COVID-19 subject UPHS-1230

2021-06-23

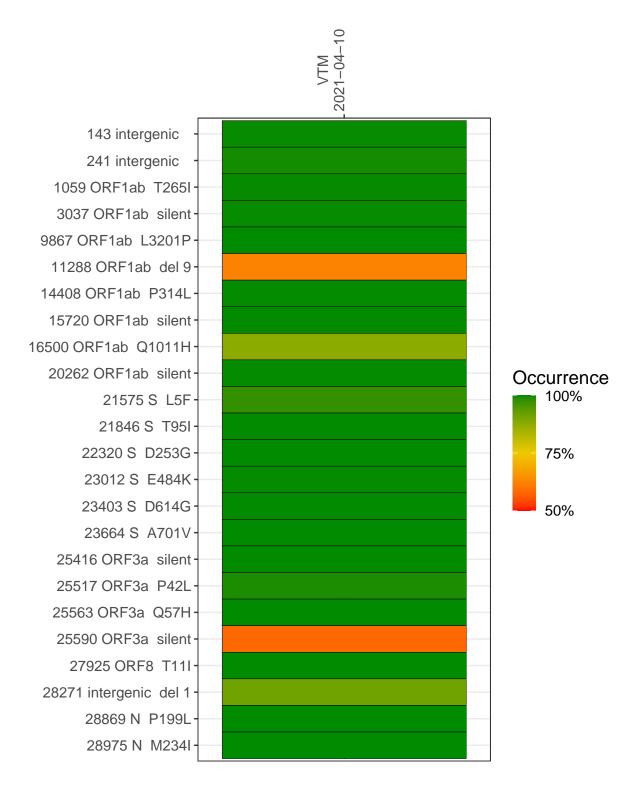
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP2484-1	single experiment	NA	VTM	2021-04-10	29.90	B.1.526	99.8%	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 2021-04-10

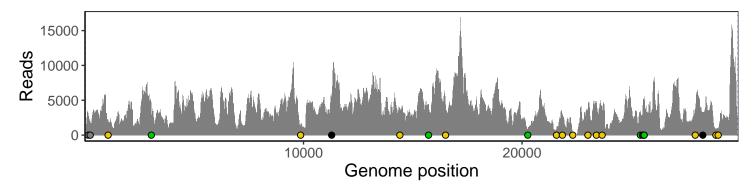
143 intergenic 241 intergenic 1587 1059 ORF1ab T265I 2019 3037 ORF1ab silent 9867 ORF1ab L3201P 11288 ORF1ab del 9 14408 ORF1ab P314L 15720 ORF1ab silent 20262 ORF1ab silent 21575 S L5F 21846 S T95I 22320 S D253G 23012 S E484K 23403 S D614G 23664 S A701V 25416 ORF3a silent 25590 ORF3a silent 27925 ORF8 T11I 28869 N P199L 28975 N M234I 890		2021 07 10
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23664 S A701V 25416 ORF3a silent 25517 ORF3a P42L 25563 ORF3a Q57H 25590 ORF3a silent 27925 ORF8 T11I 28869 N P199L 28975 N M234I 33484 3092 2548 2548 2548 25548 25548 25548 25548 25548 25548 25590 ORF3a silent 3685 28975 N M234I 3685	23012 S E484K	3421
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25563 ORF3a Q57H 5023 25590 ORF3a silent 5515 27925 ORF8 T11I 3685 28271 intergenic del 1 3175 28869 N P199L 868 28975 N M234I 890	25416 ORF3a silent	3092
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28271 intergenic del 1 28869 N P199L 28975 N M234I 890	25590 ORF3a silent	5515
28869 N P199L 868 28975 N M234I 890	27925 ORF8 T11I	3685
28975 N M234I 890	28271 intergenic del 1	3175
	28869 N P199L	868
1-48	28975 N M234I	890
VSP24		VSP2484-1



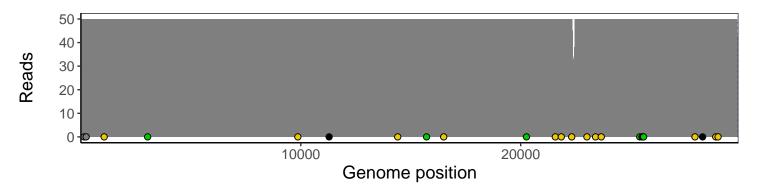
Analyses of individual experiments and composite results

VSP2484-1 | 2021-04-10 | VTM | UPHS-1230 | genomes | single experiment

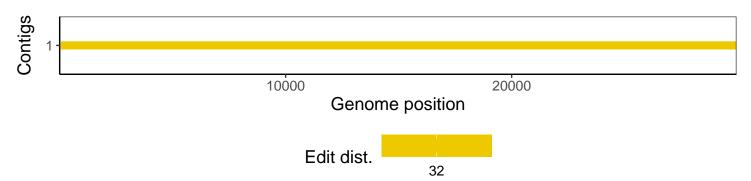
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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