

COVID-19 subject UPHS-0309

2021-06-23

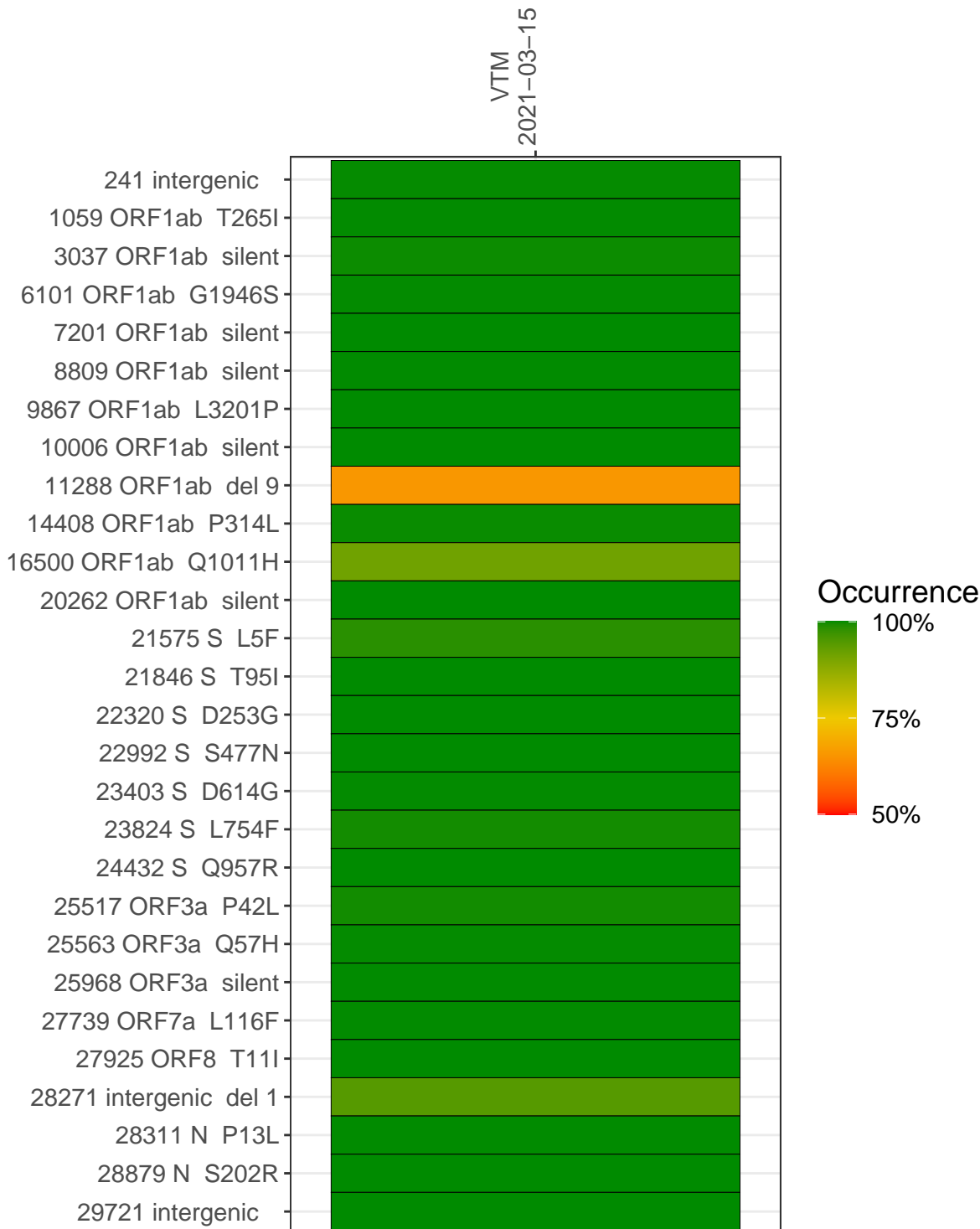
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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 (≥ 5 reads)
VSP1354-1	single experiment	NA	VTM	2021-03-15	29.84	B.1.526	99.8%	99.7%

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 2021-03-15	
241 intergenic	1684	
1059 ORF1ab T265I	1816	
3037 ORF1ab silent	3031	
6101 ORF1ab G1946S	1318	
7201 ORF1ab silent	915	
8809 ORF1ab silent	3544	
9867 ORF1ab L3201P	1610	
10006 ORF1ab silent	1541	
11288 ORF1ab del 9	3633	
14408 ORF1ab P314L	2437	
16500 ORF1ab Q1011H	8201	
20262 ORF1ab silent	1606	
21575 S L5F	850	
21846 S T95I	1928	
22320 S D253G	648	
22992 S S477N	376	
23403 S D614G	4288	
23824 S L754F	385	
24432 S Q957R	3541	
25517 ORF3a P42L	1934	
25563 ORF3a Q57H	4249	
25968 ORF3a silent	3734	
27739 ORF7a L116F	1807	
27925 ORF8 T11I	1952	
28271 intergenic del 1	2855	
28311 N P13L	3109	
28879 N S202R	717	
29721 intergenic	154	
	VSP1354-1	

