COVID-19 subject UPHS-0140

2021-03-31

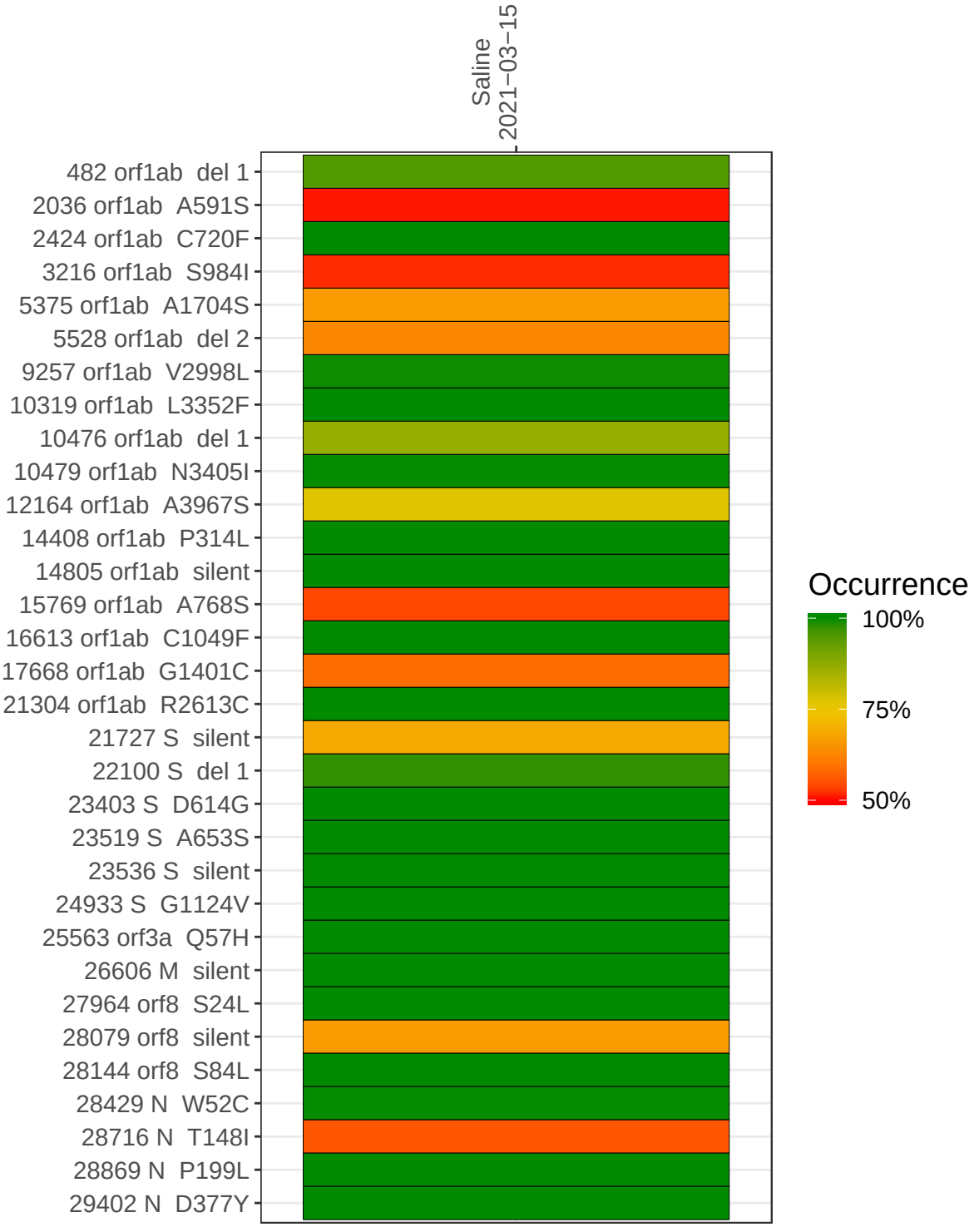
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

