COVID-19 subject HUP Q-0103

2021-06-23

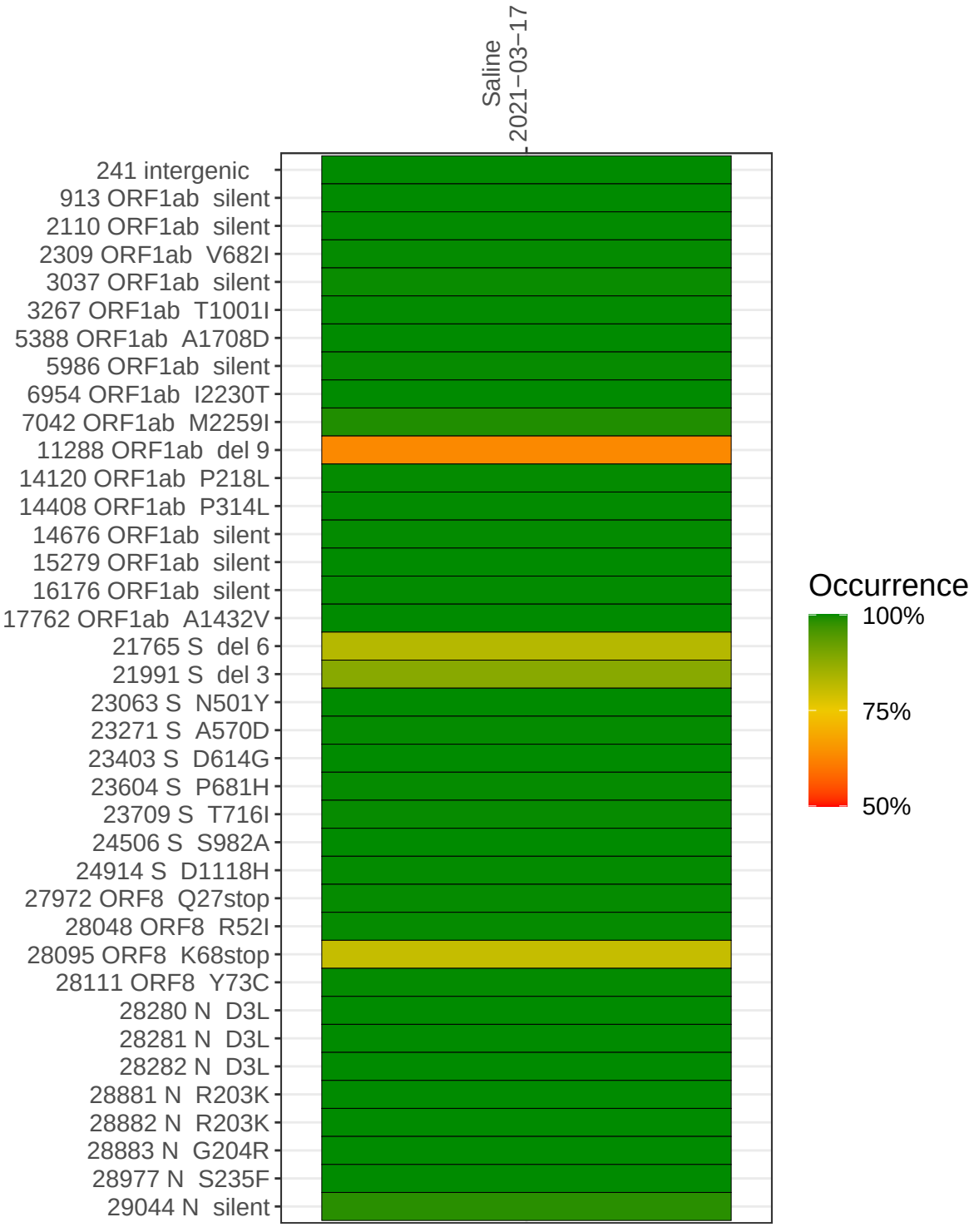
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

