COVID-19 subject UPHS- 0788

2021-05-05

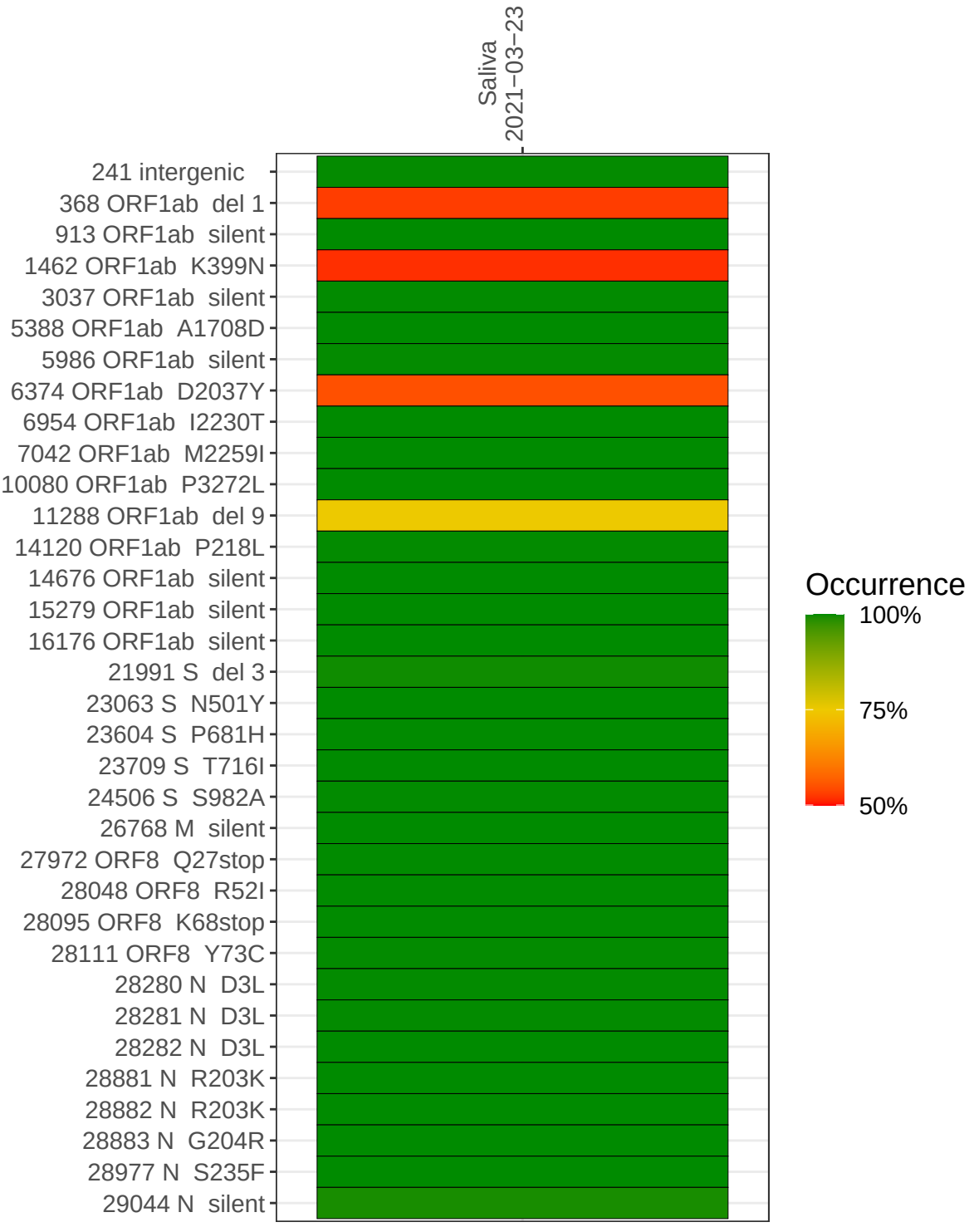
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

