COVID-19 subject UPHS-0738

2021-05-05

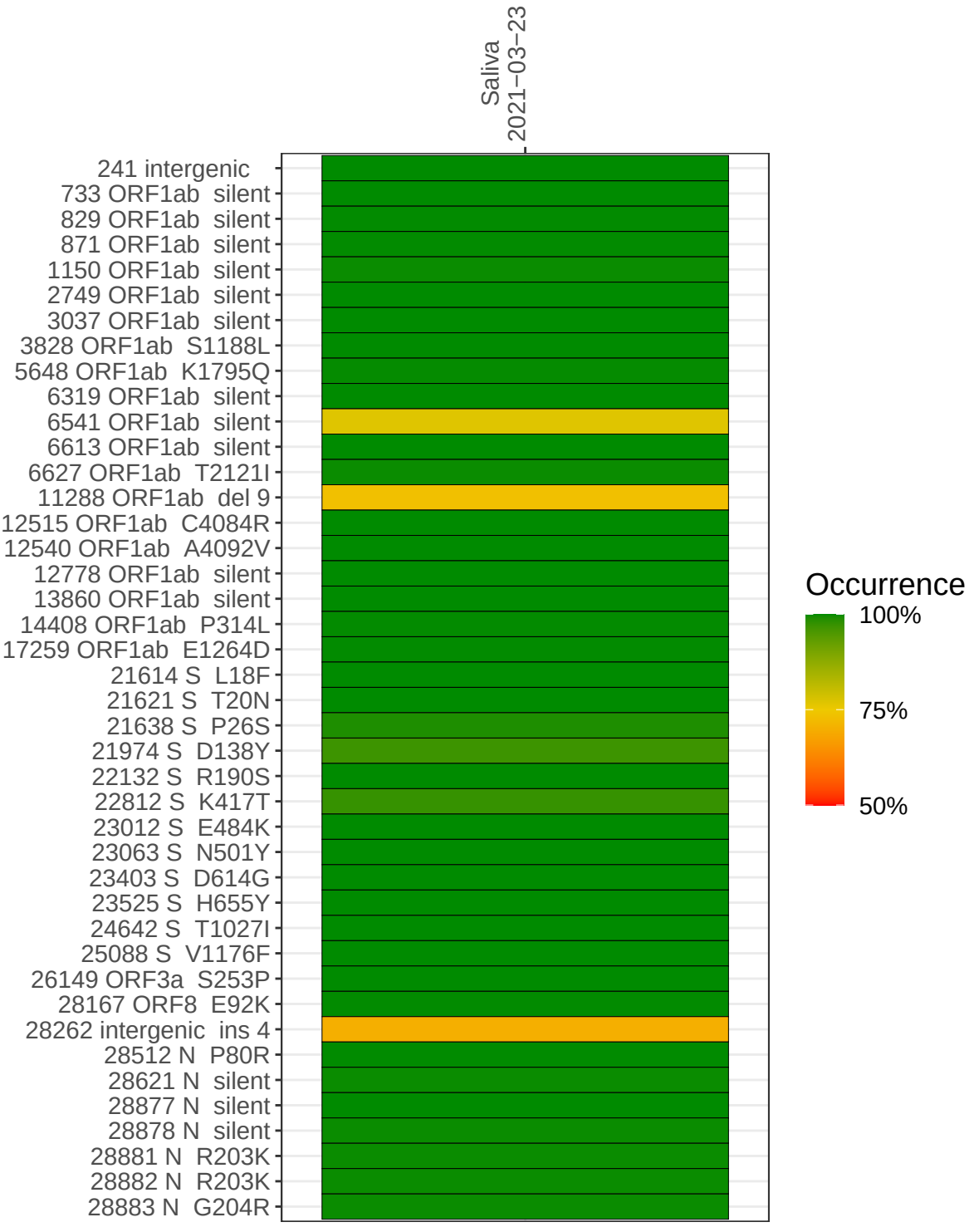
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

