COVID-19 subject UPHS-0023

2021-03-25

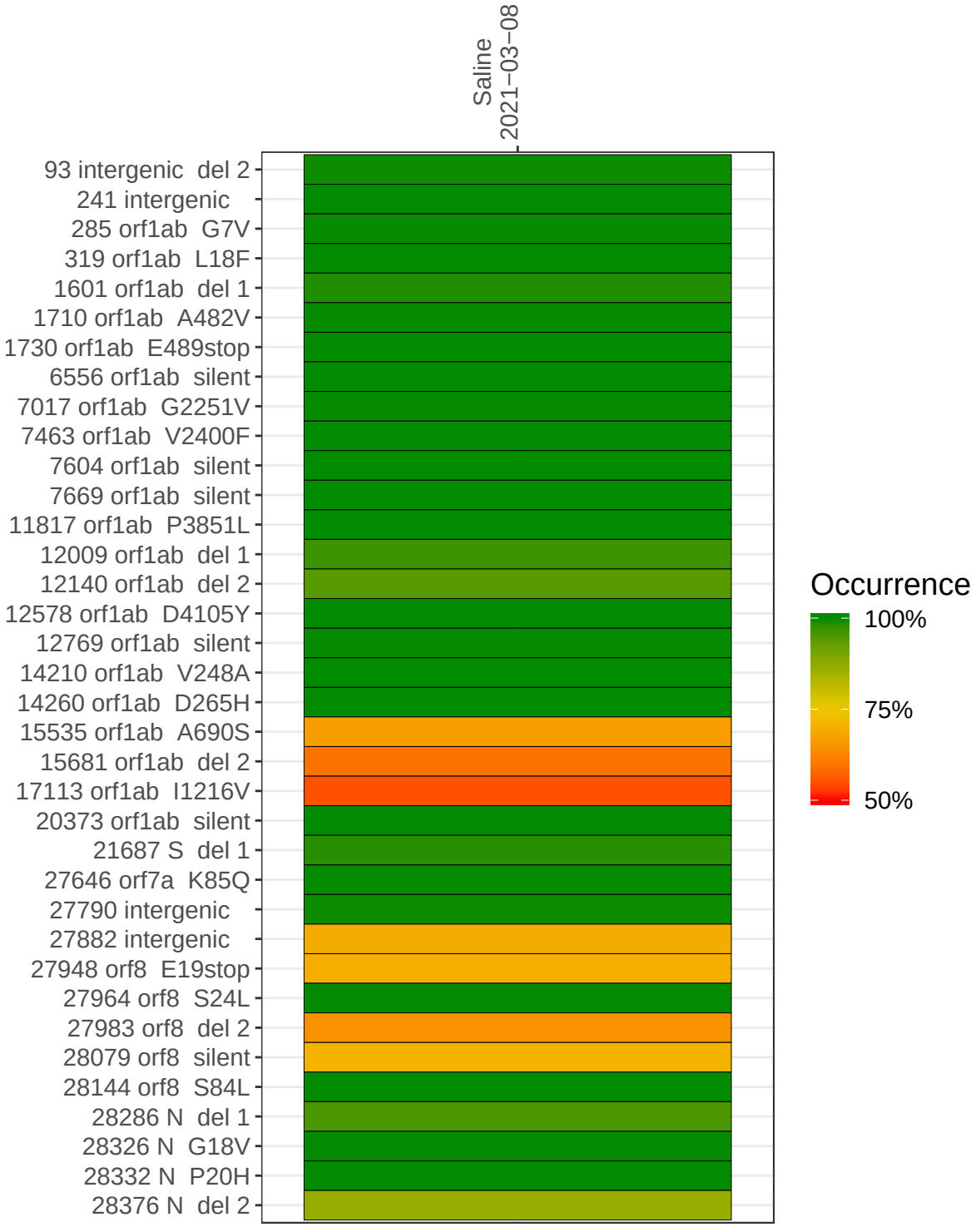
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

