COVID-19 subject HUP Q-0026

2021-04-17

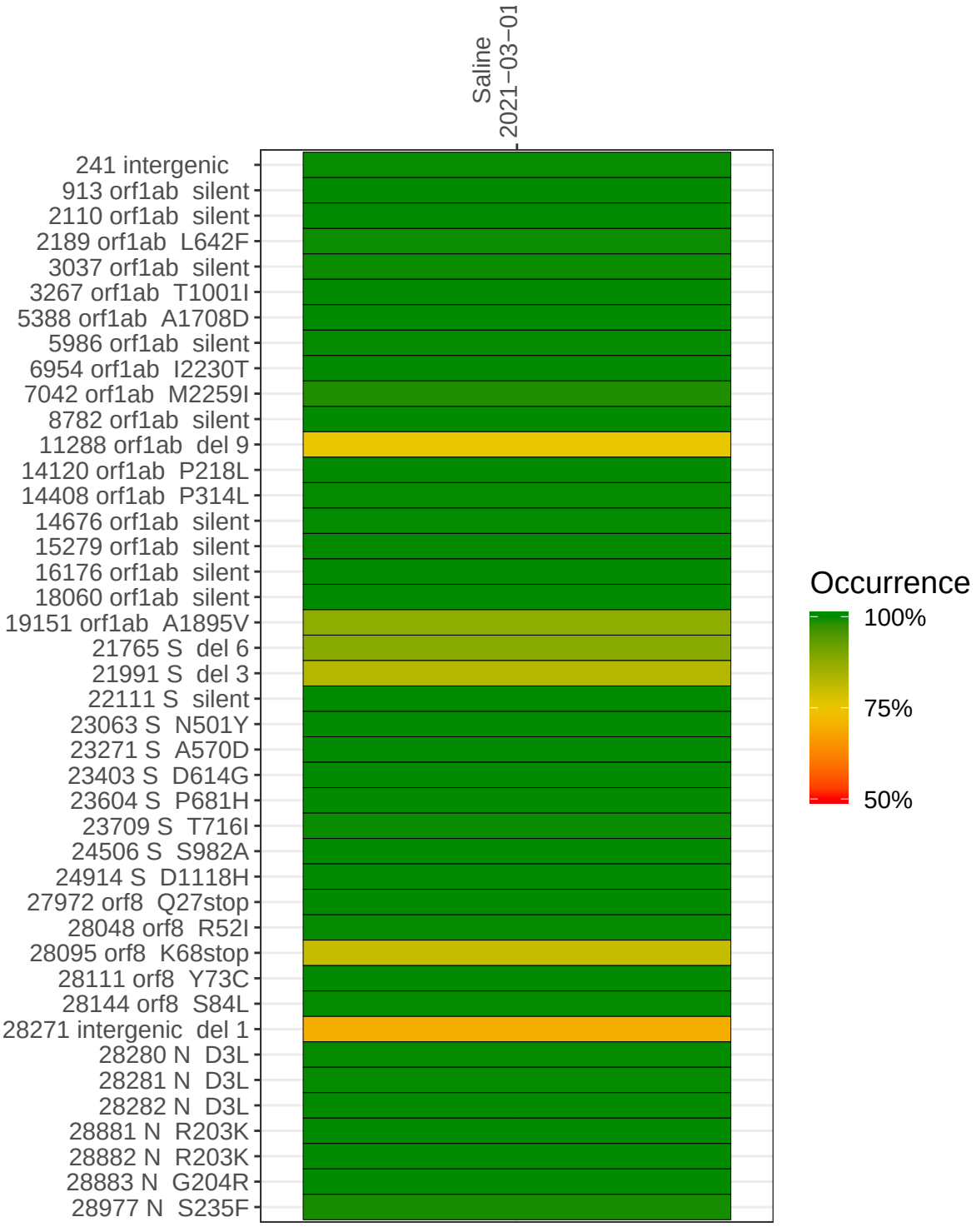
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

