COVID-19 subject UPHS-0074

2021-03-25

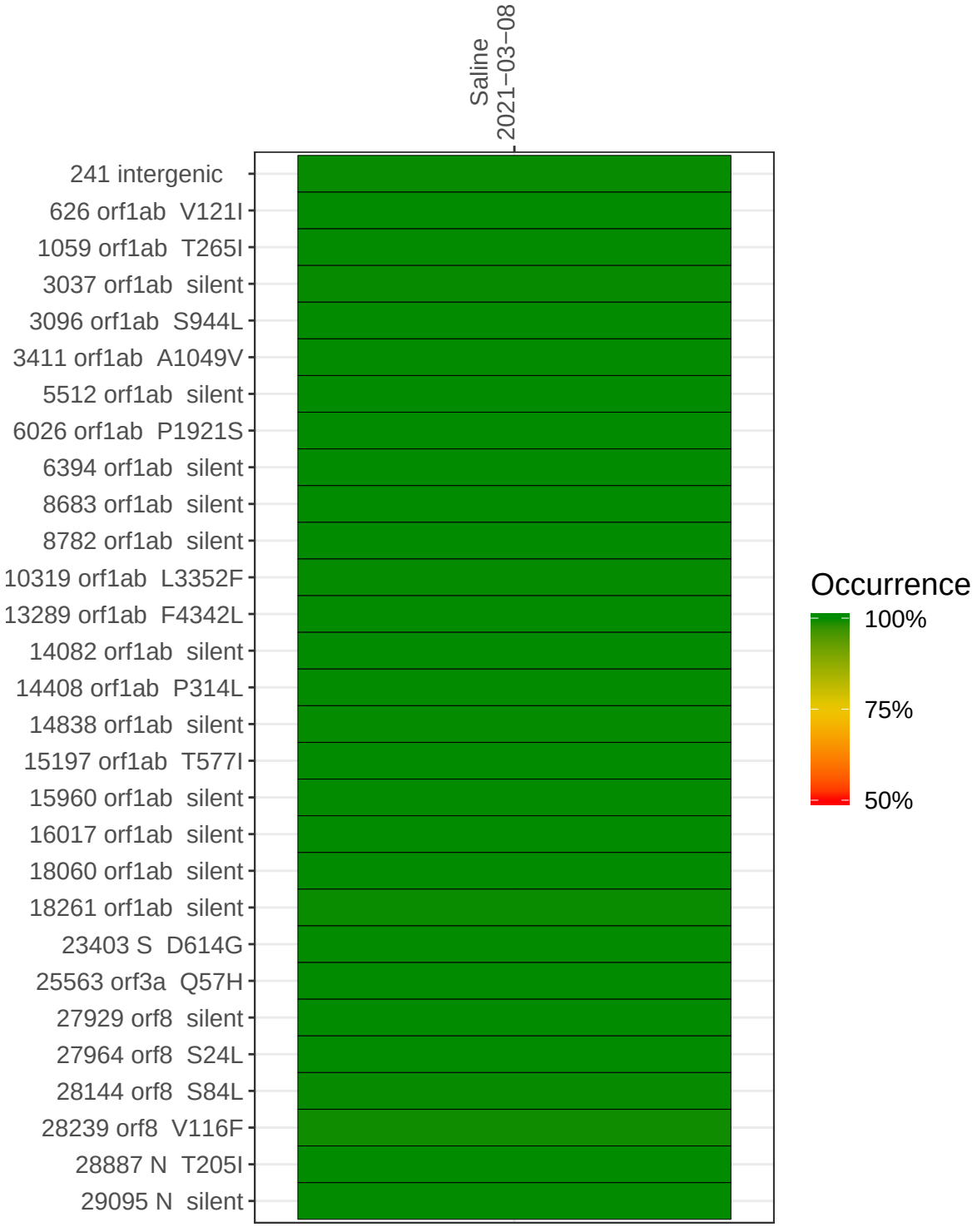
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

