COVID-19 subject UPHS-0693

2021-05-05

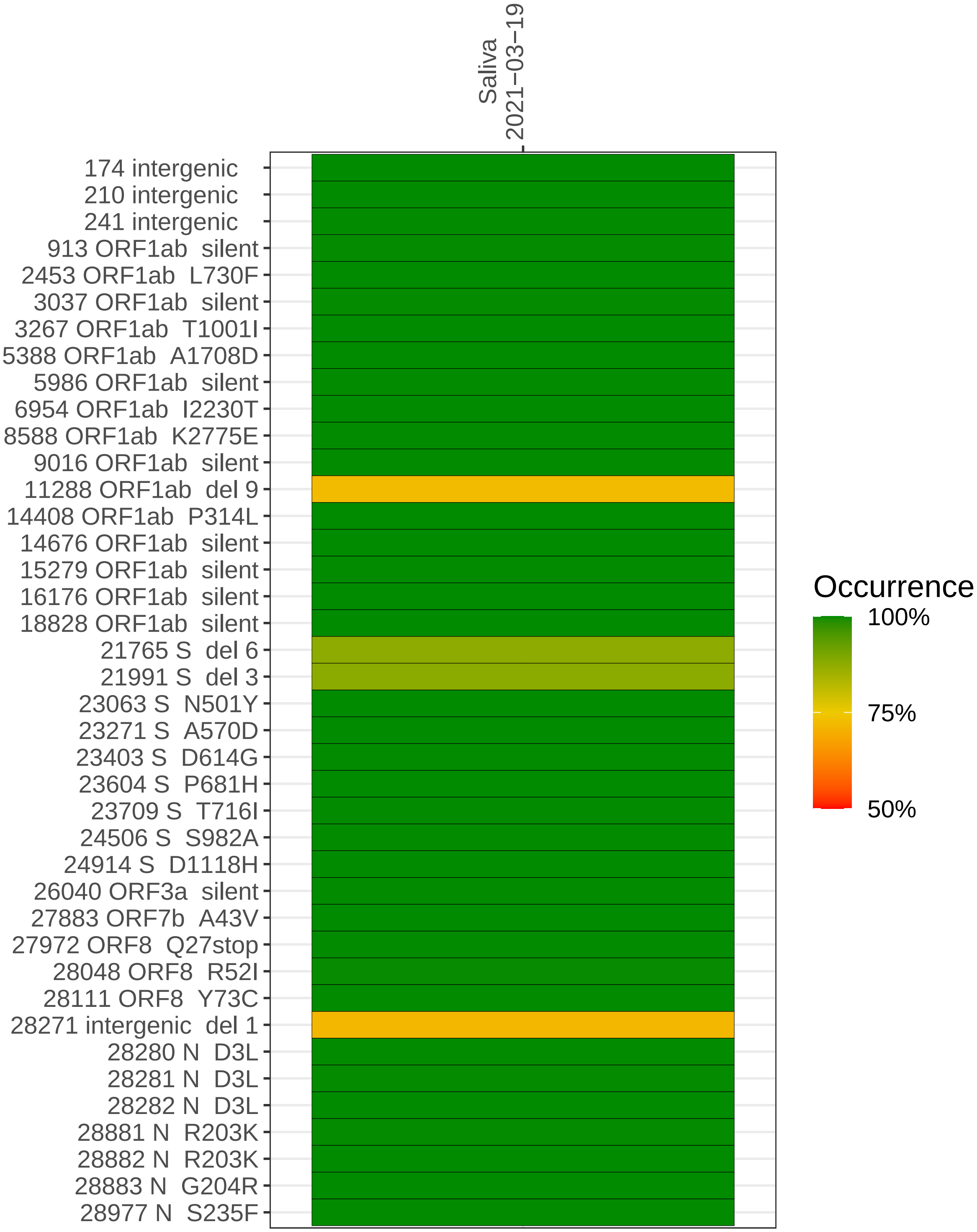
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

