COVID-19 subject UPHS-0158

2021-05-05

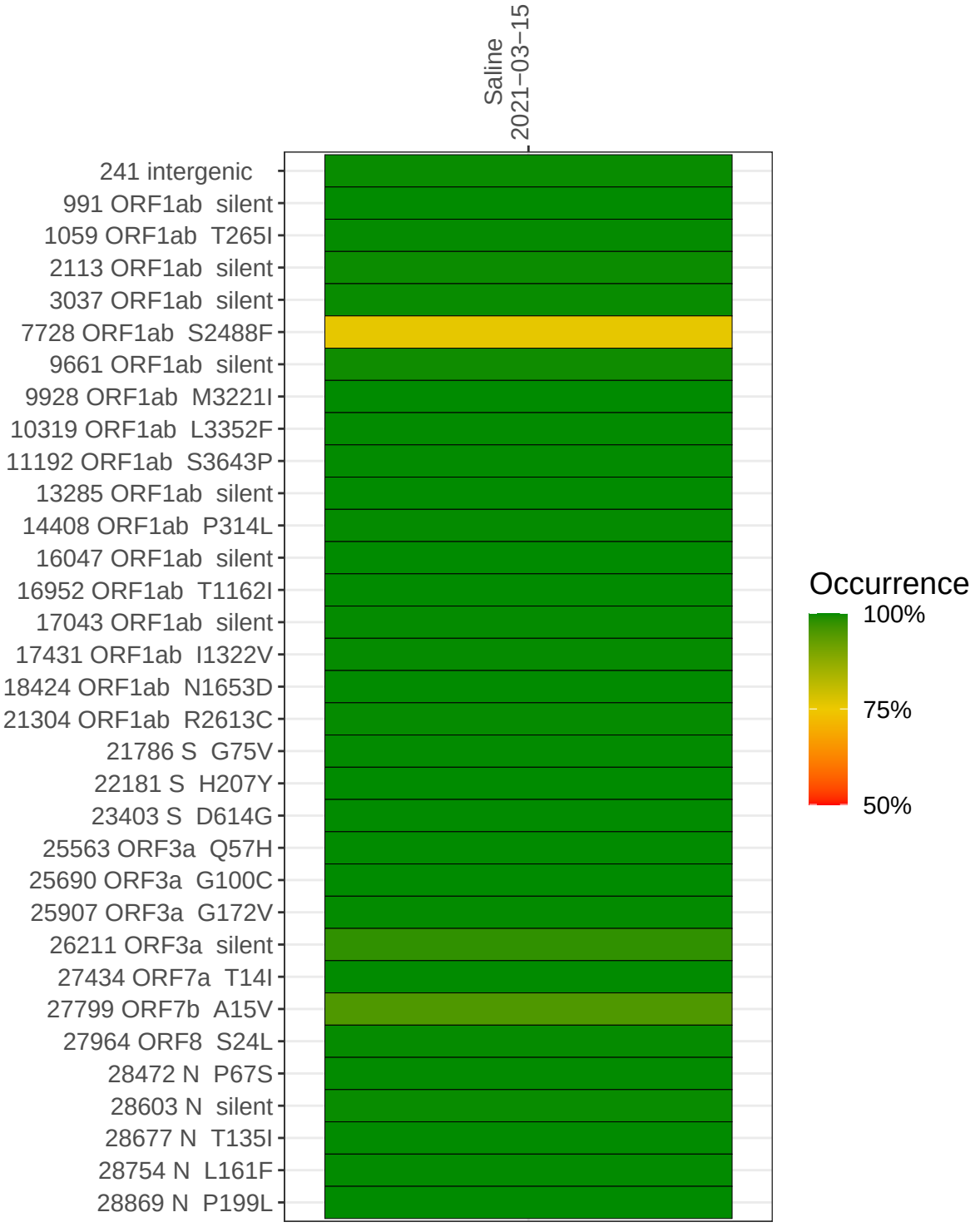
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

