COVID-19 subject UPHS-1007

2021-05-10

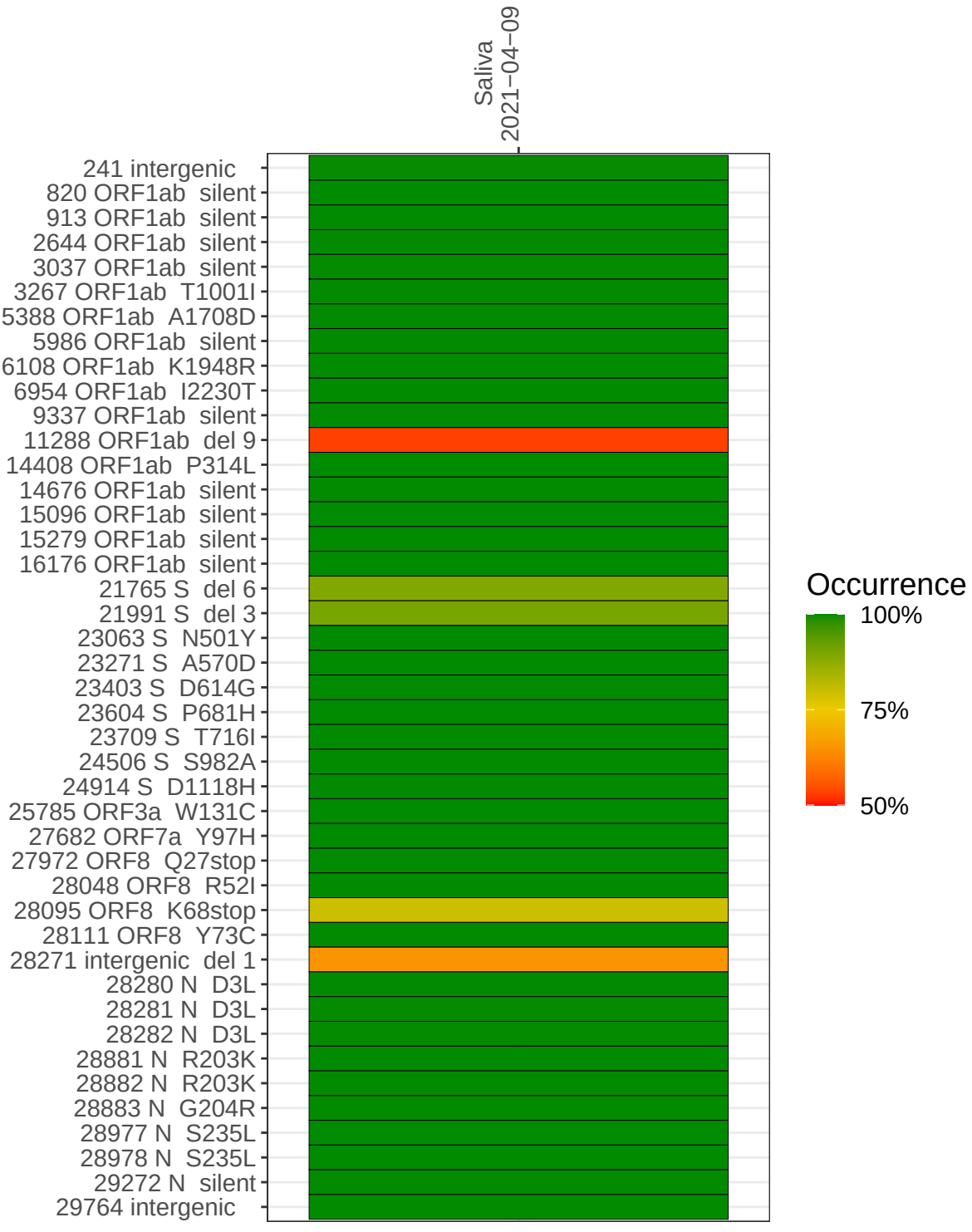
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

