COVID-19 subject HUP Q-0078

2021-06-23

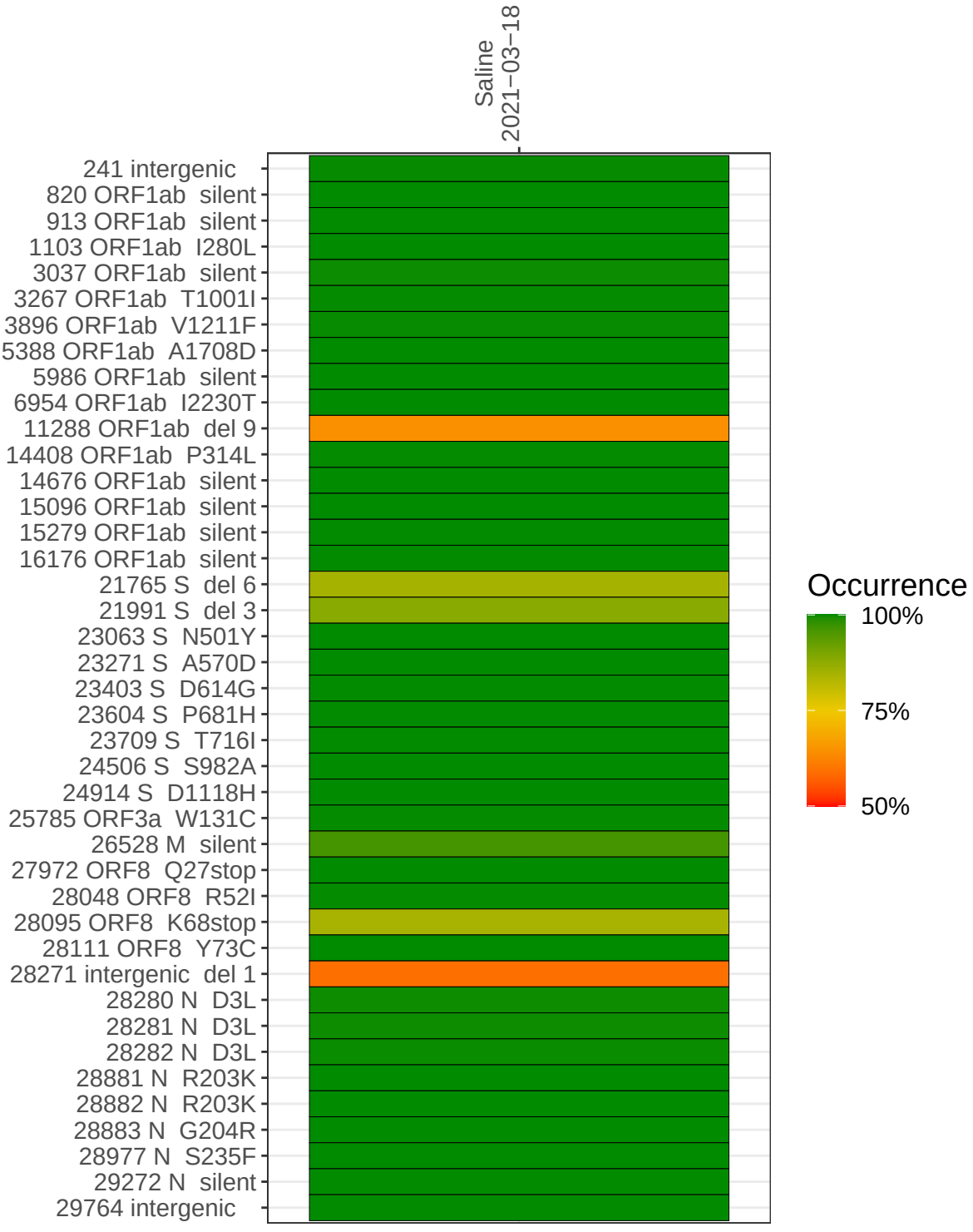
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

