

# COVID-19 subject UPHS-0235

*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.

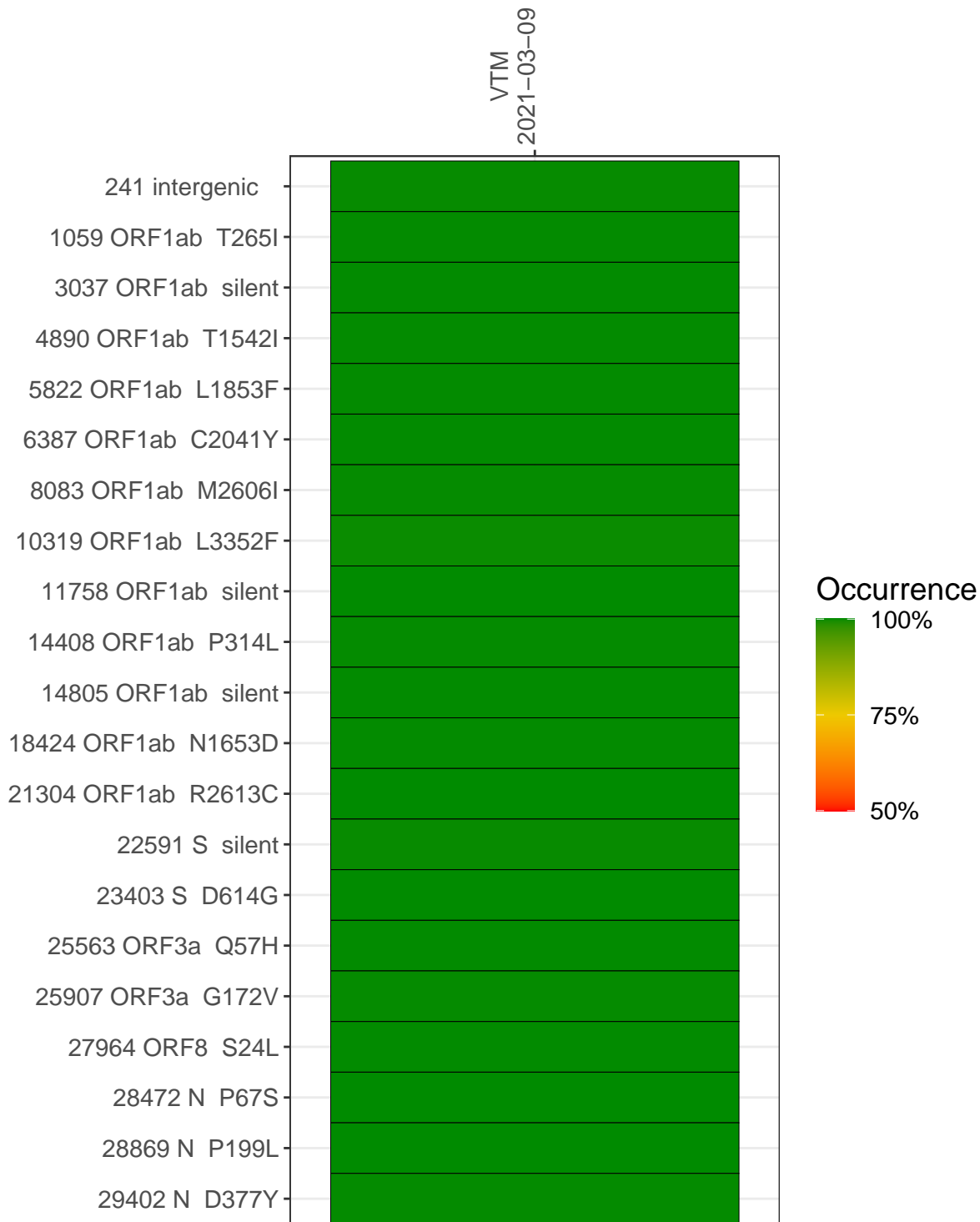
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with  $> 90\%$  sequence coverage.

Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage ( $\geq 5$ reads)
VSP1280-1	single experiment	NA	VTM	2021-03-09	29.86	B.1.2	99.9%	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  
2021-03-09

241 intergenic	653
1059 ORF1ab T265I	1432
3037 ORF1ab silent	2504
4890 ORF1ab T1542I	5709
5822 ORF1ab L1853F	8624
6387 ORF1ab C2041Y	2698
8083 ORF1ab M2606I	3028
10319 ORF1ab L3352F	2836
11758 ORF1ab silent	6589
14408 ORF1ab P314L	6837
14805 ORF1ab silent	7854
18424 ORF1ab N1653D	6710
21304 ORF1ab R2613C	3009
22591 S silent	3414
23403 S D614G	6315
25563 ORF3a Q57H	2117
25907 ORF3a G172V	4079
27964 ORF8 S24L	7399
28472 N P67S	4183
28869 N P199L	471
29402 N D377Y	990

