COVID-19 subject UPHS-1332

2021-05-21

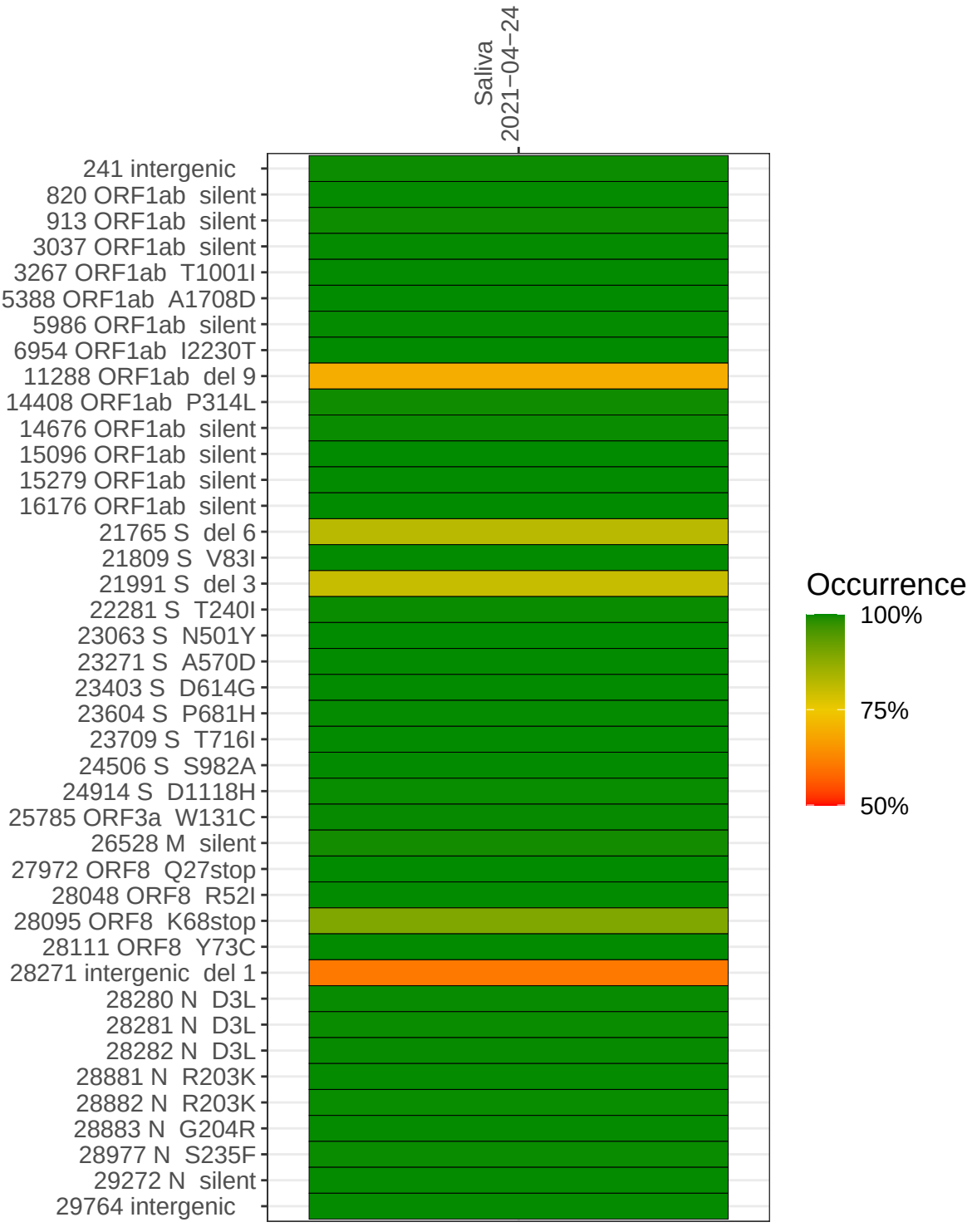
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

