COVID-19 subject 511

2021-05-21

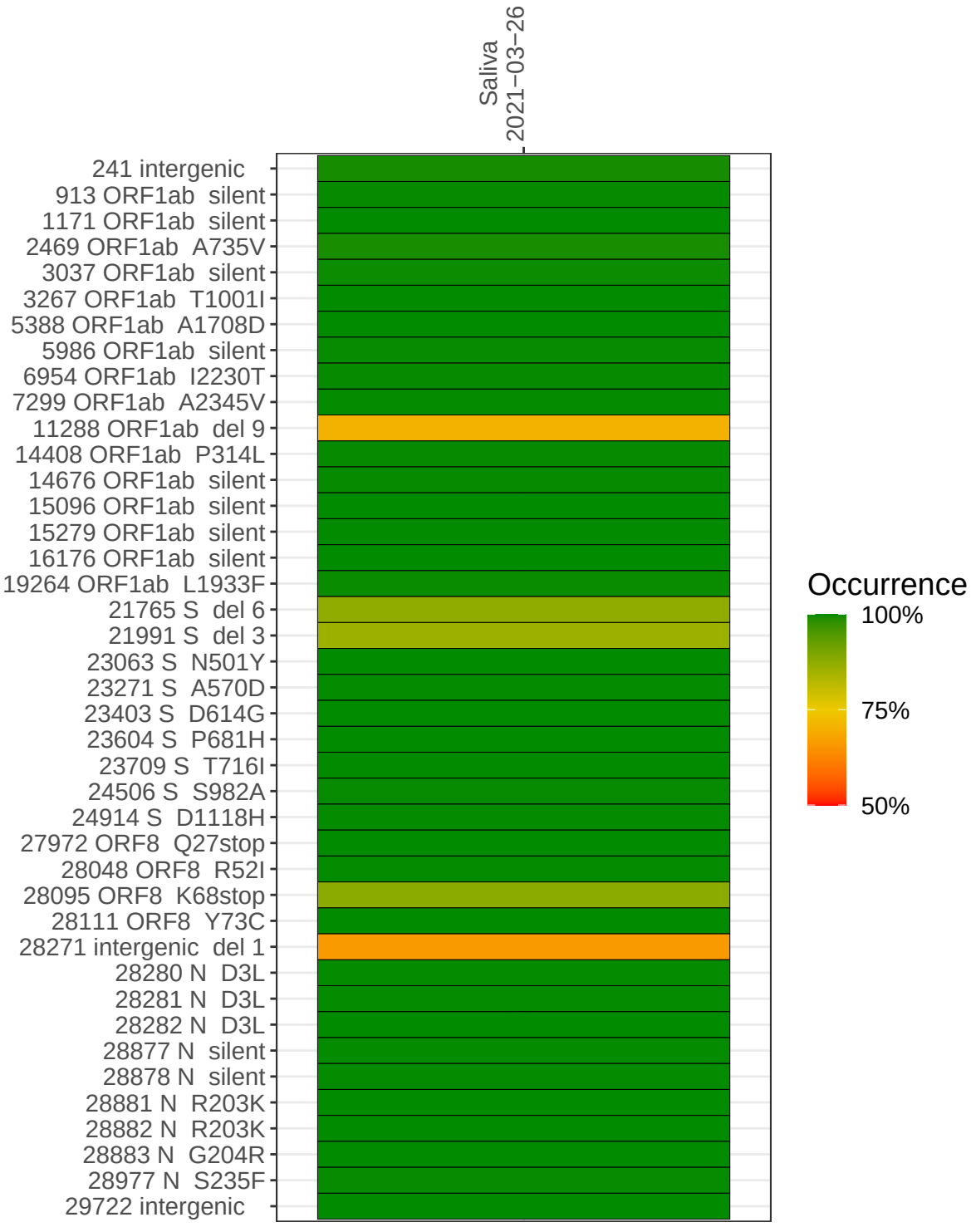
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

