COVID-19 subject UPHS-0404

2021-06-23

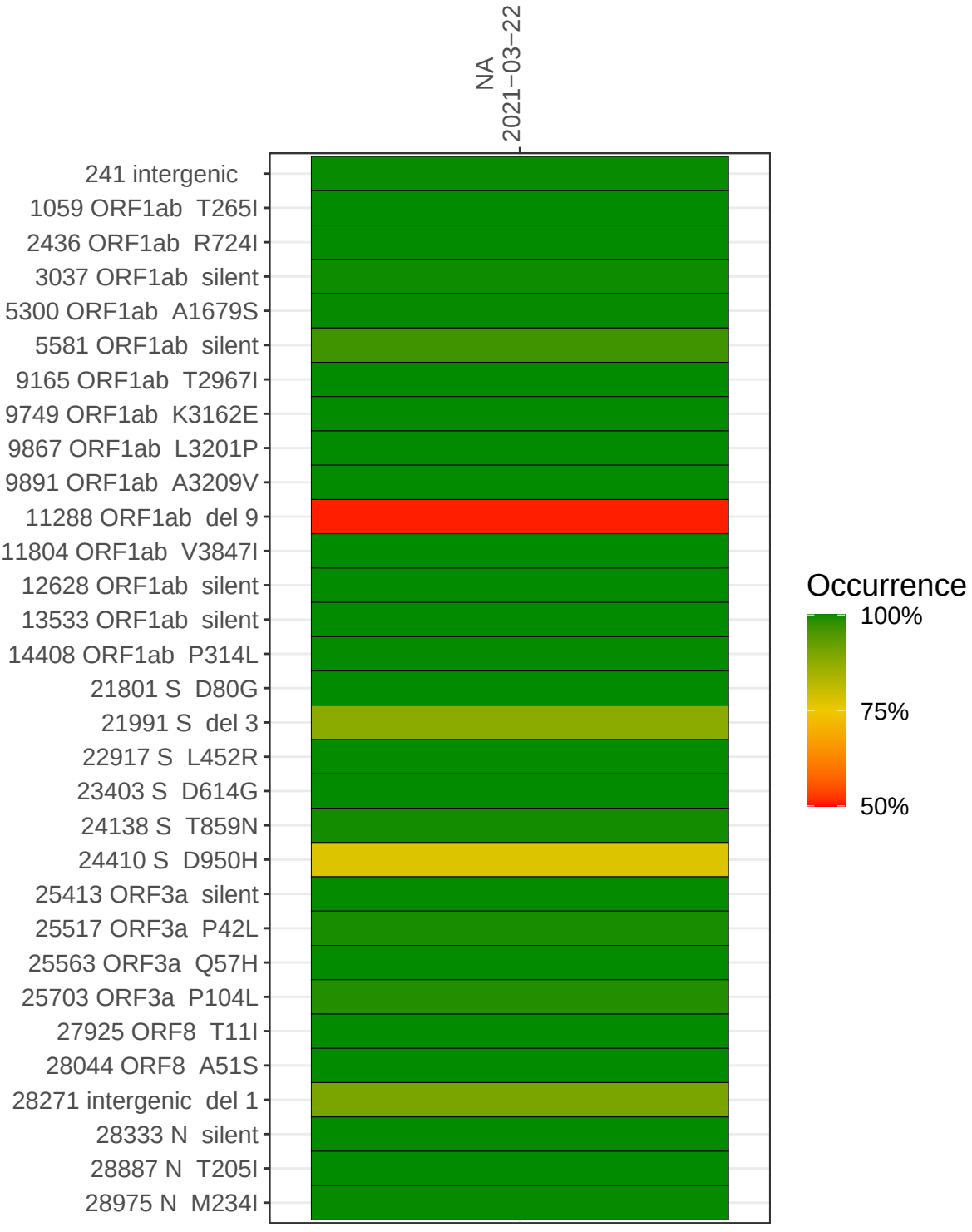
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

