# COVID-19 subject UPHS-0577

2021-06-03

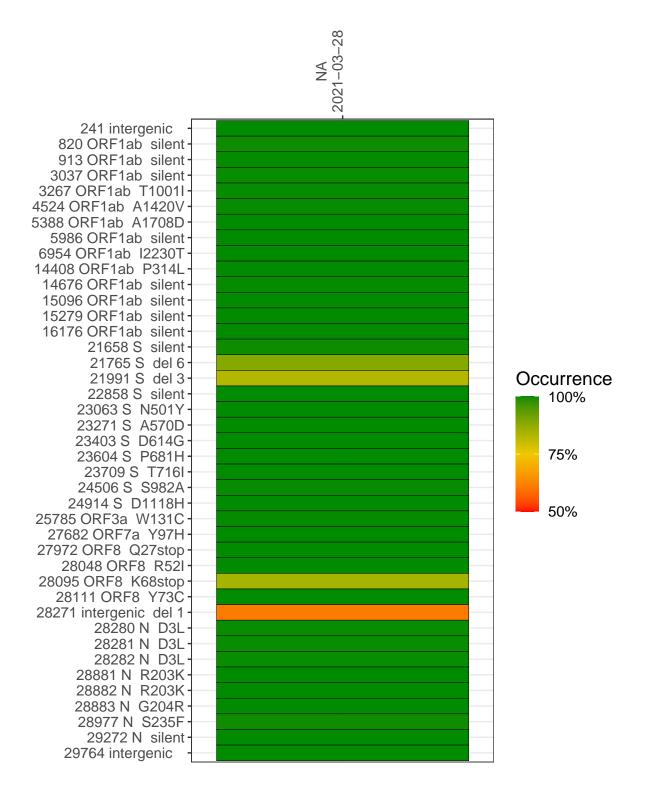
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1702-1	single experiment	NA	NA	2021-03-28	29.91	B.1.1.7	99.9%	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.



#### NA 2021-03-28

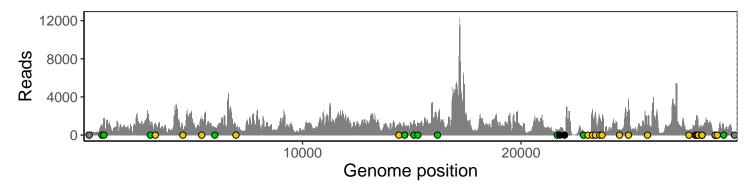
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27682 ORF7a Y97H       483         27972 ORF8 Q27stop       1422         28048 ORF8 R52I       1992         28095 ORF8 K68stop       1661         28111 ORF8 Y73C       1063         28271 intergenic del 1       311         28280 N D3L       494         28281 N D3L       494         28282 N D3L       526         28881 N R203K       165         28882 N R203K       165         28883 N G204R       165         28977 N S235F       248         29272 N silent       1190         29764 intergenic       208	24914 S D1118H	3842																																																																																																																											
27972 ORF8 Q27stop       1422         28048 ORF8 R52I       1992         28095 ORF8 K68stop       1661         28111 ORF8 Y73C       1063         28271 intergenic del 1       811         28280 N D3L       494         28281 N D3L       494         28282 N D3L       526         28881 N R203K       165         28882 N R203K       165         28883 N G204R       165         28977 N S235F       248         29272 N silent       1190         29764 intergenic       208	25785 ORF3a W131C	1102																																																																																																																											
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28271 intergenic del 1  28280 N D3L  28281 N D3L  28282 N D3L  28282 N D3L  28881 N R203K  28882 N R203K  28883 N G204R  28977 N S235F  29272 N silent  29764 intergenic  208	28095 ORF8 K68stop	1661																																																																																																																											
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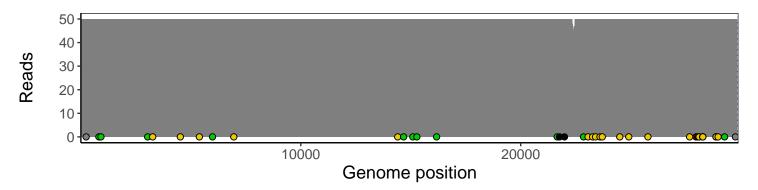
### Analyses of individual experiments and composite results

#### VSP1702-1 | 2021-03-28 | NA | UPHS-0577 | genomes | single experiment

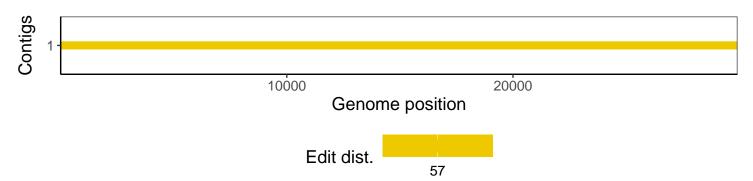
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.8
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