# COVID-19 subject UPHS-0261

2021-06-23

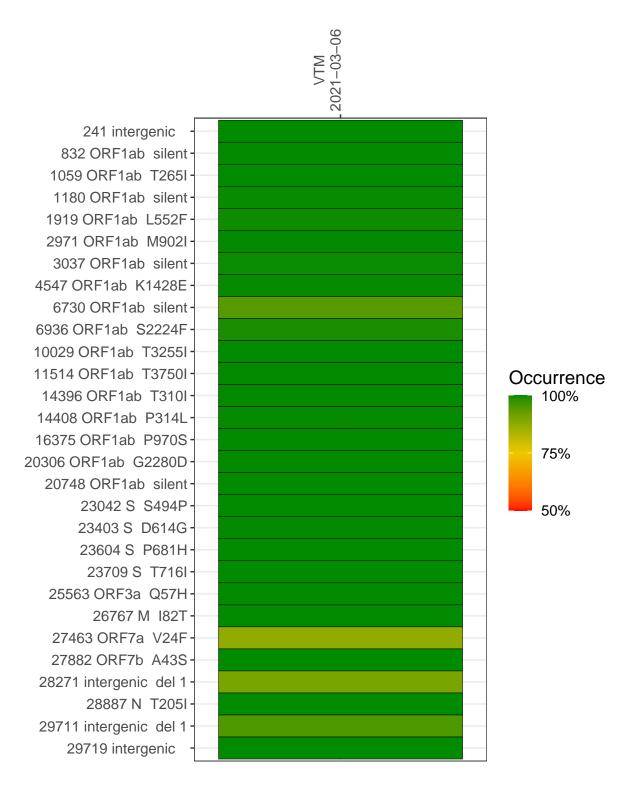
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1306-1	single experiment	NA	VTM	2021-03-06	29.88	B.1.575	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 2021-03-06

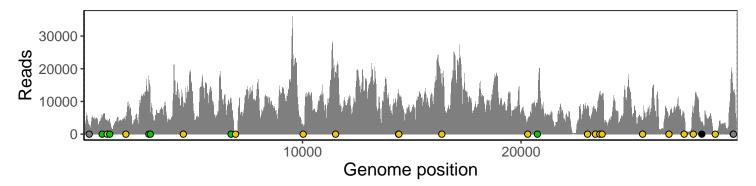
	2021-03-00
241 intergenic	2414
832 ORF1ab silent	5295
1059 ORF1ab T265I	3956
1180 ORF1ab silent	4185
1919 ORF1ab L552F	5499
2971 ORF1ab M902I	17190
3037 ORF1ab silent	8453
4547 ORF1ab K1428E	8892
6730 ORF1ab silent	10852
6936 ORF1ab S2224F	121
10029 ORF1ab T3255I	2836
11514 ORF1ab T3750I	18195
14396 ORF1ab T310I	13727
14408 ORF1ab P314L	10431
16375 ORF1ab P970S	14232
20306 ORF1ab G2280D	4327
20748 ORF1ab silent	9267
23042 S S494P	8940
23403 S D614G	7535
23604 S P681H	11767
23709 S T716I	11525
25563 ORF3a Q57H	4222
26767 M 182T	4915
27463 ORF7a V24F	6377
27882 ORF7b A43S	7156
28271 intergenic del 1	3665
28887 N T205I	606
29711 intergenic del 1	12981
29719 intergenic	11184
	06–1
	0



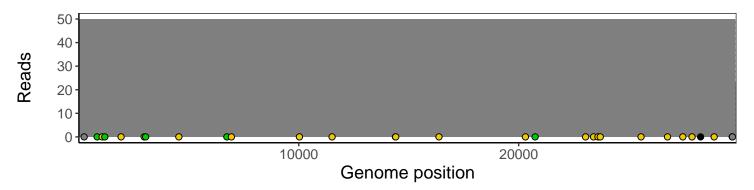
### Analyses of individual experiments and composite results

#### $VSP1306\text{-}1 \mid 2021\text{-}03\text{-}06 \mid VTM \mid UPHS\text{-}0261 \mid genomes \mid single \ experiment$

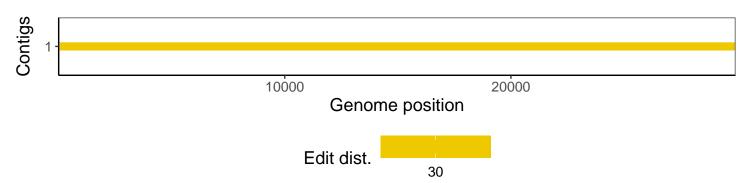
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	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				