COVID-19 subject UPHS-0597

2021-05-05

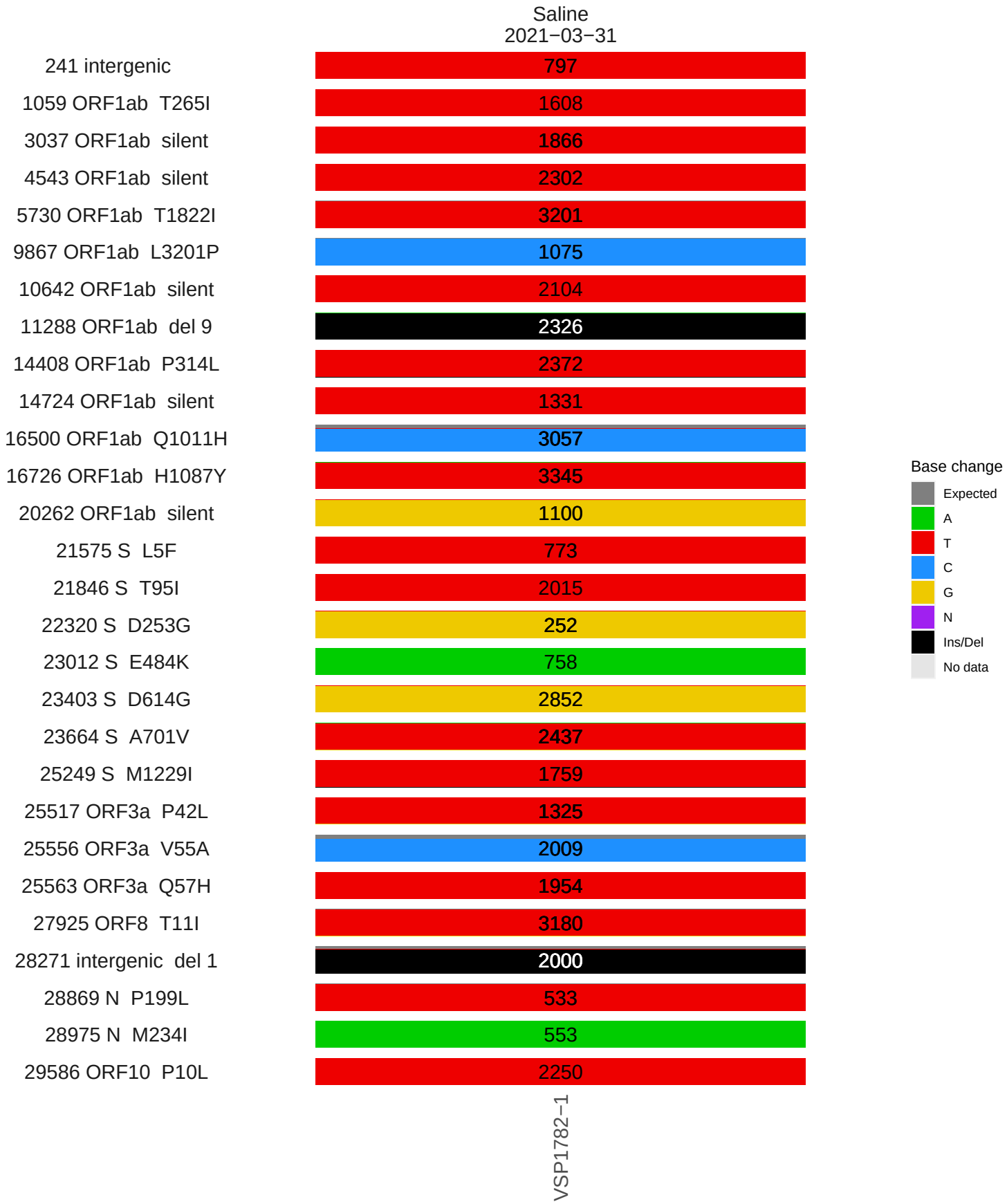
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1782-1	single experiment	NA	Saline	2021-03-31	29.81	B.1.526	99.9%	99.7%

