# COVID-19 subject UPHS-0123

2021-06-23

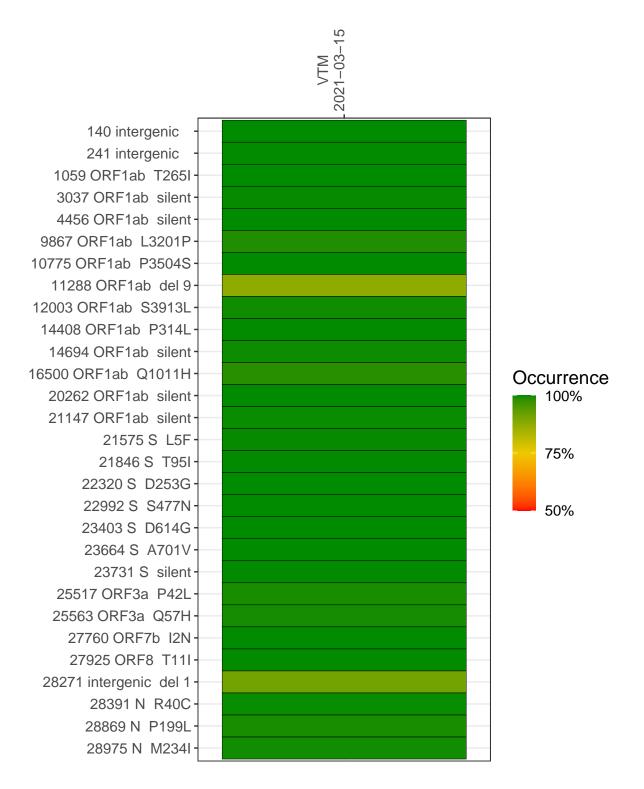
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

Table 1. Sample summary.

Experiment	Туре	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1108-1	single experiment	NA	VTM	2021-03-15	29.88	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.



#### VTM 2021-03-15

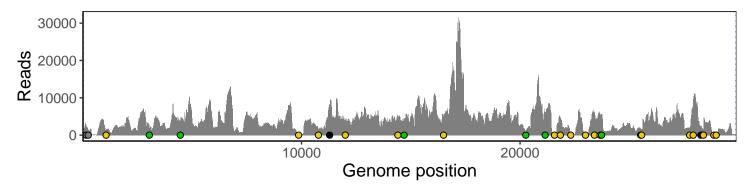
	2021-03-13
140 intergenic	2701
241 intergenic	1274
1059 ORF1ab T265I	1350
3037 ORF1ab silent	1991
4456 ORF1ab silent	3735
9867 ORF1ab L3201P	360
10775 ORF1ab P3504S	1515
11288 ORF1ab del 9	6657
12003 ORF1ab S3913L	4041
14408 ORF1ab P314L	4777
14694 ORF1ab silent	3332
16500 ORF1ab Q1011H	4811
20262 ORF1ab silent	921
21147 ORF1ab silent	6125
21575 S L5F	651
21846 S T95I	4545
22320 S D253G	312
22992 S S477N	607
23403 S D614G	6028
23664 S A701V	5176
23731 S silent	5595
25517 ORF3a P42L	1707
25563 ORF3a Q57H	1583
27760 ORF7b I2N	1905
27925 ORF8 T11I	9033
28271 intergenic del 1	2403
28391 N R40C	1468
28869 N P199L	276
28975 N M234I	211
	7-
	VSP1108-1
	/SP



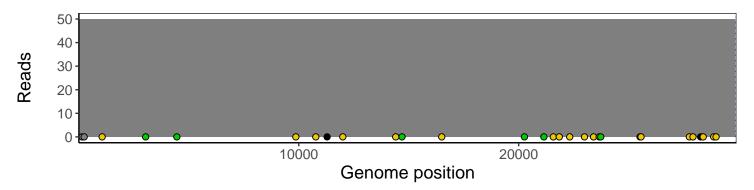
### Analyses of individual experiments and composite results

#### VSP1108-1 | 2021-03-15 | VTM | UPHS-0123 | genomes | single experiment

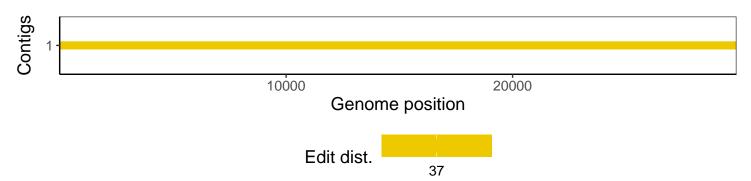
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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				
${\bf Summarized Experiment}$	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				