COVID-19 subject HUP Q-0159

2021-05-05

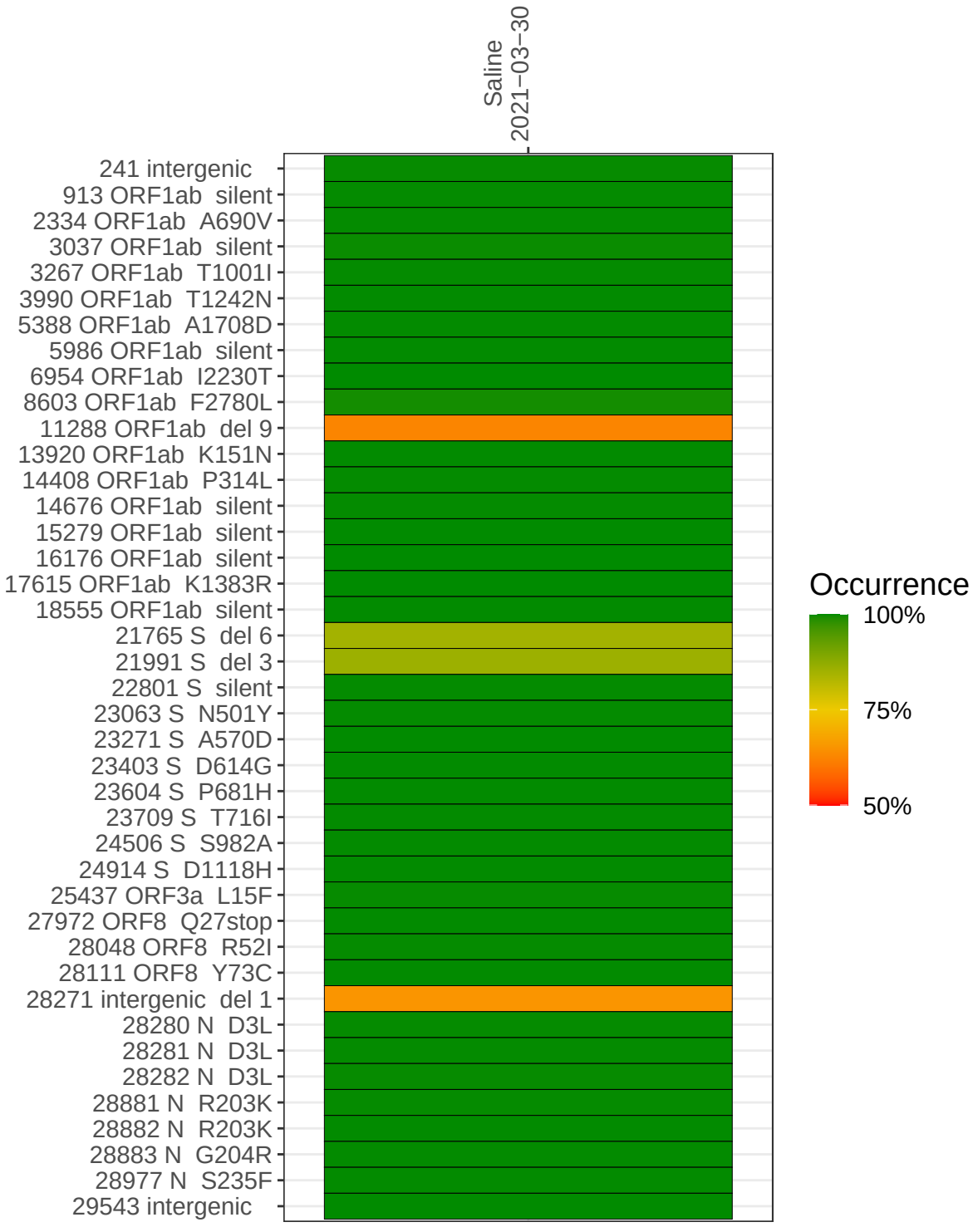
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

