COVID-19 subject UPHS-1135

2021-06-23

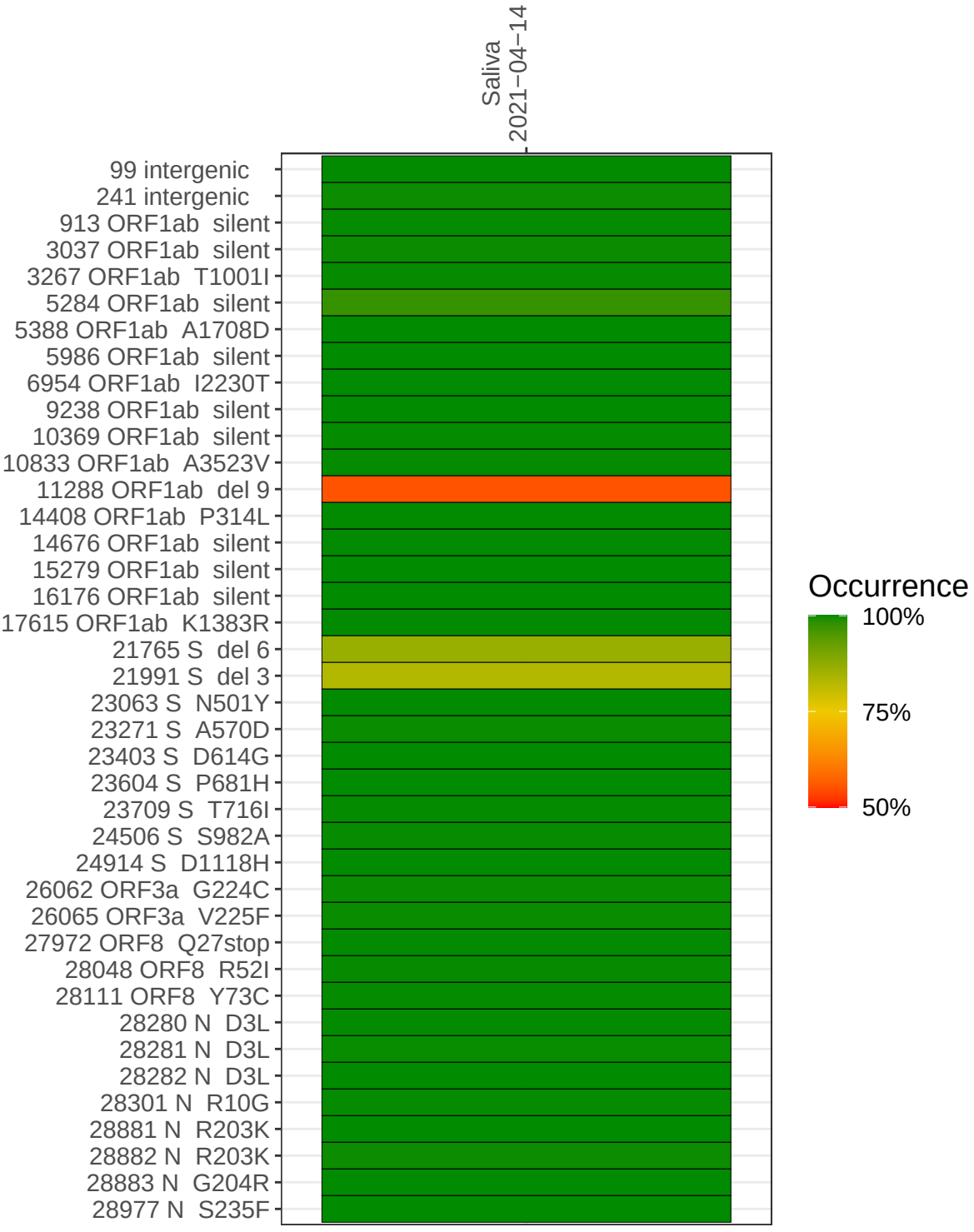
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