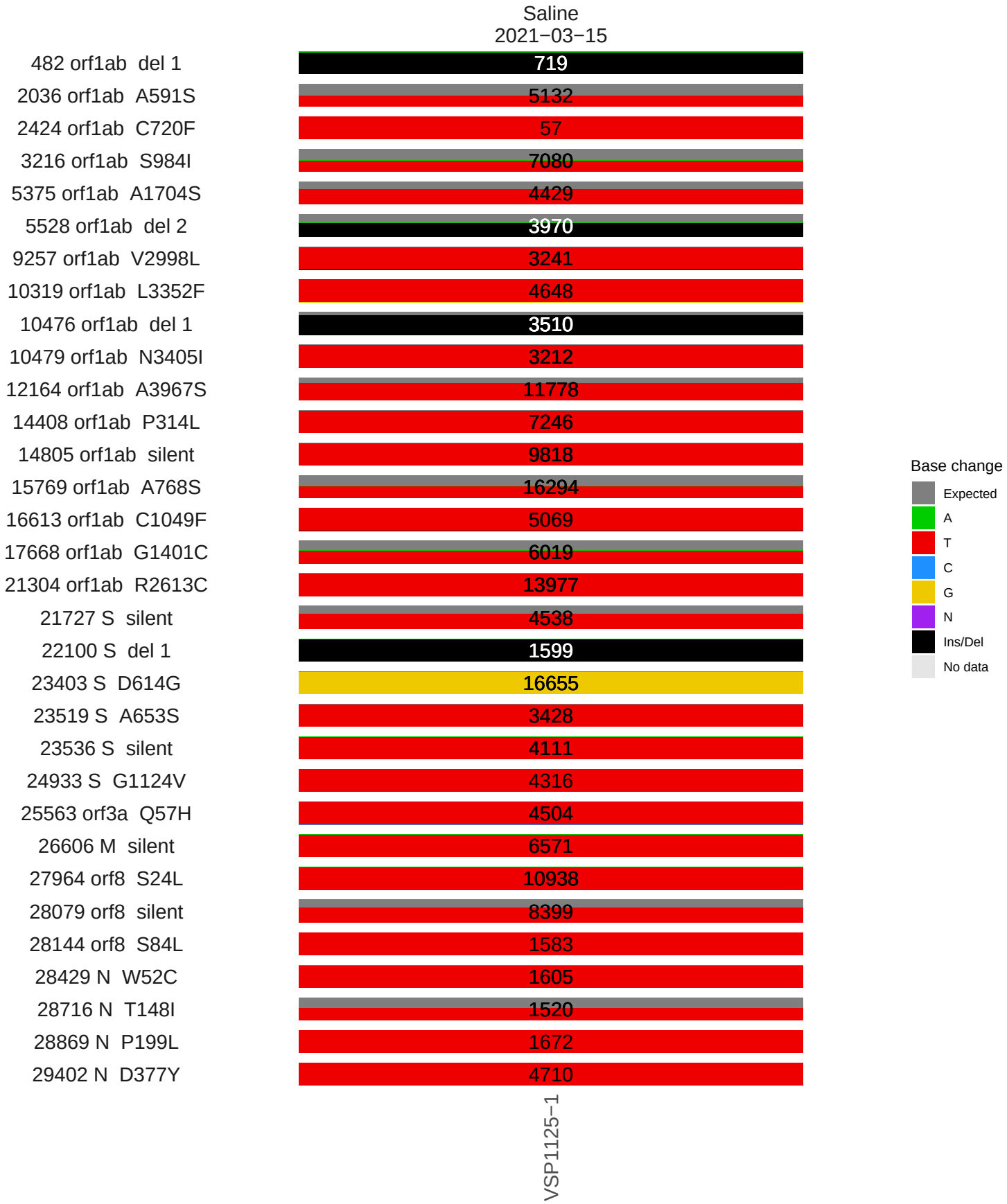
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1125-1	single experiment	NA	Saline	2021-03-15	1.72	NA	57.6%	55.7%

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.

