COVID-19 subject HUP Q-0084

2021-05-05

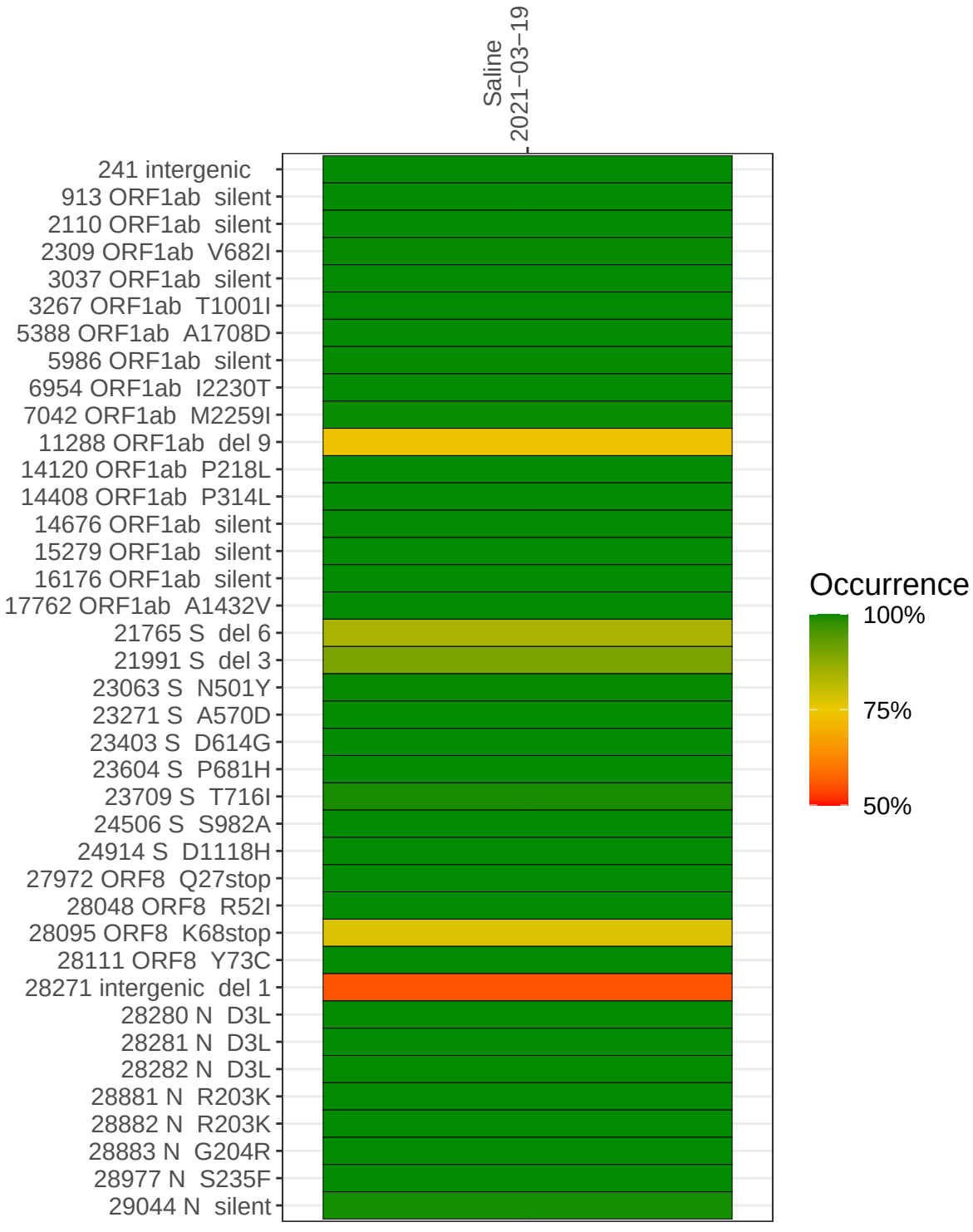
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

