COVID-19 subject HUP Q-0213

2021-06-23

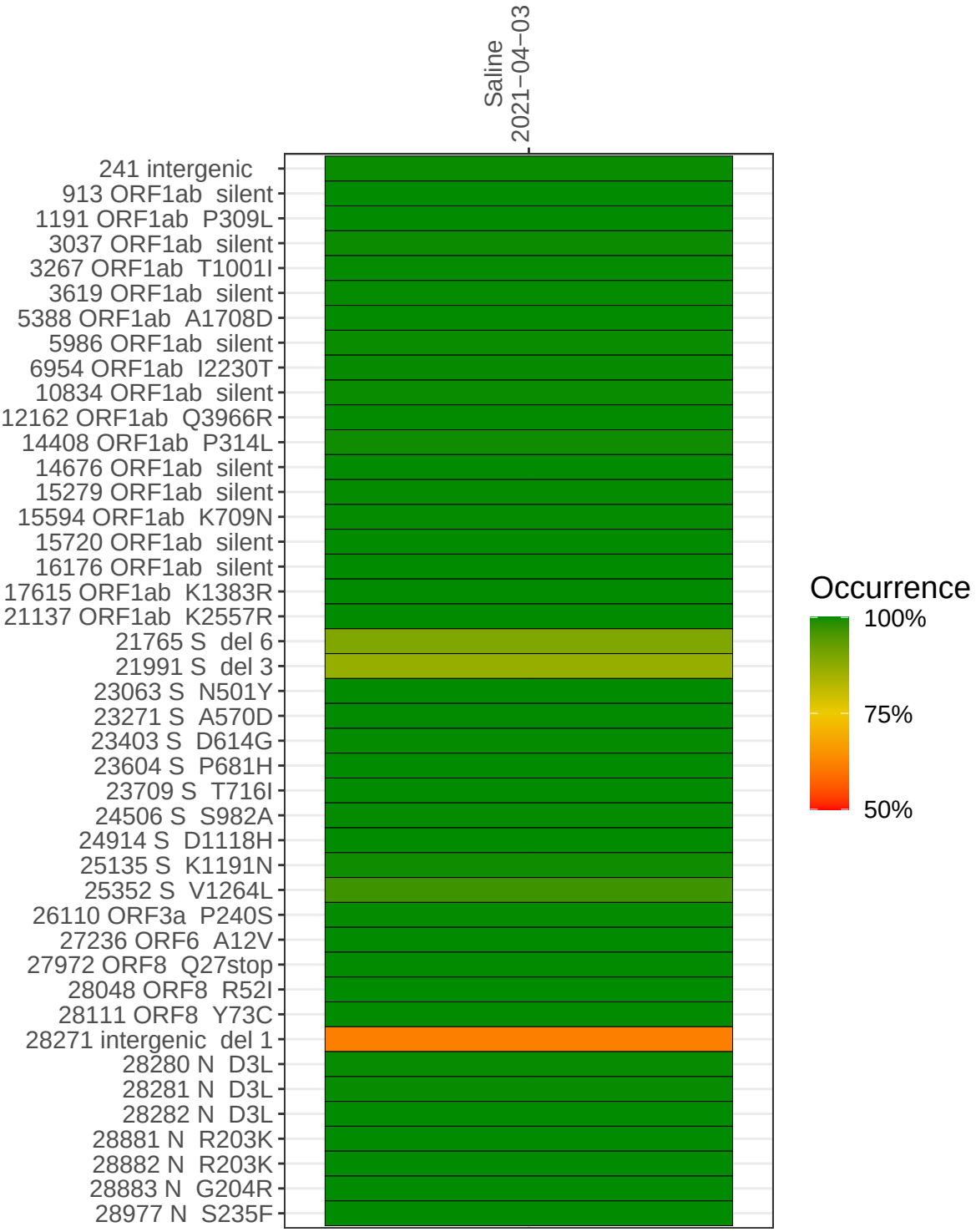
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