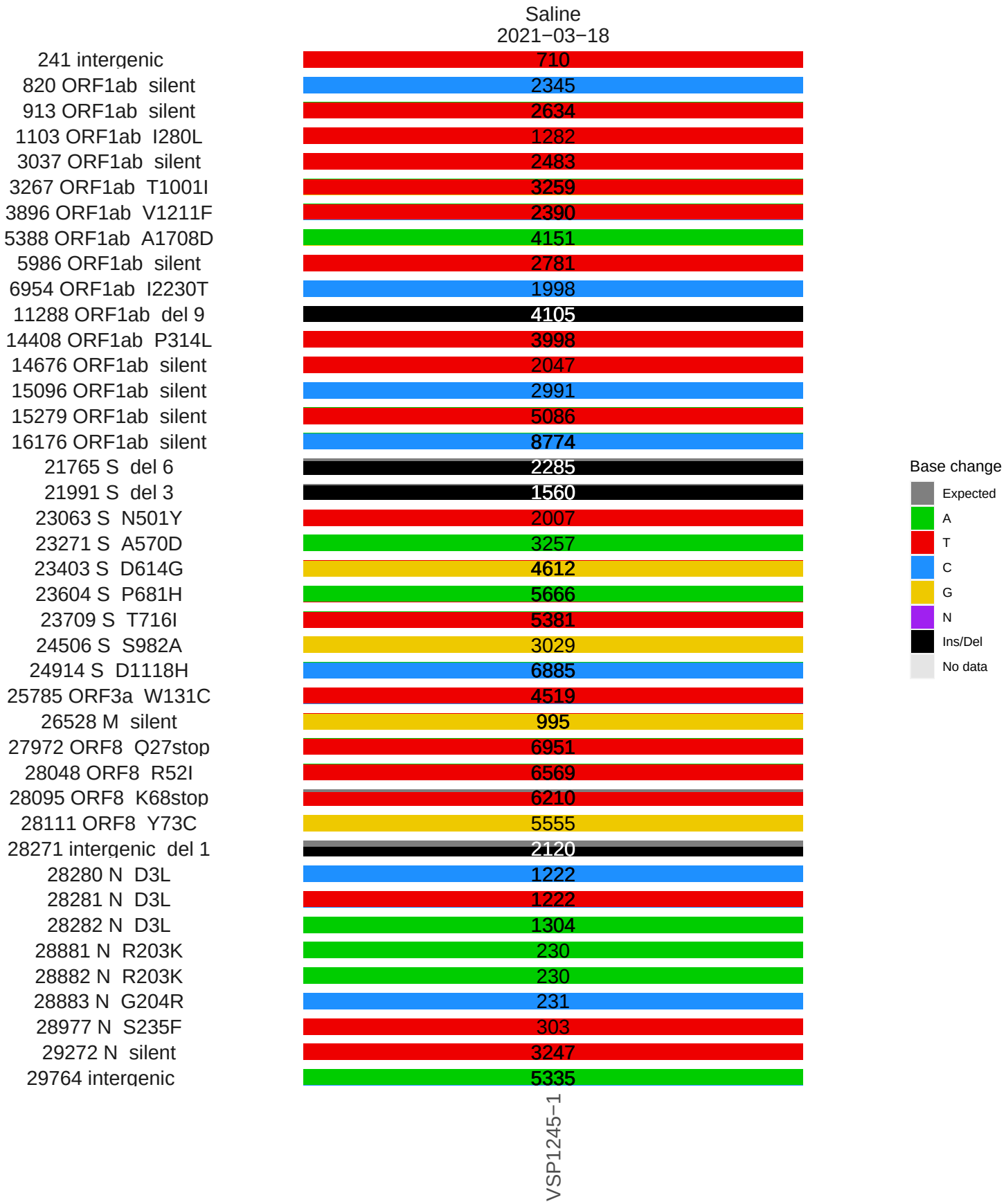
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1245-1	single experiment	NA	Saline	2021-03-18	29.85	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.

