COVID-19 subject UPHS-0679

2021-04-20

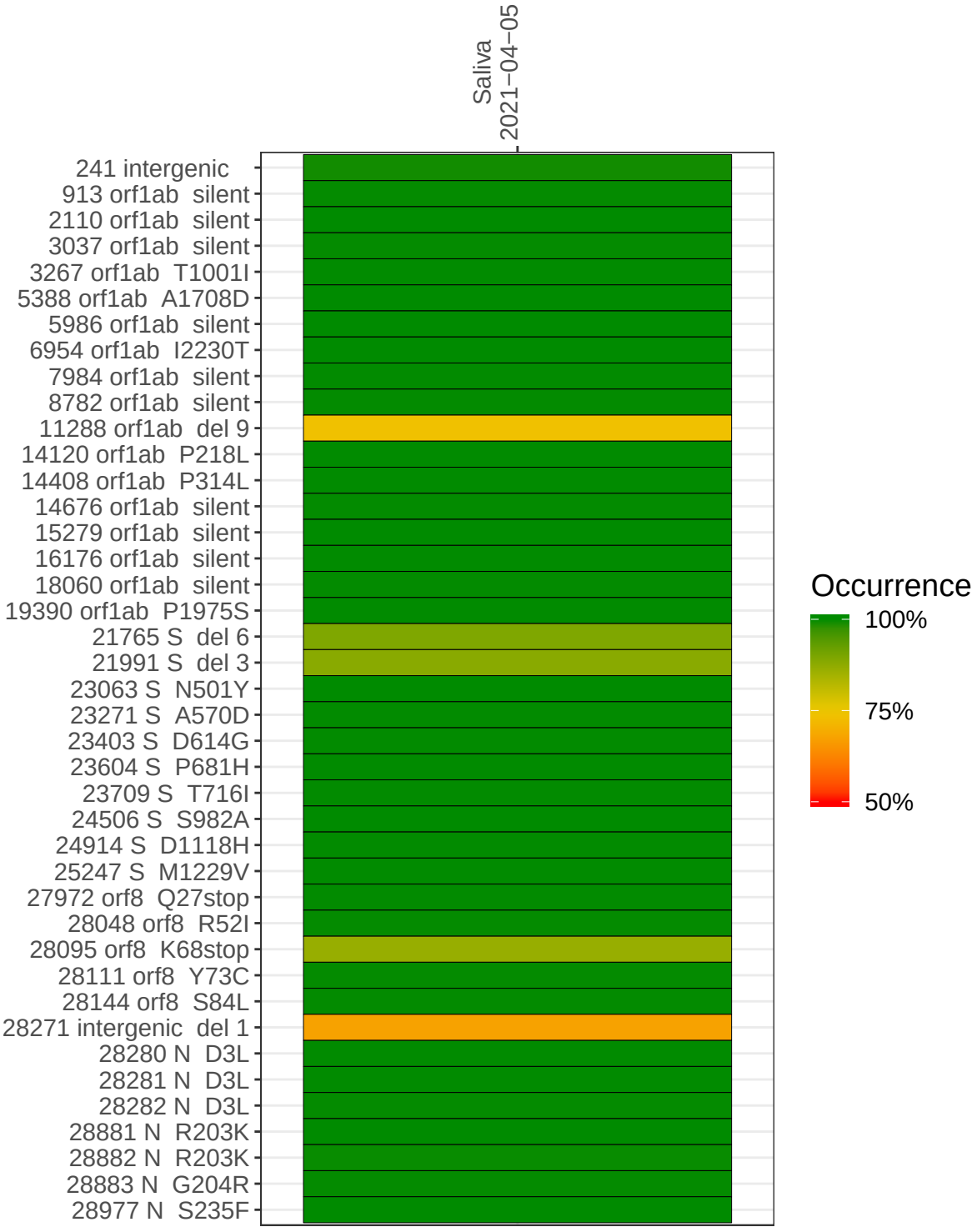
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

