

# COVID-19 subject UPHS-0510

*2021-06-23*

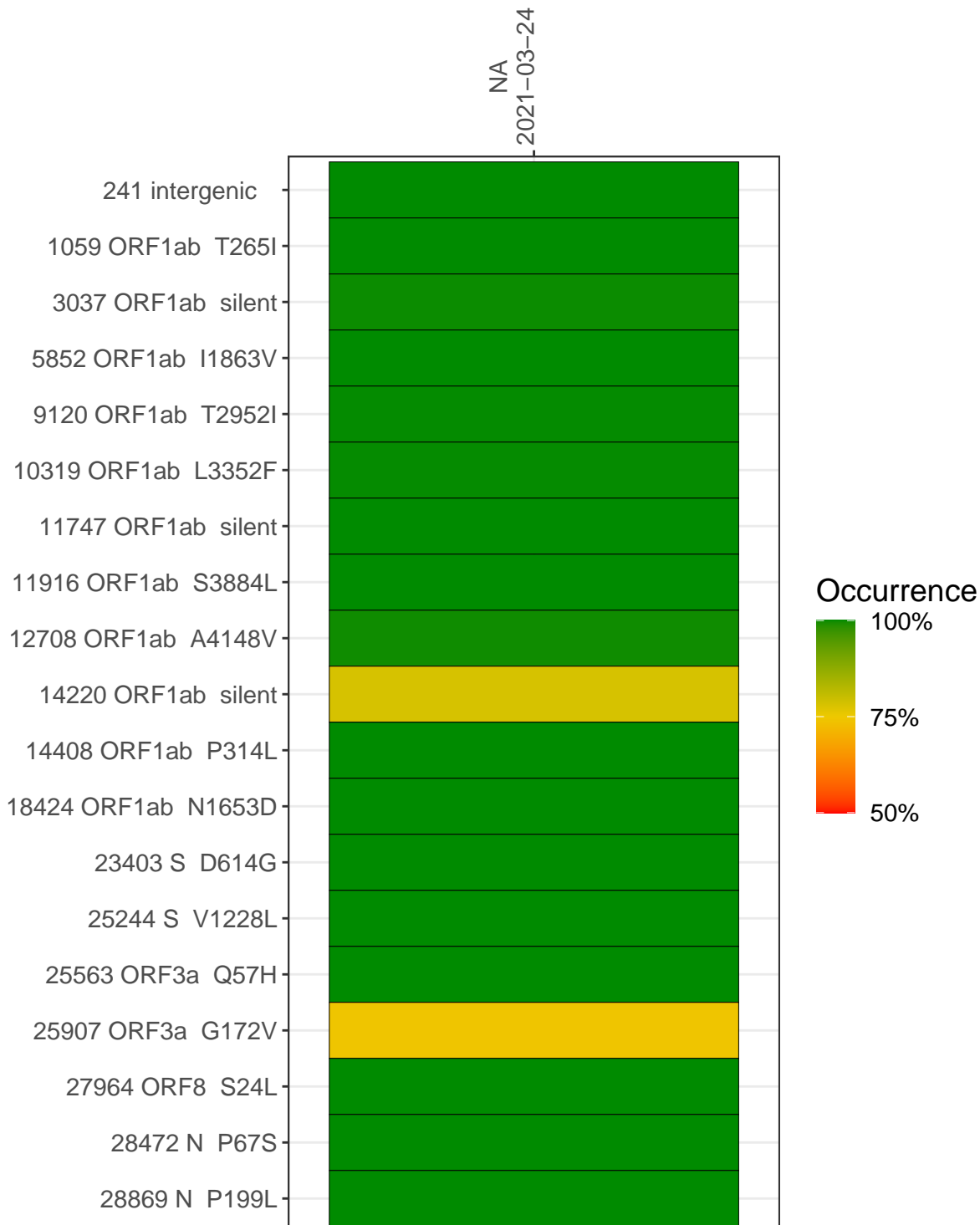
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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 ( $\geq 5$ reads)
VSP1636-1	single experiment	NA	NA	2021-03-24	29.87	B.1.596	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  
2021-03-24

241 intergenic	325
1059 ORF1ab T265I	536
3037 ORF1ab silent	389
5852 ORF1ab I1863V	590
9120 ORF1ab T2952I	1060
10319 ORF1ab L3352F	822
11747 ORF1ab silent	1700
11916 ORF1ab S3884L	661
12708 ORF1ab A4148V	524
14220 ORF1ab silent	454
14408 ORF1ab P314L	187
18424 ORF1ab N1653D	386
23403 S D614G	2110
25244 S V1228L	466
25563 ORF3a Q57H	394
25907 ORF3a G172V	450
27964 ORF8 S24L	414
28472 N P67S	527
28869 N P199L	106

