COVID-19 subject UPHS-1105

2021-06-23

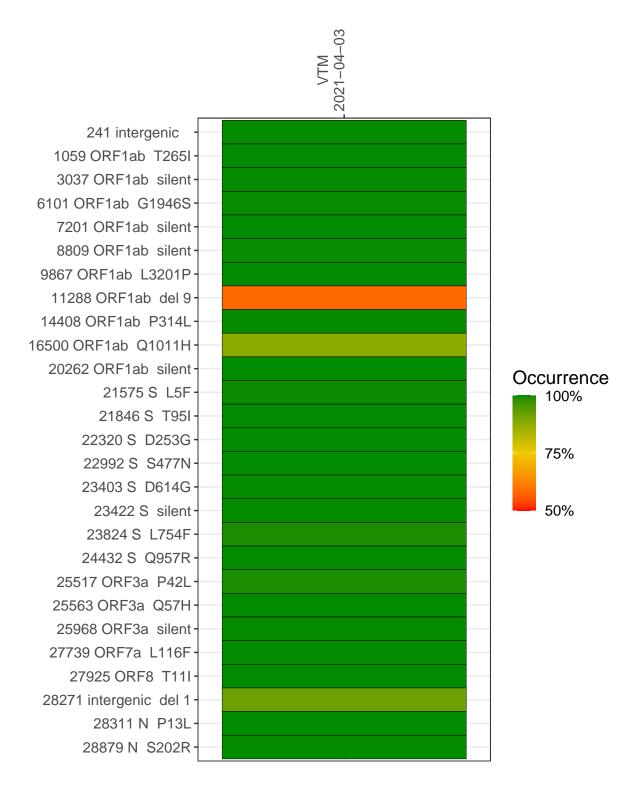
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP2316-1	single experiment	NA	VTM	2021-04-03	23.52	B.1.526	99.7%	98.9%

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 2021-04-03

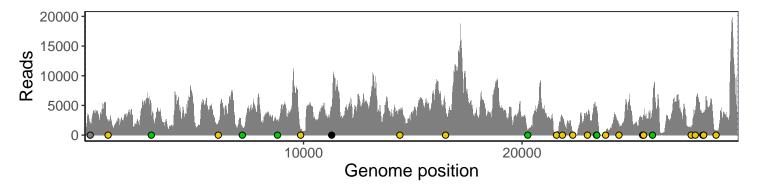
	2021 01 00
241 intergenic	1766
1059 ORF1ab T265I	2376
3037 ORF1ab silent	3373
6101 ORF1ab G1946S	1989
7201 ORF1ab silent	1111
8809 ORF1ab silent	2174
9867 ORF1ab L3201P	760
11288 ORF1ab del 9	2490
14408 ORF1ab P314L	3683
16500 ORF1ab Q1011H	4230
20262 ORF1ab silent	767
21575 S L5F	393
21846 S T95I	2788
22320 S D253G	315
22992 S S477N	3012
23403 S D614G	4705
23422 S silent	3776
23824 S L754F	227
24432 S Q957R	1697
25517 ORF3a P42L	2341
25563 ORF3a Q57H	3281
25968 ORF3a silent	4133
27739 ORF7a L116F	1294
27925 ORF8 T11I	4123
28271 intergenic del 1	3602
28311 N P13L	3761
28879 N S202R	751
	VSP2316-1



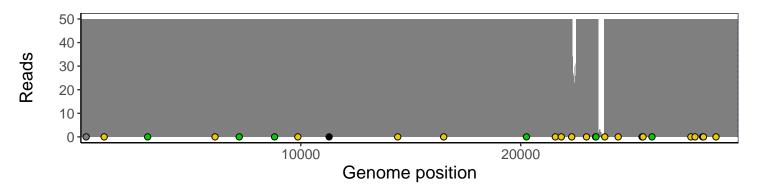
Analyses of individual experiments and composite results

$VSP2316\text{-}1 \mid 2021\text{-}04\text{-}03 \mid VTM \mid UPHS\text{-}1105 \mid genomes \mid single \ experiment$

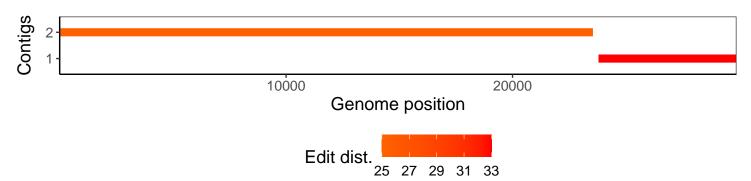
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	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				