COVID-19 subject UPHS-1134

2021-06-23

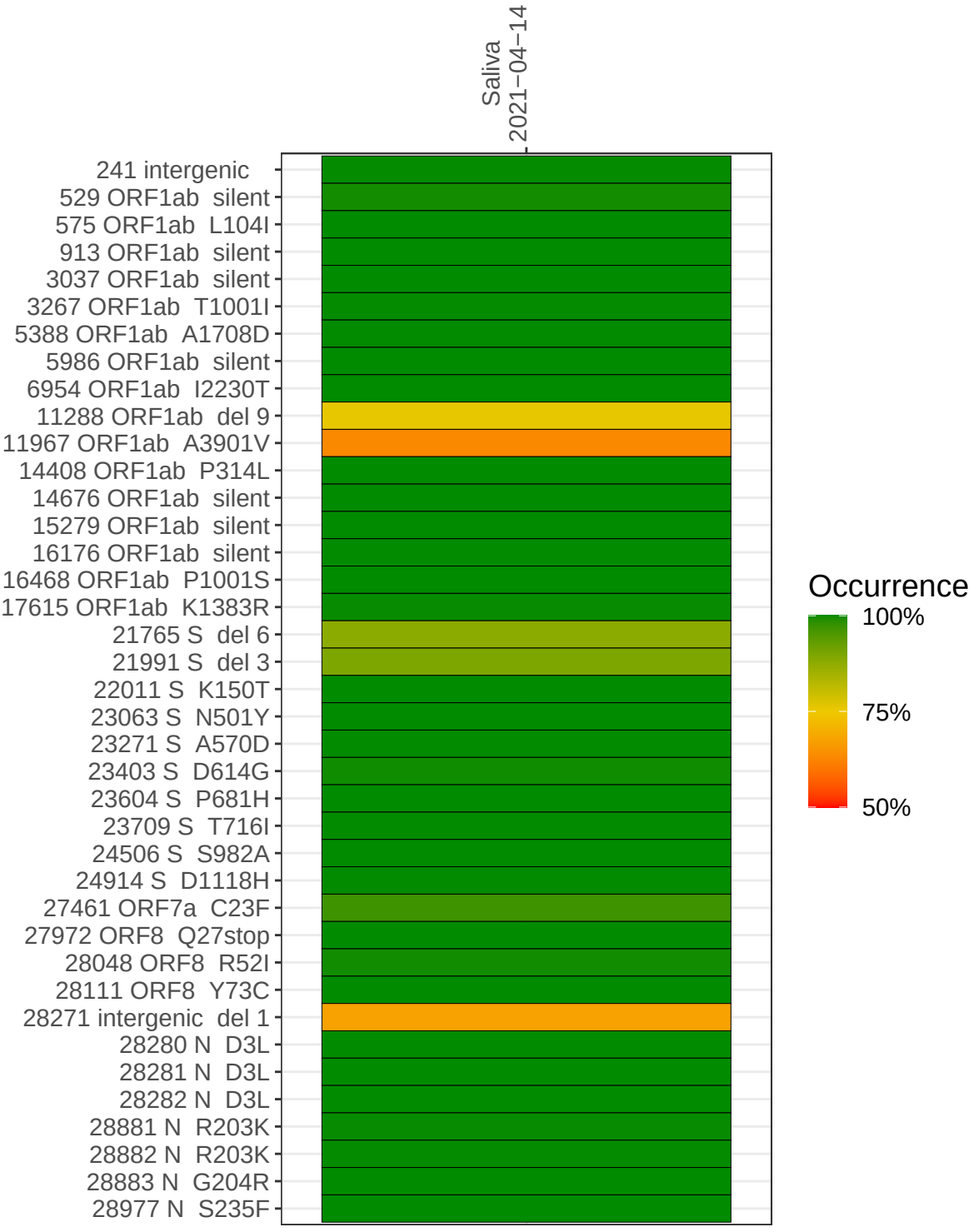
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

