COVID-19 subject UPHS-0379

2021-06-23

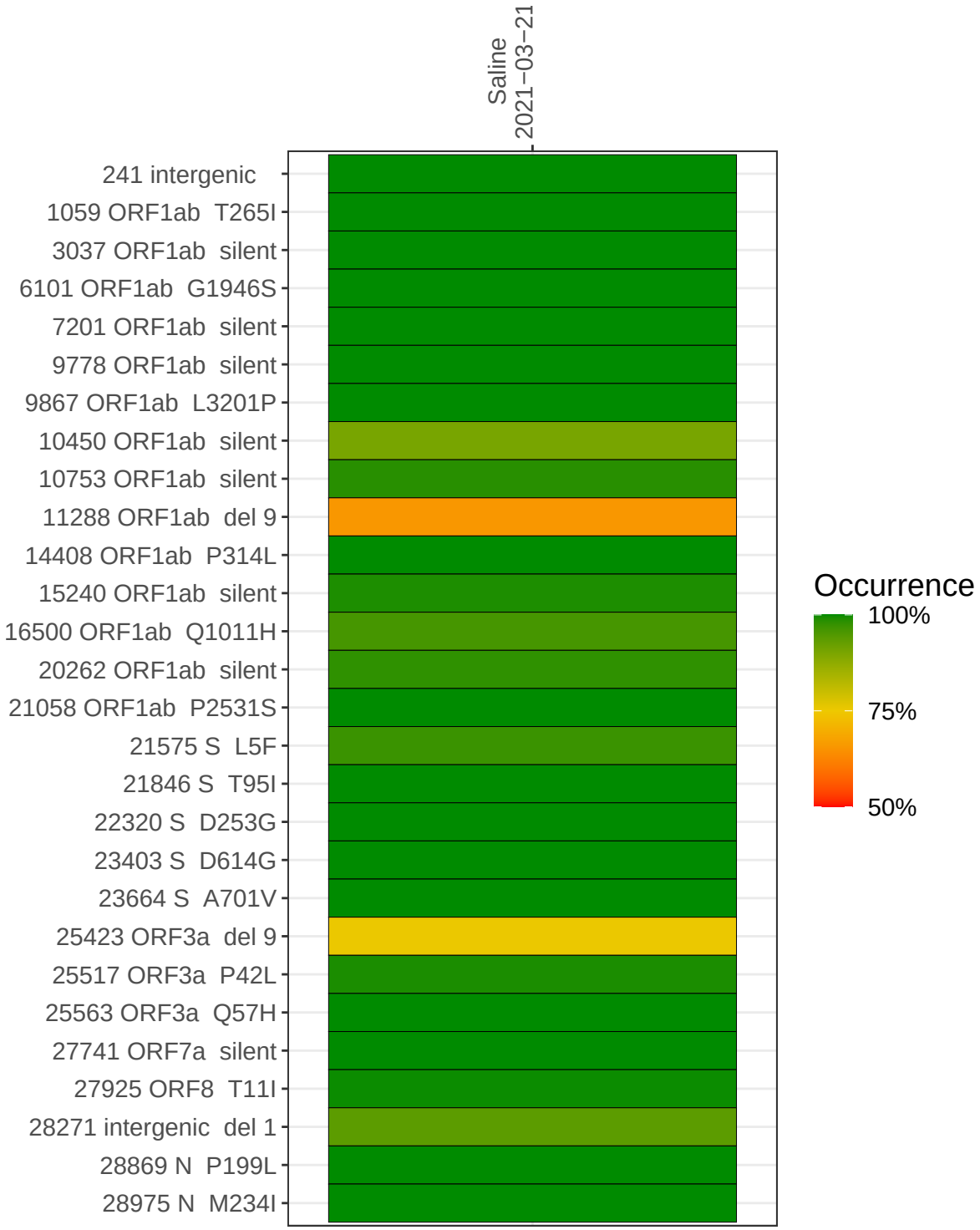
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