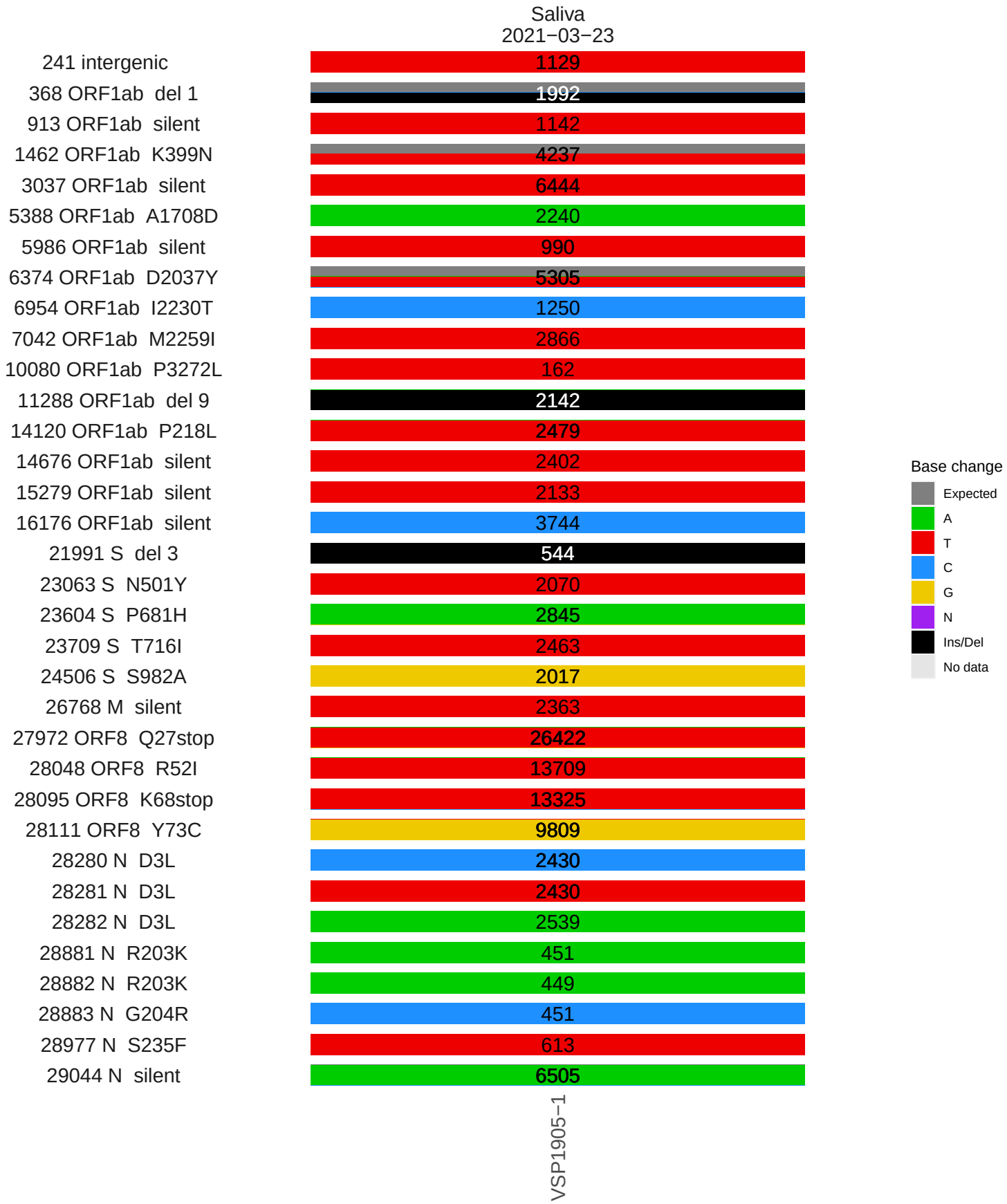
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1905-1	single experiment	NA	Saliva	2021-03-23	1.95	NA	69.2%	68.0%

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.