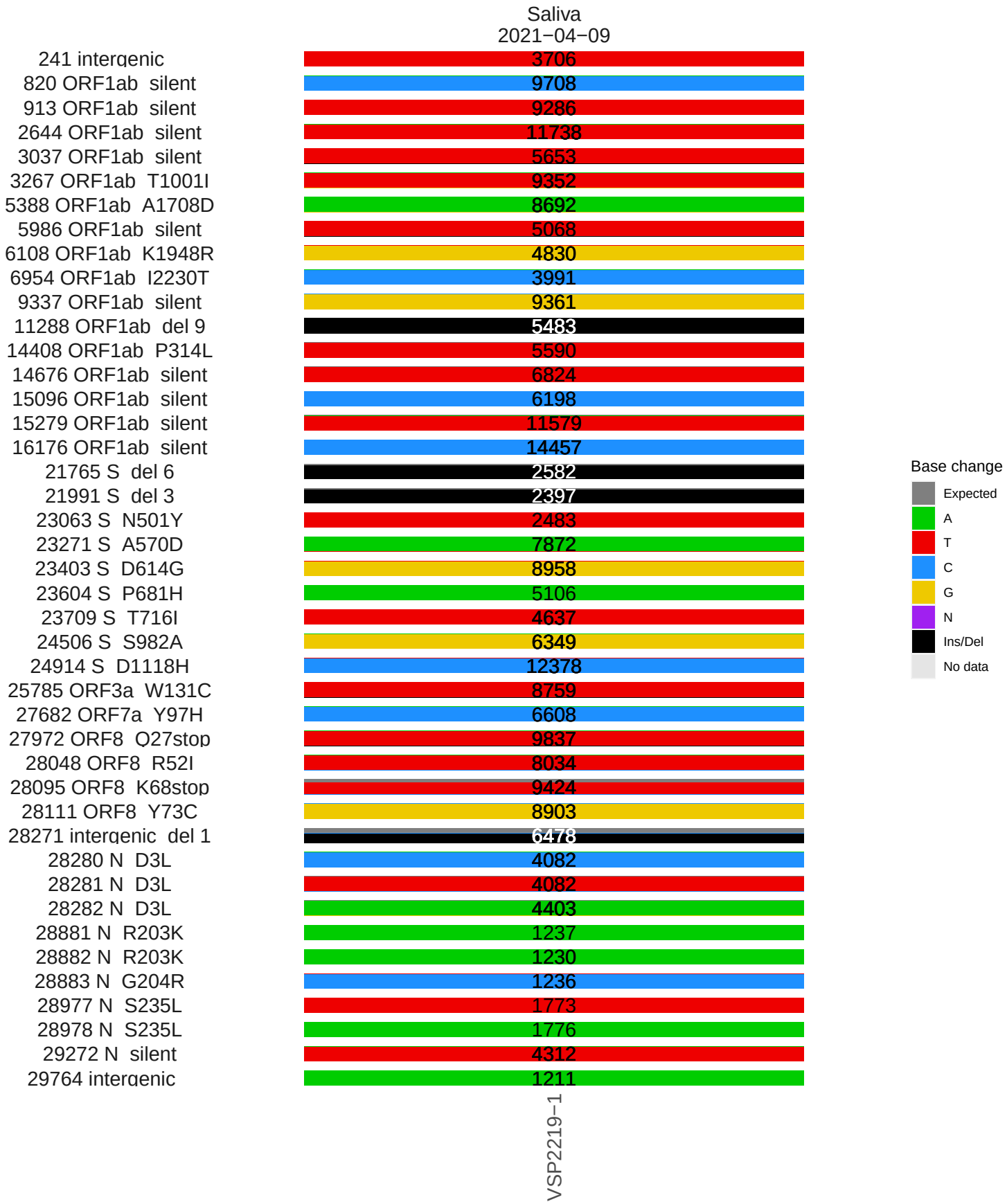
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2219-1	single experiment	NA	Saliva	2021-04-09	29.87	B.1.1.7	99.9%	99.8%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) 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.