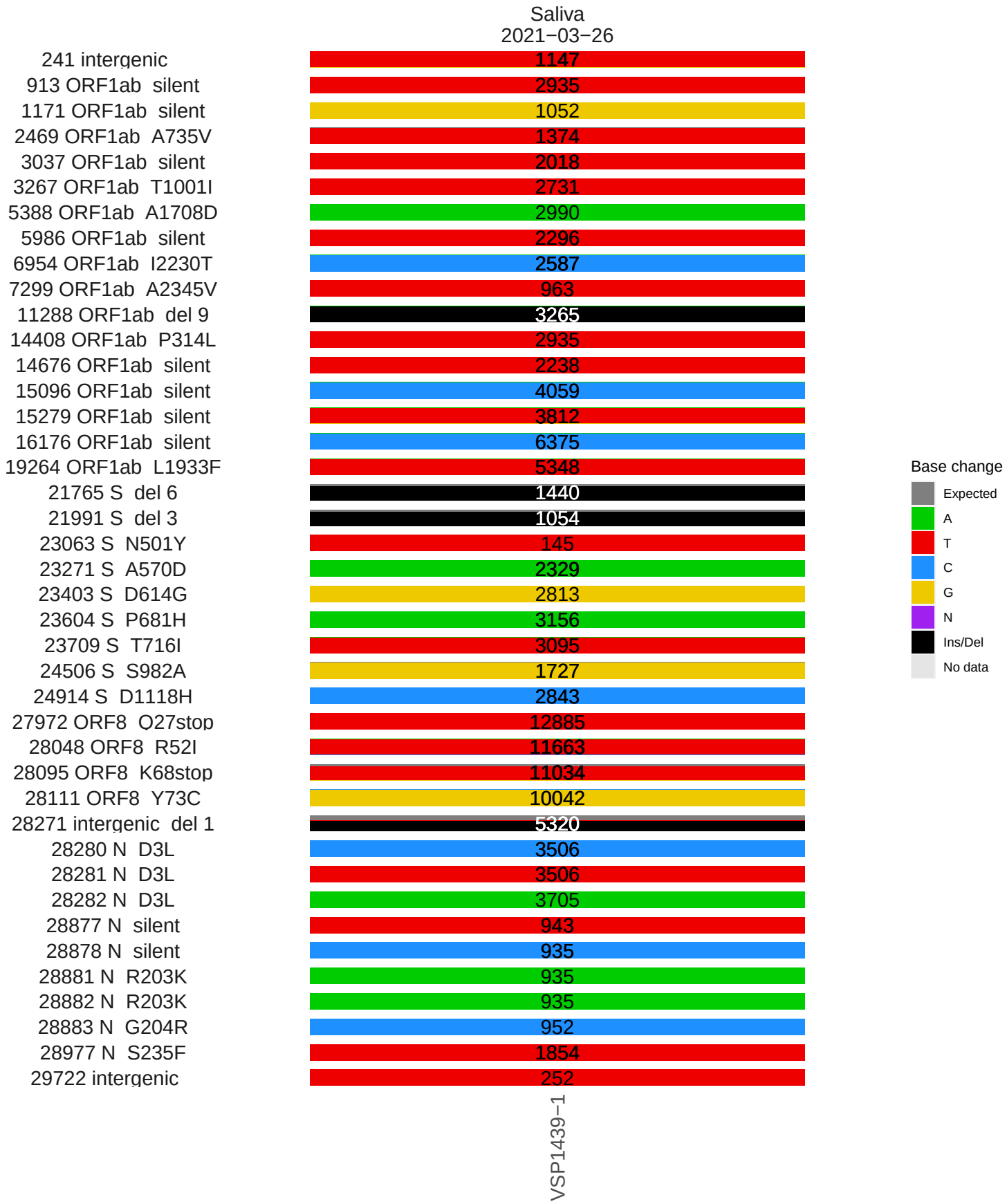
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1439-1	single experiment	NA	Saliva	2021-03-26	29.82	B.1.1.7	99.8%	99.8%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/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.