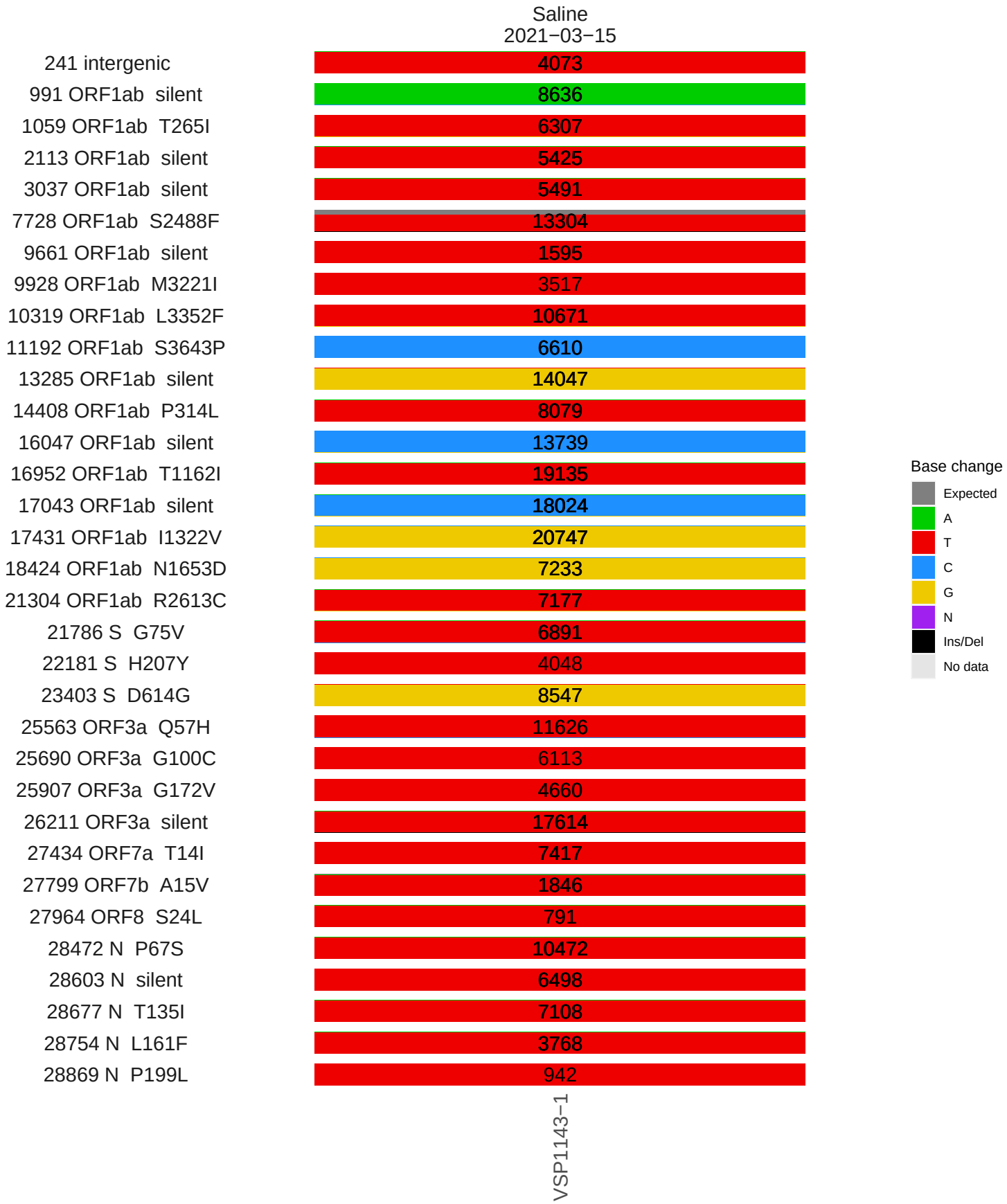
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1143-1	single experiment	NA	Saline	2021-03-15	29.86	B.1.2	99.8%	99.7%

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.

