COVID-19 subject UPHS-0511

2021-06-03

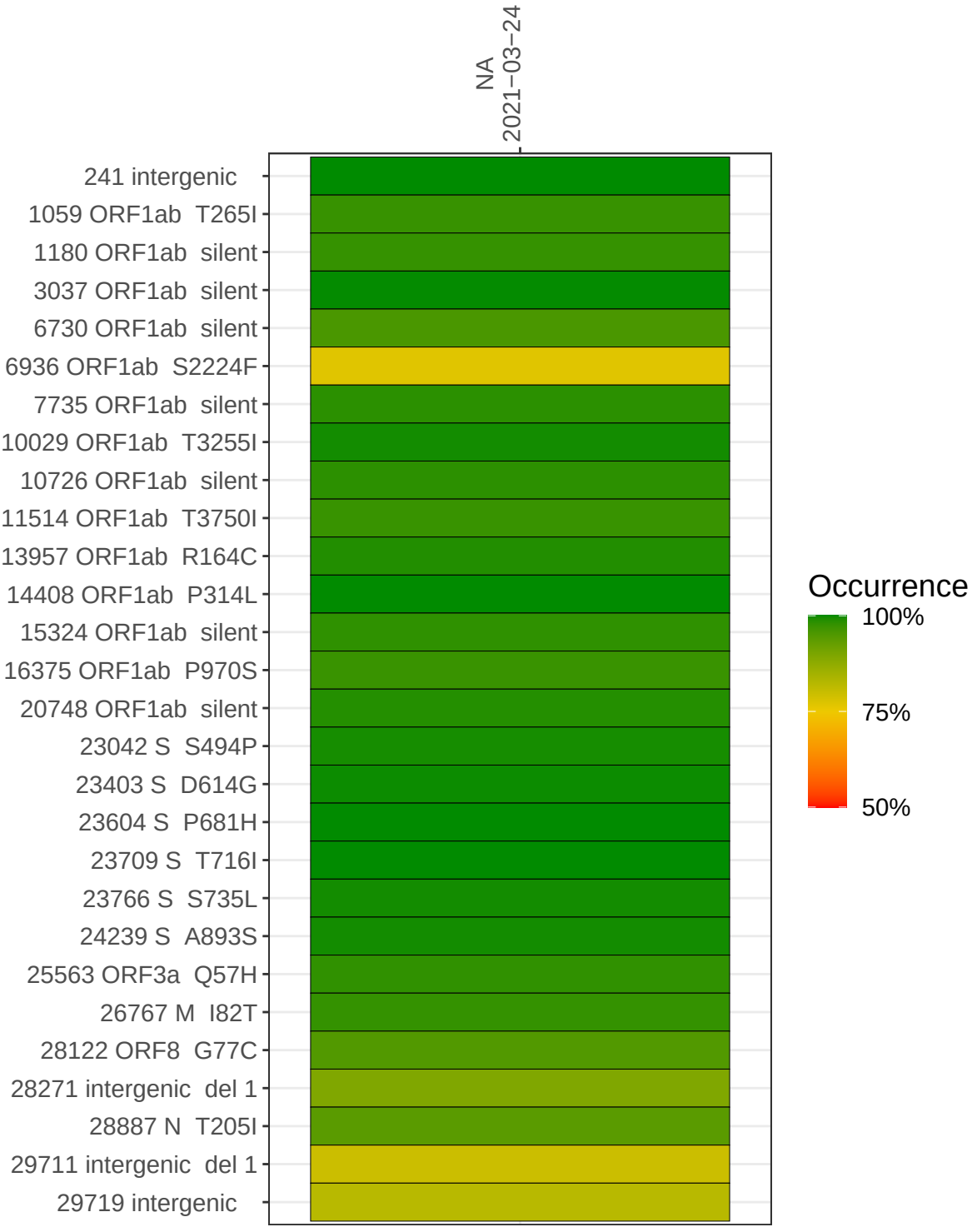
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

