COVID-19 subject UPHS-1004

2021-06-23

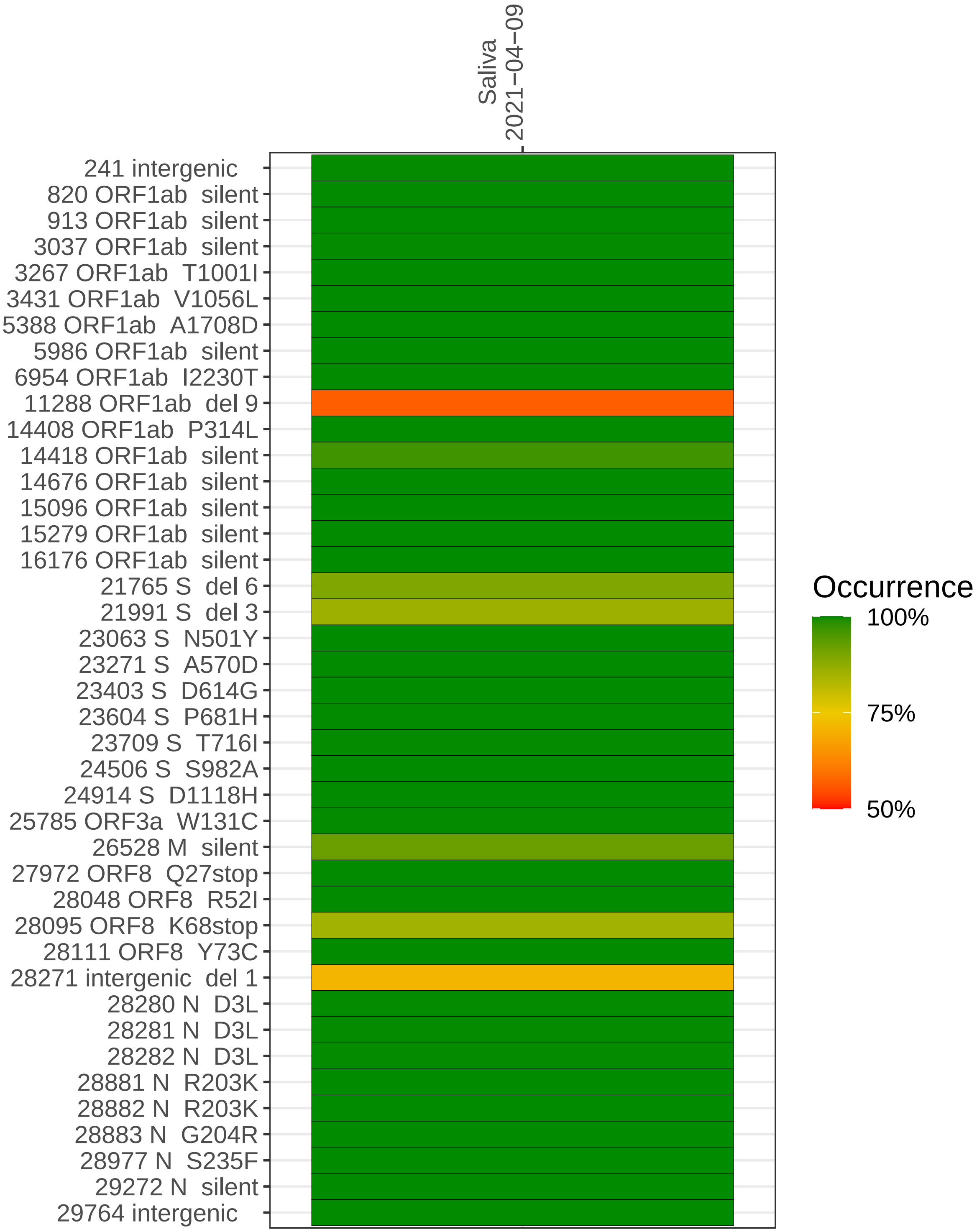
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

