COVID-19 subject UPHS-0663

2021-04-20

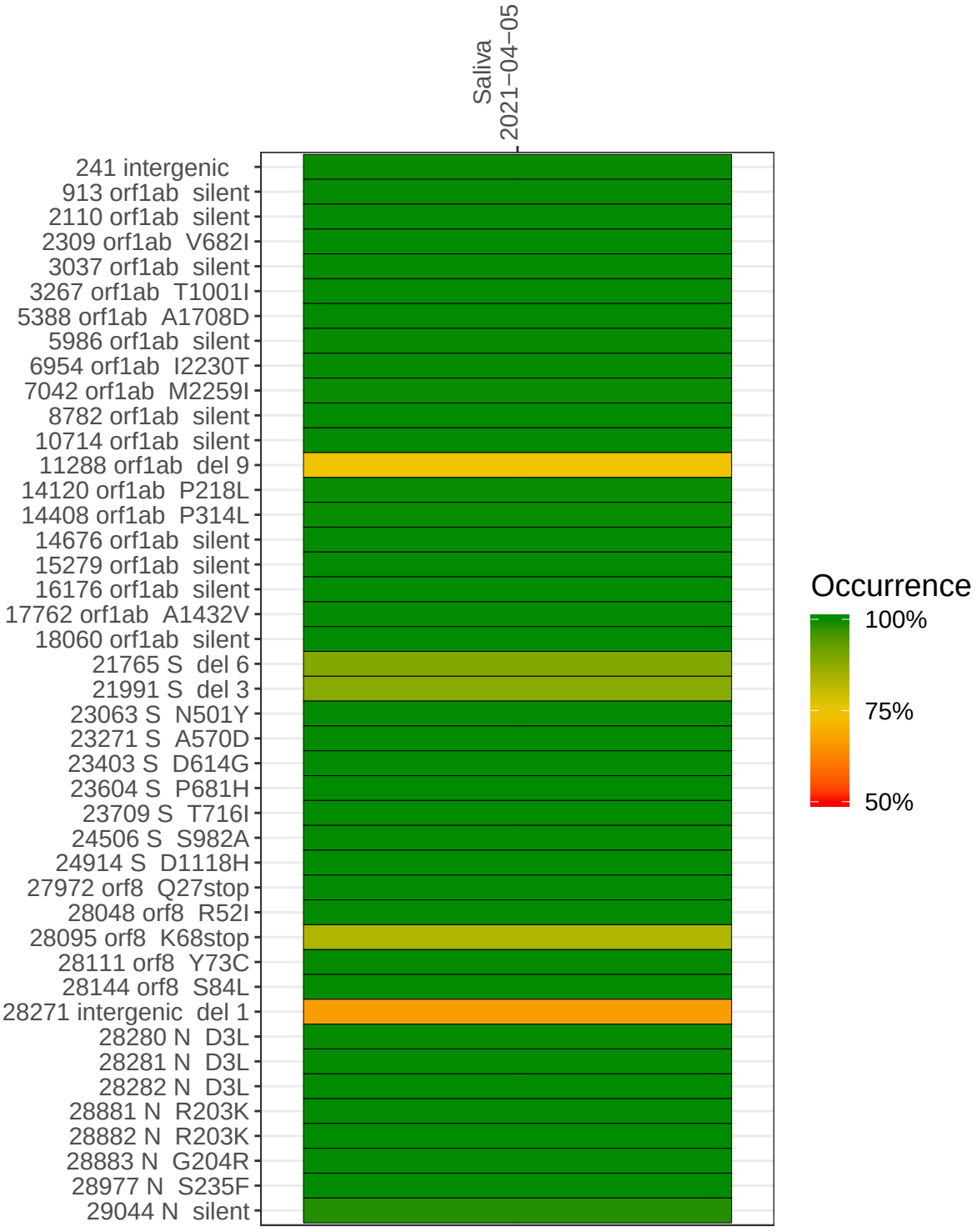
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