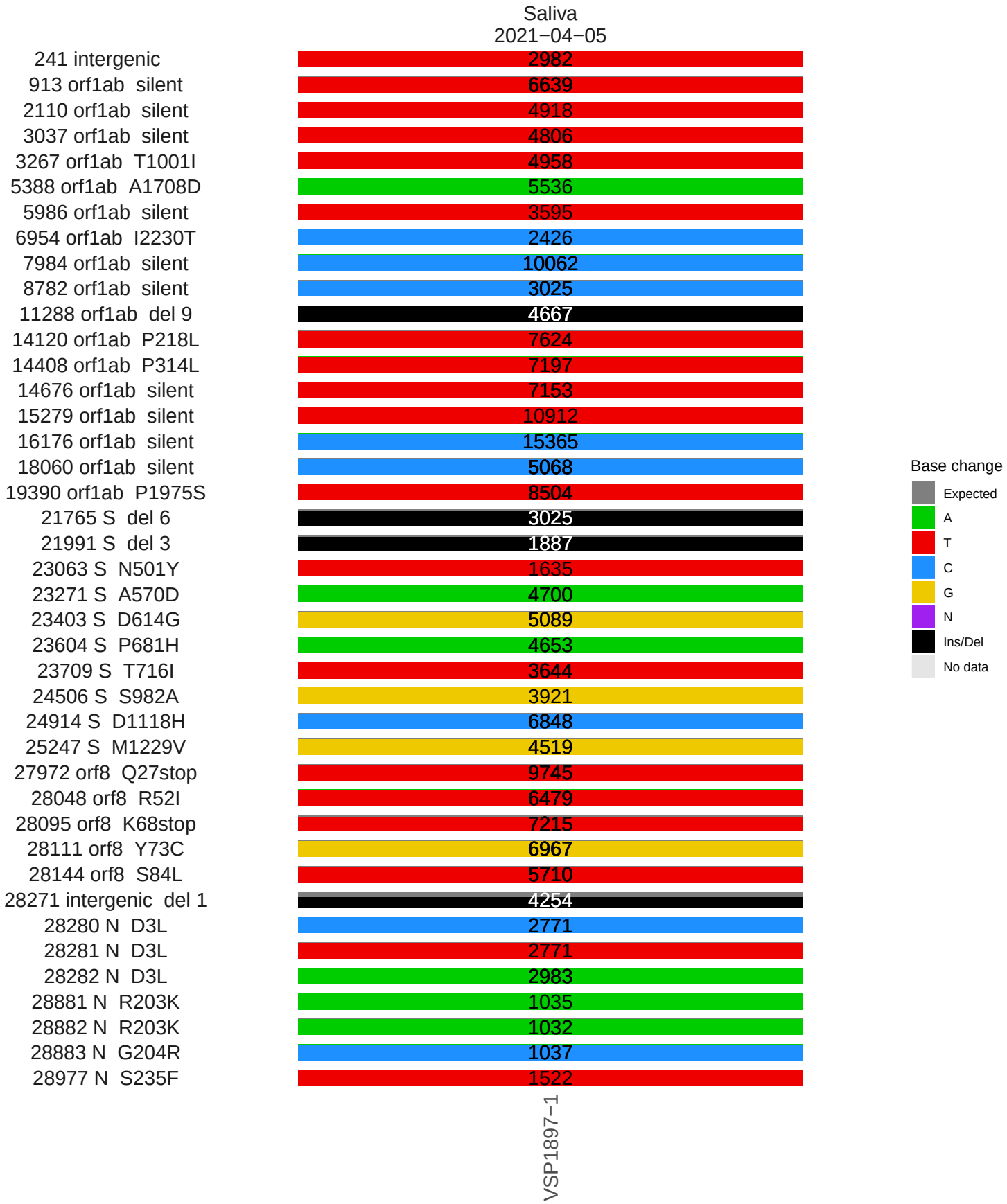
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1897-1	single experiment	NA	Saliva	2021-04-05	29.82	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.