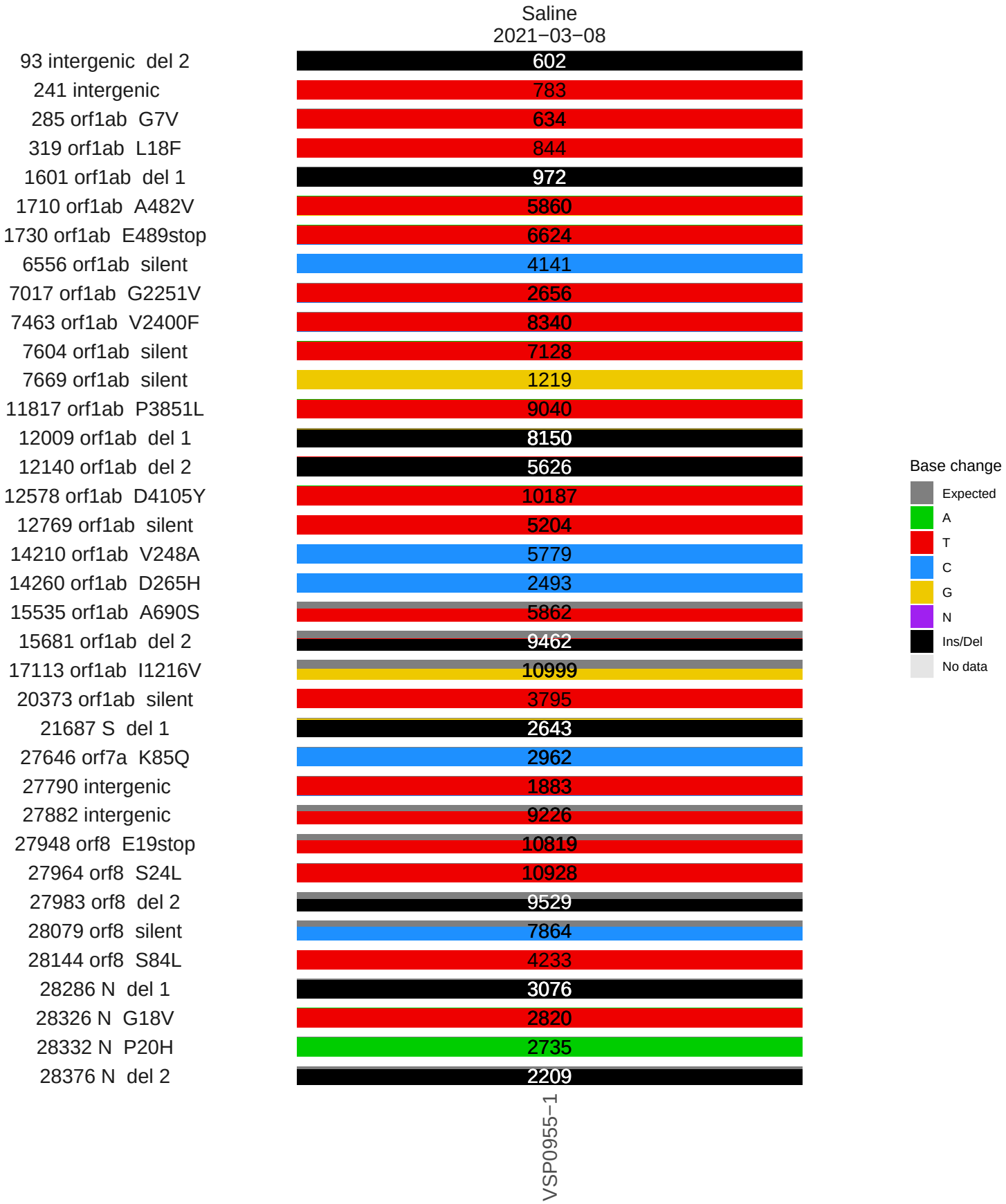
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0955-1	single experiment	NA	Saline	2021-03-08	1.03	NA	26.0%	23.7%

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.

