COVID-19 subject HUP Q-0177

2021-06-23

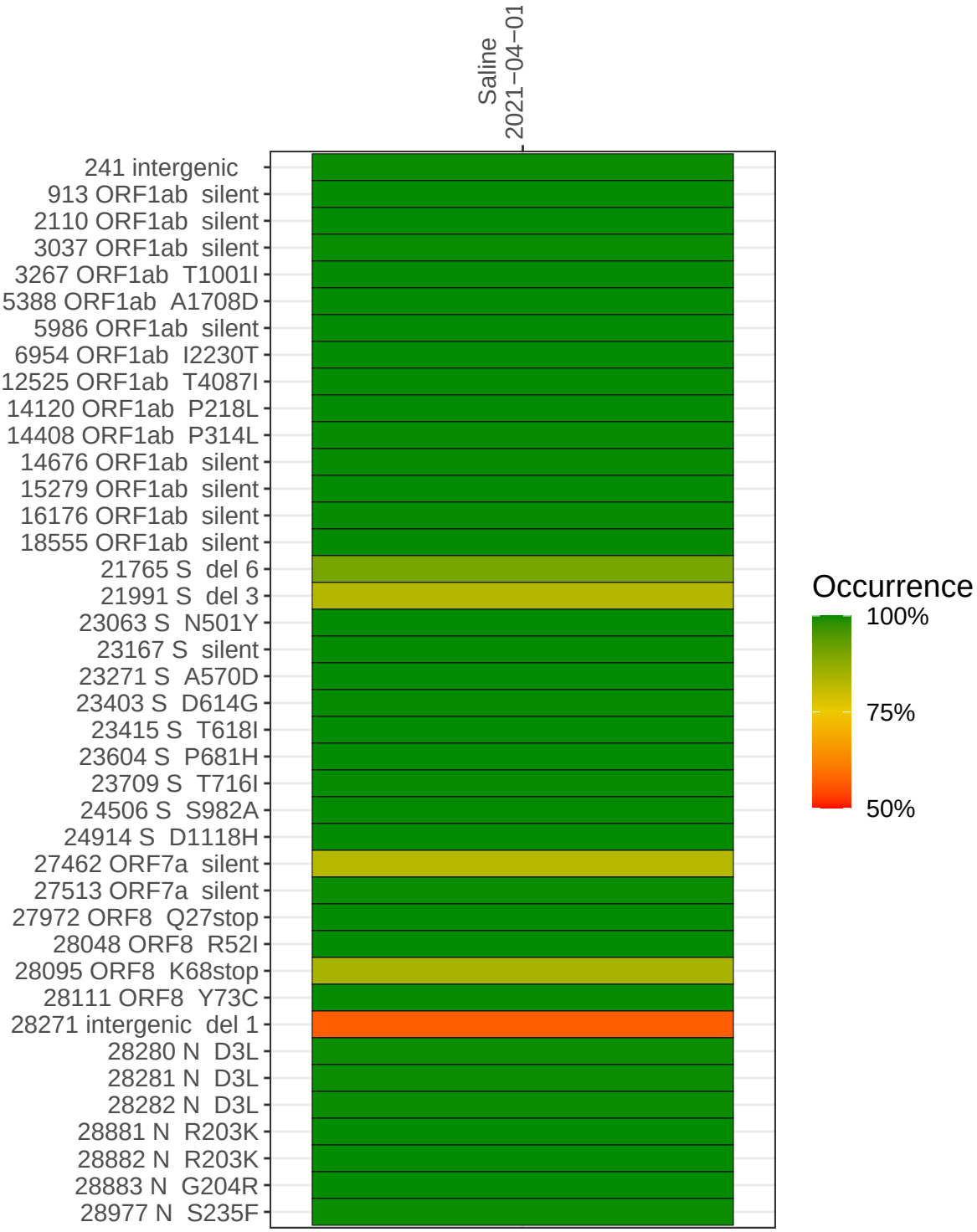
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