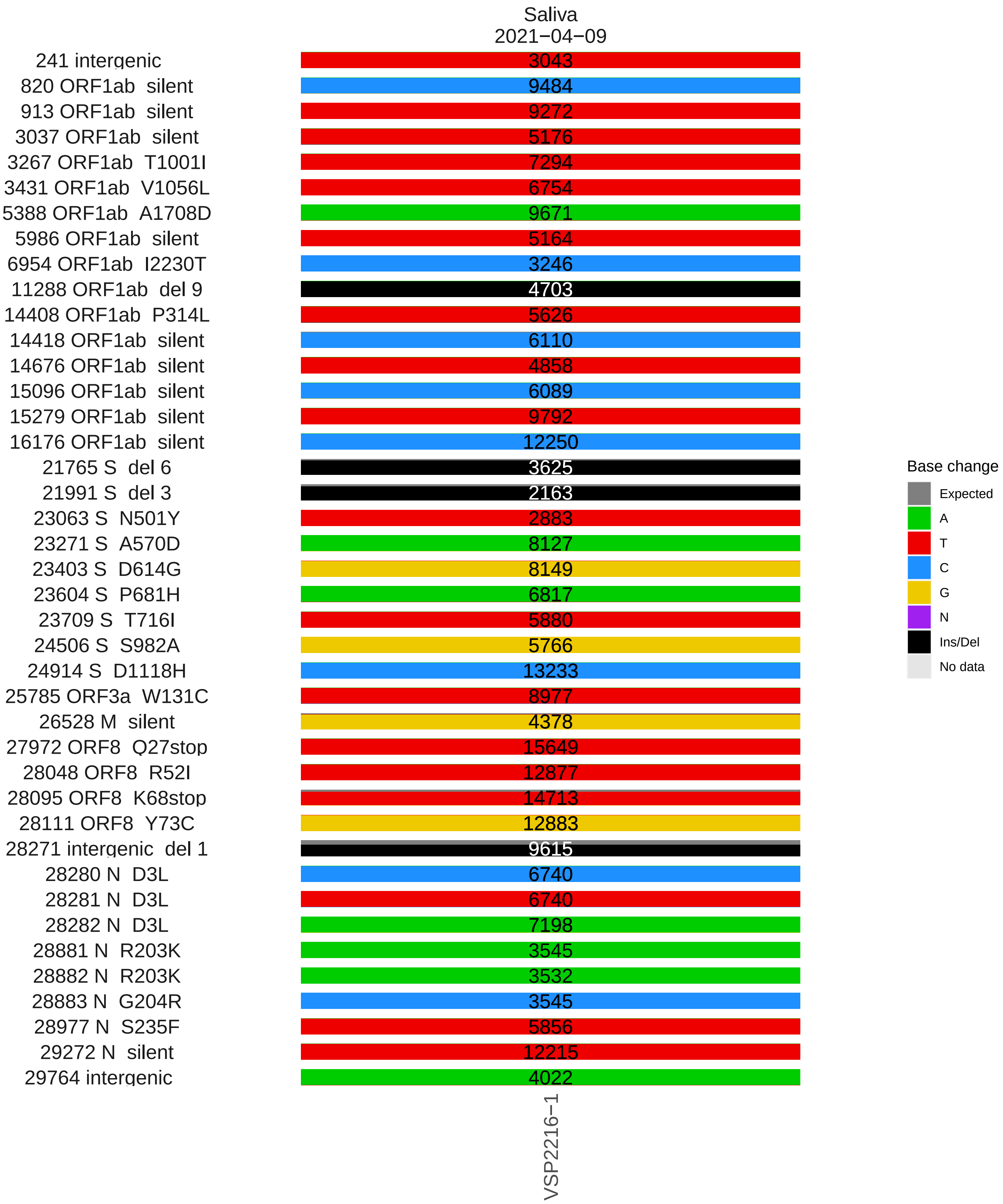
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2216-1	single experiment	NA	Saliva	2021-04-09	29.84	B.1.1.7	100.0%	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.

