COVID-19 subject HUP Q-0102

2021-05-05

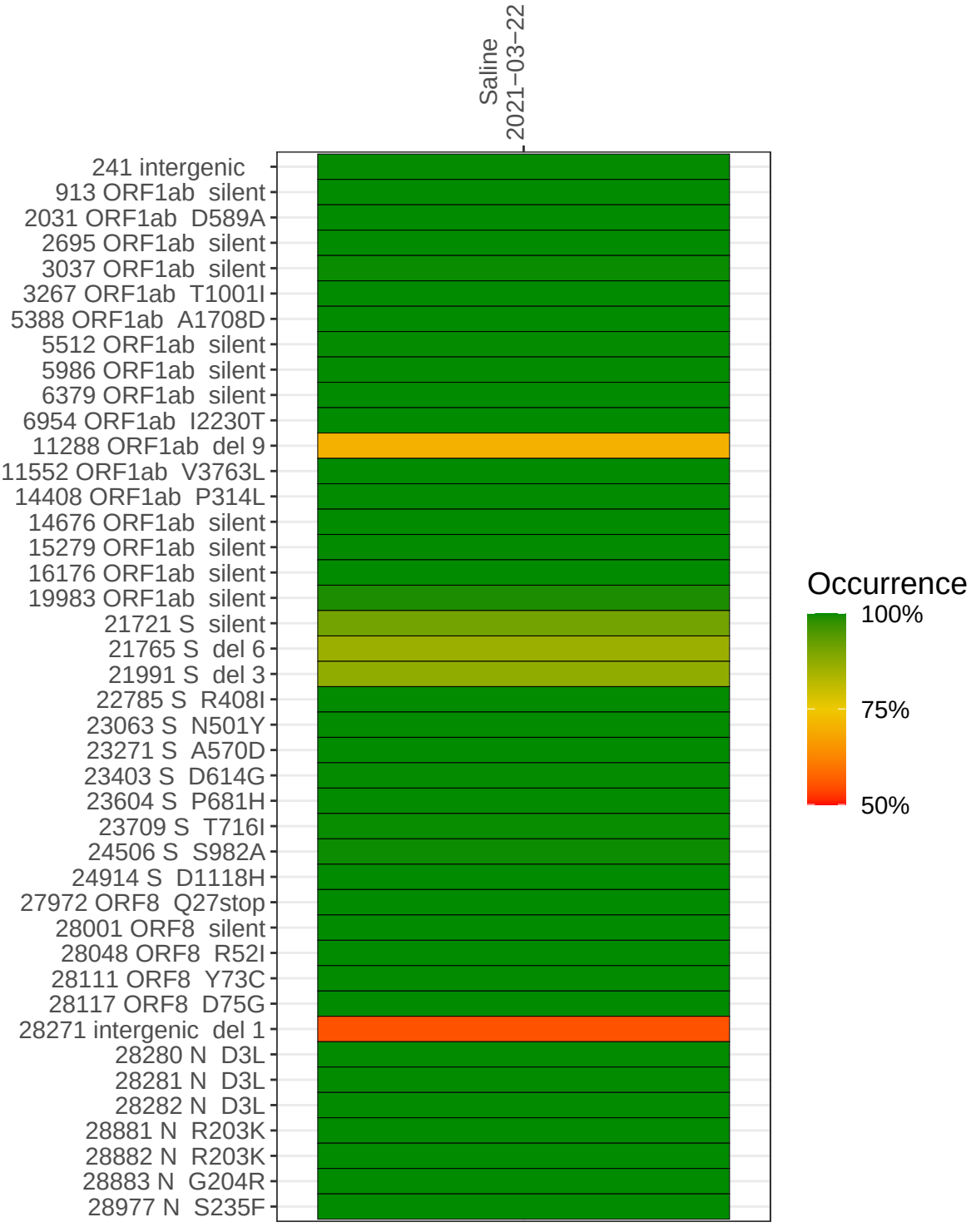
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

