COVID-19 subject UPHS-1194

2021-06-23

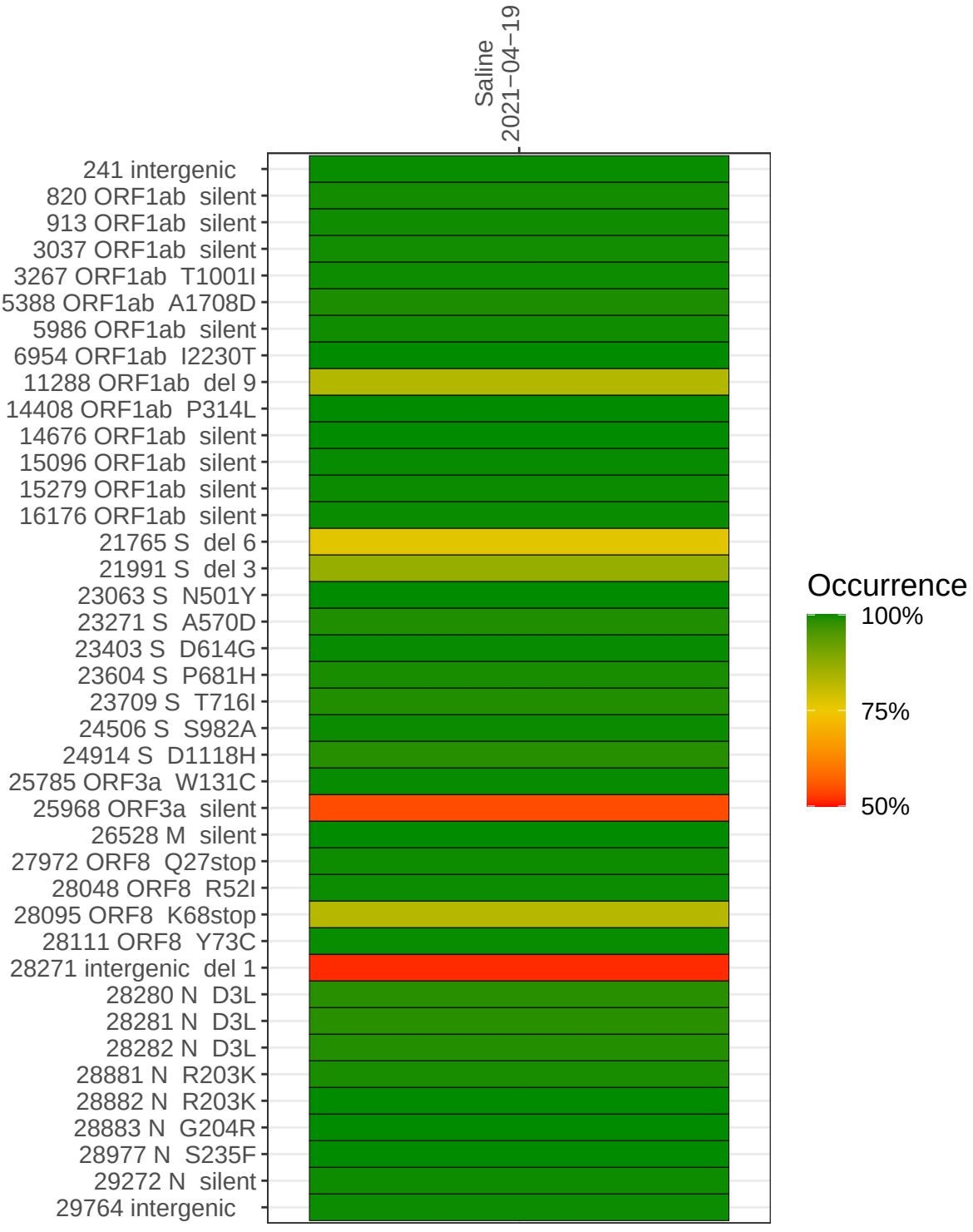
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

