COVID-19 subject HUP Q-0074

2021-04-17

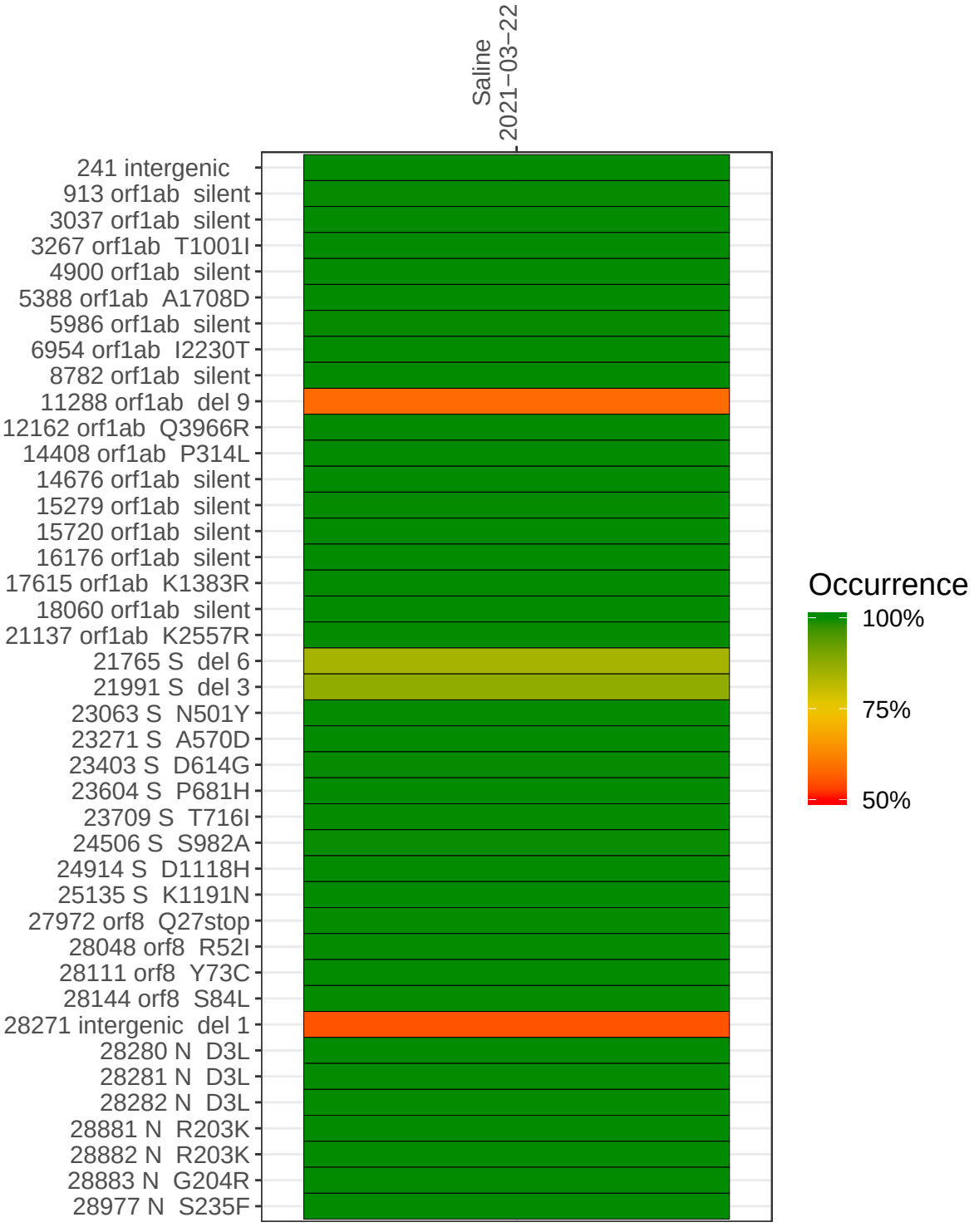
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