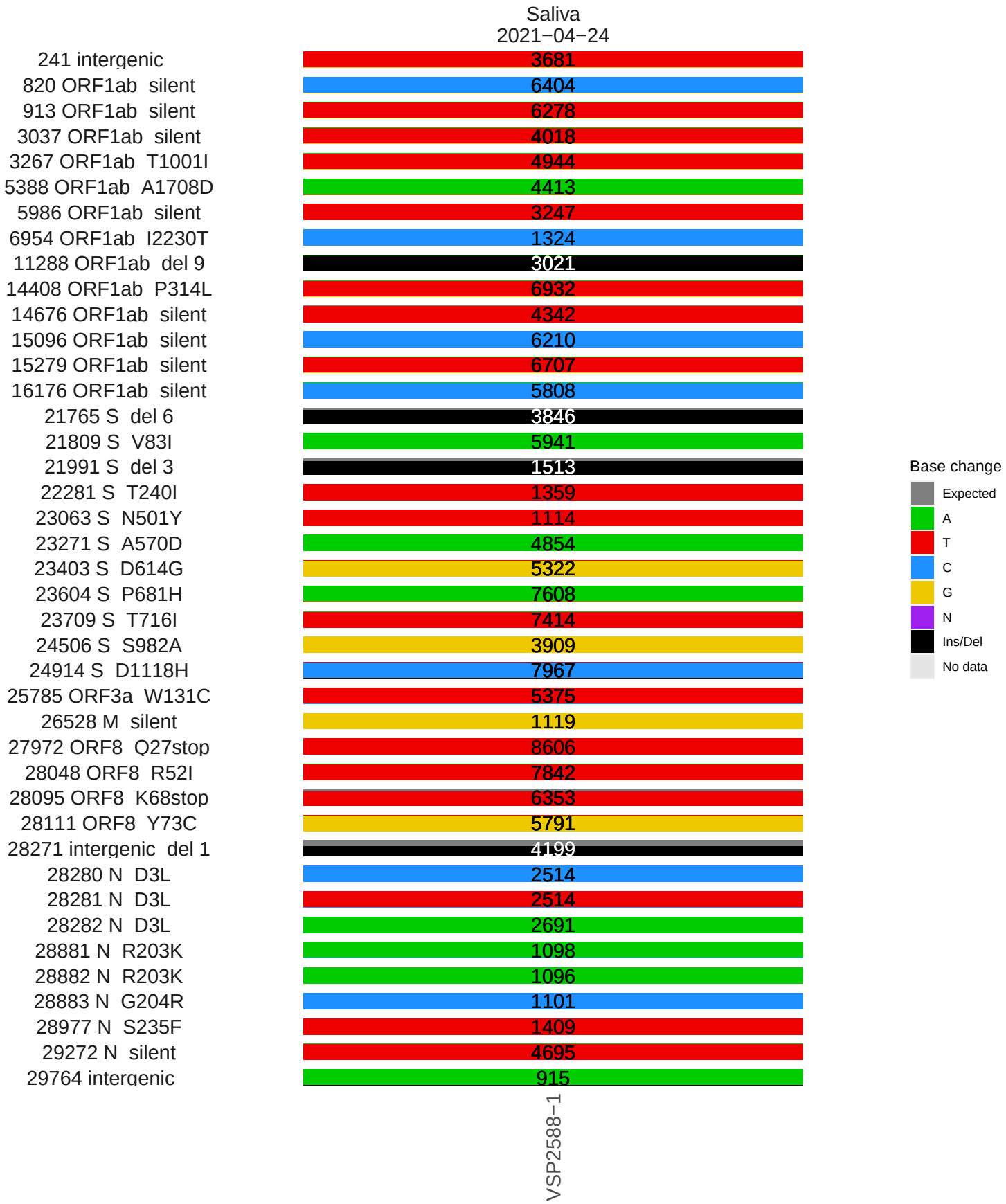
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2588-1	single experiment	NA	Saliva	2021-04-24	29.82	B.1.1.7	99.8%	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.