Base change

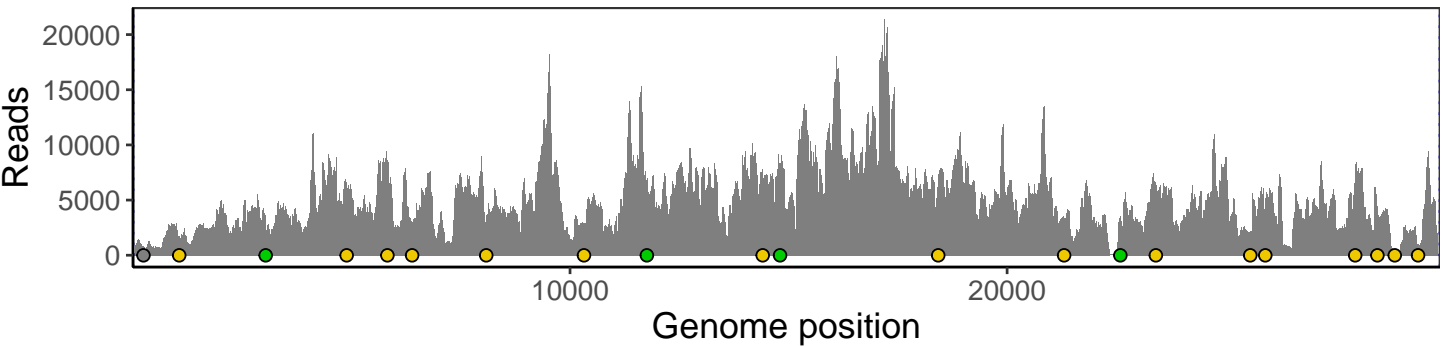
- Expected
- A
- T
- C
- G
- N
- Ins/Del
- No data

VSP1280-1

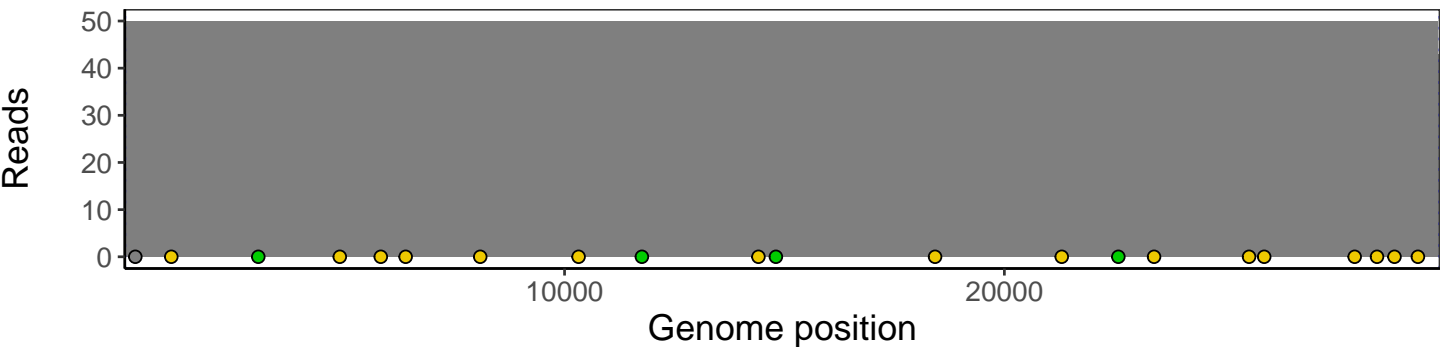
# Analyses of individual experiments and composite results

VSP1280-1 | 2021-03-09 | VTM | UPHS-0235 | genomes | single experiment

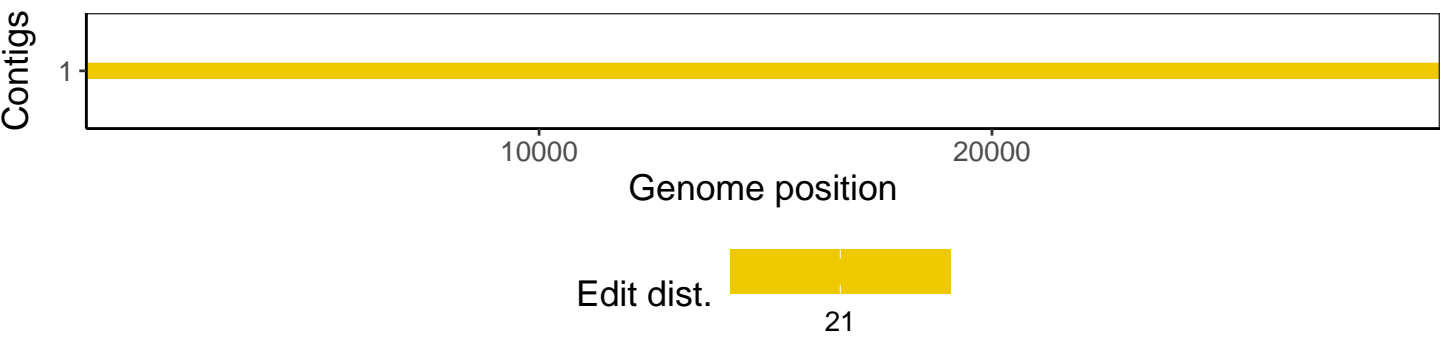
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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 htlib 1.10
bcftools	1.10.2-34-g1a12af0-dirty Using htlib 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
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