COVID-19 subject HUP Q-0117

2021-05-05

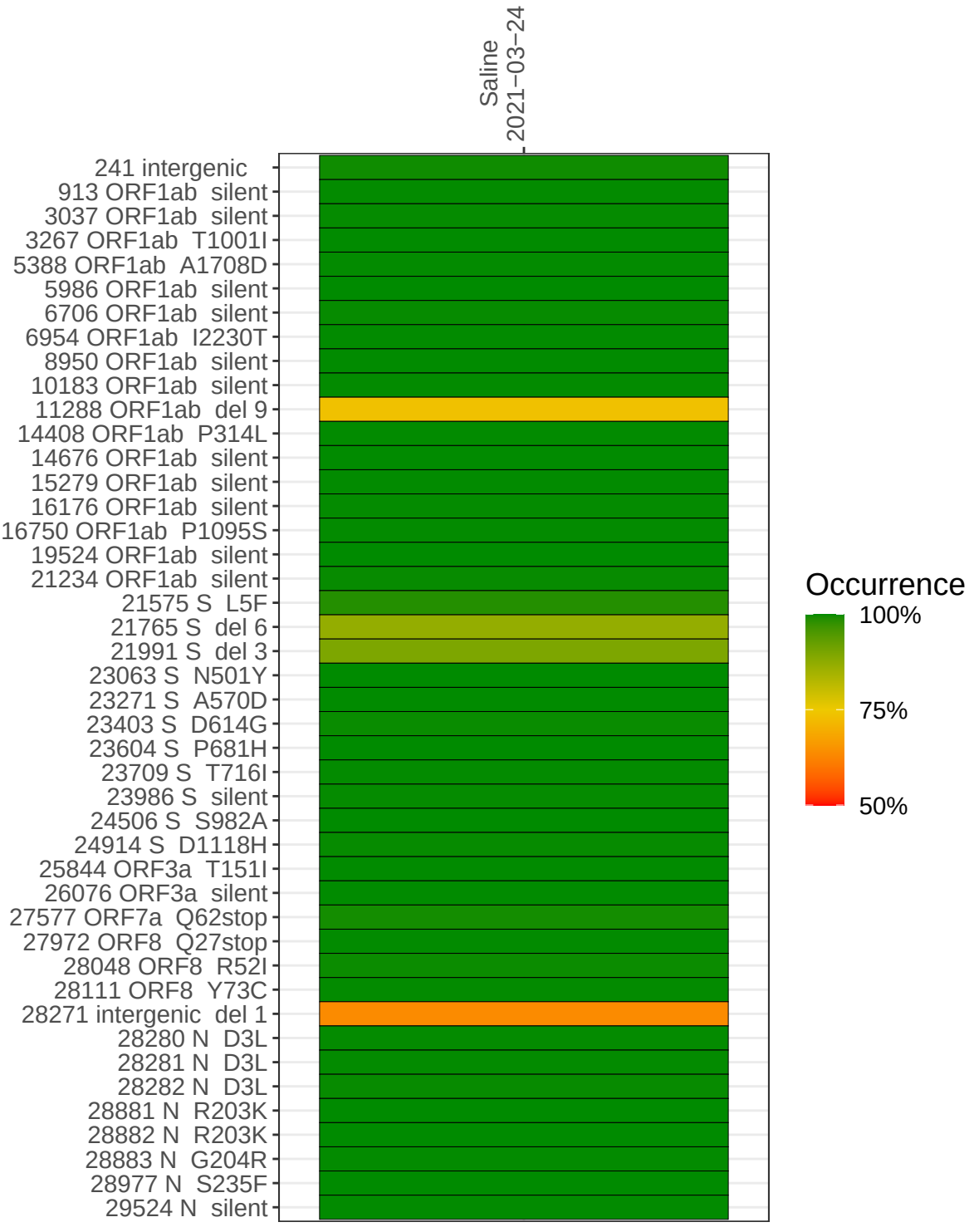
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

