COVID-19 subject UPHS-0702

2021-05-05

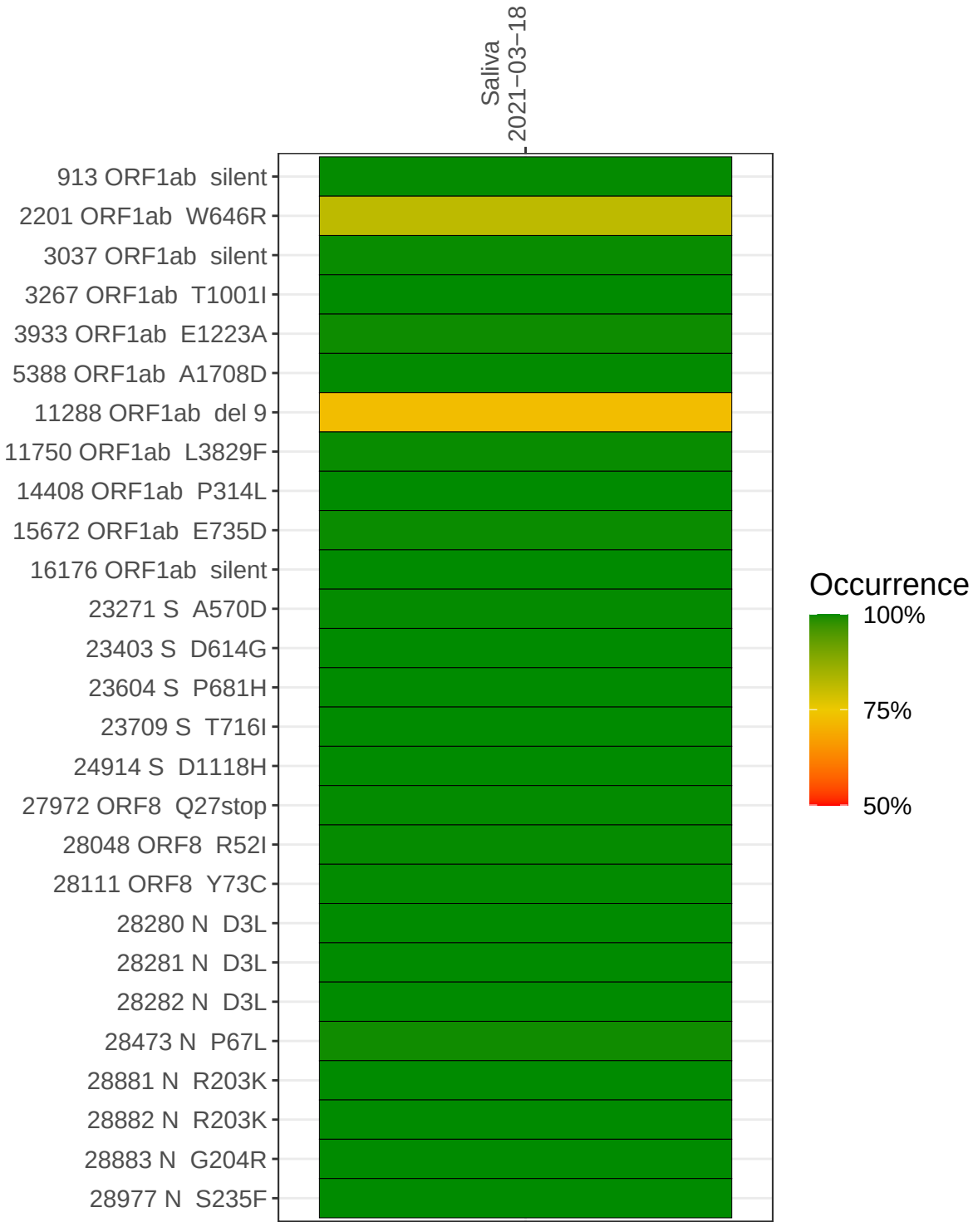
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

