# COVID-19 subject UPHS-0117

2021-04-01

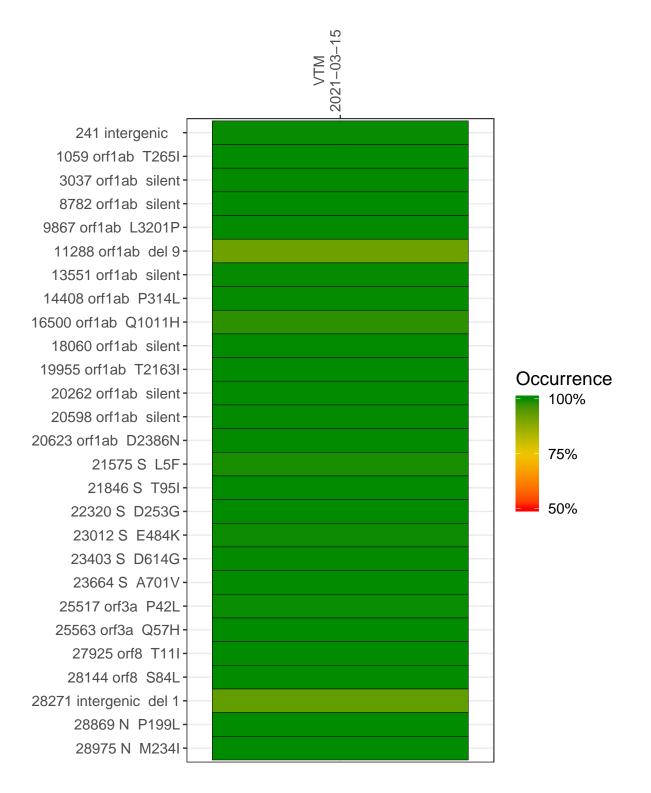
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1102-1	single experiment	NA	VTM	2021-03-15	29.89	B.1.526	99.9%	99.8%

#### Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/USA-WA1-2020) 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

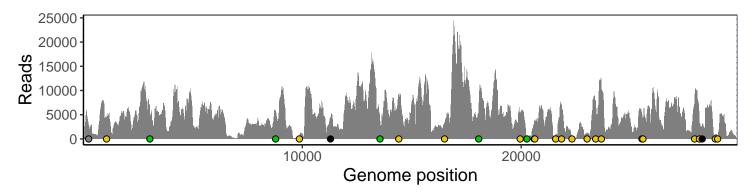
	2021-03-13
241 intergenic	2518
1059 orf1ab T265I	4294
3037 orf1ab silent	5003
8782 orf1ab silent	5553
9867 orf1ab L3201P	505
11288 orf1ab del 9	3647
13551 orf1ab silent	3603
14408 orf1ab P314L	8594
16500 orf1ab Q1011H	3278
18060 orf1ab silent	6708
19955 orf1ab T2163I	4824
20262 orf1ab silent	197
20598 orf1ab silent	3537
20623 orf1ab D2386N	3826
21575 S L5F	837
21846 S T95I	6887
22320 S D253G	356
23012 S E484K	1123
23403 S D614G	7812
23664 S A701V	9729
25517 orf3a P42L	4933
25563 orf3a Q57H	4421
27925 orf8 T11I	8690
28144 orf8 S84L	3366
28271 intergenic del 1	2940
28869 N P199L	802
28975 N M234I	678
	2-1
	VSP1102-1
	SS >



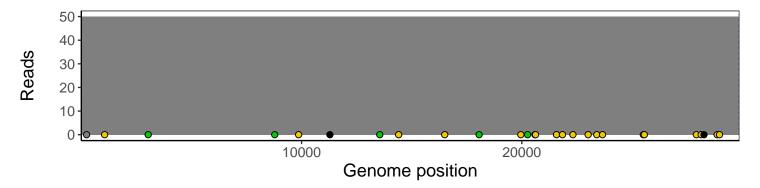
## Analyses of individual experiments and composite results

### VSP1102-1 | 2021-03-15 | VTM | UPHS-0117 | genomes | single experiment

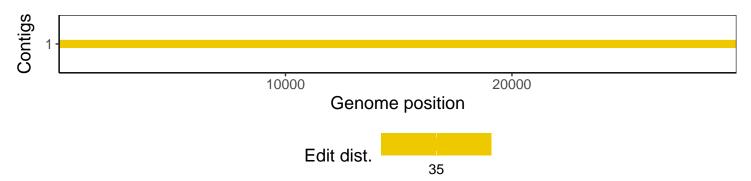
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.3
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	3.0.0
tidyverse	1.2.1
ShortRead	1.34.2
$\operatorname{GenomicAlignments}$	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
$\operatorname{GenomeInfoDb}$	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