COVID-19 subject UPHS-0509

2021-06-23

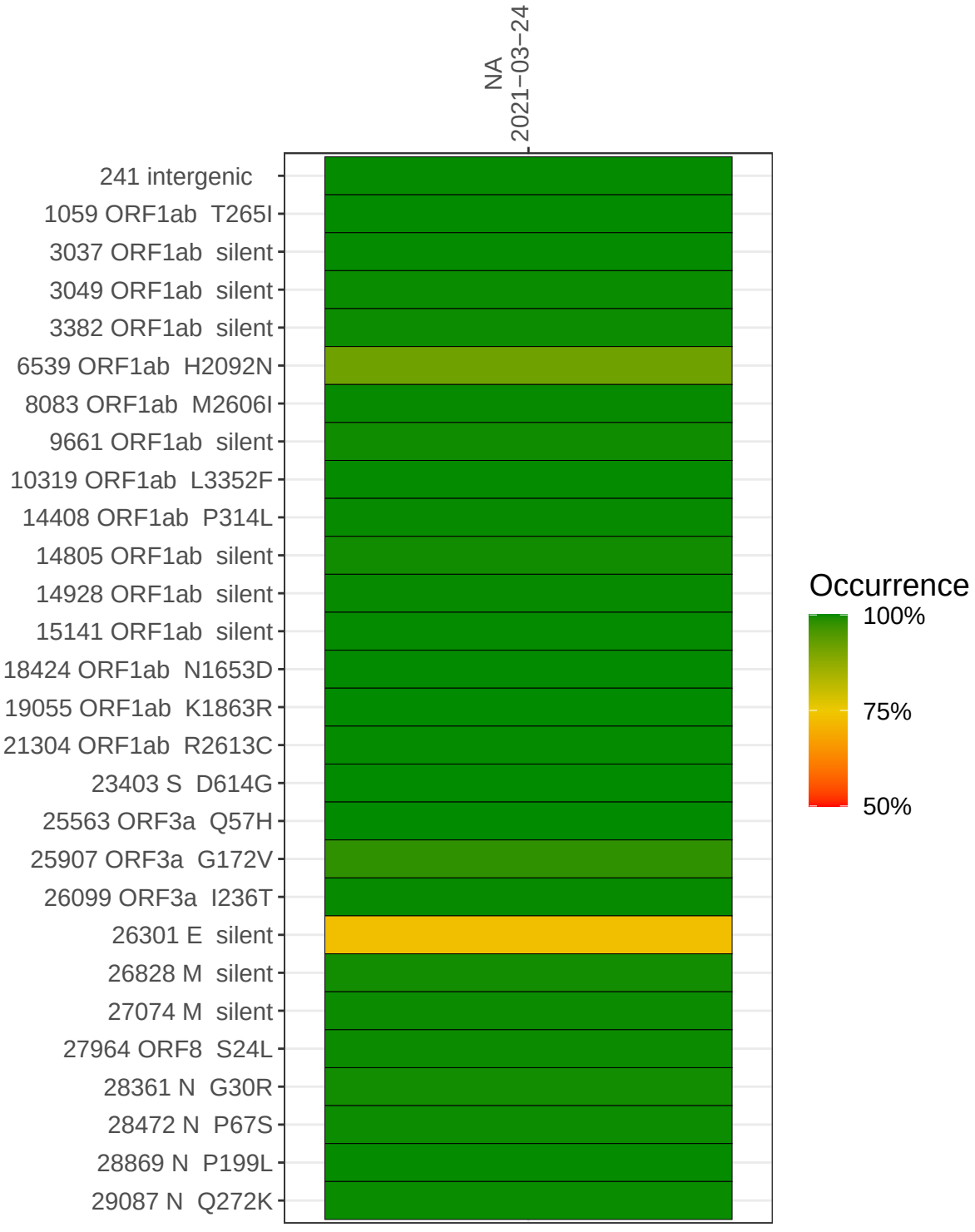
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

