COVID-19 subject HUP Q-0131

2021-05-05

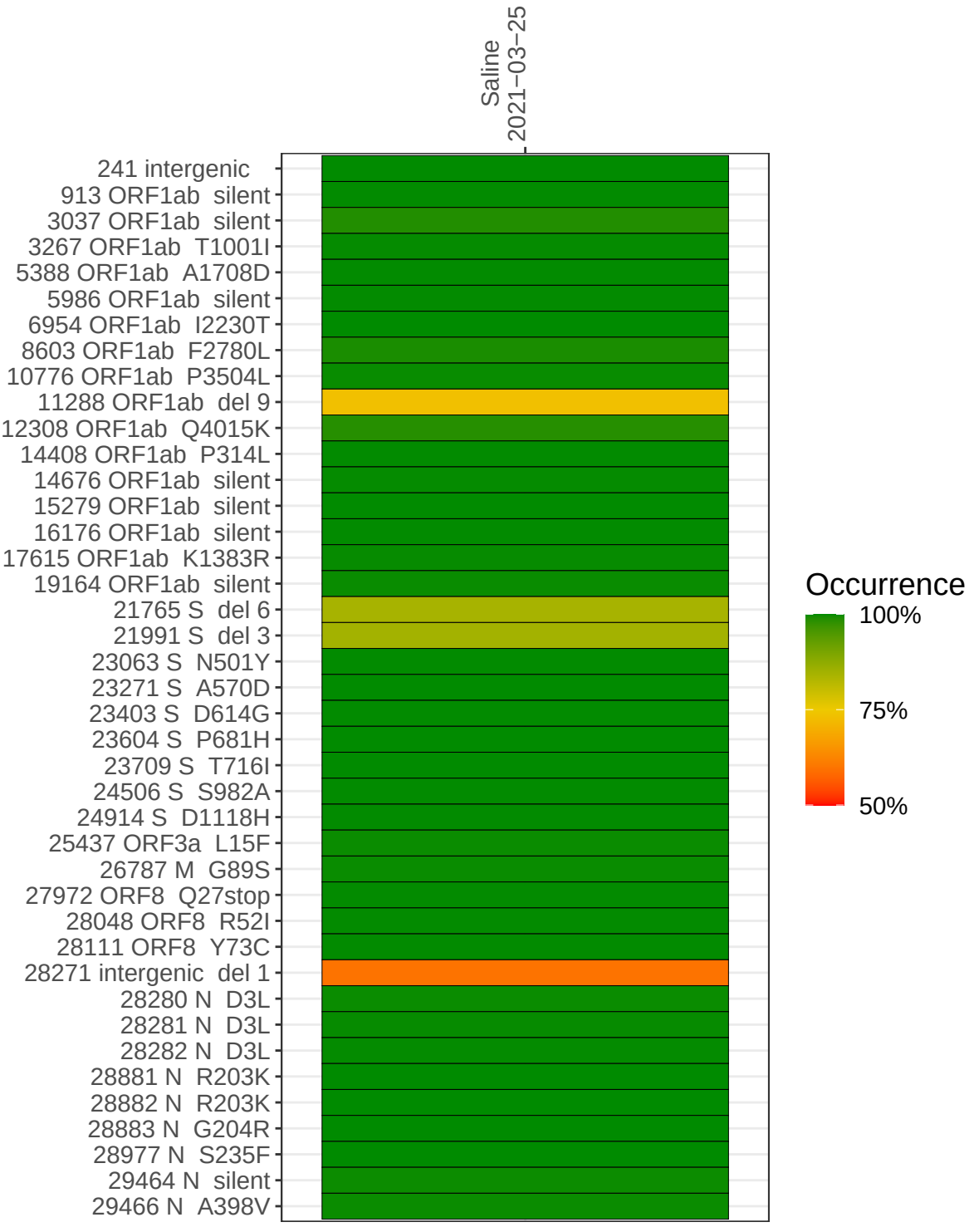
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