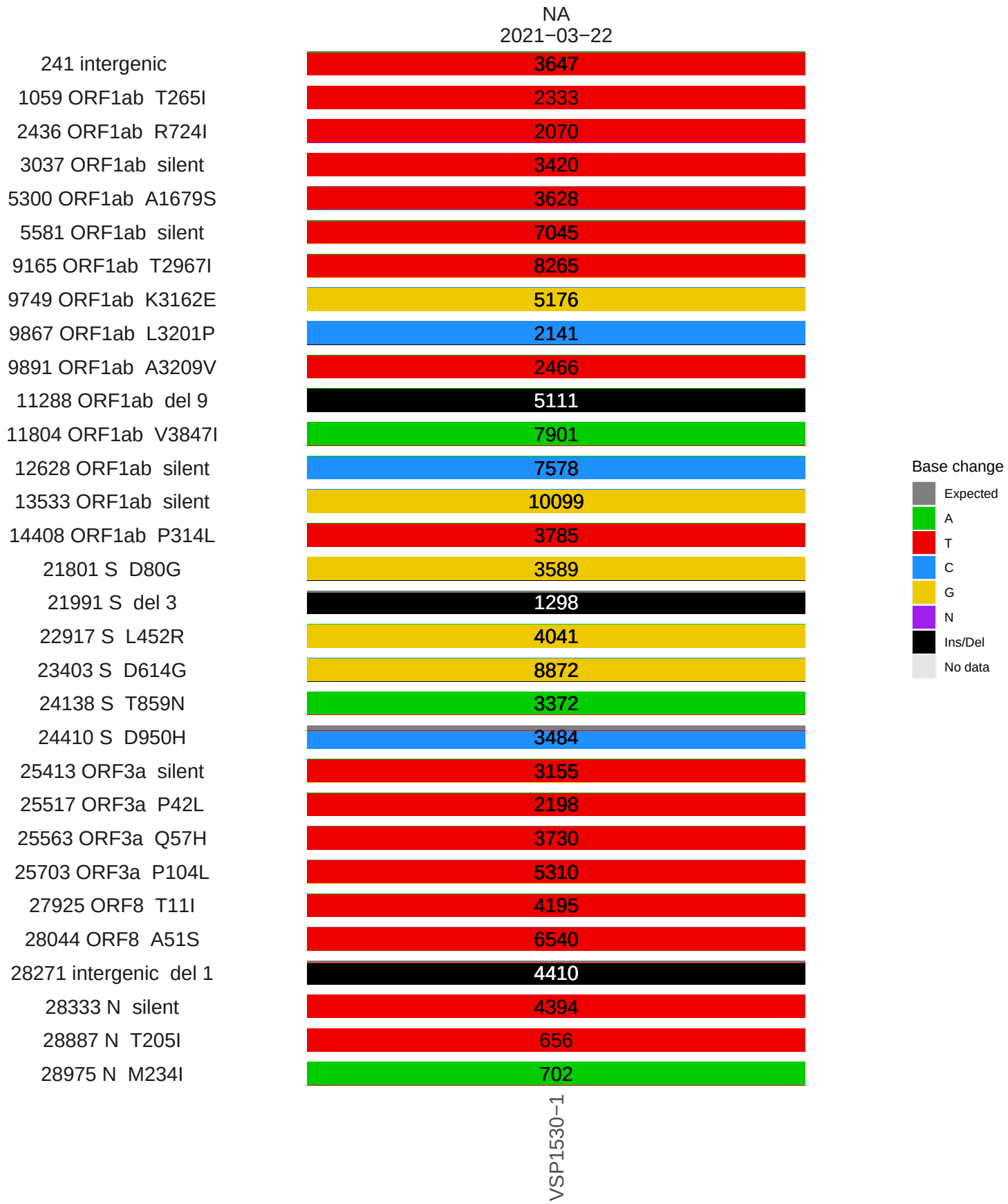
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1530-1	single experiment	NA	NA	2021-03-22	29.92	B.1.526	99.9%	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.

