COVID-19 subject UPHS-0471

2021-06-01

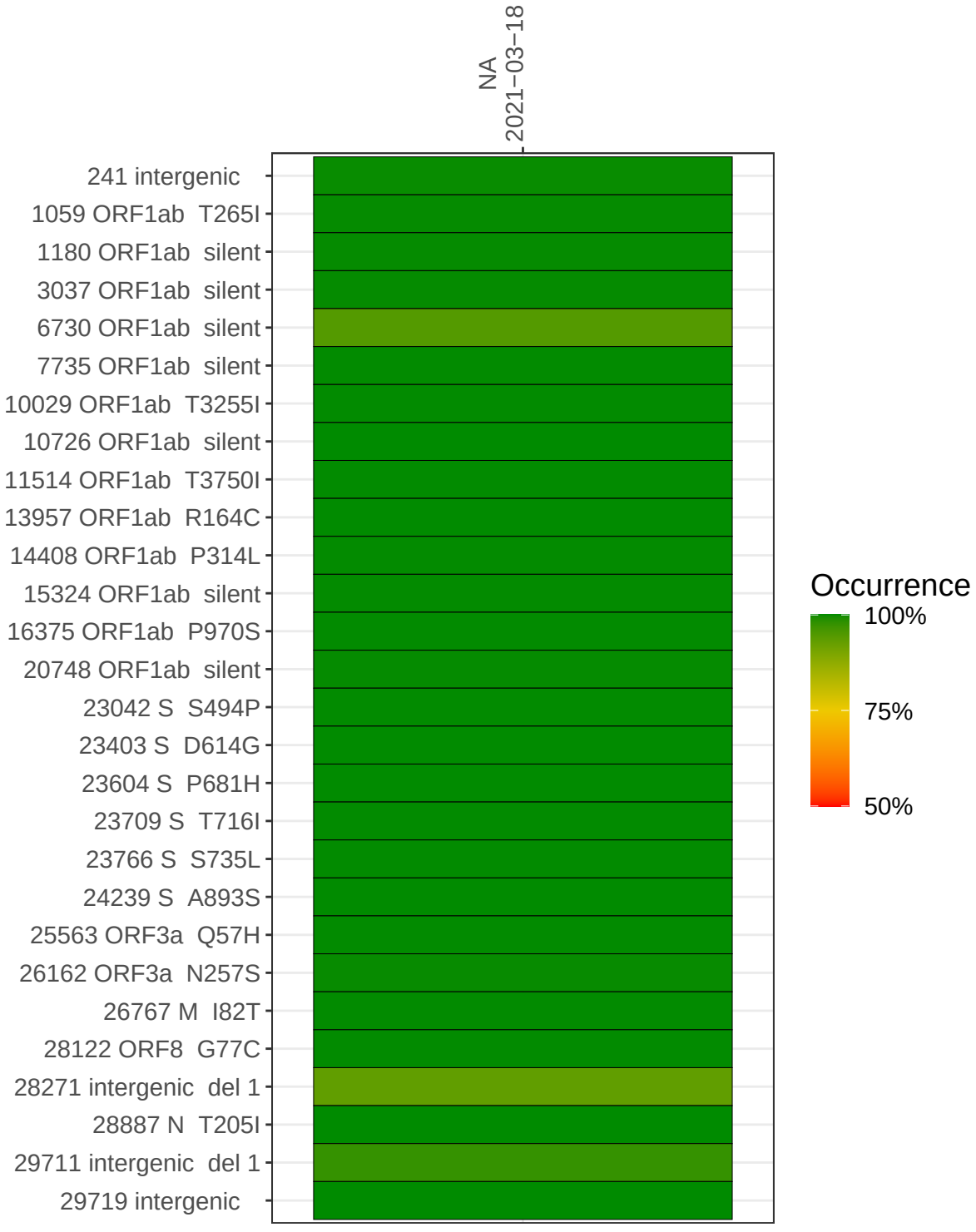
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