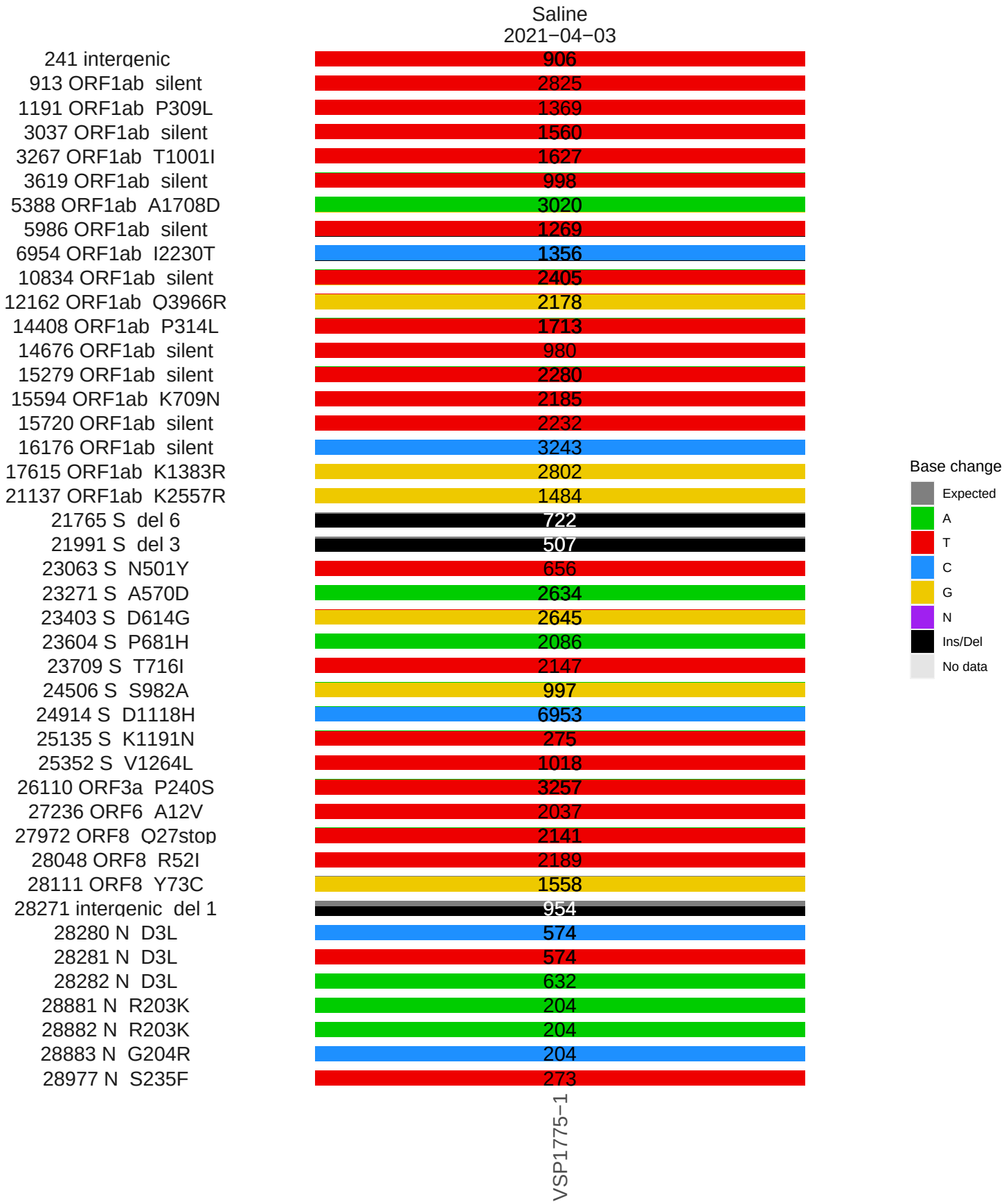
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1775-1	single experiment	NA	Saline	2021-04-03	29.92	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.

