COVID-19 subject UPHS-0705

2021-06-23

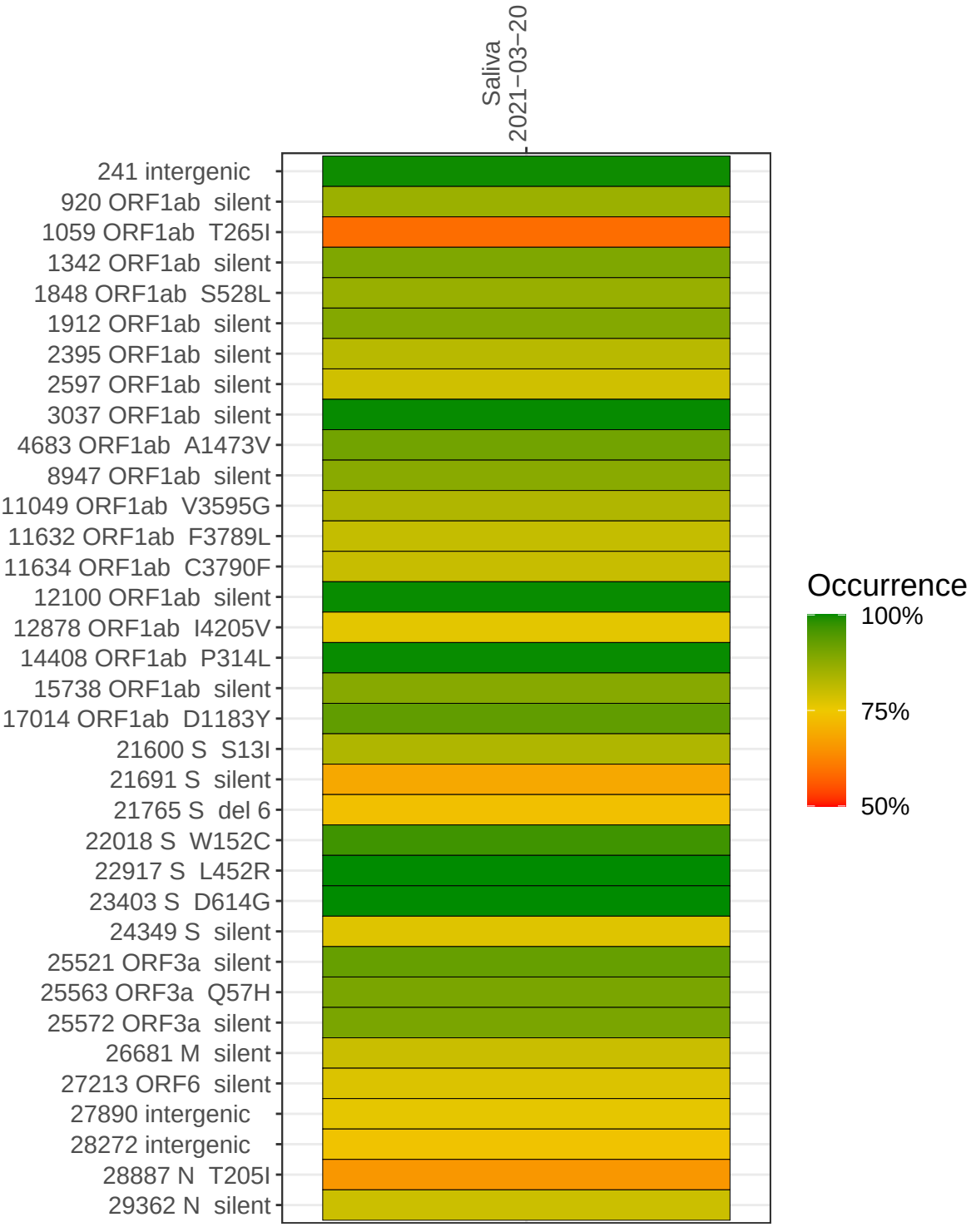
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