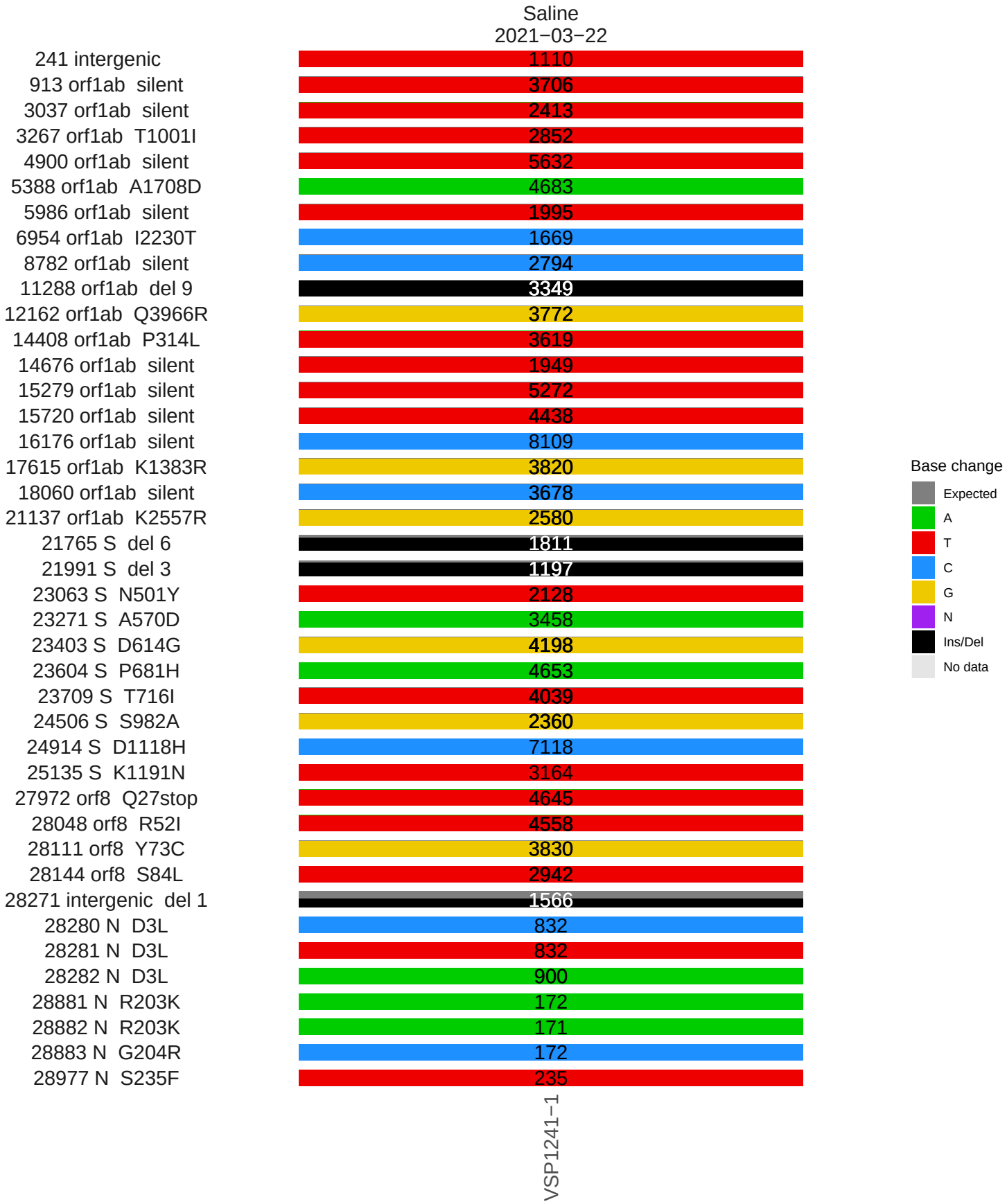
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1241-1	single experiment	NA	Saline	2021-03-22	29.88	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.

