COVID-19 subject UPHS-0110

2021-03-29

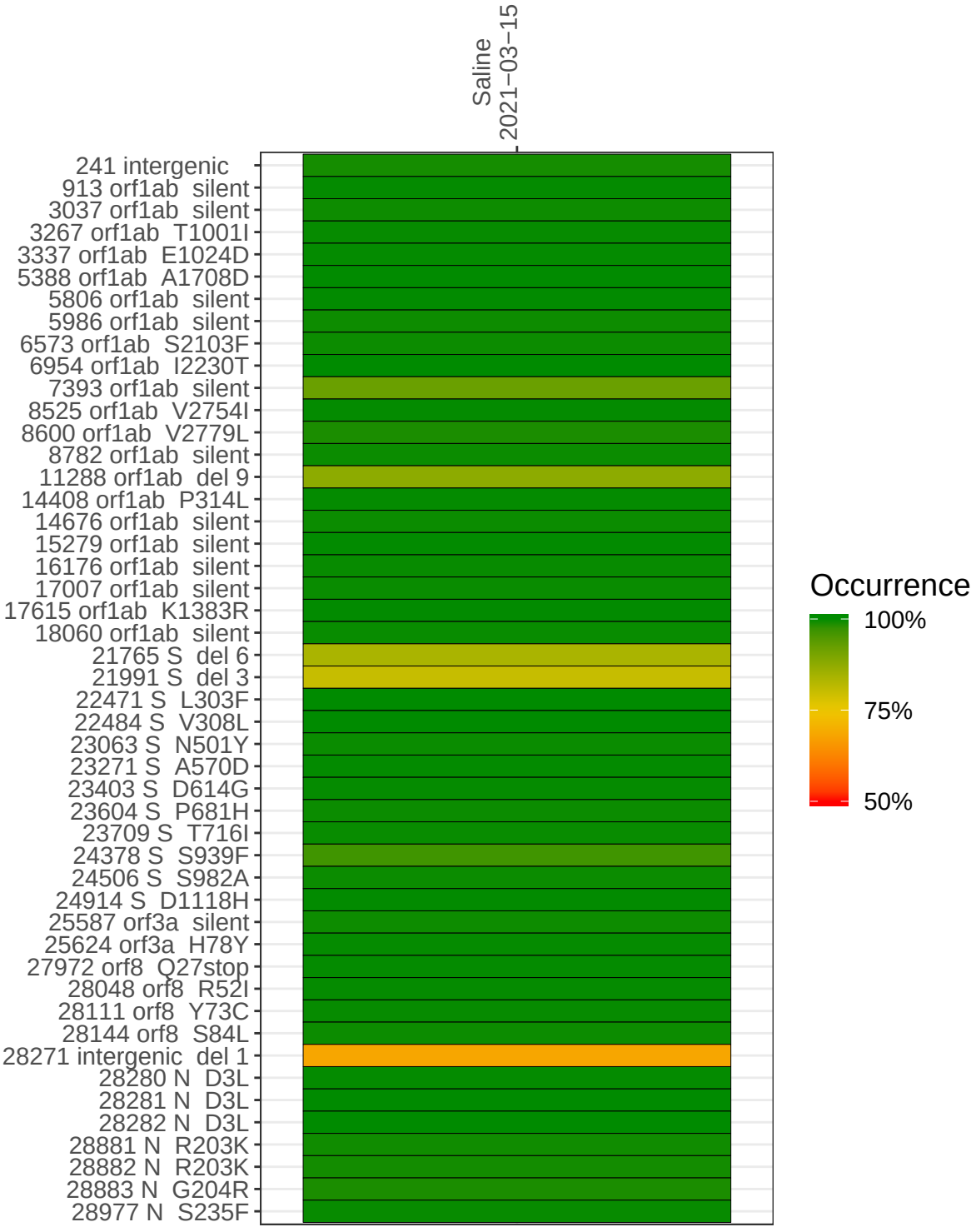
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

