# COVID-19 subject UPHS-1384

2021-06-01

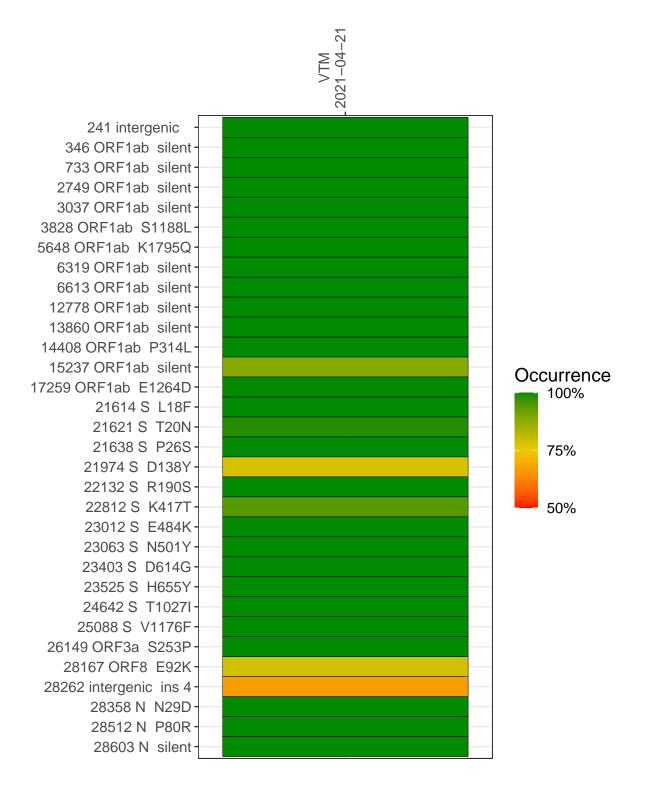
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with > 90% sequence coverage.

Table 1. Sample summary.

| Experiment | Туре              | Genomes | Sample type | Sample date | Largest contig<br>(KD) | Lineage | Reference read<br>coverage | Reference read coverage (>= 5 reads) |
|------------|-------------------|---------|-------------|-------------|------------------------|---------|----------------------------|--------------------------------------|
| VSP2639-1  | single experiment | NA      | VTM         | 2021-04-21  | 29.85                  | P.1     | 99.8%                      | 99.6%                                |

#### 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.



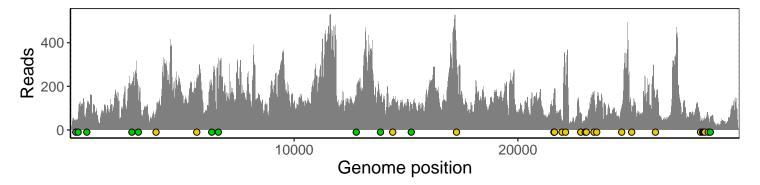
#### VTM 2021-04-21

|                        | 2021-04-21 |
|------------------------|------------|
| 241 intergenic         | 39         |
| 346 ORF1ab silent      | 67         |
| 733 ORF1ab silent      | 94         |
| 2749 ORF1ab silent     | 193        |
| 3037 ORF1ab silent     | 130        |
| 3828 ORF1ab S1188L     | 83         |
| 5648 ORF1ab K1795Q     | 220        |
| 6319 ORF1ab silent     | 193        |
| 6613 ORF1ab silent     | 318        |
| 12778 ORF1ab silent    | 145        |
| 13860 ORF1ab silent    | 147        |
| 14408 ORF1ab P314L     | 129        |
| 15237 ORF1ab silent    | 112        |
| 17259 ORF1ab E1264D    | 303        |
| 21614 S L18F           | 159        |
| 21621 S T20N           | 156        |
| 21638 S P26S           | 182        |
| 21974 S D138Y          | 41         |
| 22132 S R190S          | 202        |
| 22812 S K417T          | 68         |
| 23012 S E484K          | 40         |
| 23063 S N501Y          | 53         |
| 23403 S D614G          | 175        |
| 23525 S H655Y          | 105        |
| 24642 S T1027I         | 107        |
| 25088 S V1176F         | 79         |
| 26149 ORF3a S253P      | 139        |
| 28167 ORF8 E92K        | 33         |
| 28262 intergenic ins 4 | 33         |
| 28358 N N29D           | 59         |
| 28512 N P80R           | 61         |
| 28603 N silent         | 53         |
|                        | 9-1        |
|                        | VSP2639-1  |
|                        | SP.        |
|                        | >          |

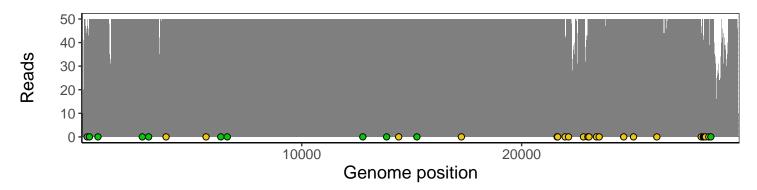
### Analyses of individual experiments and composite results

#### $VSP2639\text{-}1 \mid 2021\text{-}04\text{-}21 \mid VTM \mid UPHS\text{-}1384 \mid genomes \mid single \ experiment$

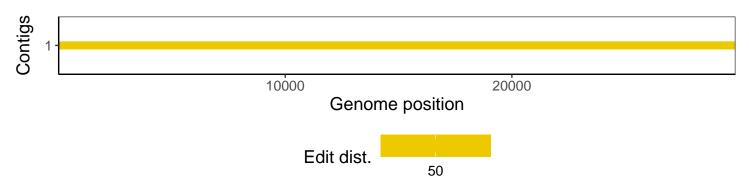
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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                      | 2.3.8  |
| 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   |
| ${\it Genomic Alignments}$    | 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   |