COVID-19 subject UPHS-0040

2021-03-25

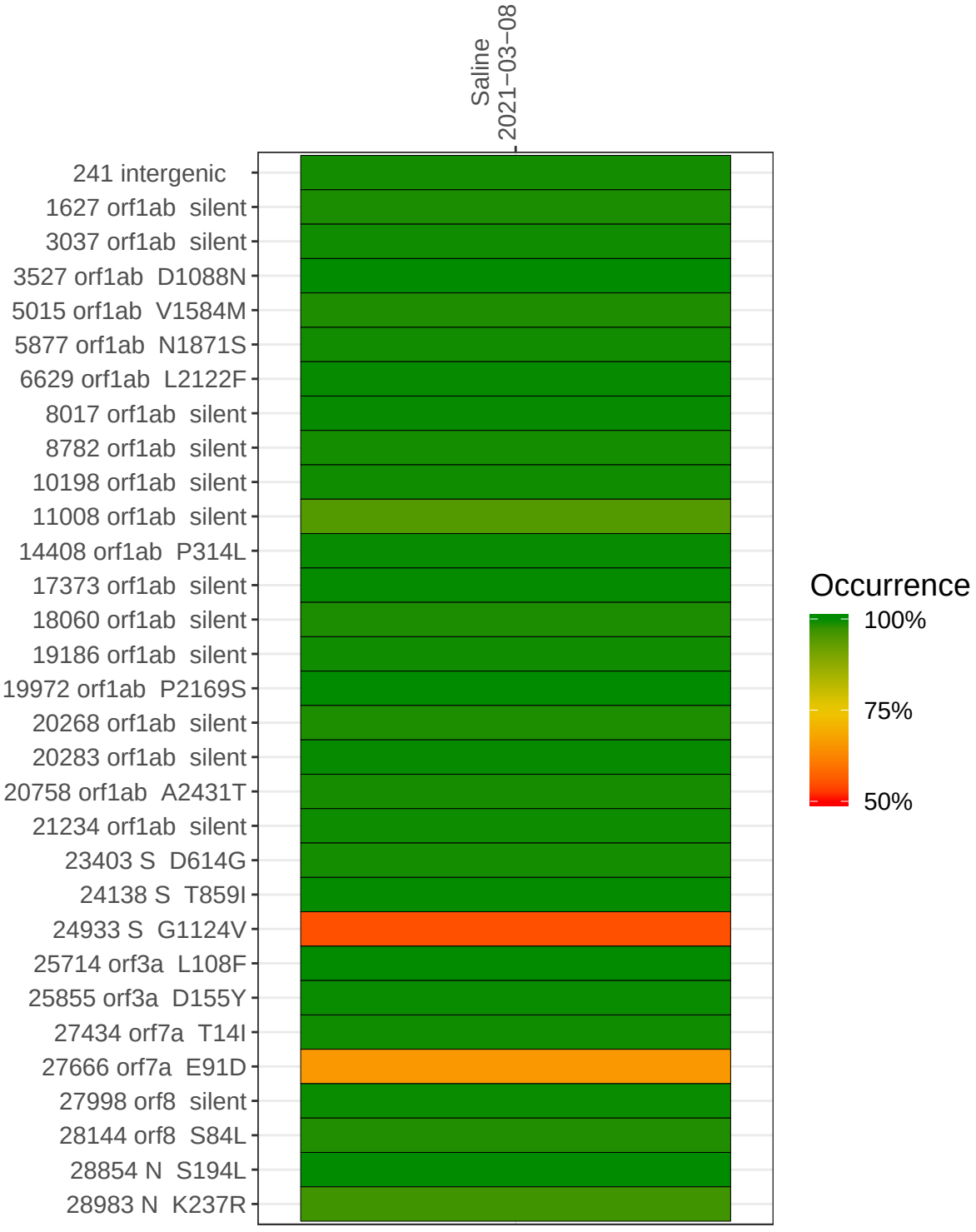
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