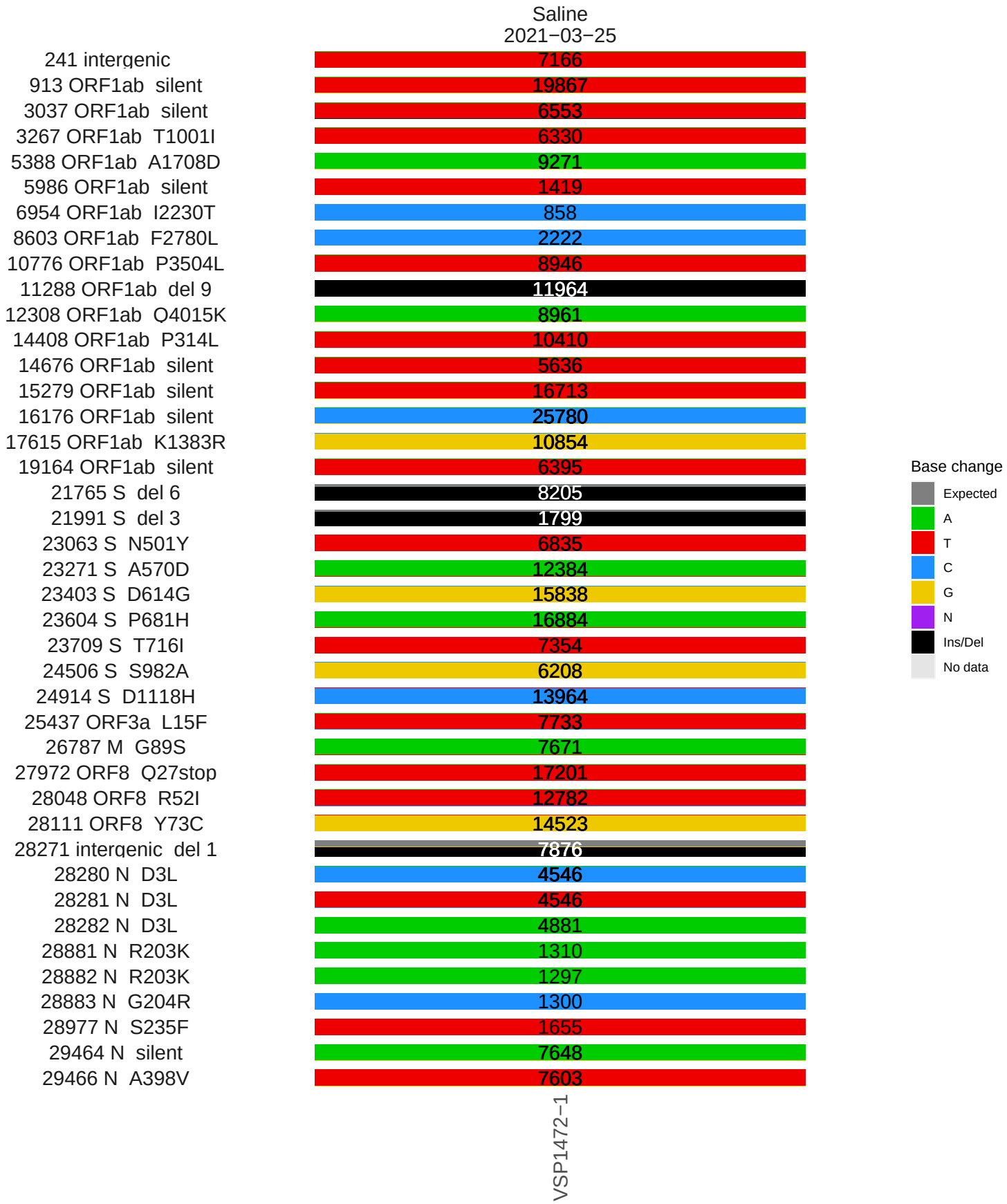
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1472-1	single experiment	NA	Saline	2021-03-25	29.84	B.1.1.7	99.9%	99.7%

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.

