COVID-19 subject UPHS-0719

2021-04-20

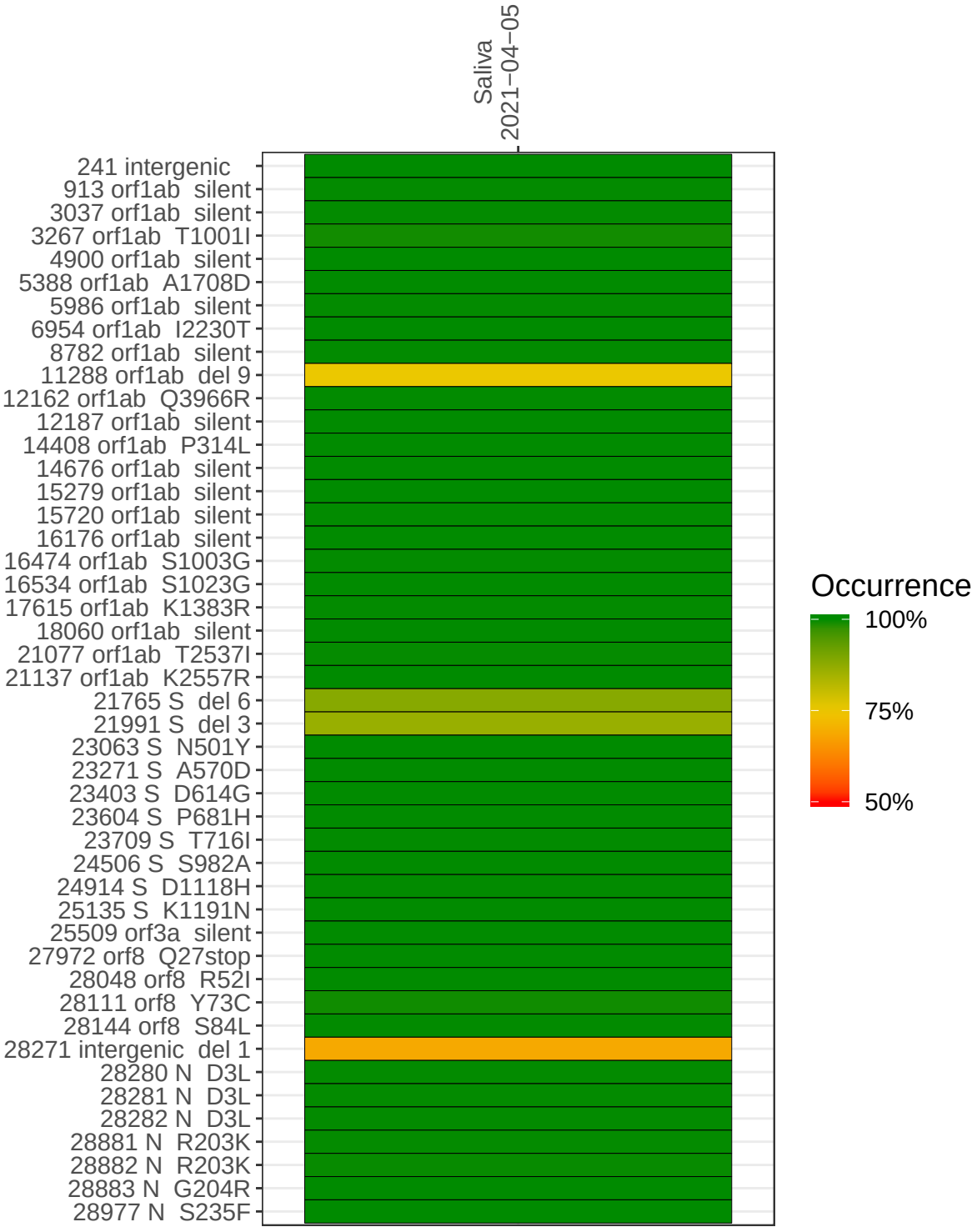
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

