COVID-19 subject UPHS-0748

2021-05-05

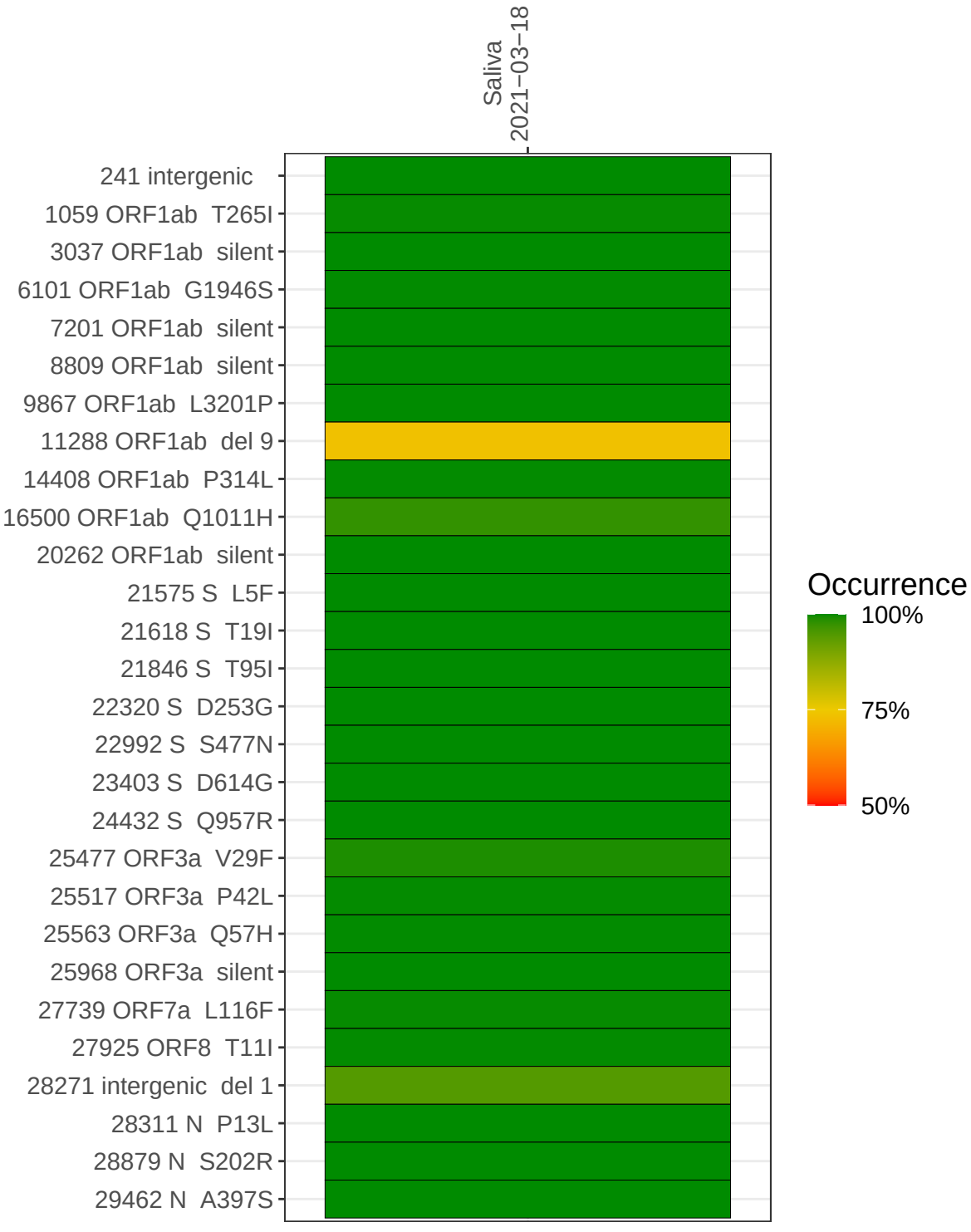
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