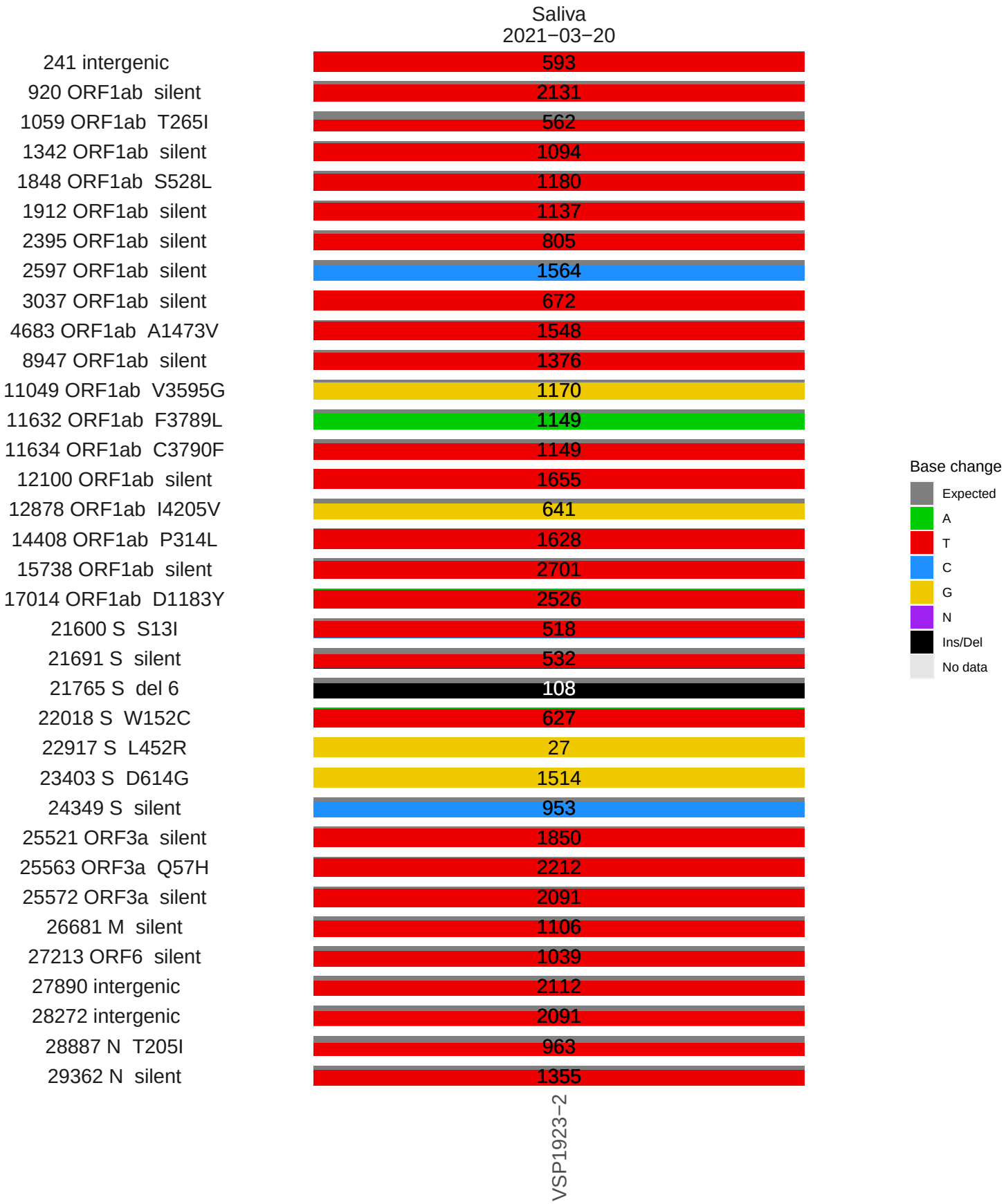
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1923-2	single experiment	NA	Saliva	2021-03-20	29.67	B.1.429	99.3%	99.3%

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.

