COVID-19 subject UPHS-0677

2021-04-20

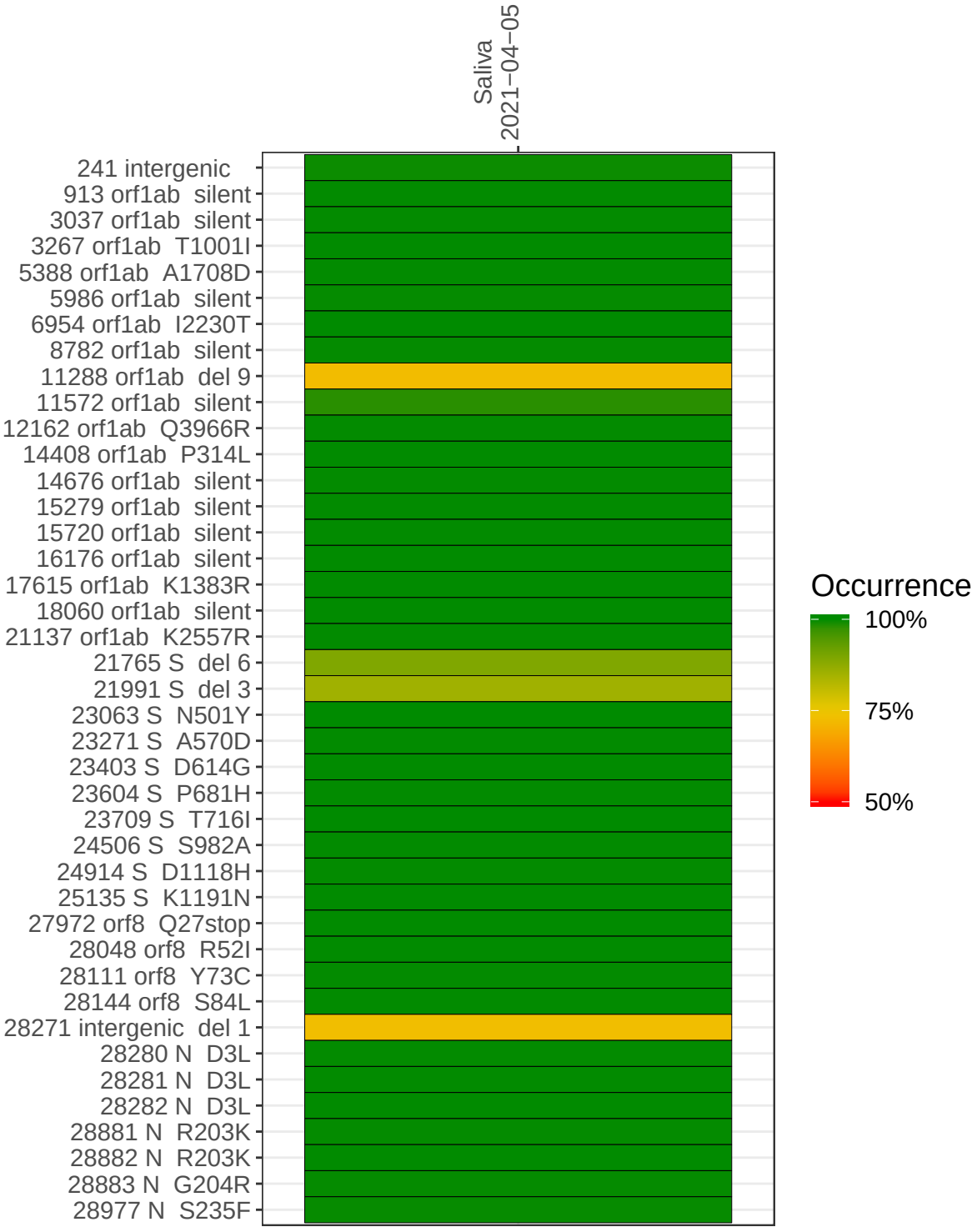
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