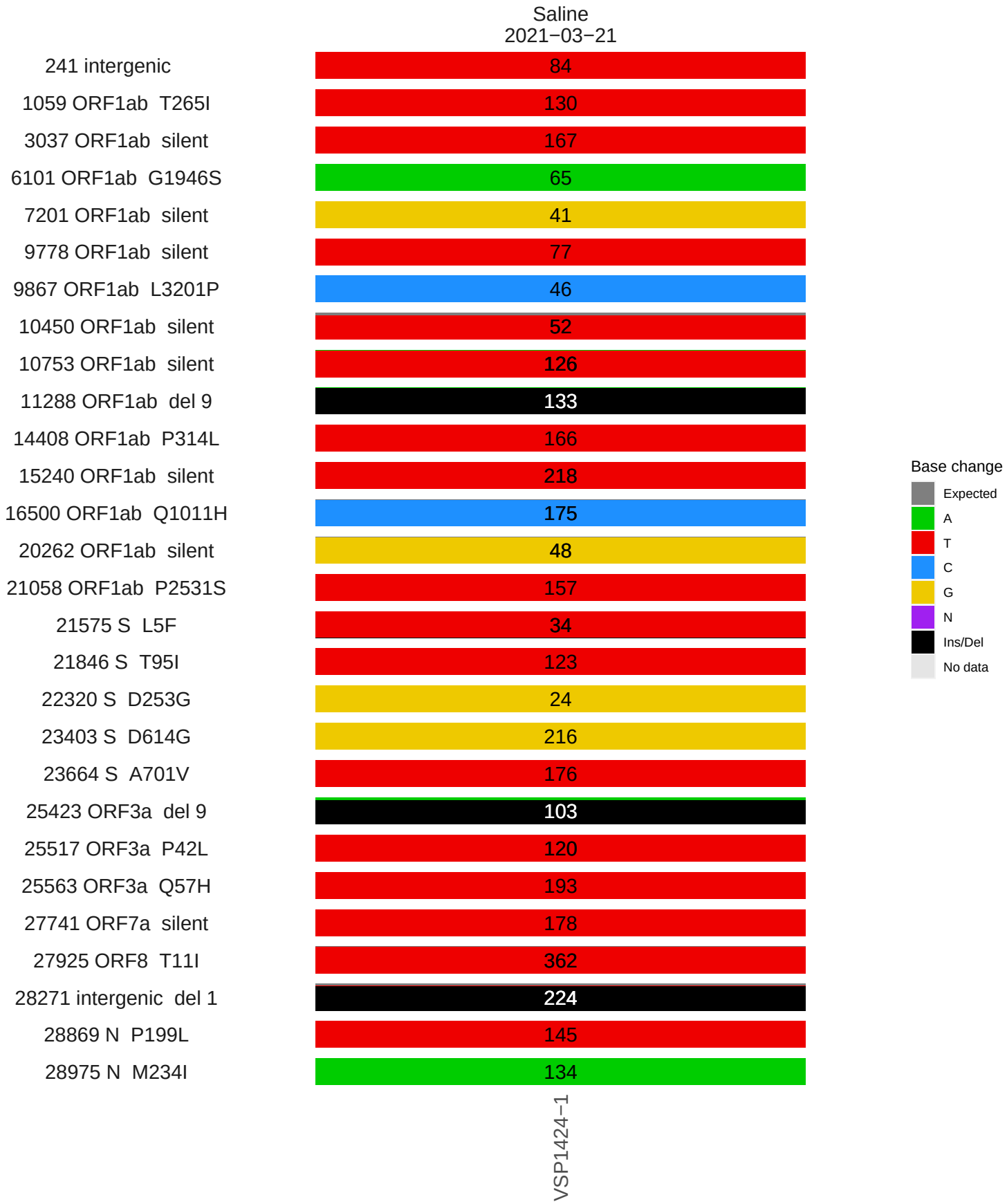
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1424-1	single experiment	NA	Saline	2021-03-21	29.79	B.1.526	99.7%	99.4%

Variants shared across samples

The heat map below shows how variants (reference genome /home/common/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.

