COVID-19 subject HUP Q-0163

2021-06-23

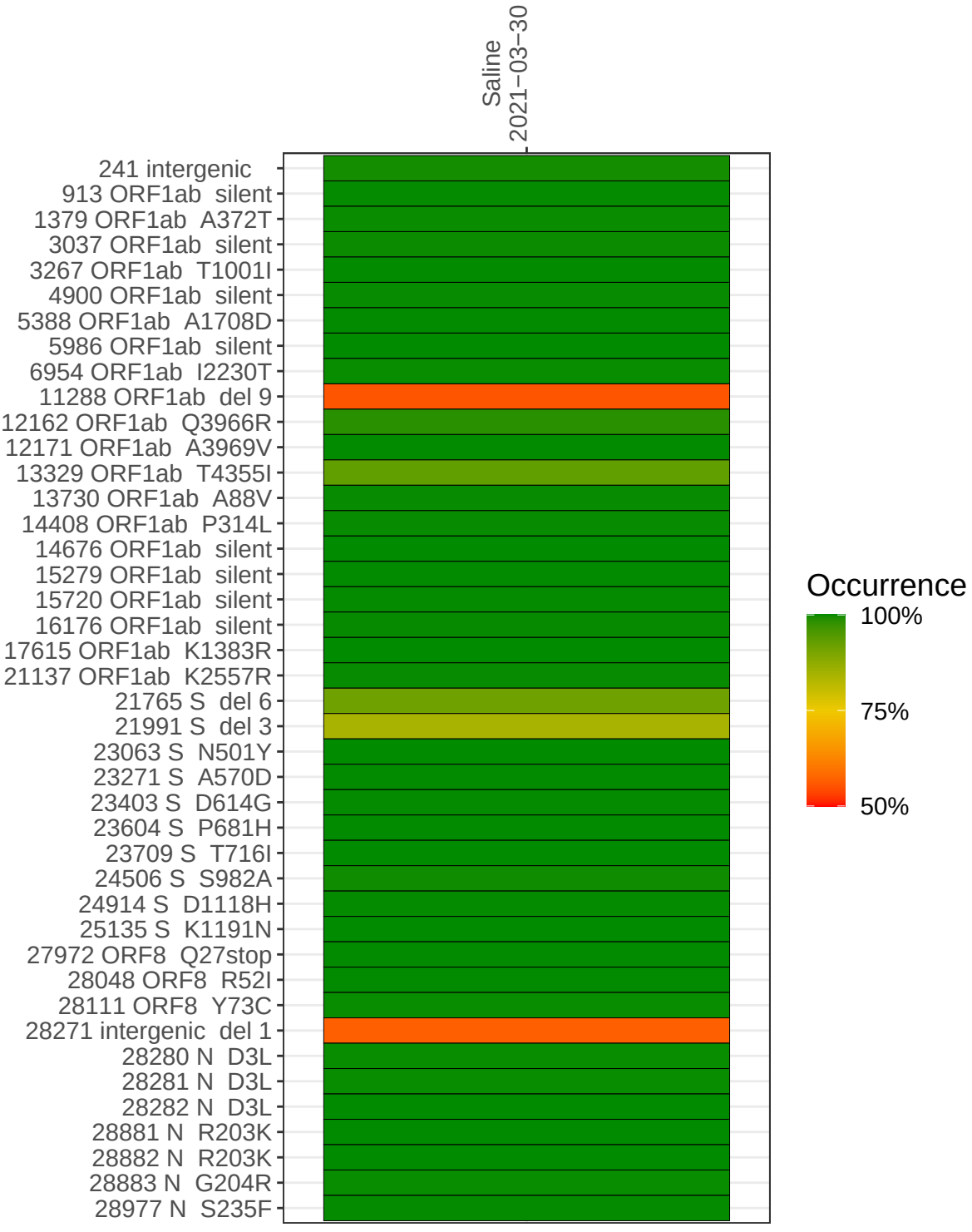
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

