COVID-19 subject HUP Q-0212

2021-05-05

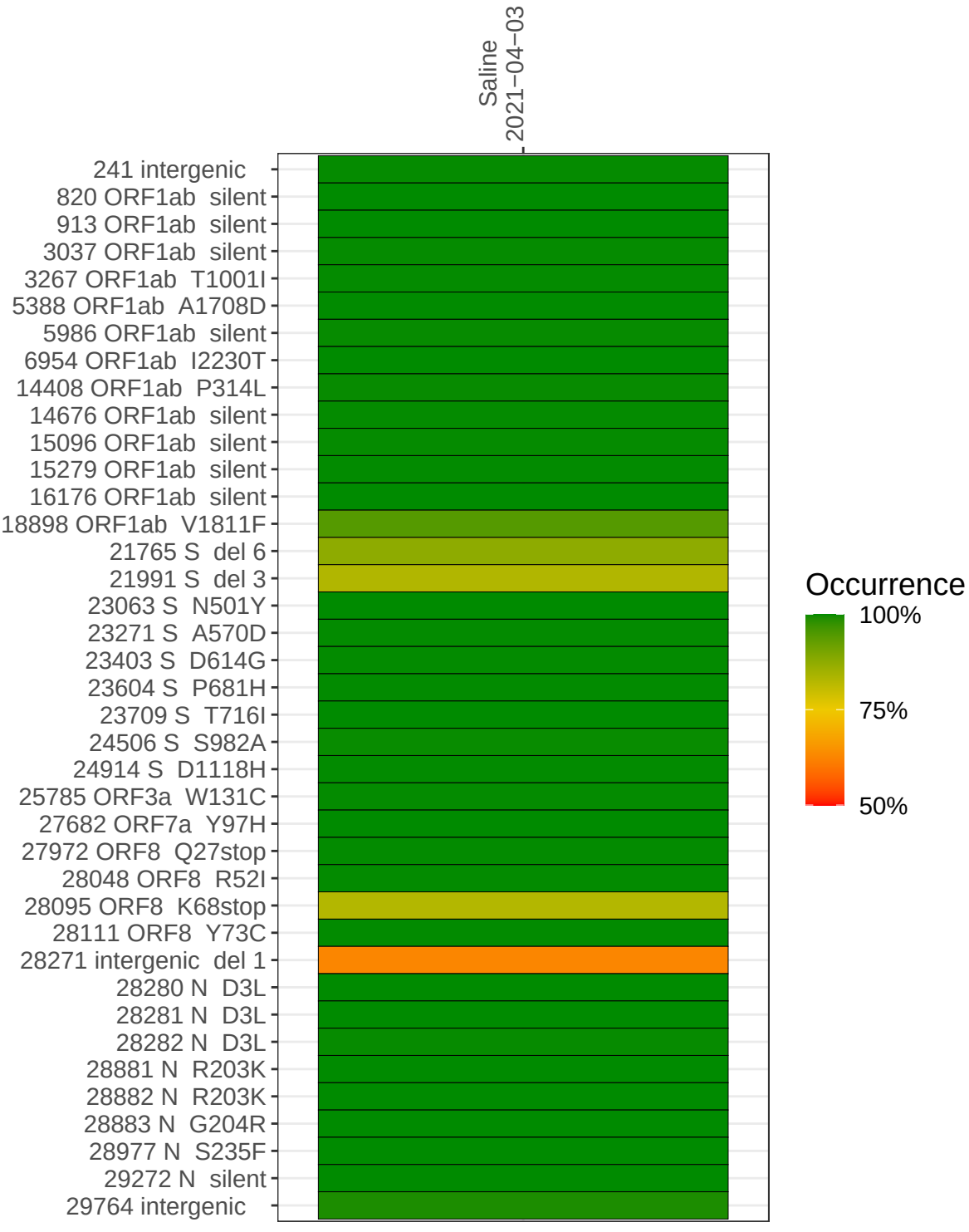
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