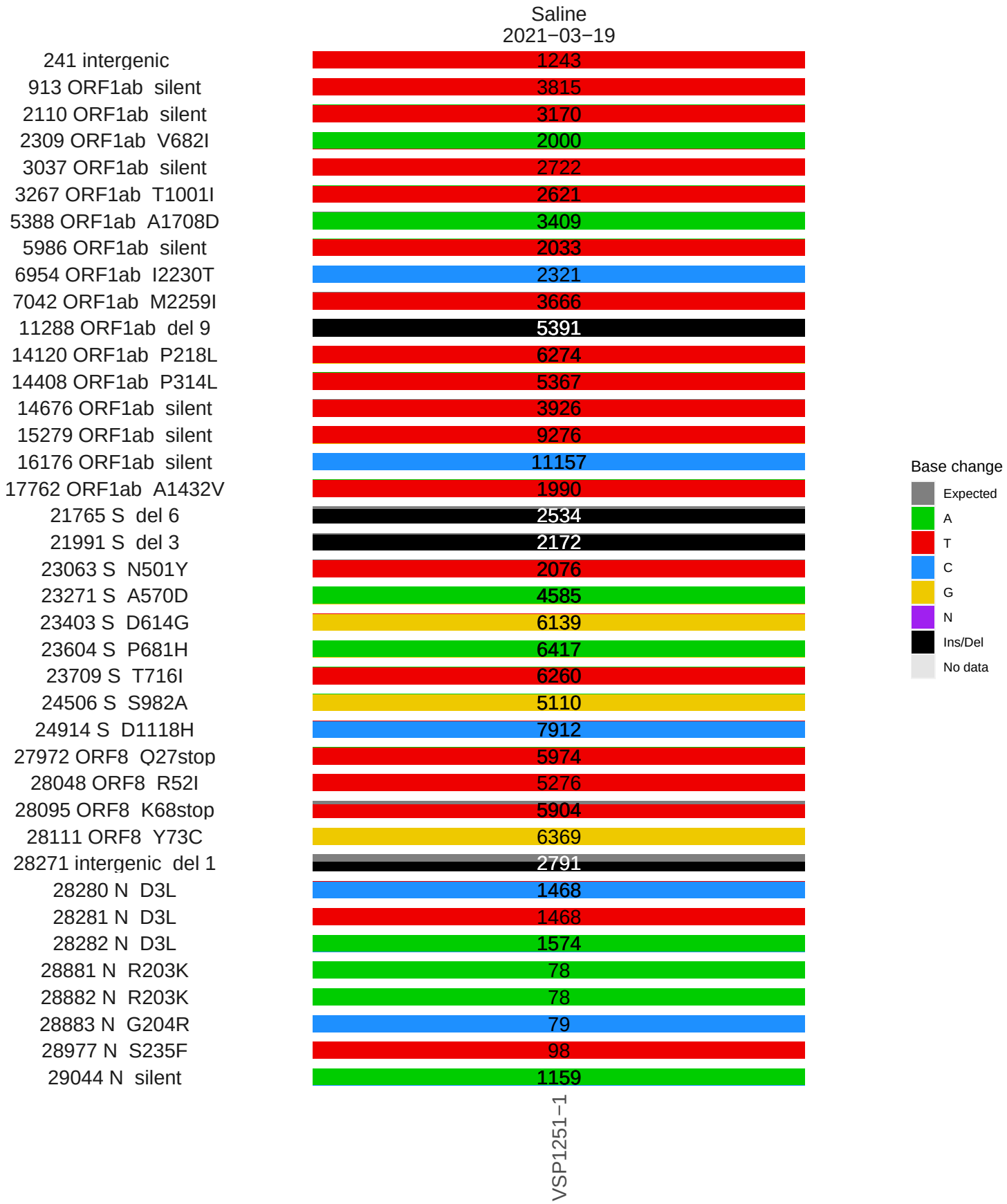
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1251-1	single experiment	NA	Saline	2021-03-19	29.88	B.1.1.7	99.9%	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.

