COVID-19 subject UPHS-0617

2021-06-01

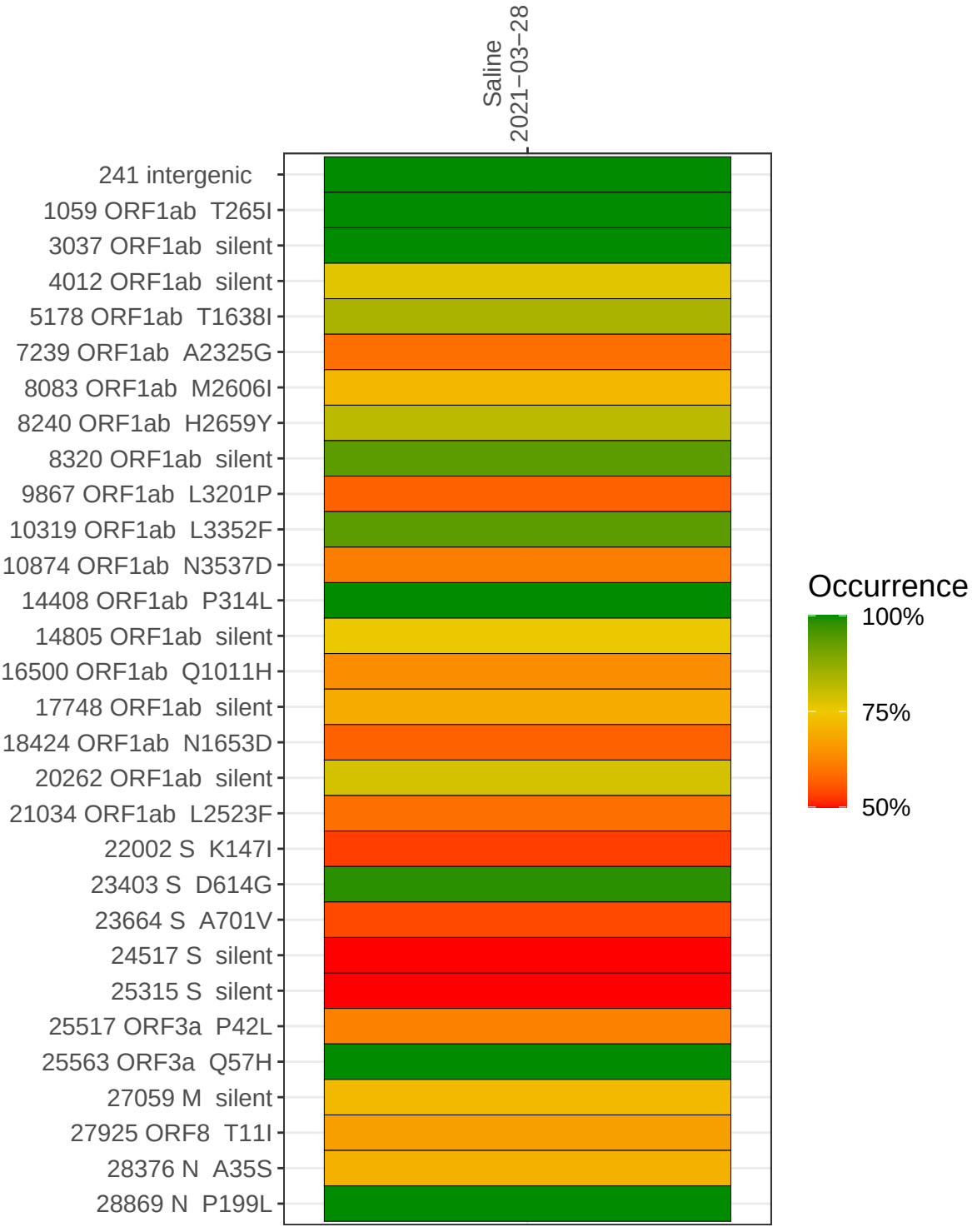
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