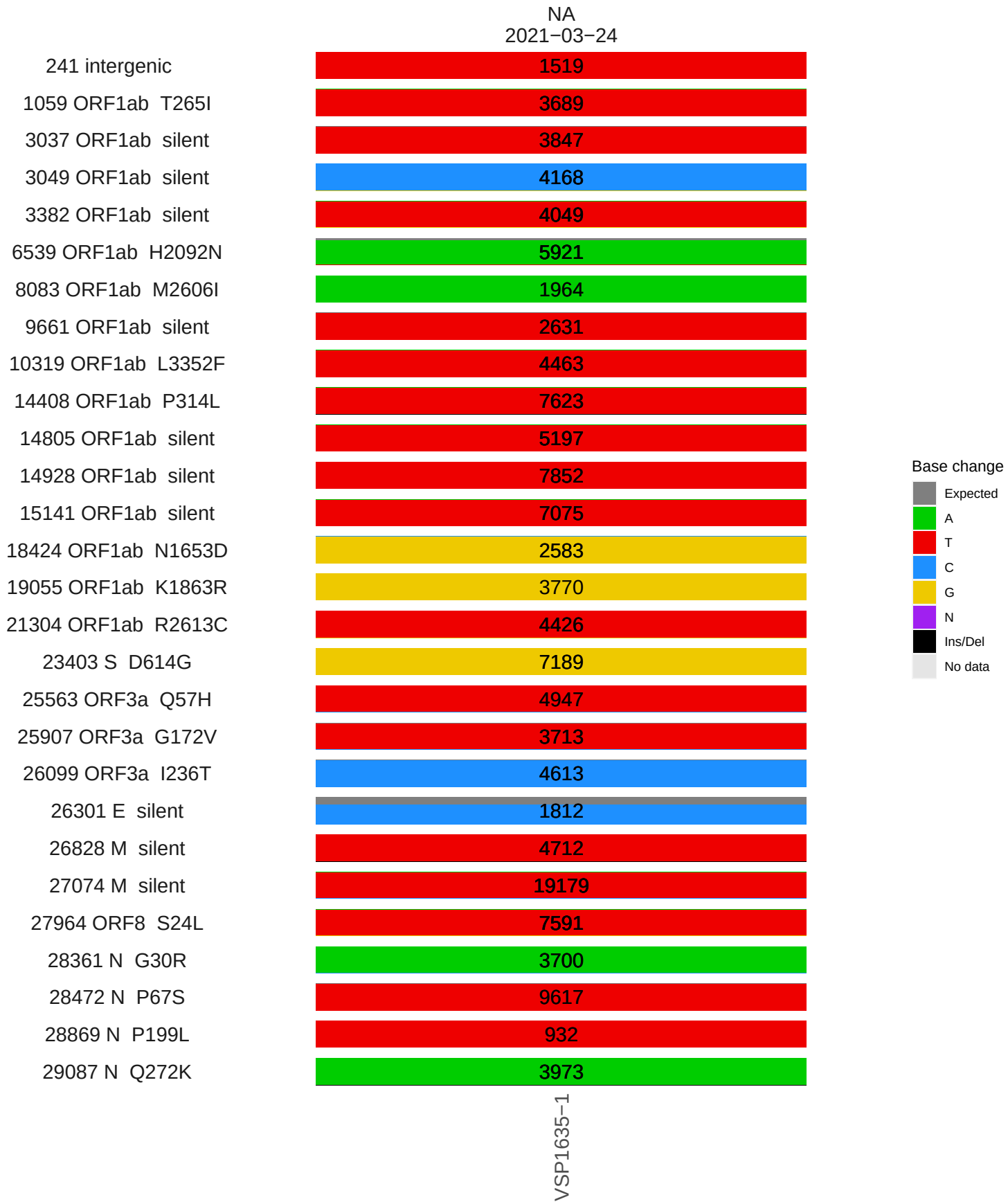
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1635-1	single experiment	NA	NA	2021-03-24	29.88	B.1.2	99.8%	99.8%

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.

