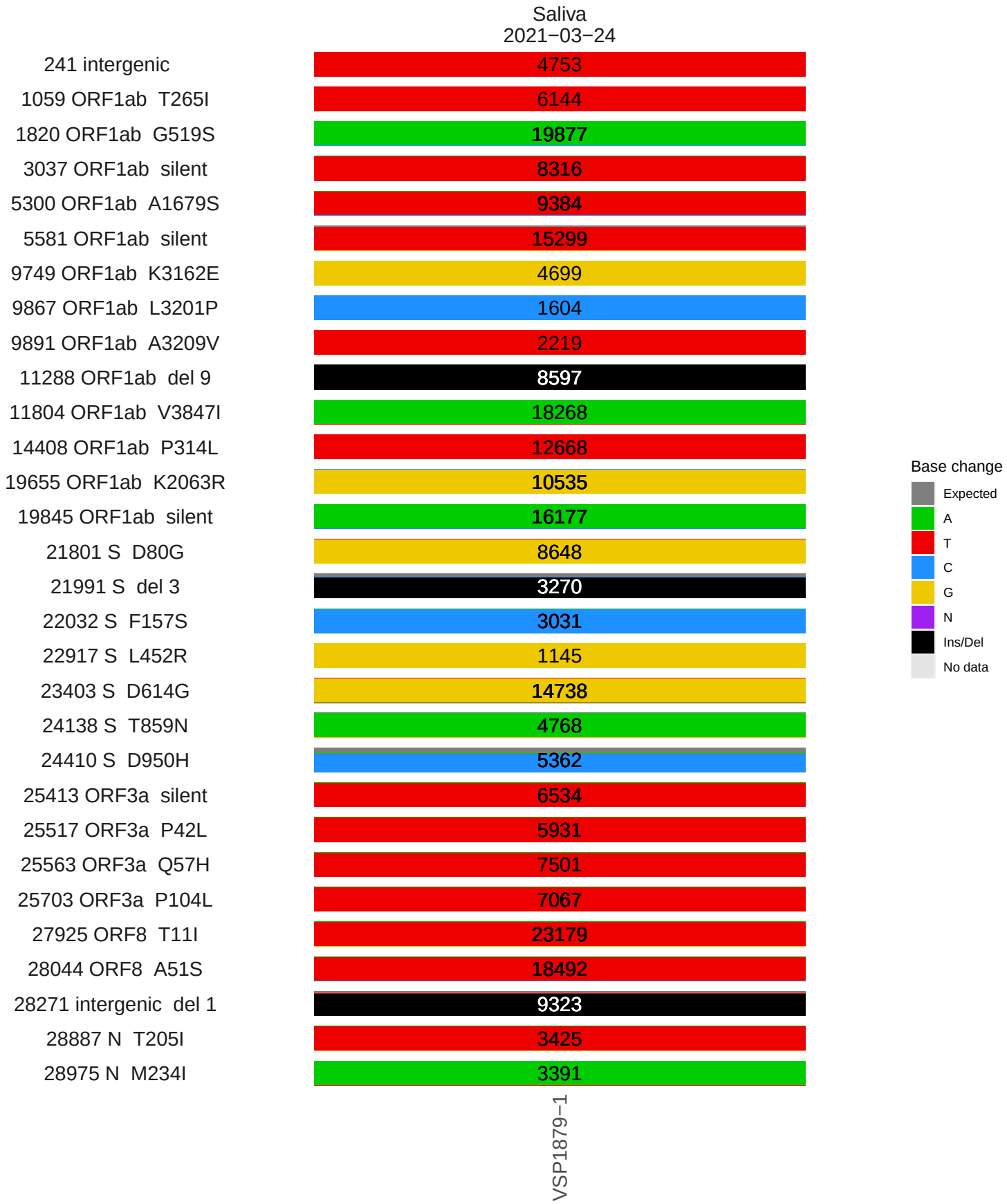
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1879-1	single experiment	NA	Saliva	2021-03-24	29.82	B.1.526	99.9%	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.