Variants shared across samples

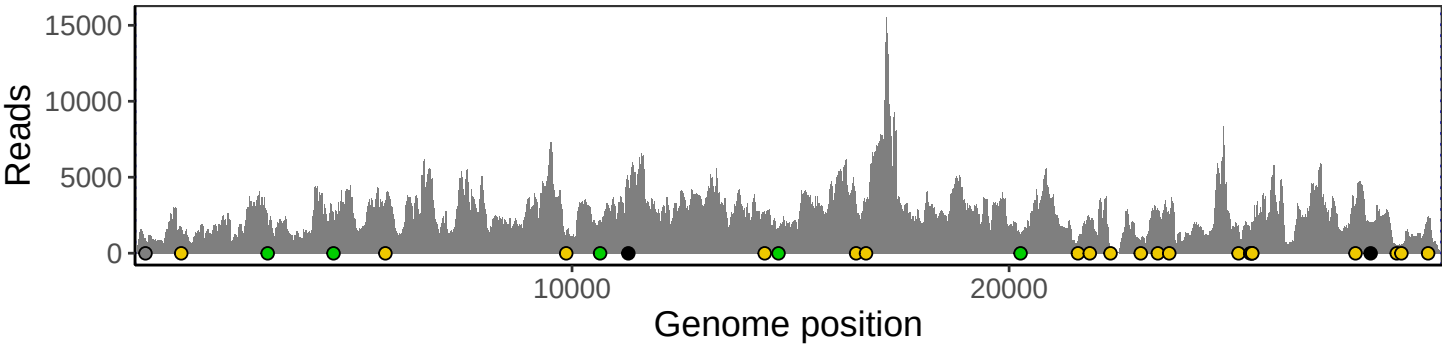
The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) are shared across subject samples where the percent variance is colored. Variants are called if a variant position is covered by 5 or more reads, the alternative base is found in > 50% of 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
2021−03−31
241 intergenic
797
1059 ORF1ab T265I
1608
3037 ORF1ab silent
1866
4543 ORF1ab silent
2302
5730 ORF1ab T1822I
3201
9867 ORF1ab L3201P
1075
10642 ORF1ab silent
2104
11288 ORF1ab del 9
2326
14408 ORF1ab P314L
2372
14724 ORF1ab silent
1331
16500 ORF1ab Q1011H
3057
16726 ORF1ab H1087Y
3345
20262 ORF1ab silent
1100
21575 S L5F
773
21846 S T95I
2015
22320 S D253G
252
23012 S E484K
758
23403 S D614G
2852
23664 S A701V
2437
25249 S M1229I
1759
25517 ORF3a P42L
1325
25556 ORF3a V55A
2009
25563 ORF3a Q57H
1954
27925 ORF8 T11I
3180
28271 intergenic del 1
2000
28869 N P199L
533
28975 N M234I
553
29586 ORF10 P10L
2250
VSP1782−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

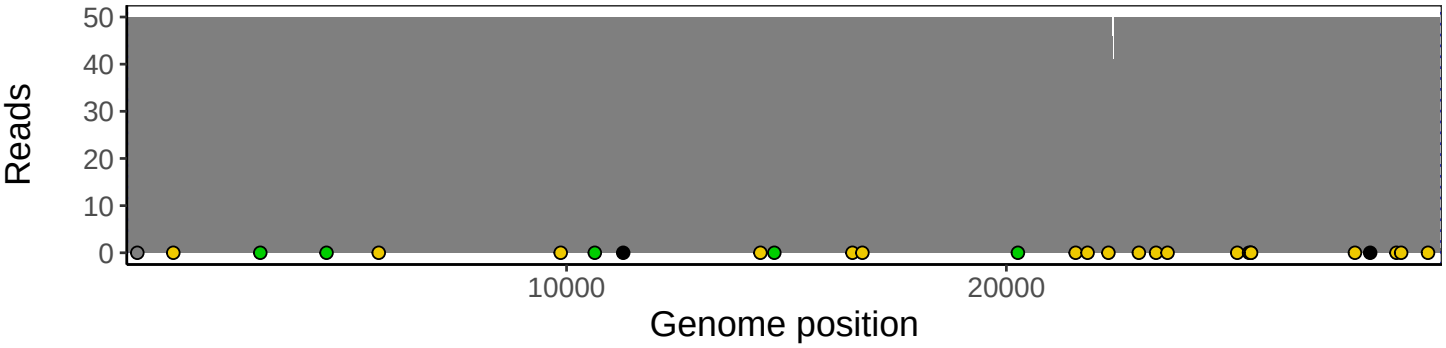
Analyses of individual experiments and composite results

VSP1782-1 | 2021-03-31 | Saline | UPHS-0597 | genomes | single experiment

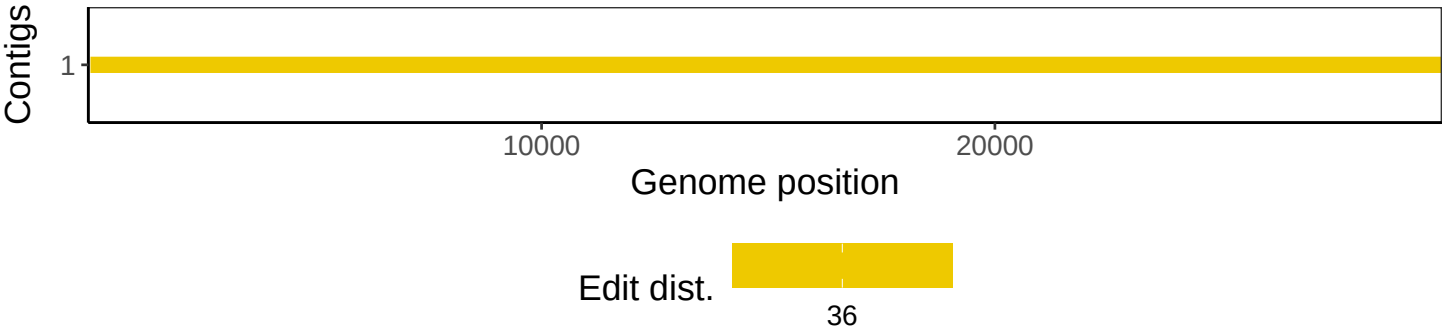
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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