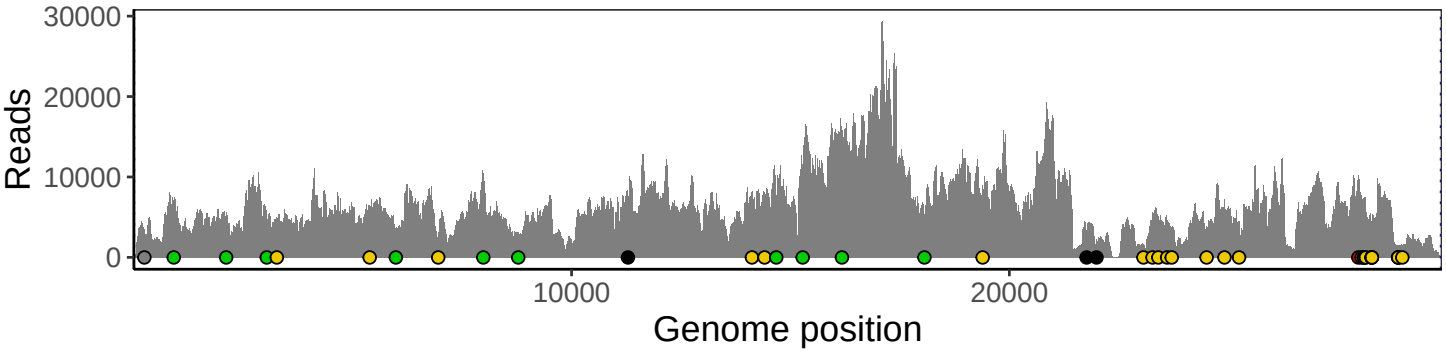



Saliva
2021−04−05
241 intergenic 2982
913 orf1ab silent 6639
2110 orf1ab silent 4918
3037 orf1ab silent 4806
3267 orf1ab T1001I 4958
5388 orf1ab A1708D 5536
5986 orf1ab silent 3595
6954 orf1ab I2230T 2426
7984 orf1ab silent 10062
8782 orf1ab silent 3025
11288 orf1ab del 9 4667
14120 orf1ab P218L 7624
14408 orf1ab P314L 7197
14676 orf1ab silent 7153
15279 orf1ab silent 10912
16176 orf1ab silent 15365
18060 orf1ab silent 5068
19390 orf1ab P1975S 8504
21765 S del 6 3025
21991 S del 3 1887
23063 S N501Y 1635
23271 S A570D 4700
23403 S D614G 5089
23604 S P681H 4653
23709 S T716I 3644
24506 S S982A 3921
24914 S D1118H 6848
25247 S M1229V 4519
27972 orf8 Q27stop 9745
28048 orf8 R52I 6479
28095 orf8 K68stop 7215
28111 orf8 Y73C 6967
28144 orf8 S84L 5710
28271 intergenic del 1 4254
28280 N D3L 2771
28281 N D3L 2771
28282 N D3L 2983
28881 N R203K 1035
28882 N R203K 1032
28883 N G204R 1037
28977 N S235F 1522
VSP1897−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

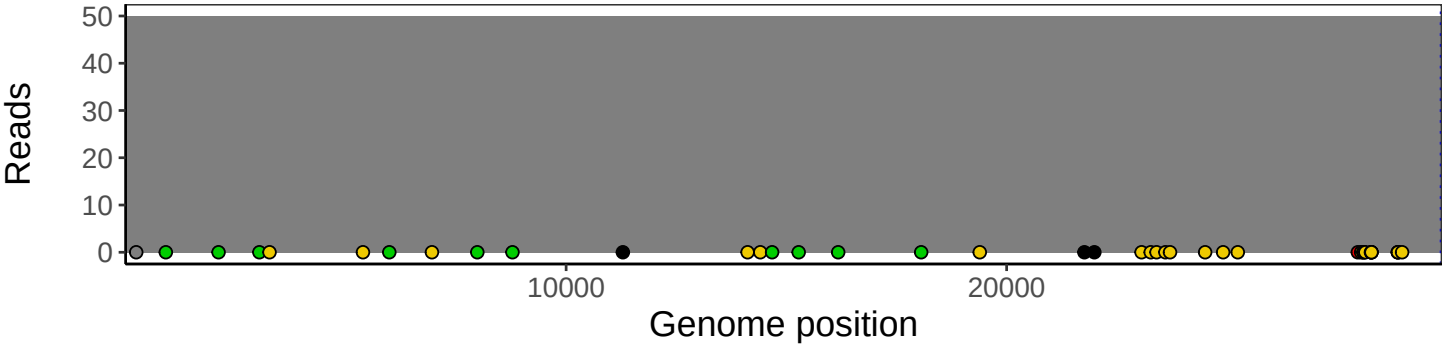
Analyses of individual experiments and composite results

VSP1897-1 | 2021-04-05 | Saliva | UPHS-0679 | genomes | single experiment

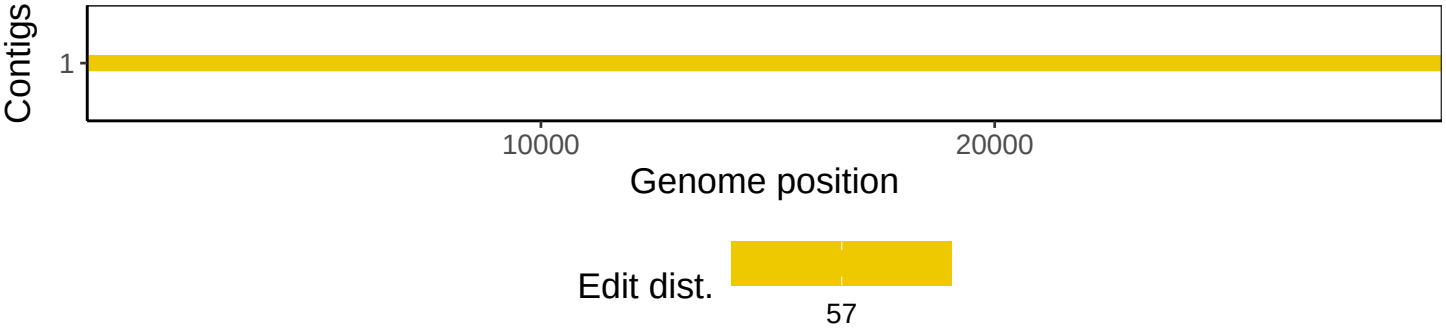
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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