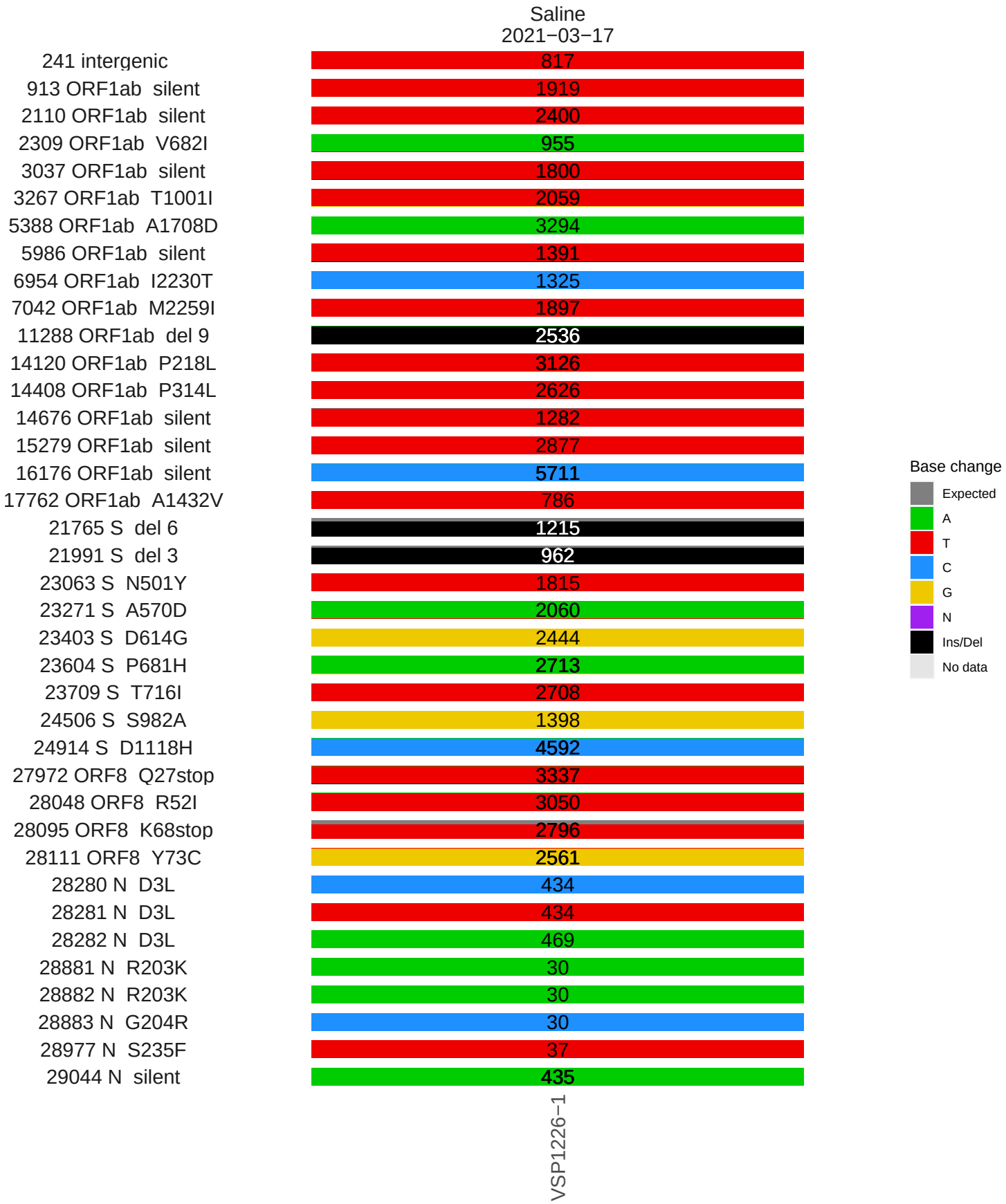
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1226-1	single experiment	NA	Saline	2021-03-17	29.80	B.1.1.7	99.8%	99.7%

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.

