COVID-19 subject UPHS-0145

2021-03-31

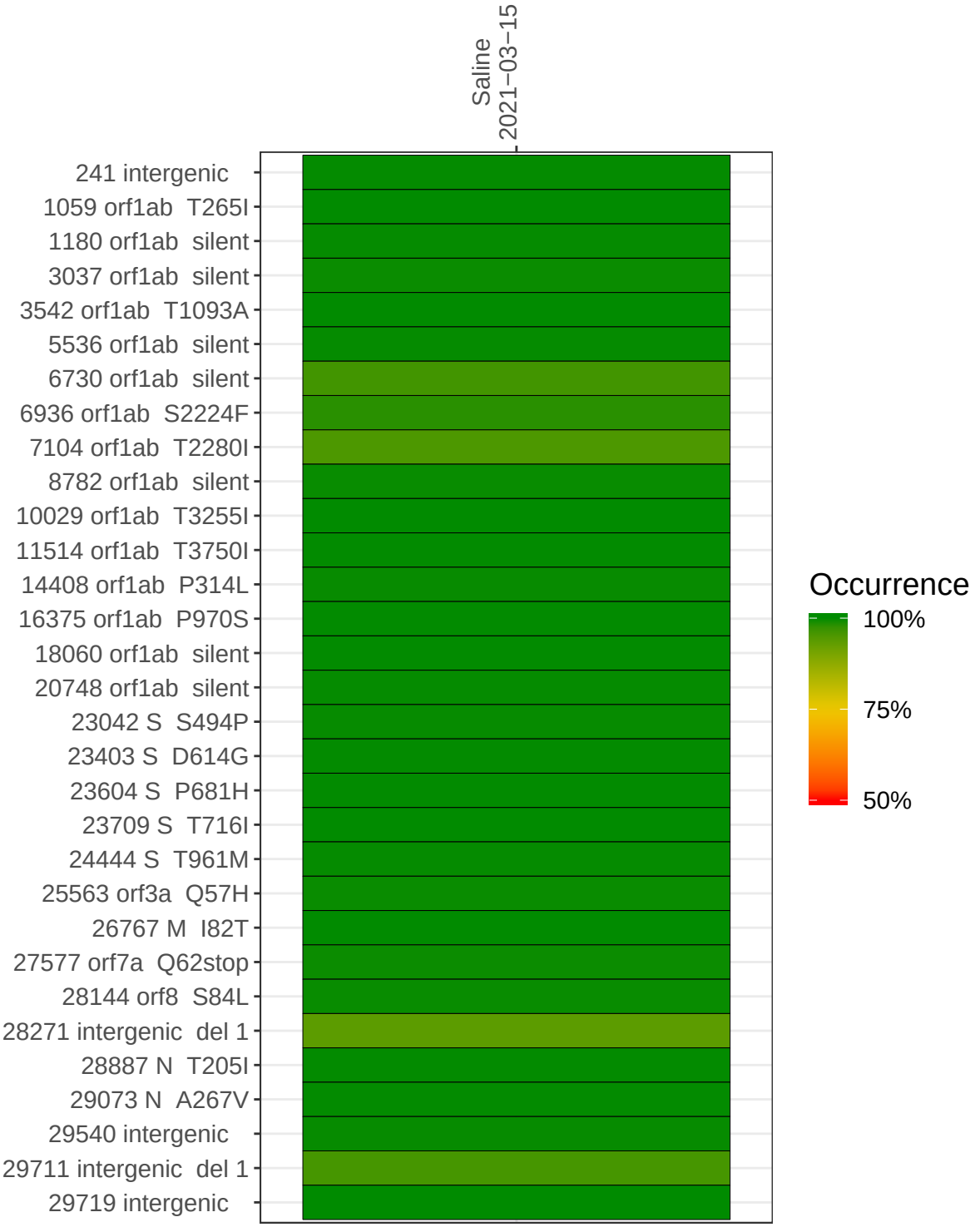
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