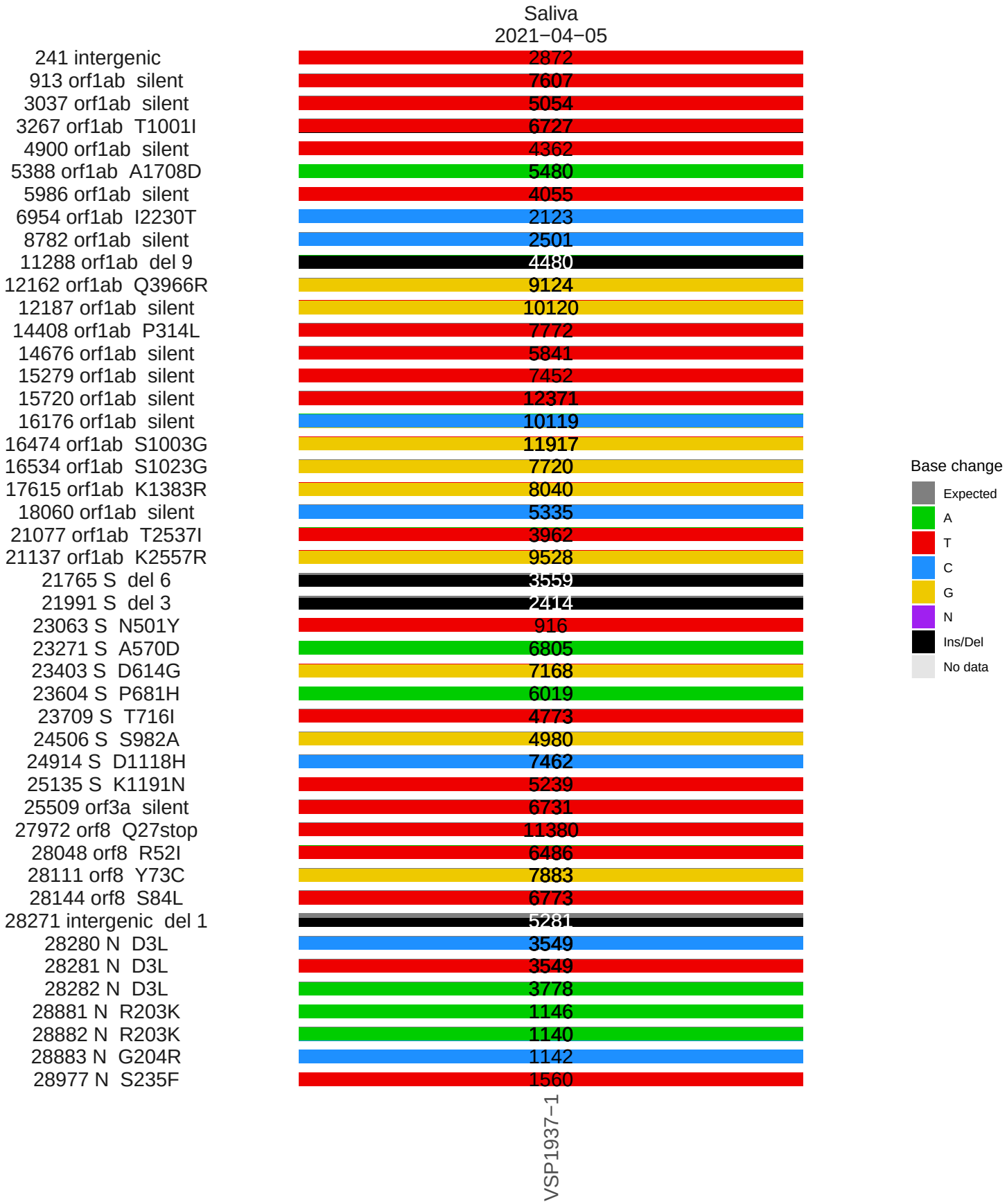
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1937-1	single experiment	NA	Saliva	2021-04-05	29.80	B.1.1.7	99.8%	99.8%

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.

