COVID-19 subject UPHS- 0786

2021-05-05

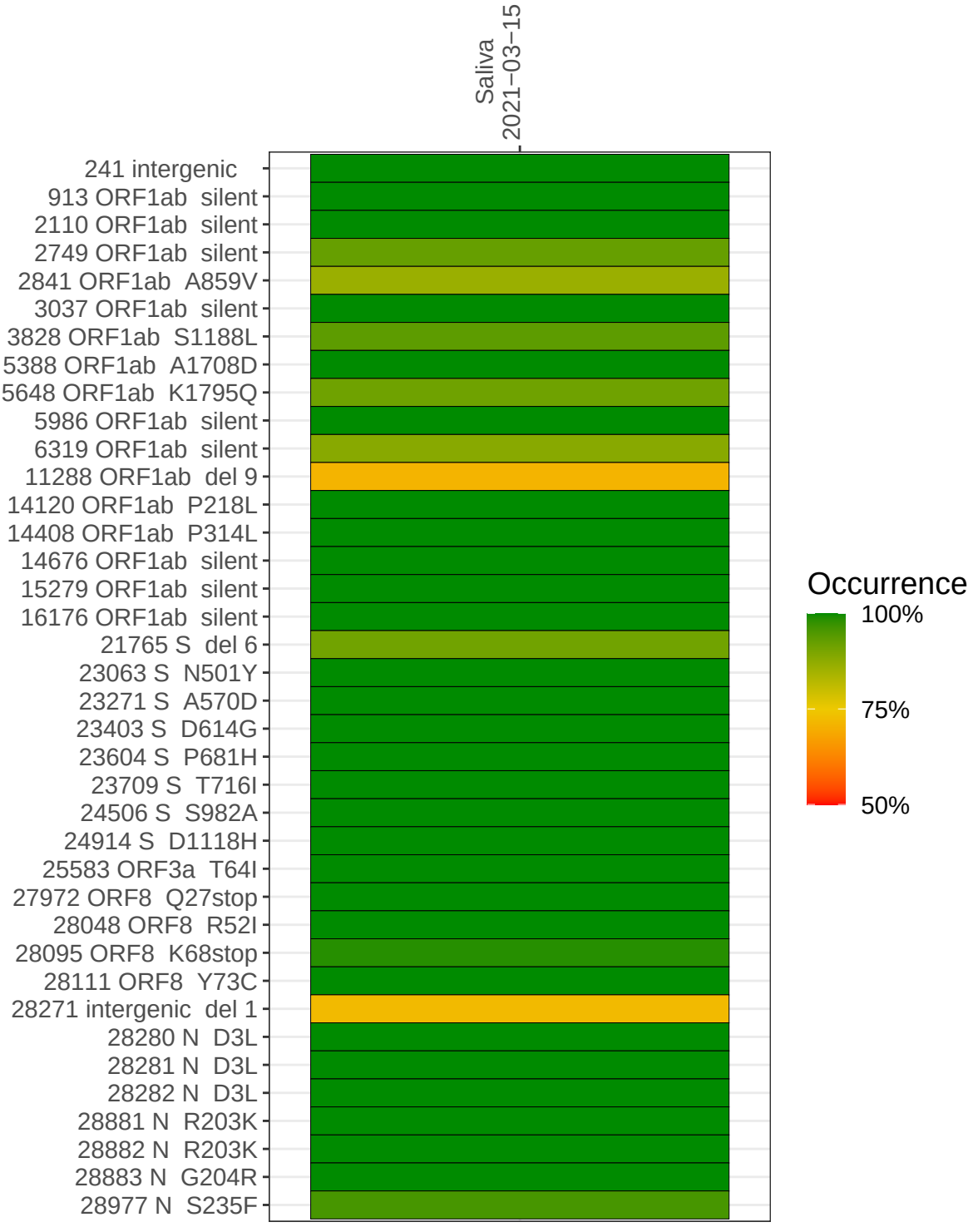
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

