COVID-19 subject UPHS-0731

2021-05-05

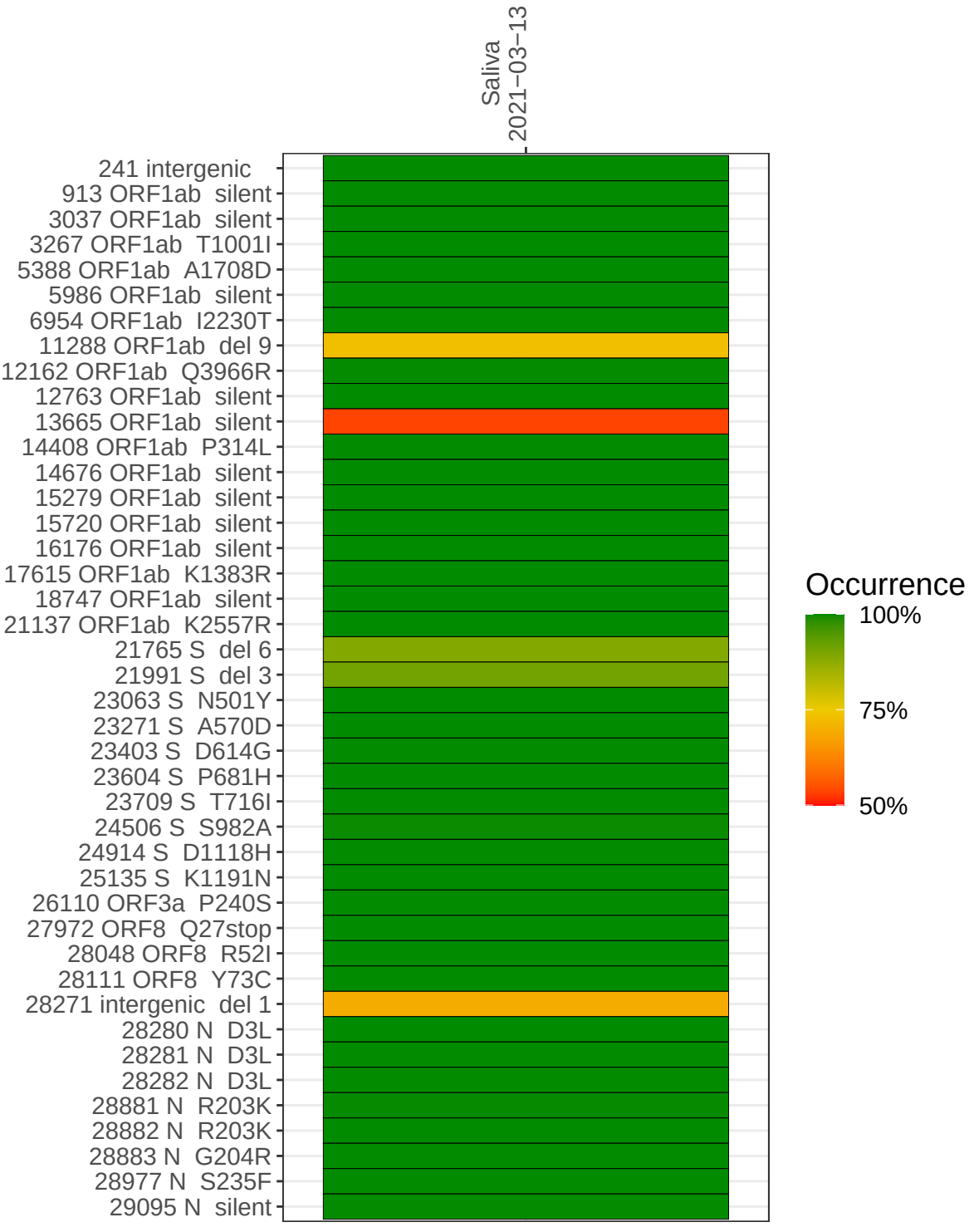
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