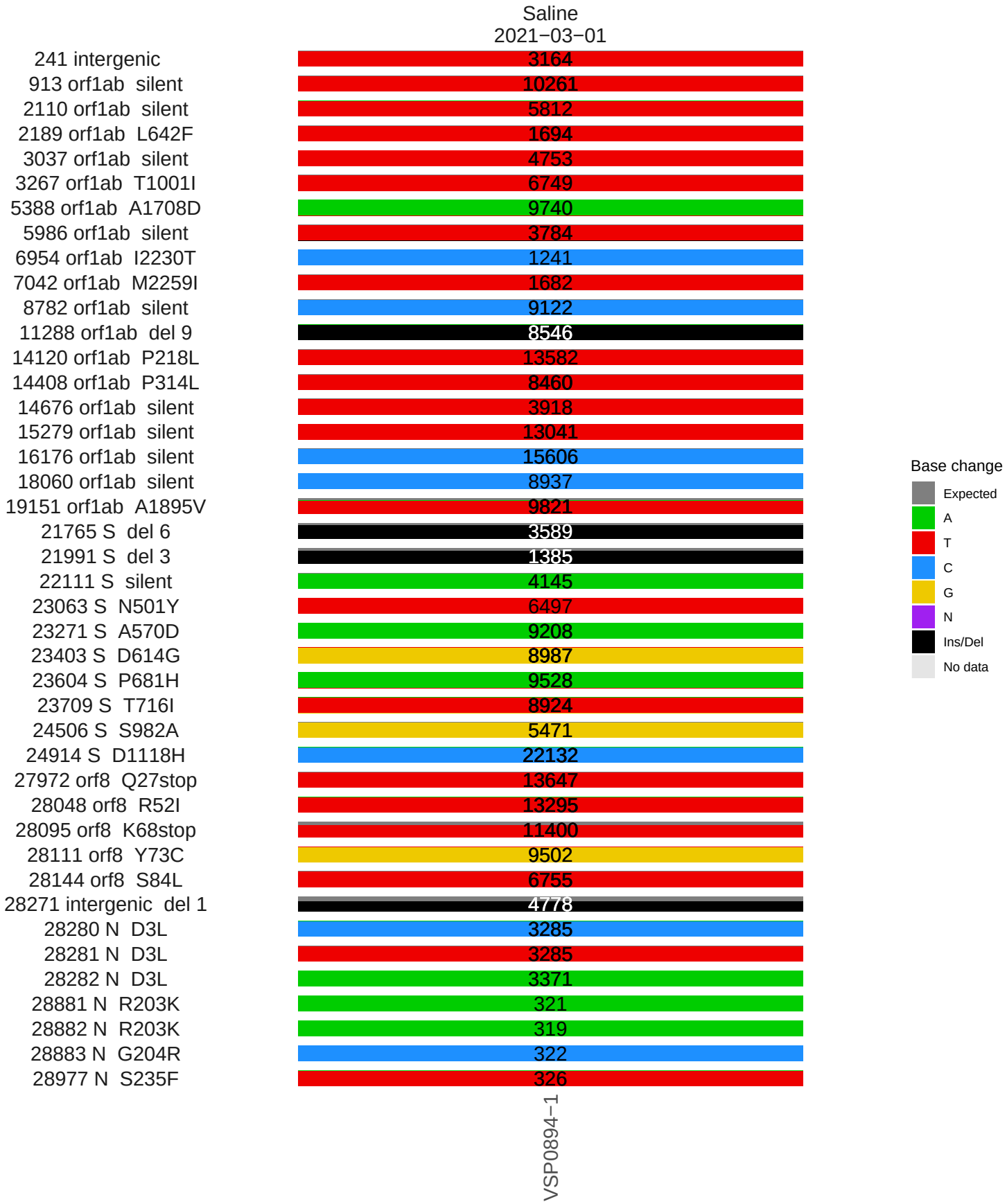
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0894-1	single experiment	NA	Saline	2021-03-01	29.80	B.1.1.7	99.8%	99.8%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/USA-WA1-2020) 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.