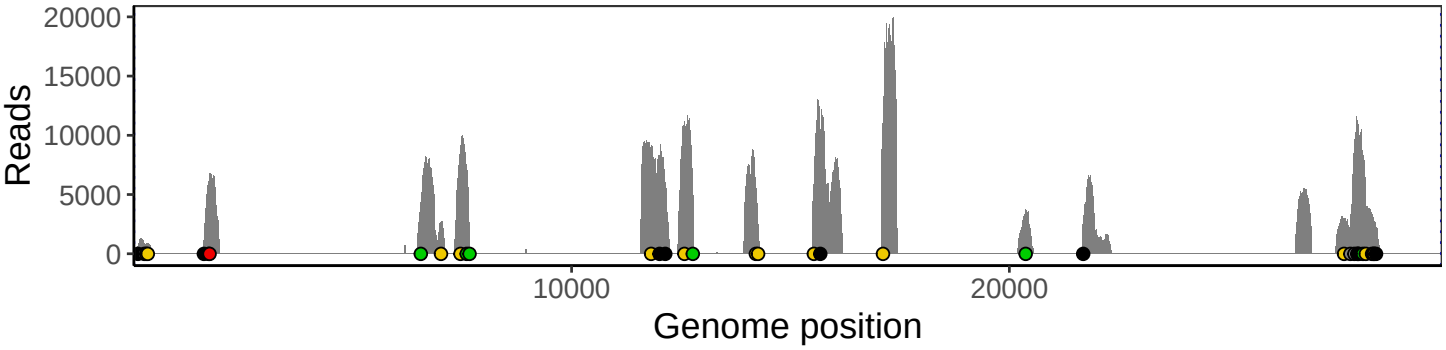



Saline
2021−03−08
93 intergenic del 2
241 intergenic
285 orf1ab G7V
319 orf1ab L18F
1601 orf1ab del 1
1710 orf1ab A482V
1730 orf1ab E489stop
6556 orf1ab silent
7017 orf1ab G2251V
7463 orf1ab V2400F
7604 orf1ab silent
7669 orf1ab silent
11817 orf1ab P3851L
12009 orf1ab del 1
12140 orf1ab del 2
12578 orf1ab D4105Y
12769 orf1ab silent
14210 orf1ab V248A
14260 orf1ab D265H
15535 orf1ab A690S
15681 orf1ab del 2
17113 orf1ab I1216V
20373 orf1ab silent
21687 S del 1
27646 orf7a K85Q
27790 intergenic
27882 intergenic
27948 orf8 E19stop
27964 orf8 S24L
27983 orf8 del 2
28079 orf8 silent
28144 orf8 S84L
28286 N del 1
28326 N G18V
28332 N P20H
28376 N del 2
602
783
634
844
972
5860
6624
4141
2656
8340
7128
1219
9040
8150
5626
10187
5204
5779
2493
5862
9462
10999
3795
2643
2962
1883
9226
10819
10928
9529
7864
4233
3076
2820
2735
2209
VSP0955−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

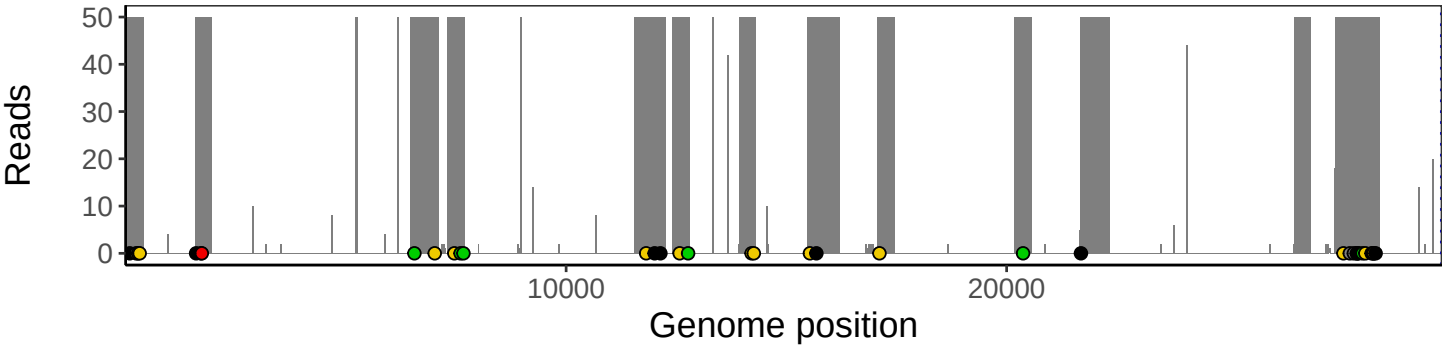
Analyses of individual experiments and composite results

VSP0955-1 | 2021-03-08 | Saline | UPHS-0023 | genomes | single experiment

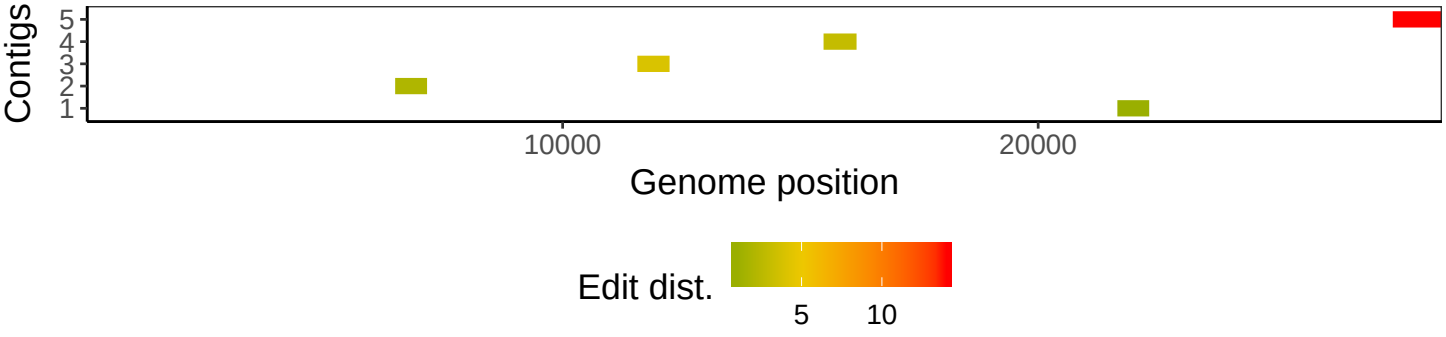
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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