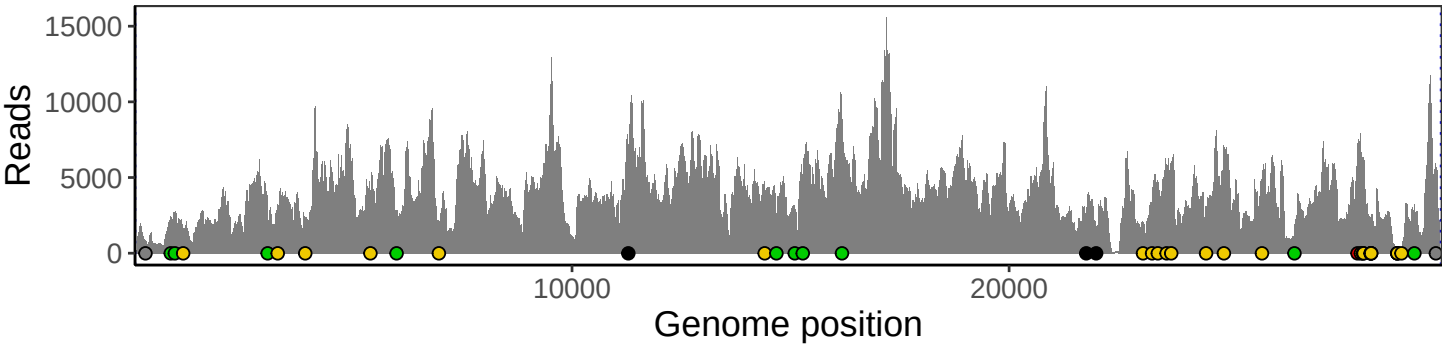



Saline
2021−03−18
241 intergenic 710
820 ORF1ab silent 2345
913 ORF1ab silent 2634
1103 ORF1ab I280L 1282
3037 ORF1ab silent 2483
3267 ORF1ab T1001I 3259
3896 ORF1ab V1211F 2390
5388 ORF1ab A1708D 4151
5986 ORF1ab silent 2781
6954 ORF1ab I2230T 1998
11288 ORF1ab del 9 4105
14408 ORF1ab P314L 3998
14676 ORF1ab silent 2047
15096 ORF1ab silent 2991
15279 ORF1ab silent 5086
16176 ORF1ab silent 8774
21765 S del 6 2285
21991 S del 3 1560
23063 S N501Y 2007
23271 S A570D 3257
23403 S D614G 4612
23604 S P681H 5666
23709 S T716I 5381
24506 S S982A 3029
24914 S D1118H 6885
25785 ORF3a W131C 4519
26528 M silent 995
27972 ORF8 Q27stop 6951
28048 ORF8 R52I 6569
28095 ORF8 K68stop 6210
28111 ORF8 Y73C 5555
28271 intergenic del 1 2120
28280 N D3L 1222
28281 N D3L 1222
28282 N D3L 1304
28881 N R203K 230
28882 N R203K 230
28883 N G204R 231
28977 N S235F 303
29272 N silent 3247
29764 intergenic 5335
VSP1245−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

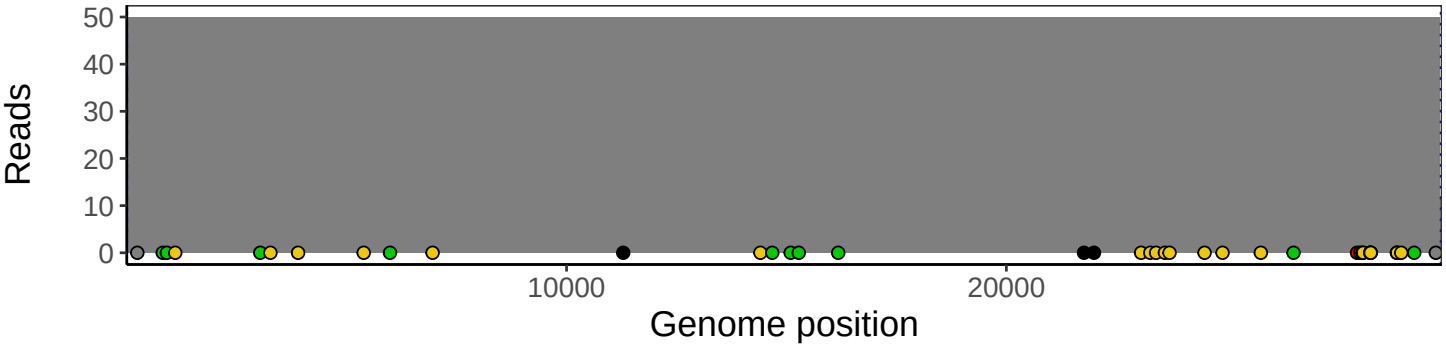
Analyses of individual experiments and composite results

VSP1245-1 | 2021-03-18 | Saline | HUP Q-0078 | genomes | single experiment

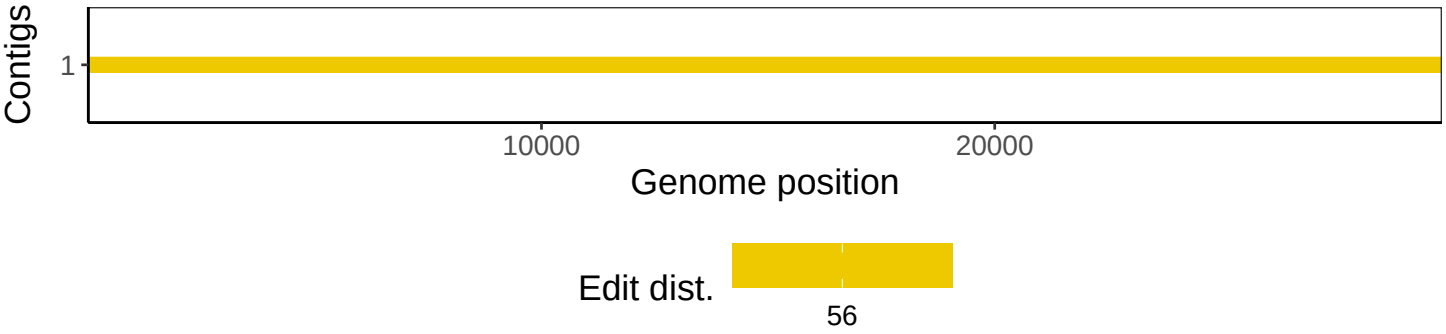
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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