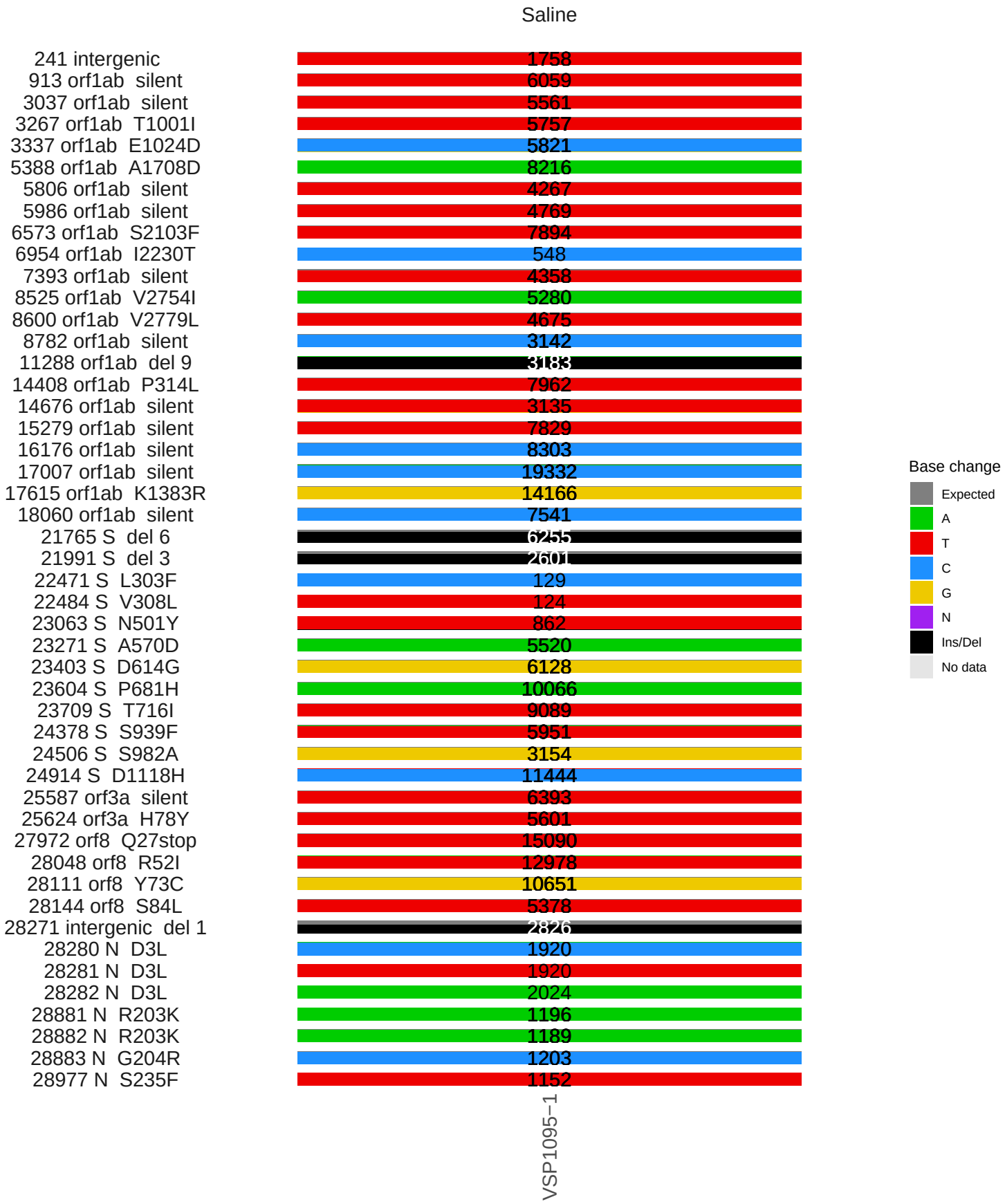
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1095-1	single experiment	NA	Saline	2021-03-15	29.82	B.1.1.7	99.8%	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.