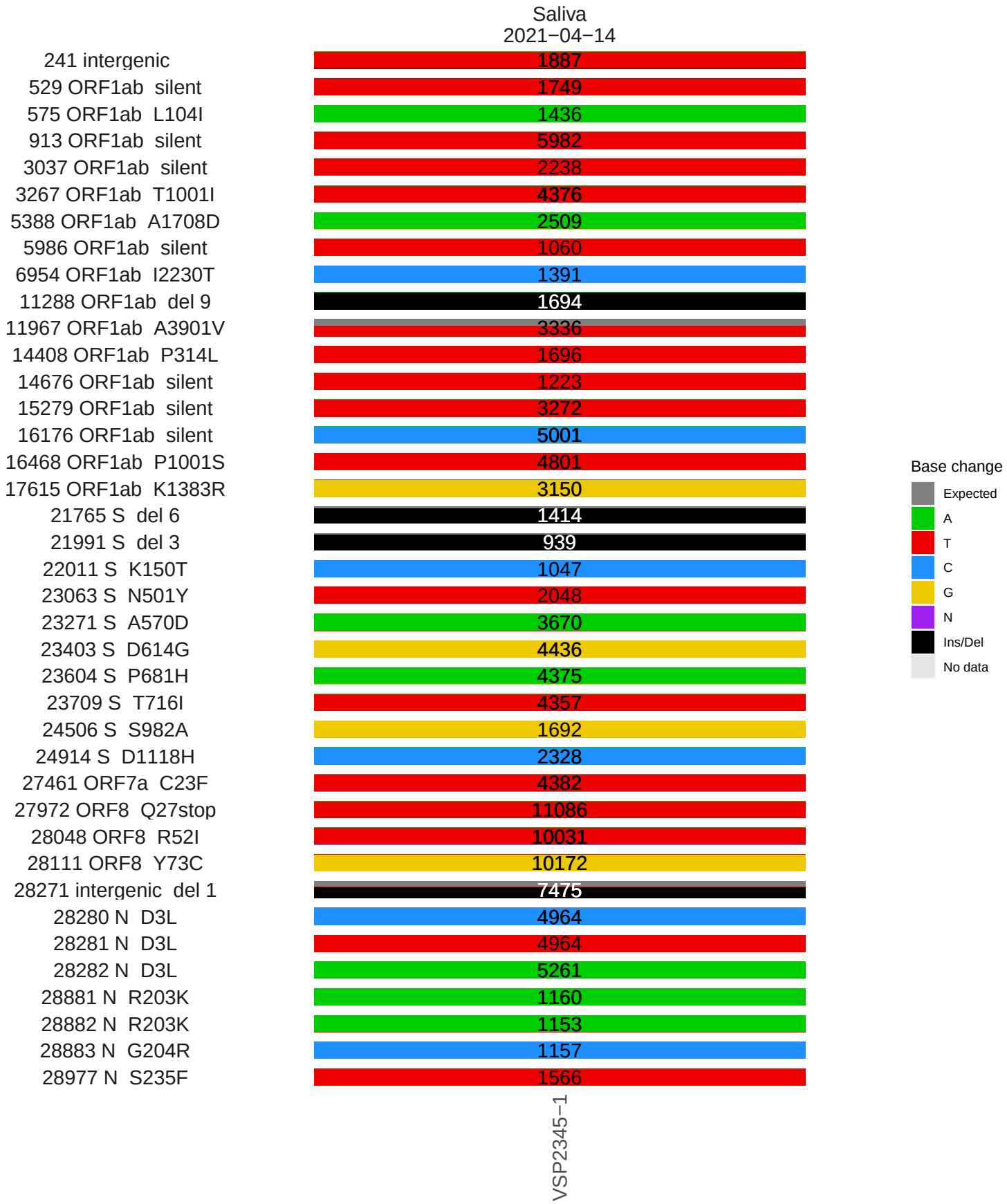
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2345-1	single experiment	NA	Saliva	2021-04-14	29.83	B.1.1.7	99.9%	99.9%

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.