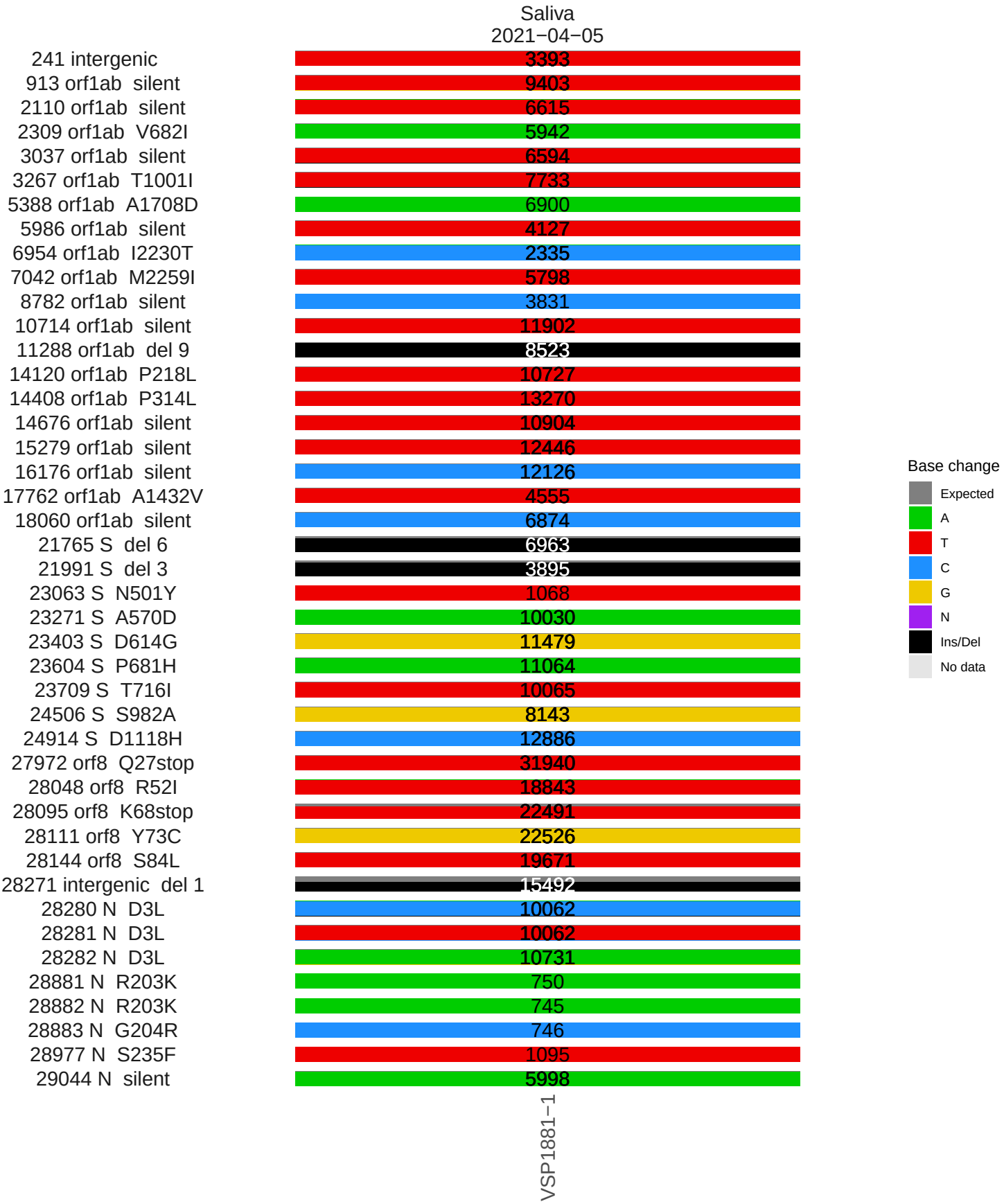
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1881-1	single experiment	NA	Saliva	2021-04-05	29.90	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.

