COVID-19 subject UPHS-0716

2021-04-20

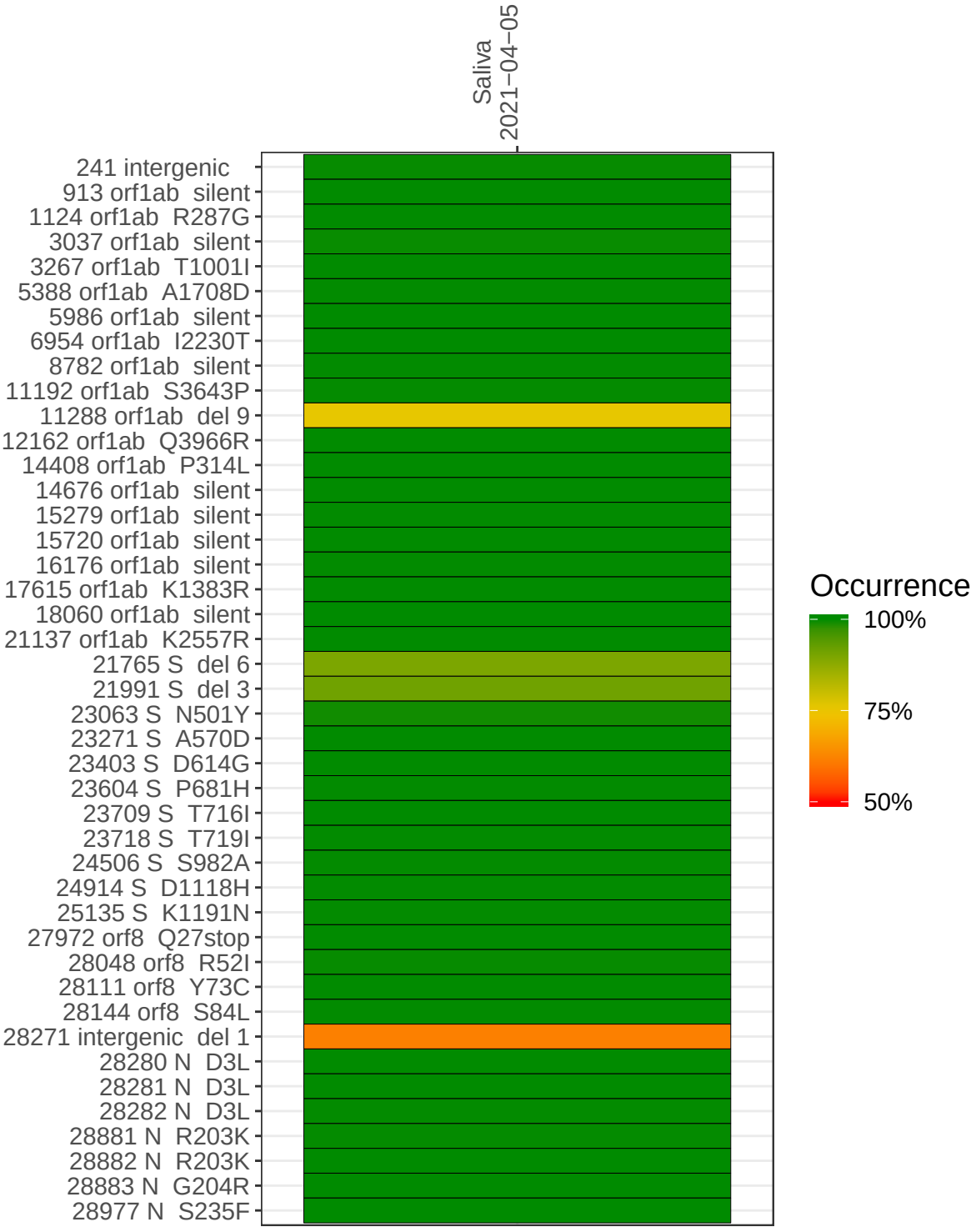
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

