COVID-19 subject HUP PH-0025

2021-03-29

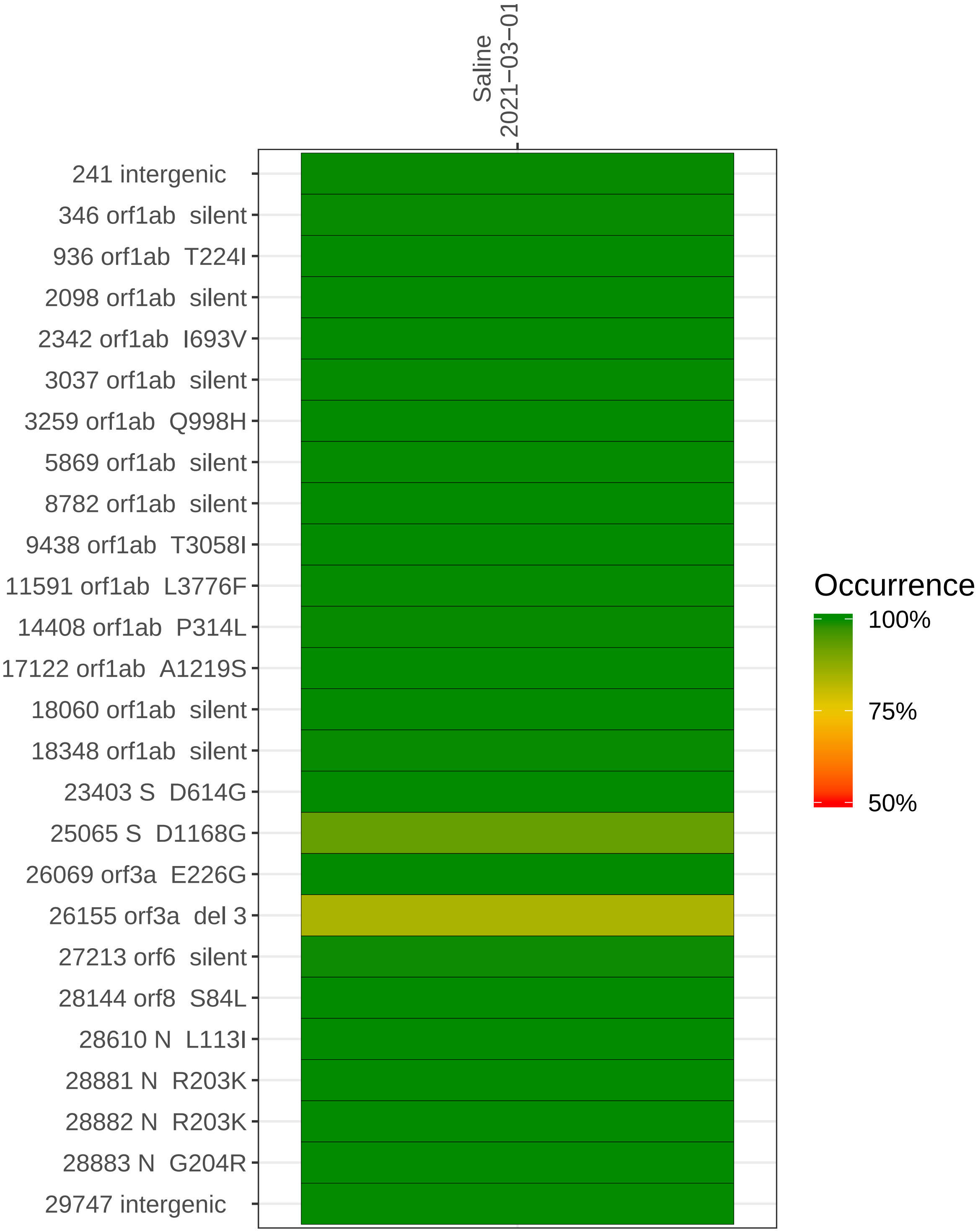
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

