COVID-19 subject UPHS-0622

2021-06-01

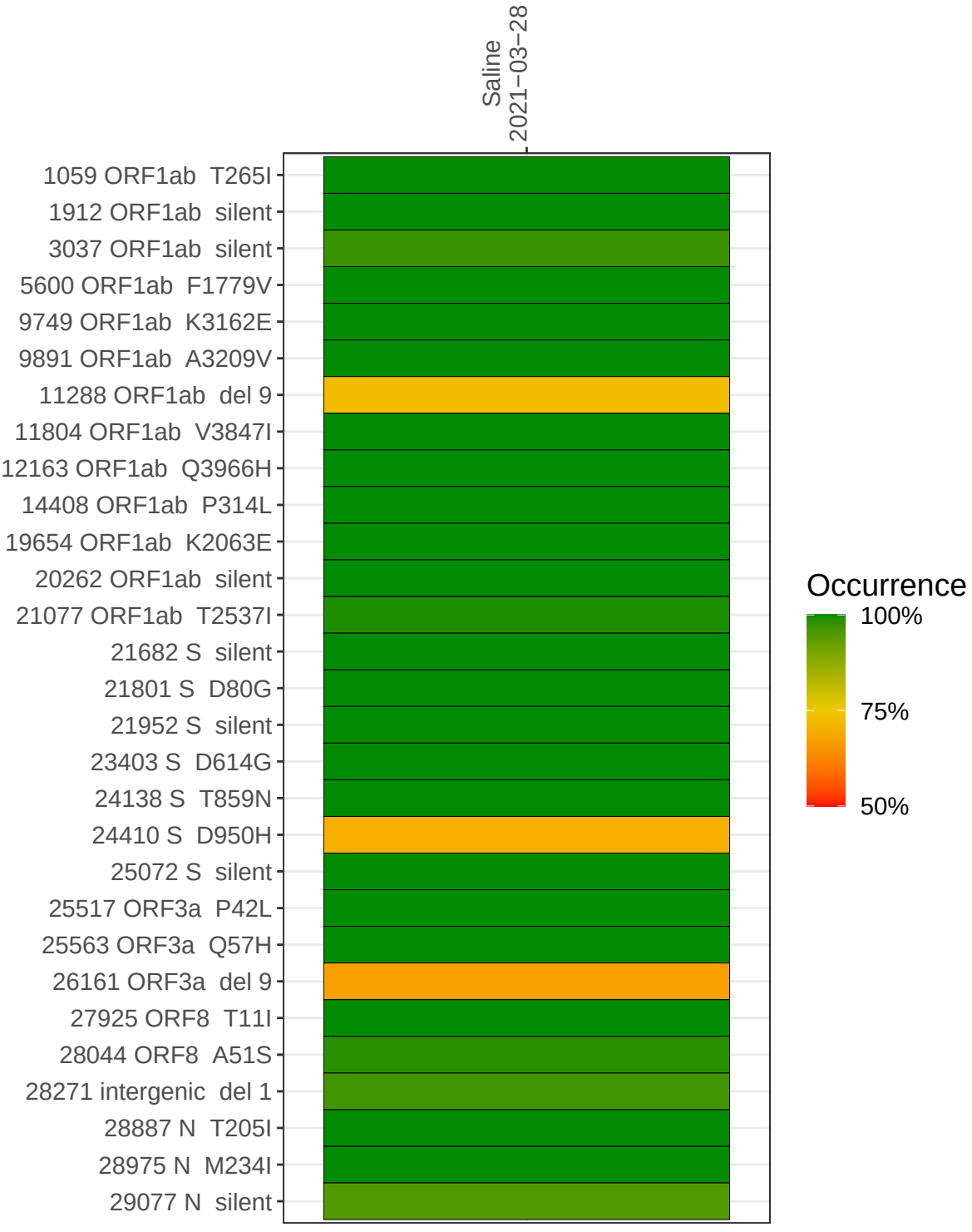
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