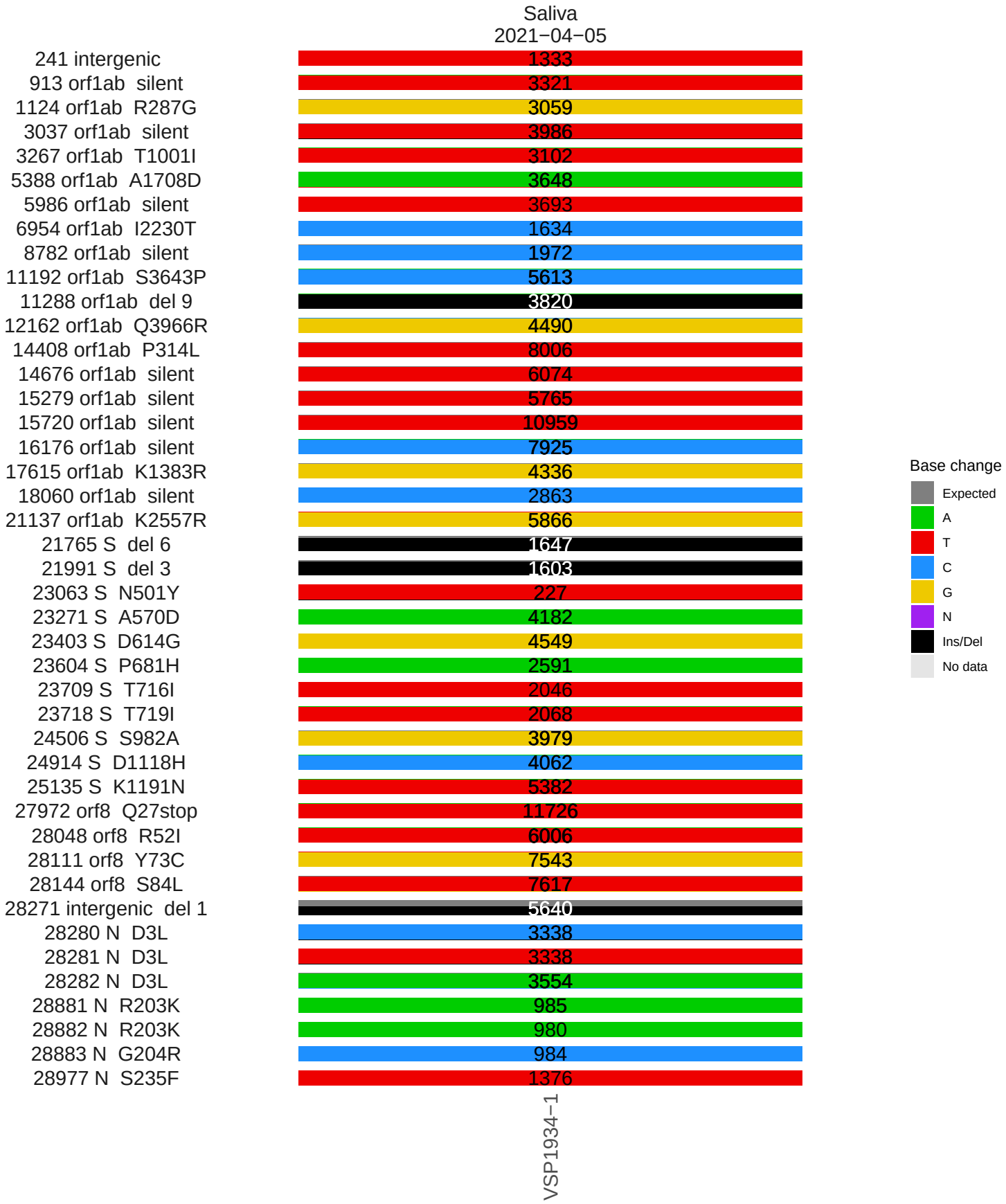
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1934-1	single experiment	NA	Saliva	2021-04-05	29.80	B.1.1.7	99.4%	99.4%

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.

