COVID-19 subject UPHS-0728

2021-05-05

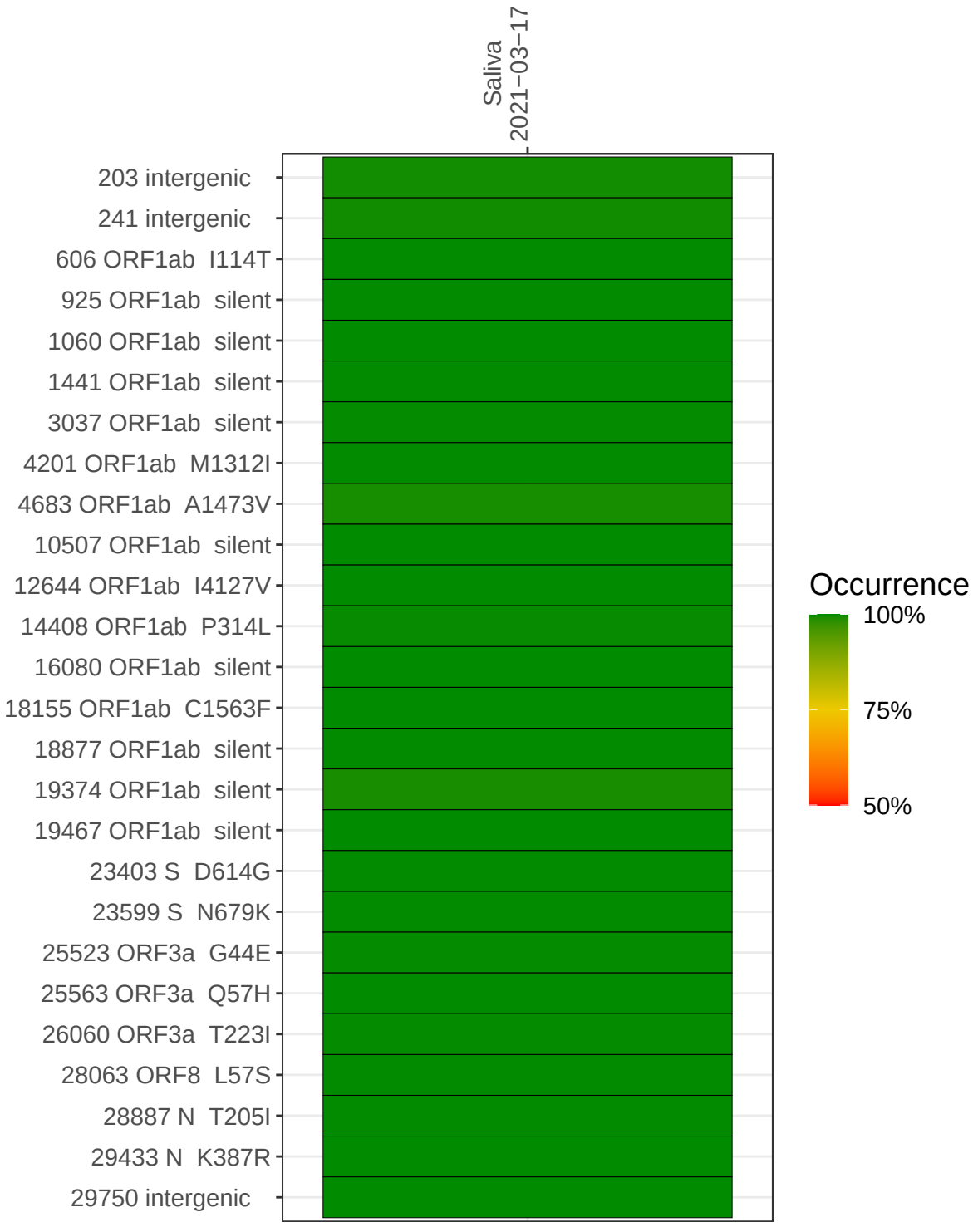
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