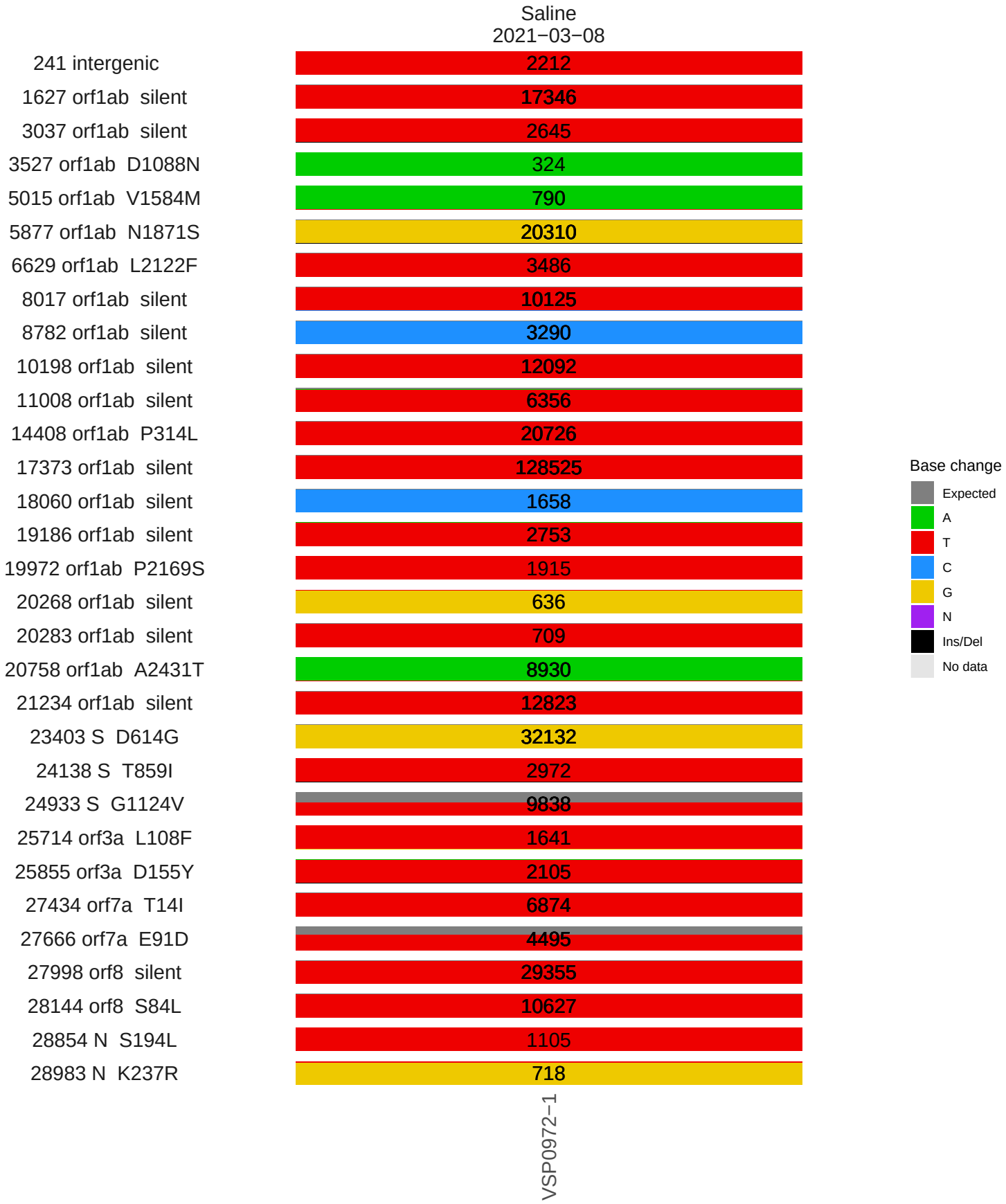
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0972-1	single experiment	NA	Saline	2021-03-08	29.86	B.1.409	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.