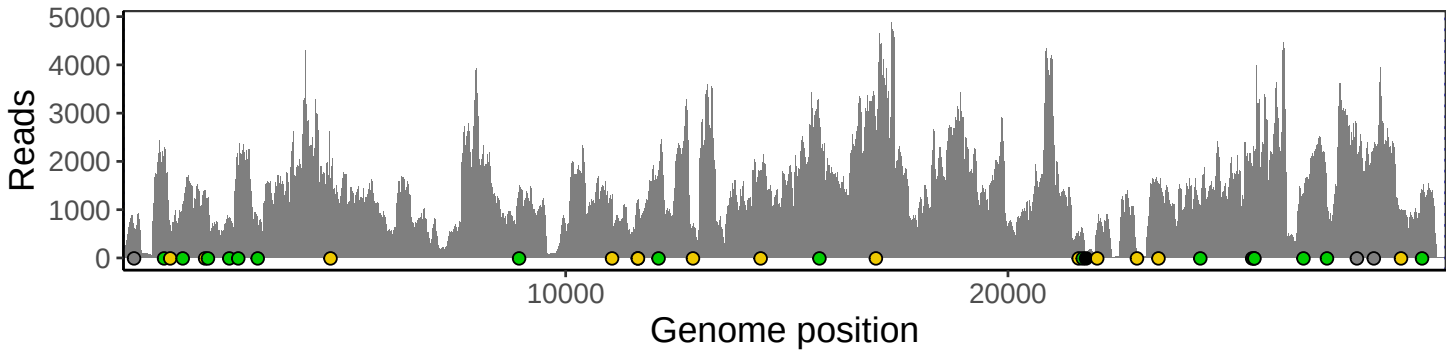



Saliva
2021−03−20
241 intergenic
920 ORF1ab silent
1059 ORF1ab T265I
1342 ORF1ab silent
1848 ORF1ab S528L
1912 ORF1ab silent
2395 ORF1ab silent
2597 ORF1ab silent
3037 ORF1ab silent
4683 ORF1ab A1473V
8947 ORF1ab silent
11049 ORF1ab V3595G
11632 ORF1ab F3789L
11634 ORF1ab C3790F
12100 ORF1ab silent
12878 ORF1ab I4205V
14408 ORF1ab P314L
15738 ORF1ab silent
17014 ORF1ab D1183Y
21600 S S13I
21691 S silent
21765 S del 6
22018 S W152C
22917 S L452R
23403 S D614G
24349 S silent
25521 ORF3a silent
25563 ORF3a Q57H
25572 ORF3a silent
26681 M silent
27213 ORF6 silent
27890 intergenic
28272 intergenic
28887 N T205I
29362 N silent
593
2131
562
1094
1180
1137
805
1564
672
1548
1376
1170
1149
1149
1655
641
1628
2701
2526
518
532
108
627
27
1514
953
1850
2212
2091
1106
1039
2112
2091
963
1355
VSP1923−2
Base change
Expected
A
T
C
G
N
Ins/Del
No data

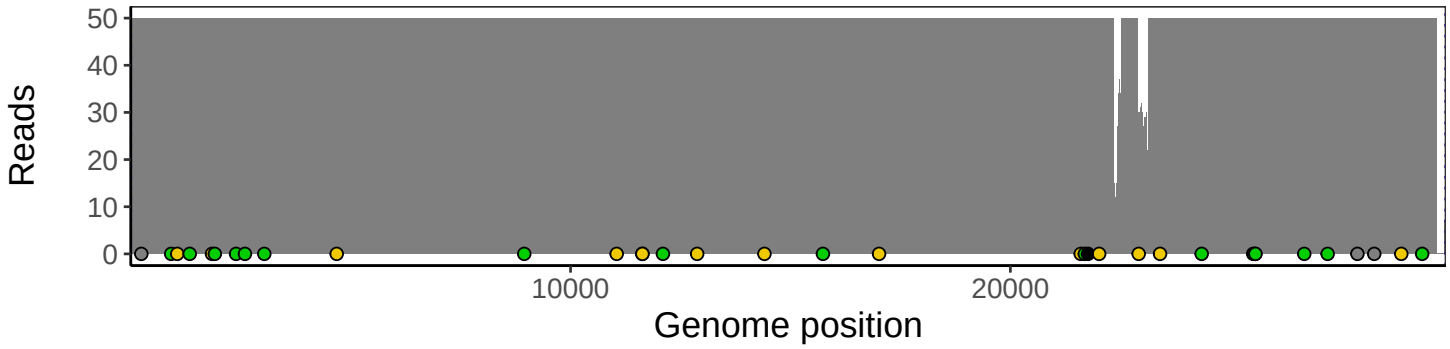
Analyses of individual experiments and composite results

VSP1923-2 | 2021-03-20 | Saliva | UPHS-0705 | genomes | single experiment

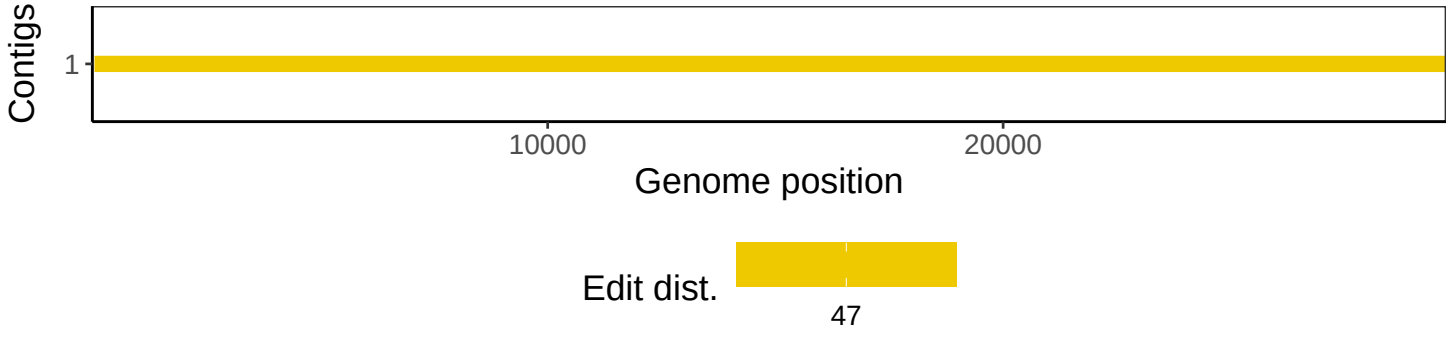
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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