# COVID-19 subject UPHS-0142

2021-03-31

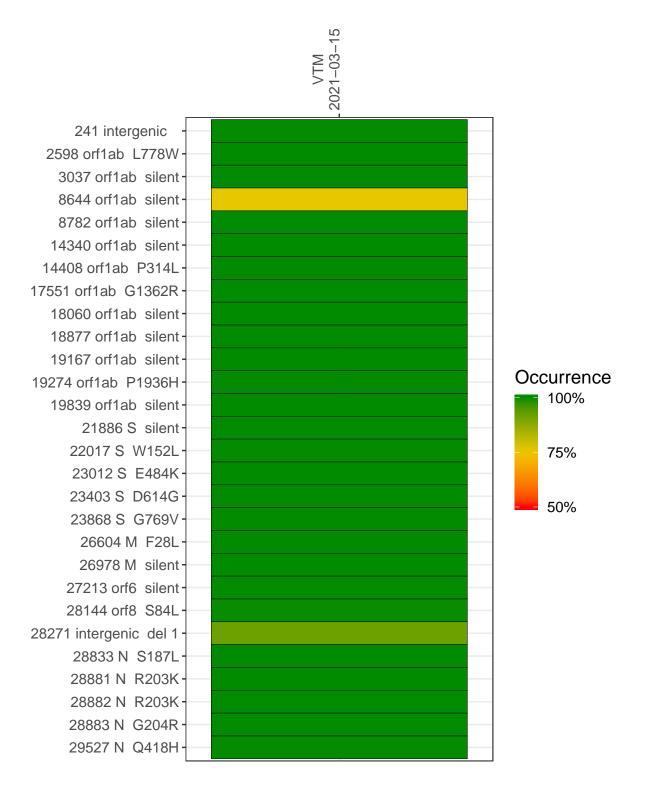
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1127-1	single experiment	NA	VTM	2021-03-15	29.83	R.1	99.8%	99.8%

#### Variants shared across samples

The heat map below shows how variants (reference genome 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

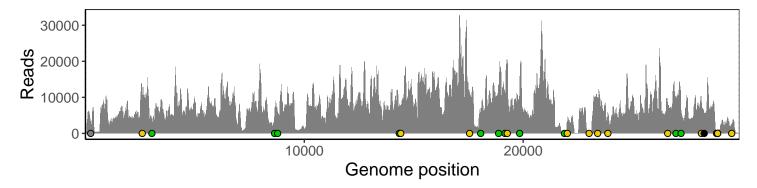
	2021-03-13
241 intergenic	2917
2598 orf1ab L778W	9237
3037 orf1ab silent	3332
8644 orf1ab silent	6447
8782 orf1ab silent	5882
14340 orf1ab silent	6920
14408 orf1ab P314L	7055
17551 orf1ab G1362R	10723
18060 orf1ab silent	5535
18877 orf1ab silent	12873
19167 orf1ab silent	10994
19274 orf1ab P1936H	18717
19839 orf1ab silent	12245
21886 S silent	268
22017 S W152L	3170
23012 S E484K	106
23403 S D614G	9696
23868 S G769V	<b>5</b> 895
26604 M F28L	8942
26978 M silent	7031
27213 orf6 silent	6341
28144 orf8 S84L	8578
28271 intergenic del 1	5360
28833 N S187L	947
28881 N R203K	646
28882 N R203K	644
28883 N G204R	648
29527 N Q418H	2253
	27-1
	· V



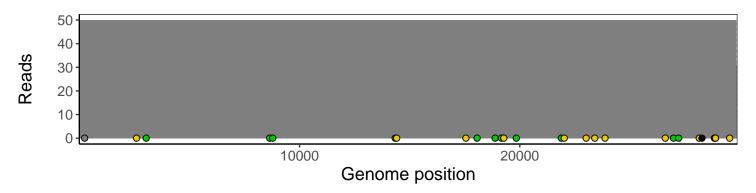
### Analyses of individual experiments and composite results

#### VSP1127-1 | 2021-03-15 | VTM | UPHS-0142 | genomes | single experiment

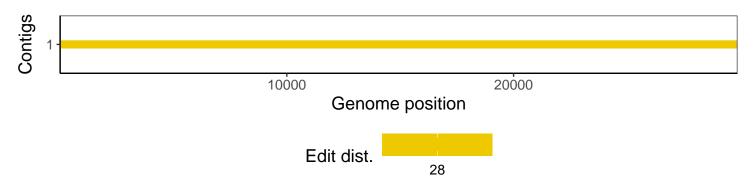
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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