COVID-19 subject HUP Q-0120

2021-05-05

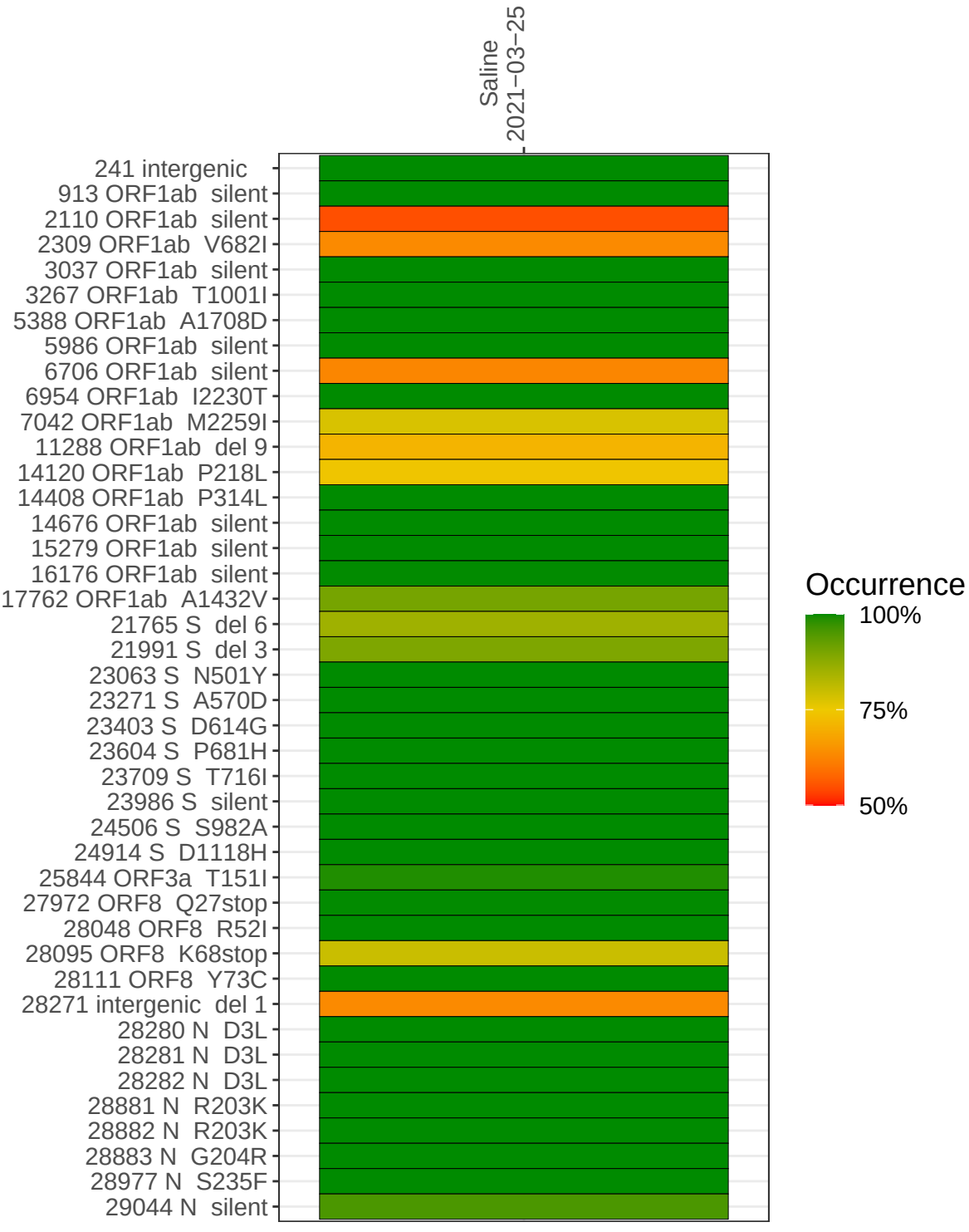
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