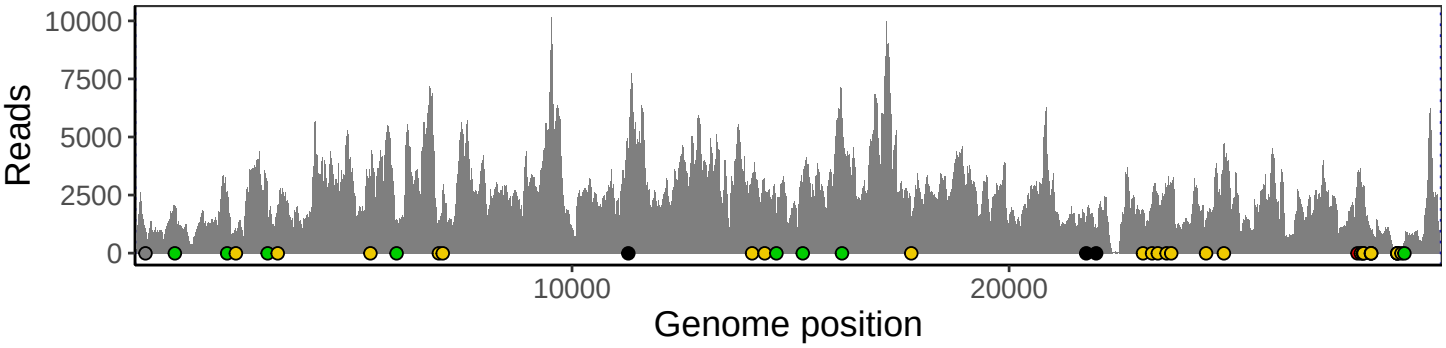



Saline
2021−03−17
241 intergenic 817
913 ORF1ab silent 1919
2110 ORF1ab silent 2400
2309 ORF1ab V682I 955
3037 ORF1ab silent 1800
3267 ORF1ab T1001I 2059
5388 ORF1ab A1708D 3294
5986 ORF1ab silent 1391
6954 ORF1ab I2230T 1325
7042 ORF1ab M2259I 1897
11288 ORF1ab del 9 2536
14120 ORF1ab P218L 3126
14408 ORF1ab P314L 2626
14676 ORF1ab silent 1282
15279 ORF1ab silent 2877
16176 ORF1ab silent 5711
17762 ORF1ab A1432V 786
21765 S del 6 1215
21991 S del 3 962
23063 S N501Y 1815
23271 S A570D 2060
23403 S D614G 2444
23604 S P681H 2713
23709 S T716I 2708
24506 S S982A 1398
24914 S D1118H 4592
27972 ORF8 Q27stop 3337
28048 ORF8 R52I 3050
28095 ORF8 K68stop 2796
28111 ORF8 Y73C 2561
28280 N D3L 434
28281 N D3L 434
28282 N D3L 469
28881 N R203K 30
28882 N R203K 30
28883 N G204R 30
28977 N S235F 37
29044 N silent 435
VSP1226−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

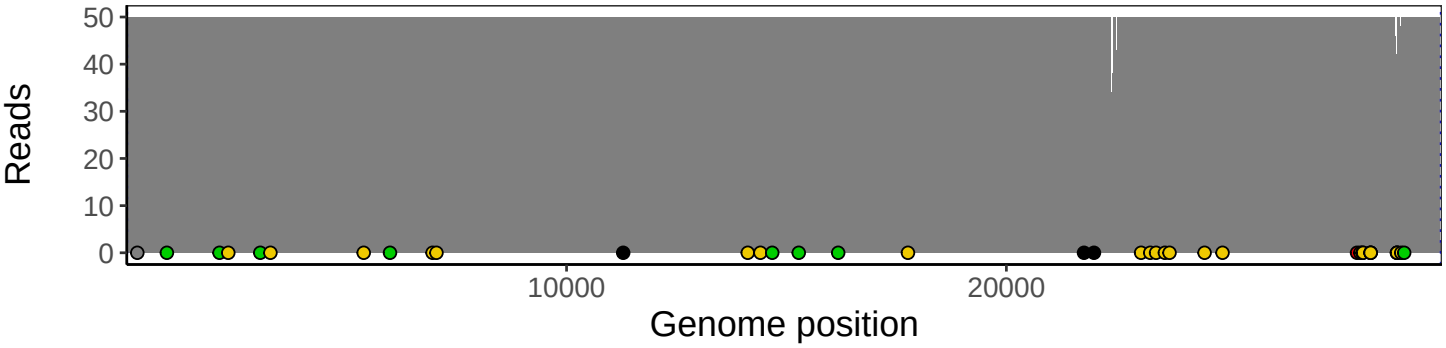
Analyses of individual experiments and composite results

VSP1226-1 | 2021-03-17 | Saline | HUP Q-0103 | genomes | single experiment

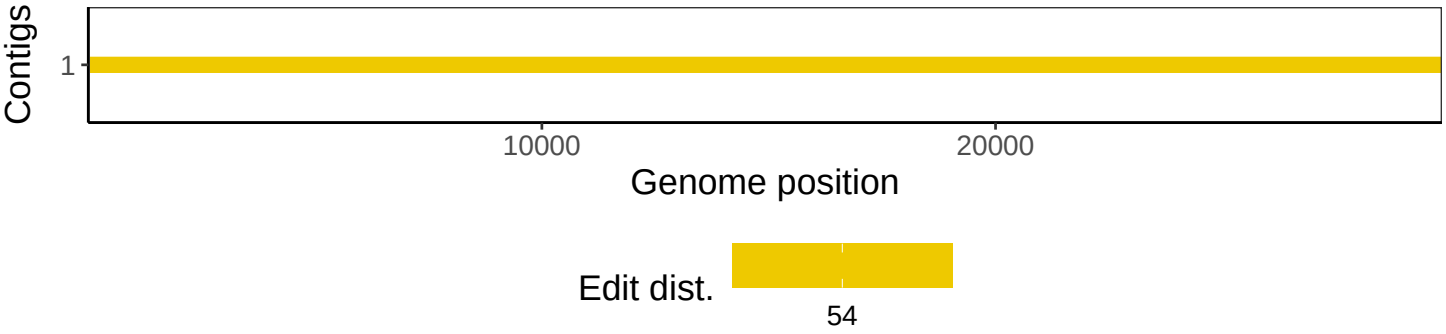
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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