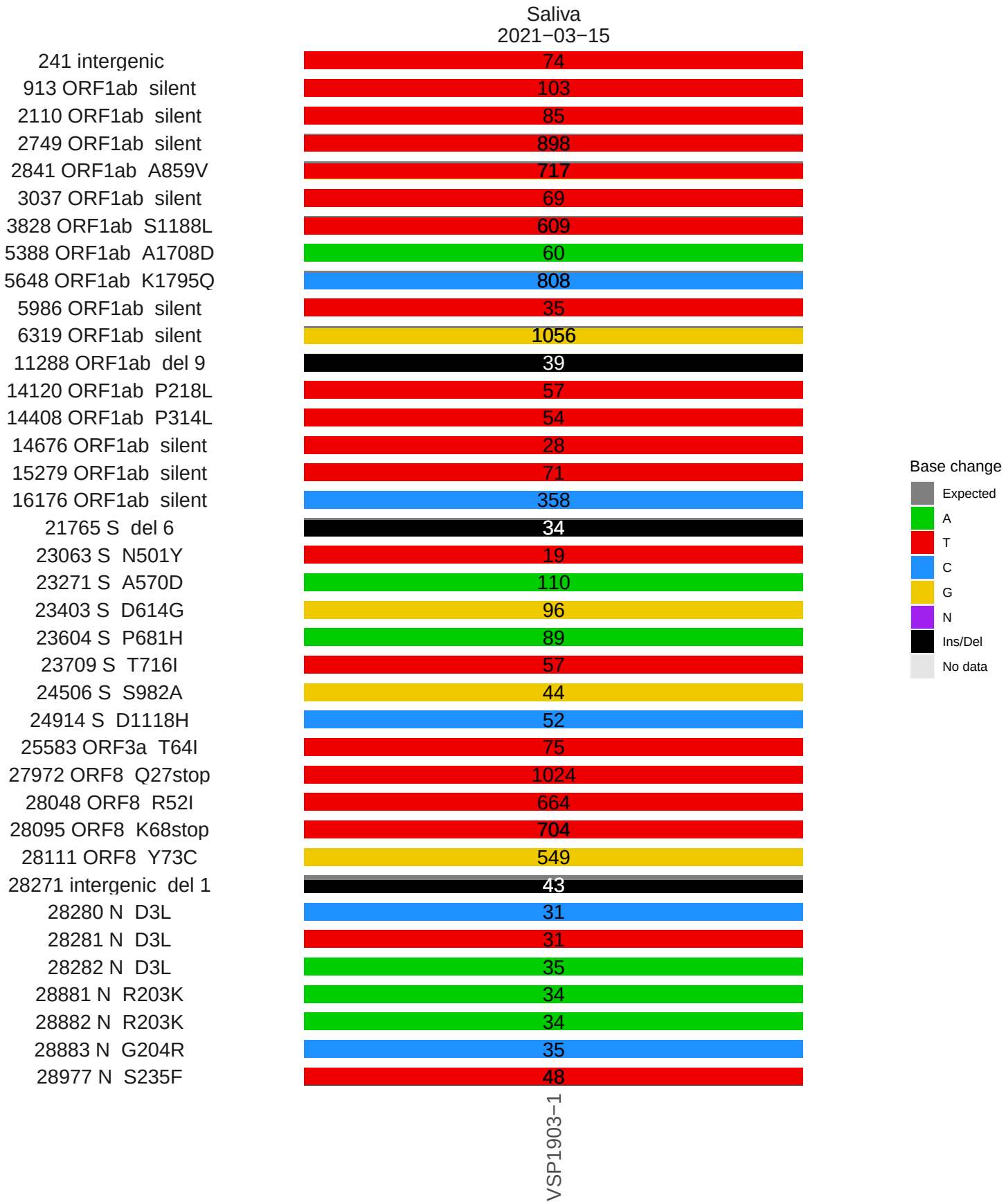
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1903-1	single experiment	NA	Saliva	2021-03-15	22.28	B.1.1.7	99.5%	98.9%

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.