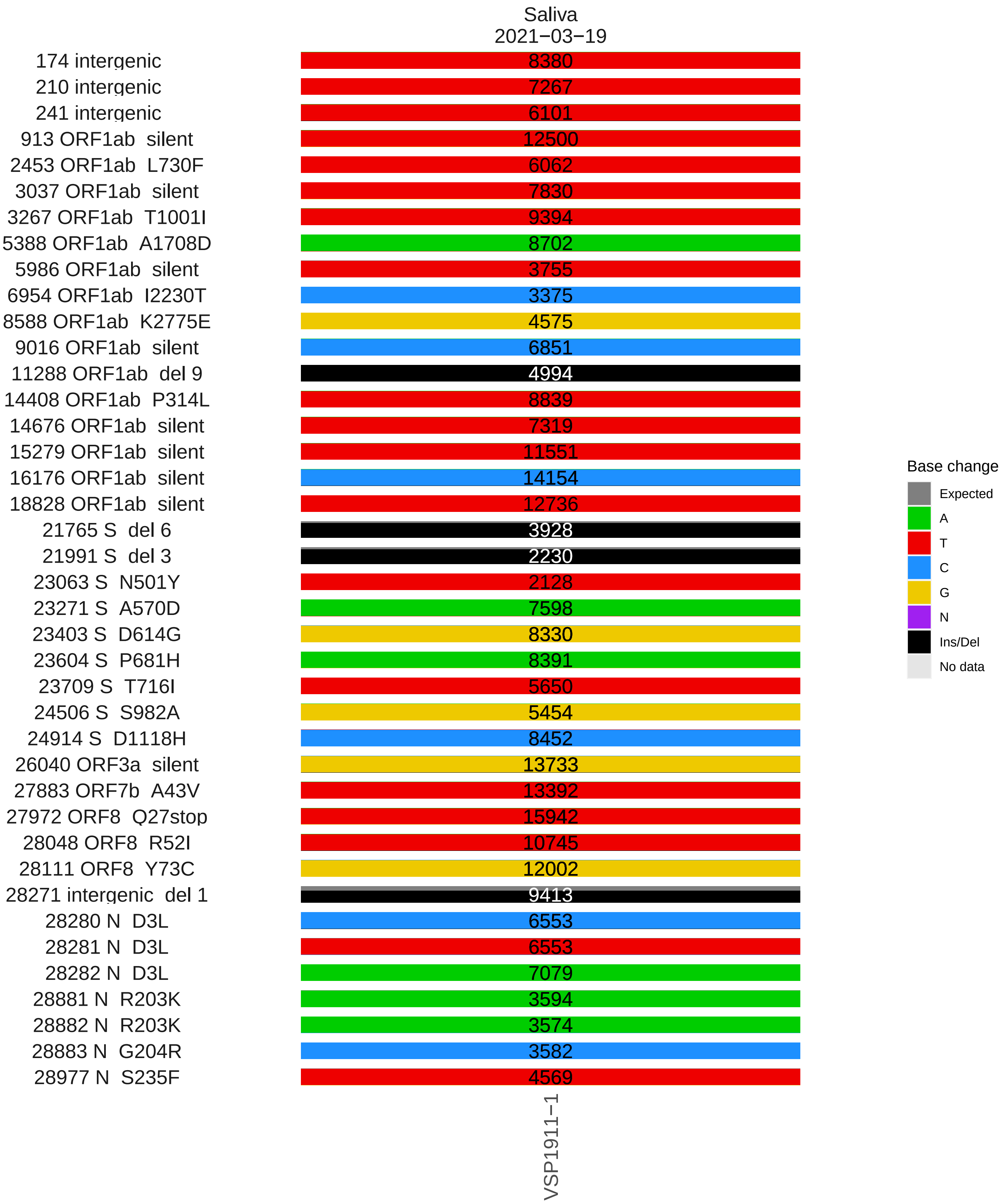
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1911-1	single experiment	NA	Saliva	2021-03-19	29.92	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.