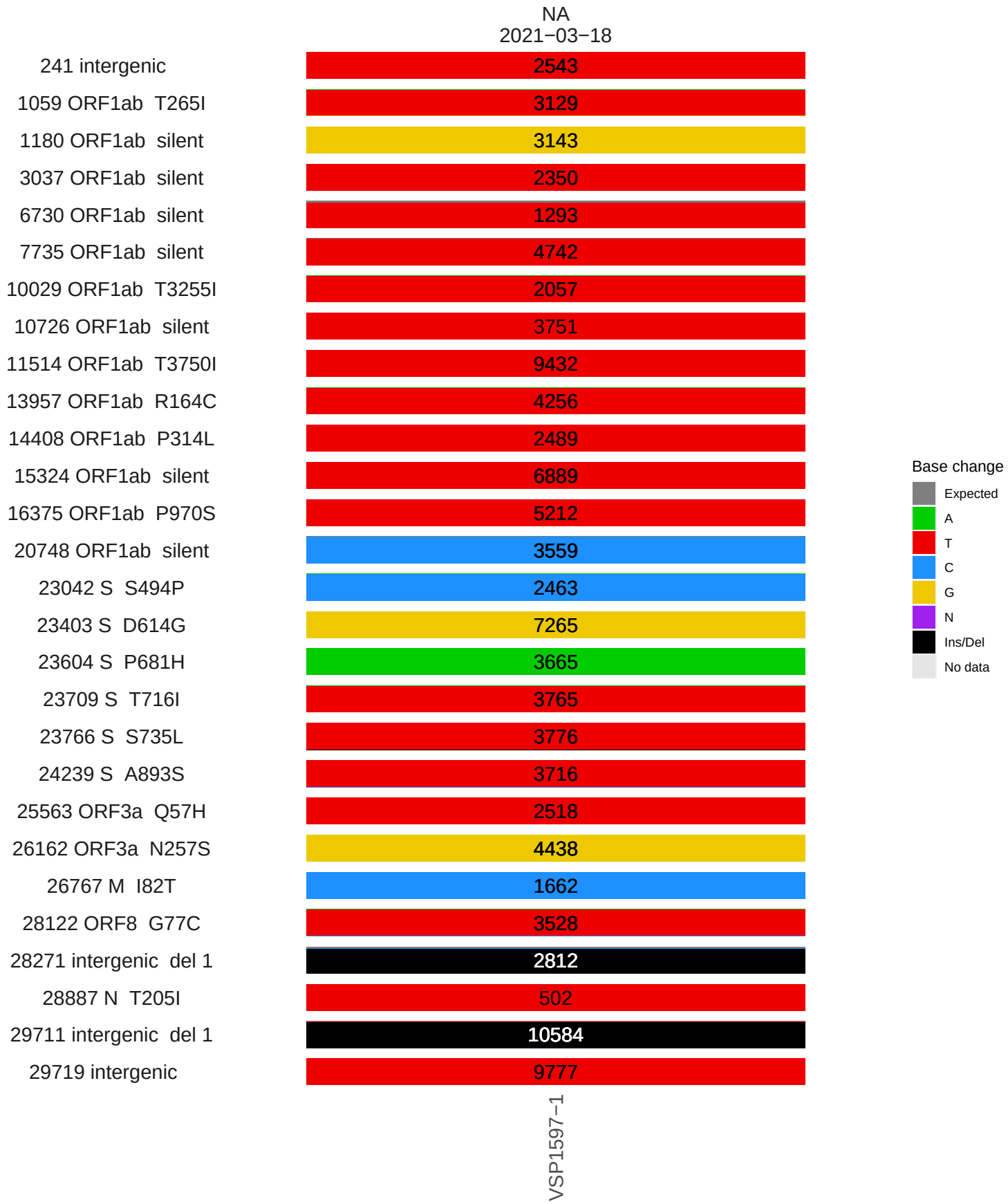
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1597-1	single experiment	NA	NA	2021-03-18	29.88	B.1.575	99.8%	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.