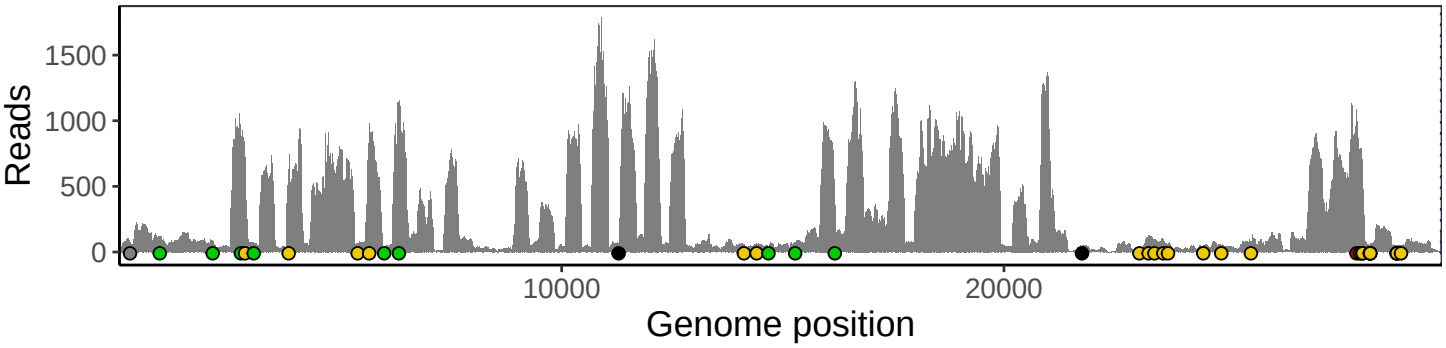



Saliva
2021−03−15
241 intergenic 74
913 ORF1ab silent 103
2110 ORF1ab silent 85
2749 ORF1ab silent 898
2841 ORF1ab A859V 717
3037 ORF1ab silent 69
3828 ORF1ab S1188L 609
5388 ORF1ab A1708D 60
5648 ORF1ab K1795Q 808
5986 ORF1ab silent 35
6319 ORF1ab silent 1056
11288 ORF1ab del 9 39
14120 ORF1ab P218L 57
14408 ORF1ab P314L 54
14676 ORF1ab silent 28
15279 ORF1ab silent 71
16176 ORF1ab silent 358
21765 S del 6 34
23063 S N501Y 19
23271 S A570D 110
23403 S D614G 96
23604 S P681H 89
23709 S T716I 57
24506 S S982A 44
24914 S D1118H 52
25583 ORF3a T64I 75
27972 ORF8 Q27stop 1024
28048 ORF8 R52I 664
28095 ORF8 K68stop 704
28111 ORF8 Y73C 549
28271 intergenic del 1 43
28280 N D3L 31
28281 N D3L 31
28282 N D3L 35
28881 N R203K 34
28882 N R203K 34
28883 N G204R 35
28977 N S235F 48
VSP1903−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

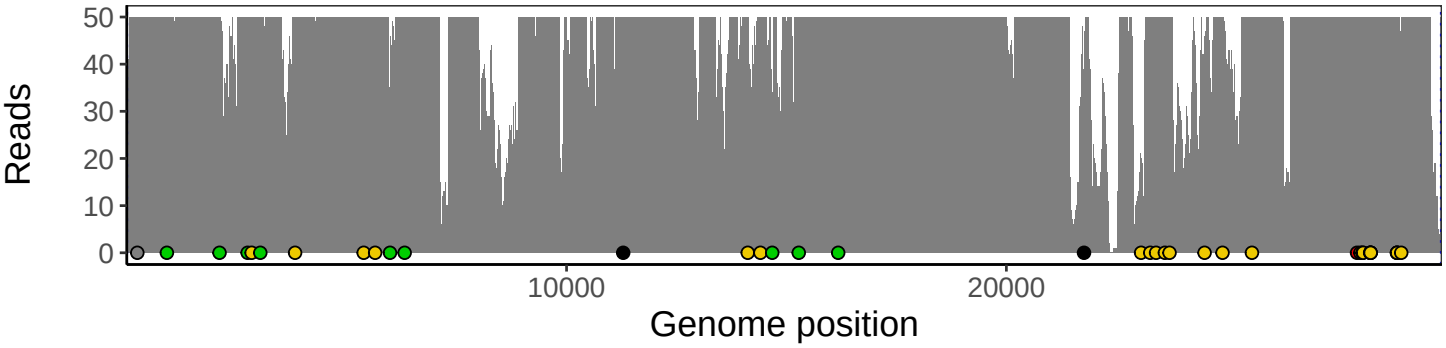
Analyses of individual experiments and composite results

VSP1903-1 | 2021-03-15 | Saliva | UPHS- 0786 | genomes | single experiment

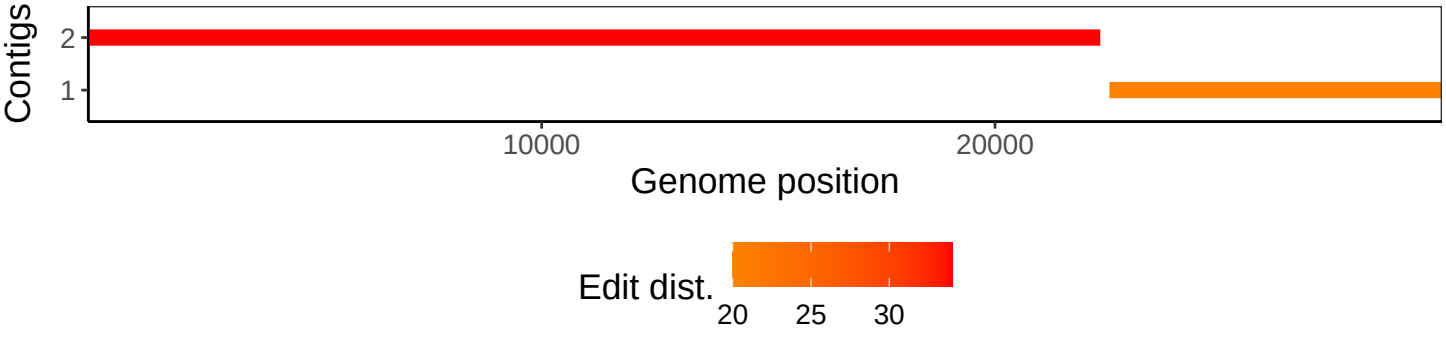
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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