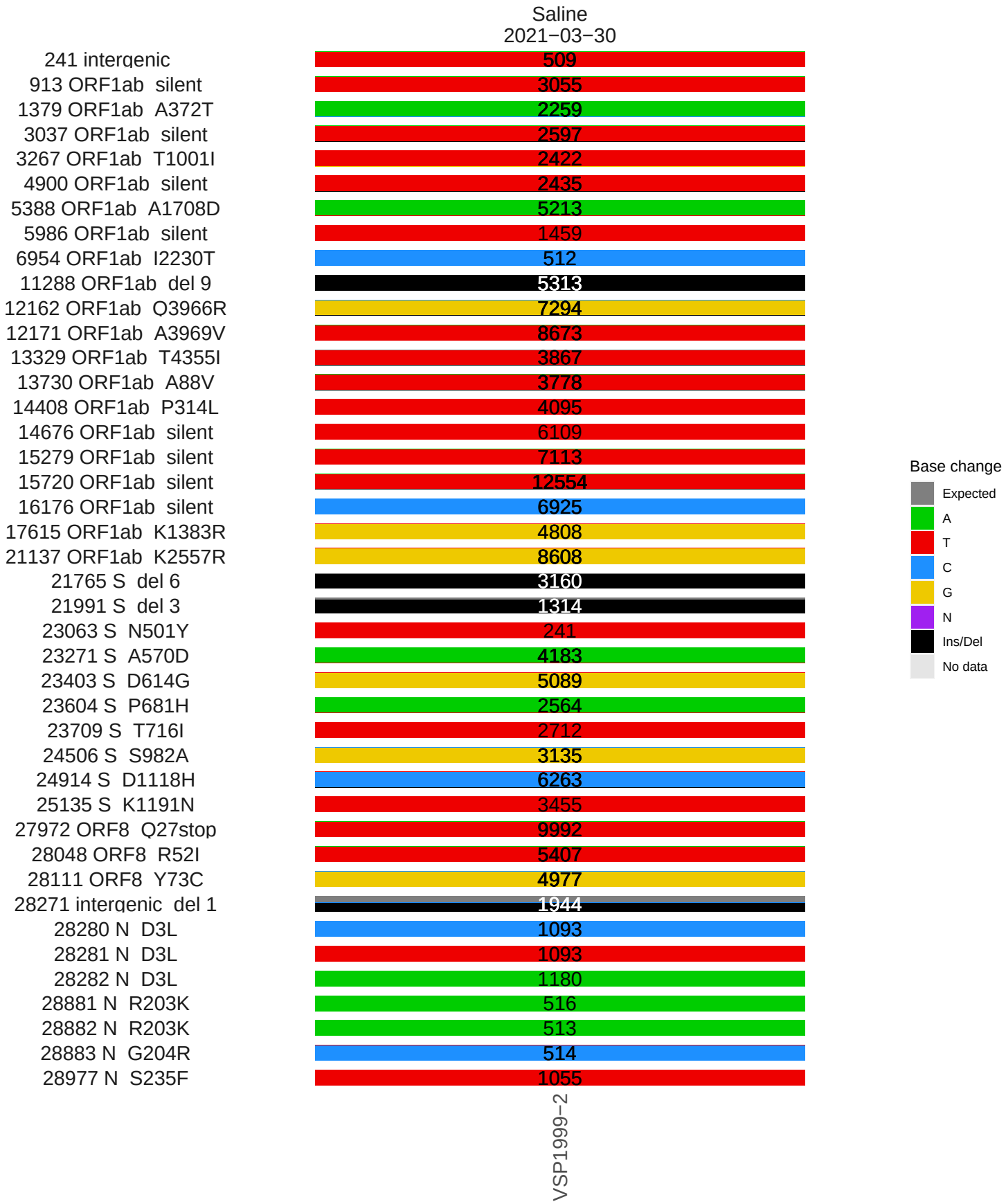
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1999-2	single experiment	NA	Saline	2021-03-30	29.82	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.