Base change

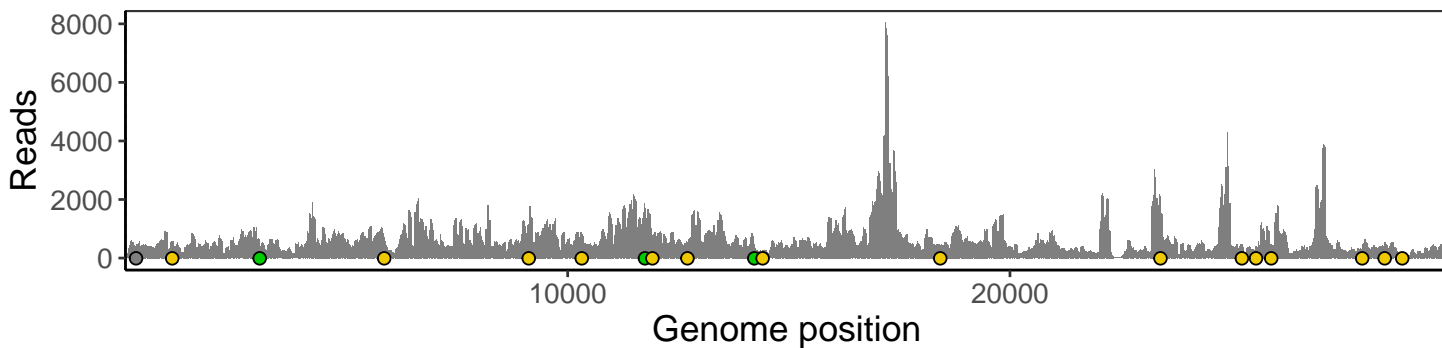
- Expected
- A
- T
- C
- G
- N
- Ins/Del
- No data

VSP1636-1

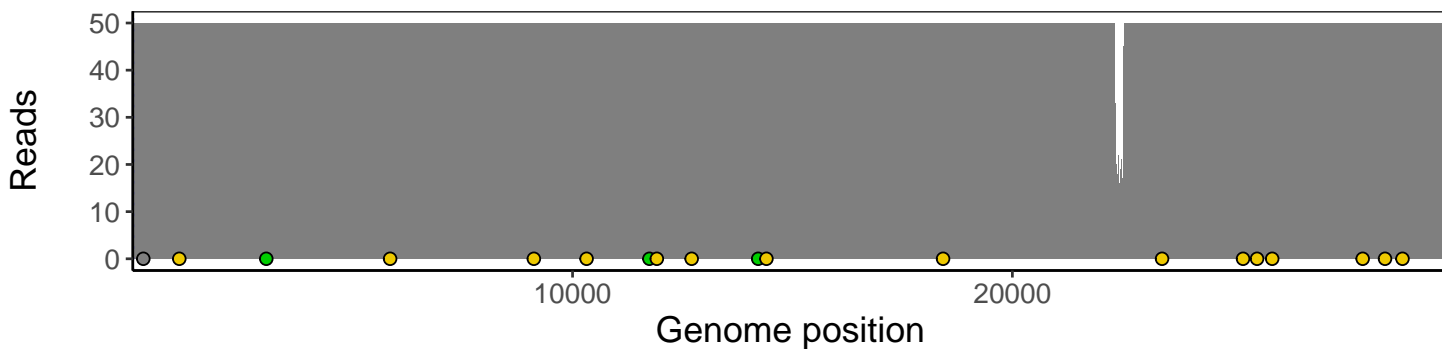
## Analyses of individual experiments and composite results

VSP1636-1 | 2021-03-24 | NA | UPHS-0510 | genomes | single experiment

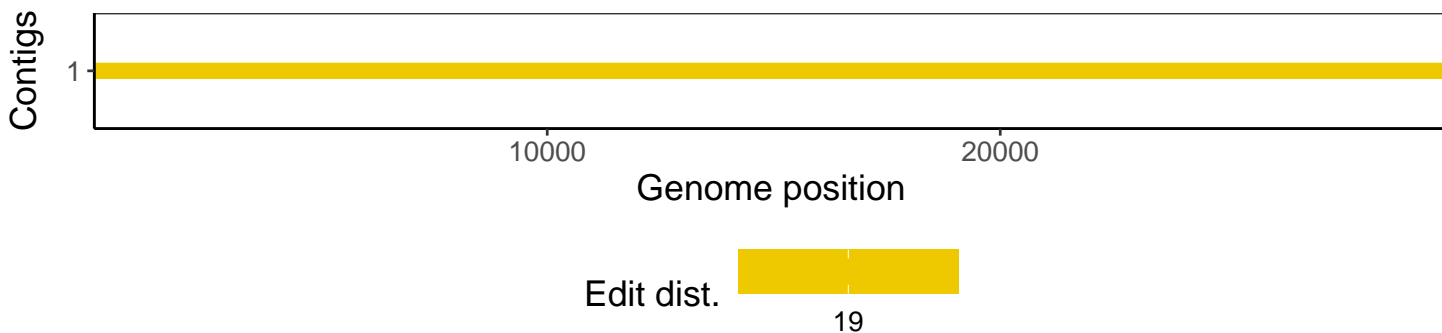
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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 htlib 1.10
bcftools	1.10.2-34-g1a12af0-dirty Using htlib 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