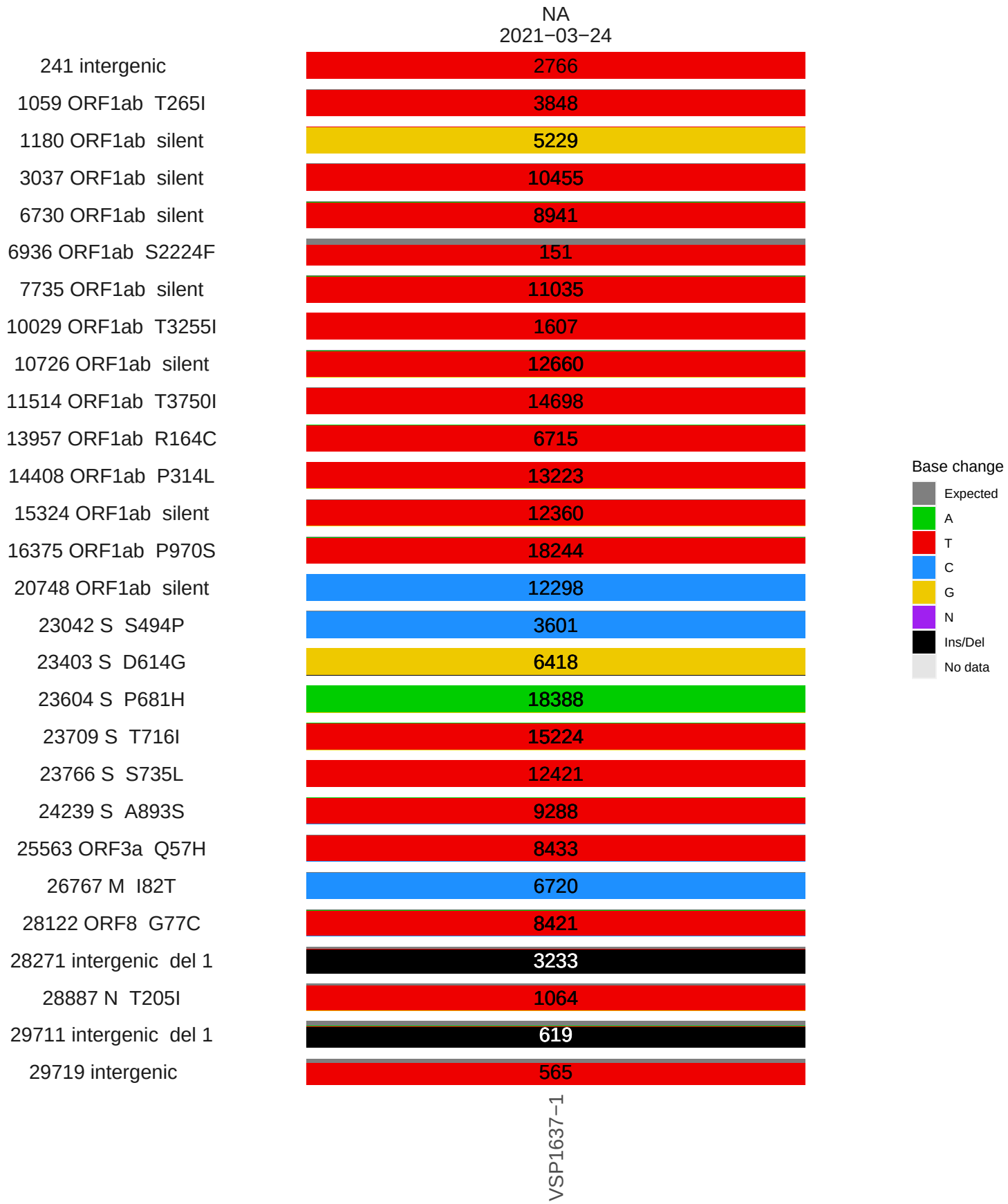
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1637-1	single experiment	NA	NA	2021-03-24	29.88	B.1.575	99.9%	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.