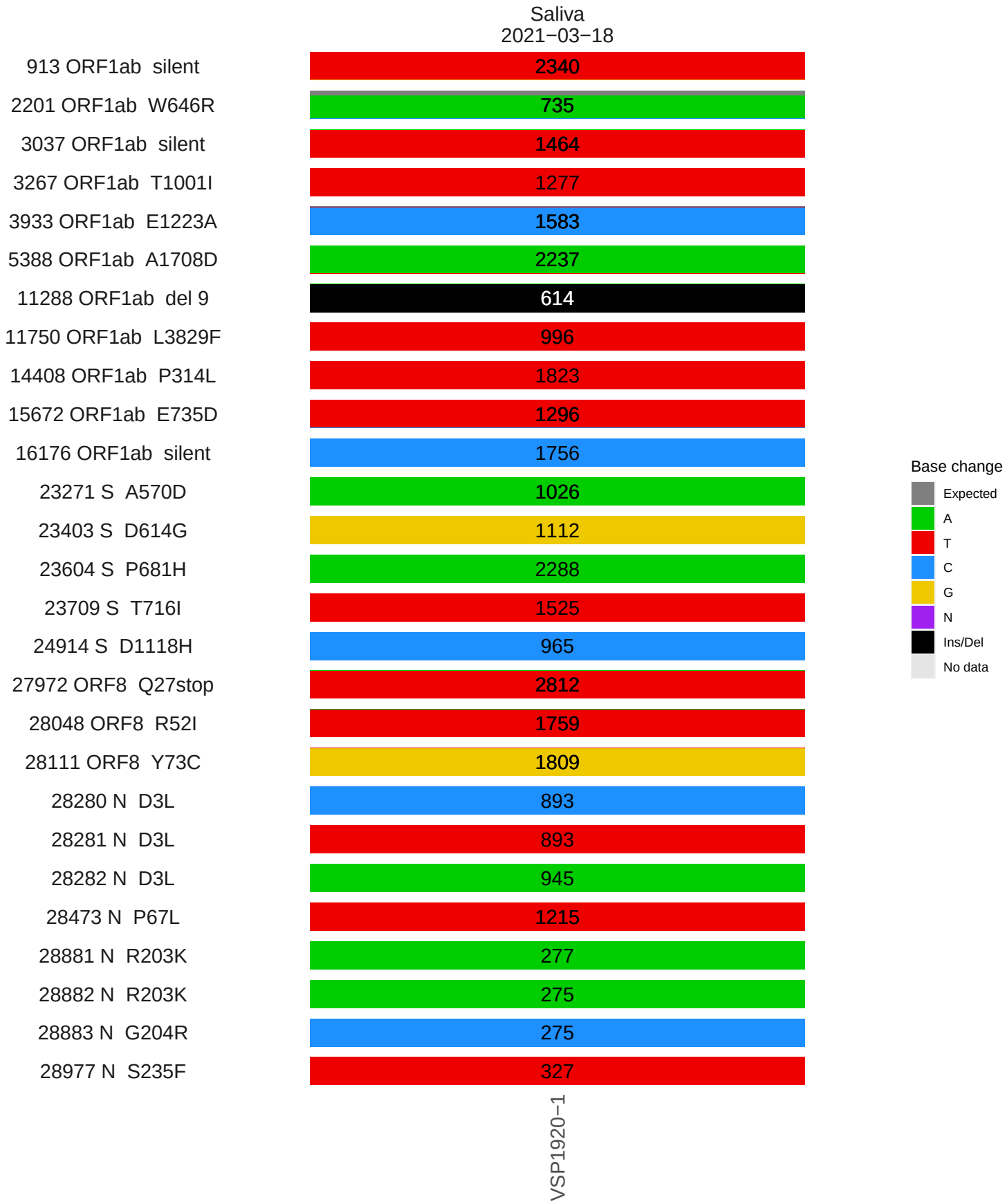
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1920-1	single experiment	NA	Saliva	2021-03-18	5.62	NA	90.7%	74.2%

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.

