COVID-19 subject UPHS-0579

2021-06-03

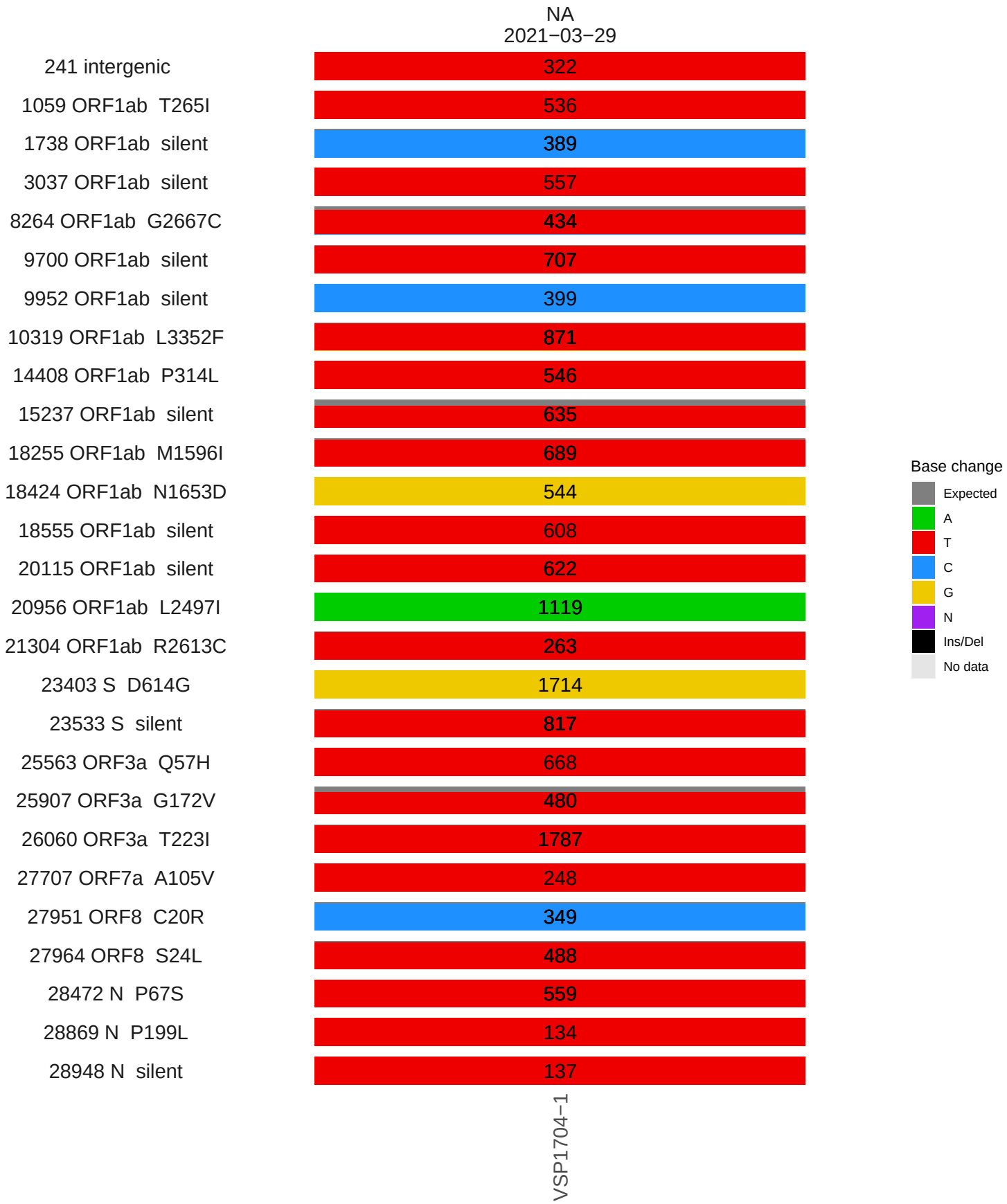
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1704-1	single experiment	NA	NA	2021-03-29	29.86	B.1.2	99.7%	99.7%

Variants shared across samples

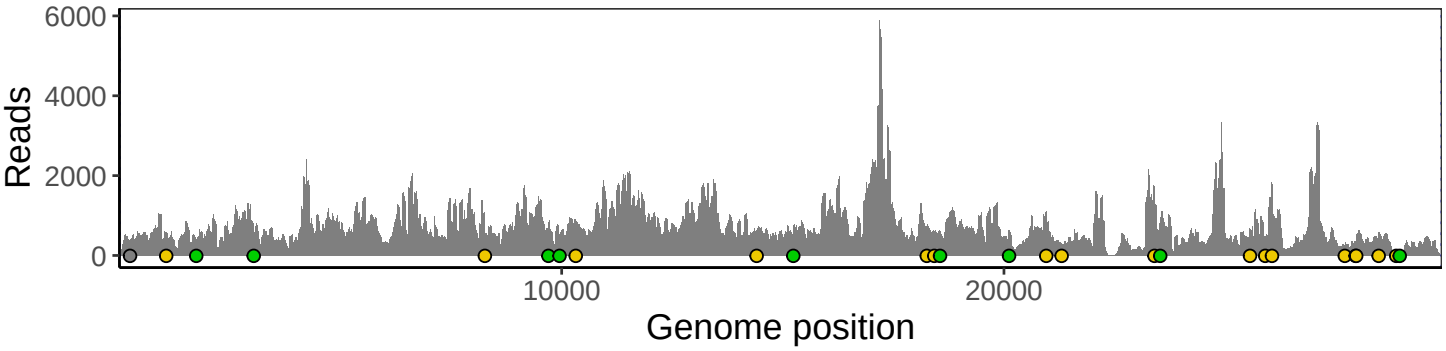
The heat map below shows how variants (reference genome /home/common/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) are shared across subject samples where the percent variance is colored. Variants are called if a variant position is covered by 5 or more reads, the alternative base is found in $> 50\%$ of read 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.