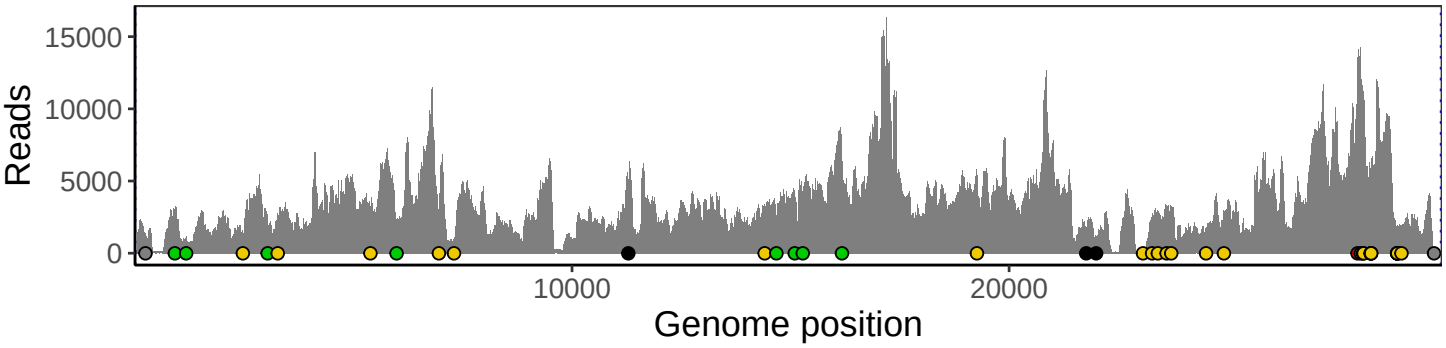



Saliva
2021−03−26
241 intergenic 1147
913 ORF1ab silent 2935
1171 ORF1ab silent 1052
2469 ORF1ab A735V 1374
3037 ORF1ab silent 2018
3267 ORF1ab T1001I 2731
5388 ORF1ab A1708D 2990
5986 ORF1ab silent 2296
6954 ORF1ab I2230T 2587
7299 ORF1ab A2345V 963
11288 ORF1ab del 9 3265
14408 ORF1ab P314L 2935
14676 ORF1ab silent 2238
15096 ORF1ab silent 4059
15279 ORF1ab silent 3812
16176 ORF1ab silent 6375
19264 ORF1ab L1933F 5348
21765 S del 6 1440
21991 S del 3 1054
23063 S N501Y 145
23271 S A570D 2329
23403 S D614G 2813
23604 S P681H 3156
23709 S T716I 3095
24506 S S982A 1727
24914 S D1118H 2843
27972 ORF8 Q27stop 12885
28048 ORF8 R52I 11663
28095 ORF8 K68stop 11034
28111 ORF8 Y73C 10042
28271 intergenic del 1 5320
28280 N D3L 3506
28281 N D3L 3506
28282 N D3L 3705
28877 N silent 943
28878 N silent 935
28881 N R203K 935
28882 N R203K 935
28883 N G204R 952
28977 N S235F 1854
29722 intergenic 252
VSP1439−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

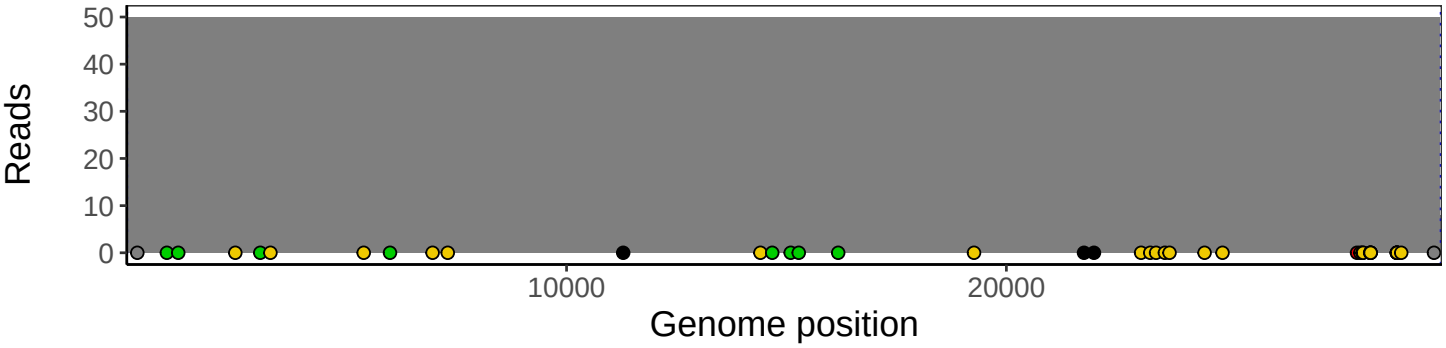
Analyses of individual experiments and composite results

VSP1439-1 | 2021-03-26 | Saliva | 511s | genomes | single experiment

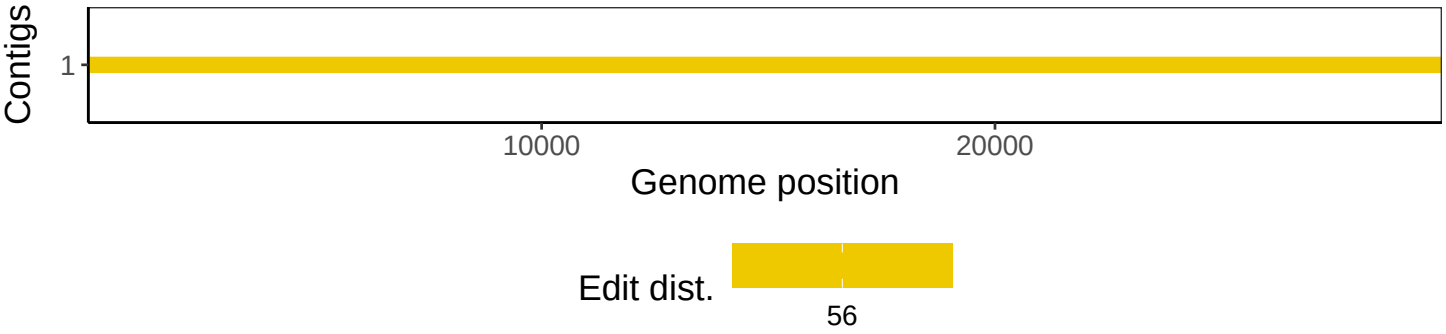
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.8
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