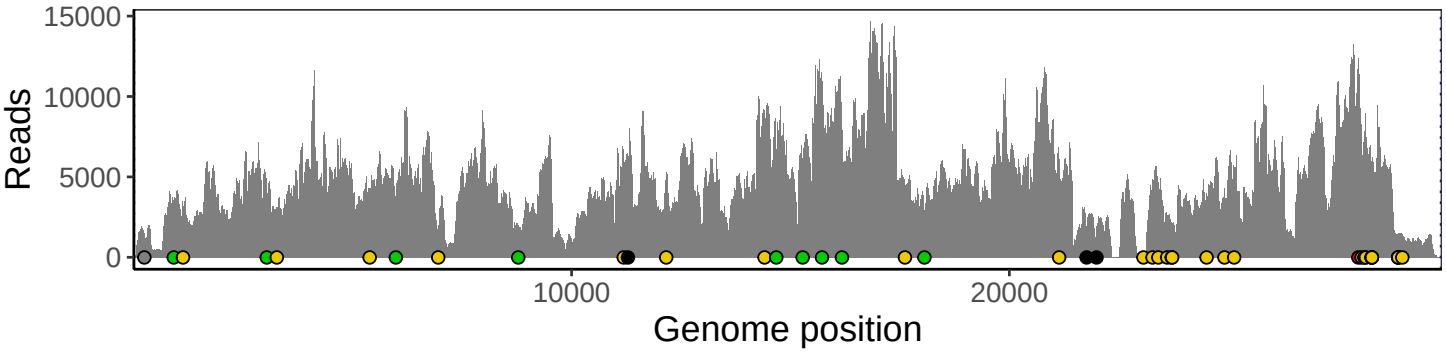



Saliva
2021−04−05
241 intergenic 1333
913 orf1ab silent 3321
1124 orf1ab R287G 3059
3037 orf1ab silent 3986
3267 orf1ab T1001I 3102
5388 orf1ab A1708D 3648
5986 orf1ab silent 3693
6954 orf1ab I2230T 1634
8782 orf1ab silent 1972
11192 orf1ab S3643P 5613
11288 orf1ab del 9 3820
12162 orf1ab Q3966R 4490
14408 orf1ab P314L 8006
14676 orf1ab silent 6074
15279 orf1ab silent 5765
15720 orf1ab silent 10959
16176 orf1ab silent 7925
17615 orf1ab K1383R 4336
18060 orf1ab silent 2863
21137 orf1ab K2557R 5866
21765 S del 6 1647
21991 S del 3 1603
23063 S N501Y 227
23271 S A570D 4182
23403 S D614G 4549
23604 S P681H 2591
23709 S T716I 2046
23718 S T719I 2068
24506 S S982A 3979
24914 S D1118H 4062
25135 S K1191N 5382
27972 orf8 Q27stop 11726
28048 orf8 R52I 6006
28111 orf8 Y73C 7543
28144 orf8 S84L 7617
28271 intergenic del 1 5640
28280 N D3L 3338
28281 N D3L 3338
28282 N D3L 3554
28881 N R203K 985
28882 N R203K 980
28883 N G204R 984
28977 N S235F 1376
VSP1934−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

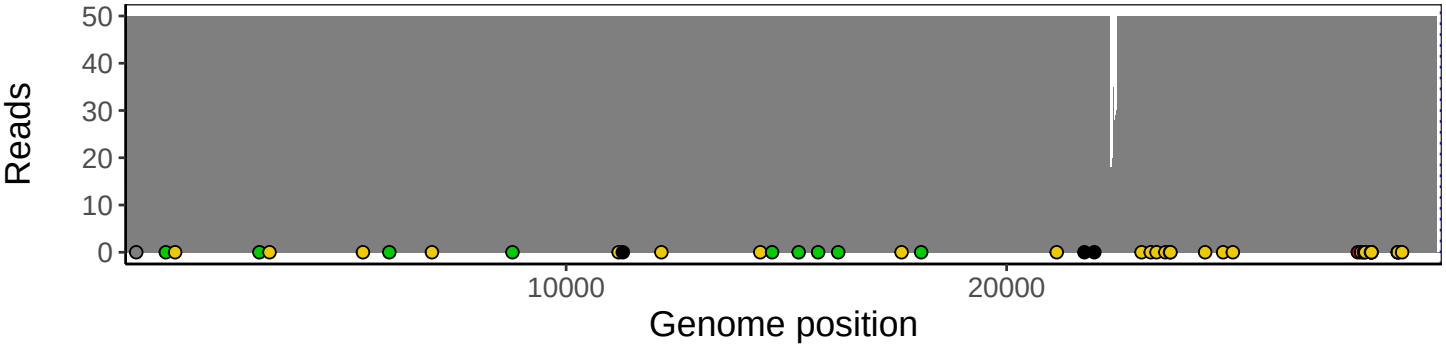
Analyses of individual experiments and composite results

VSP1934-1 | 2021-04-05 | Saliva | UPHS-0716 | genomes | single experiment

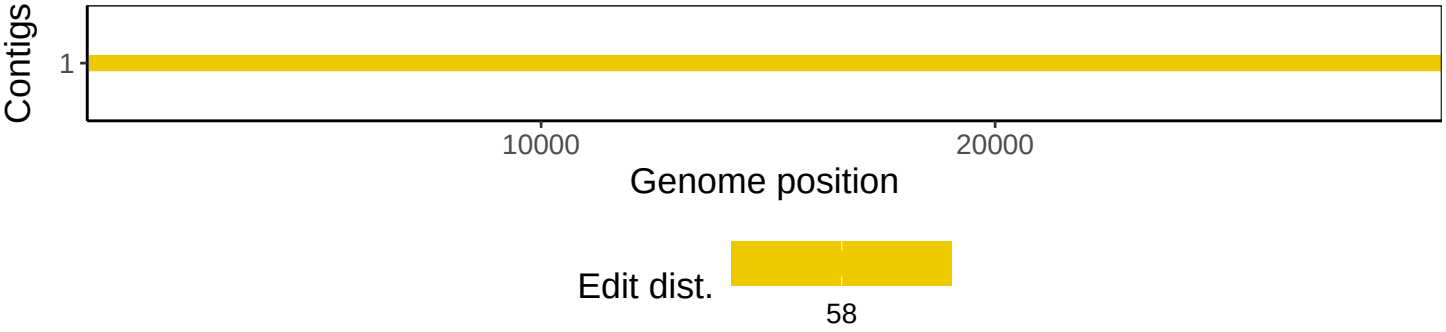
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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