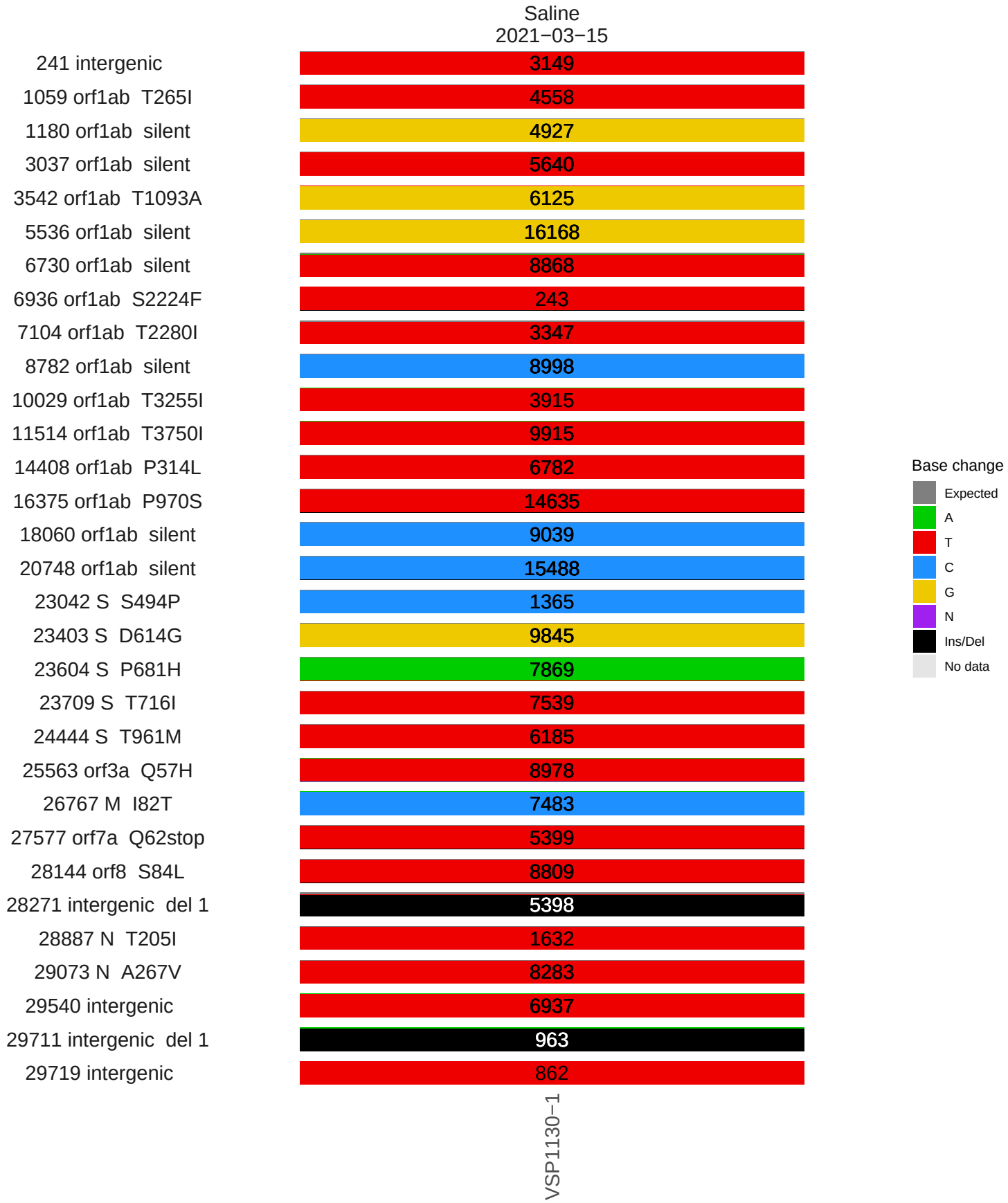
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1130-1	single experiment	NA	Saline	2021-03-15	29.90	B.1	99.9%	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.

