COVID-19 subject UPHS-0742

2021-04-20

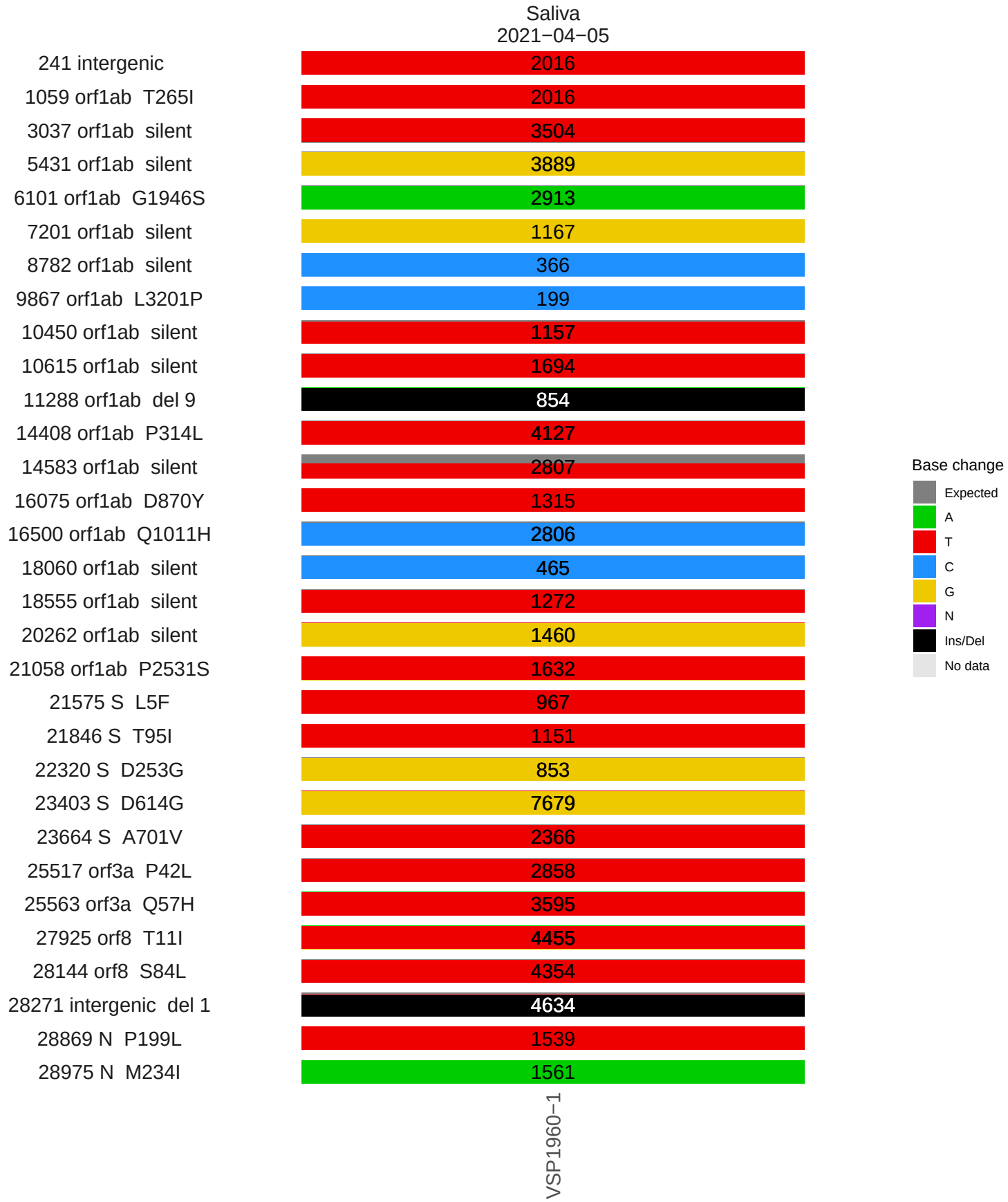
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1960-1	single experiment	NA	Saliva	2021-04-05	29.71	B.1.526	99.2%	99.2%