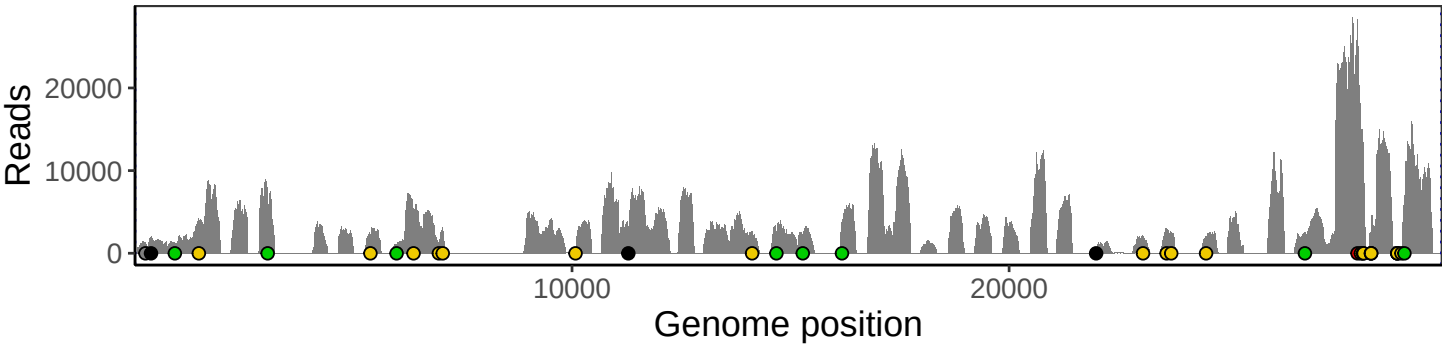



Saliva
2021−03−23
241 intergenic
368 ORF1ab del 1
913 ORF1ab silent
1462 ORF1ab K399N
3037 ORF1ab silent
5388 ORF1ab A1708D
5986 ORF1ab silent
6374 ORF1ab D2037Y
6954 ORF1ab I2230T
7042 ORF1ab M2259I
10080 ORF1ab P3272L
11288 ORF1ab del 9
14120 ORF1ab P218L
14676 ORF1ab silent
15279 ORF1ab silent
16176 ORF1ab silent
21991 S del 3
23063 S N501Y
23604 S P681H
23709 S T716I
24506 S S982A
26768 M silent
27972 ORF8 Q27stop
28048 ORF8 R52I
28095 ORF8 K68stop
28111 ORF8 Y73C
28280 N D3L
28281 N D3L
28282 N D3L
28881 N R203K
28882 N R203K
28883 N G204R
28977 N S235F
29044 N silent
1129
1992
1142
4237
6444
2240
990
5305
1250
2866
162
2142
2479
2402
2133
3744
544
2070
2845
2463
2017
2363
26422
13709
13325
9809
2430
2430
2539
451
449
451
613
6505
VSP1905−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

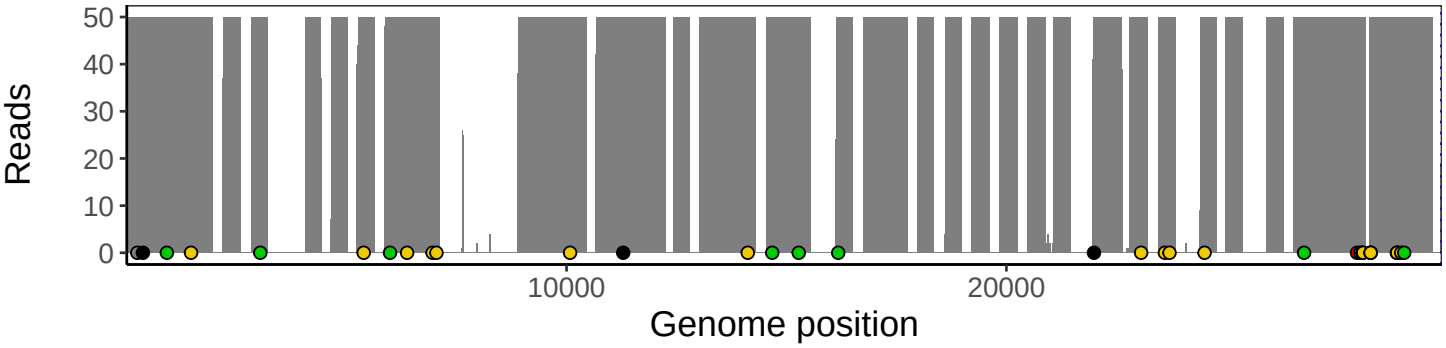
Analyses of individual experiments and composite results

VSP1905-1 | 2021-03-23 | Saliva | UPHS- 0788 | genomes | single experiment

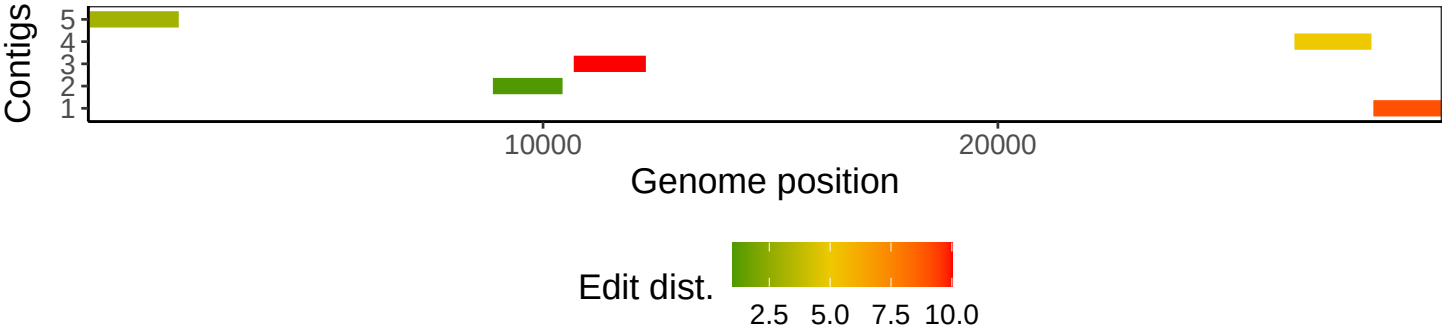
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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