

COVID-19 subject H2102100346

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.

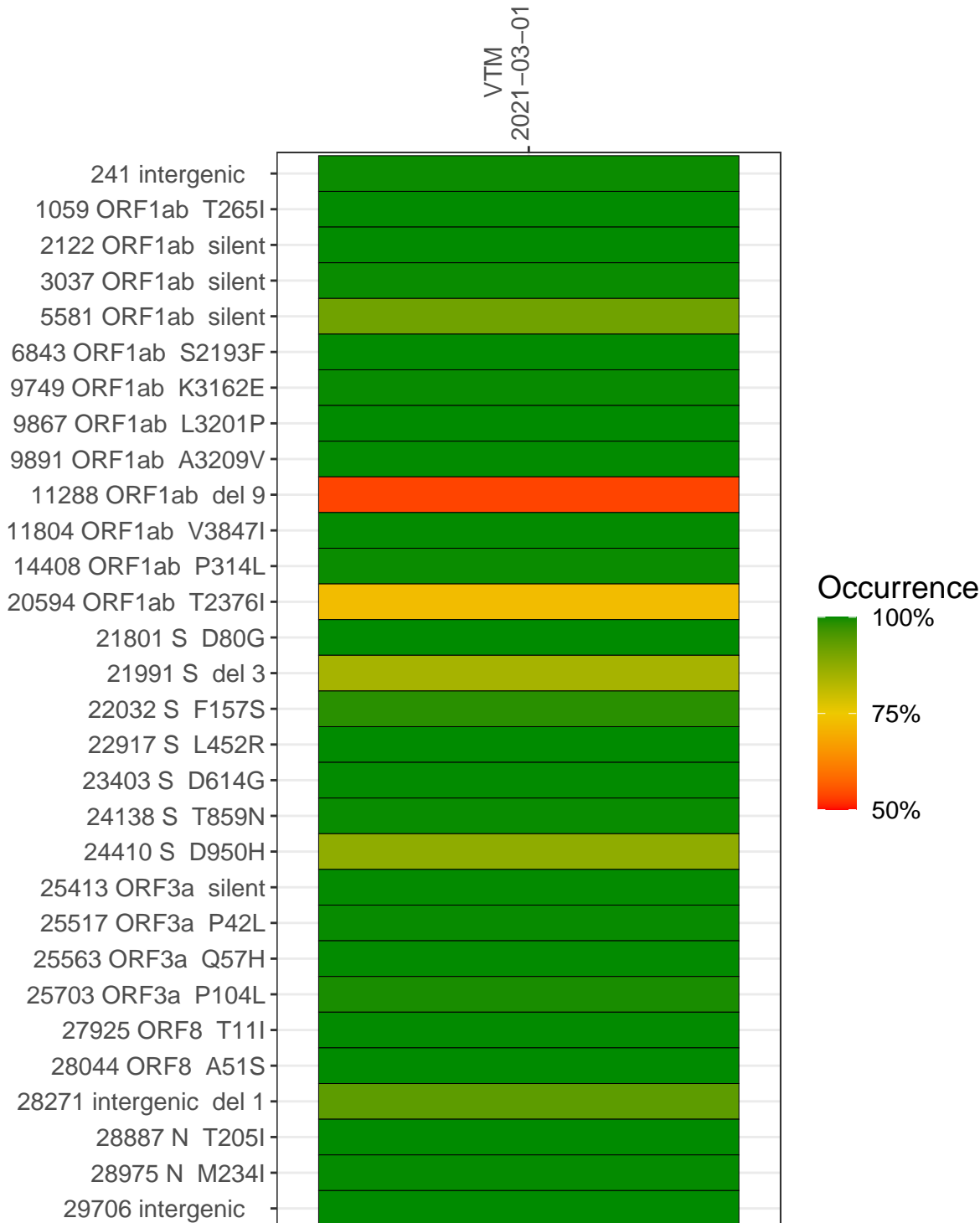
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with $> 90\%$ sequence coverage.

Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (≥ 5 reads)
VSP0696-1	single experiment	NA	VTM	2021-03-01	29.88	B.1.526	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 2021-03-01	
241 intergenic	2278	
1059 ORF1ab T265I	2871	
2122 ORF1ab silent	3304	
3037 ORF1ab silent	3622	
5581 ORF1ab silent	8054	
6843 ORF1ab S2193F	6228	
9749 ORF1ab K3162E	616	
9867 ORF1ab L3201P	1042	
9891 ORF1ab A3209V	1915	
11288 ORF1ab del 9	3229	
11804 ORF1ab V3847I	7975	
14408 ORF1ab P314L	5221	
20594 ORF1ab T2376I	11834	
21801 S D80G	3845	
21991 S del 3	1779	
22032 S F157S	1394	
22917 S L452R	189	
23403 S D614G	7190	
24138 S T859N	3713	
24410 S D950H	4950	
25413 ORF3a silent	5585	
25517 ORF3a P42L	3513	
25563 ORF3a Q57H	6184	
25703 ORF3a P104L	4064	
27925 ORF8 T11I	6110	
28044 ORF8 A51S	6951	
28271 intergenic del 1	4720	
28887 N T205I	1304	
28975 N M234I	1927	
29706 intergenic	247	
	VSP0696-1	

