COVID-19 subject HUP Q-0104

2021-04-17

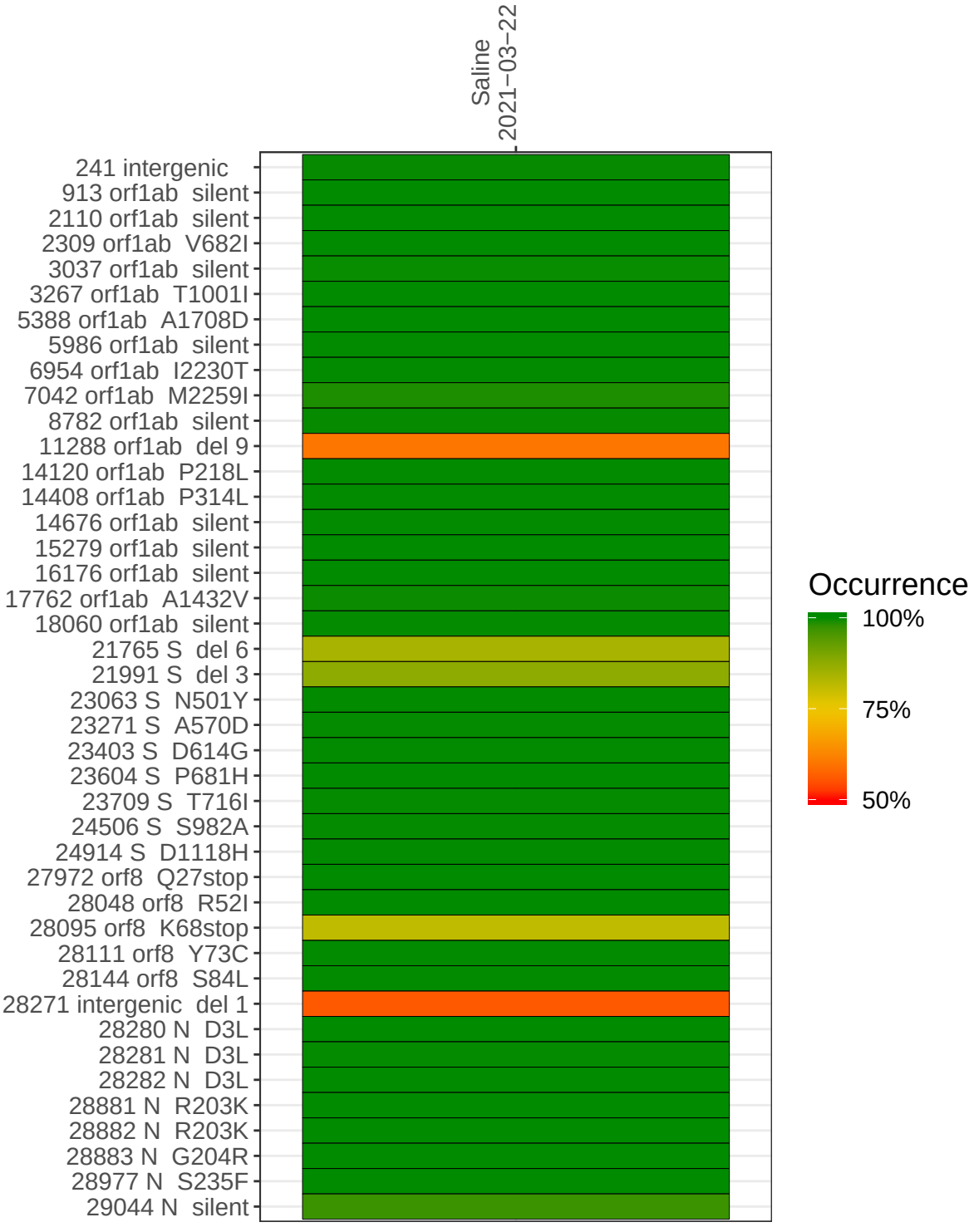
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