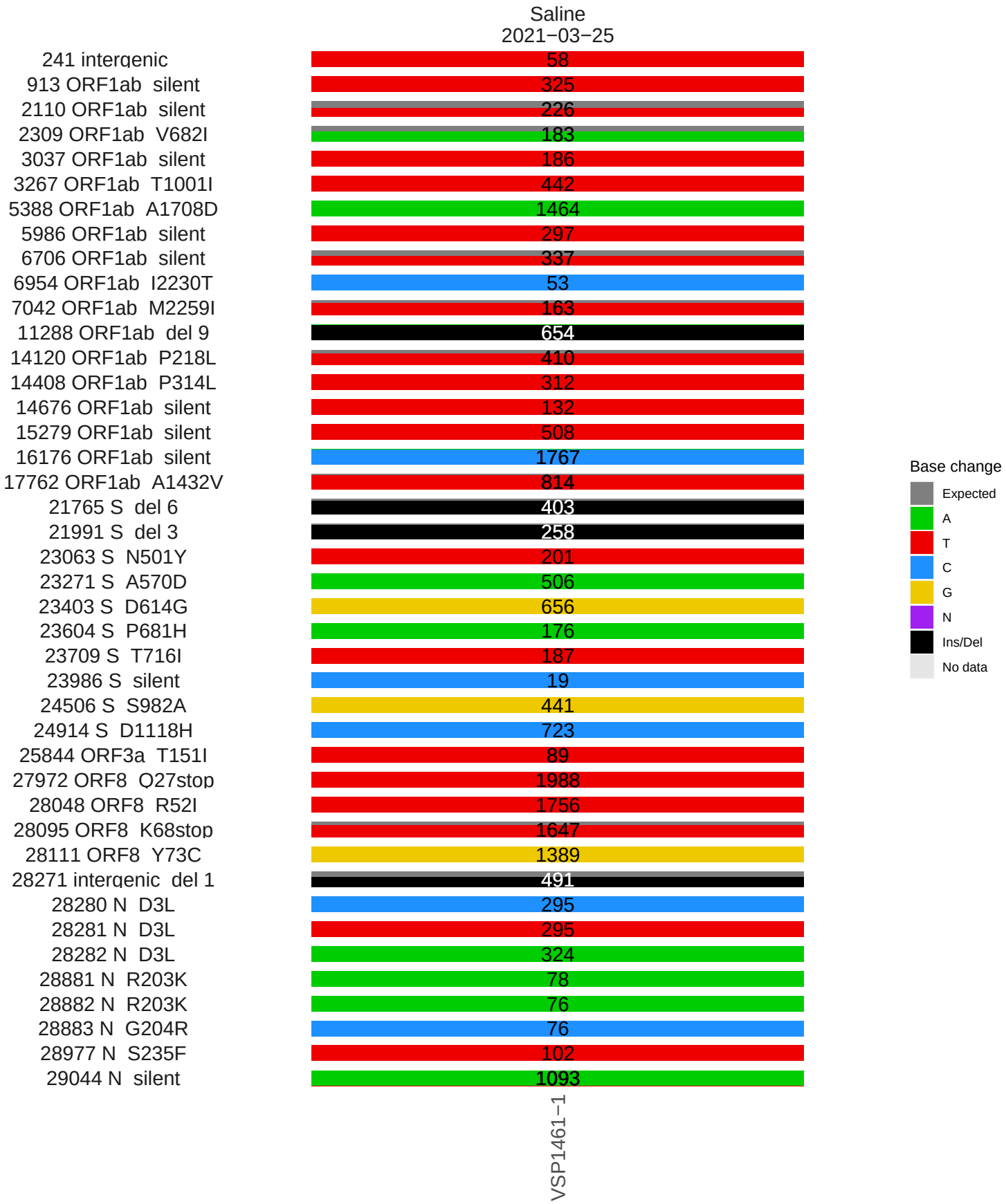
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1461-1	single experiment	NA	Saline	2021-03-25	29.85	B.1.1.7	100.0%	99.8%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/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.

