COVID-19 subject UPHS-0499

2021-06-01

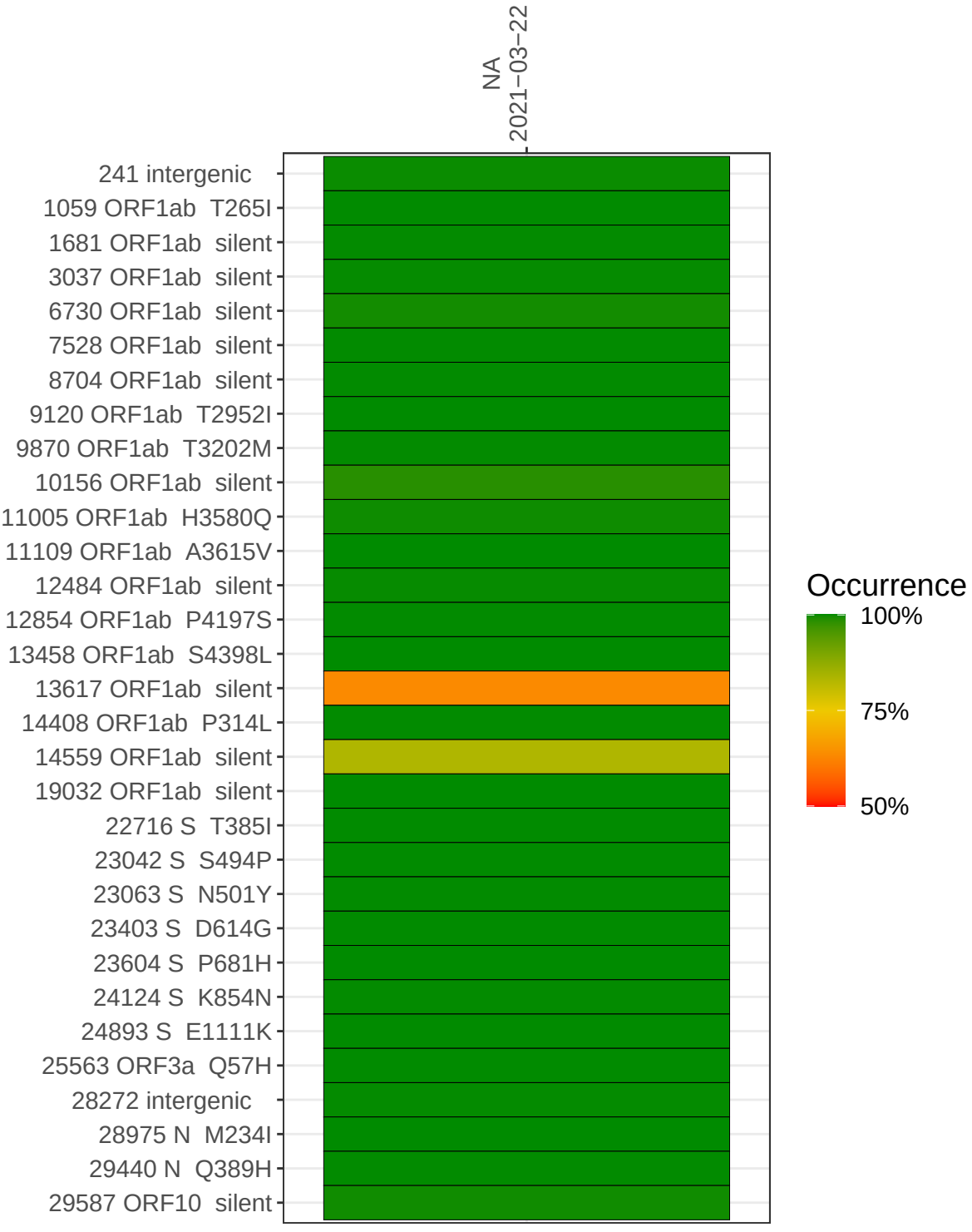
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