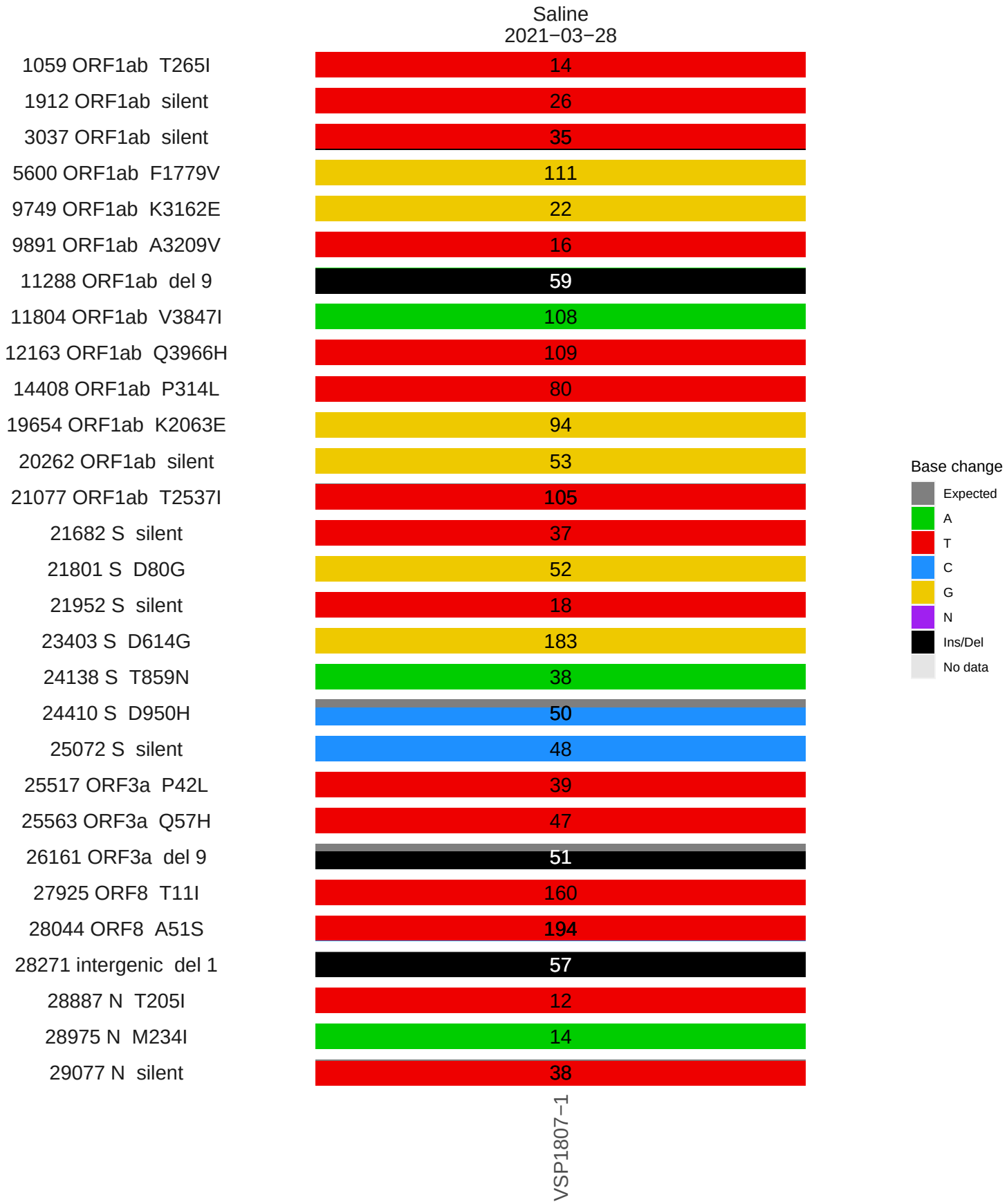
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1807-1	single experiment	NA	Saline	2021-03-28	17.13	B.1.526.1	99.5%	97.4%

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.