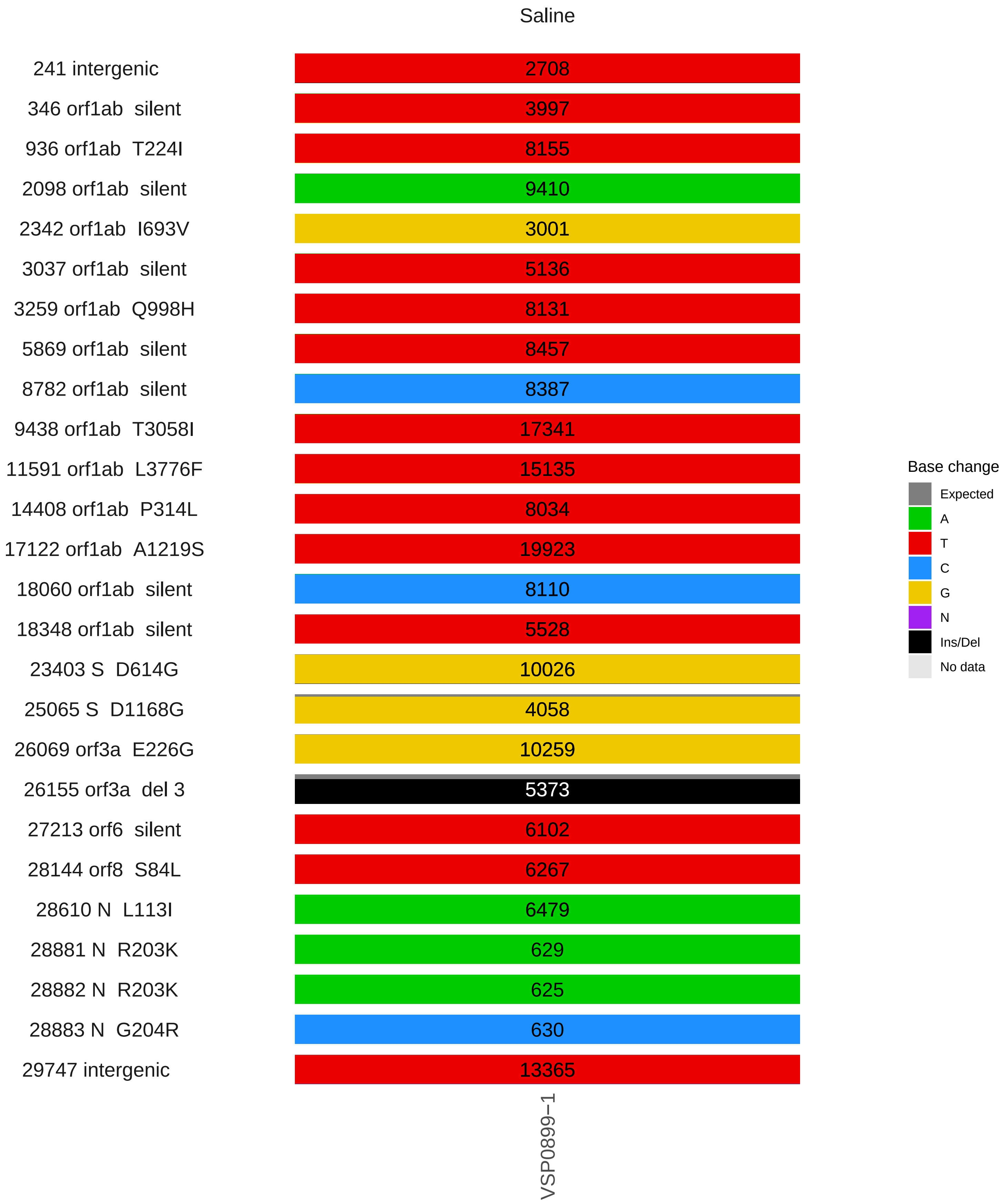
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0899-1	single experiment	NA	Saline	2021-03-01	29.89	B.1.1.304	99.9%	99.8%

Variants shared across samples

The heat map below shows how variants (reference genome 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.