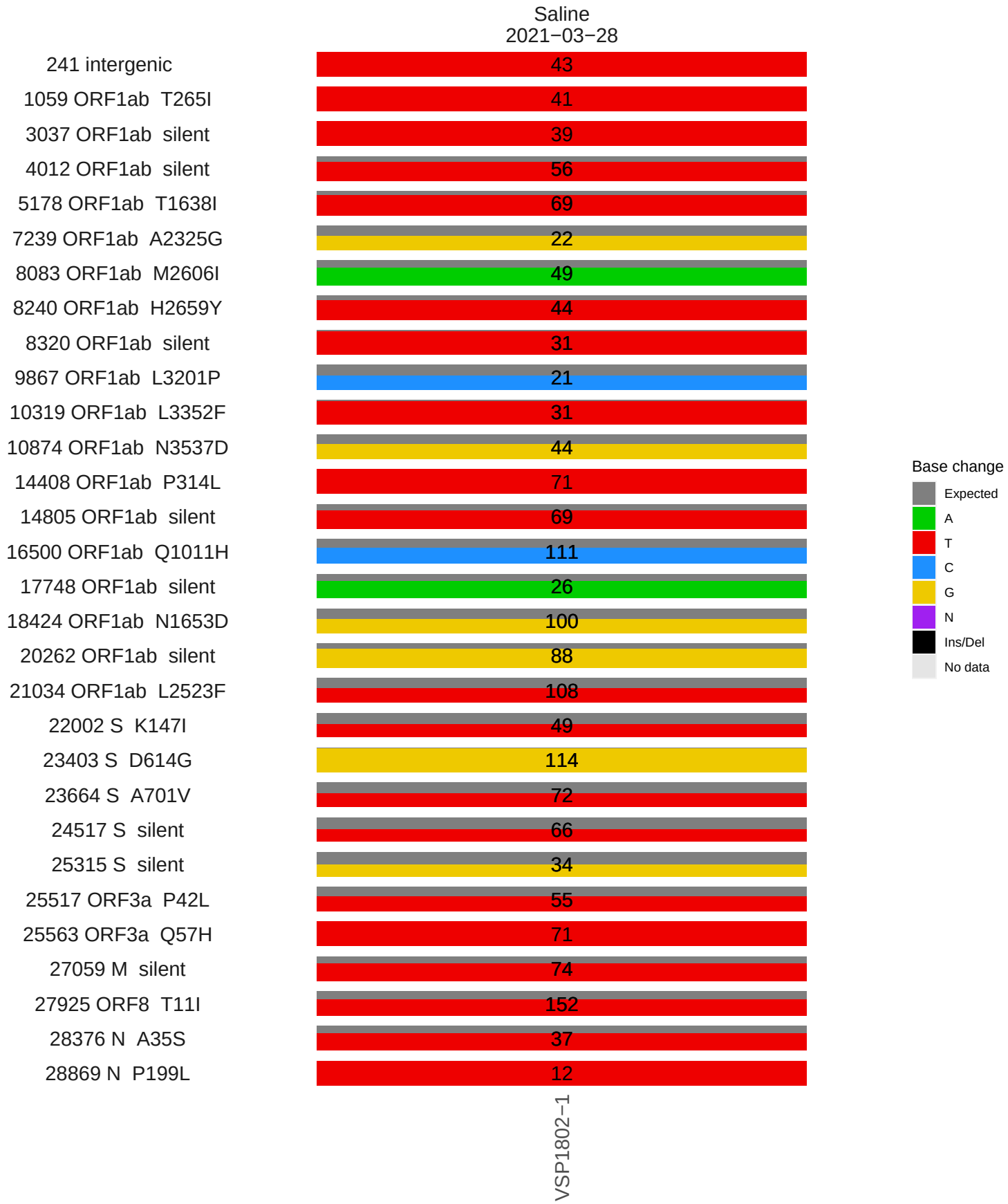
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1802-1	single experiment	NA	Saline	2021-03-28	22.50	B.1.2	99.7%	99.6%

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.