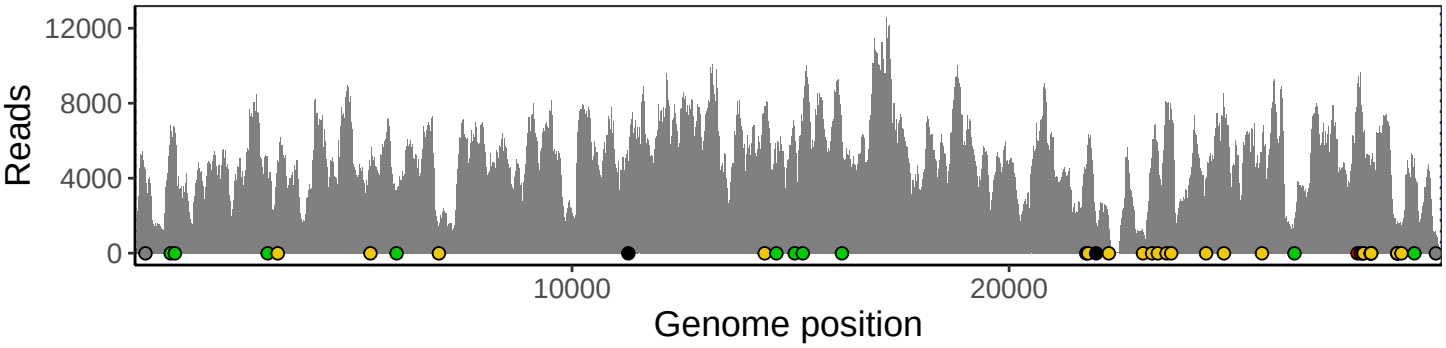



Saliva
2021−04−24
241 intergenic 3681
820 ORF1ab silent 6404
913 ORF1ab silent 6278
3037 ORF1ab silent 4018
3267 ORF1ab T1001I 4944
5388 ORF1ab A1708D 4413
5986 ORF1ab silent 3247
6954 ORF1ab I2230T 1324
11288 ORF1ab del 9 3021
14408 ORF1ab P314L 6932
14676 ORF1ab silent 4342
15096 ORF1ab silent 6210
15279 ORF1ab silent 6707
16176 ORF1ab silent 5808
21765 S del 6 3846
21809 S V83I 5941
21991 S del 3 1513
22281 S T240I 1359
23063 S N501Y 1114
23271 S A570D 4854
23403 S D614G 5322
23604 S P681H 7608
23709 S T716I 7414
24506 S S982A 3909
24914 S D1118H 7967
25785 ORF3a W131C 5375
26528 M silent 1119
27972 ORF8 Q27stop 8606
28048 ORF8 R52I 7842
28095 ORF8 K68stop 6353
28111 ORF8 Y73C 5791
28271 intergenic del 1 4199
28280 N D3L 2514
28281 N D3L 2514
28282 N D3L 2691
28881 N R203K 1098
28882 N R203K 1096
28883 N G204R 1101
28977 N S235F 1409
29272 N silent 4695
29764 intergenic 915
VSP2588−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

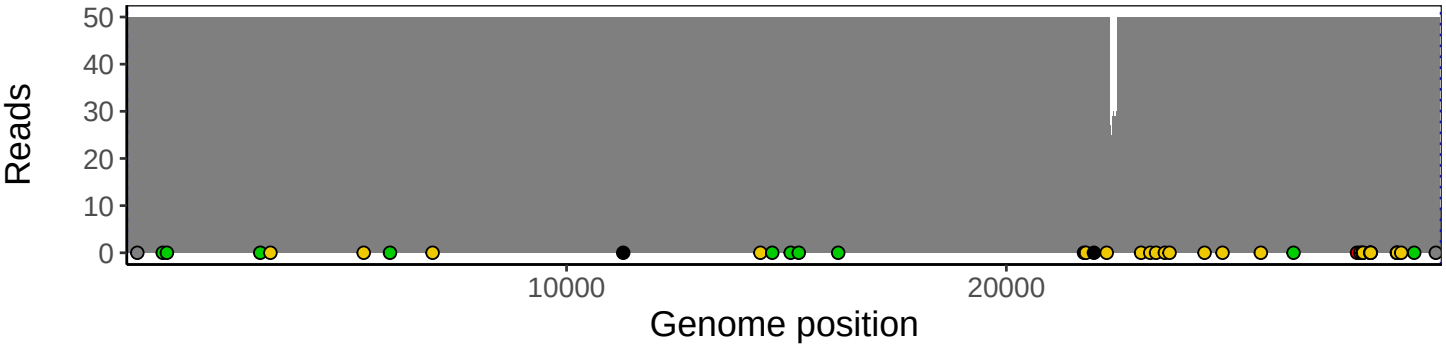
Analyses of individual experiments and composite results

VSP2588-1 | 2021-04-24 | Saliva | UPHS-1332 | genomes | single experiment

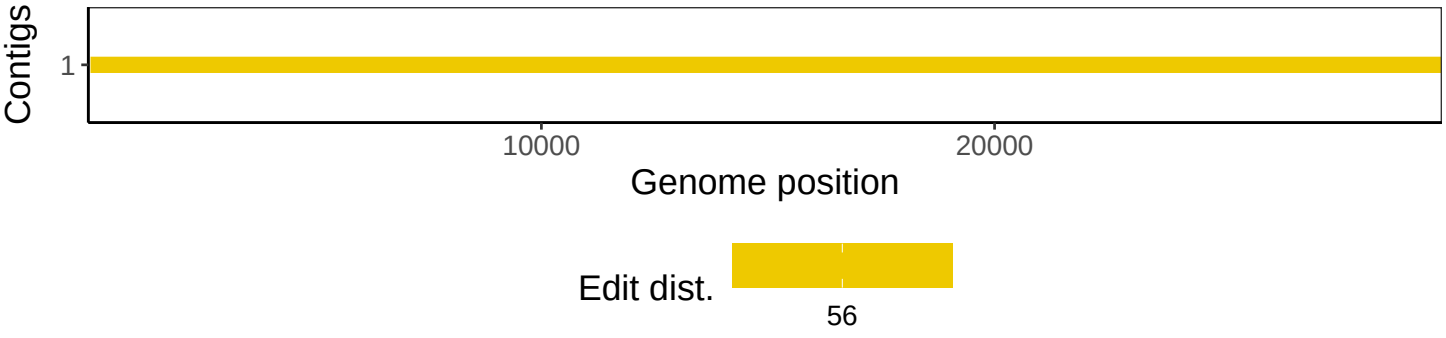
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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