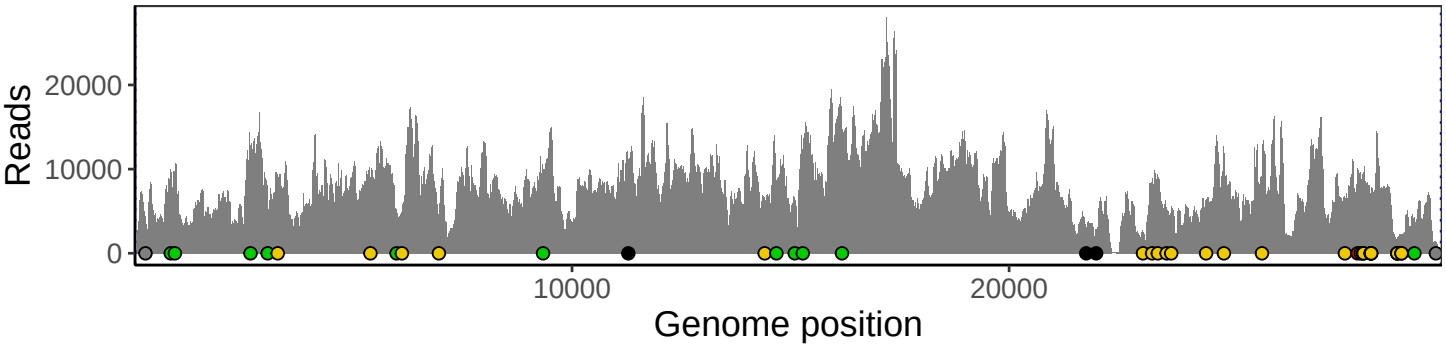



Saliva
2021−04−09
241 intergenic 3706
820 ORF1ab silent 9708
913 ORF1ab silent 9286
2644 ORF1ab silent 11738
3037 ORF1ab silent 5653
3267 ORF1ab T1001I 9352
5388 ORF1ab A1708D 8692
5986 ORF1ab silent 5068
6108 ORF1ab K1948R 4830
6954 ORF1ab I2230T 3991
9337 ORF1ab silent 9361
11288 ORF1ab del 9 5483
14408 ORF1ab P314L 5590
14676 ORF1ab silent 6824
15096 ORF1ab silent 6198
15279 ORF1ab silent 11579
16176 ORF1ab silent 14457
21765 S del 6 2582
21991 S del 3 2397
23063 S N501Y 2483
23271 S A570D 7872
23403 S D614G 8958
23604 S P681H 5106
23709 S T716I 4637
24506 S S982A 6349
24914 S D1118H 12378
25785 ORF3a W131C 8759
27682 ORF7a Y97H 6608
27972 ORF8 Q27stop 9837
28048 ORF8 R52I 8034
28095 ORF8 K68stop 9424
28111 ORF8 Y73C 8903
28271 intergenic del 1 6478
28280 N D3L 4082
28281 N D3L 4082
28282 N D3L 4403
28881 N R203K 1237
28882 N R203K 1230
28883 N G204R 1236
28977 N S235L 1773
28978 N S235L 1776
29272 N silent 4312
29764 intergenic 1211
VSP2219−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

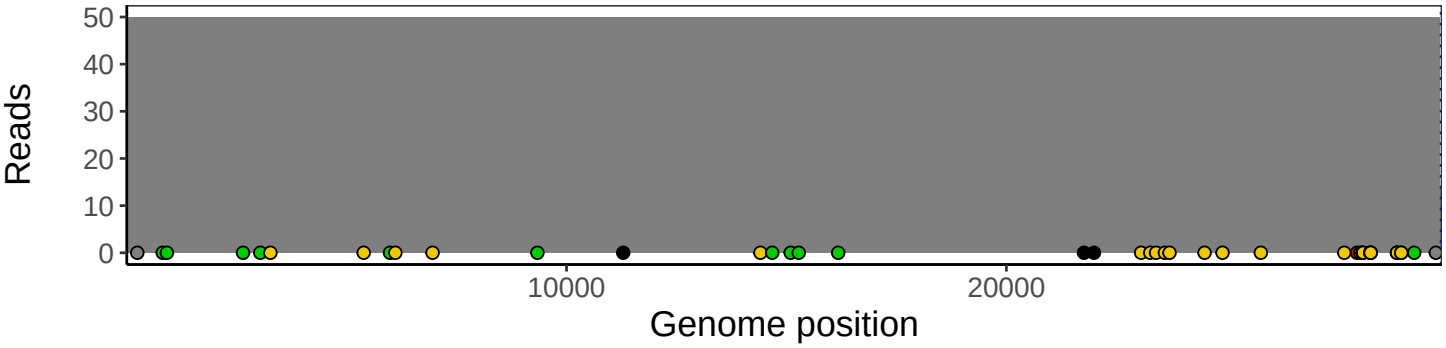
Analyses of individual experiments and composite results

VSP2219-1 | 2021-04-09 | Saliva | UPHS-1007 | genomes | single experiment

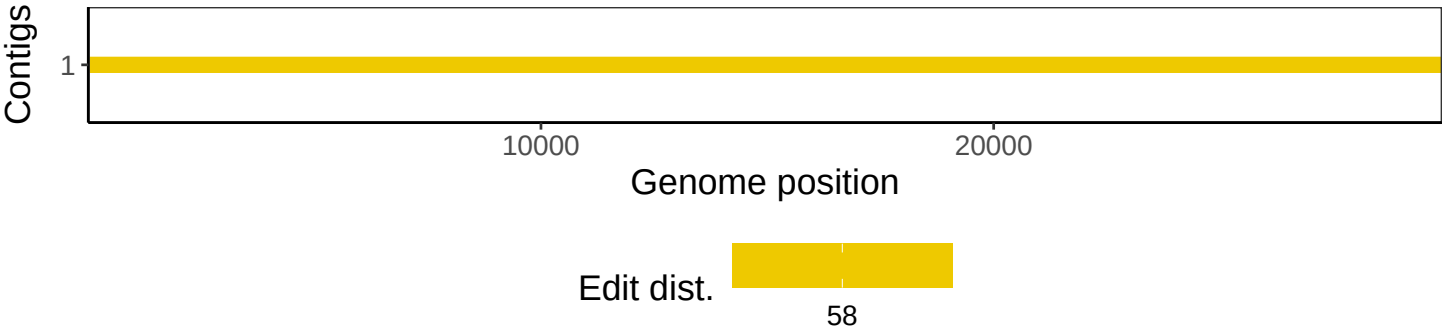
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.3.3
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