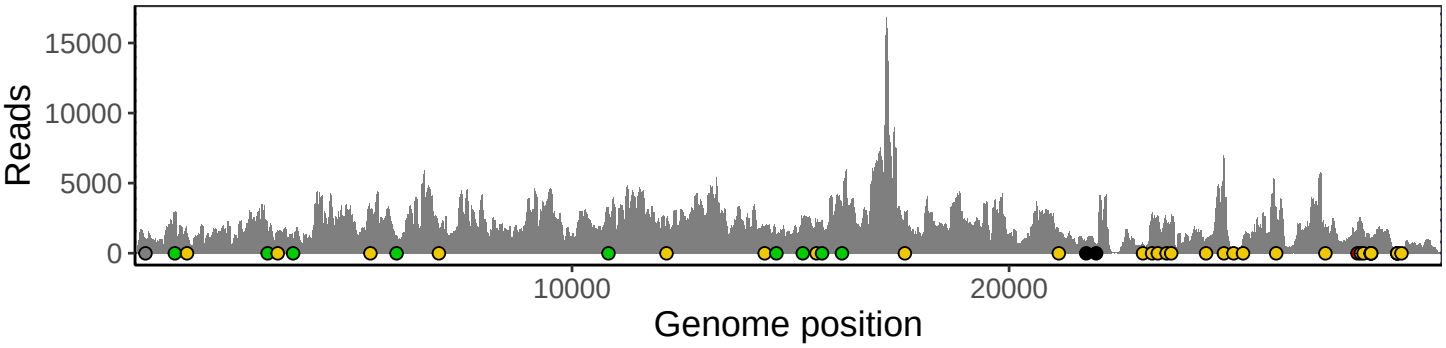



Saline
2021−04−03
241 intergenic 906
913 ORF1ab silent 2825
1191 ORF1ab P309L 1369
3037 ORF1ab silent 1560
3267 ORF1ab T1001I 1627
3619 ORF1ab silent 998
5388 ORF1ab A1708D 3020
5986 ORF1ab silent 1269
6954 ORF1ab I2230T 1356
10834 ORF1ab silent 2405
12162 ORF1ab Q3966R 2178
14408 ORF1ab P314L 1713
14676 ORF1ab silent 980
15279 ORF1ab silent 2280
15594 ORF1ab K709N 2185
15720 ORF1ab silent 2232
16176 ORF1ab silent 3243
17615 ORF1ab K1383R 2802
21137 ORF1ab K2557R 1484
21765 S del 6 722
21991 S del 3 507
23063 S N501Y 656
23271 S A570D 2634
23403 S D614G 2645
23604 S P681H 2086
23709 S T716I 2147
24506 S S982A 997
24914 S D1118H 6953
25135 S K1191N 275
25352 S V1264L 1018
26110 ORF3a P240S 3257
27236 ORF6 A12V 2037
27972 ORF8 Q27stop 2141
28048 ORF8 R52I 2189
28111 ORF8 Y73C 1558
28271 intergenic del 1 954
28280 N D3L 574
28281 N D3L 574
28282 N D3L 632
28881 N R203K 204
28882 N R203K 204
28883 N G204R 204
28977 N S235F 273
VSP1775−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

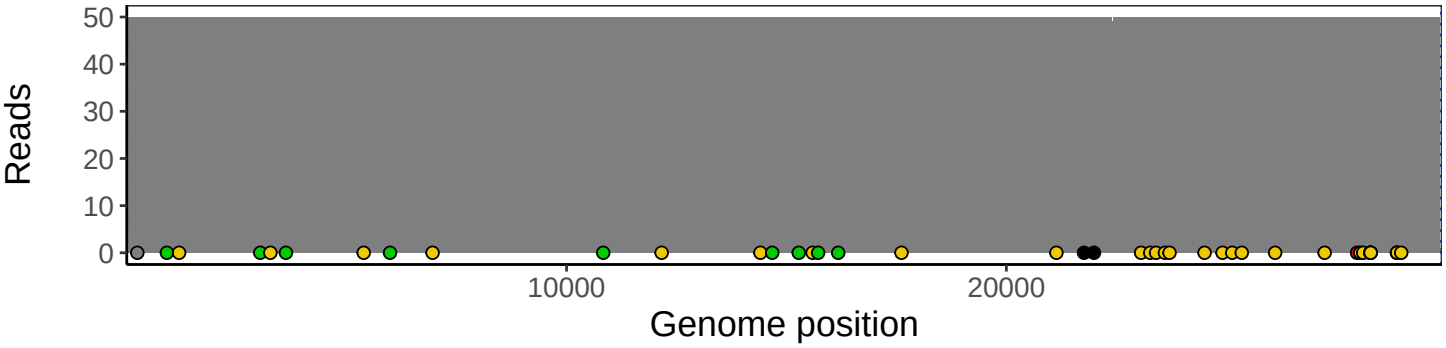
Analyses of individual experiments and composite results

VSP1775-1 | 2021-04-03 | Saline | HUP Q-0213 | genomes | single experiment

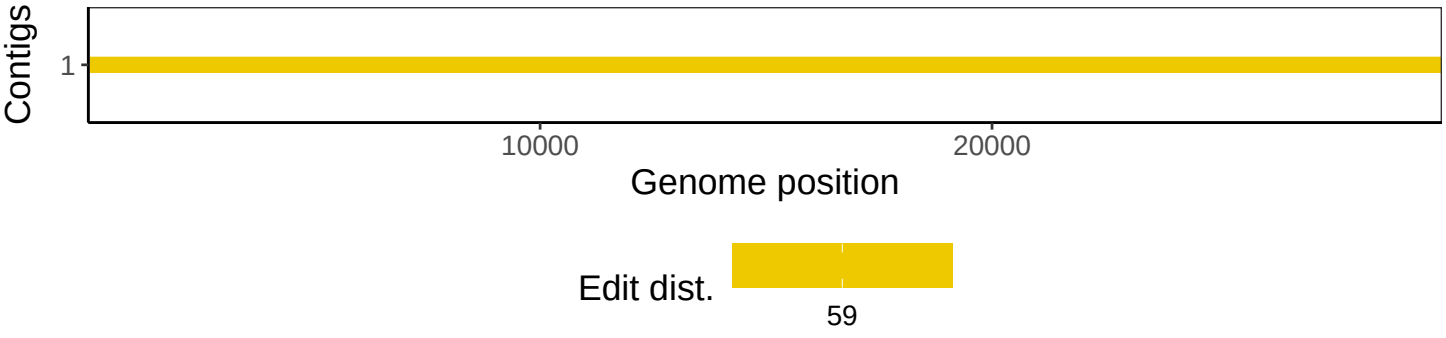
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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