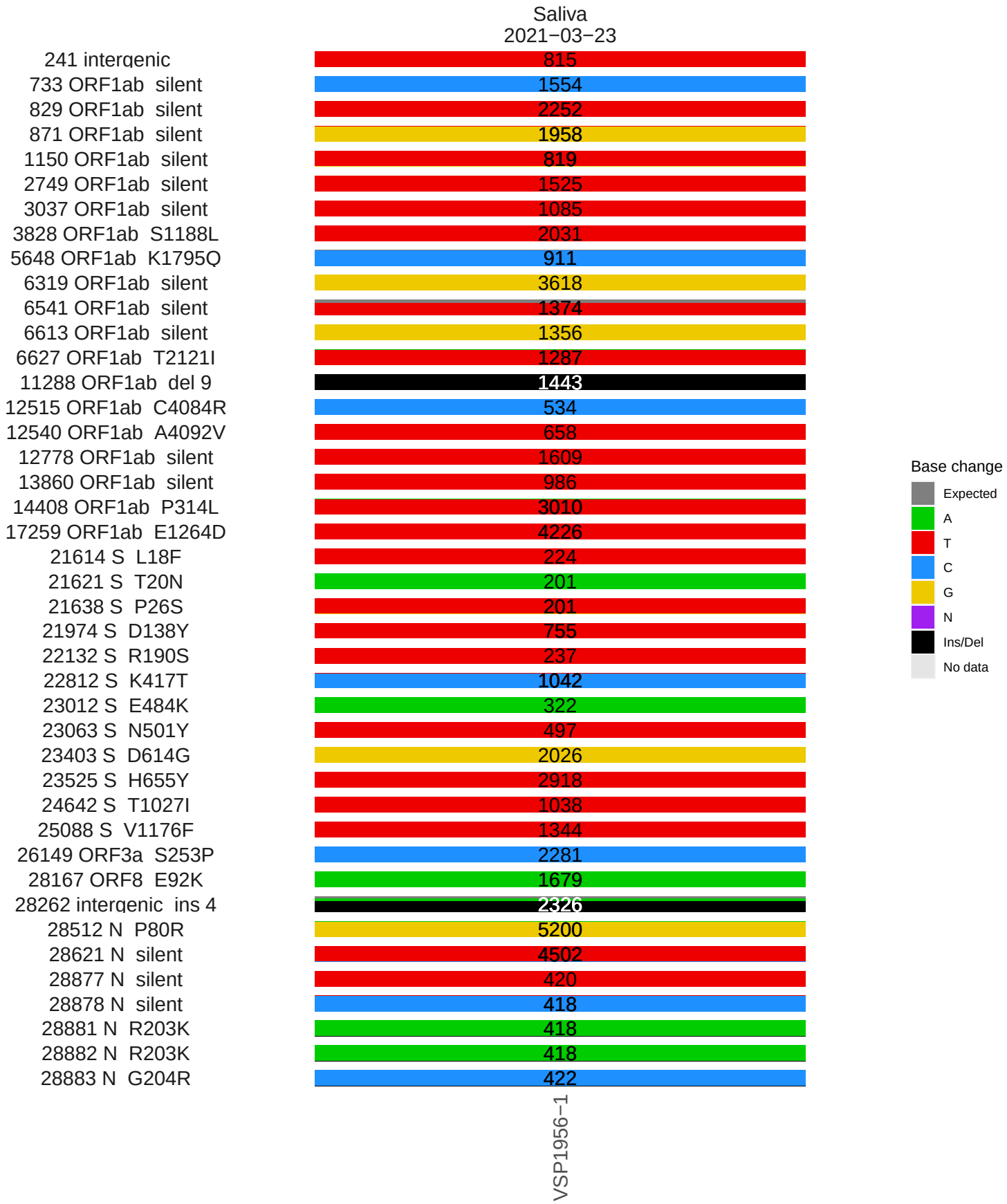
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1956-1	single experiment	NA	Saliva	2021-03-23	9.44	NA	93.9%	93.7%

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.