NA
2021−03−29
241 intergenic
322
1059 ORF1ab T265I
536
1738 ORF1ab silent
389
3037 ORF1ab silent
557
8264 ORF1ab G2667C
434
9700 ORF1ab silent
707
9952 ORF1ab silent
399
10319 ORF1ab L3352F
871
14408 ORF1ab P314L
546
15237 ORF1ab silent
635
18255 ORF1ab M1596I
689
18424 ORF1ab N1653D
544
18555 ORF1ab silent
608
20115 ORF1ab silent
622
20956 ORF1ab L2497I
1119
21304 ORF1ab R2613C
263
23403 S D614G
1714
23533 S silent
817
25563 ORF3a Q57H
668
25907 ORF3a G172V
480
26060 ORF3a T223I
1787
27707 ORF7a A105V
248
27951 ORF8 C20R
349
27964 ORF8 S24L
488
28472 N P67S
559
28869 N P199L
134
28948 N silent
137
VSP1704−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

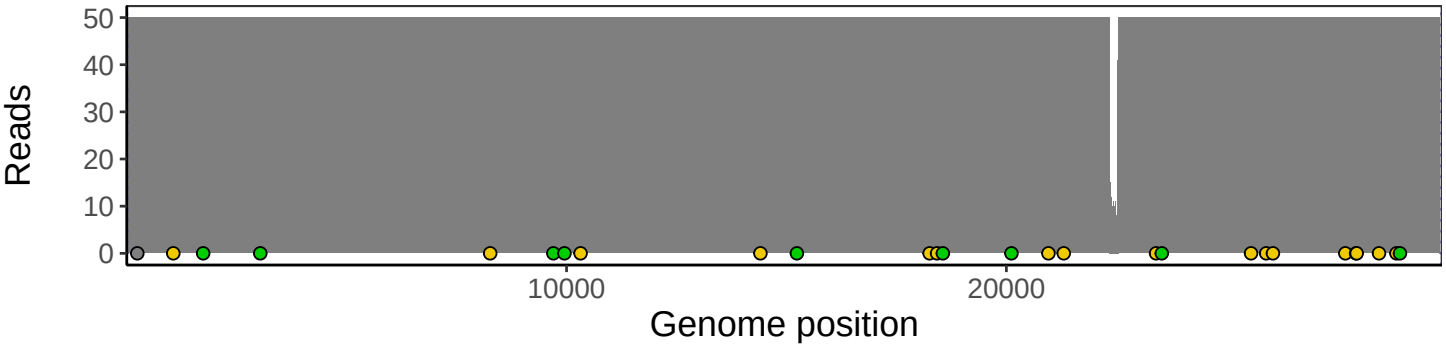
Analyses of individual experiments and composite results

VSP1704-1 | 2021-03-29 | NA | UPHS-0579 | genomes | single experiment

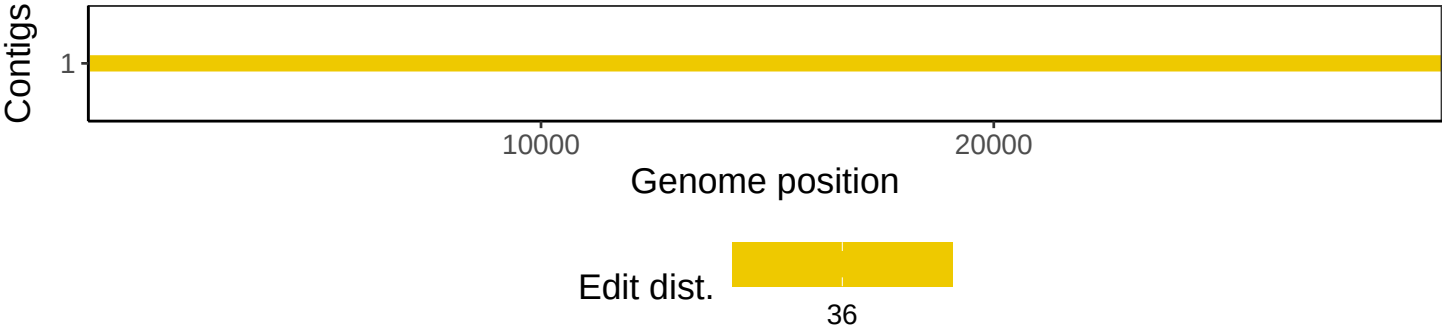
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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