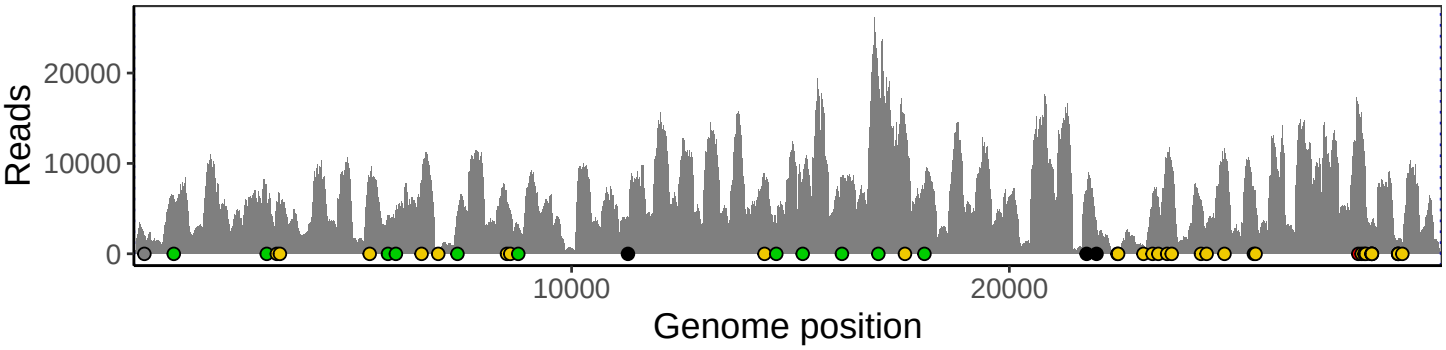



Saline
241 intergenic
913 orf1ab silent
3037 orf1ab silent
3267 orf1ab T1001I
3337 orf1ab E1024D
5388 orf1ab A1708D
5806 orf1ab silent
5986 orf1ab silent
6573 orf1ab S2103F
6954 orf1ab I2230T
7393 orf1ab silent
8525 orf1ab V2754I
8600 orf1ab V2779L
8782 orf1ab silent
11288 orf1ab del 9
14408 orf1ab P314L
14676 orf1ab silent
15279 orf1ab silent
16176 orf1ab silent
17007 orf1ab silent
17615 orf1ab K1383R
18060 orf1ab silent
21765 S del 6
21991 S del 3
22471 S L303F
22484 S V308L
23063 S N501Y
23271 S A570D
23403 S D614G
23604 S P681H
23709 S T716I
24378 S S939F
24506 S S982A
24914 S D1118H
25587 orf3a silent
25624 orf3a H78Y
27972 orf8 Q27stop
28048 orf8 R52I
28111 orf8 Y73C
28144 orf8 S84L
28271 intergenic del 1
28280 N D3L
28281 N D3L
28282 N D3L
28881 N R203K
28882 N R203K
28883 N G204R
28977 N S235F
1758
6059
5561
5757
5821
8216
4267
4769
7894
548
4358
5280
4675
3142
3183
7962
3135
7829
8303
19332
14166
7541
6255
2601
129
124
862
5520
6128
10066
9089
5951
3154
11444
6393
5601
15090
12978
10651
5378
2826
1920
1920
2024
1196
1189
1203
1152
VSP1095−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

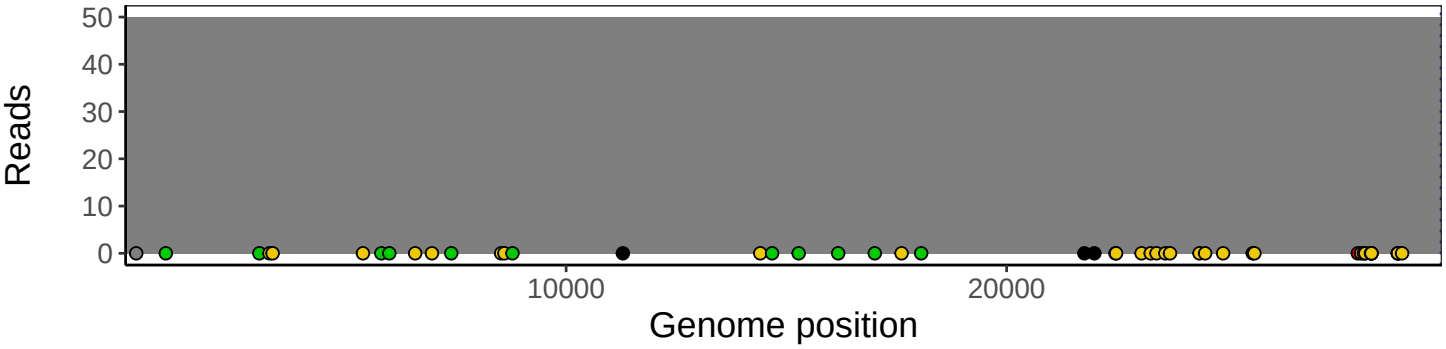
Analyses of individual experiments and composite results

VSP1095-1 | 2021-03-15 | Saline | UPHS-0110 | genomes | single experiment

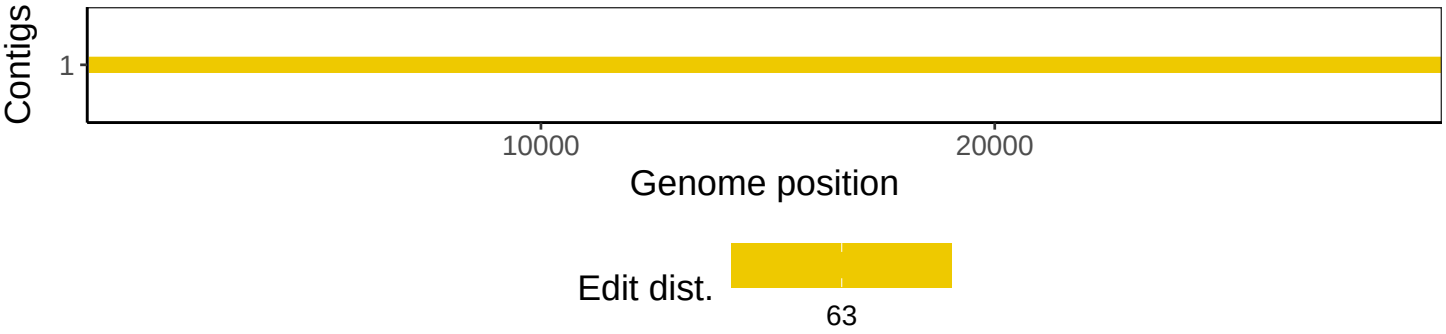
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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