COVID-19 subject UPHS-0343

2021-06-23

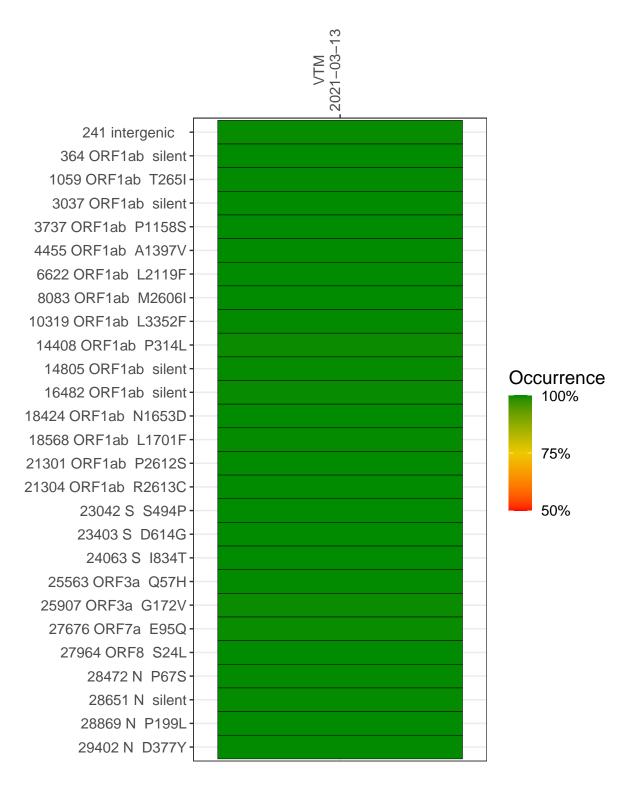
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1388-1	single experiment	NA	VTM	2021-03-13	29.85	B.1.2	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 2021-03-13

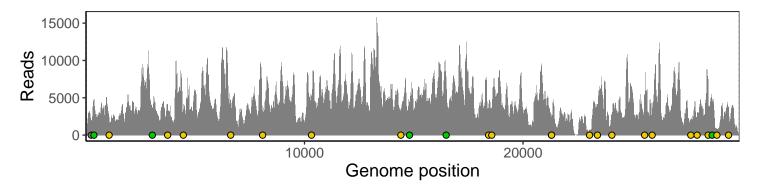
241 intergenic	1711
364 ORF1ab silent	4263
1059 ORF1ab T265I	2001
3037 ORF1ab silent	3145
3737 ORF1ab P1158S	4166
4455 ORF1ab A1397V	3190
6622 ORF1ab L2119F	3214
8083 ORF1ab M2606I	3050
10319 ORF1ab L3352F	5114
14408 ORF1ab P314L	2746
14805 ORF1ab silent	4384
16482 ORF1ab silent	7074
18424 ORF1ab N1653D	3664
18568 ORF1ab L1701F	3376
21301 ORF1ab P2612S	2201
21304 ORF1ab R2613C	2246
23042 S S494P	683
23403 S D614G	4059
24063 S 1834T	2484
25563 ORF3a Q57H	5350
25907 ORF3a G172V	2625
27676 ORF7a E95Q	1654
27964 ORF8 S24L	2791
28472 N P67S	7309
28651 N silent	4609
28869 N P199L	758
29402 N D377Y	3718
	1388-1
	138



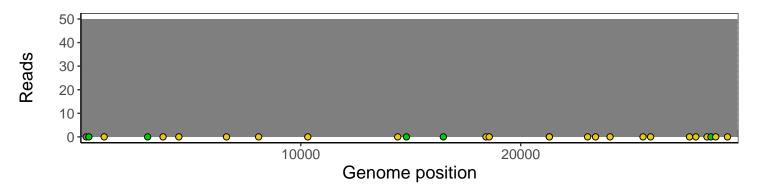
Analyses of individual experiments and composite results

VSP1388-1 | 2021-03-13 | VTM | UPHS-0343 | genomes | single experiment

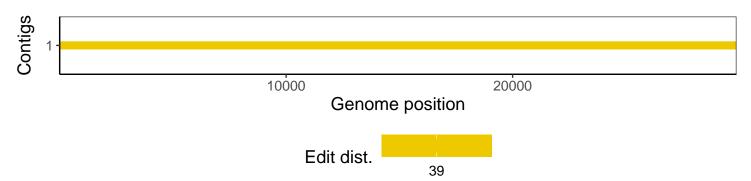
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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