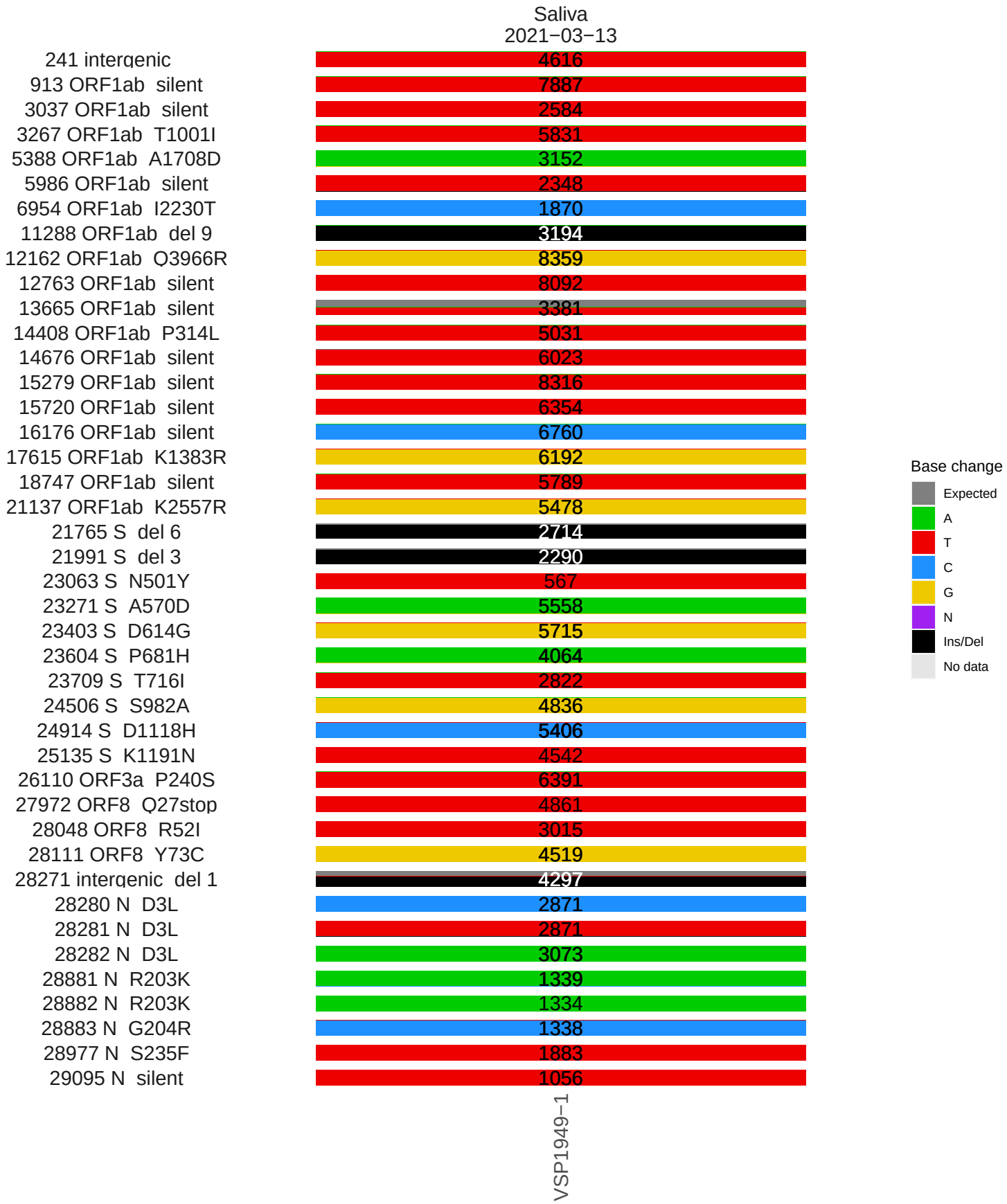
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1949-1	single experiment	NA	Saliva	2021-03-13	29.67	B.1.1.7	99.2%	99.1%

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.