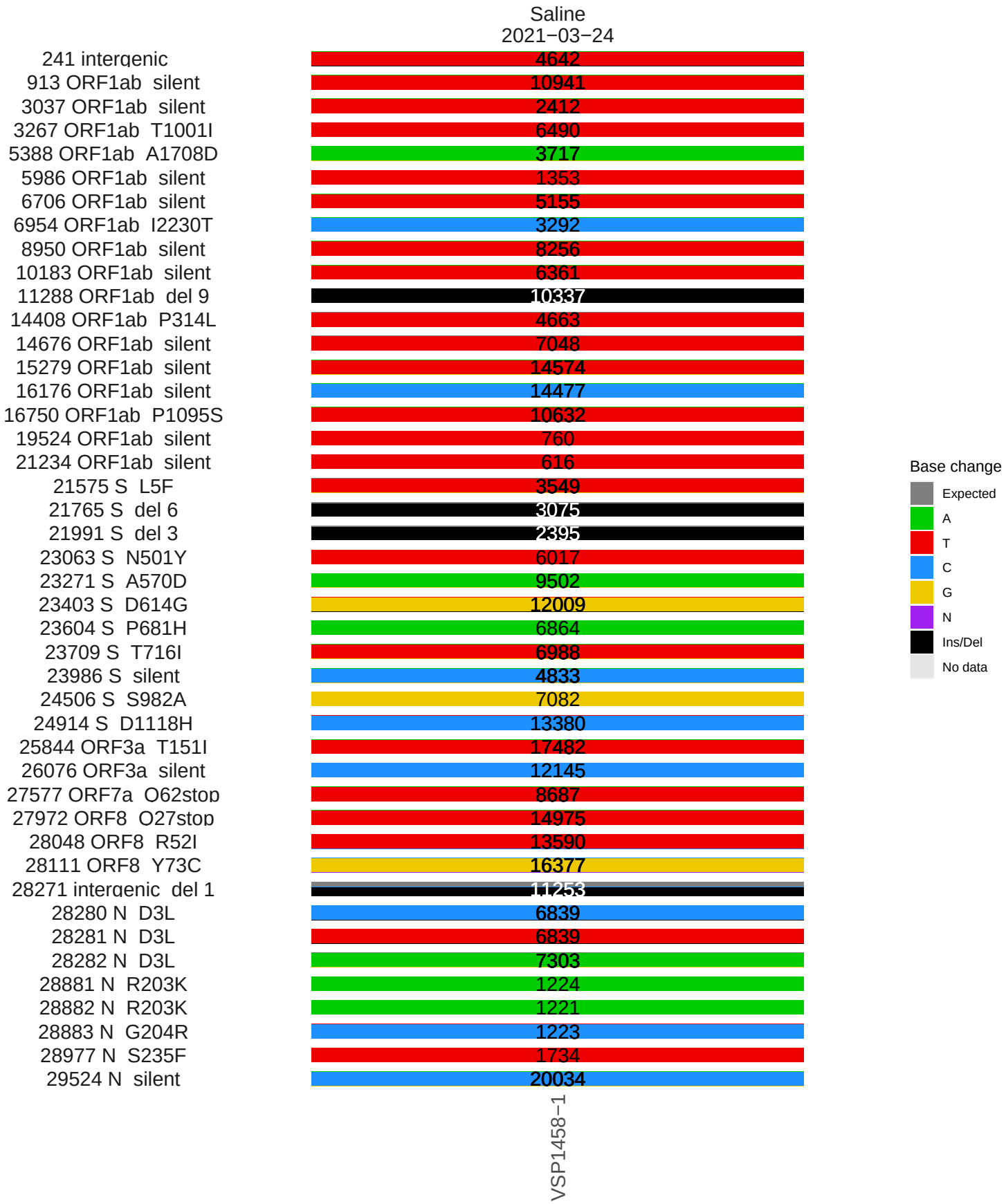
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1458-1	single experiment	NA	Saline	2021-03-24	29.86	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.