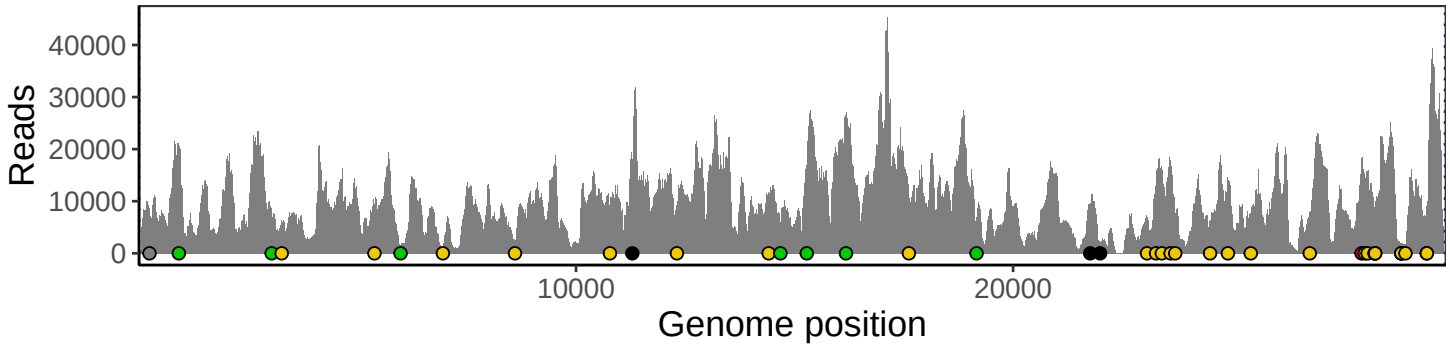



Saline
2021−03−25
241 intergenic 7166
913 ORF1ab silent 19867
3037 ORF1ab silent 6553
3267 ORF1ab T1001I 6330
5388 ORF1ab A1708D 9271
5986 ORF1ab silent 1419
6954 ORF1ab I2230T 858
8603 ORF1ab F2780L 2222
10776 ORF1ab P3504L 8946
11288 ORF1ab del 9 11964
12308 ORF1ab Q4015K 8961
14408 ORF1ab P314L 10410
14676 ORF1ab silent 5636
15279 ORF1ab silent 16713
16176 ORF1ab silent 25780
17615 ORF1ab K1383R 10854
19164 ORF1ab silent 6395
21765 S del 6 8205
21991 S del 3 1799
23063 S N501Y 6835
23271 S A570D 12384
23403 S D614G 15838
23604 S P681H 16884
23709 S T716I 7354
24506 S S982A 6208
24914 S D1118H 13964
25437 ORF3a L15F 7733
26787 M G89S 7671
27972 ORF8 Q27stop 17201
28048 ORF8 R52I 12782
28111 ORF8 Y73C 14523
28271 intergenic del 1 7876
28280 N D3L 4546
28281 N D3L 4546
28282 N D3L 4881
28881 N R203K 1310
28882 N R203K 1297
28883 N G204R 1300
28977 N S235F 1655
29464 N silent 7648
29466 N A398V 7603
VSP1472−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

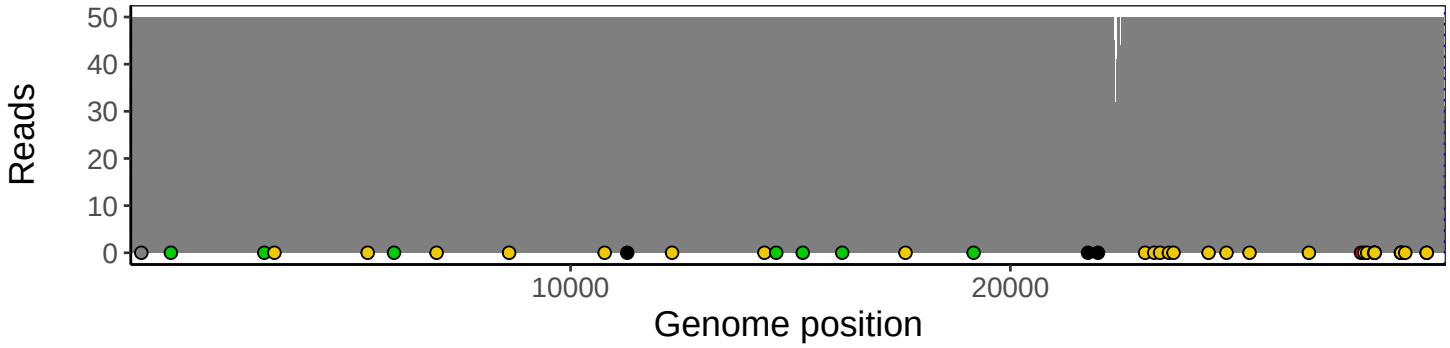
Analyses of individual experiments and composite results

VSP1472-1 | 2021-03-25 | Saline | HUP Q-0131 | genomes | single experiment

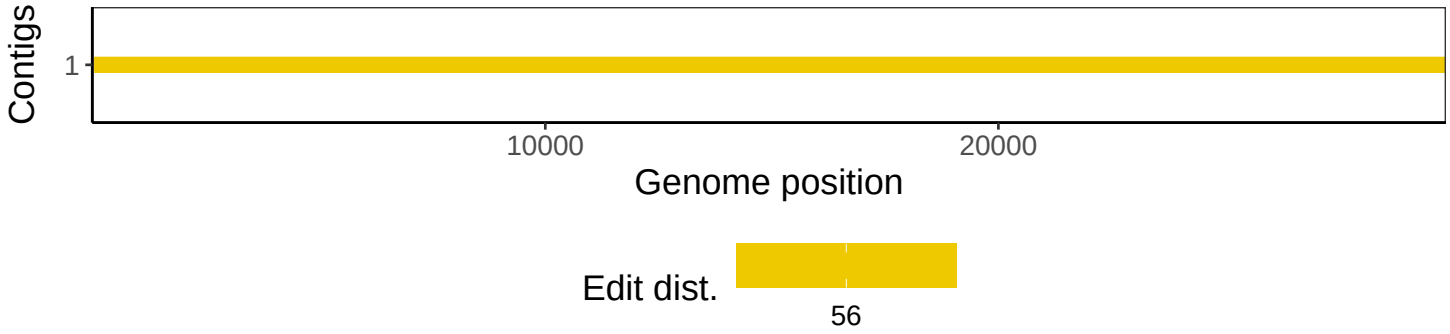
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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