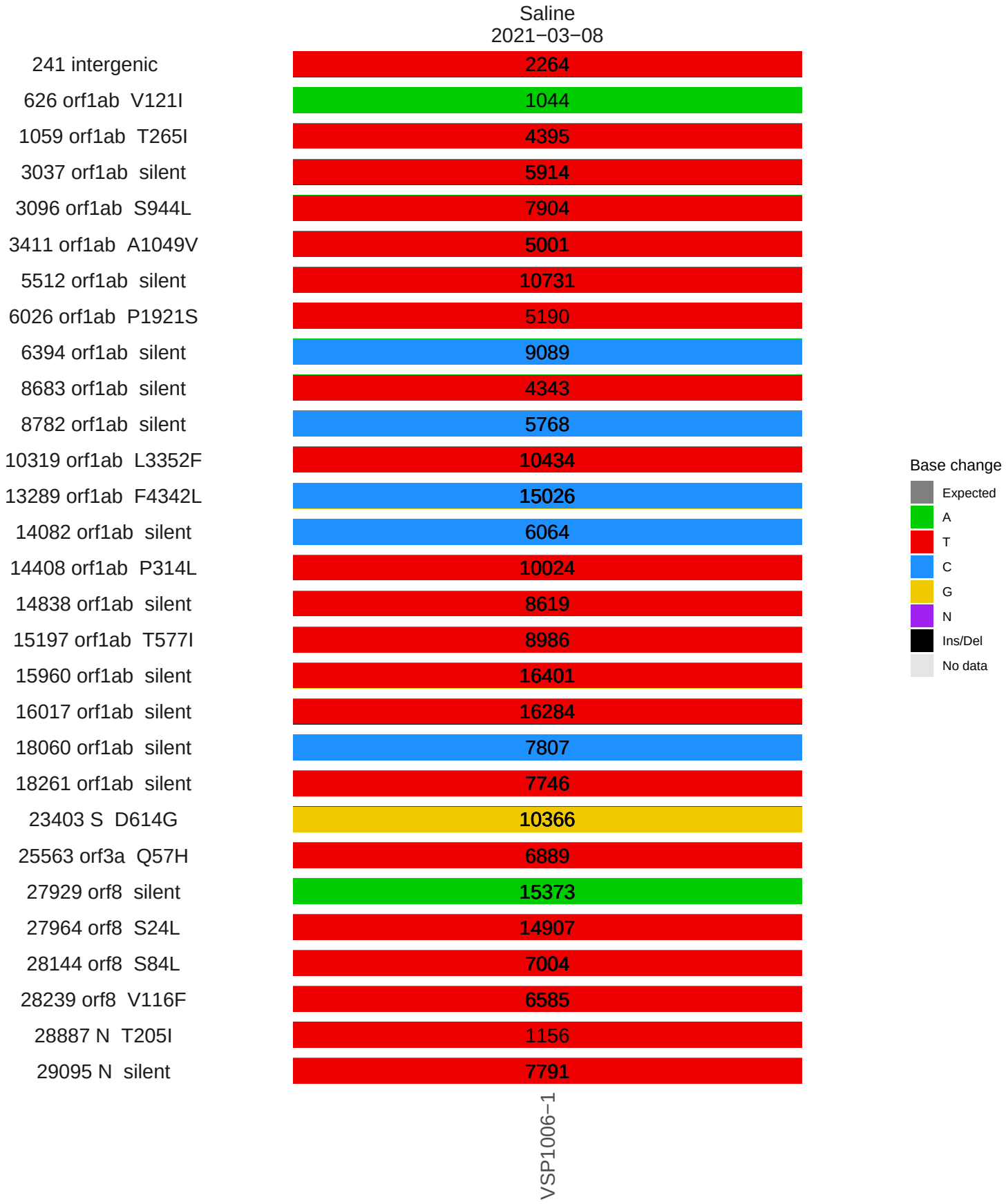
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1006-1	single experiment	NA	Saline	2021-03-08	29.84	B.1.2	99.8%	99.8%

Variants shared across samples

The heat map below shows how variants (reference genome USA-WA1-2020) 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.