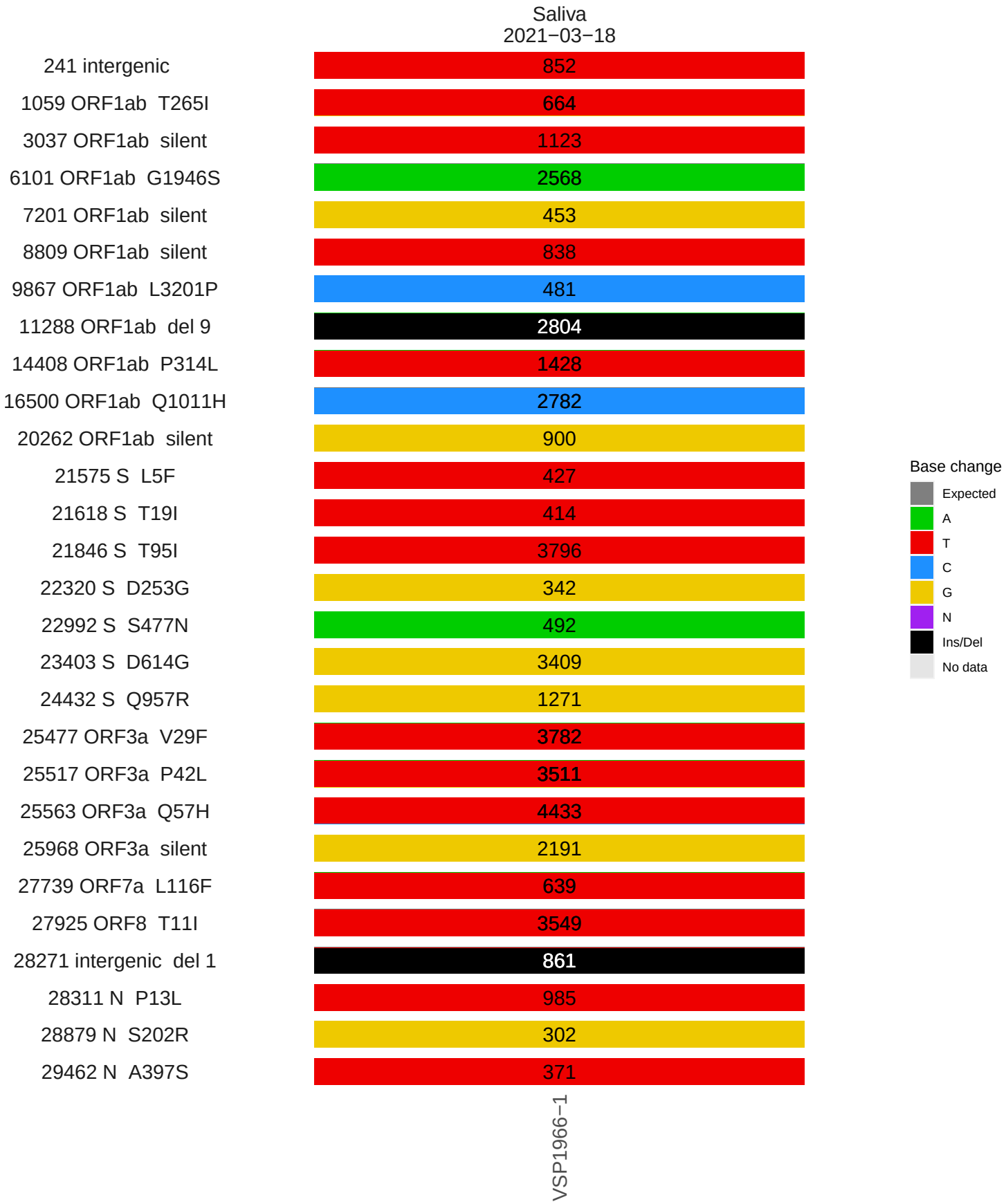
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1966-1	single experiment	NA	Saliva	2021-03-18	23.79	B.1.526.2	97.0%	96.9%

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.