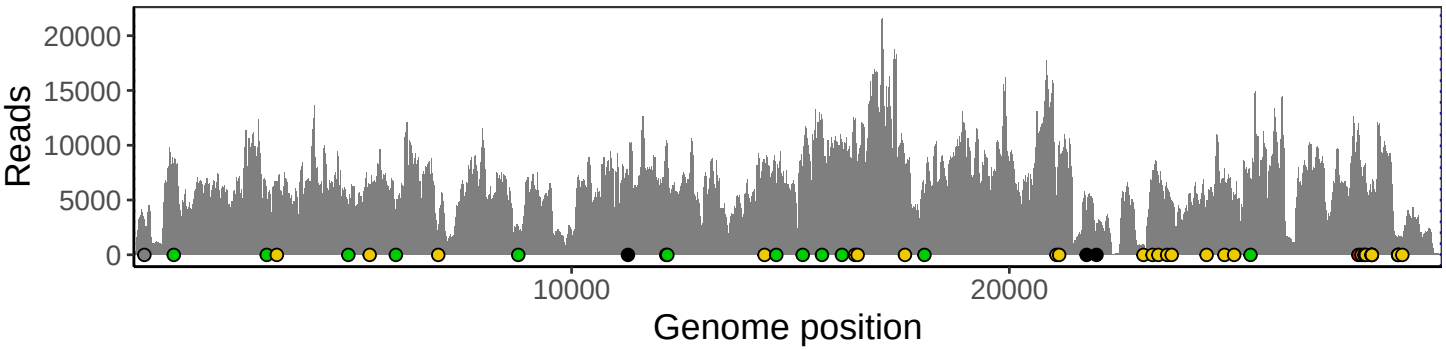



Saliva
2021−04−05
241 intergenic 2872
913 orf1ab silent 7607
3037 orf1ab silent 5054
3267 orf1ab T1001I 6727
4900 orf1ab silent 4362
5388 orf1ab A1708D 5480
5986 orf1ab silent 4055
6954 orf1ab I2230T 2123
8782 orf1ab silent 2501
11288 orf1ab del 9 4480
12162 orf1ab Q3966R 9124
12187 orf1ab silent 10120
14408 orf1ab P314L 7772
14676 orf1ab silent 5841
15279 orf1ab silent 7452
15720 orf1ab silent 12371
16176 orf1ab silent 10119
16474 orf1ab S1003G 11917
16534 orf1ab S1023G 7720
17615 orf1ab K1383R 8040
18060 orf1ab silent 5335
21077 orf1ab T2537I 3962
21137 orf1ab K2557R 9528
21765 S del 6 3559
21991 S del 3 2414
23063 S N501Y 916
23271 S A570D 6805
23403 S D614G 7168
23604 S P681H 6019
23709 S T716I 4773
24506 S S982A 4980
24914 S D1118H 7462
25135 S K1191N 5239
25509 orf3a silent 6731
27972 orf8 Q27stop 11380
28048 orf8 R52I 6486
28111 orf8 Y73C 7883
28144 orf8 S84L 6773
28271 intergenic del 1 5281
28280 N D3L 3549
28281 N D3L 3549
28282 N D3L 3778
28881 N R203K 1146
28882 N R203K 1140
28883 N G204R 1142
28977 N S235F 1560
VSP1937−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

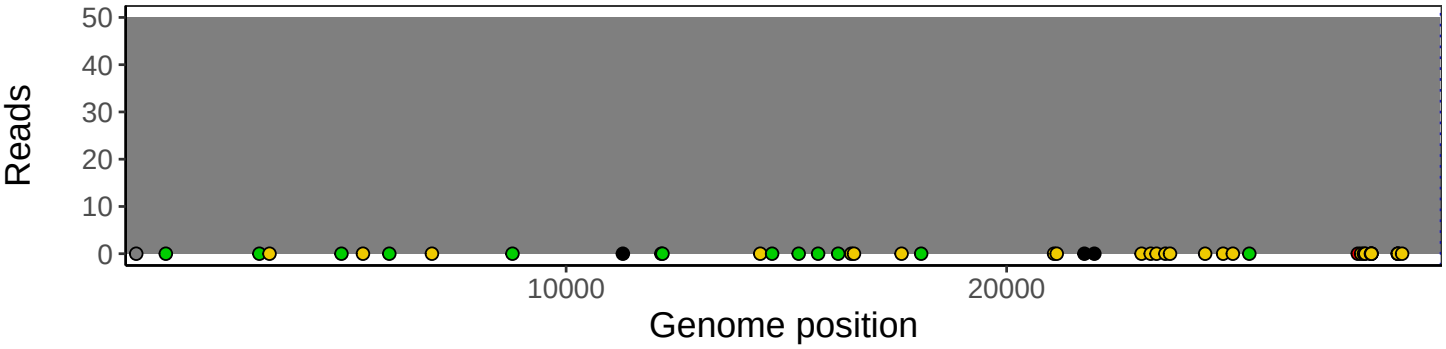
Analyses of individual experiments and composite results

VSP1937-1 | 2021-04-05 | Saliva | UPHS-0719 | genomes | single experiment

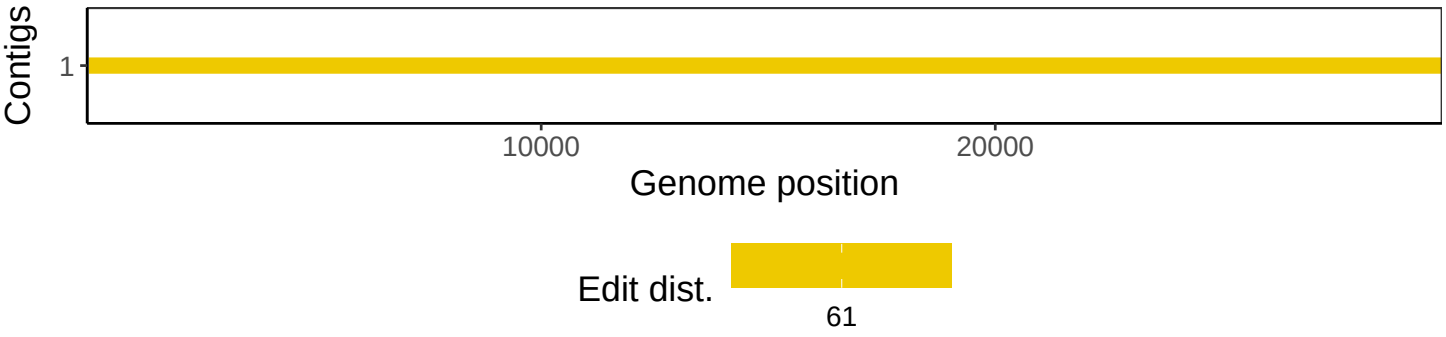
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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