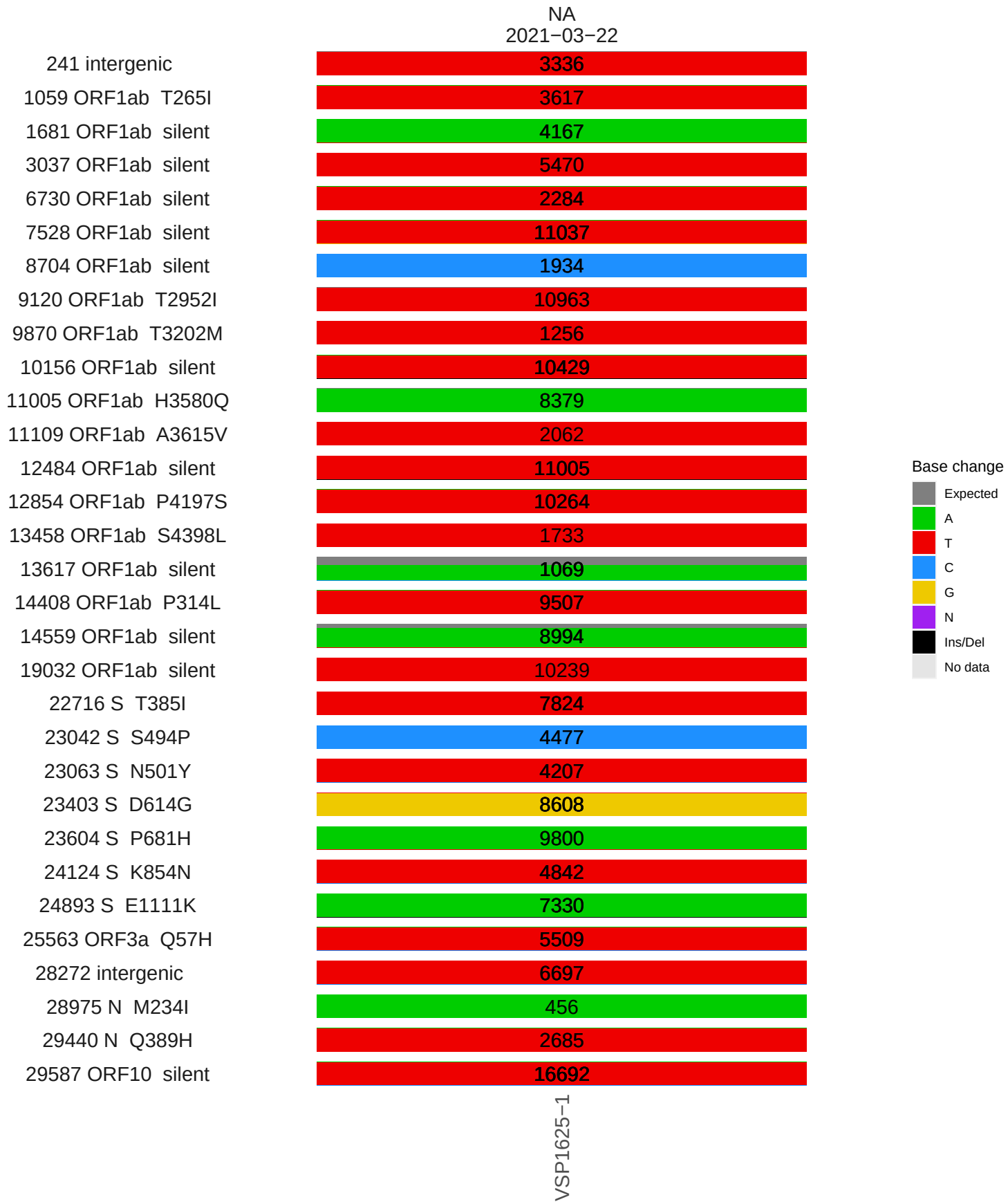
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1625-1	single experiment	NA	NA	2021-03-22	29.85	B.1.236	99.7%	99.6%

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.