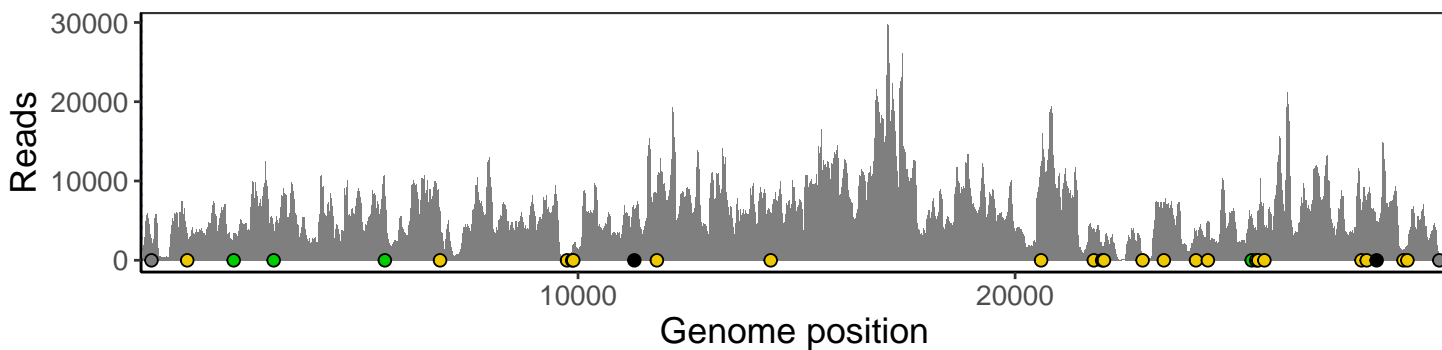
Base change

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

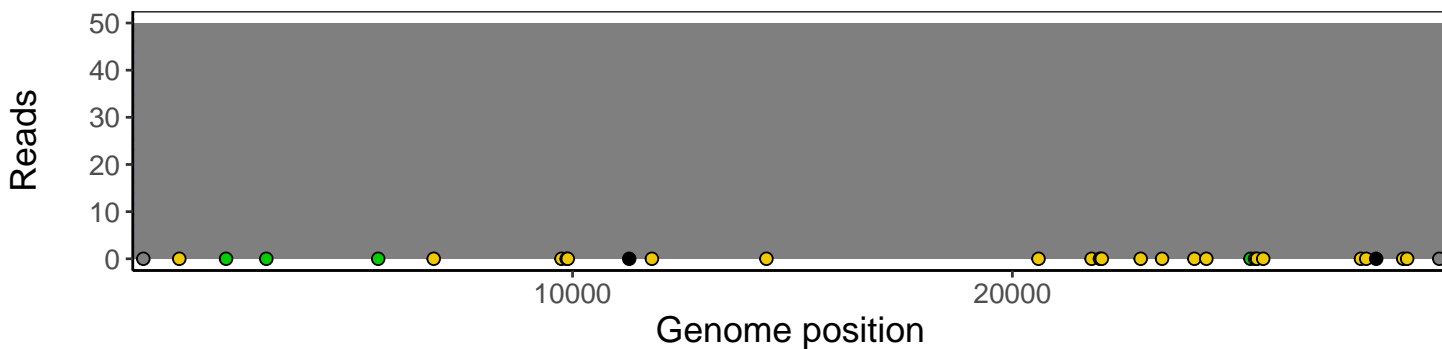
Analyses of individual experiments and composite results

VSP0696-1 | 2021-03-01 | VTM | H2102100346 | genomes | single experiment

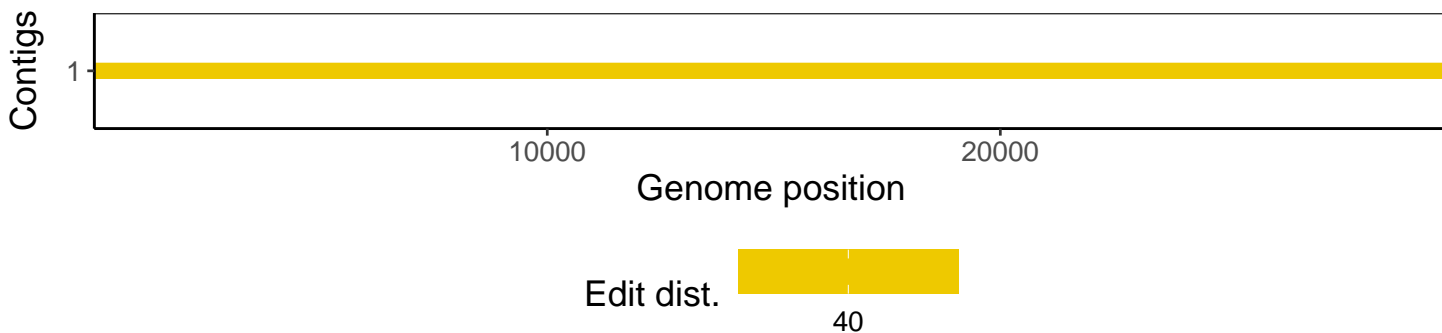
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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