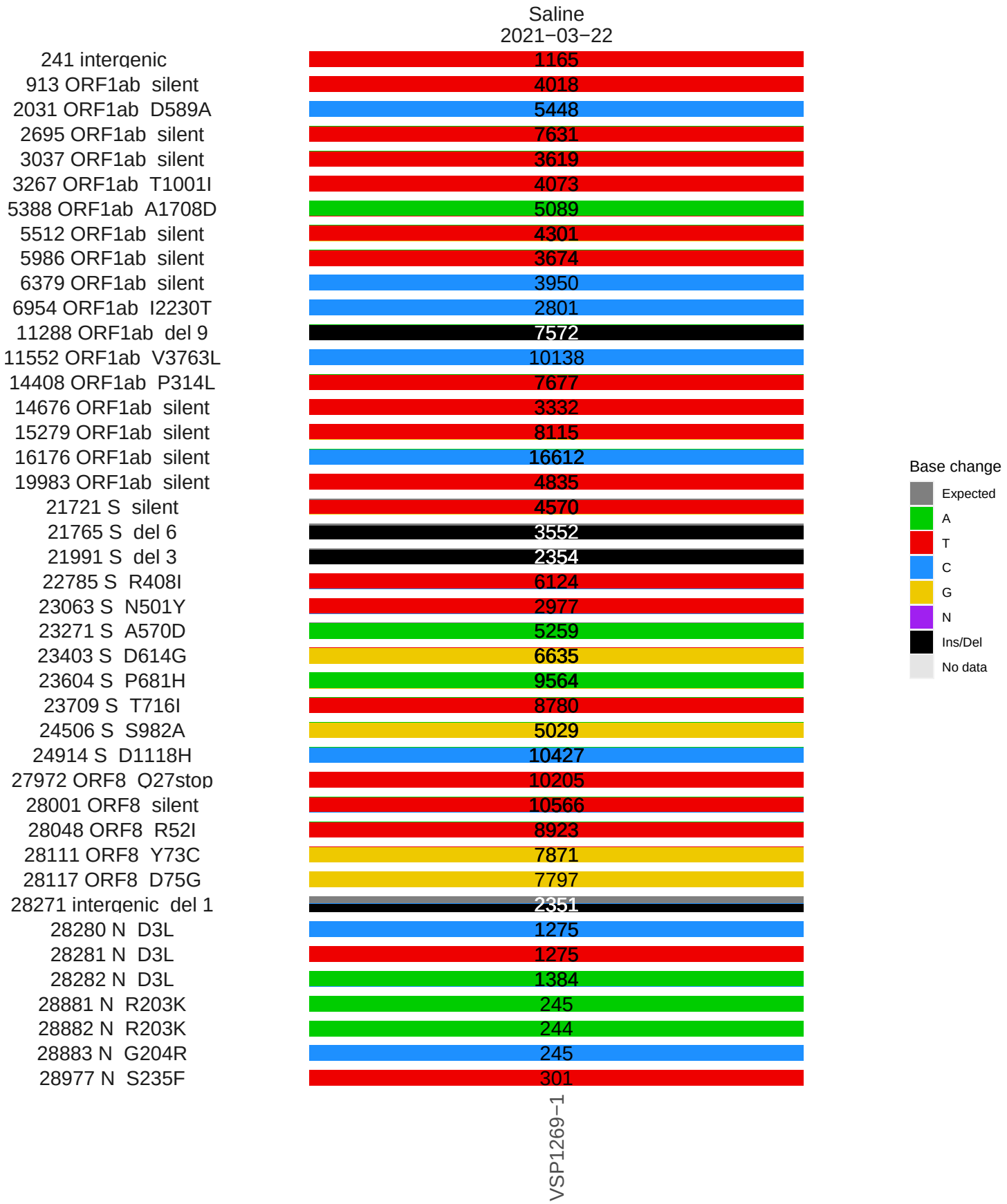
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1269-1	single experiment	NA	Saline	2021-03-22	29.86	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.