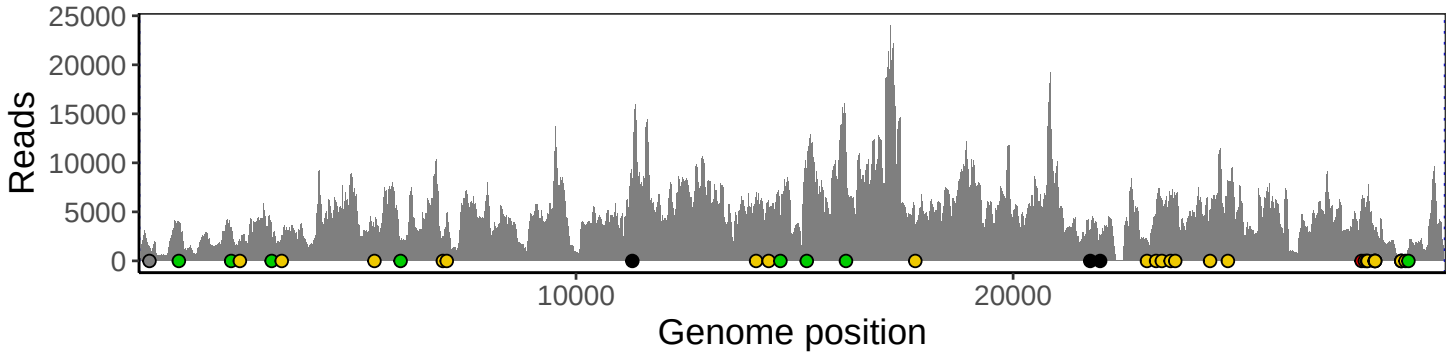



Saline
2021−03−19
241 intergenic 1243
913 ORF1ab silent 3815
2110 ORF1ab silent 3170
2309 ORF1ab V682I 2000
3037 ORF1ab silent 2722
3267 ORF1ab T1001I 2621
5388 ORF1ab A1708D 3409
5986 ORF1ab silent 2033
6954 ORF1ab I2230T 2321
7042 ORF1ab M2259I 3666
11288 ORF1ab del 9 5391
14120 ORF1ab P218L 6274
14408 ORF1ab P314L 5367
14676 ORF1ab silent 3926
15279 ORF1ab silent 9276
16176 ORF1ab silent 11157
17762 ORF1ab A1432V 1990
21765 S del 6 2534
21991 S del 3 2172
23063 S N501Y 2076
23271 S A570D 4585
23403 S D614G 6139
23604 S P681H 6417
23709 S T716I 6260
24506 S S982A 5110
24914 S D1118H 7912
27972 ORF8 Q27stop 5974
28048 ORF8 R52I 5276
28095 ORF8 K68stop 5904
28111 ORF8 Y73C 6369
28271 intergenic del 1 2791
28280 N D3L 1468
28281 N D3L 1468
28282 N D3L 1574
28881 N R203K 78
28882 N R203K 78
28883 N G204R 79
28977 N S235F 98
29044 N silent 1159
VSP1251−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

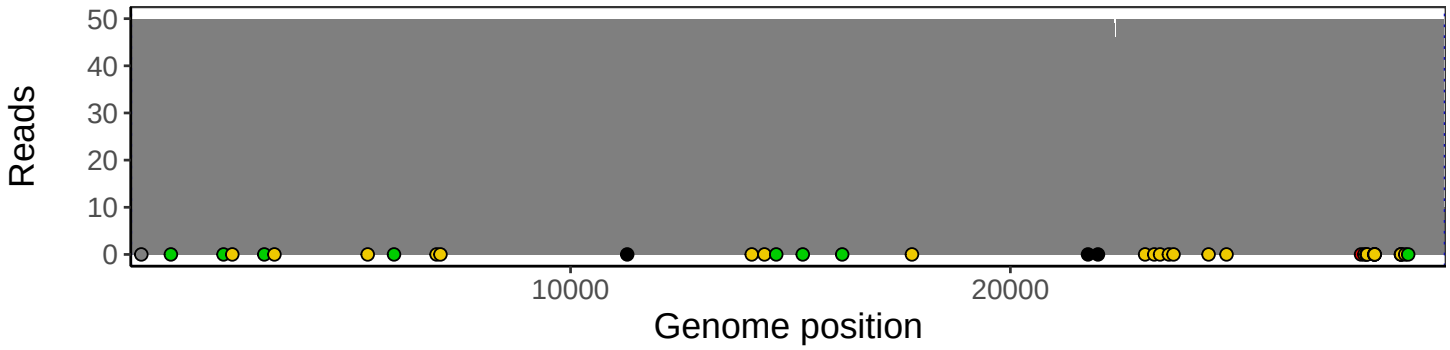
Analyses of individual experiments and composite results

VSP1251-1 | 2021-03-19 | Saline | HUP Q-0084 | genomes | single experiment

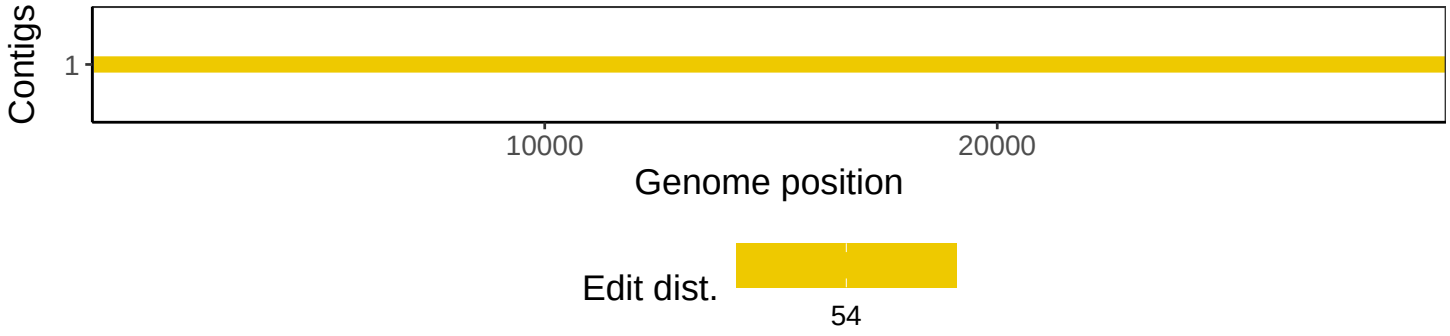
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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