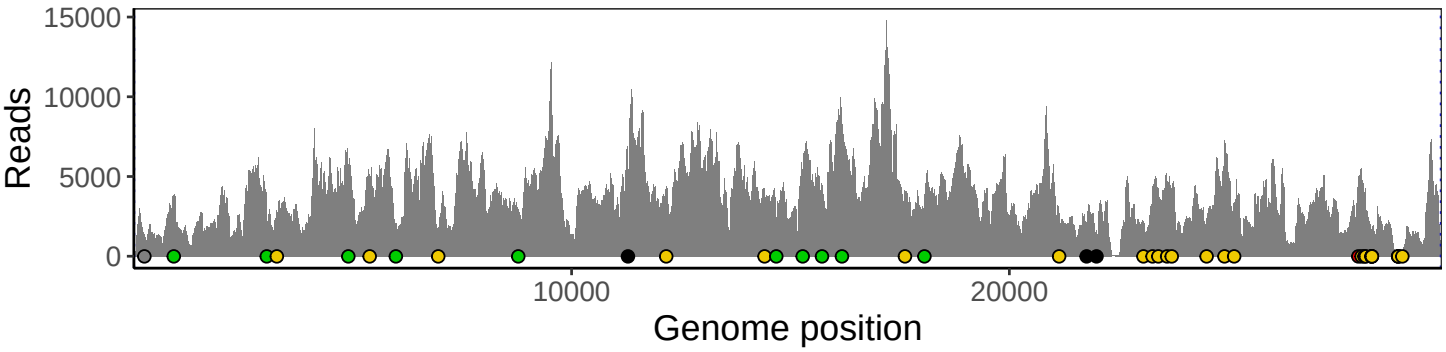



Saline
2021−03−22
241 intergenic 1110
913 orf1ab silent 3706
3037 orf1ab silent 2413
3267 orf1ab T1001I 2852
4900 orf1ab silent 5632
5388 orf1ab A1708D 4683
5986 orf1ab silent 1995
6954 orf1ab I2230T 1669
8782 orf1ab silent 2794
11288 orf1ab del 9 3349
12162 orf1ab Q3966R 3772
14408 orf1ab P314L 3619
14676 orf1ab silent 1949
15279 orf1ab silent 5272
15720 orf1ab silent 4438
16176 orf1ab silent 8109
17615 orf1ab K1383R 3820
18060 orf1ab silent 3678
21137 orf1ab K2557R 2580
21765 S del 6 1811
21991 S del 3 1197
23063 S N501Y 2128
23271 S A570D 3458
23403 S D614G 4198
23604 S P681H 4653
23709 S T716I 4039
24506 S S982A 2360
24914 S D1118H 7118
25135 S K1191N 3164
27972 orf8 Q27stop 4645
28048 orf8 R52I 4558
28111 orf8 Y73C 3830
28144 orf8 S84L 2942
28271 intergenic del 1 1566
28280 N D3L 832
28281 N D3L 832
28282 N D3L 900
28881 N R203K 172
28882 N R203K 171
28883 N G204R 172
28977 N S235F 235
VSP1241−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

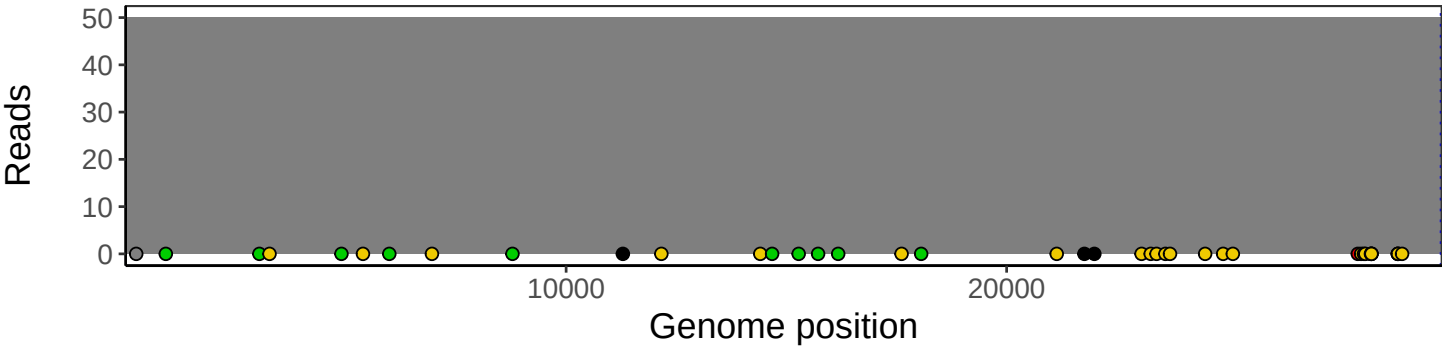
Analyses of individual experiments and composite results

VSP1241-1 | 2021-03-22 | Saline | HUP Q-0074 | genomes | single experiment

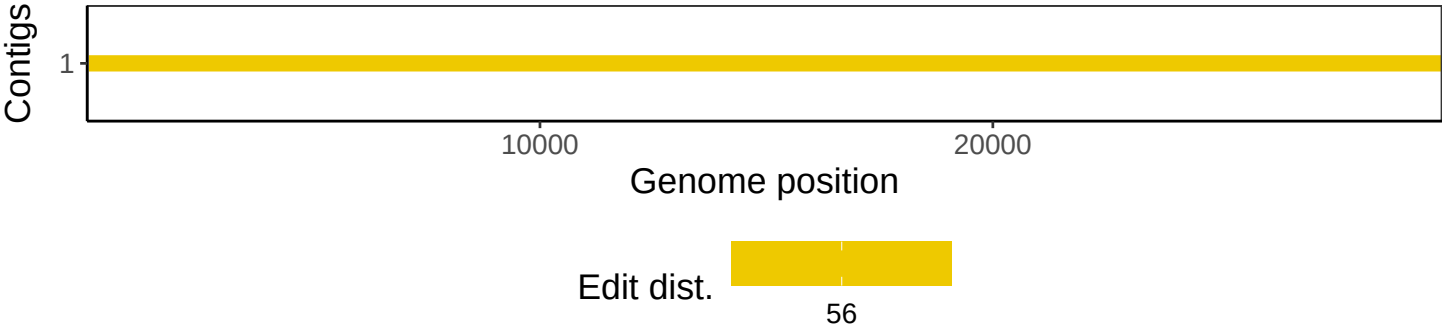
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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