COVID-19 subject UPHS-0739

2021-05-05

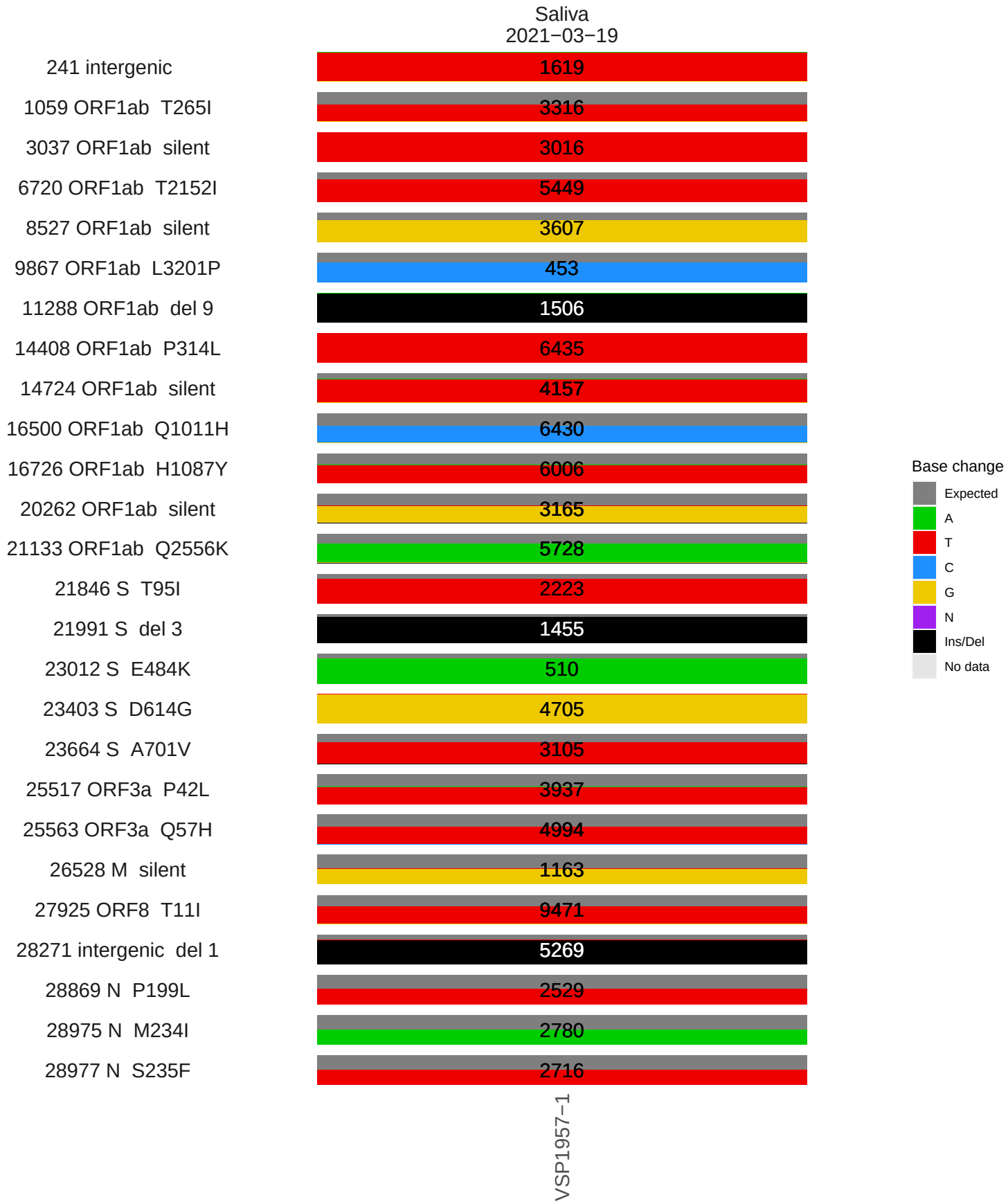
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1957-1	single experiment	NA	Saliva	2021-03-19	29.69	B.1.526	99.3%	99.3%