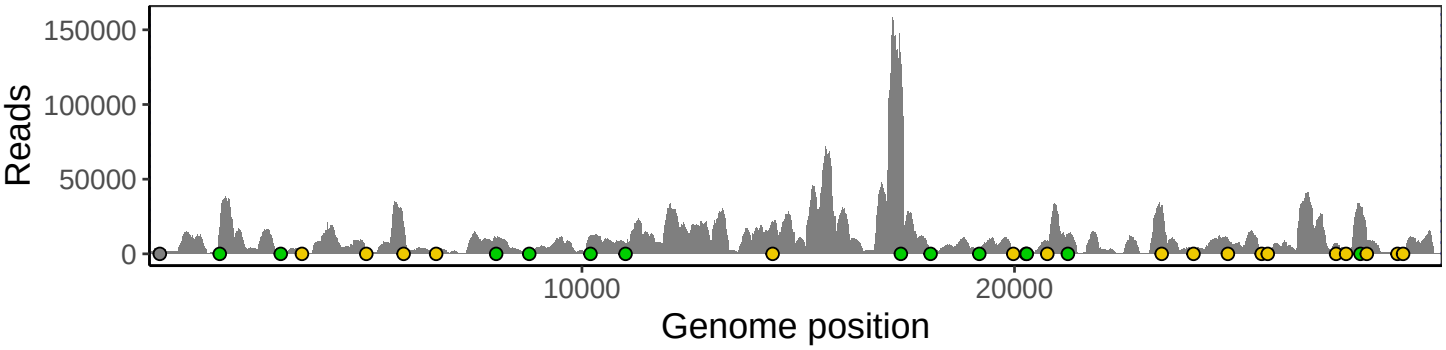



Saline
2021−03−08
241 intergenic
1627 orf1ab silent
3037 orf1ab silent
3527 orf1ab D1088N
5015 orf1ab V1584M
5877 orf1ab N1871S
6629 orf1ab L2122F
8017 orf1ab silent
8782 orf1ab silent
10198 orf1ab silent
11008 orf1ab silent
14408 orf1ab P314L
17373 orf1ab silent
18060 orf1ab silent
19186 orf1ab silent
19972 orf1ab P2169S
20268 orf1ab silent
20283 orf1ab silent
20758 orf1ab A2431T
21234 orf1ab silent
23403 S D614G
24138 S T859I
24933 S G1124V
25714 orf3a L108F
25855 orf3a D155Y
27434 orf7a T14I
27666 orf7a E91D
27998 orf8 silent
28144 orf8 S84L
28854 N S194L
28983 N K237R
2212
17346
2645
324
790
20310
3486
10125
3290
12092
6356
20726
128525
1658
2753
1915
636
709
8930
12823
32132
2972
9838
1641
2105
6874
4495
29355
10627
1105
718
VSP0972−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

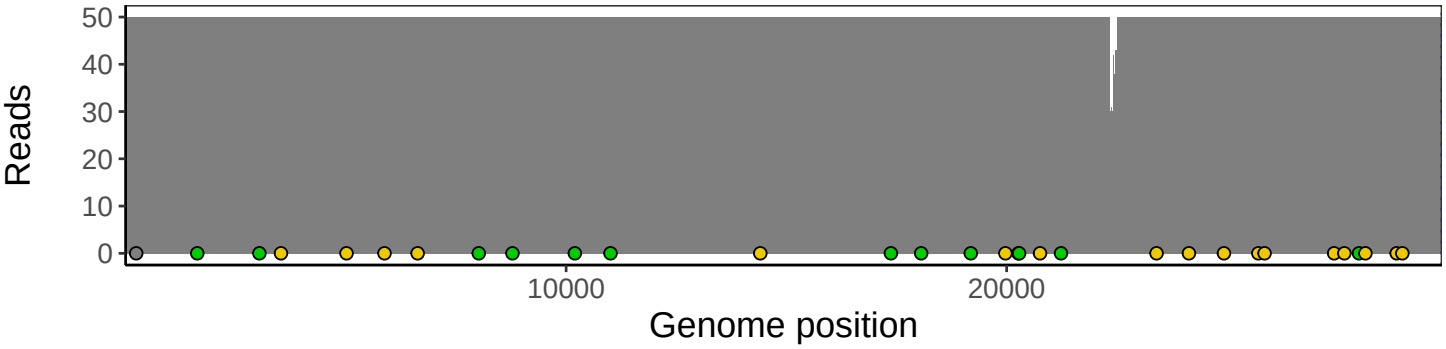
Analyses of individual experiments and composite results

VSP0972-1 | 2021-03-08 | Saline | UPHS-0040 | genomes | single experiment

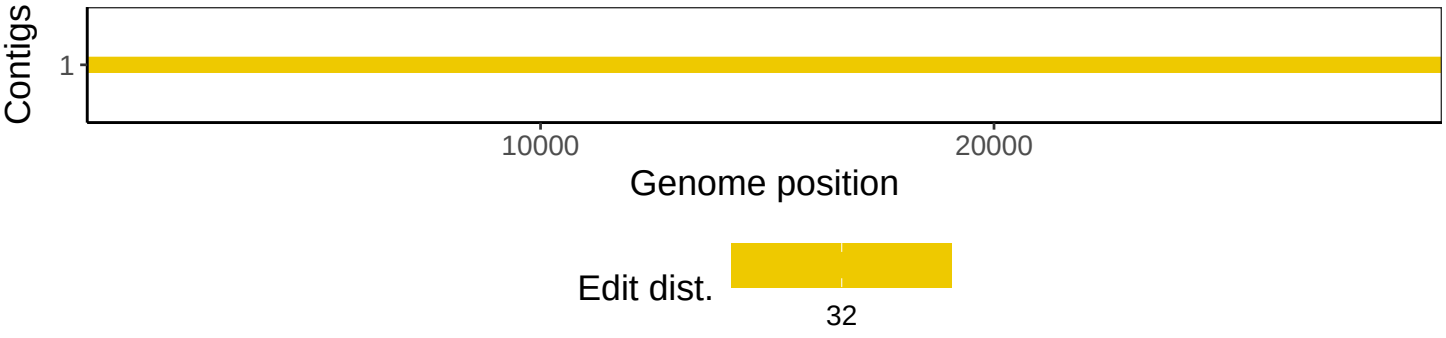
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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