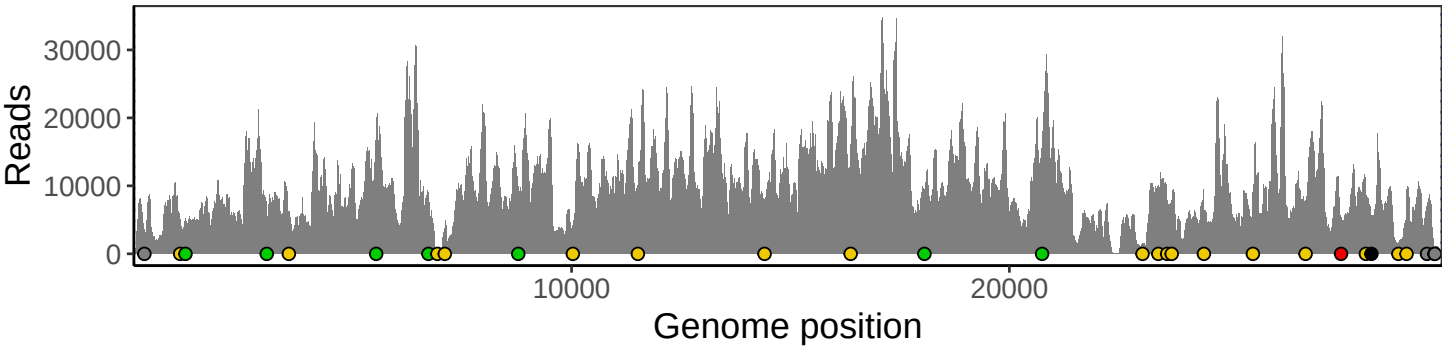



Saline
2021−03−15
241 intergenic
3149
1059 orf1ab T265I
4558
1180 orf1ab silent
4927
3037 orf1ab silent
5640
3542 orf1ab T1093A
6125
5536 orf1ab silent
16168
6730 orf1ab silent
8868
6936 orf1ab S2224F
243
7104 orf1ab T2280I
3347
8782 orf1ab silent
8998
10029 orf1ab T3255I
3915
11514 orf1ab T3750I
9915
14408 orf1ab P314L
6782
16375 orf1ab P970S
14635
18060 orf1ab silent
9039
20748 orf1ab silent
15488
23042 S S494P
1365
23403 S D614G
9845
23604 S P681H
7869
23709 S T716I
7539
24444 S T961M
6185
25563 orf3a Q57H
8978
26767 M I82T
7483
27577 orf7a Q62stop
5399
28144 orf8 S84L
8809
28271 intergenic del 1
5398
28887 N T205I
1632
29073 N A267V
8283
29540 intergenic
6937
29711 intergenic del 1
963
29719 intergenic
862
VSP1130−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

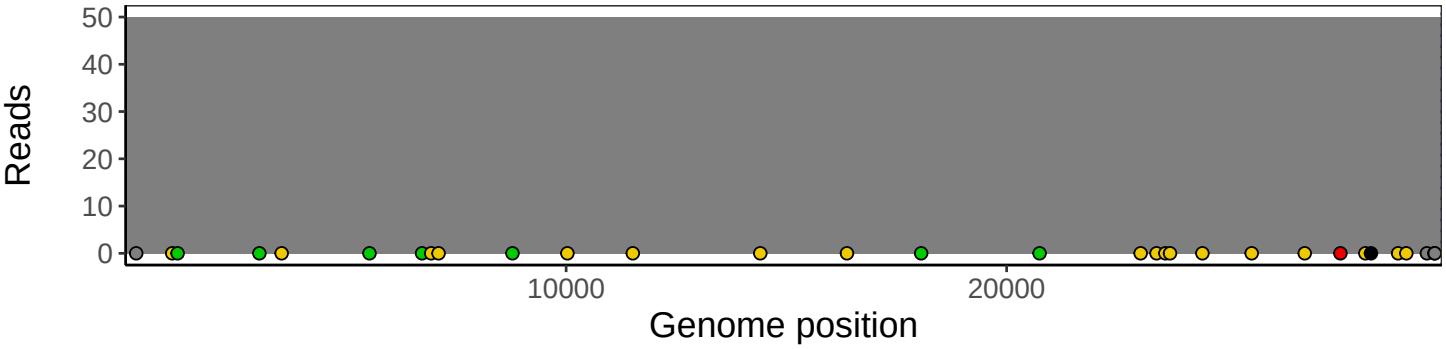
Analyses of individual experiments and composite results

VSP1130-1 | 2021-03-15 | Saline | UPHS-0145 | genomes | single experiment

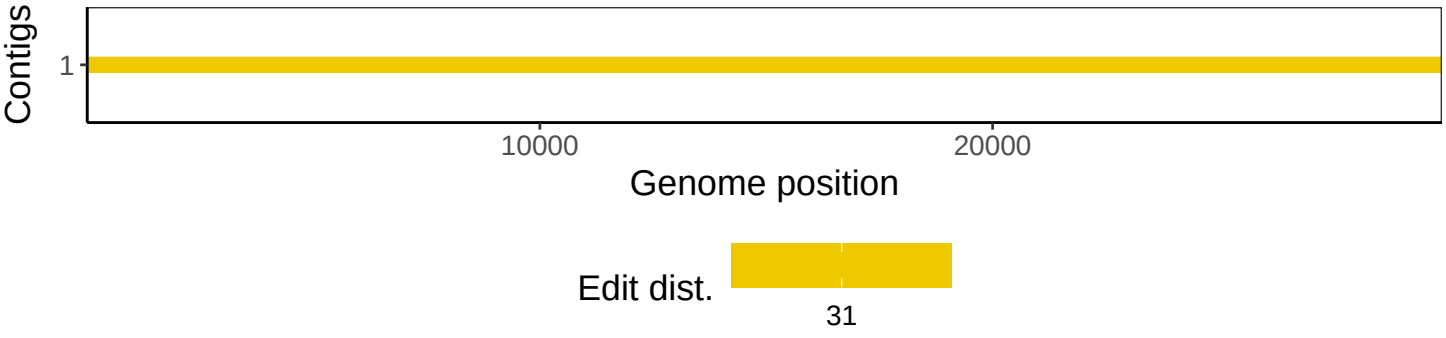
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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