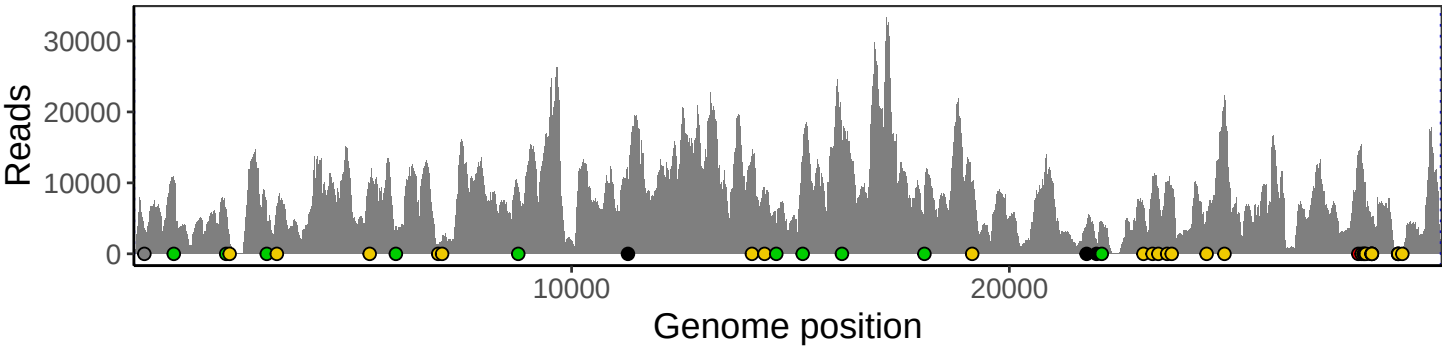



Saline
2021−03−01
241 intergenic 3164
913 orf1ab silent 10261
2110 orf1ab silent 5812
2189 orf1ab L642F 1694
3037 orf1ab silent 4753
3267 orf1ab T1001I 6749
5388 orf1ab A1708D 9740
5986 orf1ab silent 3784
6954 orf1ab I2230T 1241
7042 orf1ab M2259I 1682
8782 orf1ab silent 9122
11288 orf1ab del 9 8546
14120 orf1ab P218L 13582
14408 orf1ab P314L 8460
14676 orf1ab silent 3918
15279 orf1ab silent 13041
16176 orf1ab silent 15606
18060 orf1ab silent 8937
19151 orf1ab A1895V 9821
21765 S del 6 3589
21991 S del 3 1385
22111 S silent 4145
23063 S N501Y 6497
23271 S A570D 9208
23403 S D614G 8987
23604 S P681H 9528
23709 S T716I 8924
24506 S S982A 5471
24914 S D1118H 22132
27972 orf8 Q27stop 13647
28048 orf8 R52I 13295
28095 orf8 K68stop 11400
28111 orf8 Y73C 9502
28144 orf8 S84L 6755
28271 intergenic del 1 4778
28280 N D3L 3285
28281 N D3L 3285
28282 N D3L 3371
28881 N R203K 321
28882 N R203K 319
28883 N G204R 322
28977 N S235F 326
VSP0894−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

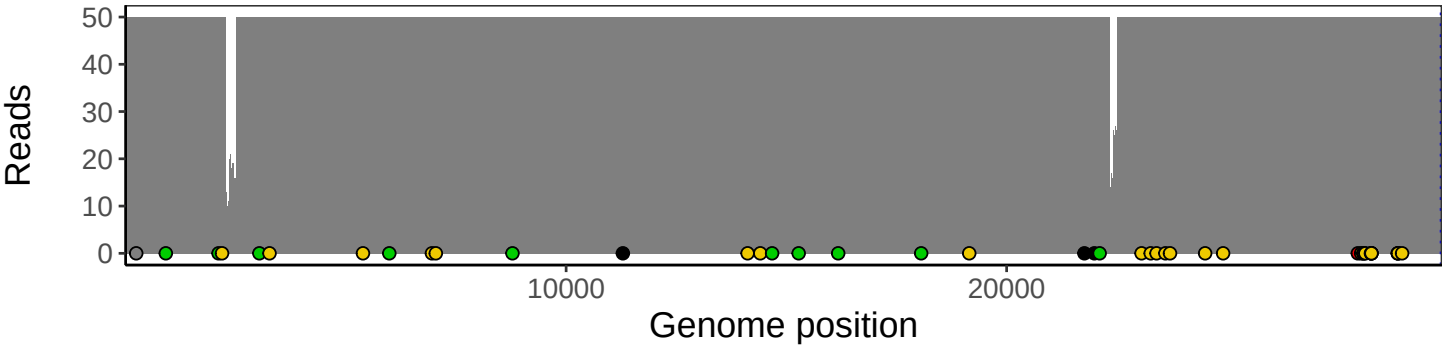
Analyses of individual experiments and composite results

VSP0894-1 | 2021-03-01 | Saline | HUP Q-0026 | genomes | single experiment

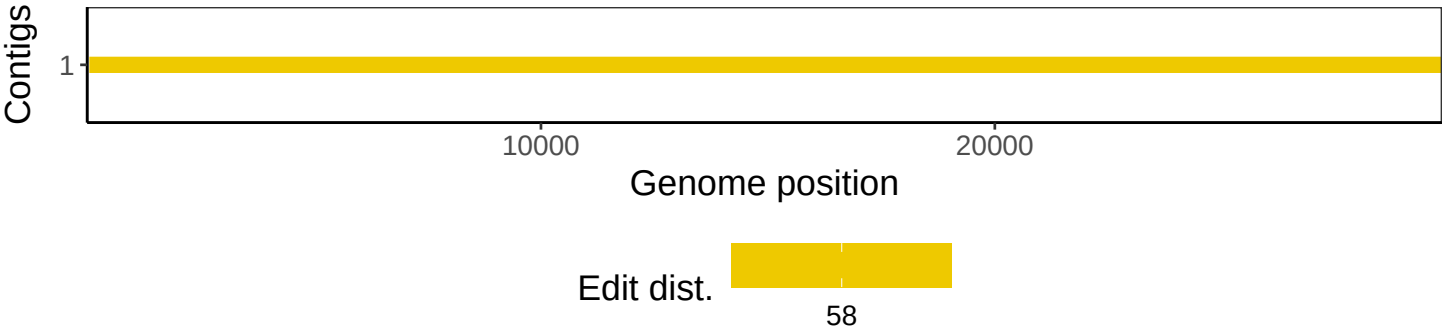
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.0.0
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