# COVID-19 subject UPHS-0248

2021-06-23

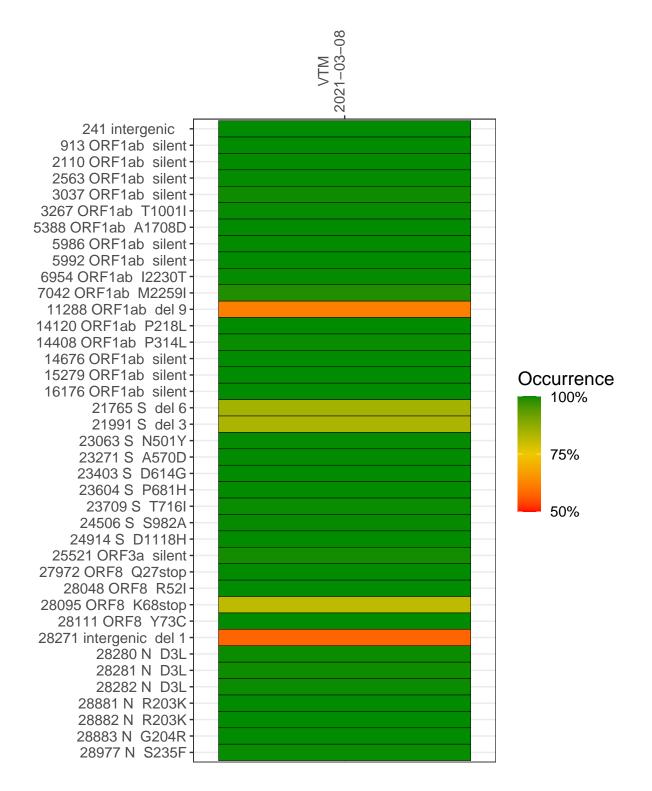
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1293-1	single experiment	NA	VTM	2021-03-08	29.90	B.1.1.7	99.9%	99.8%

#### 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 2021-03-08

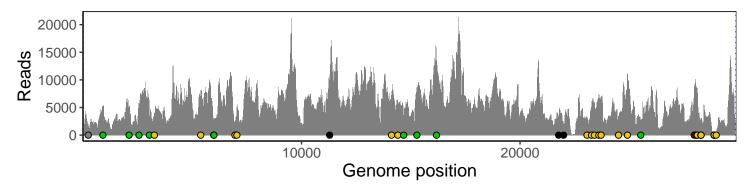
	2021-03-00
241 intergenic	1594
913 ORF1ab silent	5162
2110 ORF1ab silent	4736
2563 ORF1ab silent	5727
3037 ORF1ab silent	3943
3267 ORF1ab T1001I	4063
5388 ORF1ab A1708D	7022
5986 ORF1ab silent	2922
5992 ORF1ab silent	2817
6954 ORF1ab I2230T	2323
7042 ORF1ab M2259I	3696
11288 ORF1ab del 9	5567
14120 ORF1ab P218L	7027
14408 ORF1ab P314L	5430
14676 ORF1ab silent	2809
15279 ORF1ab silent	7398
16176 ORF1ab silent	13334
21765 S del 6	2876
21991 S del 3	1875
23063 S N501Y	3269
23271 S A570D	4926
23403 S D614G	5840
23604 S P681H	6427
23709 S T716I	6306
24506 S S982A	3392
24914 S D1118H	10935
25521 ORF3a silent	2791
27972 ORF8 Q27stop	8293
28048 ORF8 R52I	8522
28095 ORF8 K68stop	8360
28111 ORF8 Y73C	6987
28271 intergenic del 1	2573
28280 N D3L	1449
28281 N D3L	1449
28282 N D3L	1549
28881 N R203K	334
28882 N R203K	328
28883 N G204R	333
28977 N S235F	534
	<u></u>



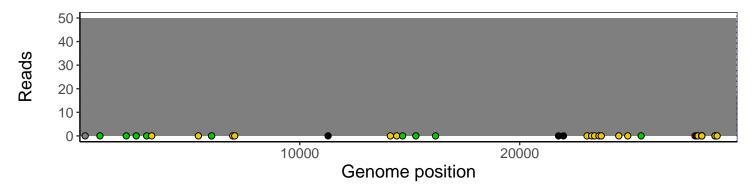
### Analyses of individual experiments and composite results

#### VSP1293-1 | 2021-03-08 | VTM | UPHS-0248 | genomes | single experiment

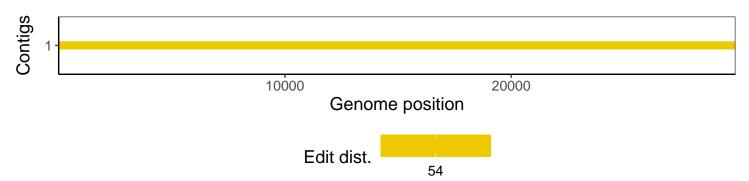
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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				