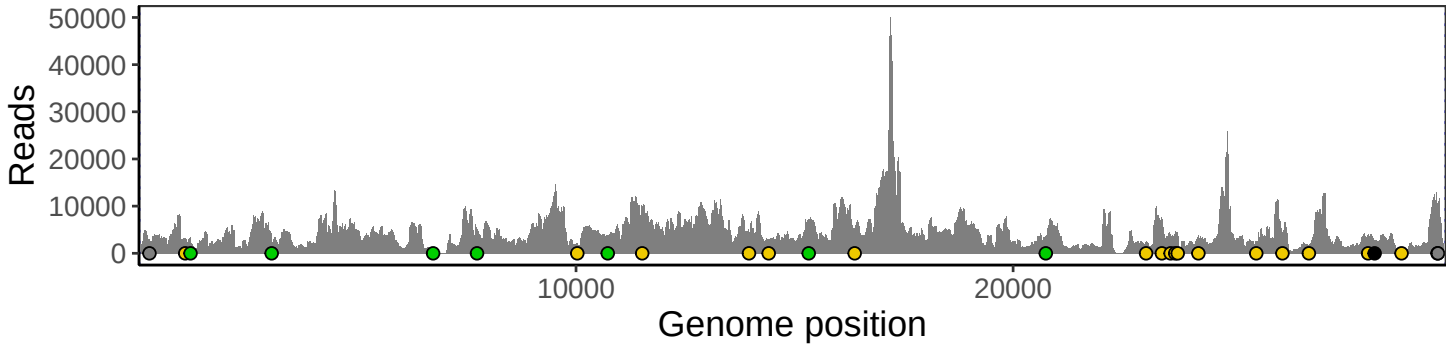



NA
2021−03−18
241 intergenic
2543
1059 ORF1ab T265I
3129
1180 ORF1ab silent
3143
3037 ORF1ab silent
2350
6730 ORF1ab silent
1293
7735 ORF1ab silent
4742
10029 ORF1ab T3255I
2057
10726 ORF1ab silent
3751
11514 ORF1ab T3750I
9432
13957 ORF1ab R164C
4256
14408 ORF1ab P314L
2489
15324 ORF1ab silent
6889
16375 ORF1ab P970S
5212
20748 ORF1ab silent
3559
23042 S S494P
2463
23403 S D614G
7265
23604 S P681H
3665
23709 S T716I
3765
23766 S S735L
3776
24239 S A893S
3716
25563 ORF3a Q57H
2518
26162 ORF3a N257S
4438
26767 M I82T
1662
28122 ORF8 G77C
3528
28271 intergenic del 1
2812
28887 N T205I
502
29711 intergenic del 1
10584
29719 intergenic
9777
VSP1597−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

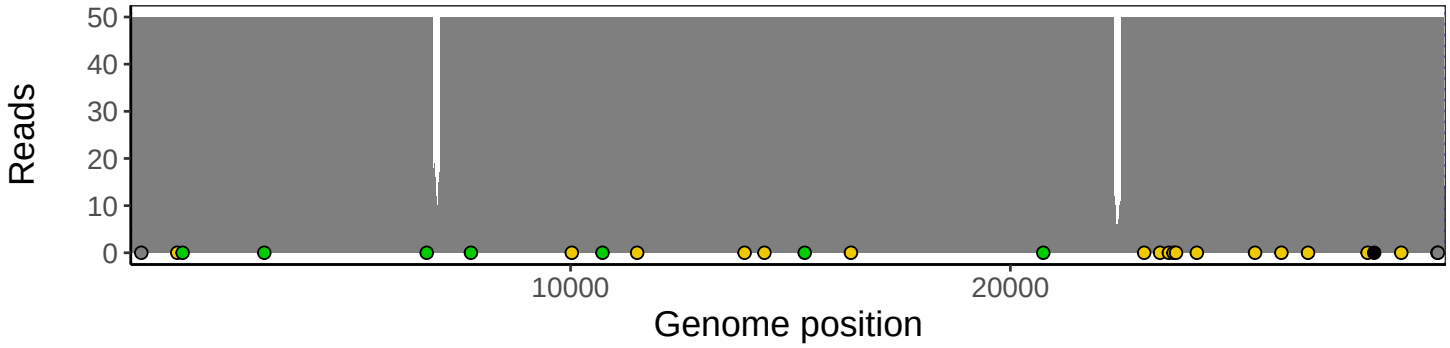
Analyses of individual experiments and composite results

VSP1597-1 | 2021-03-18 | NA | UPHS-0471 | genomes | single experiment

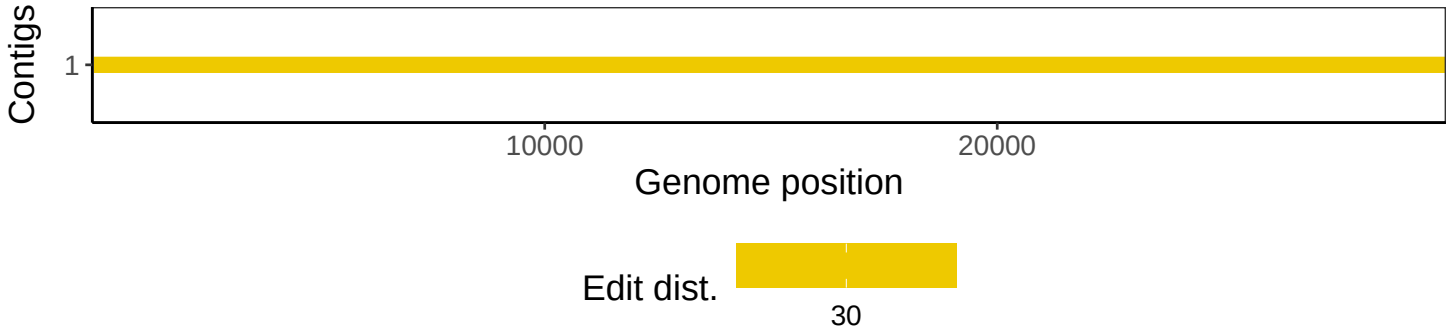
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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