COVID-19 subject UPHS-0212

2021-04-17

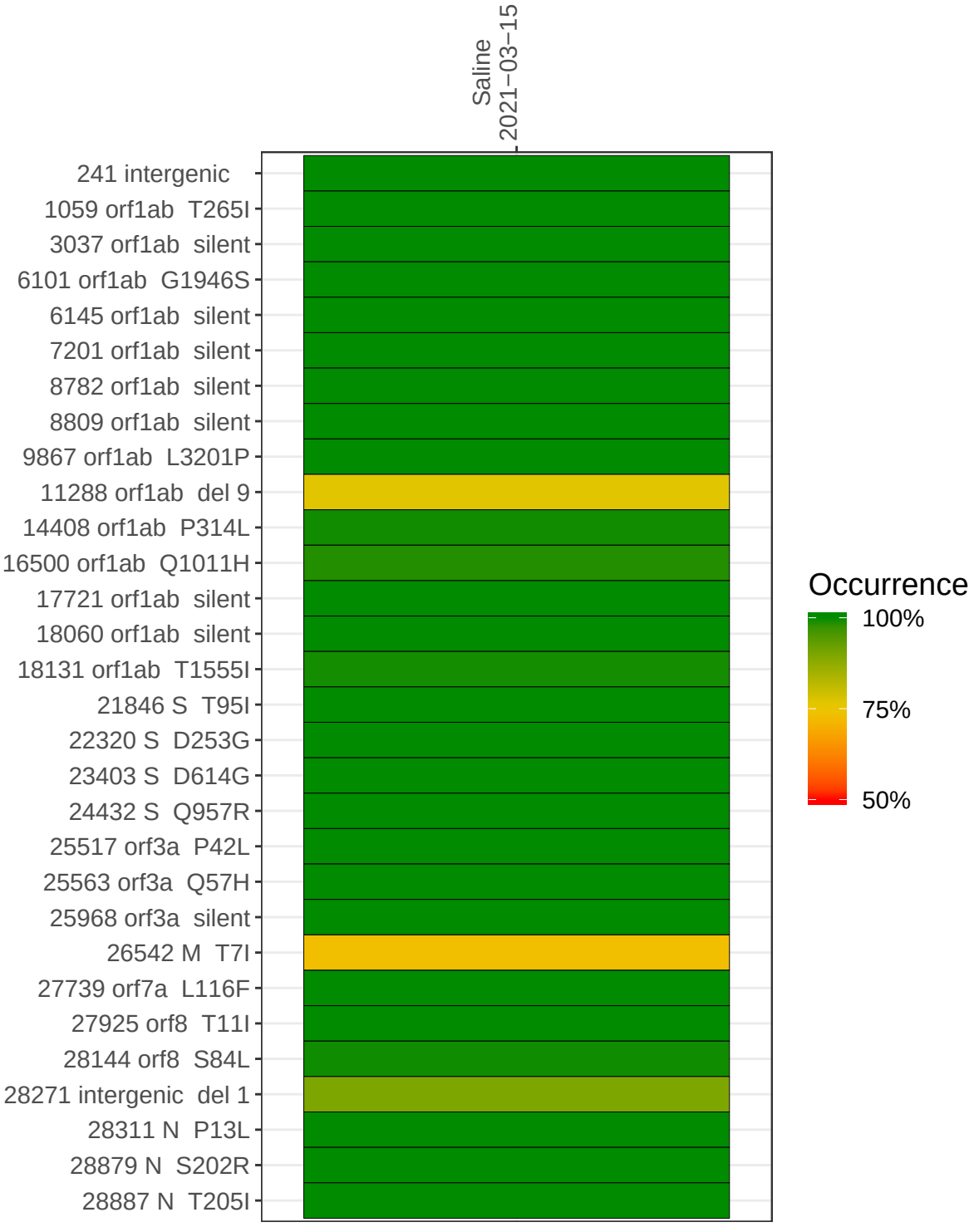
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

