

# COVID-19 subject UPHS-0122

*2021-03-29*

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.

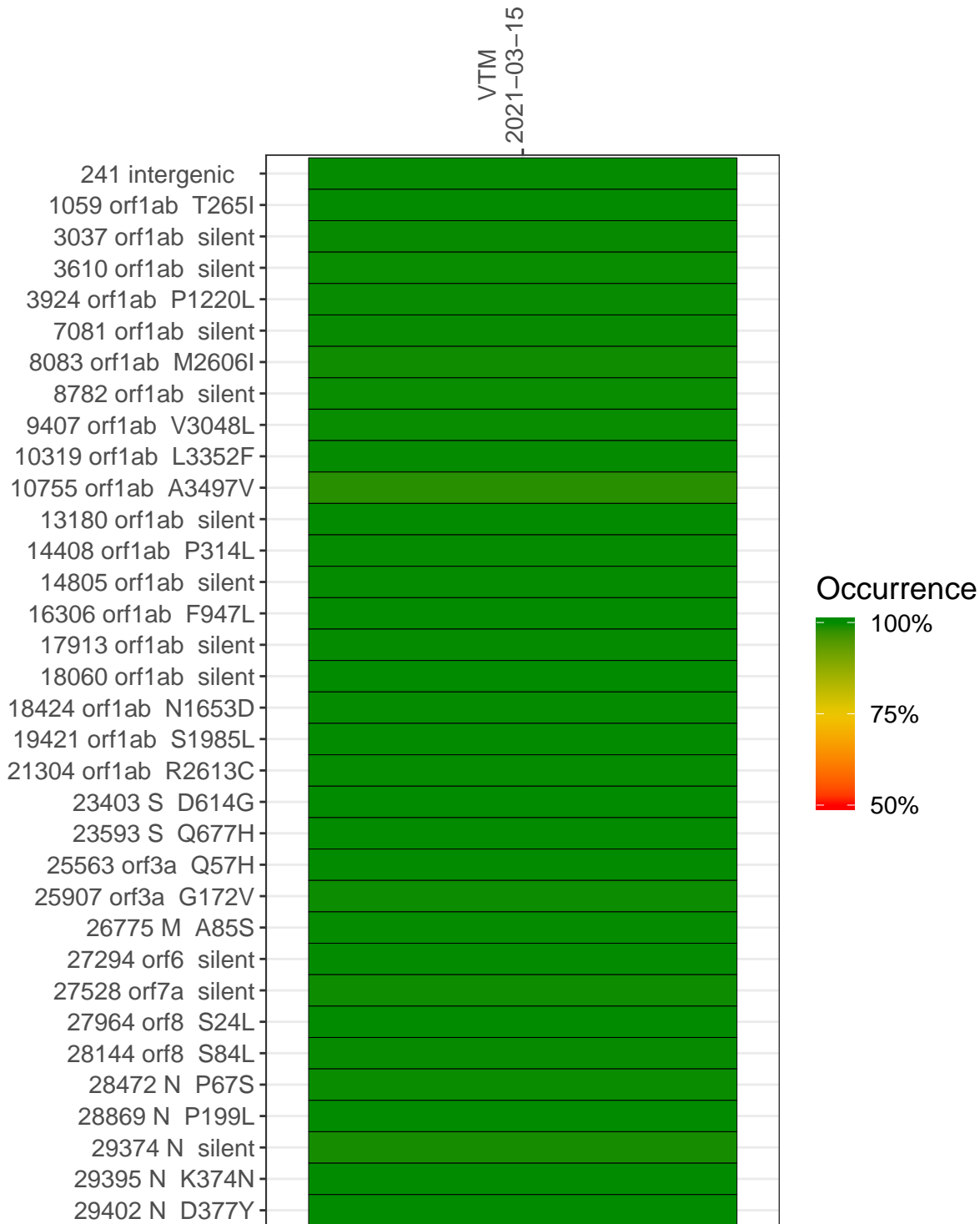
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with  $> 90\%$  sequence coverage.

Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage ( $\geq 5$ reads)
VSP1107-1	single experiment	NA	VTM	2021-03-15	29.83	B.1.2	99.9%	99.8%

## Variants shared across samples

The heat map below shows how variants (reference genome USA-WA1-2020) 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

241 intergenic	2000
1059 orf1ab T265I	4804
3037 orf1ab silent	7006
3610 orf1ab silent	6597
3924 orf1ab P1220L	1226
7081 orf1ab silent	4618
8083 orf1ab M2606I	3745
8782 orf1ab silent	5257
9407 orf1ab V3048L	10540
10319 orf1ab L3352F	13085
10755 orf1ab A3497V	9251
13180 orf1ab silent	17412
14408 orf1ab P314L	12234
14805 orf1ab silent	6407
16306 orf1ab F947L	11665
17913 orf1ab silent	6440
18060 orf1ab silent	8843
18424 orf1ab N1653D	4985
19421 orf1ab S1985L	12546
21304 orf1ab R2613C	9550
23403 S D614G	5481
23593 S Q677H	12226
25563 orf3a Q57H	4871
25907 orf3a G172V	3186
26775 M A85S	6206
27294 orf6 silent	6021
27528 orf7a silent	1599
27964 orf8 S24L	13877
28144 orf8 S84L	5217
28472 N P67S	5712
28869 N P199L	733
29374 N silent	988
29395 N K374N	1129
29402 N D377Y	1129

