

# COVID-19 subject UPHS-0553

*2021-06-03*

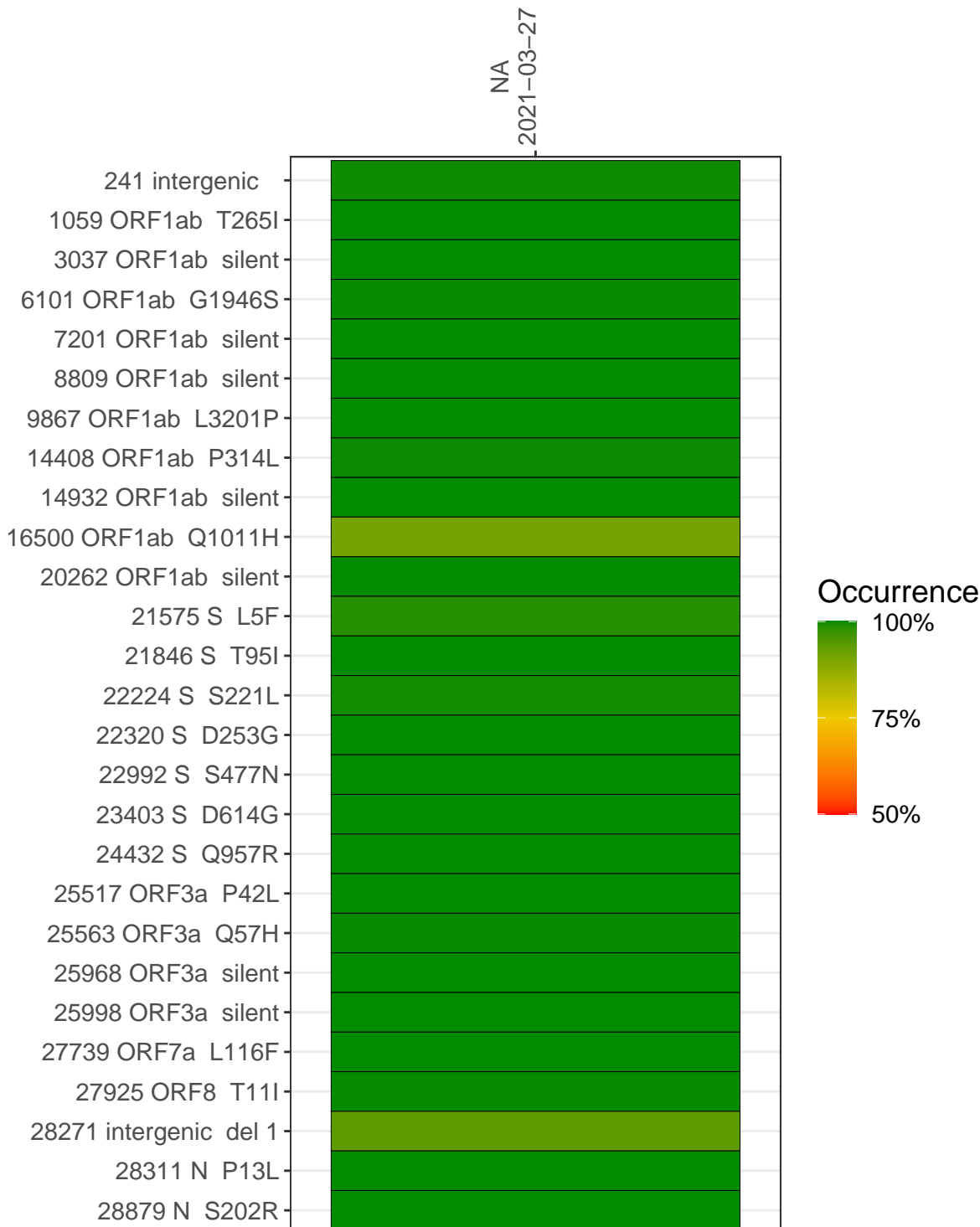
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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 ( $\geq 5$ reads)
VSP1679-1	single experiment	NA	NA	2021-03-27	29.78	B.1.526.2	99.7%	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 2021-03-27	
241 intergenic	320	
1059 ORF1ab T265I	2764	
3037 ORF1ab silent	2236	
6101 ORF1ab G1946S	2075	
7201 ORF1ab silent	394	
8809 ORF1ab silent	494	
9867 ORF1ab L3201P	960	
14408 ORF1ab P314L	1517	
14932 ORF1ab silent	2628	
16500 ORF1ab Q1011H	2491	
20262 ORF1ab silent	489	
21575 S L5F	492	
21846 S T95I	1855	
22224 S S221L	3969	
22320 S D253G	285	
22992 S S477N	176	
23403 S D614G	4254	
24432 S Q957R	932	
25517 ORF3a P42L	1336	
25563 ORF3a Q57H	2496	
25968 ORF3a silent	1874	
25998 ORF3a silent	4619	
27739 ORF7a L116F	883	
27925 ORF8 T11I	1845	
28271 intergenic del 1	1271	
28311 N P13L	1318	
28879 N S202R	253	
	VSP1679-1	