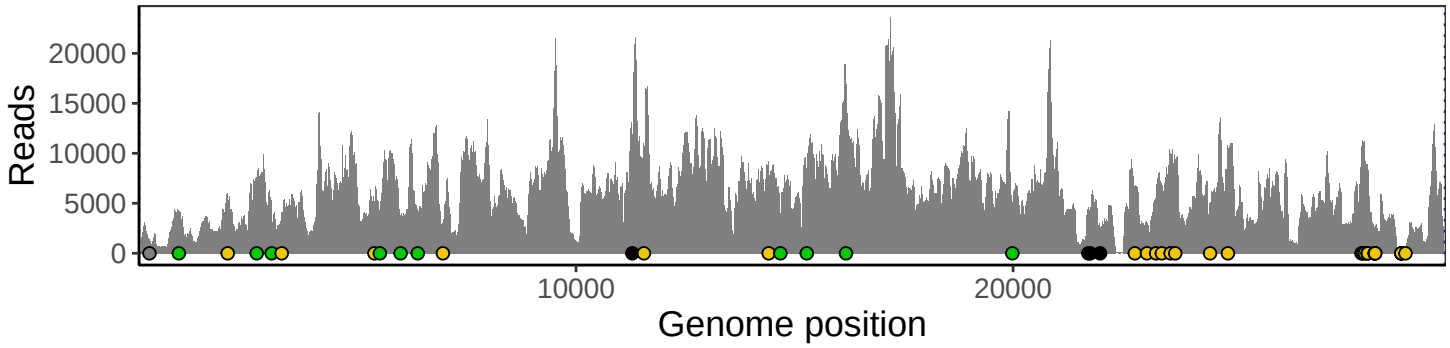



Saline
2021−03−22
241 intergenic 1165
913 ORF1ab silent 4018
2031 ORF1ab D589A 5448
2695 ORF1ab silent 7631
3037 ORF1ab silent 3619
3267 ORF1ab T1001I 4073
5388 ORF1ab A1708D 5089
5512 ORF1ab silent 4301
5986 ORF1ab silent 3674
6379 ORF1ab silent 3950
6954 ORF1ab I2230T 2801
11288 ORF1ab del 9 7572
11552 ORF1ab V3763L 10138
14408 ORF1ab P314L 7677
14676 ORF1ab silent 3332
15279 ORF1ab silent 8115
16176 ORF1ab silent 16612
19983 ORF1ab silent 4835
21721 S silent 4570
21765 S del 6 3552
21991 S del 3 2354
22785 S R408I 6124
23063 S N501Y 2977
23271 S A570D 5259
23403 S D614G 6635
23604 S P681H 9564
23709 S T716I 8780
24506 S S982A 5029
24914 S D1118H 10427
27972 ORF8 Q27stop 10205
28001 ORF8 silent 10566
28048 ORF8 R52I 8923
28111 ORF8 Y73C 7871
28117 ORF8 D75G 7797
28271 intergenic del 1 2351
28280 N D3L 1275
28281 N D3L 1275
28282 N D3L 1384
28881 N R203K 245
28882 N R203K 244
28883 N G204R 245
28977 N S235F 301
VSP1269−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

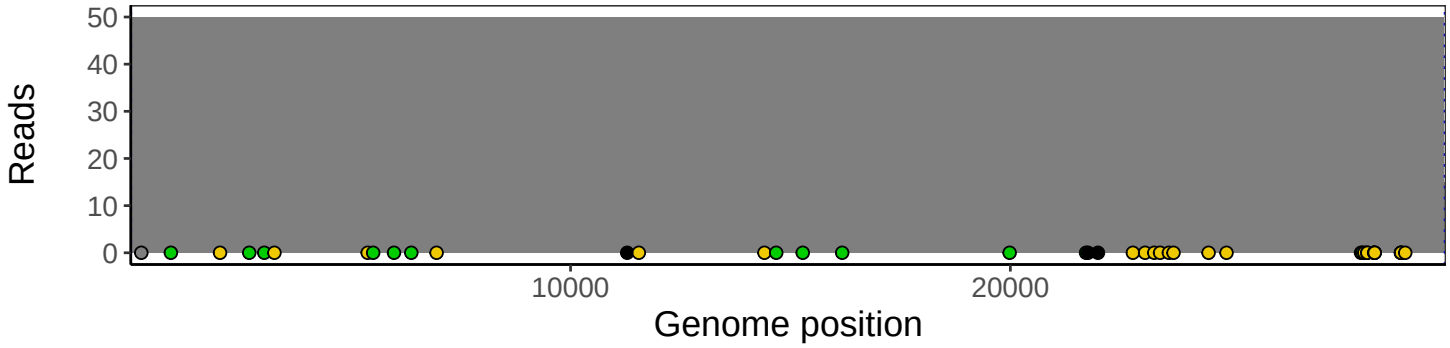
Analyses of individual experiments and composite results

VSP1269-1 | 2021-03-22 | Saline | HUP Q-0102 | genomes | single experiment

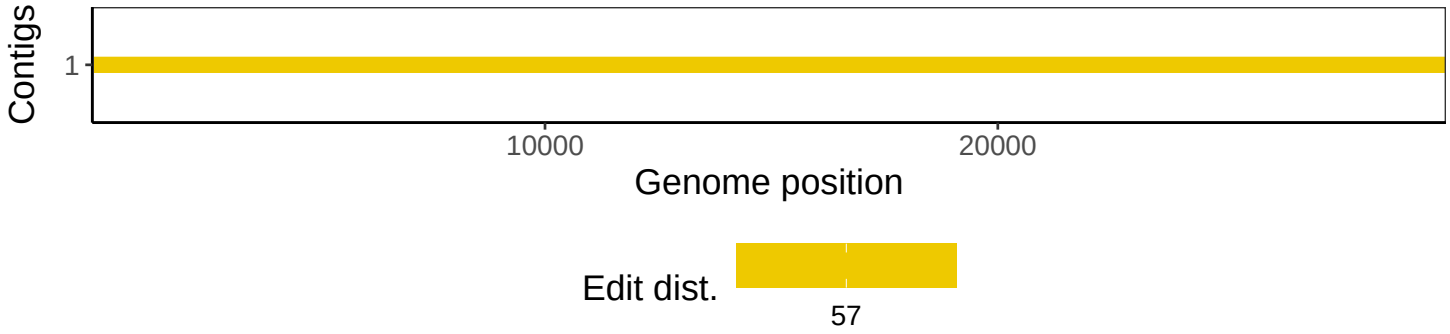
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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