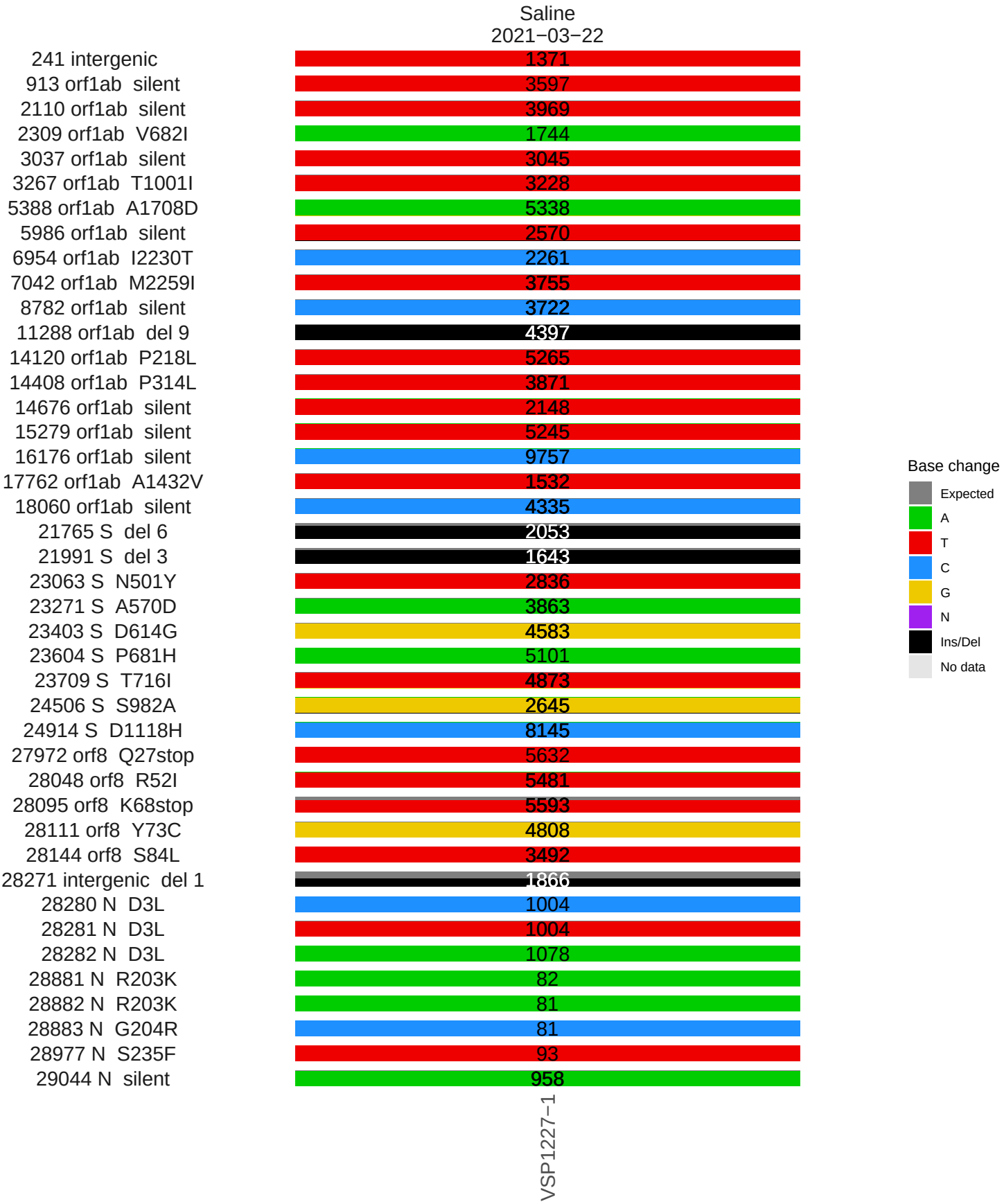
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1227-1	single experiment	NA	Saline	2021-03-22	29.85	B.1.1.7	99.9%	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.