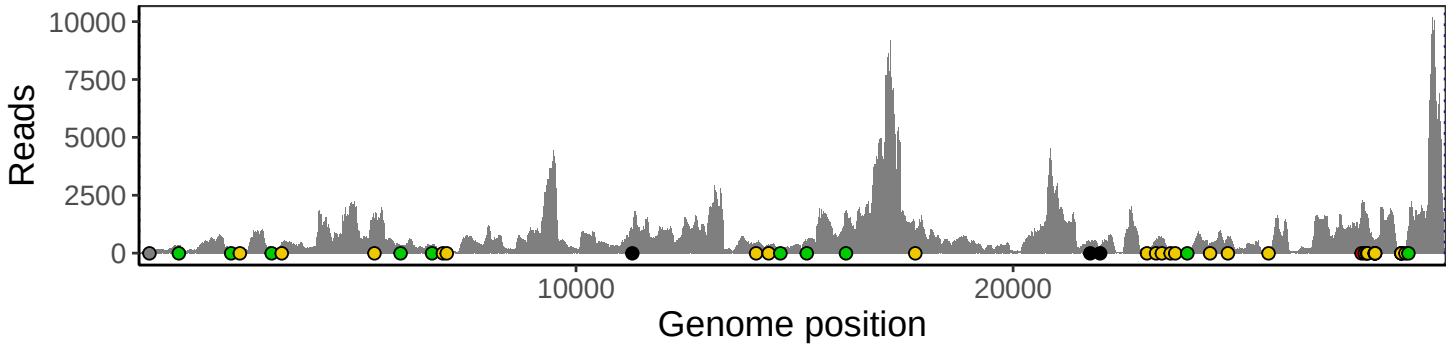



Saline
2021−03−25
241 intergenic 58
913 ORF1ab silent 325
2110 ORF1ab silent 226
2309 ORF1ab V682I 183
3037 ORF1ab silent 186
3267 ORF1ab T1001I 442
5388 ORF1ab A1708D 1464
5986 ORF1ab silent 297
6706 ORF1ab silent 337
6954 ORF1ab I2230T 53
7042 ORF1ab M2259I 163
11288 ORF1ab del 9 654
14120 ORF1ab P218L 410
14408 ORF1ab P314L 312
14676 ORF1ab silent 132
15279 ORF1ab silent 508
16176 ORF1ab silent 1767
17762 ORF1ab A1432V 814
21765 S del 6 403
21991 S del 3 258
23063 S N501Y 201
23271 S A570D 506
23403 S D614G 656
23604 S P681H 176
23709 S T716I 187
23986 S silent 19
24506 S S982A 441
24914 S D1118H 723
25844 ORF3a T151I 89
27972 ORF8 Q27stop 1988
28048 ORF8 R52I 1756
28095 ORF8 K68stop 1647
28111 ORF8 Y73C 1389
28271 intergenic del 1 491
28280 N D3L 295
28281 N D3L 295
28282 N D3L 324
28881 N R203K 78
28882 N R203K 76
28883 N G204R 76
28977 N S235F 102
29044 N silent 1093
VSP1461−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

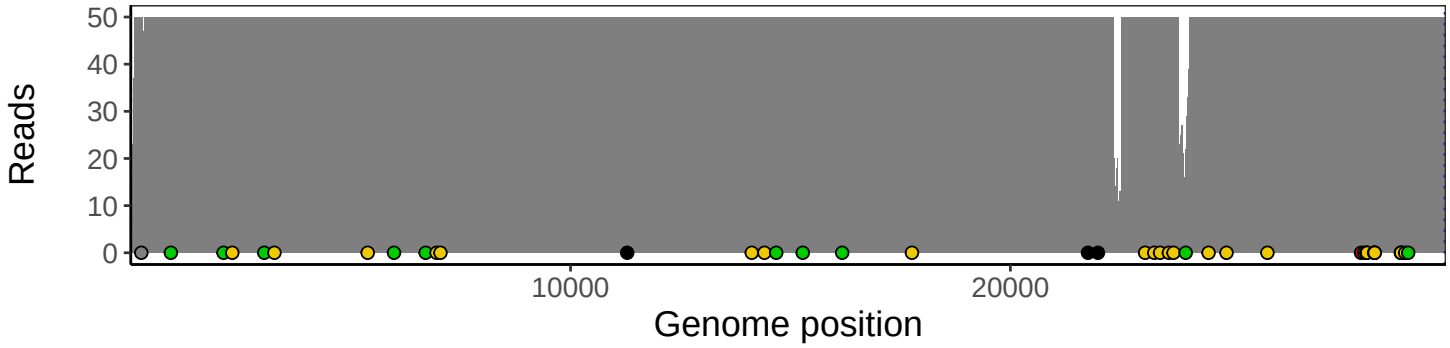
Analyses of individual experiments and composite results

VSP1461-1 | 2021-03-25 | Saline | HUP Q-0120 | genomes | single experiment

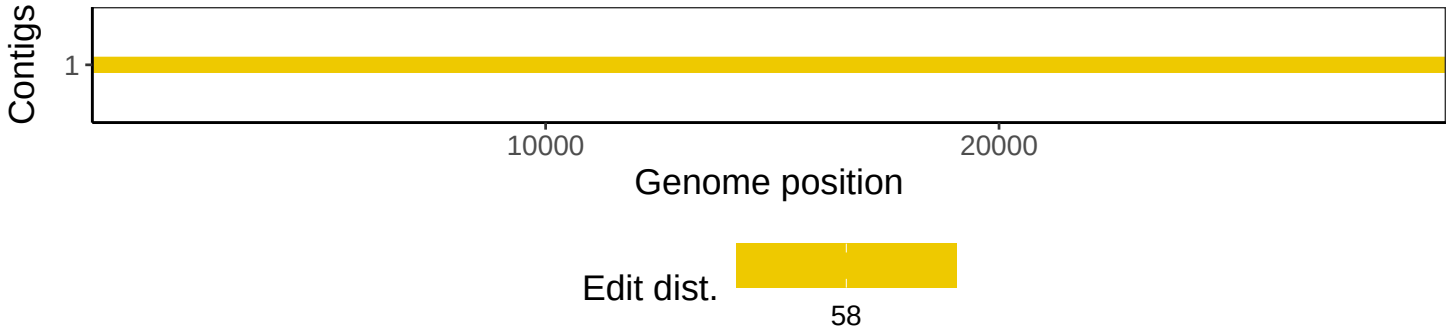
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.3.3
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