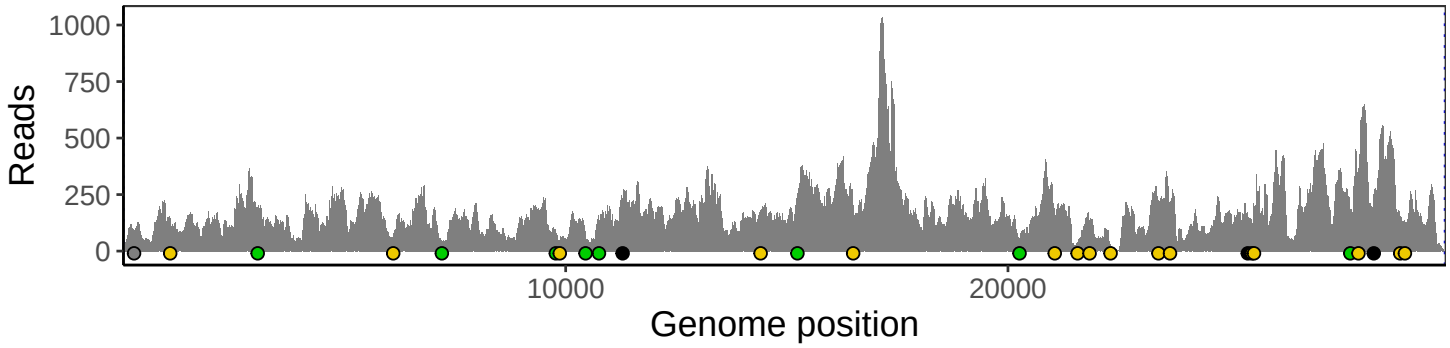



Saline
2021−03−21
241 intergenic
84
1059 ORF1ab T265I
130
3037 ORF1ab silent
167
6101 ORF1ab G1946S
65
7201 ORF1ab silent
41
9778 ORF1ab silent
77
9867 ORF1ab L3201P
46
10450 ORF1ab silent
52
10753 ORF1ab silent
126
11288 ORF1ab del 9
133
14408 ORF1ab P314L
166
15240 ORF1ab silent
218
16500 ORF1ab Q1011H
175
20262 ORF1ab silent
48
21058 ORF1ab P2531S
157
21575 S L5F
34
21846 S T95I
123
22320 S D253G
24
23403 S D614G
216
23664 S A701V
176
25423 ORF3a del 9
103
25517 ORF3a P42L
120
25563 ORF3a Q57H
193
27741 ORF7a silent
178
27925 ORF8 T11I
362
28271 intergenic del 1
224
28869 N P199L
145
28975 N M234I
134
VSP1424−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

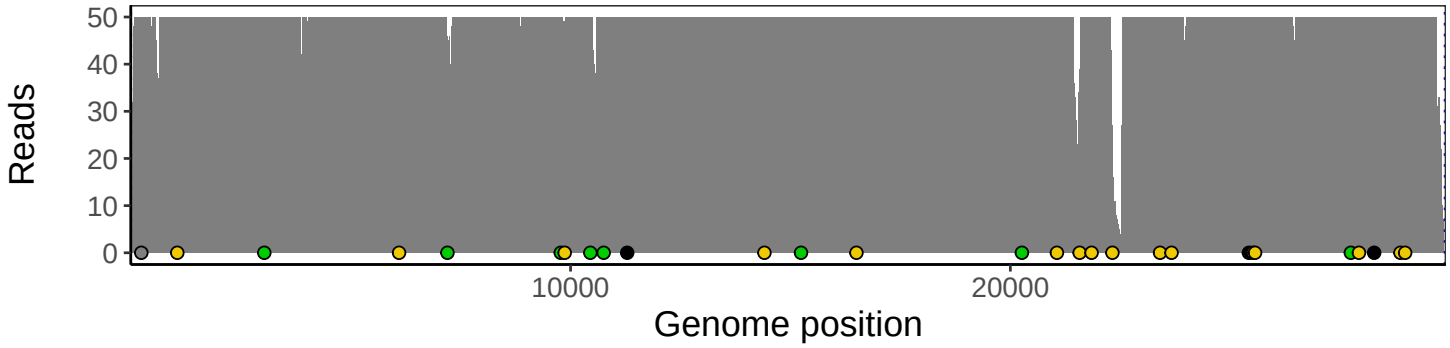
Analyses of individual experiments and composite results

VSP1424-1 | 2021-03-21 | Saline | UPHS-0379 | genomes | single experiment

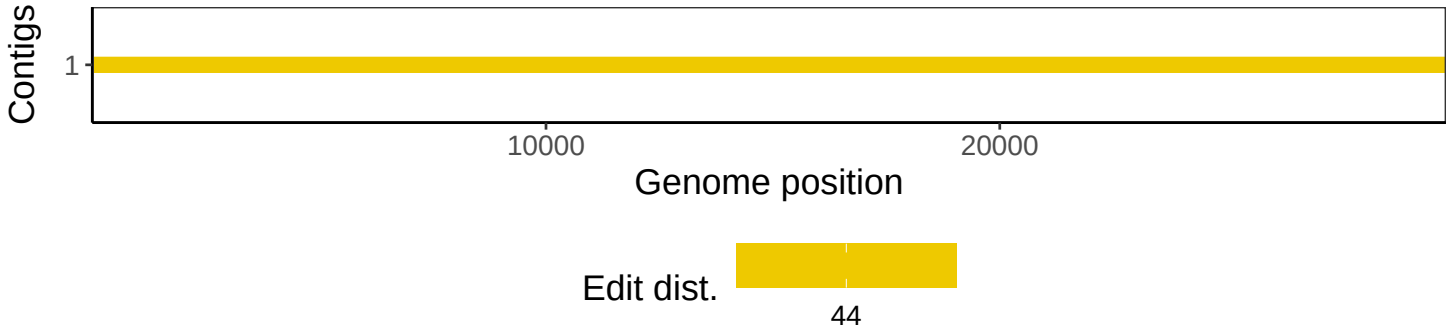
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.1.3
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	3.3.3
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