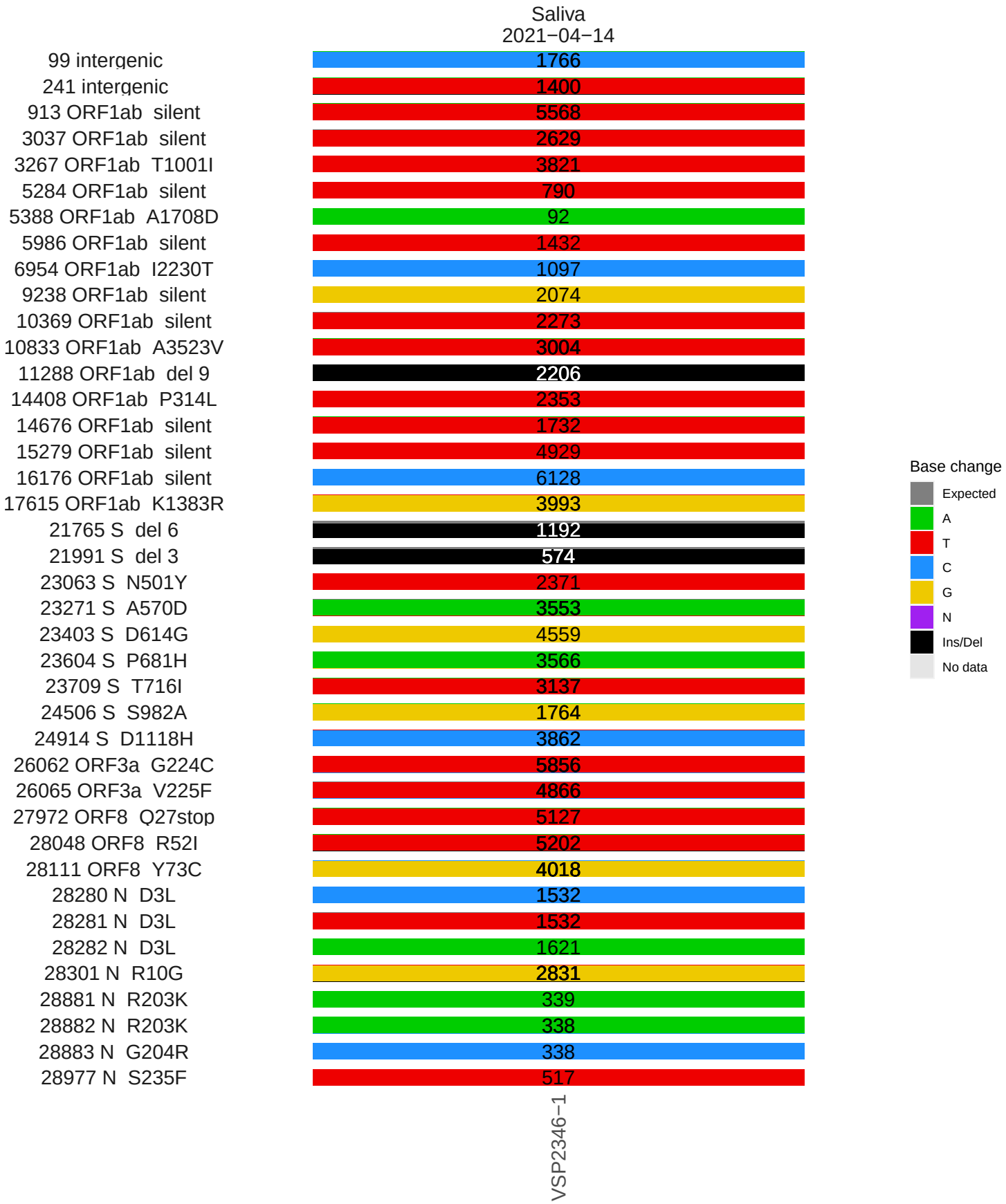
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2346-1	single experiment	NA	Saliva	2021-04-14	29.80	B.1.1.7	99.9%	99.7%

Variants shared across samples

The heat map below shows how variants (reference genome /home/common/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.