Variants shared across samples

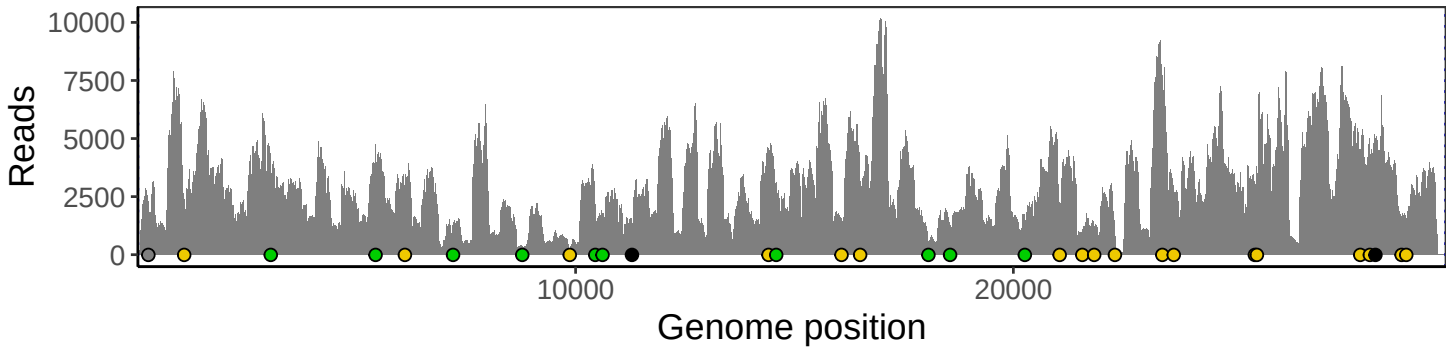
The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/USA-WA1-2020) are shared across subject samples where the percent variance is colored. Variants are called if a variant position is covered by 5 or more reads, the alternative base is found in > 50% 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
2021−04−05
241 intergenic
2016
1059 orf1ab T265I
2016
3037 orf1ab silent
3504
5431 orf1ab silent
3889
6101 orf1ab G1946S
2913
7201 orf1ab silent
1167
8782 orf1ab silent
366
9867 orf1ab L3201P
199
10450 orf1ab silent
1157
10615 orf1ab silent
1694
11288 orf1ab del 9
854
14408 orf1ab P314L
4127
14583 orf1ab silent
2807
16075 orf1ab D870Y
1315
16500 orf1ab Q1011H
2806
18060 orf1ab silent
465
18555 orf1ab silent
1272
20262 orf1ab silent
1460
21058 orf1ab P2531S
1632
21575 S L5F
967
21846 S T95I
1151
22320 S D253G
853
23403 S D614G
7679
23664 S A701V
2366
25517 orf3a P42L
2858
25563 orf3a Q57H
3595
27925 orf8 T11I
4455
28144 orf8 S84L
4354
28271 intergenic del 1
4634
28869 N P199L
1539
28975 N M234I
1561
VSP1960−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

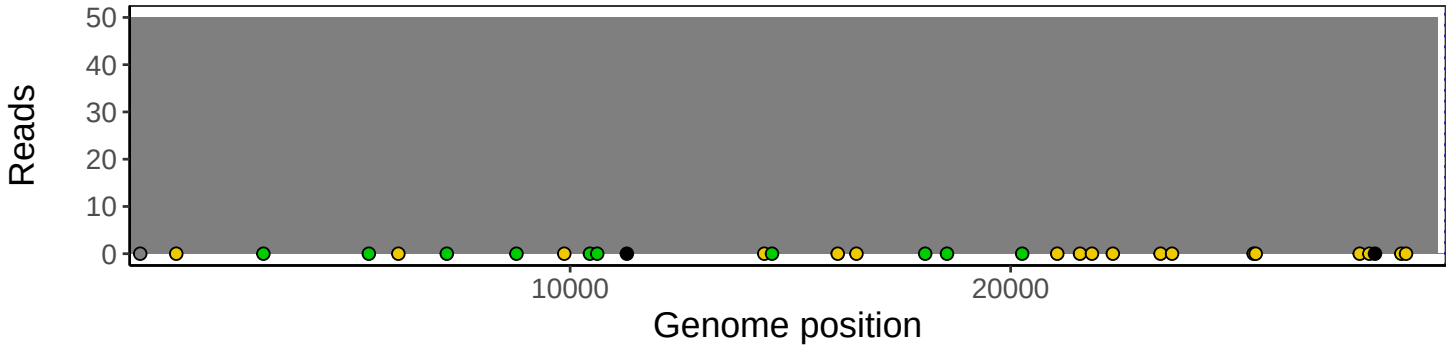
Analyses of individual experiments and composite results

VSP1960-1 | 2021-04-05 | Saliva | UPHS-0742 | genomes | single experiment

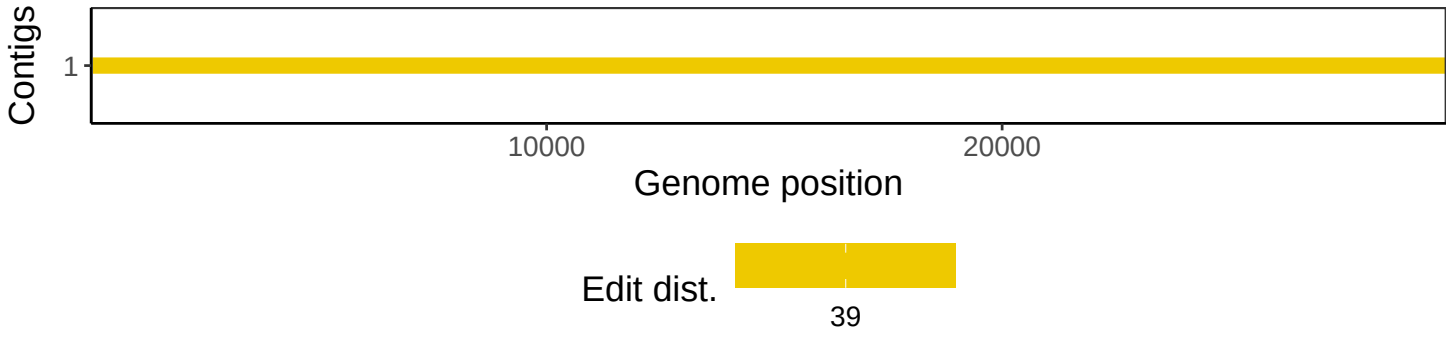
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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