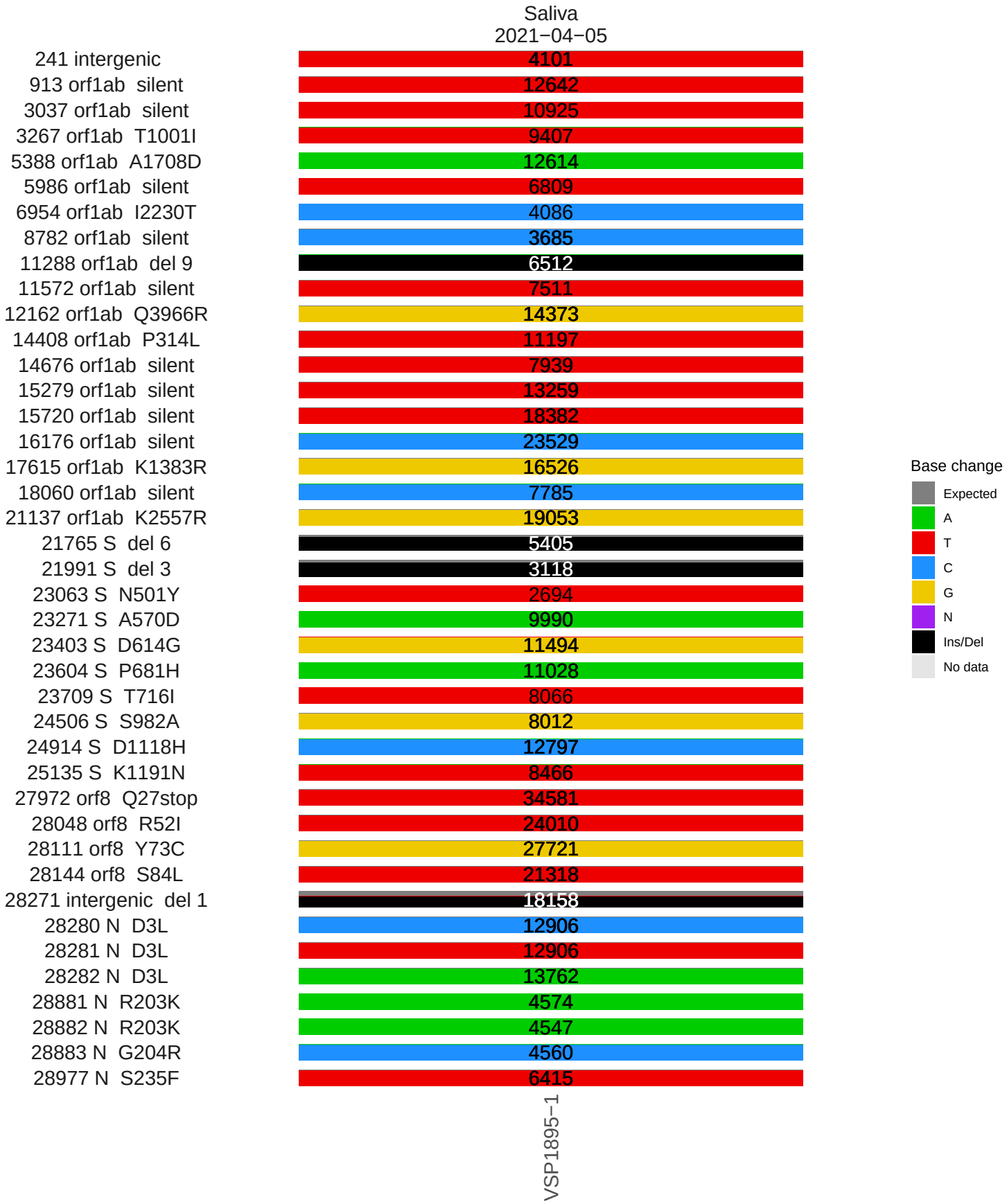
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1895-1	single experiment	NA	Saliva	2021-04-05	29.93	B.1.1.7	99.9%	99.9%

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.