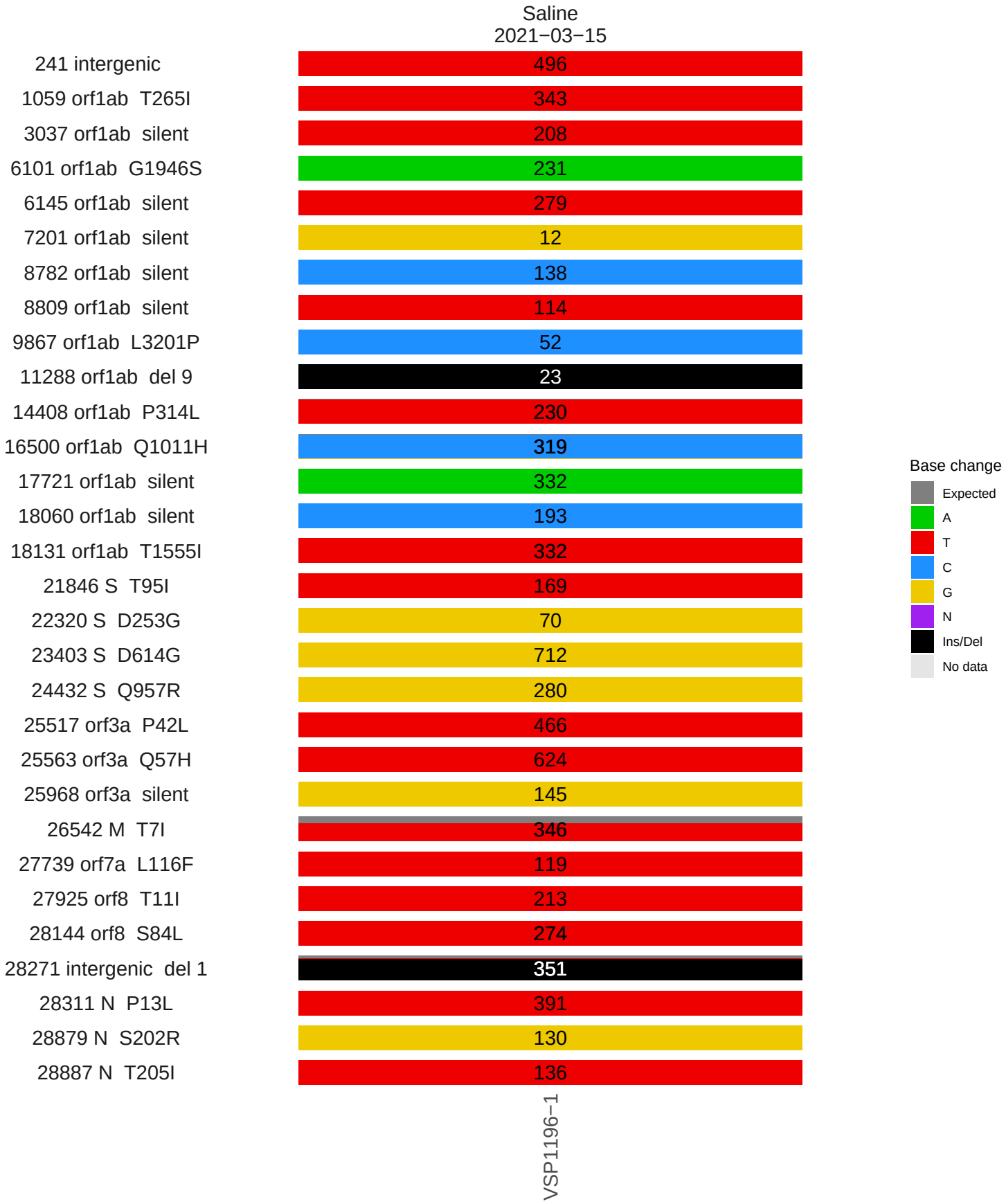
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1196-1	single experiment	NA	Saline	2021-03-15	12.55	B.1.526.2	99.7%	97.4%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/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.