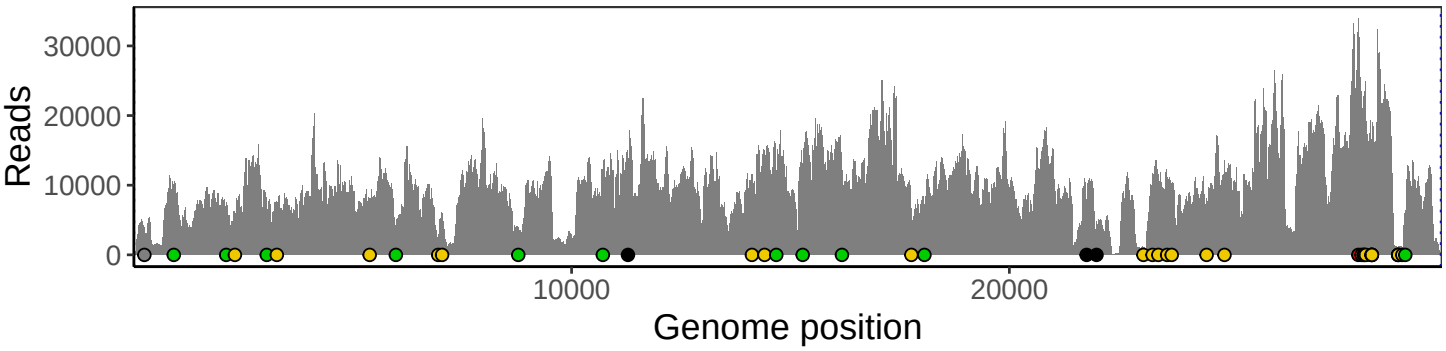



Saliva
2021−04−05
241 intergenic 3393
913 orf1ab silent 9403
2110 orf1ab silent 6615
2309 orf1ab V682I 5942
3037 orf1ab silent 6594
3267 orf1ab T1001I 7733
5388 orf1ab A1708D 6900
5986 orf1ab silent 4127
6954 orf1ab I2230T 2335
7042 orf1ab M2259I 5798
8782 orf1ab silent 3831
10714 orf1ab silent 11902
11288 orf1ab del 9 8523
14120 orf1ab P218L 10727
14408 orf1ab P314L 13270
14676 orf1ab silent 10904
15279 orf1ab silent 12446
16176 orf1ab silent 12126
17762 orf1ab A1432V 4555
18060 orf1ab silent 6874
21765 S del 6 6963
21991 S del 3 3895
23063 S N501Y 1068
23271 S A570D 10030
23403 S D614G 11479
23604 S P681H 11064
23709 S T716I 10065
24506 S S982A 8143
24914 S D1118H 12886
27972 orf8 Q27stop 31940
28048 orf8 R52I 18843
28095 orf8 K68stop 22491
28111 orf8 Y73C 22526
28144 orf8 S84L 19671
28271 intergenic del 1 15492
28280 N D3L 10062
28281 N D3L 10062
28282 N D3L 10731
28881 N R203K 750
28882 N R203K 745
28883 N G204R 746
28977 N S235F 1095
29044 N silent 5998
VSP1881−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

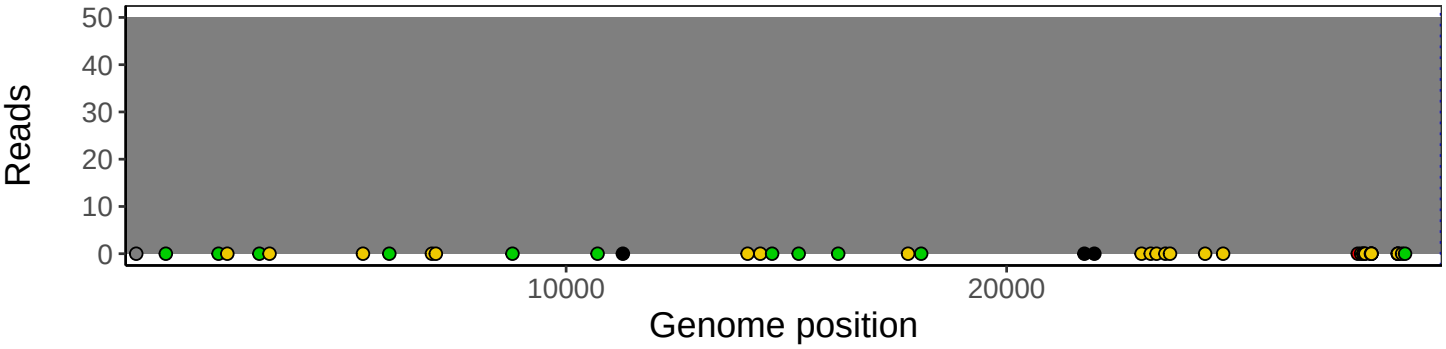
Analyses of individual experiments and composite results

VSP1881-1 | 2021-04-05 | Saliva | UPHS-0663 | genomes | single experiment

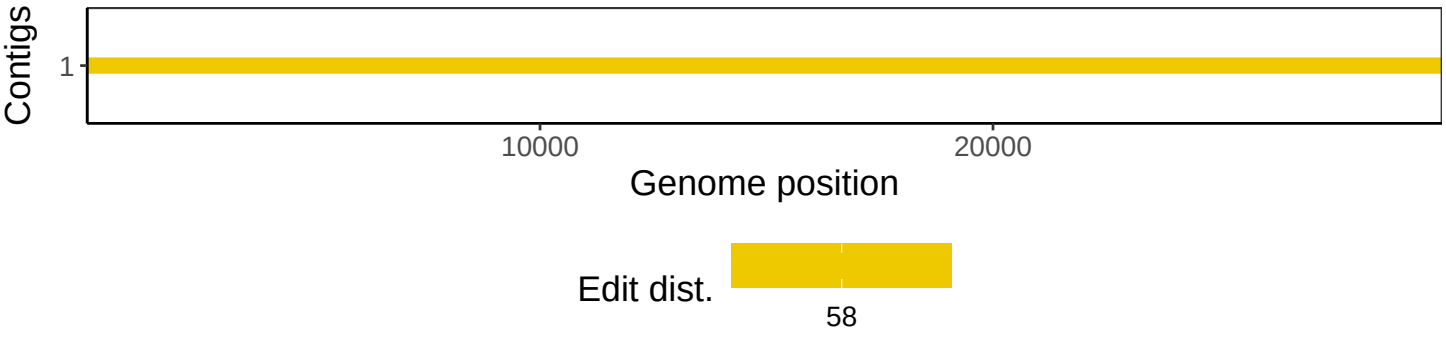
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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