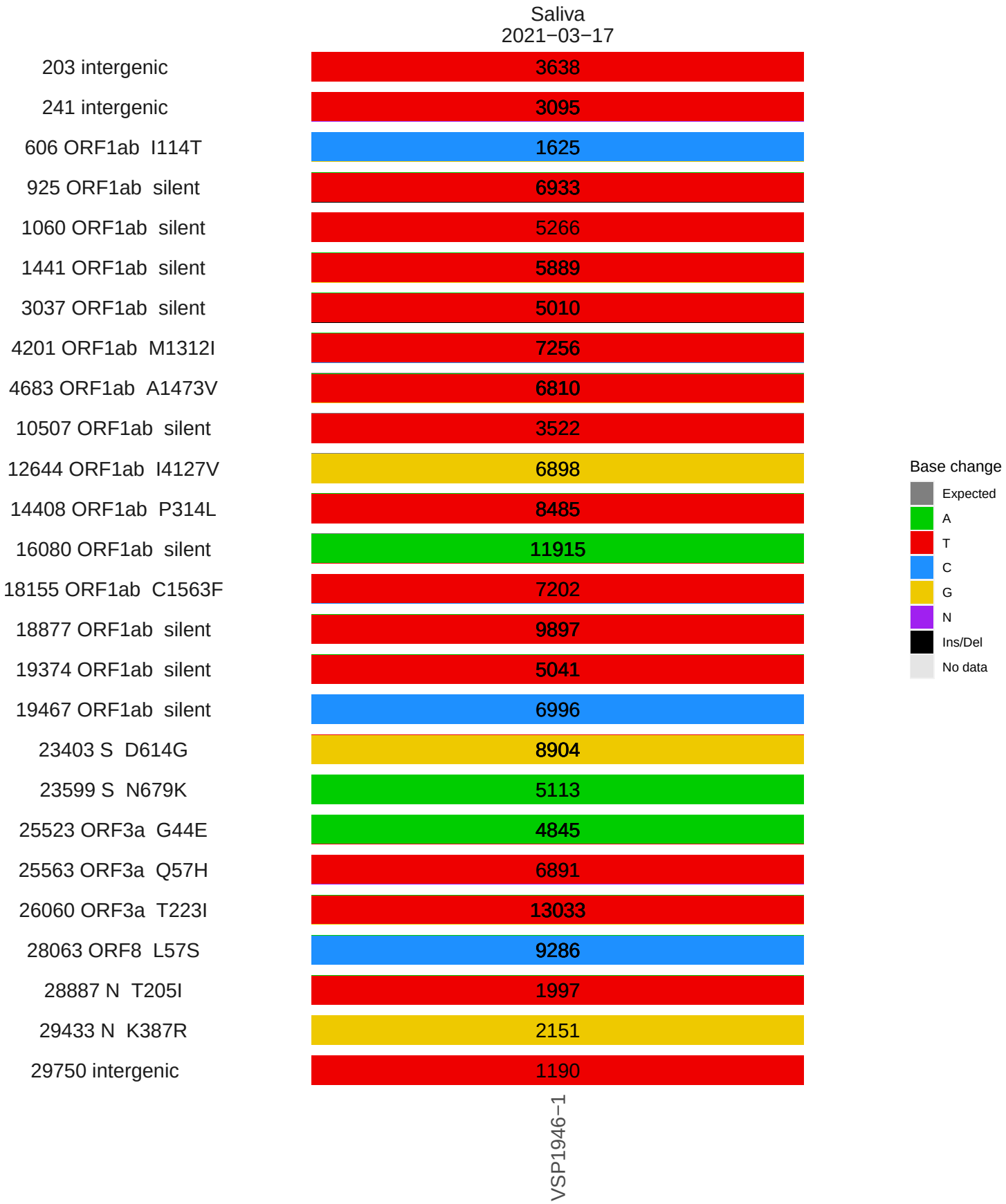
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1946-1	single experiment	NA	Saliva	2021-03-17	29.89	B.1.111	99.8%	99.7%

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.