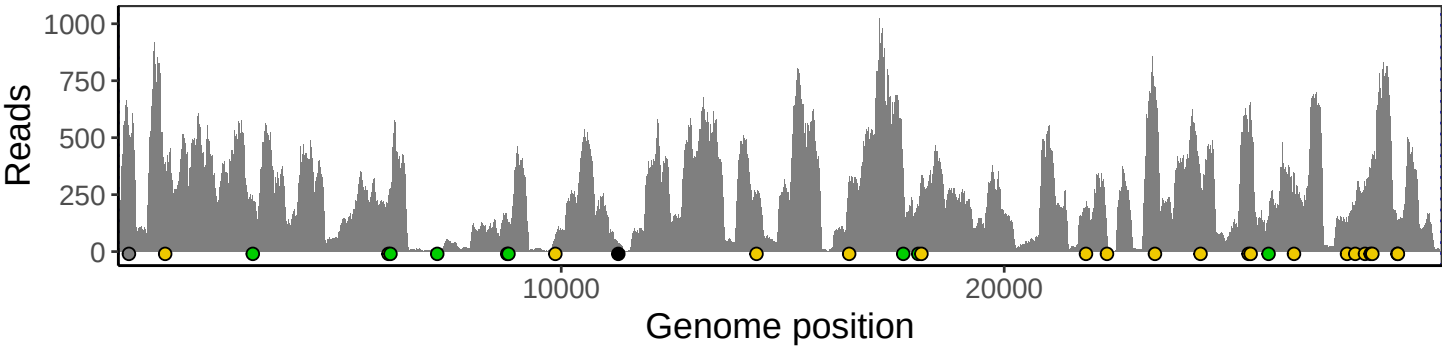



Saline
2021−03−15
241 intergenic
496
1059 orf1ab T265I
343
3037 orf1ab silent
208
6101 orf1ab G1946S
231
6145 orf1ab silent
279
7201 orf1ab silent
12
8782 orf1ab silent
138
8809 orf1ab silent
114
9867 orf1ab L3201P
52
11288 orf1ab del 9
23
14408 orf1ab P314L
230
16500 orf1ab Q1011H
319
17721 orf1ab silent
332
18060 orf1ab silent
193
18131 orf1ab T1555I
332
21846 S T95I
169
22320 S D253G
70
23403 S D614G
712
24432 S Q957R
280
25517 orf3a P42L
466
25563 orf3a Q57H
624
25968 orf3a silent
145
26542 M T7I
346
27739 orf7a L116F
119
27925 orf8 T11I
213
28144 orf8 S84L
274
28271 intergenic del 1
351
28311 N P13L
391
28879 N S202R
130
28887 N T205I
136
VSP1196−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

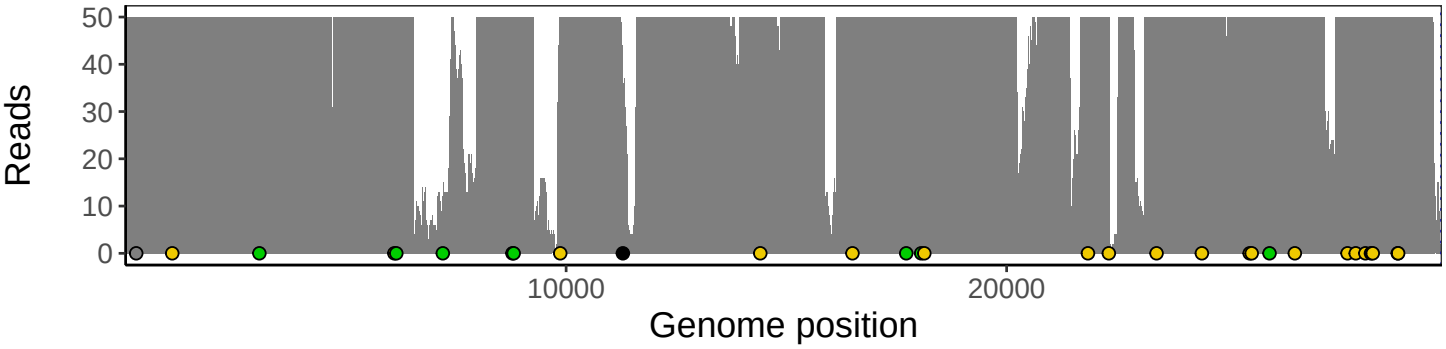
Analyses of individual experiments and composite results

VSP1196-1 | 2021-03-15 | Saline | UPHS-0212 | genomes | single experiment

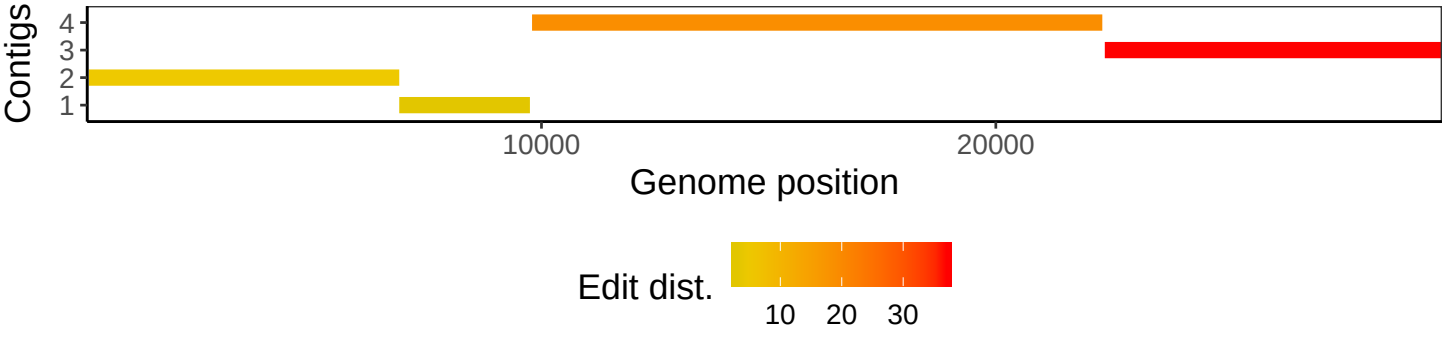
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.8
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