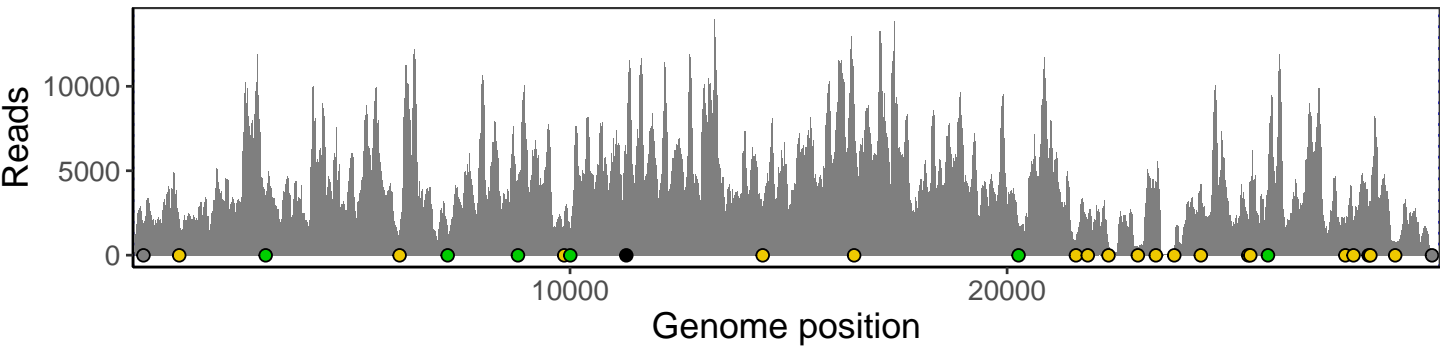
Base change

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

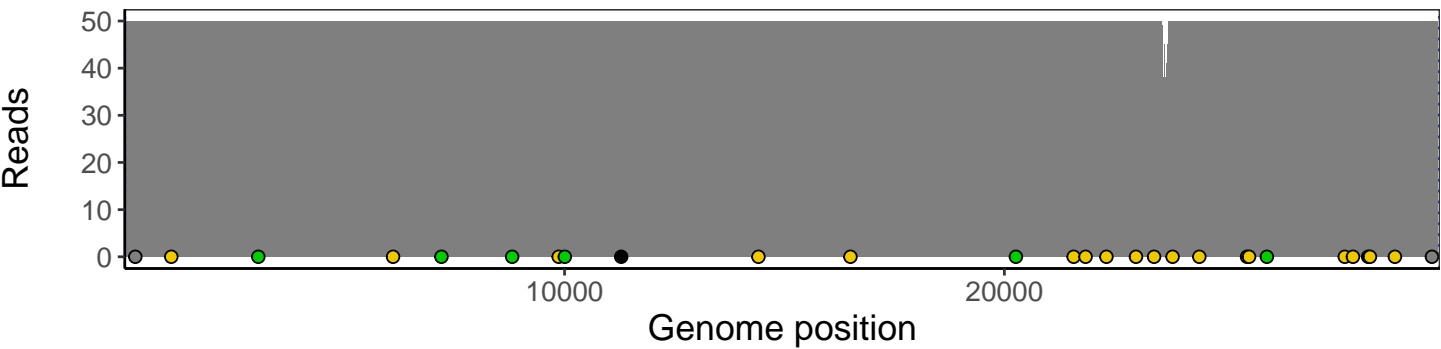
Analyses of individual experiments and composite results

VSP1354-1 | 2021-03-15 | VTM | UPHS-0309 | genomes | single experiment

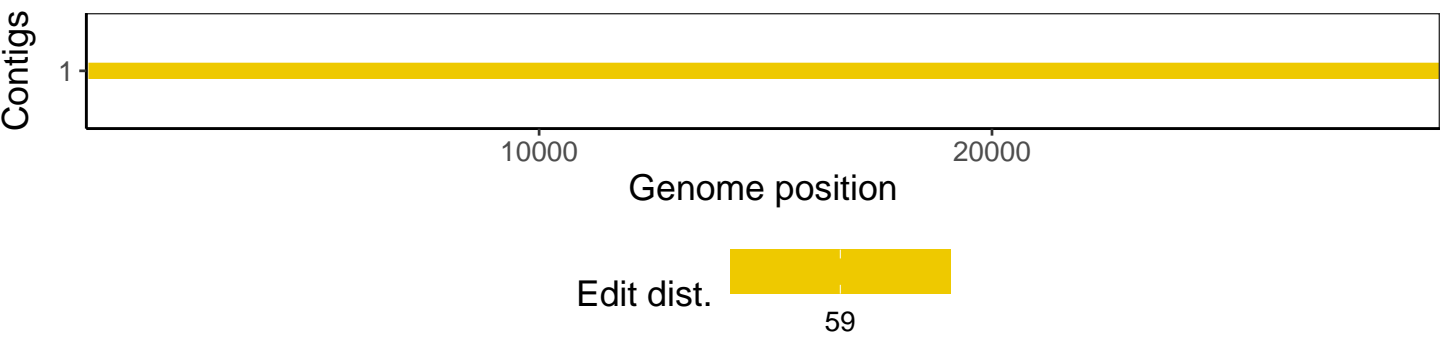
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	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