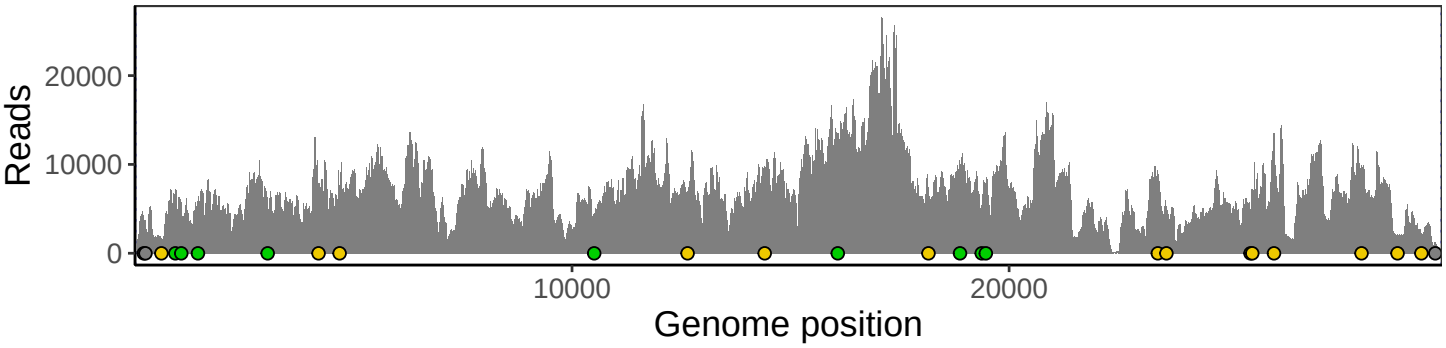



Saliva
2021−03−17
203 intergenic
241 intergenic
606 ORF1ab I114T
925 ORF1ab silent
1060 ORF1ab silent
1441 ORF1ab silent
3037 ORF1ab silent
4201 ORF1ab M1312I
4683 ORF1ab A1473V
10507 ORF1ab silent
12644 ORF1ab I4127V
14408 ORF1ab P314L
16080 ORF1ab silent
18155 ORF1ab C1563F
18877 ORF1ab silent
19374 ORF1ab silent
19467 ORF1ab silent
23403 S D614G
23599 S N679K
25523 ORF3a G44E
25563 ORF3a Q57H
26060 ORF3a T223I
28063 ORF8 L57S
28887 N T205I
29433 N K387R
29750 intergenic
3638
3095
1625
6933
5266
5889
5010
7256
6810
3522
6898
8485
11915
7202
9897
5041
6996
8904
5113
4845
6891
13033
9286
1997
2151
1190
VSP1946−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

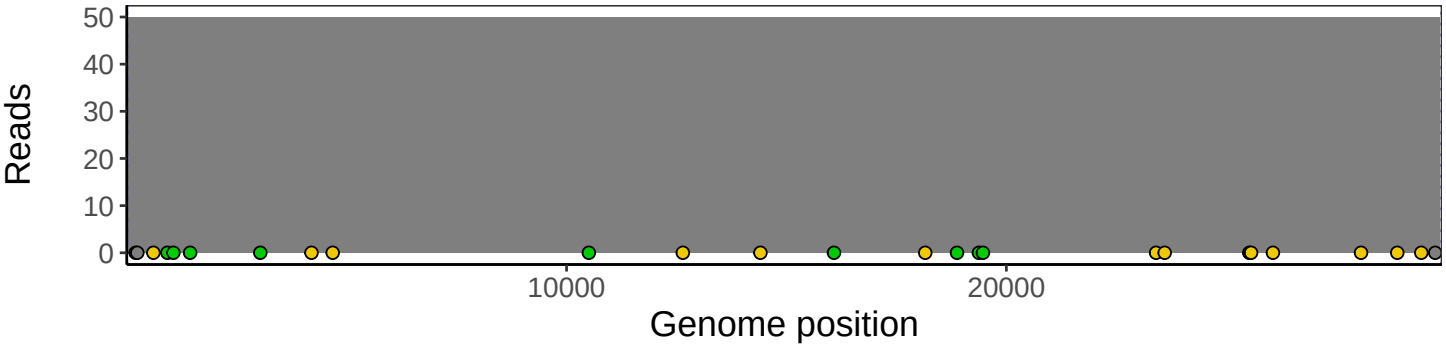
Analyses of individual experiments and composite results

VSP1946-1 | 2021-03-17 | Saliva | UPHS-0728 | genomes | single experiment

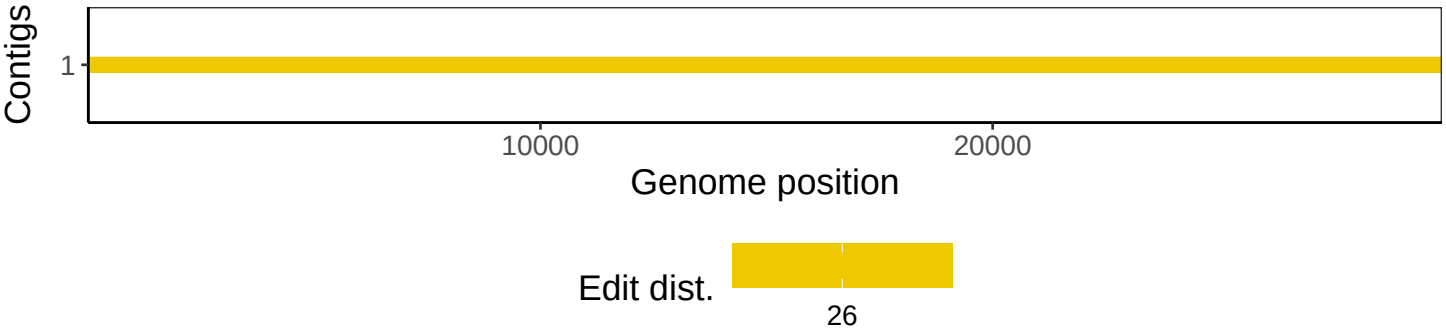
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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