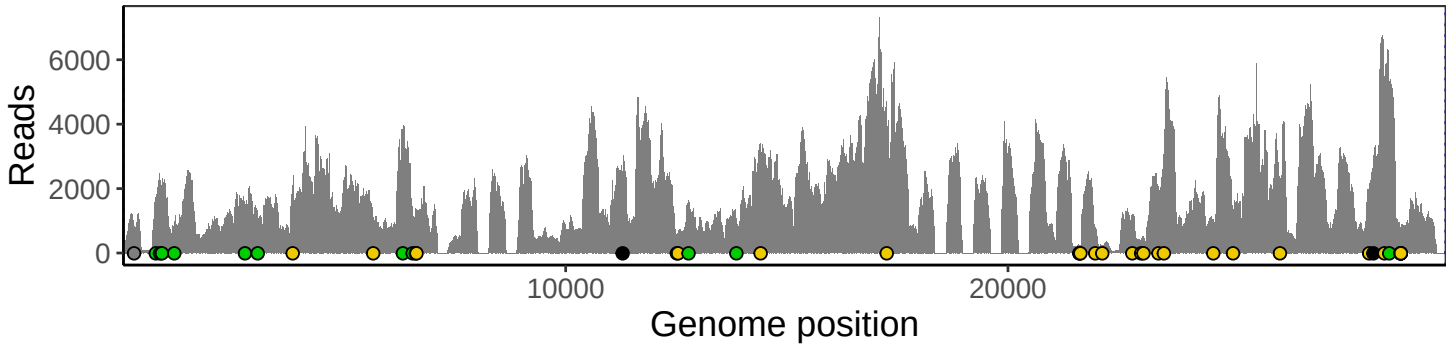



Saliva
2021−03−23
241 intergenic
733 ORF1ab silent
829 ORF1ab silent
871 ORF1ab silent
1150 ORF1ab silent
2749 ORF1ab silent
3037 ORF1ab silent
3828 ORF1ab S1188L
5648 ORF1ab K1795Q
6319 ORF1ab silent
6541 ORF1ab silent
6613 ORF1ab silent
6627 ORF1ab T2121I
11288 ORF1ab del 9
12515 ORF1ab C4084R
12540 ORF1ab A4092V
12778 ORF1ab silent
13860 ORF1ab silent
14408 ORF1ab P314L
17259 ORF1ab E1264D
21614 S L18F
21621 S T20N
21638 S P26S
21974 S D138Y
22132 S R190S
22812 S K417T
23012 S E484K
23063 S N501Y
23403 S D614G
23525 S H655Y
24642 S T1027I
25088 S V1176F
26149 ORF3a S253P
28167 ORF8 E92K
28262 intergenic ins 4
28512 N P80R
28621 N silent
28877 N silent
28878 N silent
28881 N R203K
28882 N R203K
28883 N G204R
815
1554
2252
1958
819
1525
1085
2031
911
3618
1374
1356
1287
1443
534
658
1609
986
3010
4226
224
201
201
755
237
1042
322
497
2026
2918
1038
1344
2281
1679
2326
5200
4502
420
418
418
418
422
VSP1956−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

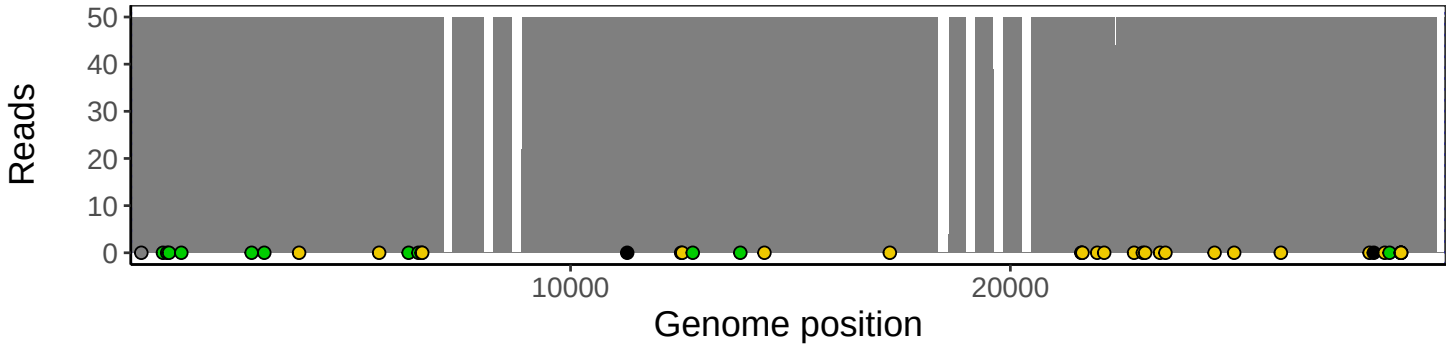
Analyses of individual experiments and composite results

VSP1956-1 | 2021-03-23 | Saliva | UPHS-0738 | genomes | single experiment

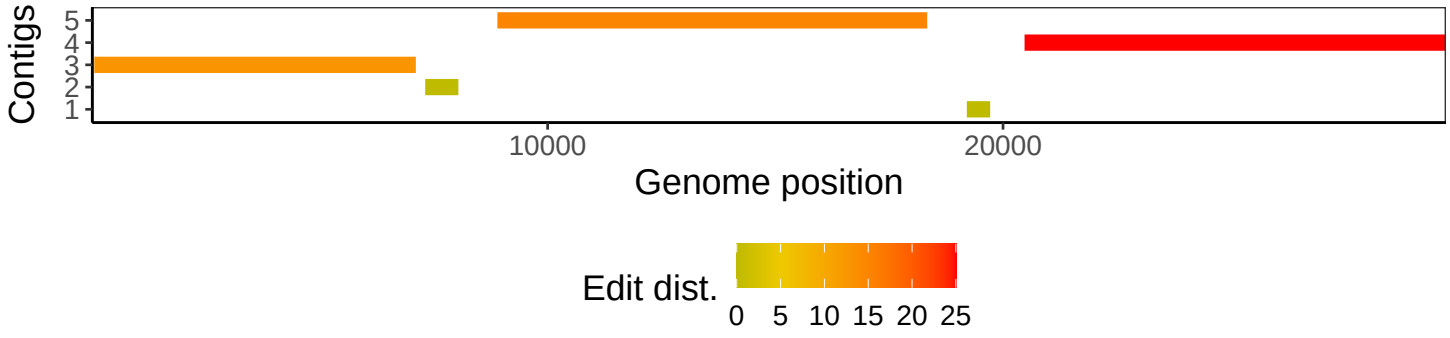
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.0.0
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