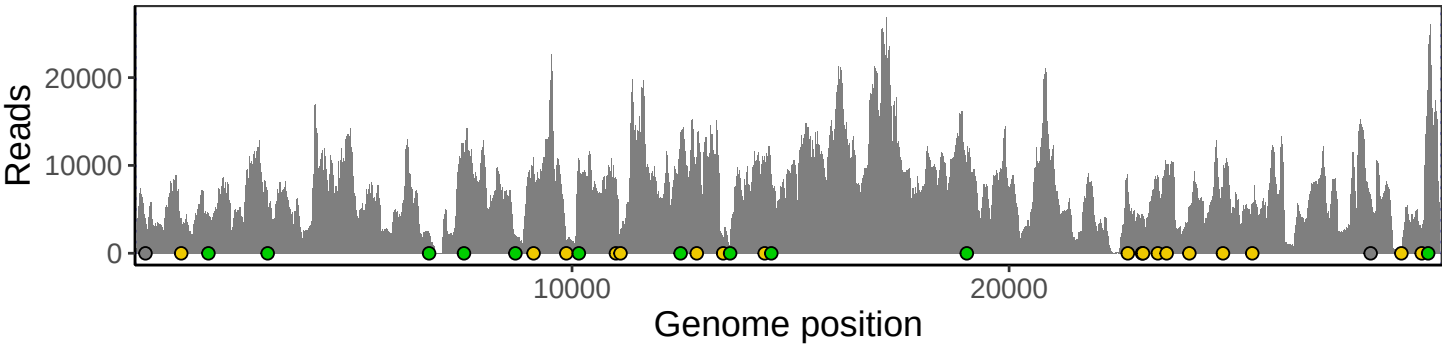



NA
2021−03−22
241 intergenic
1059 ORF1ab T265I
1681 ORF1ab silent
3037 ORF1ab silent
6730 ORF1ab silent
7528 ORF1ab silent
8704 ORF1ab silent
9120 ORF1ab T2952I
9870 ORF1ab T3202M
10156 ORF1ab silent
11005 ORF1ab H3580Q
11109 ORF1ab A3615V
12484 ORF1ab silent
12854 ORF1ab P4197S
13458 ORF1ab S4398L
13617 ORF1ab silent
14408 ORF1ab P314L
14559 ORF1ab silent
19032 ORF1ab silent
22716 S T385I
23042 S S494P
23063 S N501Y
23403 S D614G
23604 S P681H
24124 S K854N
24893 S E1111K
25563 ORF3a Q57H
28272 intergenic
28975 N M234I
29440 N Q389H
29587 ORF10 silent
3336
3617
4167
5470
2284
11037
1934
10963
1256
10429
8379
2062
11005
10264
1733
1069
9507
8994
10239
7824
4477
4207
8608
9800
4842
7330
5509
6697
456
2685
16692
VSP1625−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

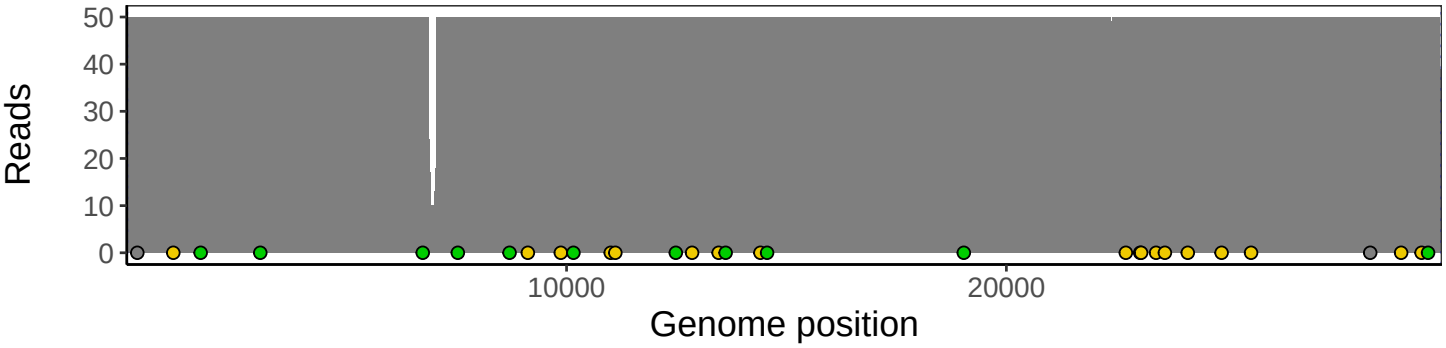
Analyses of individual experiments and composite results

VSP1625-1 | 2021-03-22 | NA | UPHS-0499 | genomes | single experiment

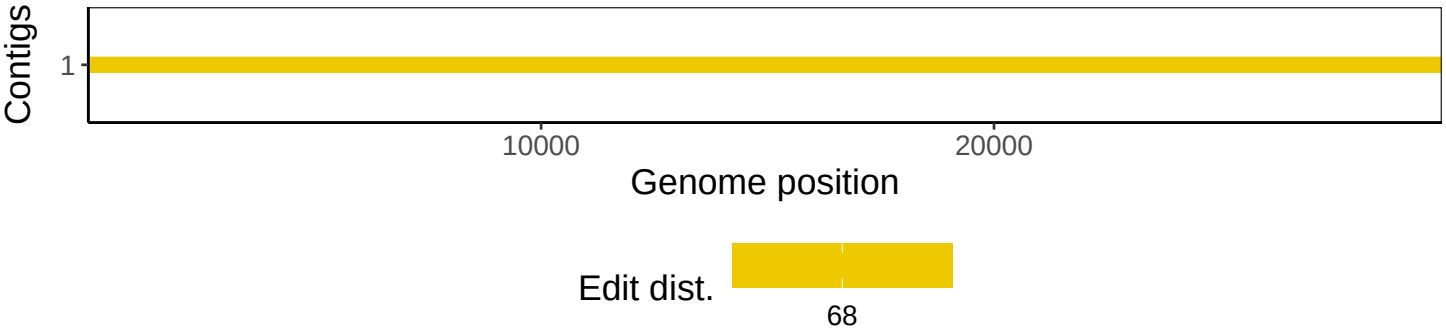
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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