# COVID-19 subject UPHS-0008

2021-05-05

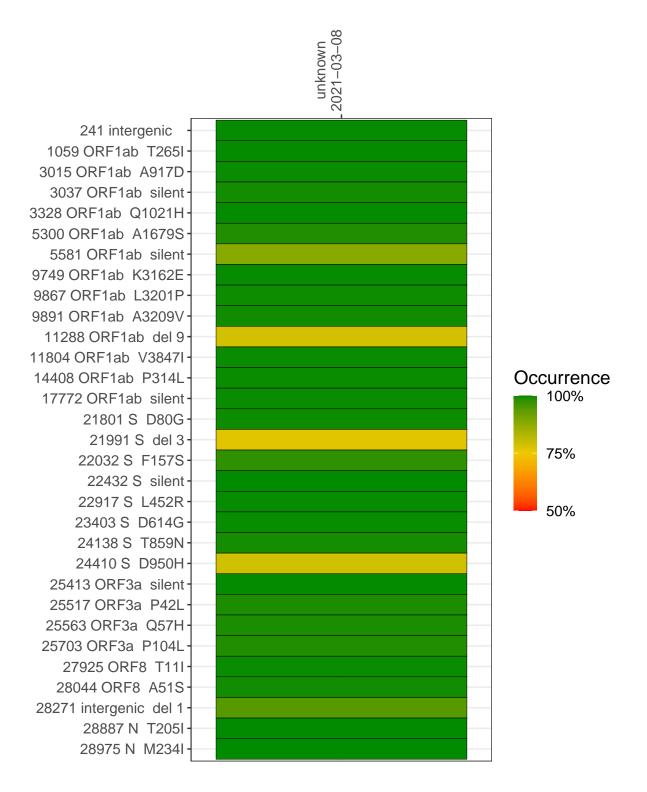
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP0941-1	single experiment	NA	unknown	2021-03-08	29.82	B.1.526.1	99.8%	99.7%

#### Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/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.



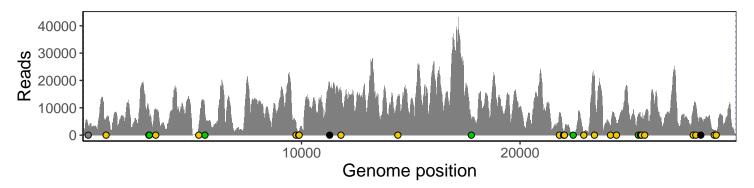
#### unknown 2021-03-08

	2021 00 00
241 intergenic	3394
1059 ORF1ab T265I	5880
3015 ORF1ab A917D	8985
3037 ORF1ab silent	7140
3328 ORF1ab Q1021H	9461
5300 ORF1ab A1679S	3035
5581 ORF1ab silent	7743
9749 ORF1ab K3162E	4726
9867 ORF1ab L3201P	982
9891 ORF1ab A3209V	1568
11288 ORF1ab del 9	14634
11804 ORF1ab V3847I	16471
14408 ORF1ab P314L	13918
17772 ORF1ab silent	5712
21801 S D80G	7804
21991 S del 3	1199
22032 S F157S	1499
22432 S silent	119
22917 S L452R	1135
23403 S D614G	21718
24138 S T859N	3663
24410 S D950H	4172
25413 ORF3a silent	7405
25517 ORF3a P42L	6678
25563 ORF3a Q57H	6467
25703 ORF3a P104L	6612
27925 ORF8 T11I	10000
28044 ORF8 A51S	11003
28271 intergenic del 1	6207
28887 N T205I	1776
28975 N M234I	1454
	1-146
	.46

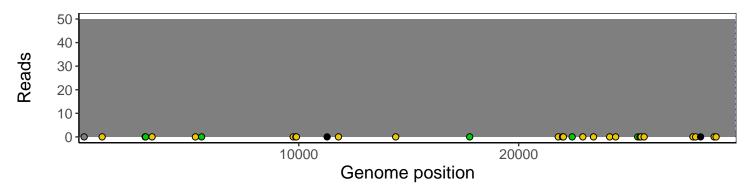
## Analyses of individual experiments and composite results

### $VSP0941\text{-}1 \mid 2021\text{-}03\text{-}08 \mid unknown \mid UPHS\text{-}0008 \mid genomes \mid single \; experiment$

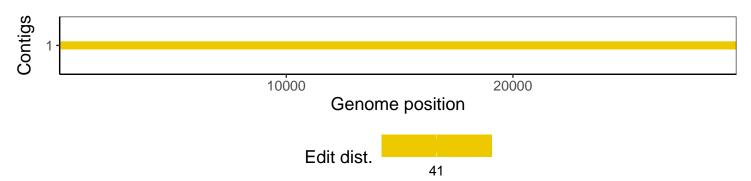
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.0.0
tidyverse	1.2.1
ShortRead	1.34.2
${\it Genomic Alignments}$	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
$\operatorname{GenomeInfoDb}$	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