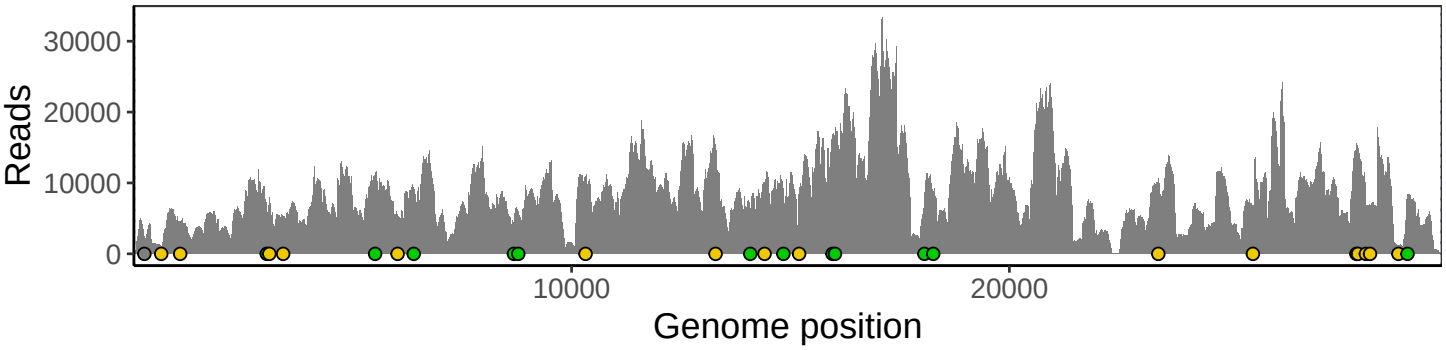



Saline
2021−03−08
241 intergenic
626 orf1ab V121I
1059 orf1ab T265I
3037 orf1ab silent
3096 orf1ab S944L
3411 orf1ab A1049V
5512 orf1ab silent
6026 orf1ab P1921S
6394 orf1ab silent
8683 orf1ab silent
8782 orf1ab silent
10319 orf1ab L3352F
13289 orf1ab F4342L
14082 orf1ab silent
14408 orf1ab P314L
14838 orf1ab silent
15197 orf1ab T577I
15960 orf1ab silent
16017 orf1ab silent
18060 orf1ab silent
18261 orf1ab silent
23403 S D614G
25563 orf3a Q57H
27929 orf8 silent
27964 orf8 S24L
28144 orf8 S84L
28239 orf8 V116F
28887 N T205I
29095 N silent
2264
1044
4395
5914
7904
5001
10731
5190
9089
4343
5768
10434
15026
6064
10024
8619
8986
16401
16284
7807
7746
10366
6889
15373
14907
7004
6585
1156
7791
VSP1006−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

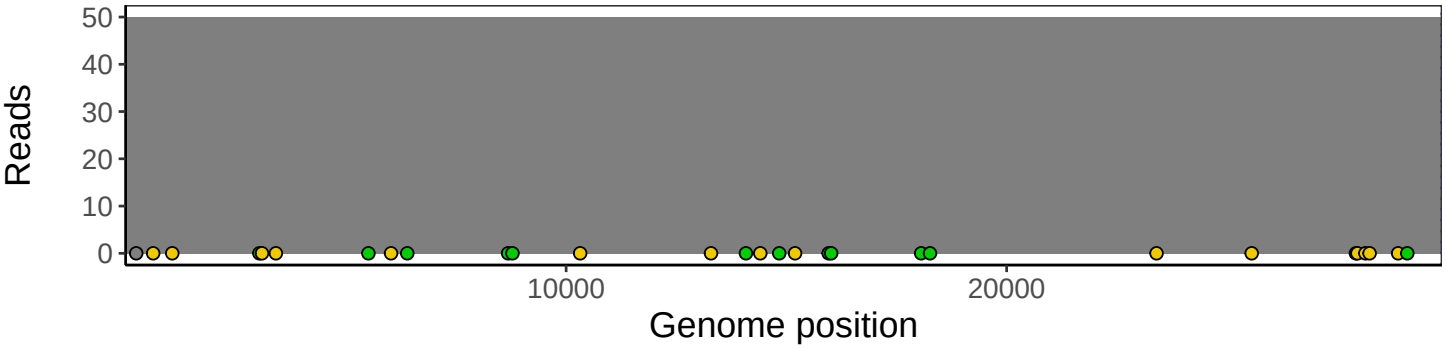
Analyses of individual experiments and composite results

VSP1006-1 | 2021-03-08 | Saline | UPHS-0074 | genomes | single experiment

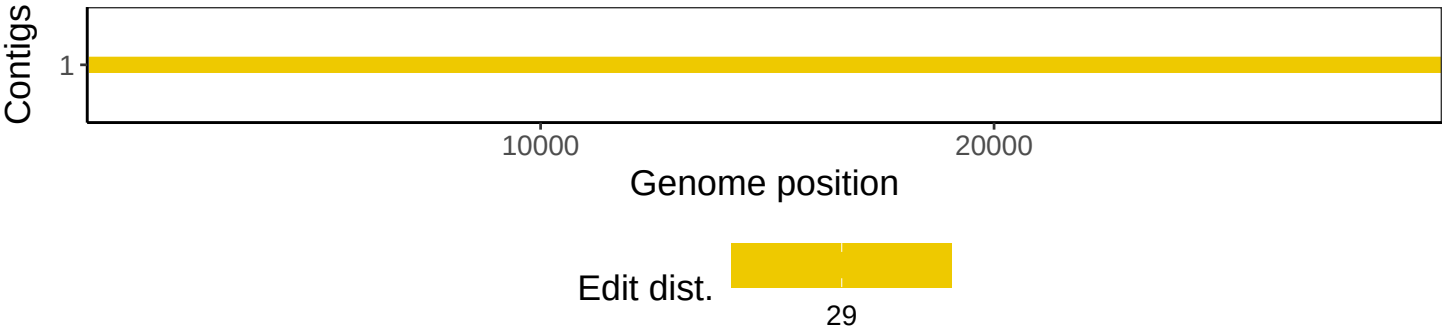
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.3
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	3.0.0
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