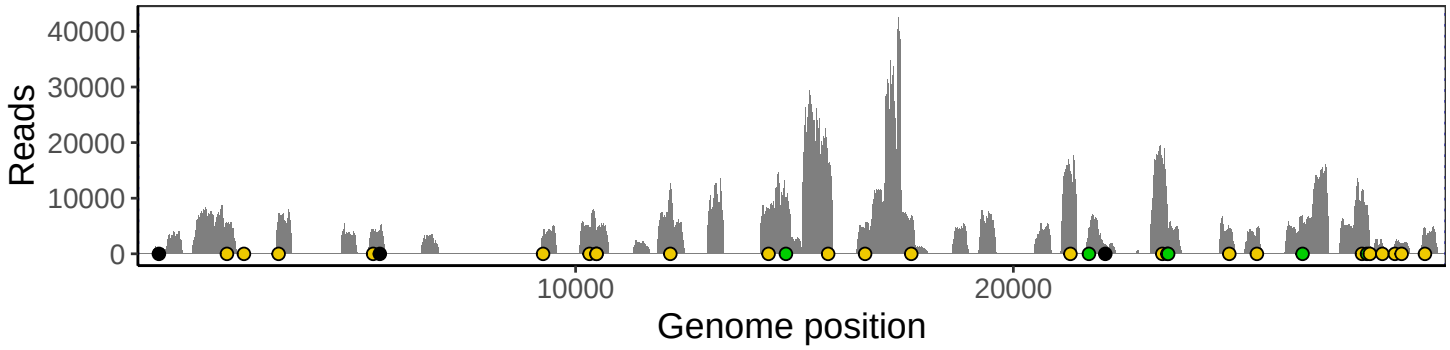



Saline
2021−03−15
482 orf1ab del 1
719
2036 orf1ab A591S
5132
2424 orf1ab C720F
57
3216 orf1ab S984I
7080
5375 orf1ab A1704S
4429
5528 orf1ab del 2
3970
9257 orf1ab V2998L
3241
10319 orf1ab L3352F
4648
10476 orf1ab del 1
3510
10479 orf1ab N3405I
3212
12164 orf1ab A3967S
11778
14408 orf1ab P314L
7246
14805 orf1ab silent
9818
15769 orf1ab A768S
16294
16613 orf1ab C1049F
5069
17668 orf1ab G1401C
6019
21304 orf1ab R2613C
13977
21727 S silent
4538
22100 S del 1
1599
23403 S D614G
16655
23519 S A653S
3428
23536 S silent
4111
24933 S G1124V
4316
25563 orf3a Q57H
4504
26606 M silent
6571
27964 orf8 S24L
10938
28079 orf8 silent
8399
28144 orf8 S84L
1583
28429 N W52C
1605
28716 N T148I
1520
28869 N P199L
1672
29402 N D377Y
4710
VSP1125−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

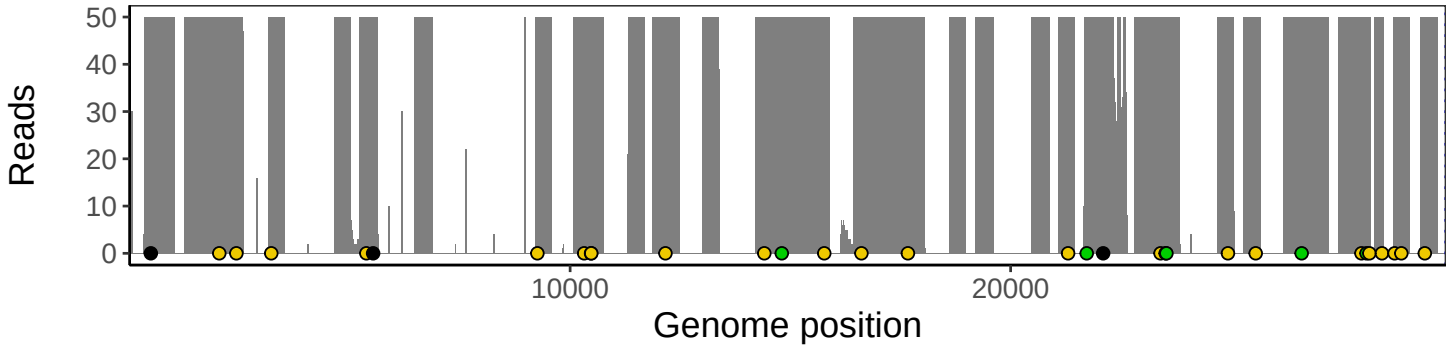
Analyses of individual experiments and composite results

VSP1125-1 | 2021-03-15 | Saline | UPHS-0140 | genomes | single experiment

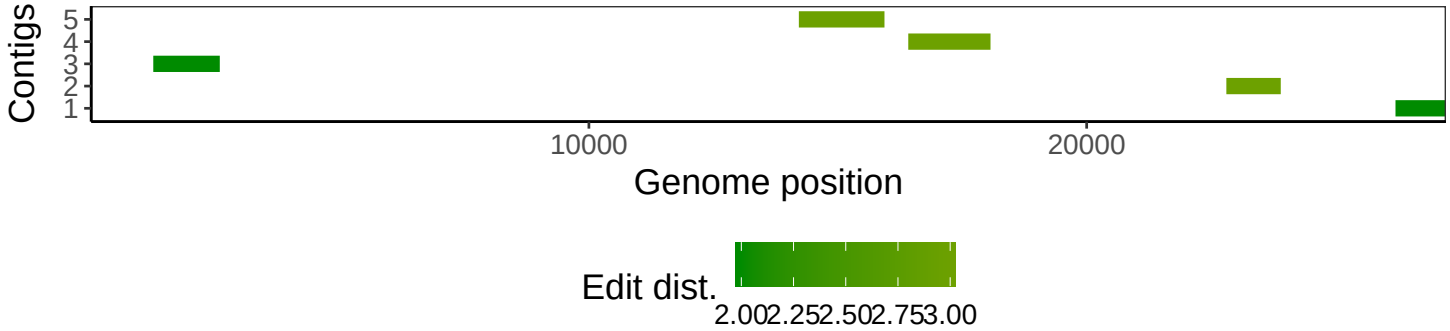
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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