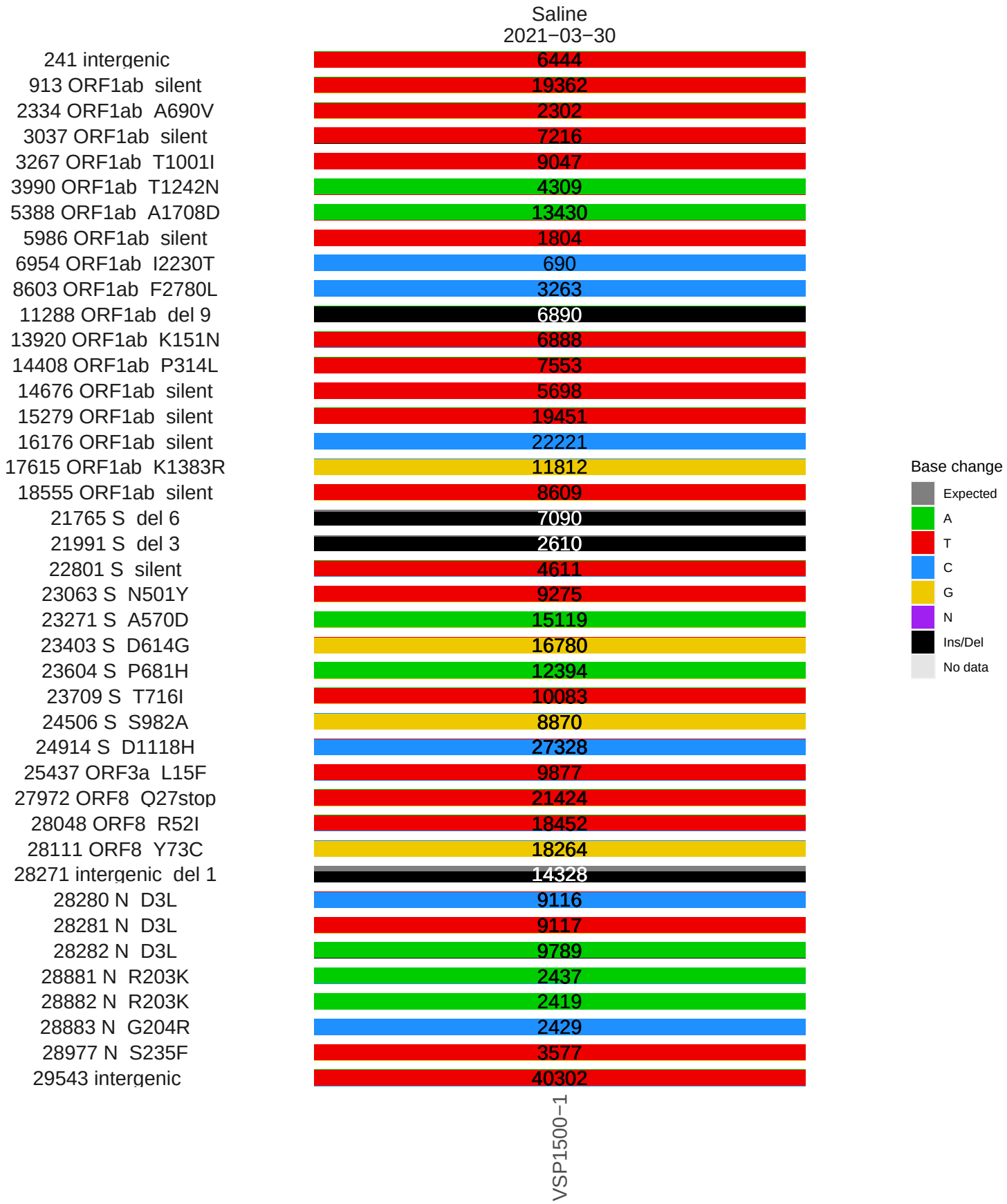
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1500-1	single experiment	NA	Saline	2021-03-30	29.86	B.1.1.7	100.0%	99.8%

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.