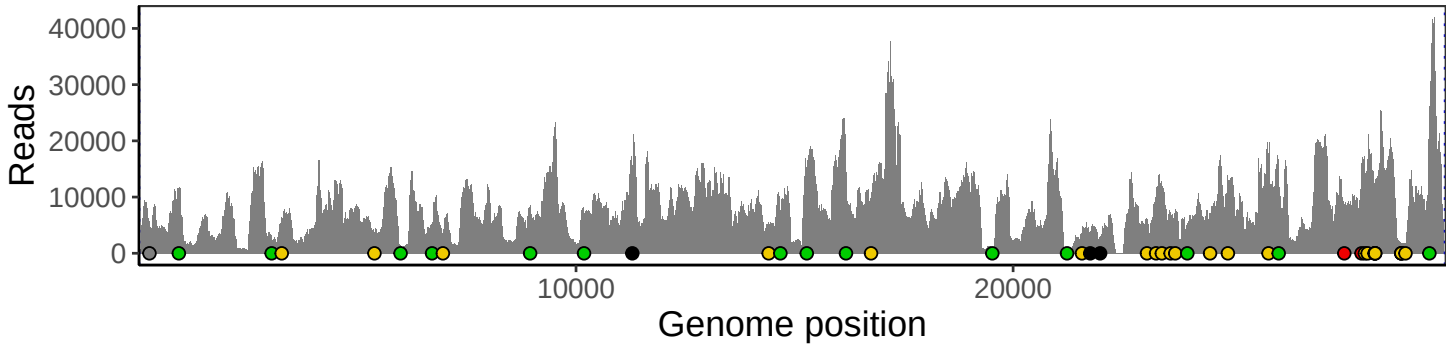



Saline
2021−03−24
241 intergenic 4642
913 ORF1ab silent 10941
3037 ORF1ab silent 2412
3267 ORF1ab T1001I 6490
5388 ORF1ab A1708D 3717
5986 ORF1ab silent 1353
6706 ORF1ab silent 5155
6954 ORF1ab I2230T 3292
8950 ORF1ab silent 8256
10183 ORF1ab silent 6361
11288 ORF1ab del 9 10337
14408 ORF1ab P314L 4663
14676 ORF1ab silent 7048
15279 ORF1ab silent 14574
16176 ORF1ab silent 14477
16750 ORF1ab P1095S 10632
19524 ORF1ab silent 760
21234 ORF1ab silent 616
21575 S L5F 3549
21765 S del 6 3075
21991 S del 3 2395
23063 S N501Y 6017
23271 S A570D 9502
23403 S D614G 12009
23604 S P681H 6864
23709 S T716I 6988
23986 S silent 4833
24506 S S982A 7082
24914 S D1118H 13380
25844 ORF3a T151I 17482
26076 ORF3a silent 12145
27577 ORF7a O62stop 8687
27972 ORF8 O27stop 14975
28048 ORF8 R52I 13590
28111 ORF8 Y73C 16377
28271 intergenic del 1 11253
28280 N D3L 6839
28281 N D3L 6839
28282 N D3L 7303
28881 N R203K 1224
28882 N R203K 1221
28883 N G204R 1223
28977 N S235F 1734
29524 N silent 20034
VSP1458−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

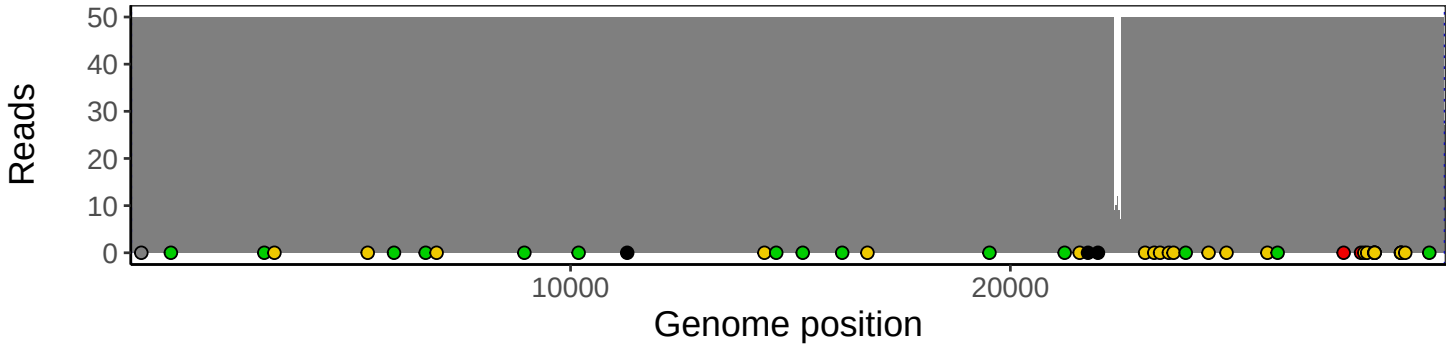
Analyses of individual experiments and composite results

VSP1458-1 | 2021-03-24 | Saline | HUP Q-0117 | genomes | single experiment

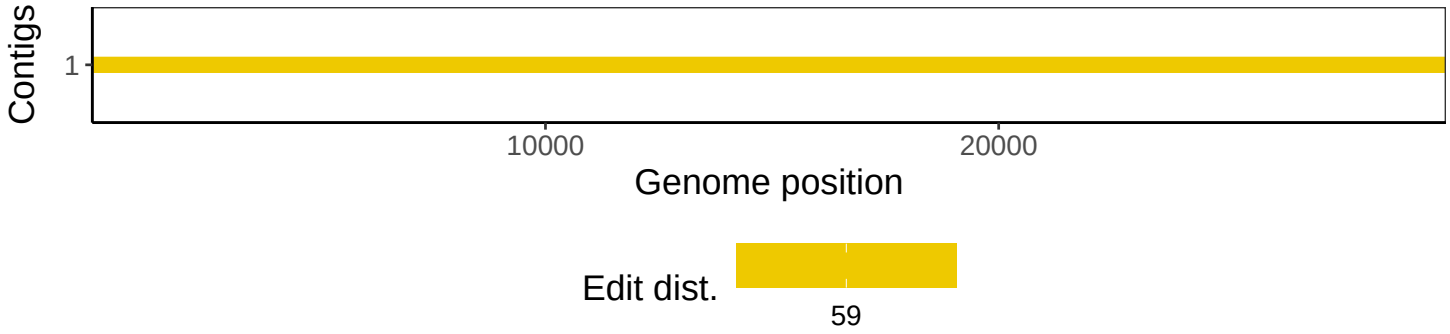
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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