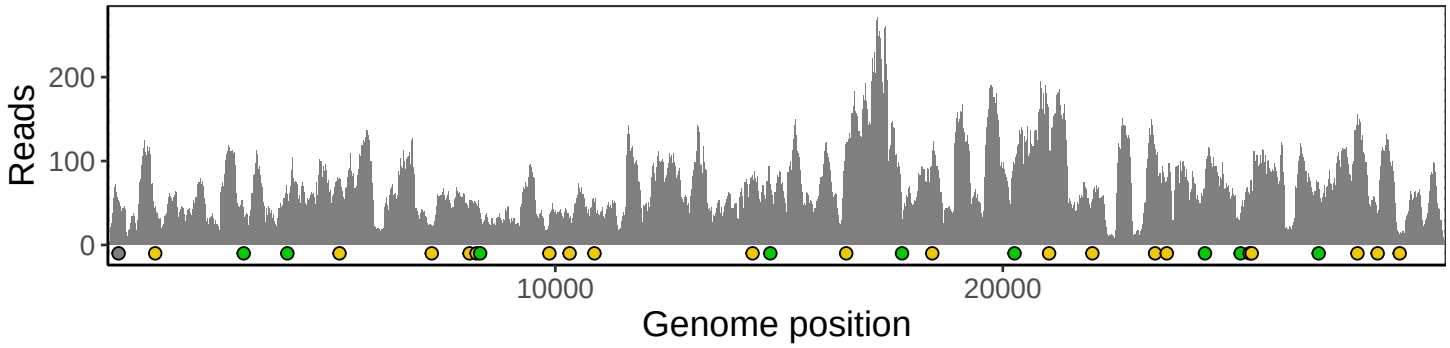



Saline
2021−03−28
241 intergenic
1059 ORF1ab T265I
3037 ORF1ab silent
4012 ORF1ab silent
5178 ORF1ab T1638I
7239 ORF1ab A2325G
8083 ORF1ab M2606I
8240 ORF1ab H2659Y
8320 ORF1ab silent
9867 ORF1ab L3201P
10319 ORF1ab L3352F
10874 ORF1ab N3537D
14408 ORF1ab P314L
14805 ORF1ab silent
16500 ORF1ab Q1011H
17748 ORF1ab silent
18424 ORF1ab N1653D
20262 ORF1ab silent
21034 ORF1ab L2523F
22002 S K147I
23403 S D614G
23664 S A701V
24517 S silent
25315 S silent
25517 ORF3a P42L
25563 ORF3a Q57H
27059 M silent
27925 ORF8 T11I
28376 N A35S
28869 N P199L
43
41
39
56
69
22
49
44
31
21
31
44
71
69
111
26
100
88
108
49
114
72
66
34
55
71
74
152
37
12
VSP1802−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

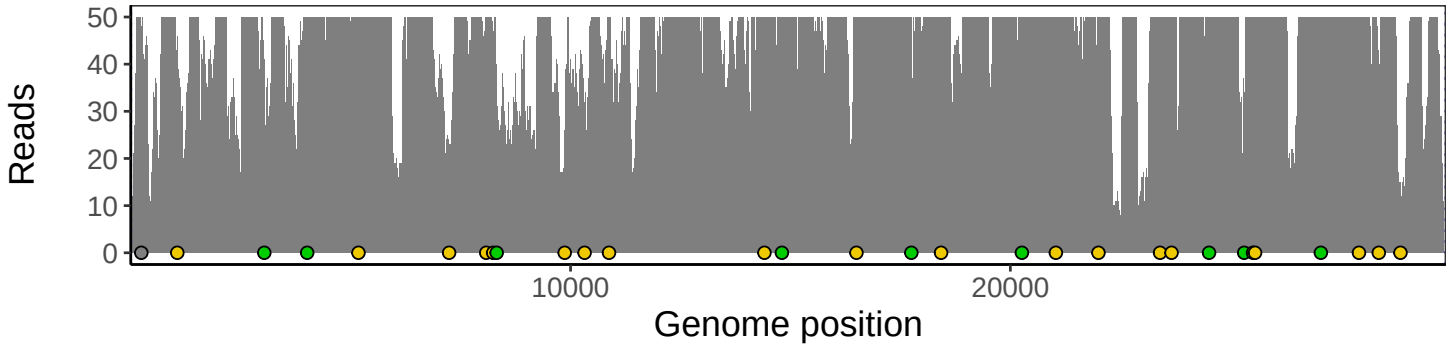
Analyses of individual experiments and composite results

VSP1802-1 | 2021-03-28 | Saline | UPHS-0617 | genomes | single experiment

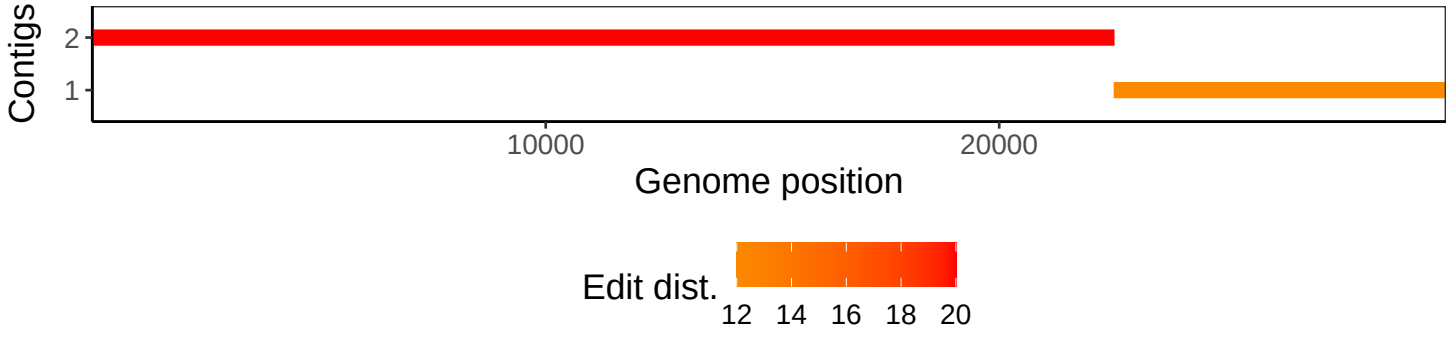
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.3.3
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