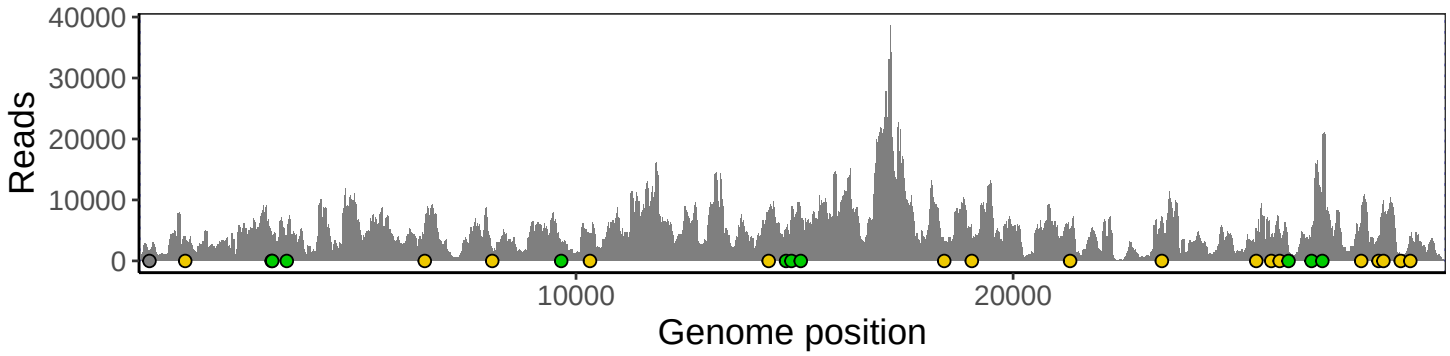



NA
2021−03−24
241 intergenic
1059 ORF1ab T265I
3037 ORF1ab silent
3049 ORF1ab silent
3382 ORF1ab silent
6539 ORF1ab H2092N
8083 ORF1ab M2606I
9661 ORF1ab silent
10319 ORF1ab L3352F
14408 ORF1ab P314L
14805 ORF1ab silent
14928 ORF1ab silent
15141 ORF1ab silent
18424 ORF1ab N1653D
19055 ORF1ab K1863R
21304 ORF1ab R2613C
23403 S D614G
25563 ORF3a Q57H
25907 ORF3a G172V
26099 ORF3a I236T
26301 E silent
26828 M silent
27074 M silent
27964 ORF8 S24L
28361 N G30R
28472 N P67S
28869 N P199L
29087 N Q272K
1519
3689
3847
4168
4049
5921
1964
2631
4463
7623
5197
7852
7075
2583
3770
4426
7189
4947
3713
4613
1812
4712
19179
7591
3700
9617
932
3973
VSP1635−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

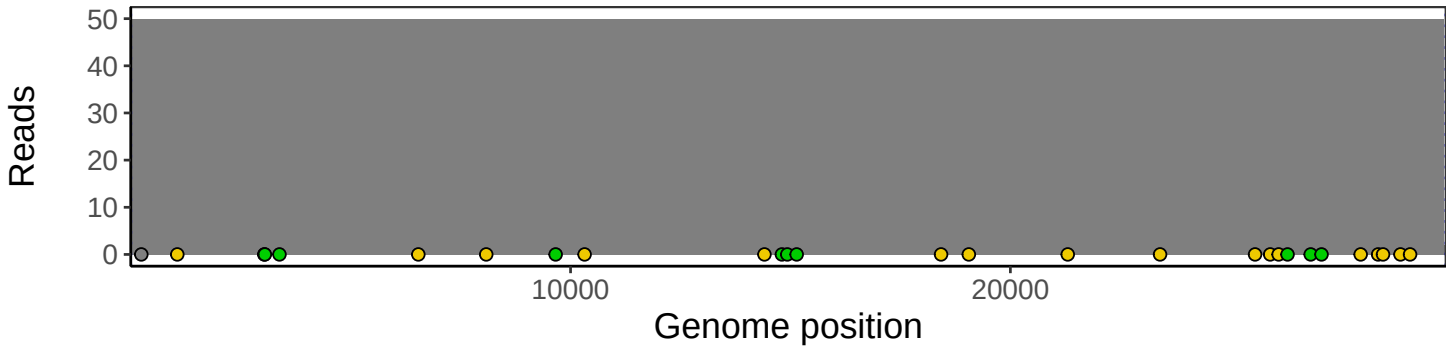
Analyses of individual experiments and composite results

VSP1635-1 | 2021-03-24 | NA | UPHS-0509 | genomes | single experiment

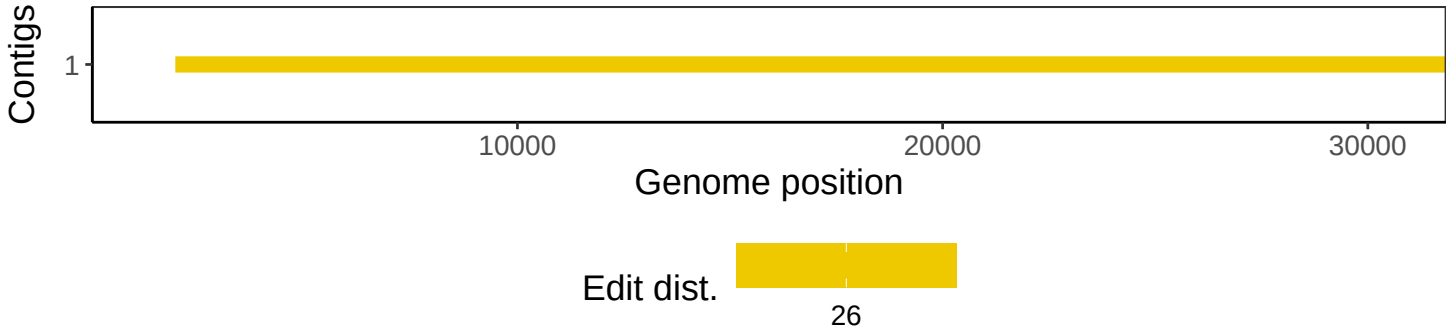
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.1.3
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	3.3.3
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