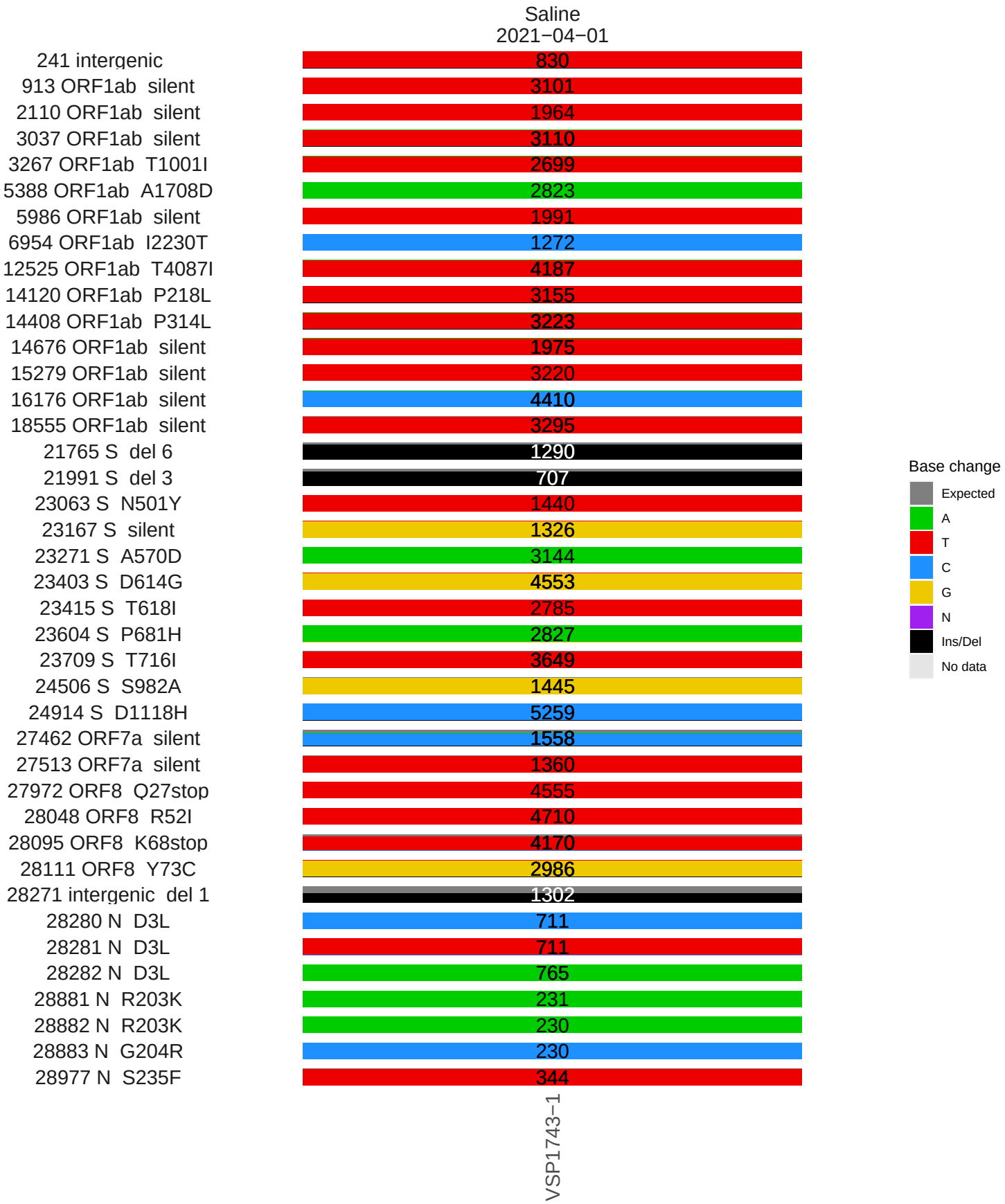
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1743-1	single experiment	NA	Saline	2021-04-01	29.82	B.1.1.7	99.9%	99.8%

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.