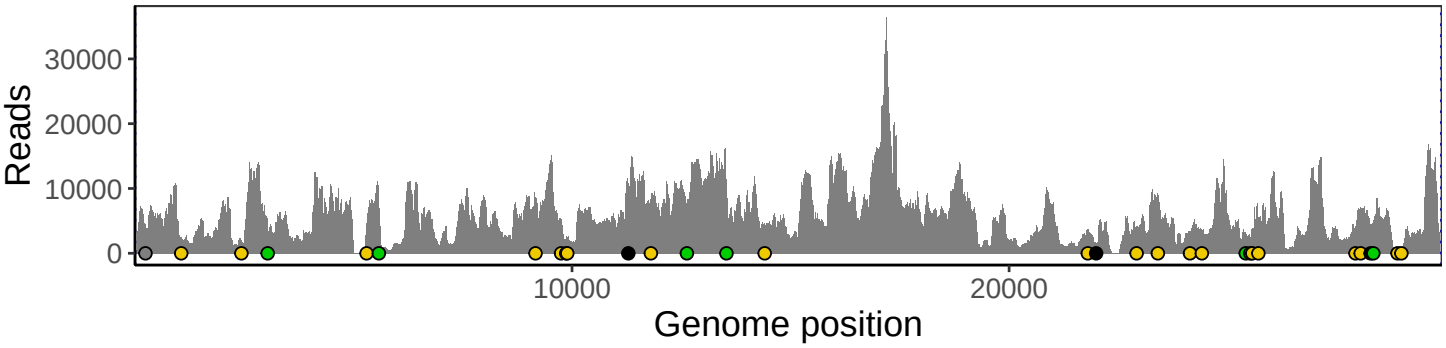



NA
2021−03−22
241 intergenic
1059 ORF1ab T265I
2436 ORF1ab R724I
3037 ORF1ab silent
5300 ORF1ab A1679S
5581 ORF1ab silent
9165 ORF1ab T2967I
9749 ORF1ab K3162E
9867 ORF1ab L3201P
9891 ORF1ab A3209V
11288 ORF1ab del 9
11804 ORF1ab V3847I
12628 ORF1ab silent
13533 ORF1ab silent
14408 ORF1ab P314L
21801 S D80G
21991 S del 3
22917 S L452R
23403 S D614G
24138 S T859N
24410 S D950H
25413 ORF3a silent
25517 ORF3a P42L
25563 ORF3a Q57H
25703 ORF3a P104L
27925 ORF8 T11I
28044 ORF8 A51S
28271 intergenic del 1
28333 N silent
28887 N T205I
28975 N M234I
3647
2333
2070
3420
3628
7045
8265
5176
2141
2466
5111
7901
7578
10099
3785
3589
1298
4041
8872
3372
3484
3155
2198
3730
5310
4195
6540
4410
4394
656
702
VSP1530−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

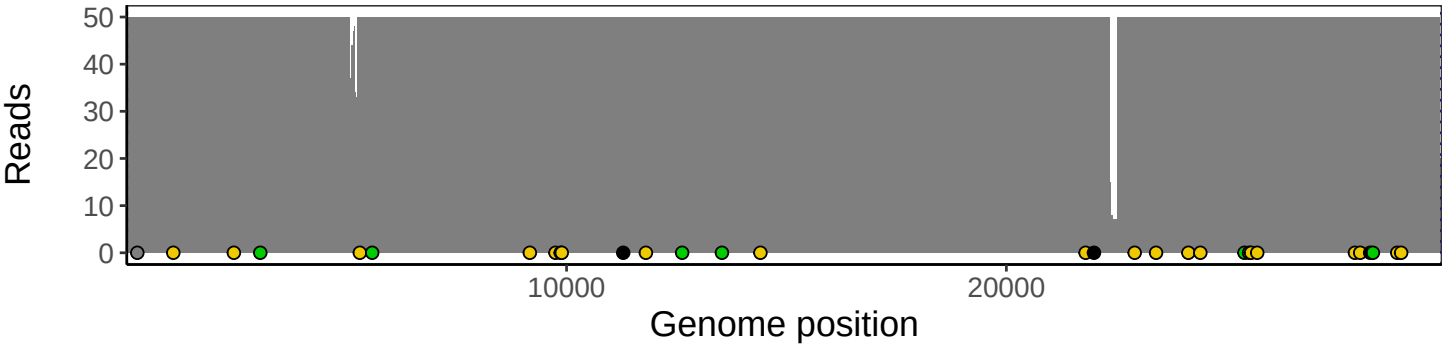
Analyses of individual experiments and composite results

VSP1530-1 | 2021-03-22 | NA | UPHS-0404 | genomes | single experiment

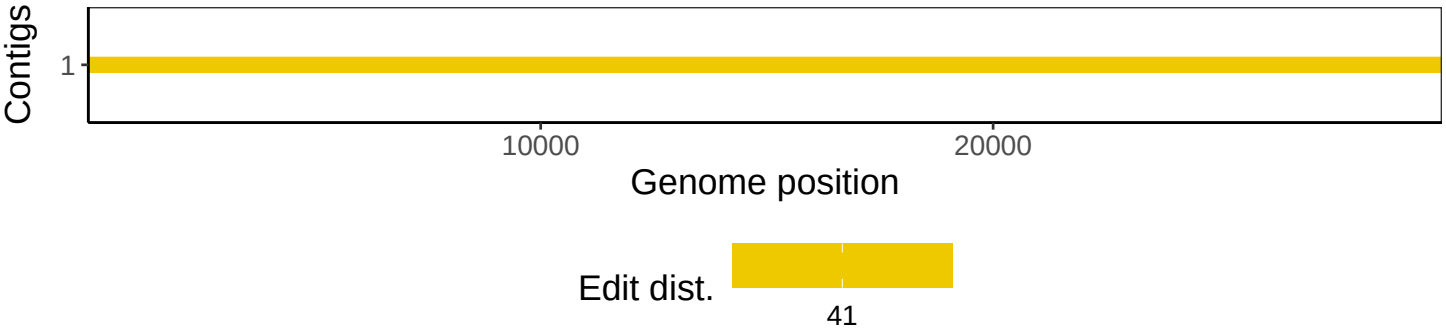
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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