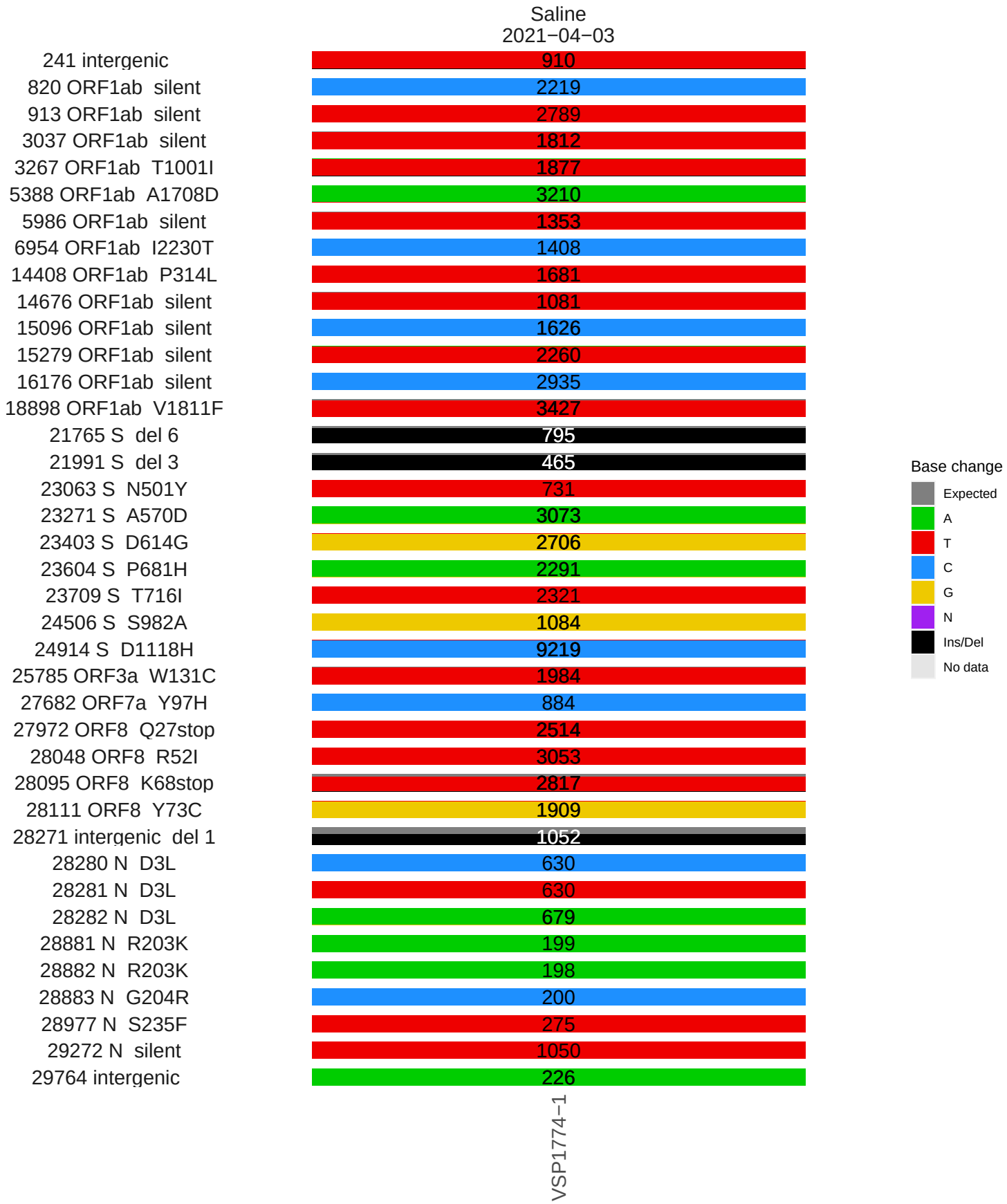
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1774-1	single experiment	NA	Saline	2021-04-03	29.82	B.1.1.7	99.9%	99.7%

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.