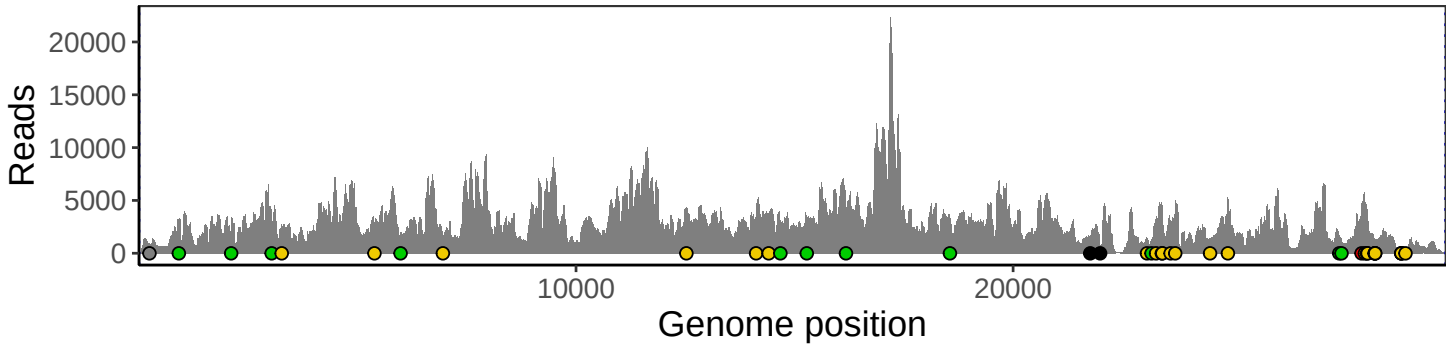



Saline
2021−04−01
241 intergenic 830
913 ORF1ab silent 3101
2110 ORF1ab silent 1964
3037 ORF1ab silent 3110
3267 ORF1ab T1001I 2699
5388 ORF1ab A1708D 2823
5986 ORF1ab silent 1991
6954 ORF1ab I2230T 1272
12525 ORF1ab T4087I 4187
14120 ORF1ab P218L 3155
14408 ORF1ab P314L 3223
14676 ORF1ab silent 1975
15279 ORF1ab silent 3220
16176 ORF1ab silent 4410
18555 ORF1ab silent 3295
21765 S del 6 1290
21991 S del 3 707
23063 S N501Y 1440
23167 S silent 1326
23271 S A570D 3144
23403 S D614G 4553
23415 S T618I 2785
23604 S P681H 2827
23709 S T716I 3649
24506 S S982A 1445
24914 S D1118H 5259
27462 ORF7a silent 1558
27513 ORF7a silent 1360
27972 ORF8 Q27stop 4555
28048 ORF8 R52I 4710
28095 ORF8 K68stop 4170
28111 ORF8 Y73C 2986
28271 intergenic del 1 1302
28280 N D3L 711
28281 N D3L 711
28282 N D3L 765
28881 N R203K 231
28882 N R203K 230
28883 N G204R 230
28977 N S235F 344
VSP1743−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

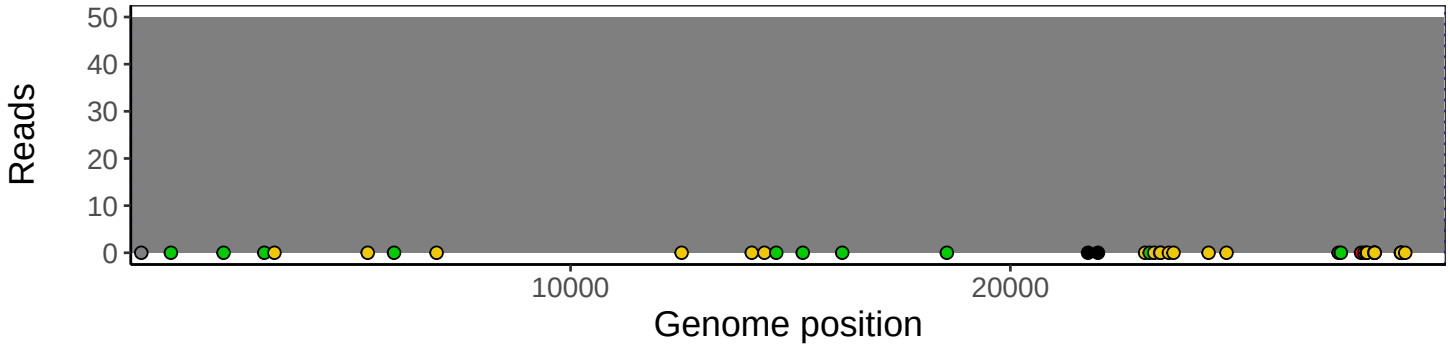
Analyses of individual experiments and composite results

VSP1743-1 | 2021-04-01 | Saline | HUP Q-0177 | genomes | single experiment

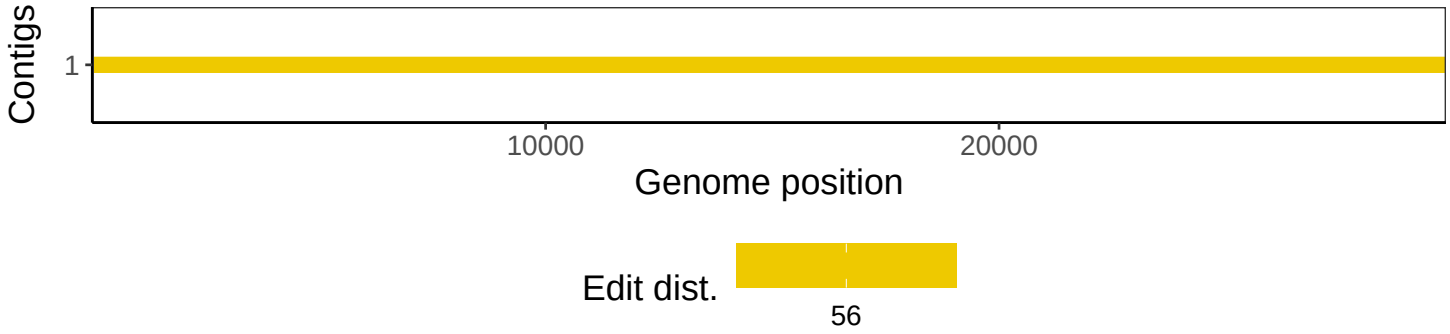
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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