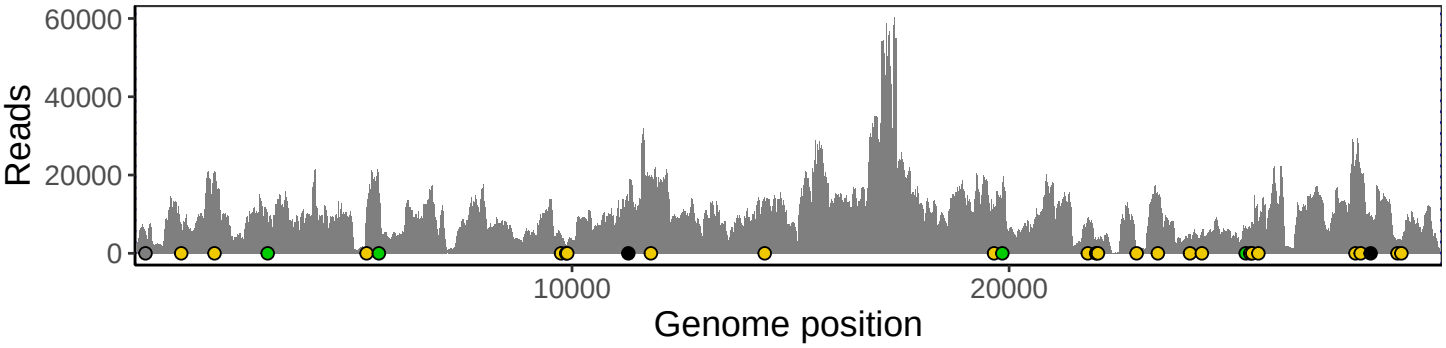



Saliva
2021−03−24
241 intergenic
4753
1059 ORF1ab T265I
6144
1820 ORF1ab G519S
19877
3037 ORF1ab silent
8316
5300 ORF1ab A1679S
9384
5581 ORF1ab silent
15299
9749 ORF1ab K3162E
4699
9867 ORF1ab L3201P
1604
9891 ORF1ab A3209V
2219
11288 ORF1ab del 9
8597
11804 ORF1ab V3847I
18268
14408 ORF1ab P314L
12668
19655 ORF1ab K2063R
10535
19845 ORF1ab silent
16177
21801 S D80G
8648
21991 S del 3
3270
22032 S F157S
3031
22917 S L452R
1145
23403 S D614G
14738
24138 S T859N
4768
24410 S D950H
5362
25413 ORF3a silent
6534
25517 ORF3a P42L
5931
25563 ORF3a Q57H
7501
25703 ORF3a P104L
7067
27925 ORF8 T11I
23179
28044 ORF8 A51S
18492
28271 intergenic del 1
9323
28887 N T205I
3425
28975 N M234I
3391
VSP1879−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

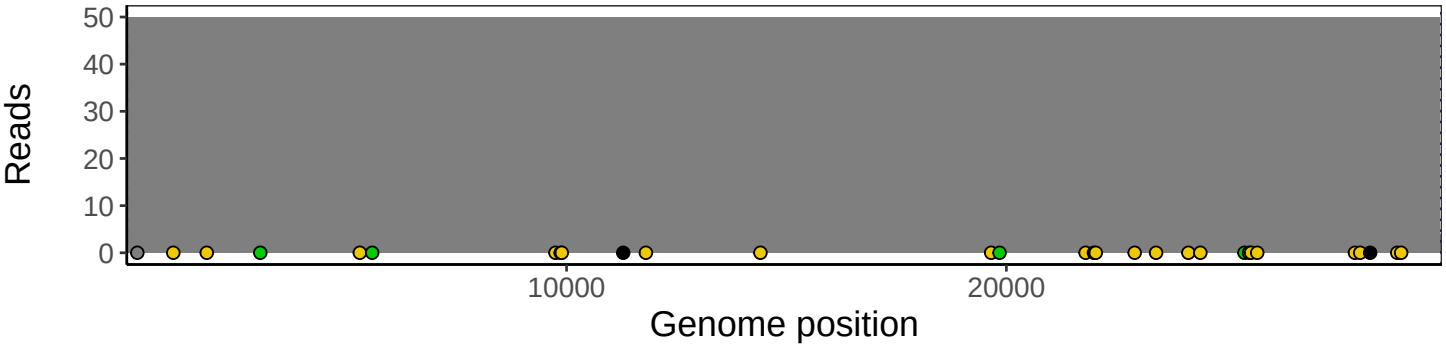
Analyses of individual experiments and composite results

VSP1879-1 | 2021-03-24 | Saliva | UPHS-0661 | genomes | single experiment

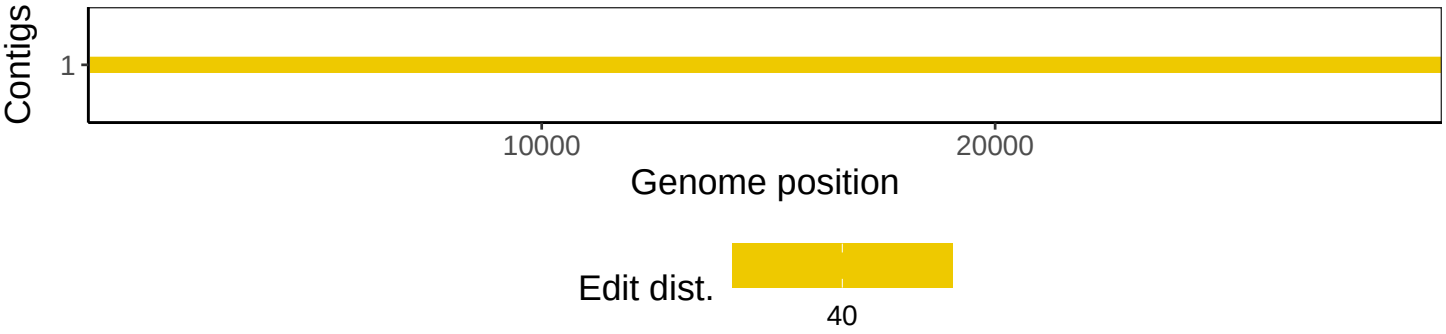
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	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