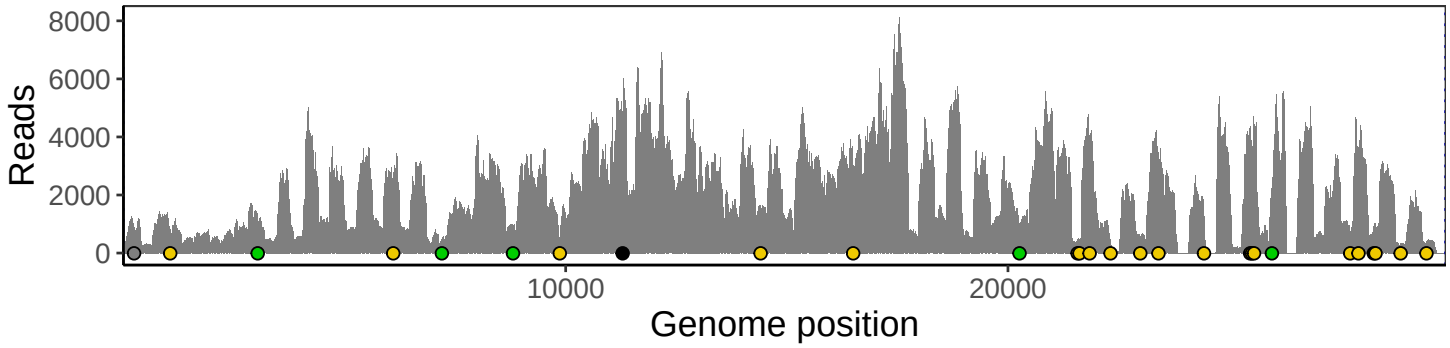



Saliva
2021−03−18
241 intergenic
852
1059 ORF1ab T265I
664
3037 ORF1ab silent
1123
6101 ORF1ab G1946S
2568
7201 ORF1ab silent
453
8809 ORF1ab silent
838
9867 ORF1ab L3201P
481
11288 ORF1ab del 9
2804
14408 ORF1ab P314L
1428
16500 ORF1ab Q1011H
2782
20262 ORF1ab silent
900
21575 S L5F
427
21618 S T19I
414
21846 S T95I
3796
22320 S D253G
342
22992 S S477N
492
23403 S D614G
3409
24432 S Q957R
1271
25477 ORF3a V29F
3782
25517 ORF3a P42L
3511
25563 ORF3a Q57H
4433
25968 ORF3a silent
2191
27739 ORF7a L116F
639
27925 ORF8 T11I
3549
28271 intergenic del 1
861
28311 N P13L
985
28879 N S202R
302
29462 N A397S
371
VSP1966−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

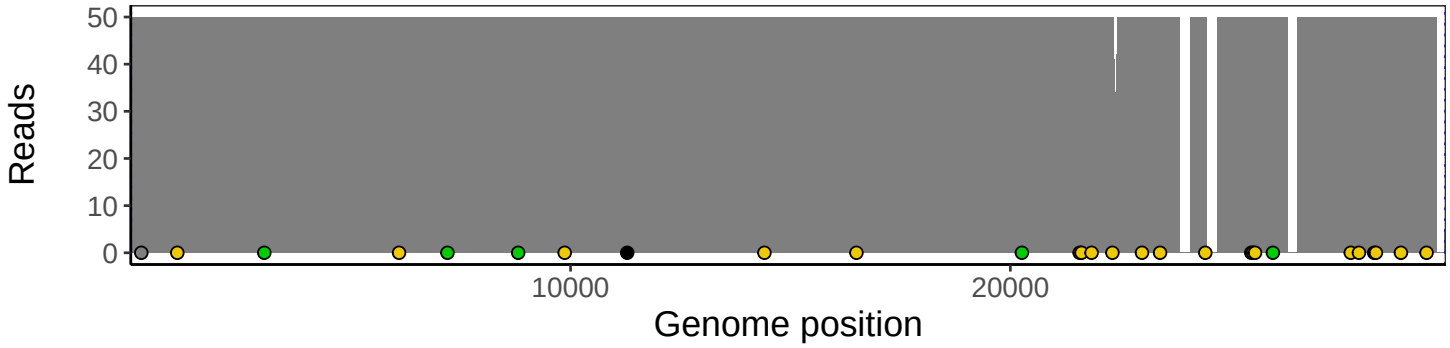
Analyses of individual experiments and composite results

VSP1966-1 | 2021-03-18 | Saliva | UPHS-0748 | genomes | single experiment

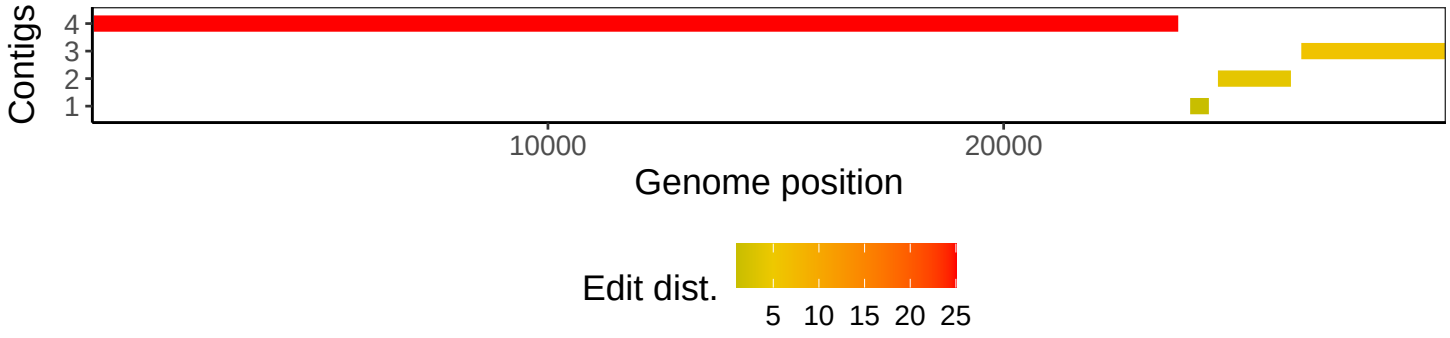
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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