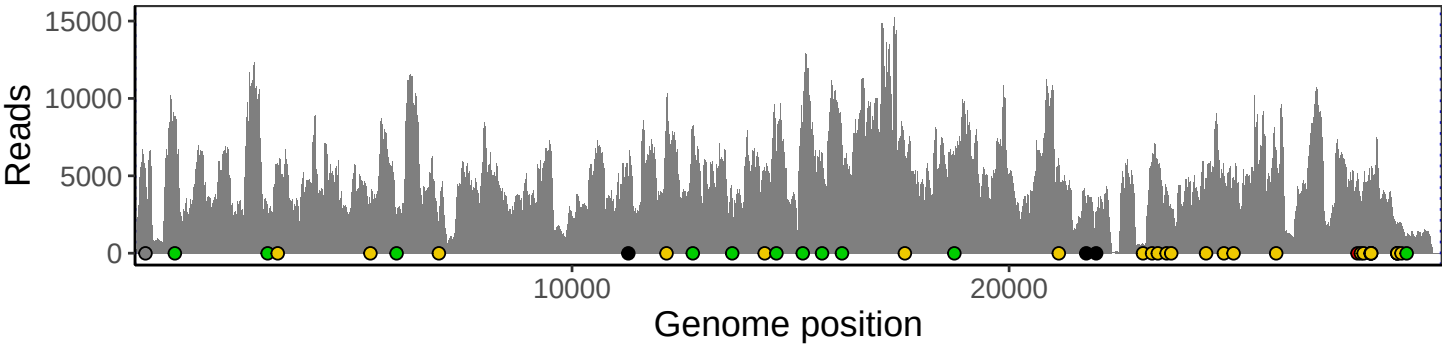



Saliva
2021−03−13
241 intergenic 4616
913 ORF1ab silent 7887
3037 ORF1ab silent 2584
3267 ORF1ab T1001I 5831
5388 ORF1ab A1708D 3152
5986 ORF1ab silent 2348
6954 ORF1ab I2230T 1870
11288 ORF1ab del 9 3194
12162 ORF1ab Q3966R 8359
12763 ORF1ab silent 8092
13665 ORF1ab silent 3381
14408 ORF1ab P314L 5031
14676 ORF1ab silent 6023
15279 ORF1ab silent 8316
15720 ORF1ab silent 6354
16176 ORF1ab silent 6760
17615 ORF1ab K1383R 6192
18747 ORF1ab silent 5789
21137 ORF1ab K2557R 5478
21765 S del 6 2714
21991 S del 3 2290
23063 S N501Y 567
23271 S A570D 5558
23403 S D614G 5715
23604 S P681H 4064
23709 S T716I 2822
24506 S S982A 4836
24914 S D1118H 5406
25135 S K1191N 4542
26110 ORF3a P240S 6391
27972 ORF8 Q27stop 4861
28048 ORF8 R52I 3015
28111 ORF8 Y73C 4519
28271 intergenic del 1 4297
28280 N D3L 2871
28281 N D3L 2871
28282 N D3L 3073
28881 N R203K 1339
28882 N R203K 1334
28883 N G204R 1338
28977 N S235F 1883
29095 N silent 1056
VSP1949−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

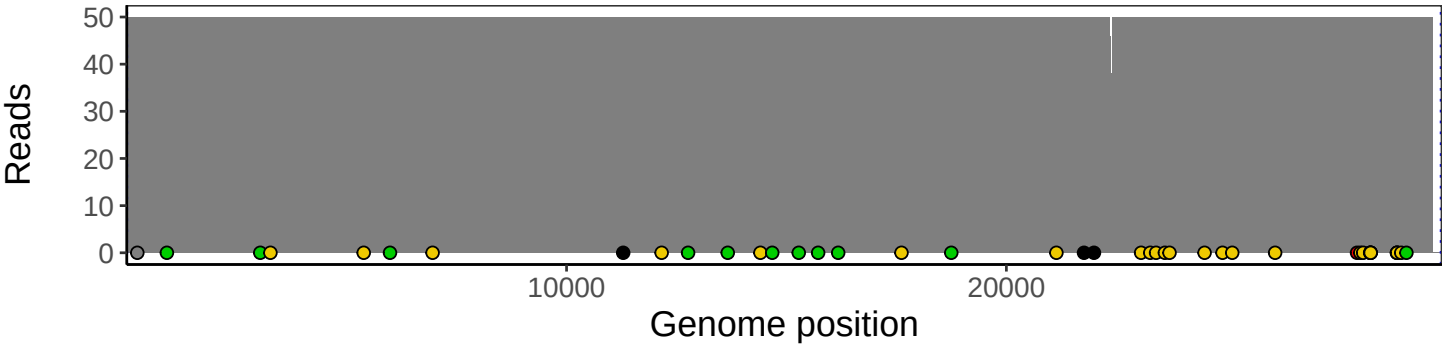
Analyses of individual experiments and composite results

VSP1949-1 | 2021-03-13 | Saliva | UPHS-0731 | genomes | single experiment

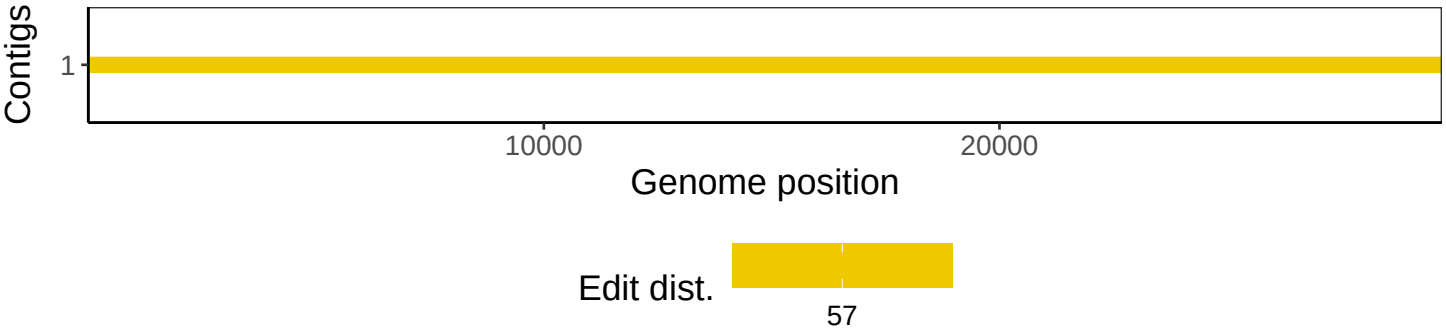
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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