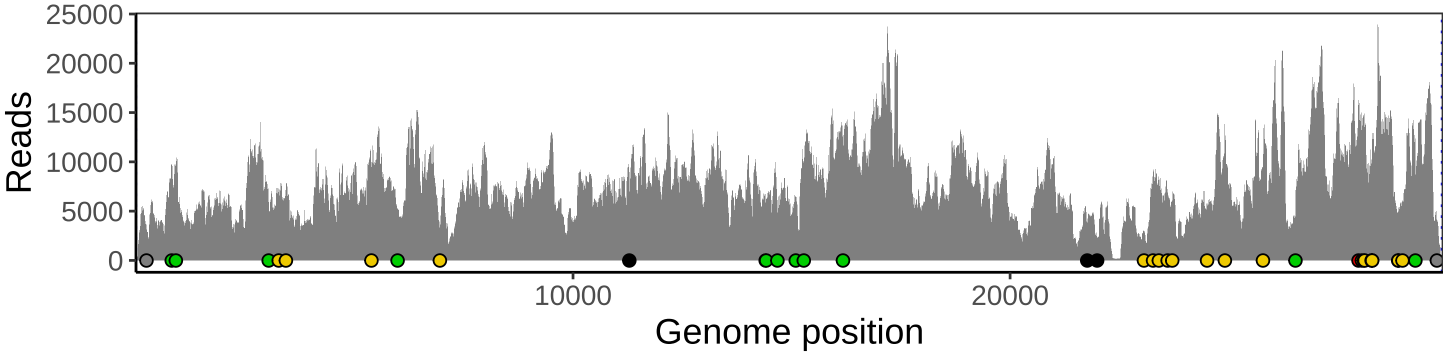



Saliva
2021−04−09
241 intergenic 3043
820 ORF1ab silent 9484
913 ORF1ab silent 9272
3037 ORF1ab silent 5176
3267 ORF1ab T1001I 7294
3431 ORF1ab V1056L 6754
5388 ORF1ab A1708D 9671
5986 ORF1ab silent 5164
6954 ORF1ab I2230T 3246
11288 ORF1ab del 9 4703
14408 ORF1ab P314L 5626
14418 ORF1ab silent 6110
14676 ORF1ab silent 4858
15096 ORF1ab silent 6089
15279 ORF1ab silent 9792
16176 ORF1ab silent 12250
21765 S del 6 3625
21991 S del 3 2163
23063 S N501Y 2883
23271 S A570D 8127
23403 S D614G 8149
23604 S P681H 6817
23709 S T716I 5880
24506 S S982A 5766
24914 S D1118H 13233
25785 ORF3a W131C 8977
26528 M silent 4378
27972 ORF8 Q27stop 15649
28048 ORF8 R52I 12877
28095 ORF8 K68stop 14713
28111 ORF8 Y73C 12883
28271 intergenic del 1 9615
28280 N D3L 6740
28281 N D3L 6740
28282 N D3L 7198
28881 N R203K 3545
28882 N R203K 3532
28883 N G204R 3545
28977 N S235F 5856
29272 N silent 12215
29764 intergenic 4022
VSP2216−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

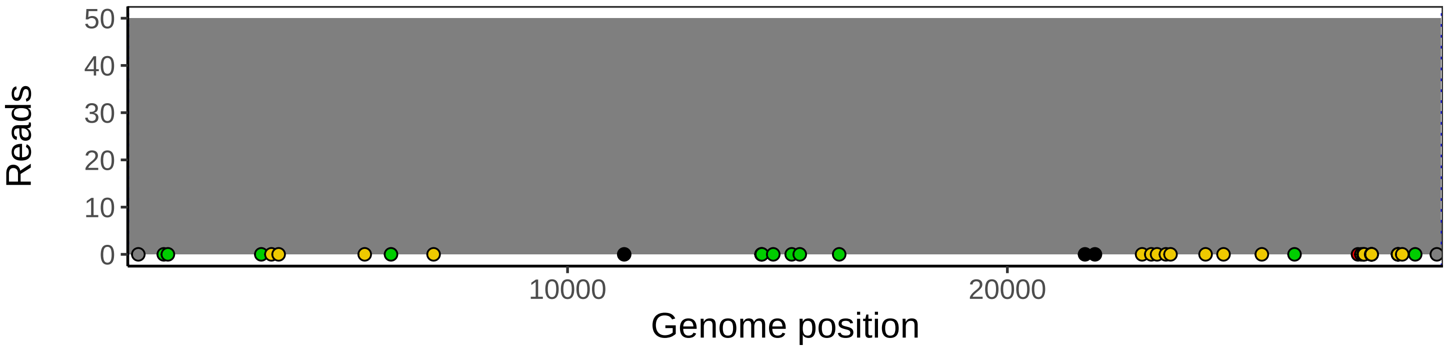
Analyses of individual experiments and composite results

VSP2216-1 | 2021-04-09 | Saliva | UPHS-1004 | genomes | single experiment

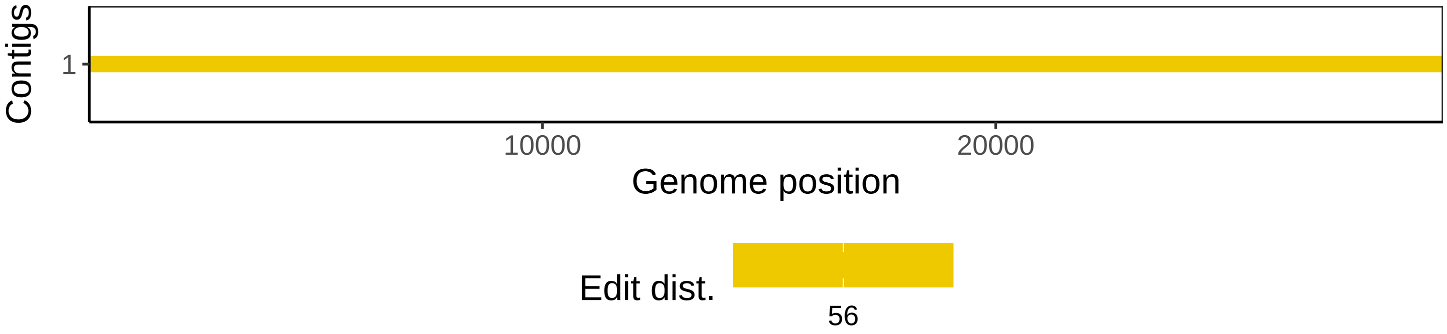
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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