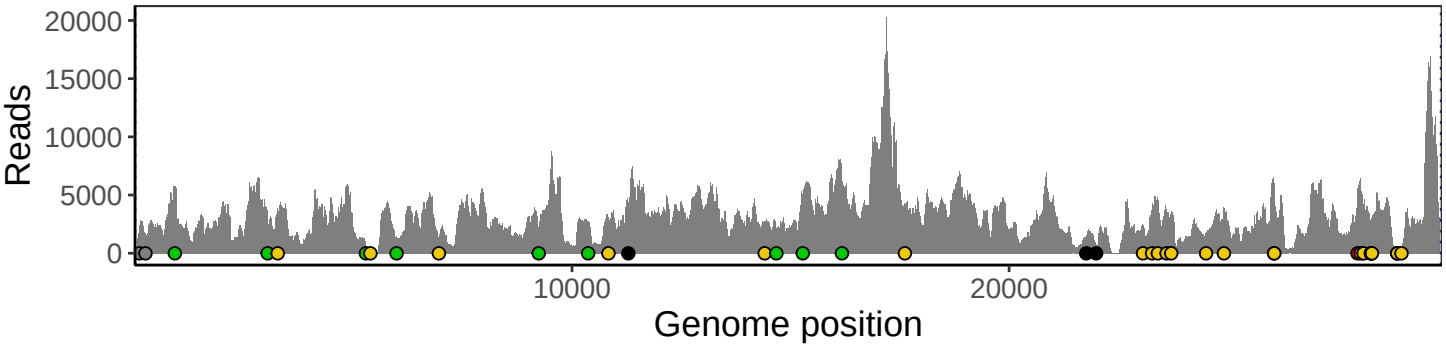



Saliva
2021−04−14
99 intergenic 1766
241 intergenic 1400
913 ORF1ab silent 5568
3037 ORF1ab silent 2629
3267 ORF1ab T1001I 3821
5284 ORF1ab silent 790
5388 ORF1ab A1708D 92
5986 ORF1ab silent 1432
6954 ORF1ab I2230T 1097
9238 ORF1ab silent 2074
10369 ORF1ab silent 2273
10833 ORF1ab A3523V 3004
11288 ORF1ab del 9 2206
14408 ORF1ab P314L 2353
14676 ORF1ab silent 1732
15279 ORF1ab silent 4929
16176 ORF1ab silent 6128
17615 ORF1ab K1383R 3993
21765 S del 6 1192
21991 S del 3 574
23063 S N501Y 2371
23271 S A570D 3553
23403 S D614G 4559
23604 S P681H 3566
23709 S T716I 3137
24506 S S982A 1764
24914 S D1118H 3862
26062 ORF3a G224C 5856
26065 ORF3a V225F 4866
27972 ORF8 Q27stop 5127
28048 ORF8 R52I 5202
28111 ORF8 Y73C 4018
28280 N D3L 1532
28281 N D3L 1532
28282 N D3L 1621
28301 N R10G 2831
28881 N R203K 339
28882 N R203K 338
28883 N G204R 338
28977 N S235F 517
VSP2346−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

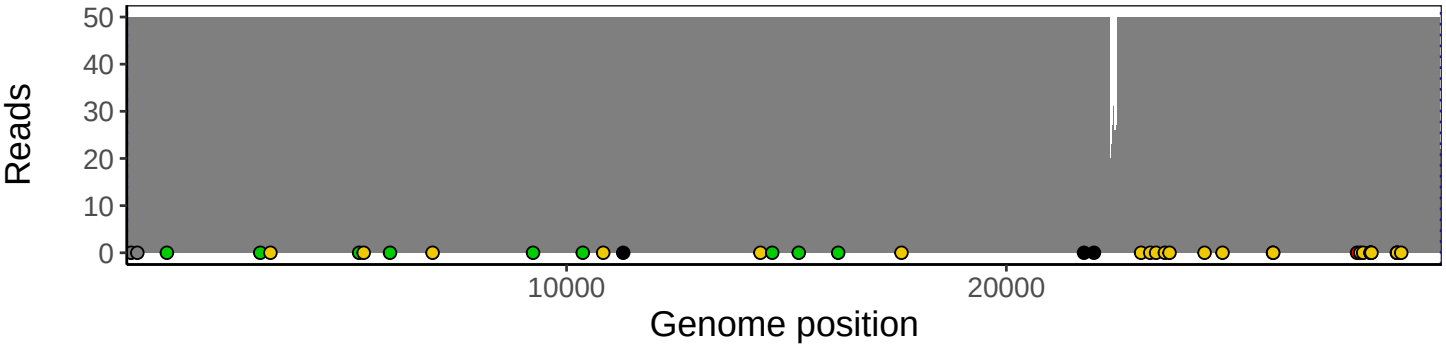
Analyses of individual experiments and composite results

VSP2346-1 | 2021-04-14 | Saliva | UPHS-1135 | genomes | single experiment

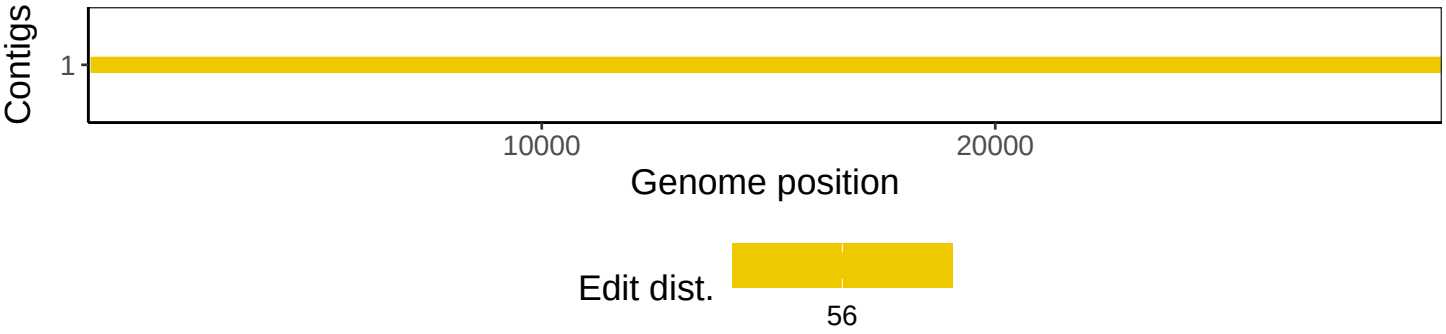
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.1.3
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