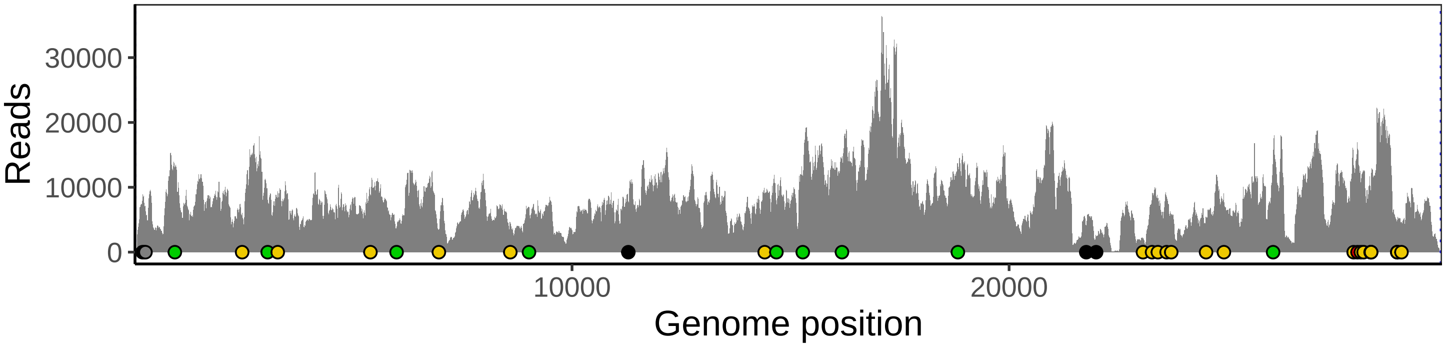



Saliva
2021−03−19
174 intergenic 8380
210 intergenic 7267
241 intergenic 6101
913 ORF1ab silent 12500
2453 ORF1ab L730F 6062
3037 ORF1ab silent 7830
3267 ORF1ab T1001I 9394
5388 ORF1ab A1708D 8702
5986 ORF1ab silent 3755
6954 ORF1ab I2230T 3375
8588 ORF1ab K2775E 4575
9016 ORF1ab silent 6851
11288 ORF1ab del 9 4994
14408 ORF1ab P314L 8839
14676 ORF1ab silent 7319
15279 ORF1ab silent 11551
16176 ORF1ab silent 14154
18828 ORF1ab silent 12736
21765 S del 6 3928
21991 S del 3 2230
23063 S N501Y 2128
23271 S A570D 7598
23403 S D614G 8330
23604 S P681H 8391
23709 S T716I 5650
24506 S S982A 5454
24914 S D1118H 8452
26040 ORF3a silent 13733
27883 ORF7b A43V 13392
27972 ORF8 Q27stop 15942
28048 ORF8 R52I 10745
28111 ORF8 Y73C 12002
28271 intergenic del 1 9413
28280 N D3L 6553
28281 N D3L 6553
28282 N D3L 7079
28881 N R203K 3594
28882 N R203K 3574
28883 N G204R 3582
28977 N S235F 4569
VSP1911−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

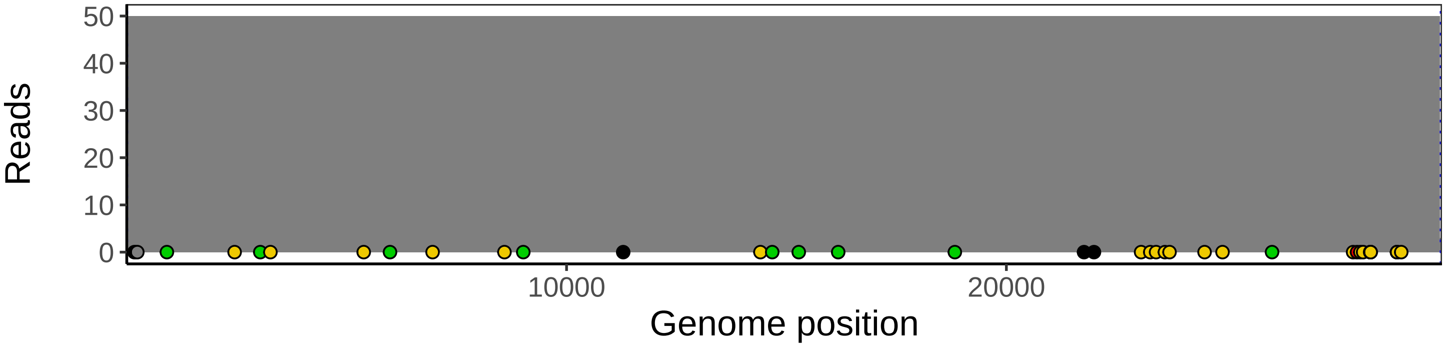
Analyses of individual experiments and composite results

VSP1911-1 | 2021-03-19 | Saliva | UPHS-0693 | genomes | single experiment

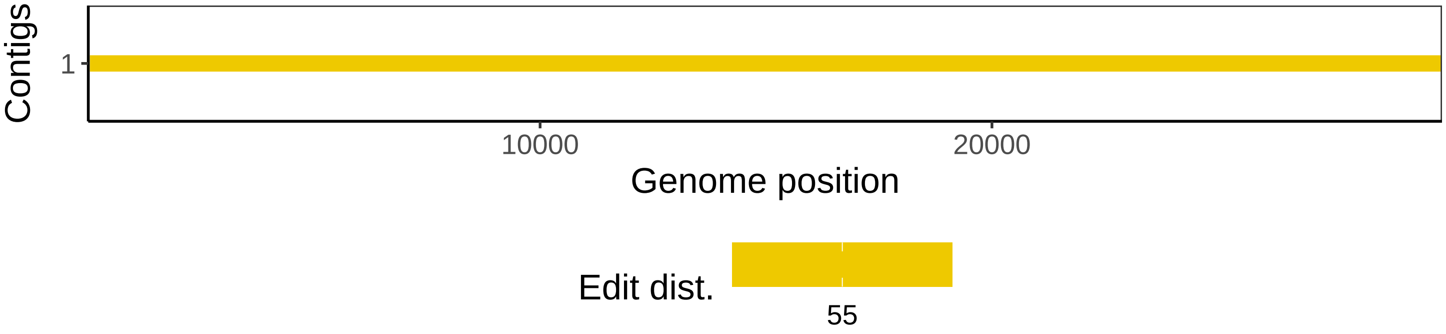
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.0.0
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