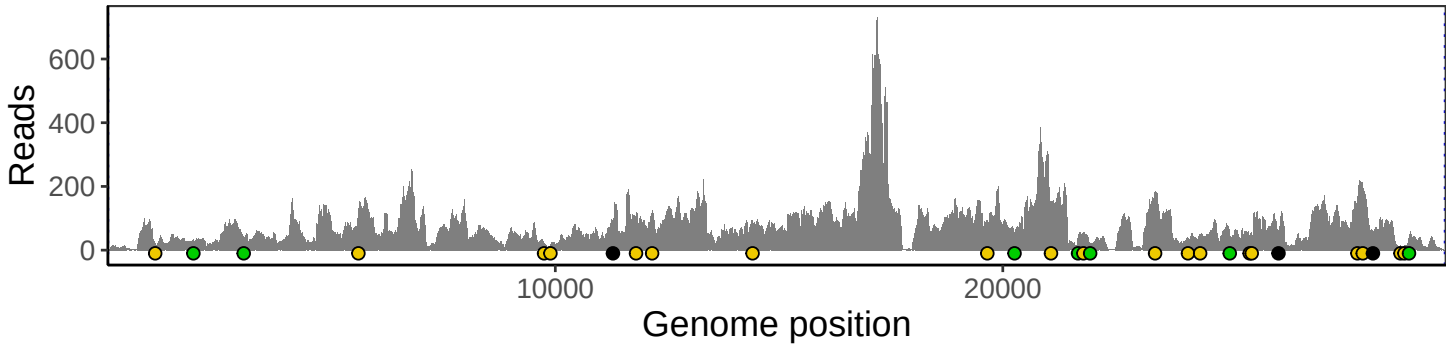



Saline
2021−03−28
1059 ORF1ab T265I
1912 ORF1ab silent
3037 ORF1ab silent
5600 ORF1ab F1779V
9749 ORF1ab K3162E
9891 ORF1ab A3209V
11288 ORF1ab del 9
11804 ORF1ab V3847I
12163 ORF1ab Q3966H
14408 ORF1ab P314L
19654 ORF1ab K2063E
20262 ORF1ab silent
21077 ORF1ab T2537I
21682 S silent
21801 S D80G
21952 S silent
23403 S D614G
24138 S T859N
24410 S D950H
25072 S silent
25517 ORF3a P42L
25563 ORF3a Q57H
26161 ORF3a del 9
27925 ORF8 T11I
28044 ORF8 A51S
28271 intergenic del 1
28887 N T205I
28975 N M234I
29077 N silent
14
26
35
111
22
16
59
108
109
80
94
53
105
37
52
18
183
38
50
48
39
47
51
160
194
57
12
14
38
VSP1807−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

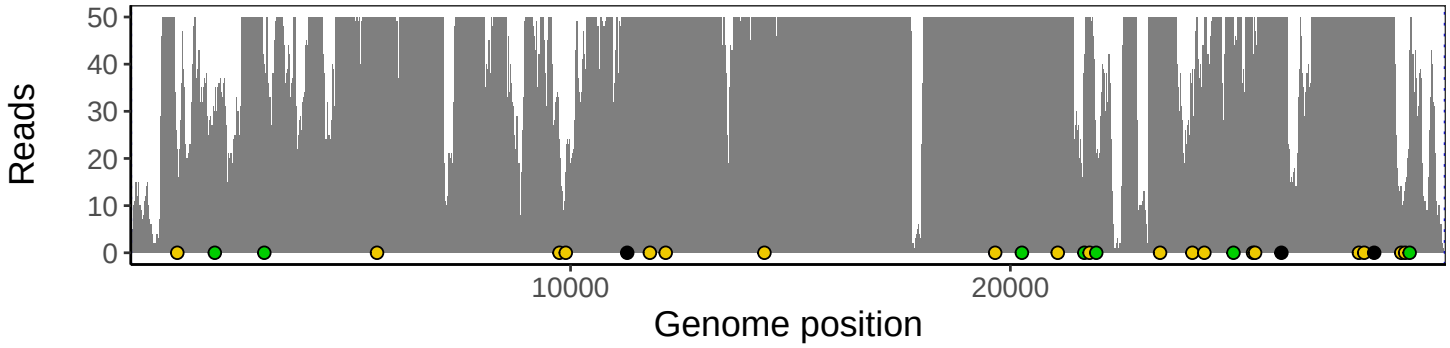
Analyses of individual experiments and composite results

VSP1807-1 | 2021-03-28 | Saline | UPHS-0622 | genomes | single experiment

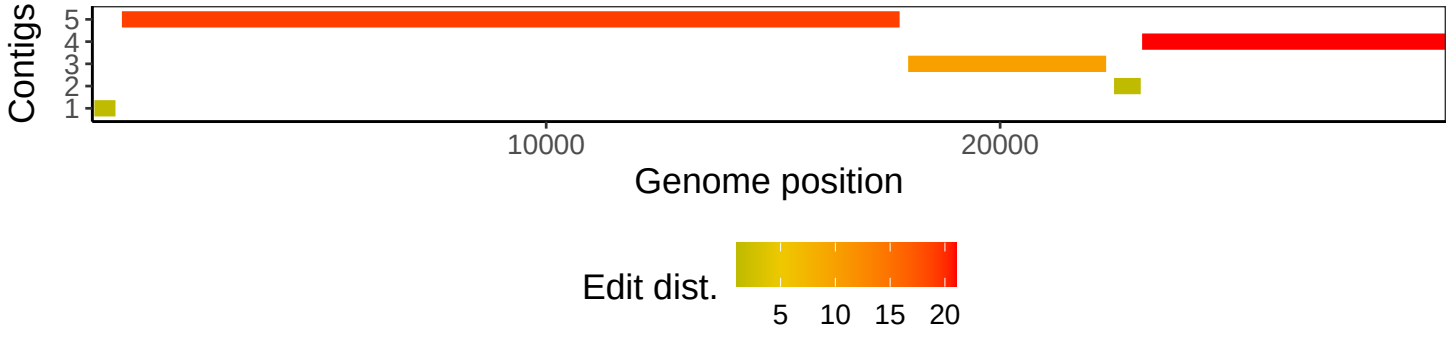
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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