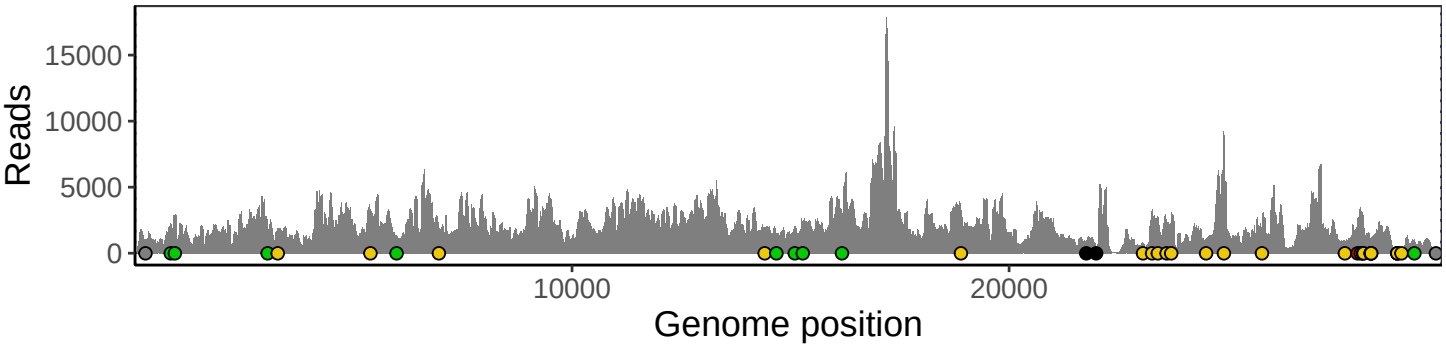



Saline
2021−04−03
241 intergenic 910
820 ORF1ab silent 2219
913 ORF1ab silent 2789
3037 ORF1ab silent 1812
3267 ORF1ab T1001I 1877
5388 ORF1ab A1708D 3210
5986 ORF1ab silent 1353
6954 ORF1ab I2230T 1408
14408 ORF1ab P314L 1681
14676 ORF1ab silent 1081
15096 ORF1ab silent 1626
15279 ORF1ab silent 2260
16176 ORF1ab silent 2935
18898 ORF1ab V1811F 3427
21765 S del 6 795
21991 S del 3 465
23063 S N501Y 731
23271 S A570D 3073
23403 S D614G 2706
23604 S P681H 2291
23709 S T716I 2321
24506 S S982A 1084
24914 S D1118H 9219
25785 ORF3a W131C 1984
27682 ORF7a Y97H 884
27972 ORF8 Q27stop 2514
28048 ORF8 R52I 3053
28095 ORF8 K68stop 2817
28111 ORF8 Y73C 1909
28271 intergenic del 1 1052
28280 N D3L 630
28281 N D3L 630
28282 N D3L 679
28881 N R203K 199
28882 N R203K 198
28883 N G204R 200
28977 N S235F 275
29272 N silent 1050
29764 intergenic 226
VSP1774−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

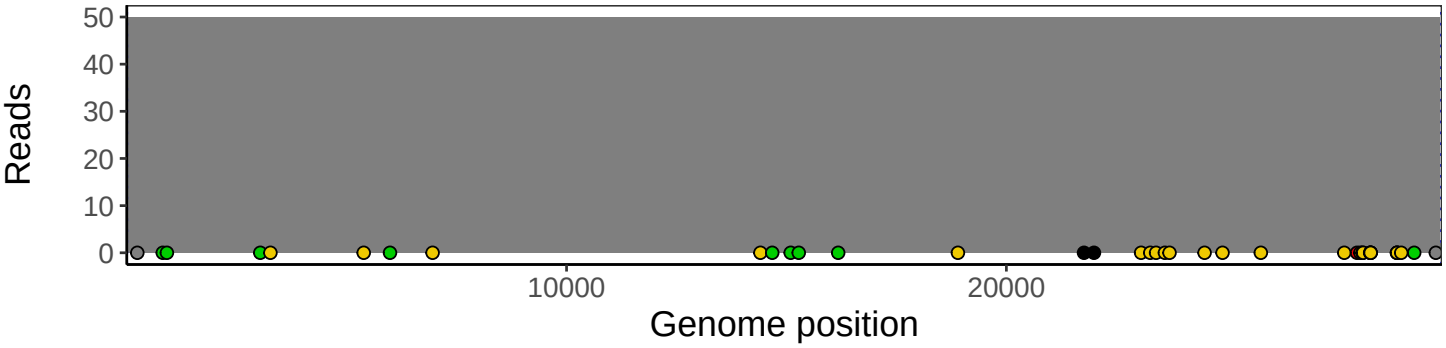
Analyses of individual experiments and composite results

VSP1774-1 | 2021-04-03 | Saline | HUP Q-0212 | genomes | single experiment

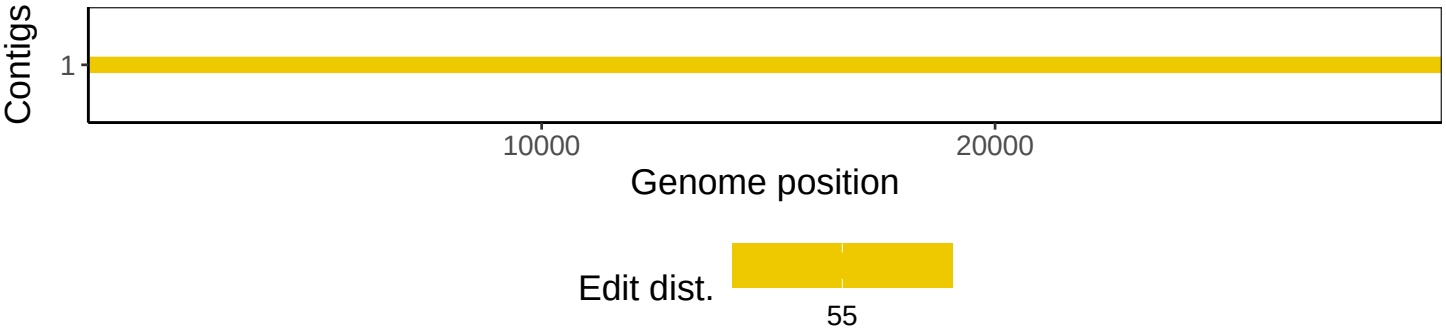
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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