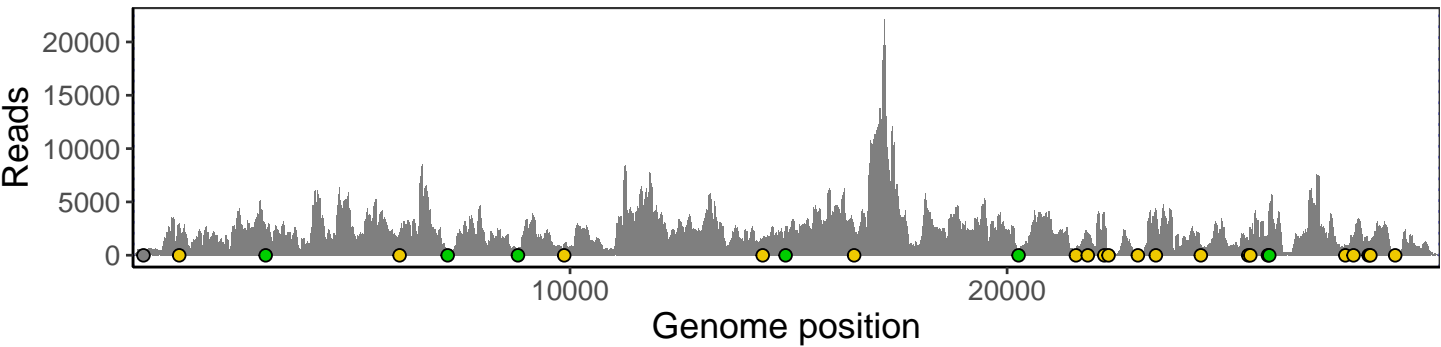
Base change

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

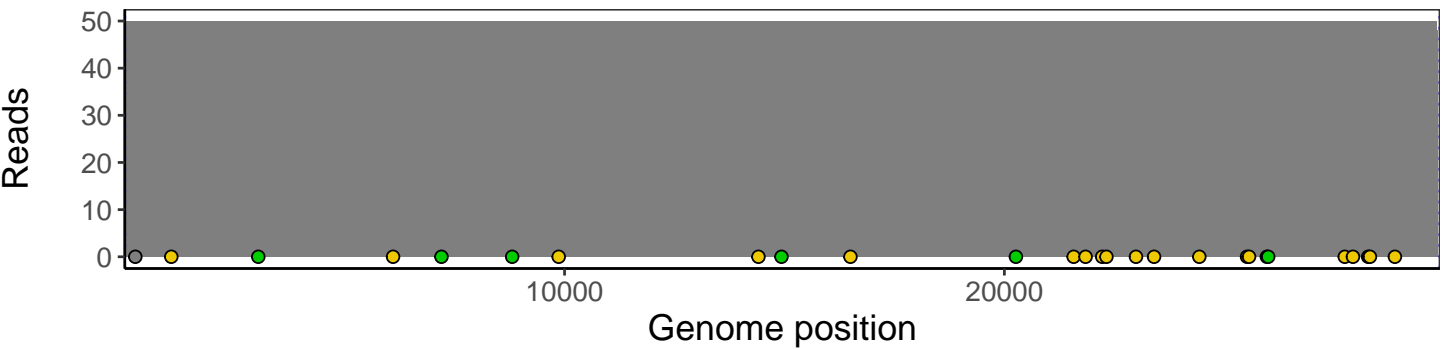
# Analyses of individual experiments and composite results

VSP1679-1 | 2021-03-27 | NA | UPHS-0553 | genomes | single experiment

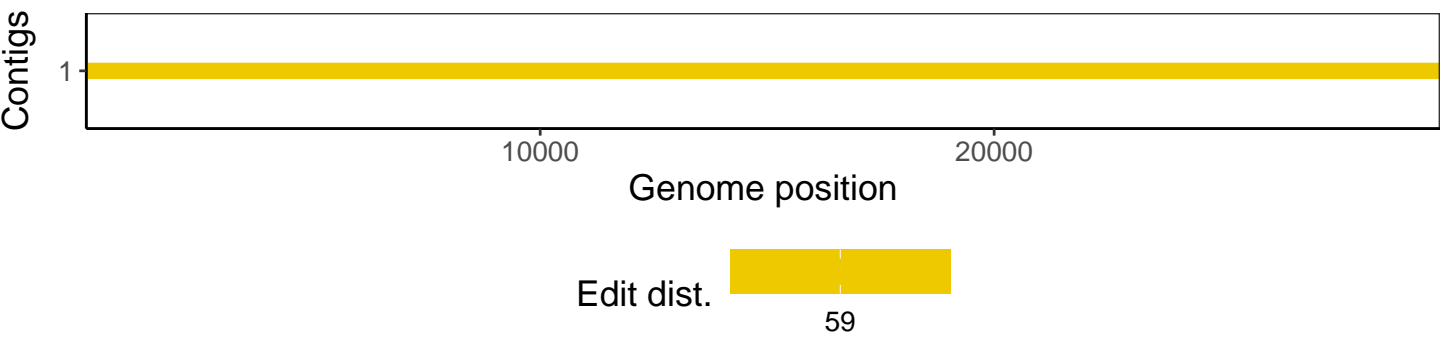
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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