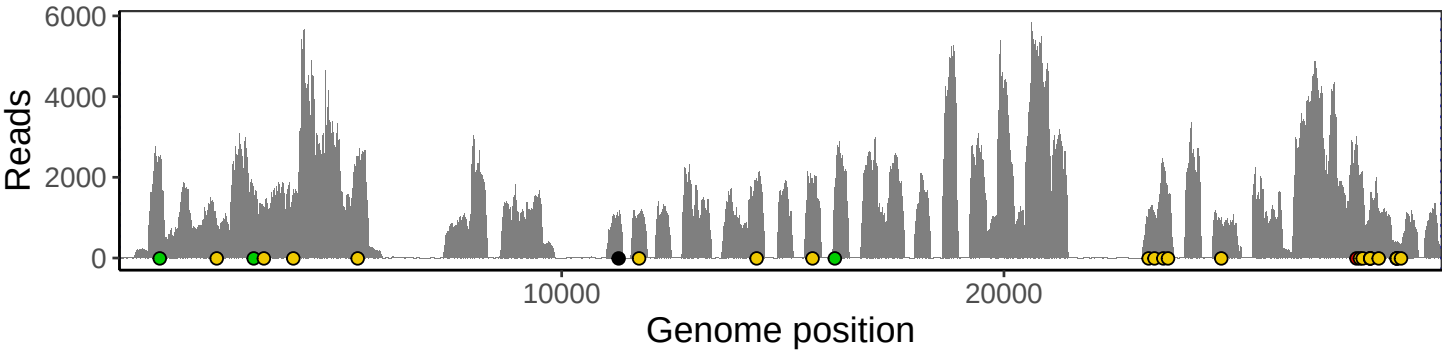



Saliva
2021−03−18
913 ORF1ab silent
2201 ORF1ab W646R
3037 ORF1ab silent
3267 ORF1ab T1001I
3933 ORF1ab E1223A
5388 ORF1ab A1708D
11288 ORF1ab del 9
11750 ORF1ab L3829F
14408 ORF1ab P314L
15672 ORF1ab E735D
16176 ORF1ab silent
23271 S A570D
23403 S D614G
23604 S P681H
23709 S T716I
24914 S D1118H
27972 ORF8 Q27stop
28048 ORF8 R52I
28111 ORF8 Y73C
28280 N D3L
28281 N D3L
28282 N D3L
28473 N P67L
28881 N R203K
28882 N R203K
28883 N G204R
28977 N S235F
2340
735
1464
1277
1583
2237
614
996
1823
1296
1756
1026
1112
2288
1525
965
2812
1759
1809
893
893
945
1215
277
275
275
327
VSP1920−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

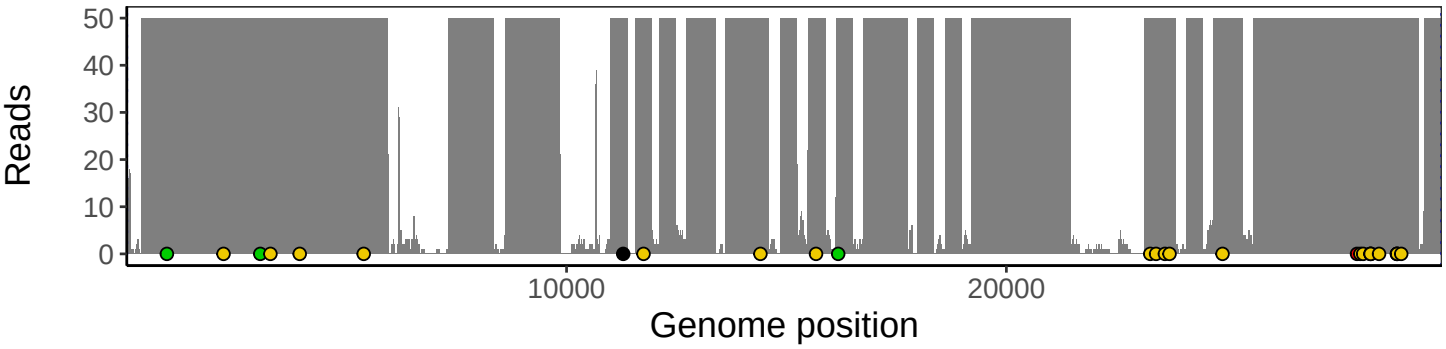
Analyses of individual experiments and composite results

VSP1920-1 | 2021-03-18 | Saliva | UPHS-0702 | genomes | single experiment

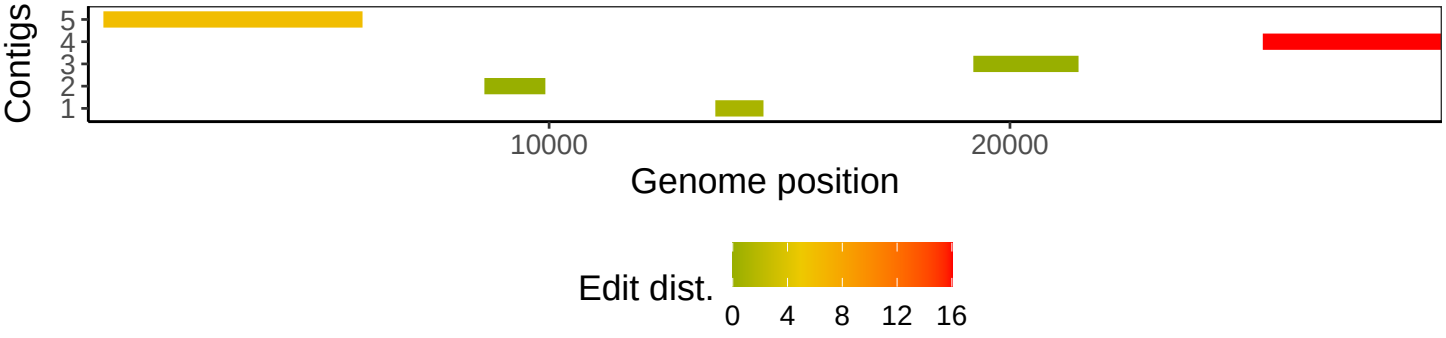
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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