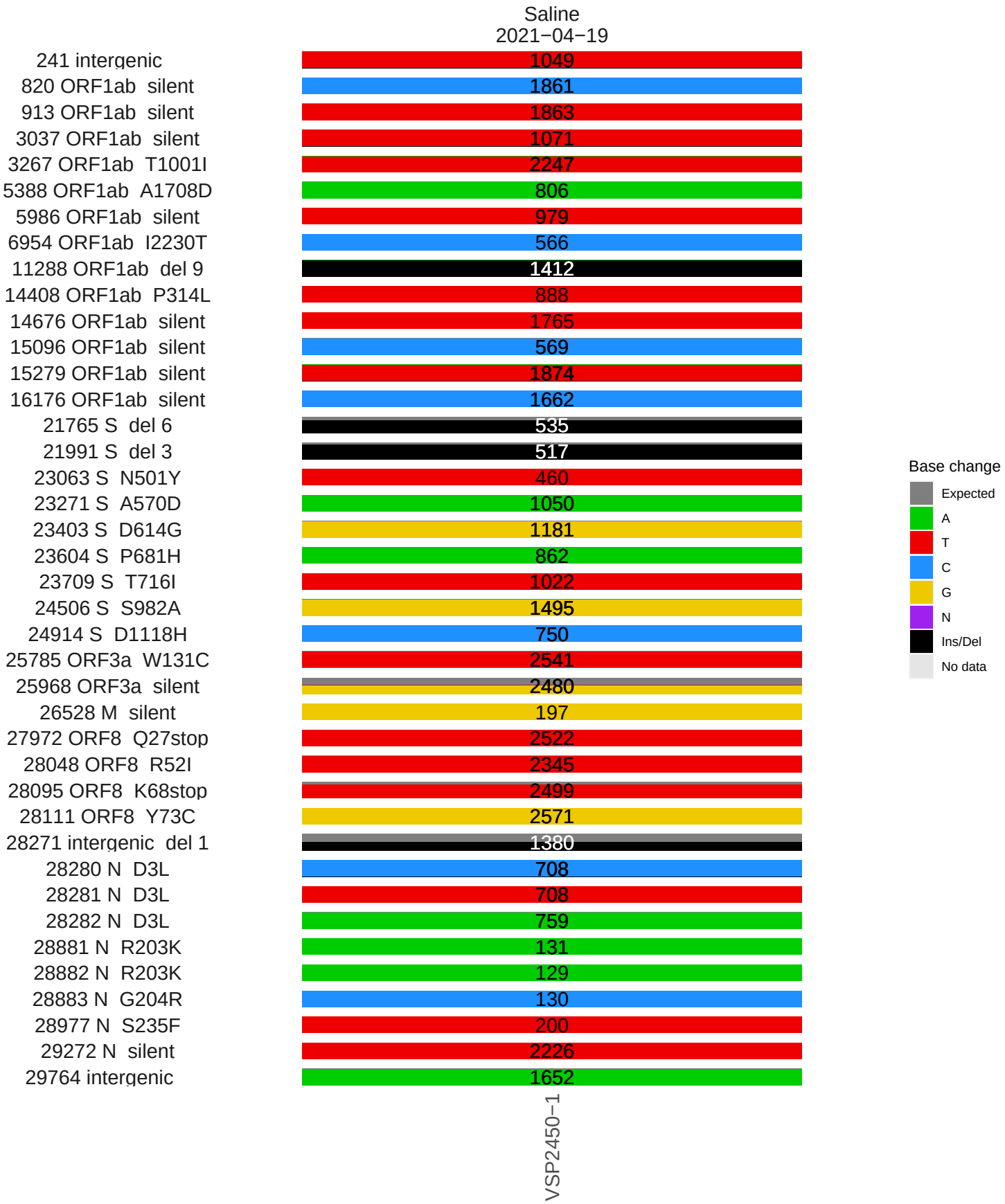
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2450-1	single experiment	NA	Saline	2021-04-19	22.38	B.1.1.7	99.9%	99.8%

Variants shared across samples

The heat map below shows how variants (reference genome /home/common/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) 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.