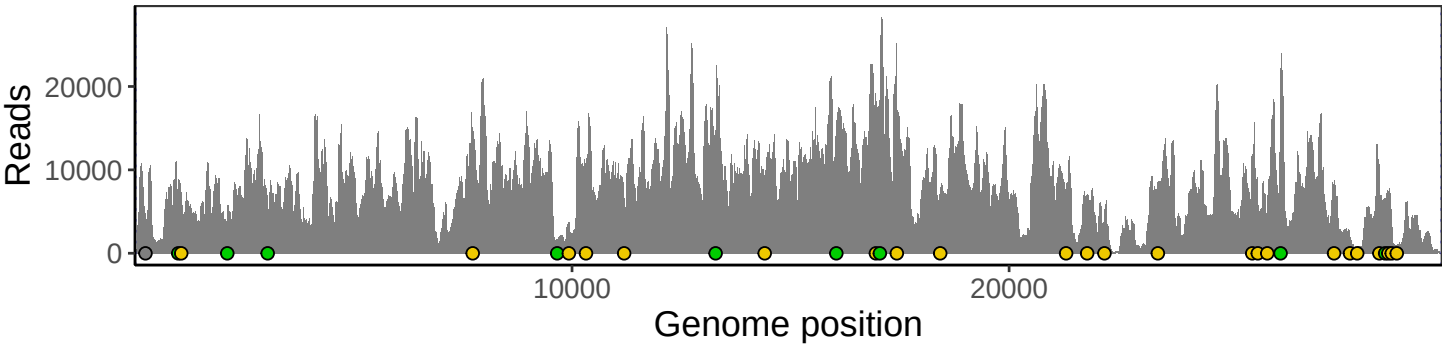



Saline
2021−03−15
241 intergenic
4073
991 ORF1ab silent
8636
1059 ORF1ab T265I
6307
2113 ORF1ab silent
5425
3037 ORF1ab silent
5491
7728 ORF1ab S2488F
13304
9661 ORF1ab silent
1595
9928 ORF1ab M3221I
3517
10319 ORF1ab L3352F
10671
11192 ORF1ab S3643P
6610
13285 ORF1ab silent
14047
14408 ORF1ab P314L
8079
16047 ORF1ab silent
13739
16952 ORF1ab T1162I
19135
17043 ORF1ab silent
18024
17431 ORF1ab I1322V
20747
18424 ORF1ab N1653D
7233
21304 ORF1ab R2613C
7177
21786 S G75V
6891
22181 S H207Y
4048
23403 S D614G
8547
25563 ORF3a Q57H
11626
25690 ORF3a G100C
6113
25907 ORF3a G172V
4660
26211 ORF3a silent
17614
27434 ORF7a T14I
7417
27799 ORF7b A15V
1846
27964 ORF8 S24L
791
28472 N P67S
10472
28603 N silent
6498
28677 N T135I
7108
28754 N L161F
3768
28869 N P199L
942
VSP1143−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

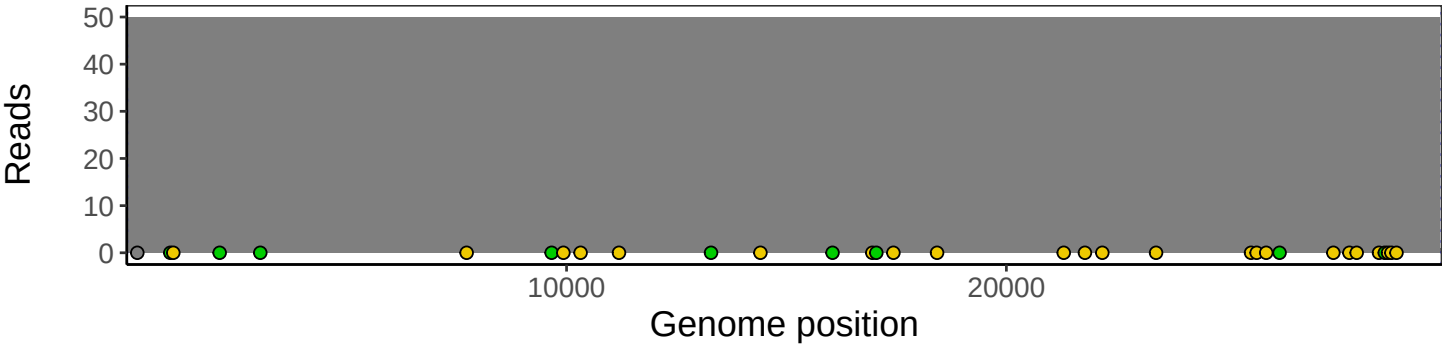
Analyses of individual experiments and composite results

VSP1143-1 | 2021-03-15 | Saline | UPHS-0158 | genomes | single experiment

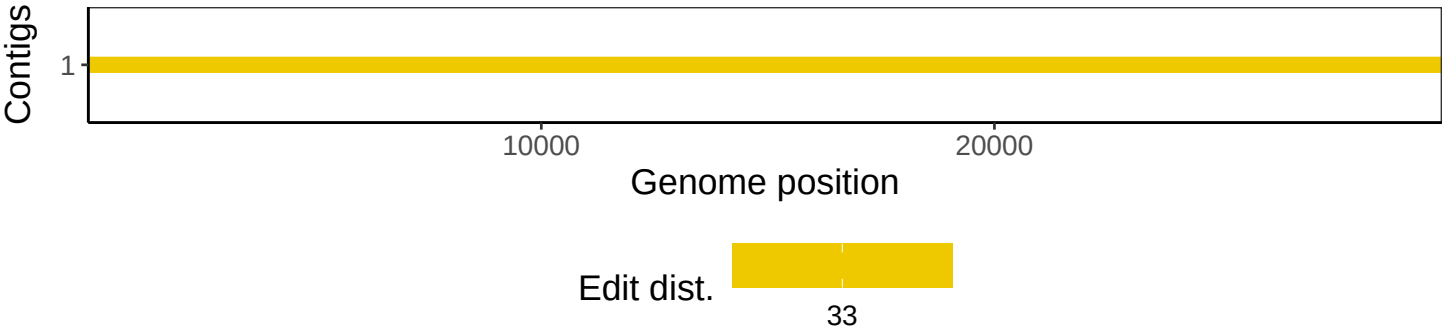
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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