Base change

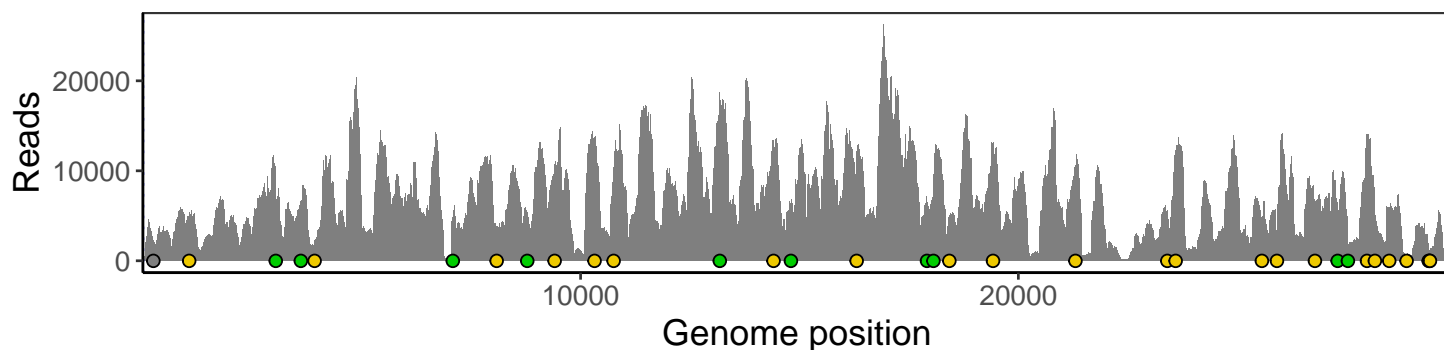
Expected
A
T
C
G
N
Ins/Del
No data

VSP1107-1

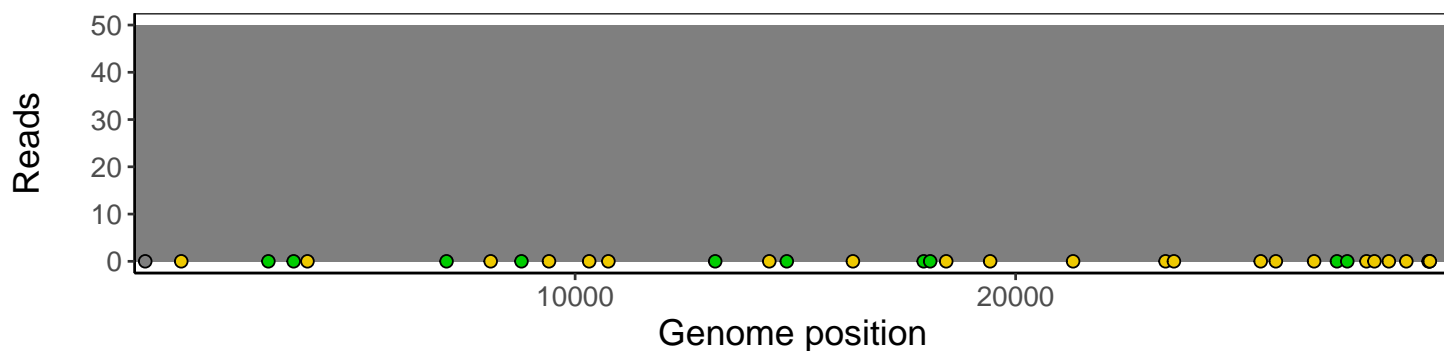
## Analyses of individual experiments and composite results

VSP1107-1 | 2021-03-15 | VTM | UPHS-0122 | genomes | single experiment

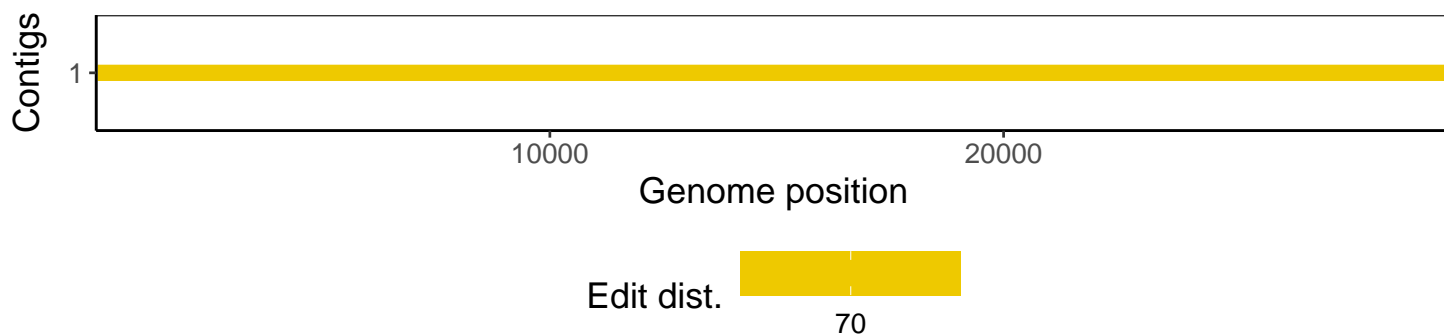
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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 htlib 1.10
bcftools	1.10.2-34-g1a12af0-dirty Using htlib 1.10.2-57-gf58a6f3
pangolin	2.3.3
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	3.0.0
tidyverse	1.2.1
ShortRead	1.34.2
GenomicAlignments	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
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