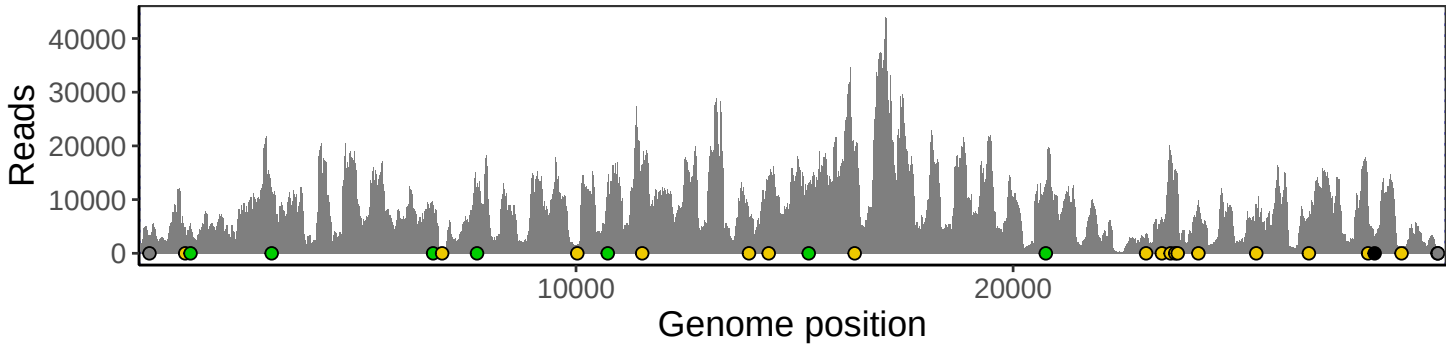



NA
2021−03−24
241 intergenic
2766
1059 ORF1ab T265I
3848
1180 ORF1ab silent
5229
3037 ORF1ab silent
10455
6730 ORF1ab silent
8941
6936 ORF1ab S2224F
151
7735 ORF1ab silent
11035
10029 ORF1ab T3255I
1607
10726 ORF1ab silent
12660
11514 ORF1ab T3750I
14698
13957 ORF1ab R164C
6715
14408 ORF1ab P314L
13223
15324 ORF1ab silent
12360
16375 ORF1ab P970S
18244
20748 ORF1ab silent
12298
23042 S S494P
3601
23403 S D614G
6418
23604 S P681H
18388
23709 S T716I
15224
23766 S S735L
12421
24239 S A893S
9288
25563 ORF3a Q57H
8433
26767 M I82T
6720
28122 ORF8 G77C
8421
28271 intergenic del 1
3233
28887 N T205I
1064
29711 intergenic del 1
619
29719 intergenic
565
VSP1637−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

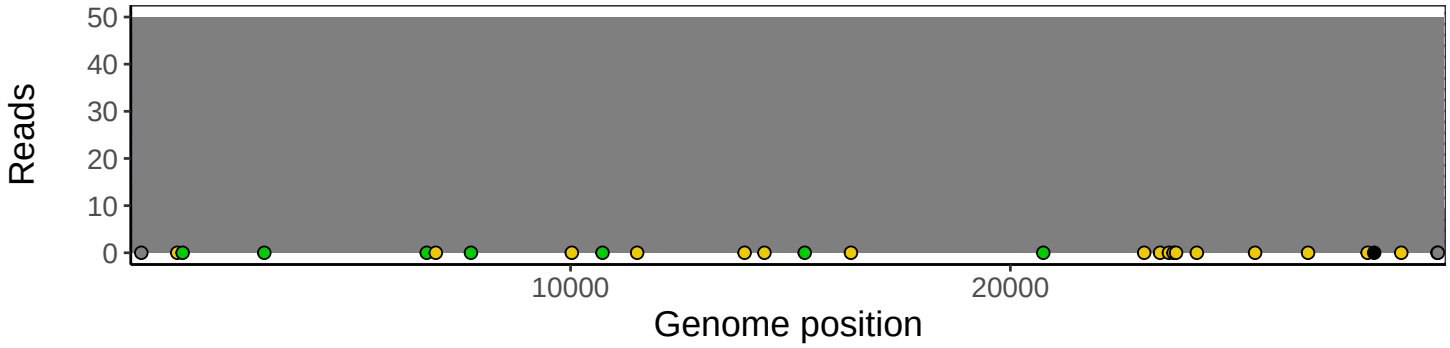
Analyses of individual experiments and composite results

VSP1637-1 | 2021-03-24 | NA | UPHS-0511 | genomes | single experiment

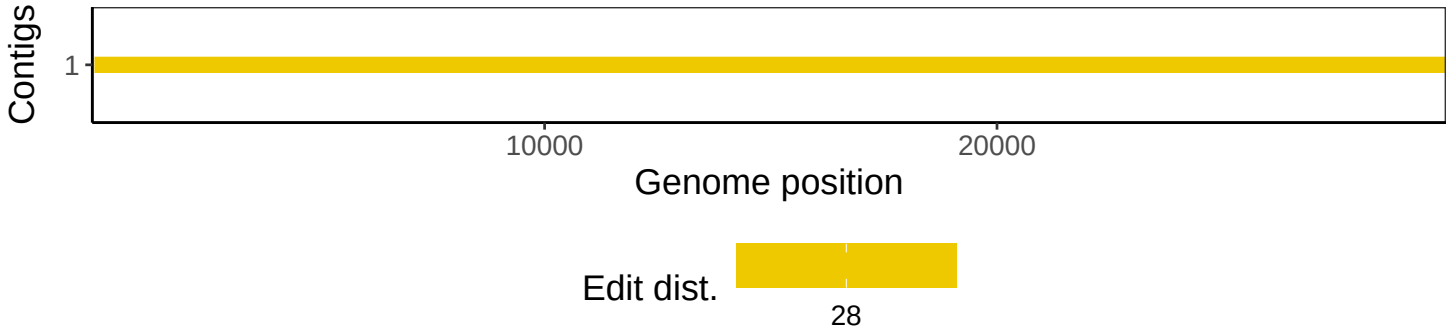
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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