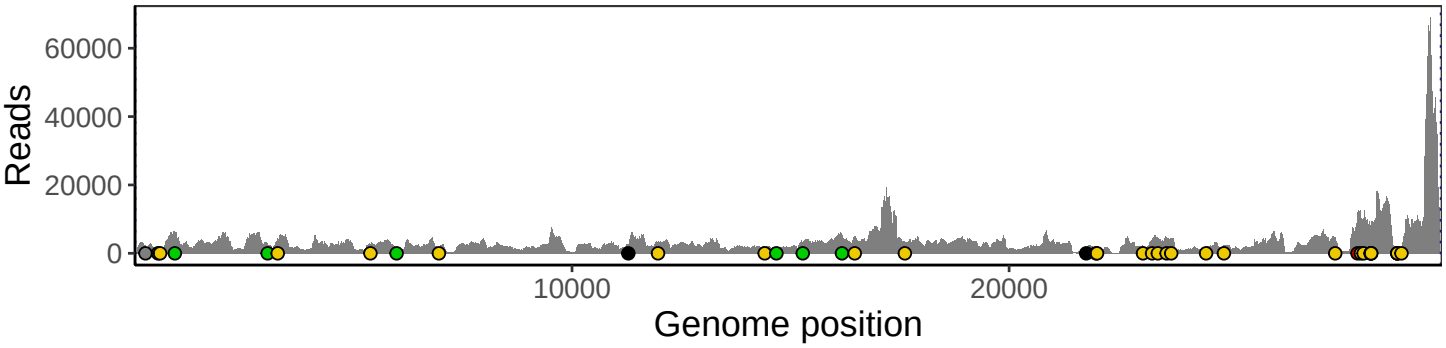



Saliva
2021−04−14
241 intergenic 1887
529 ORF1ab silent 1749
575 ORF1ab L104I 1436
913 ORF1ab silent 5982
3037 ORF1ab silent 2238
3267 ORF1ab T1001I 4376
5388 ORF1ab A1708D 2509
5986 ORF1ab silent 1060
6954 ORF1ab I2230T 1391
11288 ORF1ab del 9 1694
11967 ORF1ab A3901V 3336
14408 ORF1ab P314L 1696
14676 ORF1ab silent 1223
15279 ORF1ab silent 3272
16176 ORF1ab silent 5001
16468 ORF1ab P1001S 4801
17615 ORF1ab K1383R 3150
21765 S del 6 1414
21991 S del 3 939
22011 S K150T 1047
23063 S N501Y 2048
23271 S A570D 3670
23403 S D614G 4436
23604 S P681H 4375
23709 S T716I 4357
24506 S S982A 1692
24914 S D1118H 2328
27461 ORF7a C23F 4382
27972 ORF8 Q27stop 11086
28048 ORF8 R52I 10031
28111 ORF8 Y73C 10172
28271 intergenic del 1 7475
28280 N D3L 4964
28281 N D3L 4964
28282 N D3L 5261
28881 N R203K 1160
28882 N R203K 1153
28883 N G204R 1157
28977 N S235F 1566
VSP2345−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

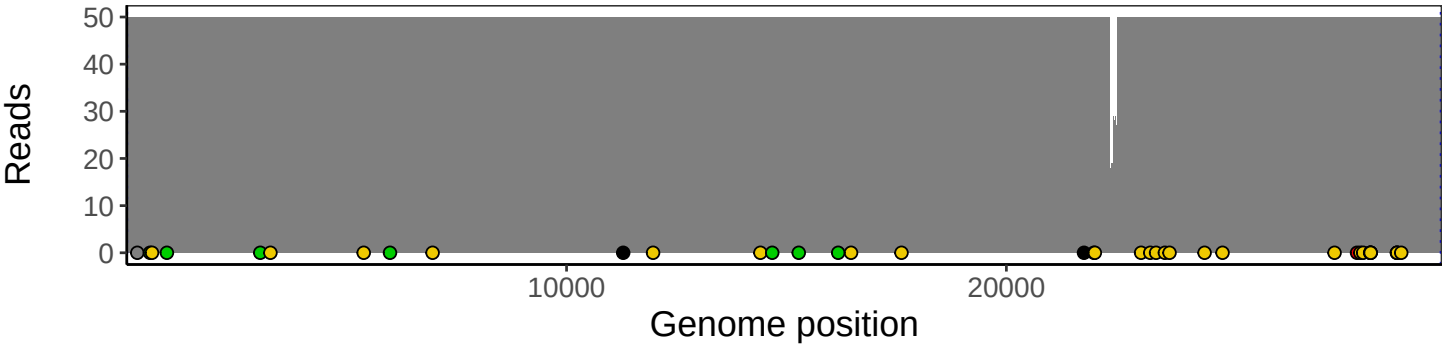
Analyses of individual experiments and composite results

VSP2345-1 | 2021-04-14 | Saliva | UPHS-1134 | genomes | single experiment

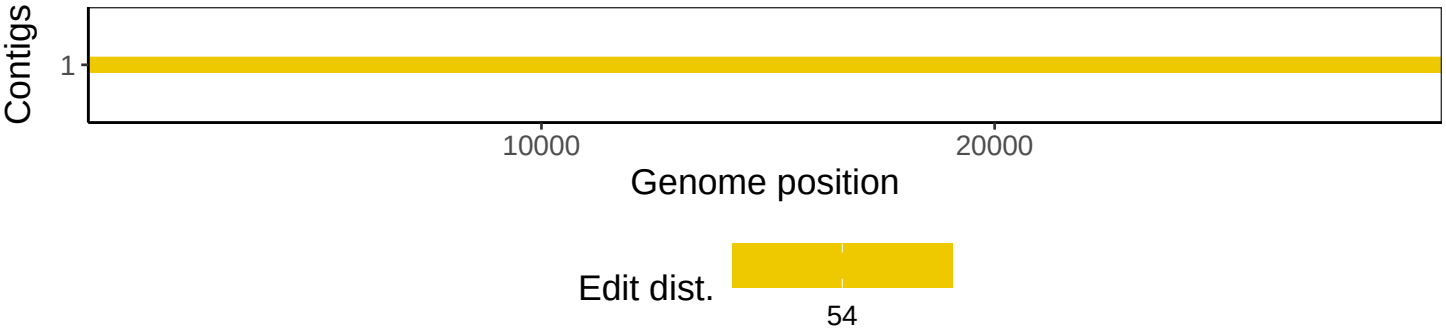
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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