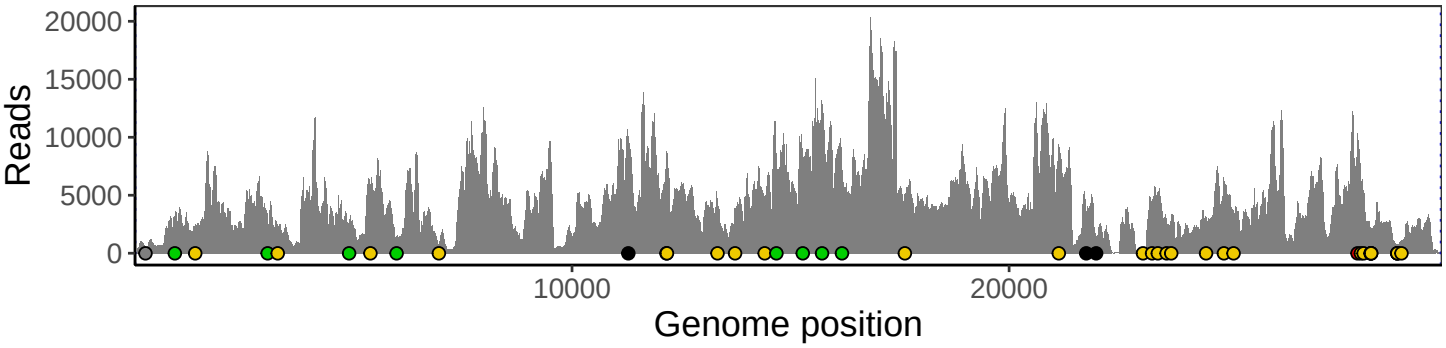



Saline
2021−03−30
241 intergenic 509
913 ORF1ab silent 3055
1379 ORF1ab A372T 2259
3037 ORF1ab silent 2597
3267 ORF1ab T1001I 2422
4900 ORF1ab silent 2435
5388 ORF1ab A1708D 5213
5986 ORF1ab silent 1459
6954 ORF1ab I2230T 512
11288 ORF1ab del 9 5313
12162 ORF1ab Q3966R 7294
12171 ORF1ab A3969V 8673
13329 ORF1ab T4355I 3867
13730 ORF1ab A88V 3778
14408 ORF1ab P314L 4095
14676 ORF1ab silent 6109
15279 ORF1ab silent 7113
15720 ORF1ab silent 12554
16176 ORF1ab silent 6925
17615 ORF1ab K1383R 4808
21137 ORF1ab K2557R 8608
21765 S del 6 3160
21991 S del 3 1314
23063 S N501Y 241
23271 S A570D 4183
23403 S D614G 5089
23604 S P681H 2564
23709 S T716I 2712
24506 S S982A 3135
24914 S D1118H 6263
25135 S K1191N 3455
27972 ORF8 Q27stop 9992
28048 ORF8 R52I 5407
28111 ORF8 Y73C 4977
28271 intergenic del 1 1944
28280 N D3L 1093
28281 N D3L 1093
28282 N D3L 1180
28881 N R203K 516
28882 N R203K 513
28883 N G204R 514
28977 N S235F 1055
VSP1999−2
Base change
Expected
A
T
C
G
N
Ins/Del
No data

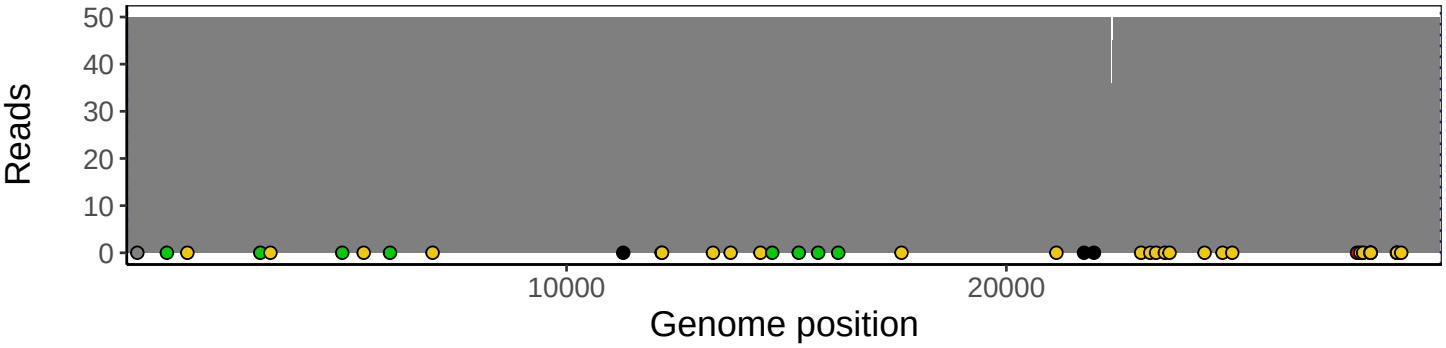
Analyses of individual experiments and composite results

VSP1999-2 | 2021-03-30 | Saline | HUP Q-0163 | genomes | single experiment

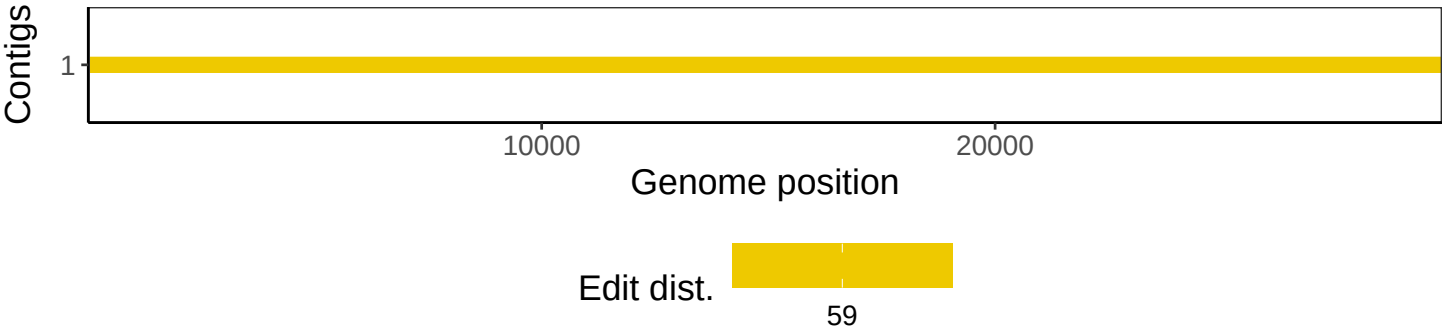
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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