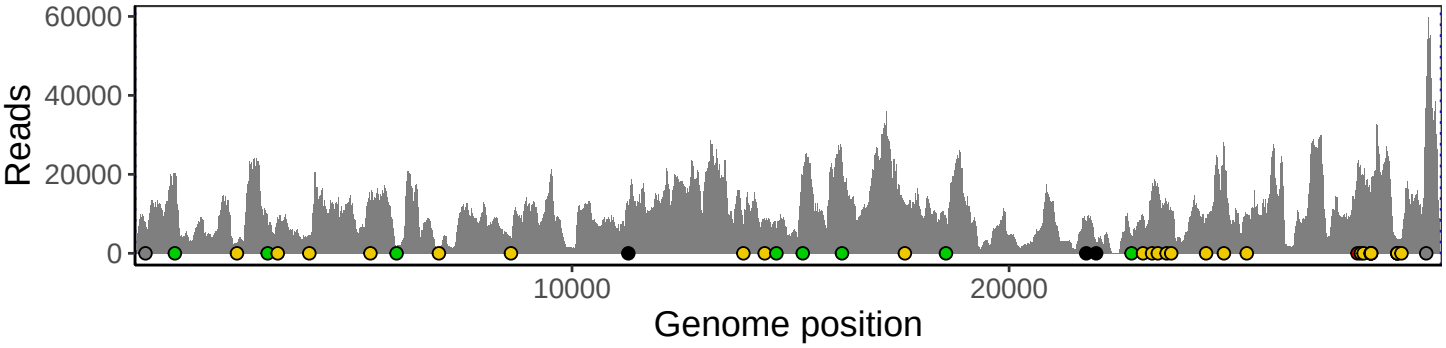



Saline
2021−03−30
241 intergenic 6444
913 ORF1ab silent 19362
2334 ORF1ab A690V 2302
3037 ORF1ab silent 7216
3267 ORF1ab T1001I 9047
3990 ORF1ab T1242N 4309
5388 ORF1ab A1708D 13430
5986 ORF1ab silent 1804
6954 ORF1ab I2230T 690
8603 ORF1ab F2780L 3263
11288 ORF1ab del 9 6890
13920 ORF1ab K151N 6888
14408 ORF1ab P314L 7553
14676 ORF1ab silent 5698
15279 ORF1ab silent 19451
16176 ORF1ab silent 22221
17615 ORF1ab K1383R 11812
18555 ORF1ab silent 8609
21765 S del 6 7090
21991 S del 3 2610
22801 S silent 4611
23063 S N501Y 9275
23271 S A570D 15119
23403 S D614G 16780
23604 S P681H 12394
23709 S T716I 10083
24506 S S982A 8870
24914 S D1118H 27328
25437 ORF3a L15F 9877
27972 ORF8 Q27stop 21424
28048 ORF8 R52I 18452
28111 ORF8 Y73C 18264
28271 intergenic del 1 14328
28280 N D3L 9116
28281 N D3L 9117
28282 N D3L 9789
28881 N R203K 2437
28882 N R203K 2419
28883 N G204R 2429
28977 N S235F 3577
29543 intergenic 40302
VSP1500−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

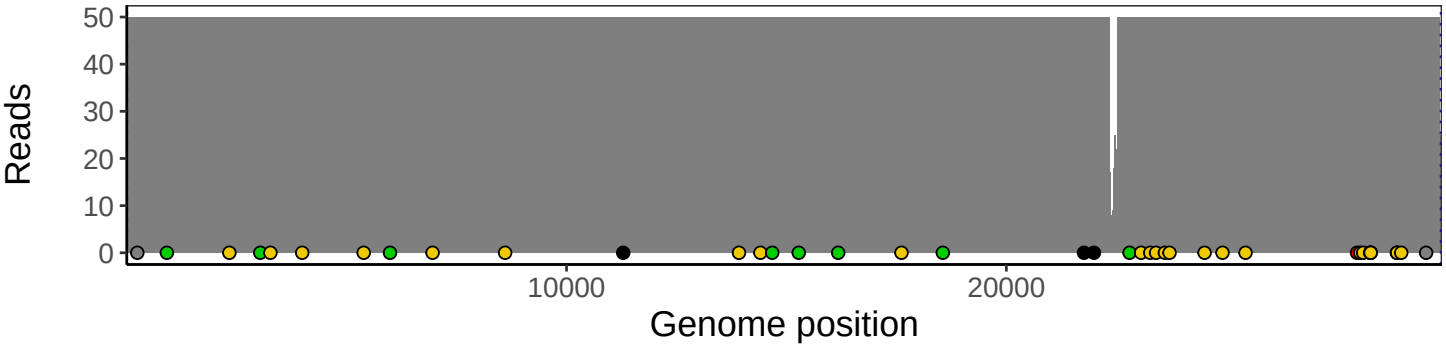
Analyses of individual experiments and composite results

VSP1500-1 | 2021-03-30 | Saline | HUP Q-0159 | genomes | single experiment

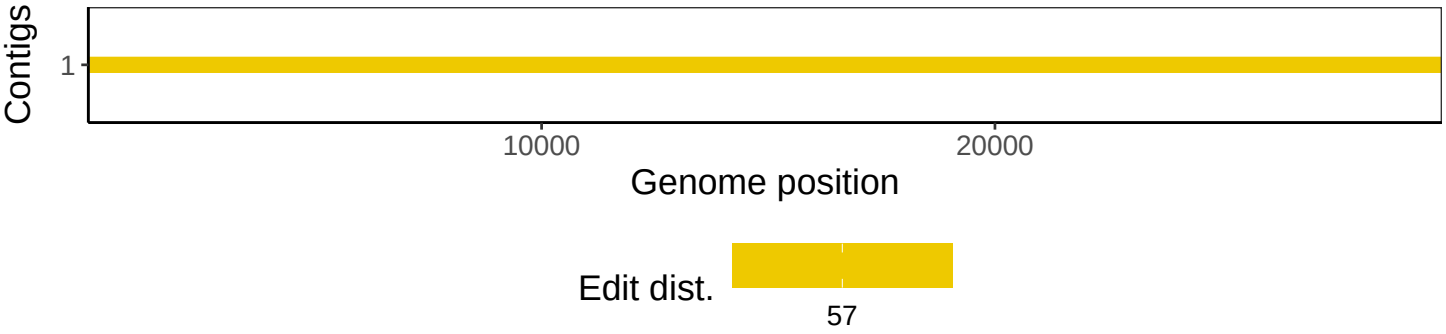
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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