Variants shared across samples

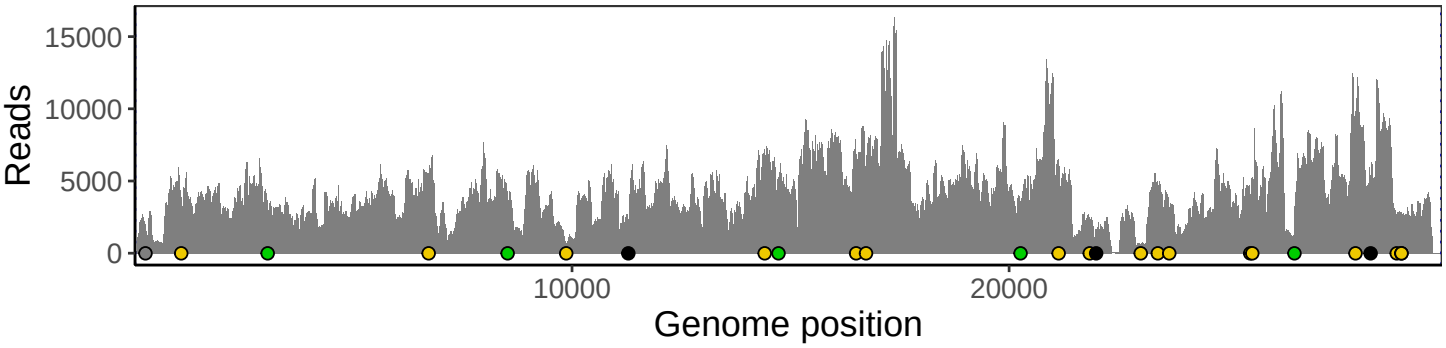
The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) are shared across subject samples where the percent variance is colored. Variants are called if a variant position is covered by 5 or more reads, the alternative base is found in > 50% of 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
2021−03−19
241 intergenic
1059 ORF1ab T265I
3037 ORF1ab silent
6720 ORF1ab T2152I
8527 ORF1ab silent
9867 ORF1ab L3201P
11288 ORF1ab del 9
14408 ORF1ab P314L
14724 ORF1ab silent
16500 ORF1ab Q1011H
16726 ORF1ab H1087Y
20262 ORF1ab silent
21133 ORF1ab Q2556K
21846 S T95I
21991 S del 3
23012 S E484K
23403 S D614G
23664 S A701V
25517 ORF3a P42L
25563 ORF3a Q57H
26528 M silent
27925 ORF8 T11I
28271 intergenic del 1
28869 N P199L
28975 N M234I
28977 N S235F
1619
3316
3016
5449
3607
453
1506
6435
4157
6430
6006
3165
5728
2223
1455
510
4705
3105
3937
4994
1163
9471
5269
2529
2780
2716
VSP1957−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

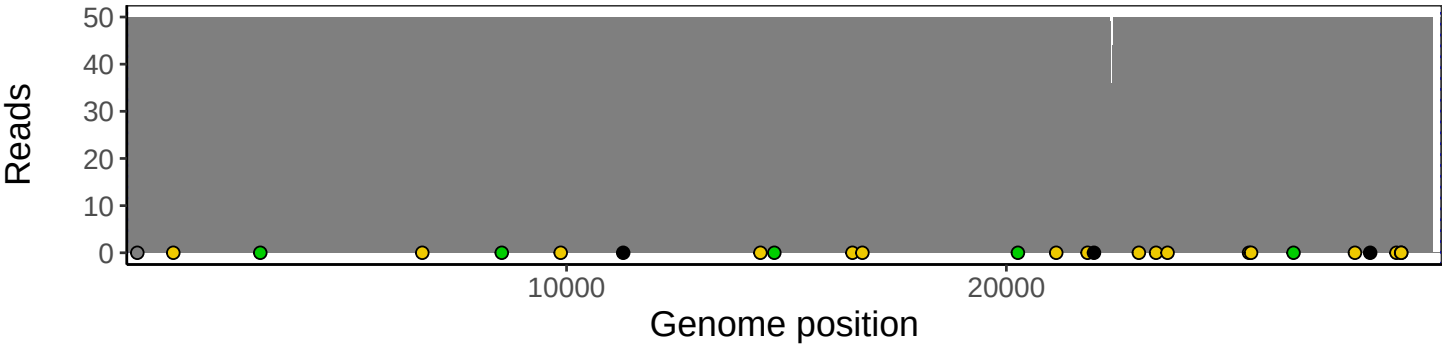
Analyses of individual experiments and composite results

VSP1957-1 | 2021-03-19 | Saliva | UPHS-0739 | genomes | single experiment

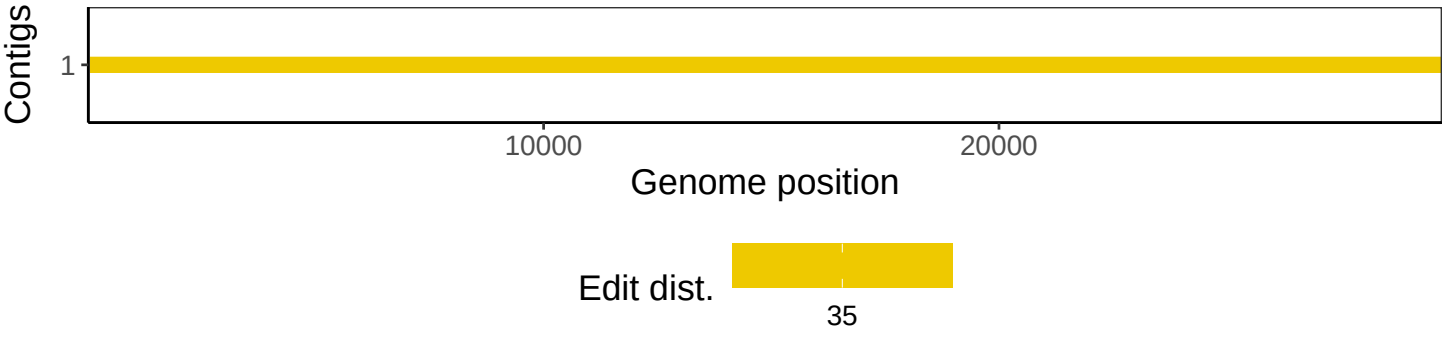
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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