# COVID-19 subject UPHS-1117

2021-06-23

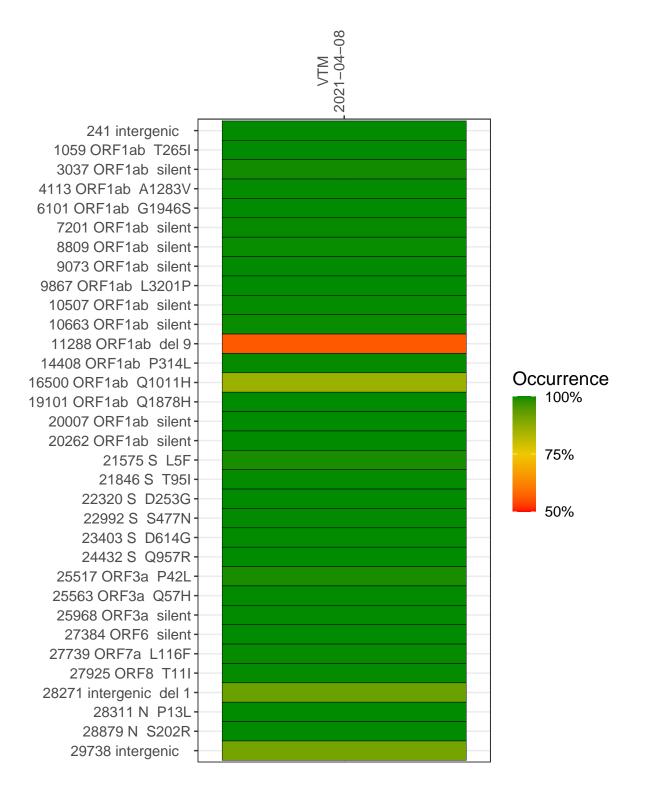
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP2328-1	single experiment	NA	VTM	2021-04-08	29.88	B.1.526	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.



## VTM 2021-04-08

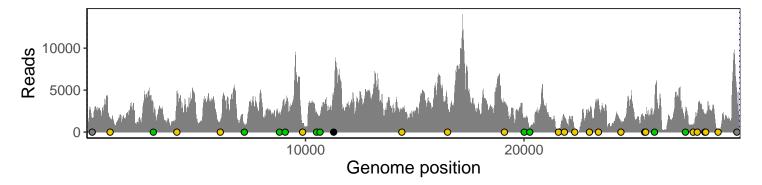
241 intergenic 1059 ORF1ab T2651 3037 ORF1ab silent 4113 ORF1ab A1283V 6101 ORF1ab G1946S 7201 ORF1ab silent 9073 ORF1ab silent 9073 ORF1ab silent 10507 ORF1ab silent 11288 ORF1ab del 9 14408 ORF1ab Q1011H 19101 ORF1ab Q1878H 20262 ORF1ab silent 21575 S L5F 21846 S T95I 22320 S D253G 22992 S S477N 23403 S D614G 24432 S Q957R 2576 ORF2 L116F 27925 ORF8 T111 28271 intergenic 2065 29738 intergenic		202: 0: 00
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20262 ORF1ab silent       479         21575 S L5F       286         21846 S T95I       1671         22320 S D253G       209         22992 S S477N       2118         23403 S D614G       3833         24432 S Q957R       1130         25517 ORF3a P42L       2077         25563 ORF3a Q57H       2077         25968 ORF3a silent       2584         27739 ORF7a L116F       835         27925 ORF8 T11I       2217         28271 intergenic del 1       2052         28311 N P13L       2065         2879 N S202R       364         29738 intergenic       2057	19101 ORF1ab Q1878H	3600
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21846 S T95I       1671         22320 S D253G       209         22992 S S477N       2118         23403 S D614G       3833         24432 S Q957R       1130         25517 ORF3a P42L       1359         25563 ORF3a Q57H       2077         25968 ORF3a silent       2584         27384 ORF6 silent       2125         27739 ORF7a L116F       835         27925 ORF8 T11I       2217         28271 intergenic del 1       2052         28311 N P13L       2065         28879 N S202R       364         29738 intergenic       2057	20262 ORF1ab silent	479
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22992 S S477N       2118         23403 S D614G       3833         24432 S Q957R       1130         25517 ORF3a P42L       1359         25563 ORF3a Q57H       2077         25968 ORF3a silent       2584         27384 ORF6 silent       2125         27739 ORF7a L116F       835         27925 ORF8 T11I       2217         28271 intergenic del 1       2052         28311 N P13L       2065         2879 N S202R       364         29738 intergenic       2057	21846 S T95I	1671
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27384 ORF6 silent       2125         27739 ORF7a L116F       835         27925 ORF8 T11I       2217         28271 intergenic del 1       2052         28311 N P13L       2065         28879 N S202R       364         29738 intergenic       2057	25563 ORF3a Q57H	2077
27739 ORF7a L116F       835         27925 ORF8 T11I       2217         28271 intergenic del 1       2052         28311 N P13L       2065         28879 N S202R       364         29738 intergenic       2057	25968 ORF3a silent	2584
27925 ORF8 T11I       2217         28271 intergenic del 1       2052         28311 N P13L       2065         28879 N S202R       364         29738 intergenic       2057	27384 ORF6 silent	2125
28271 intergenic del 1       2052         28311 N P13L       2065         28879 N S202R       364         29738 intergenic       2057	27739 ORF7a L116F	835
28311 N P13L 2065 28879 N S202R 364 29738 intergenic 2057	27925 ORF8 T11I	2217
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29738 intergenic <b>2057</b>	28311 N P13L	2065
<u> </u>	28879 N S202R	364
7	29738 intergenic	2057
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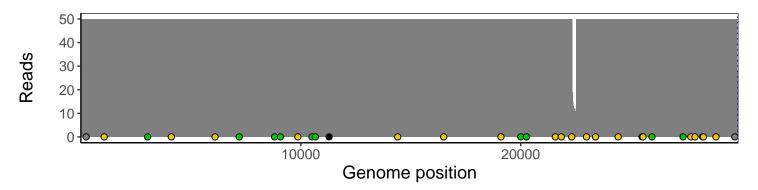
## Analyses of individual experiments and composite results

### VSP2328-1 | 2021-04-08 | VTM | UPHS-1117 | genomes | single experiment

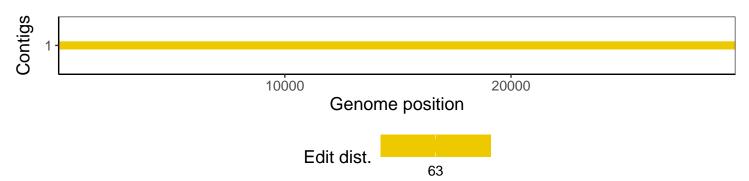
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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