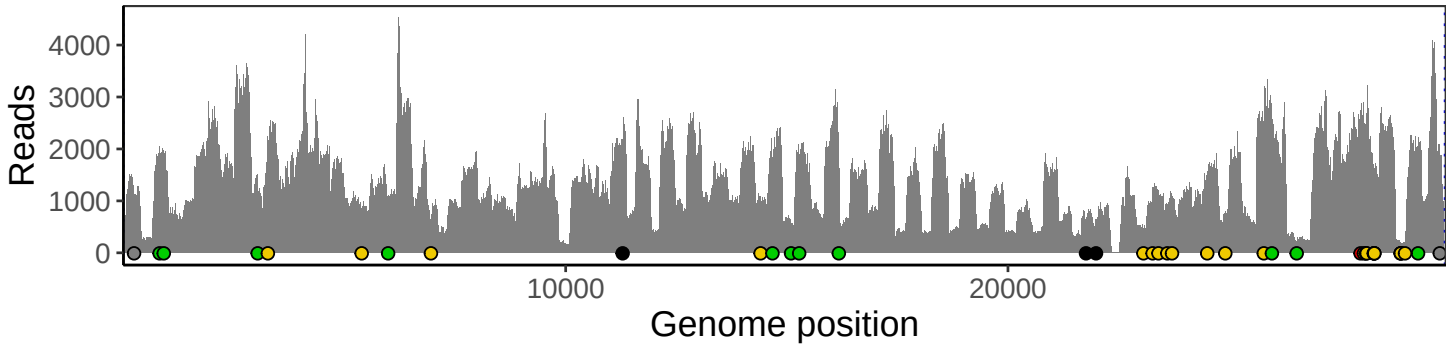



Saline
2021−04−19
241 intergenic 1049
820 ORF1ab silent 1861
913 ORF1ab silent 1863
3037 ORF1ab silent 1071
3267 ORF1ab T1001I 2247
5388 ORF1ab A1708D 806
5986 ORF1ab silent 979
6954 ORF1ab I2230T 566
11288 ORF1ab del 9 1412
14408 ORF1ab P314L 888
14676 ORF1ab silent 1765
15096 ORF1ab silent 569
15279 ORF1ab silent 1874
16176 ORF1ab silent 1662
21765 S del 6 535
21991 S del 3 517
23063 S N501Y 460
23271 S A570D 1050
23403 S D614G 1181
23604 S P681H 862
23709 S T716I 1022
24506 S S982A 1495
24914 S D1118H 750
25785 ORF3a W131C 2541
25968 ORF3a silent 2480
26528 M silent 197
27972 ORF8 Q27stop 2522
28048 ORF8 R52I 2345
28095 ORF8 K68stop 2499
28111 ORF8 Y73C 2571
28271 intergenic del 1 1380
28280 N D3L 708
28281 N D3L 708
28282 N D3L 759
28881 N R203K 131
28882 N R203K 129
28883 N G204R 130
28977 N S235F 200
29272 N silent 2226
29764 intergenic 1652
VSP2450−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

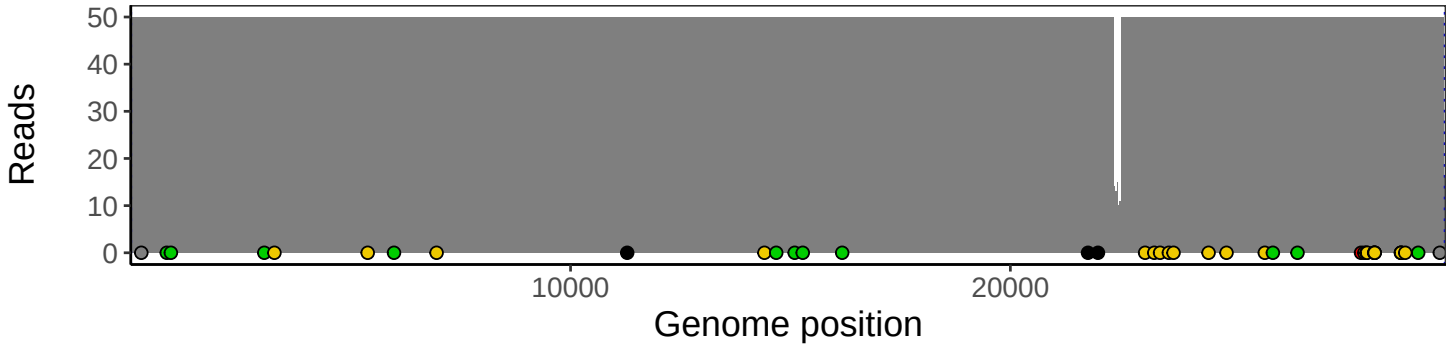
Analyses of individual experiments and composite results

VSP2450-1 | 2021-04-19 | Saline | UPHS-1194 | genomes | single experiment

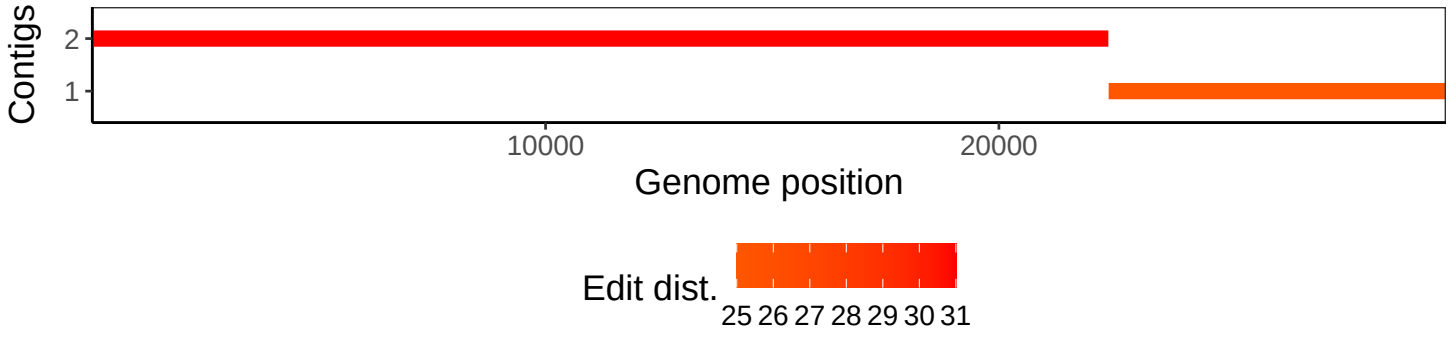
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.1.3
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	3.3.3
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