COVID-19 subject UPHS-0129

2021-05-05

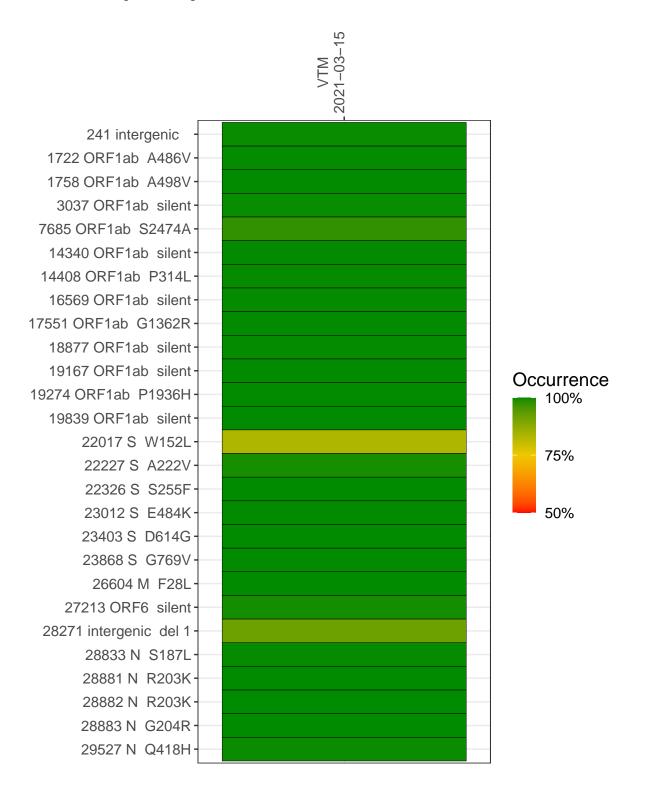
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1114-1	single experiment	NA	VTM	2021-03-15	29.83	R.1	100.0%	99.7%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/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 2021-03-15

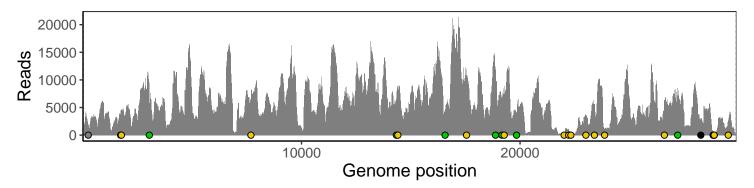
241 intergenic	1691
1722 ORF1ab A486V	3819
1758 ORF1ab A498V	4224
3037 ORF1ab silent	5996
7685 ORF1ab S2474A	6199
14340 ORF1ab silent	6386
14408 ORF1ab P314L	8104
16569 ORF1ab silent	4361
17551 ORF1ab G1362R	10761
18877 ORF1ab silent	11721
19167 ORF1ab silent	7177
19274 ORF1ab P1936H	7661
19839 ORF1ab silent	4033
22017 S W152L	348
22227 S A222V	1064
22326 S S255F	169
23012 S E484K	3240
23403 S D614G	5548
23868 S G769V	1225
26604 M F28L	6012
27213 ORF6 silent	6661
28271 intergenic del 1	2900
28833 N S187L	663
28881 N R203K	454
28882 N R203K	451
28883 N G204R	454
29527 N Q418H	2367
	14 1
	VSP1114-1
	S>



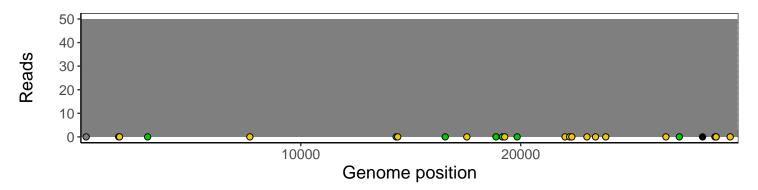
Analyses of individual experiments and composite results

VSP1114-1 | 2021-03-15 | VTM | UPHS-0129 | genomes | single experiment

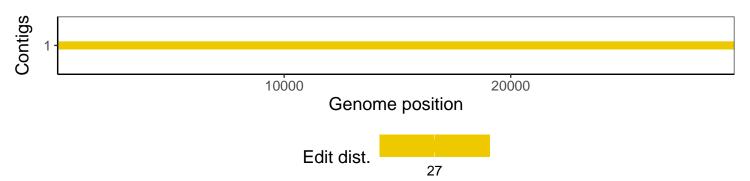
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.0.0
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