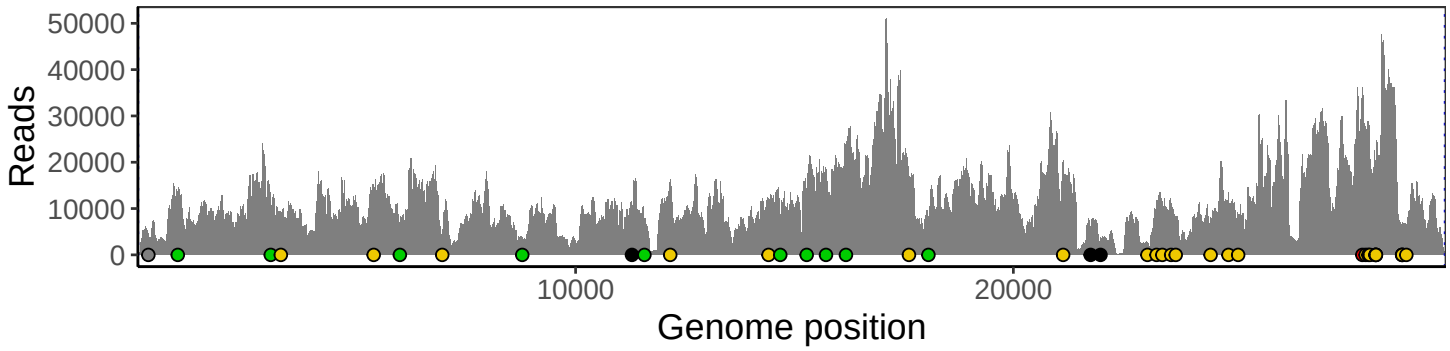



Saliva
2021−04−05
241 intergenic 4101
913 orf1ab silent 12642
3037 orf1ab silent 10925
3267 orf1ab T1001I 9407
5388 orf1ab A1708D 12614
5986 orf1ab silent 6809
6954 orf1ab I2230T 4086
8782 orf1ab silent 3685
11288 orf1ab del 9 6512
11572 orf1ab silent 7511
12162 orf1ab Q3966R 14373
14408 orf1ab P314L 11197
14676 orf1ab silent 7939
15279 orf1ab silent 13259
15720 orf1ab silent 18382
16176 orf1ab silent 23529
17615 orf1ab K1383R 16526
18060 orf1ab silent 7785
21137 orf1ab K2557R 19053
21765 S del 6 5405
21991 S del 3 3118
23063 S N501Y 2694
23271 S A570D 9990
23403 S D614G 11494
23604 S P681H 11028
23709 S T716I 8066
24506 S S982A 8012
24914 S D1118H 12797
25135 S K1191N 8466
27972 orf8 Q27stop 34581
28048 orf8 R52I 24010
28111 orf8 Y73C 27721
28144 orf8 S84L 21318
28271 intergenic del 1 18158
28280 N D3L 12906
28281 N D3L 12906
28282 N D3L 13762
28881 N R203K 4574
28882 N R203K 4547
28883 N G204R 4560
28977 N S235F 6415
VSP1895−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

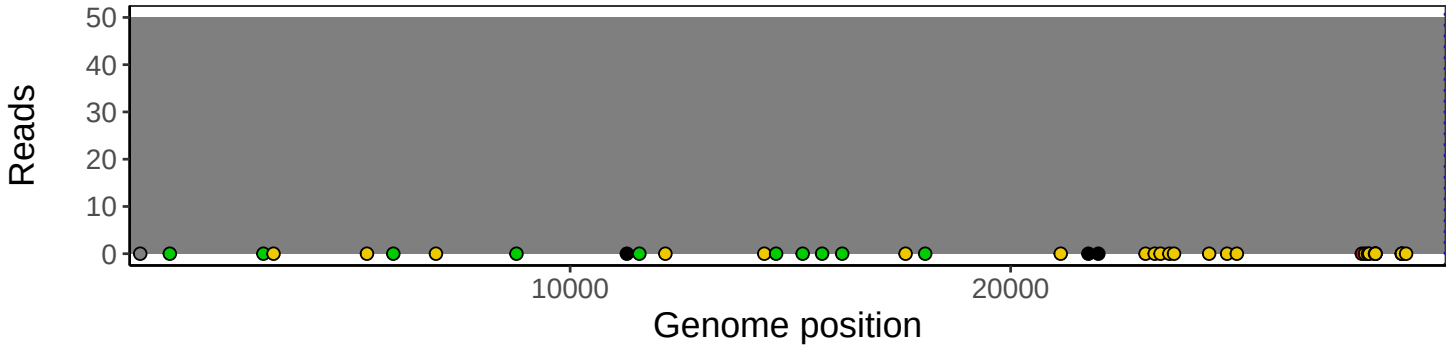
Analyses of individual experiments and composite results

VSP1895-1 | 2021-04-05 | Saliva | UPHS-0677 | genomes | single experiment

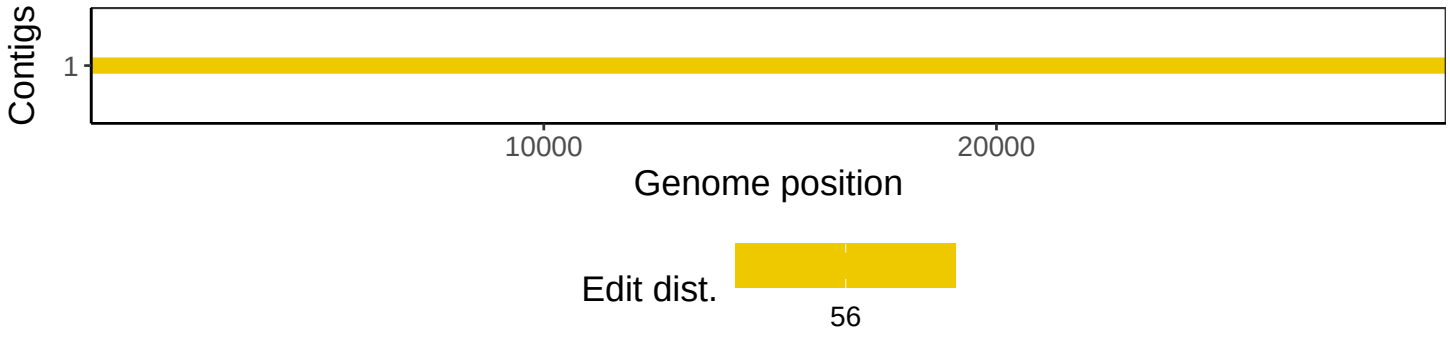
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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