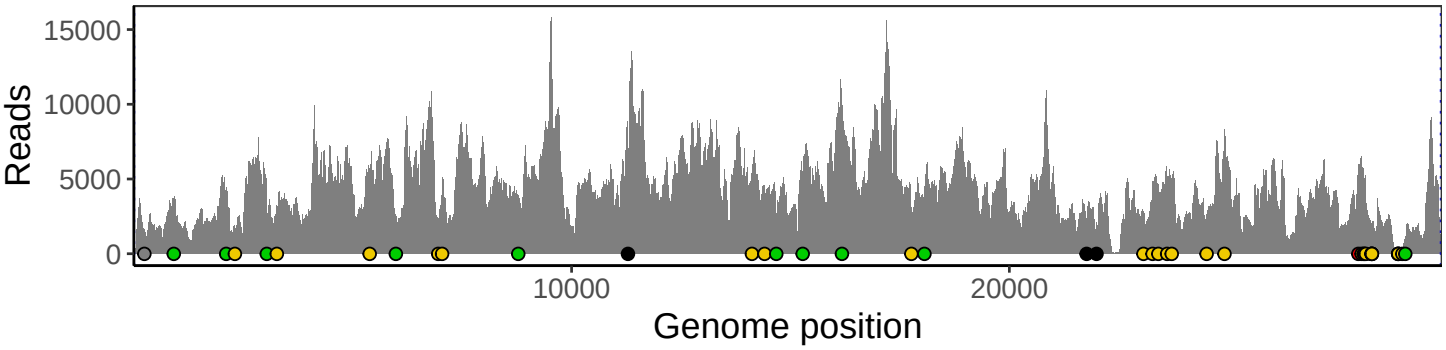



Saline
2021−03−22
241 intergenic 1371
913 orf1ab silent 3597
2110 orf1ab silent 3969
2309 orf1ab V682I 1744
3037 orf1ab silent 3045
3267 orf1ab T1001I 3228
5388 orf1ab A1708D 5338
5986 orf1ab silent 2570
6954 orf1ab I2230T 2261
7042 orf1ab M2259I 3755
8782 orf1ab silent 3722
11288 orf1ab del 9 4397
14120 orf1ab P218L 5265
14408 orf1ab P314L 3871
14676 orf1ab silent 2148
15279 orf1ab silent 5245
16176 orf1ab silent 9757
17762 orf1ab A1432V 1532
18060 orf1ab silent 4335
21765 S del 6 2053
21991 S del 3 1643
23063 S N501Y 2836
23271 S A570D 3863
23403 S D614G 4583
23604 S P681H 5101
23709 S T716I 4873
24506 S S982A 2645
24914 S D1118H 8145
27972 orf8 Q27stop 5632
28048 orf8 R52I 5481
28095 orf8 K68stop 5593
28111 orf8 Y73C 4808
28144 orf8 S84L 3492
28271 intergenic del 1 1866
28280 N D3L 1004
28281 N D3L 1004
28282 N D3L 1078
28881 N R203K 82
28882 N R203K 81
28883 N G204R 81
28977 N S235F 93
29044 N silent 958
VSP1227−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

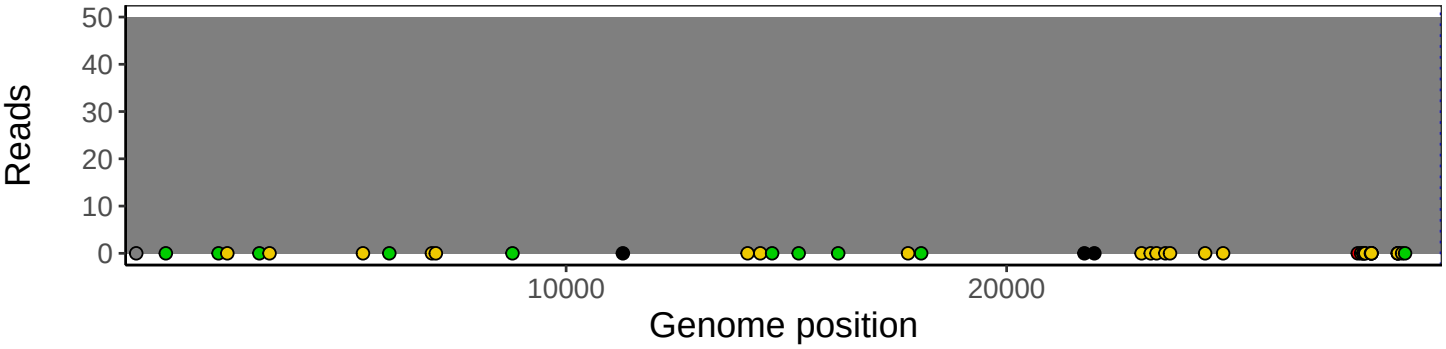
Analyses of individual experiments and composite results

VSP1227-1 | 2021-03-22 | Saline | HUP Q-0104 | genomes | single experiment

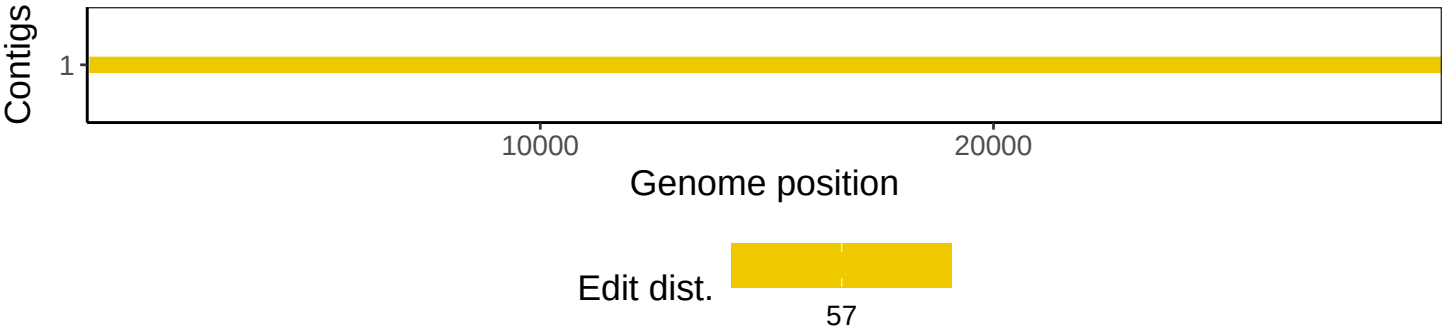
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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