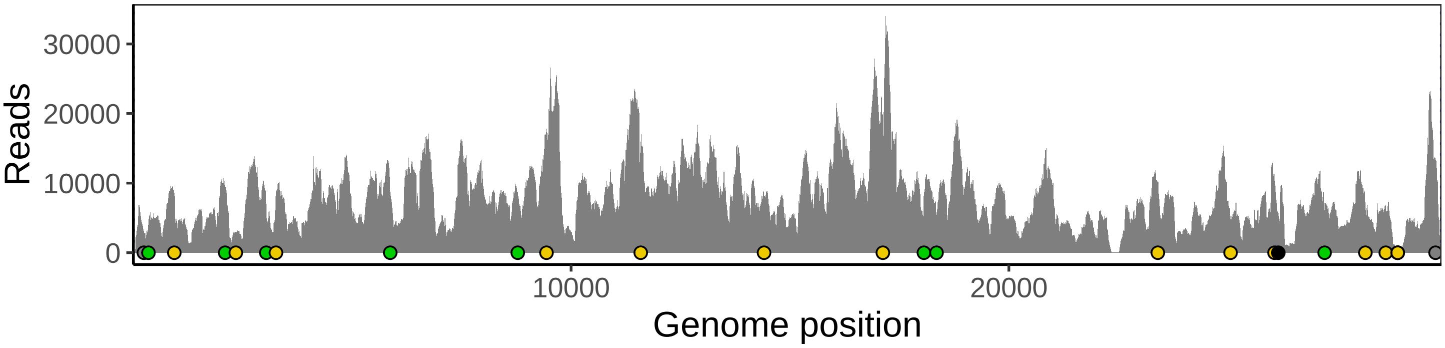



Saline
241 intergenic
2708
346 orf1ab silent
3997
936 orf1ab T224I
8155
2098 orf1ab silent
9410
2342 orf1ab I693V
3001
3037 orf1ab silent
5136
3259 orf1ab Q998H
8131
5869 orf1ab silent
8457
8782 orf1ab silent
8387
9438 orf1ab T3058I
17341
11591 orf1ab L3776F
15135
14408 orf1ab P314L
8034
17122 orf1ab A1219S
19923
18060 orf1ab silent
8110
18348 orf1ab silent
5528
23403 S D614G
10026
25065 S D1168G
4058
26069 orf3a E226G
10259
26155 orf3a del 3
5373
27213 orf6 silent
6102
28144 orf8 S84L
6267
28610 N L113I
6479
28881 N R203K
629
28882 N R203K
625
28883 N G204R
630
29747 intergenic
13365
VSP0899–1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

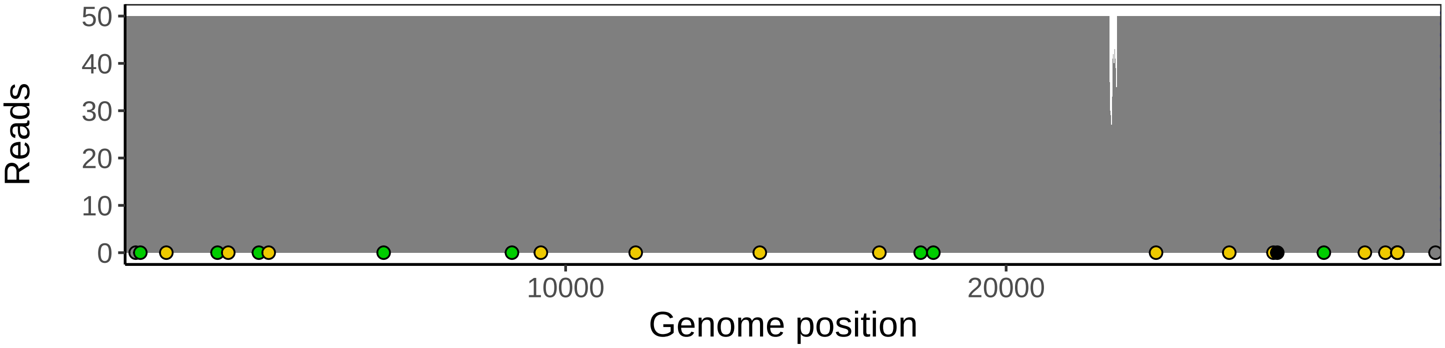
Analyses of individual experiments and composite results

VSP0899-1 | 2021-03-01 | Saline | HUP PH-0025 | genomes | single experiment

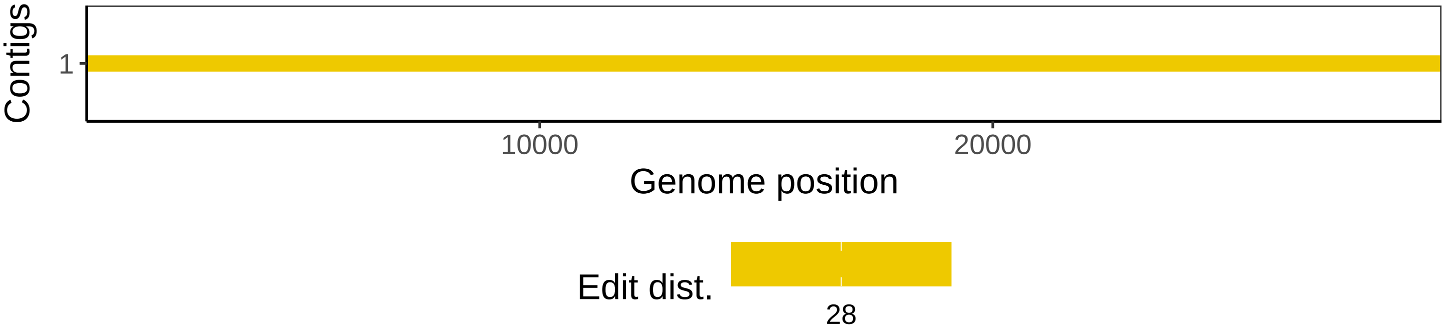
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.3
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