COVID-19 subject H2102170736

2021-04-01

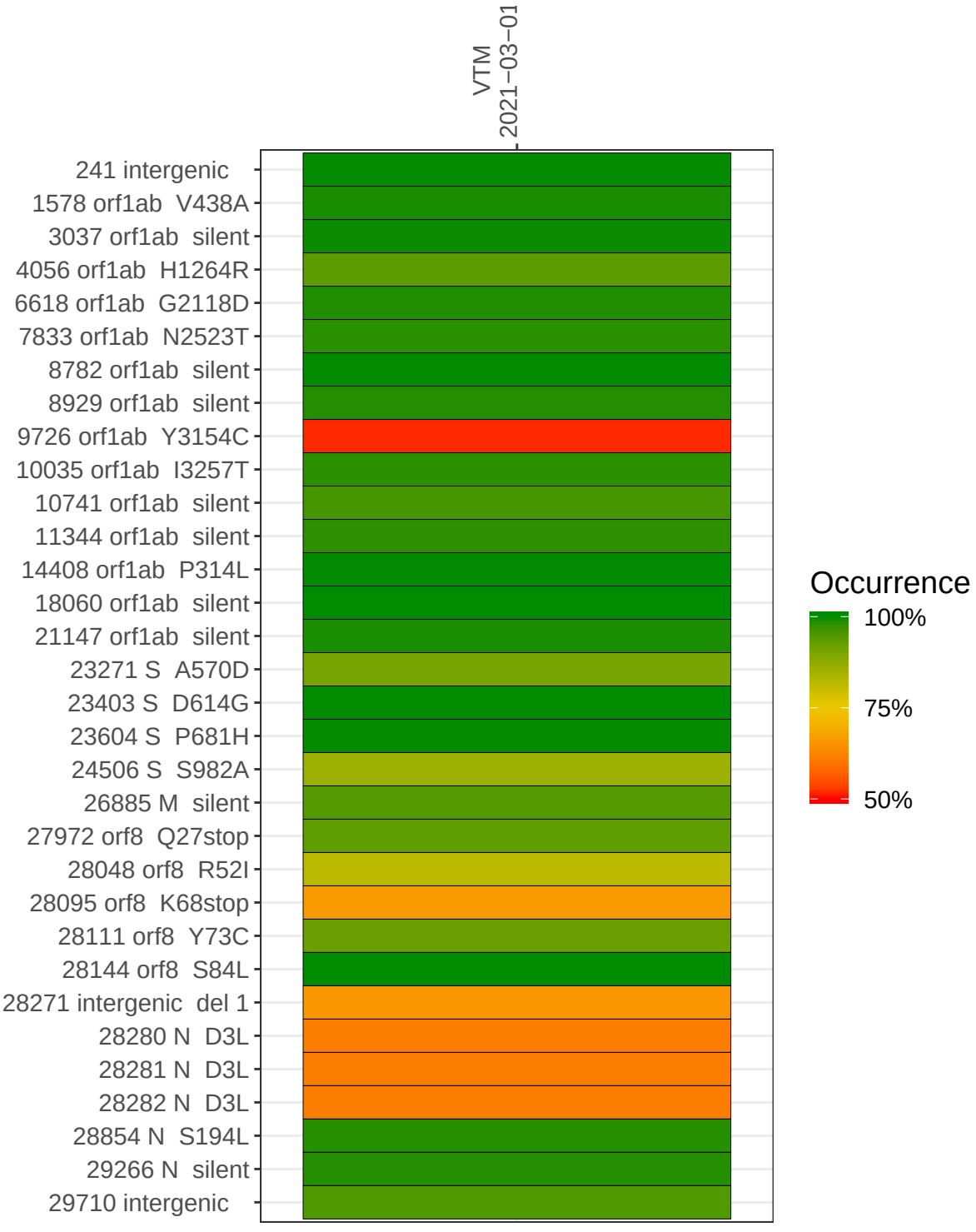
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with > 90% sequence coverage.

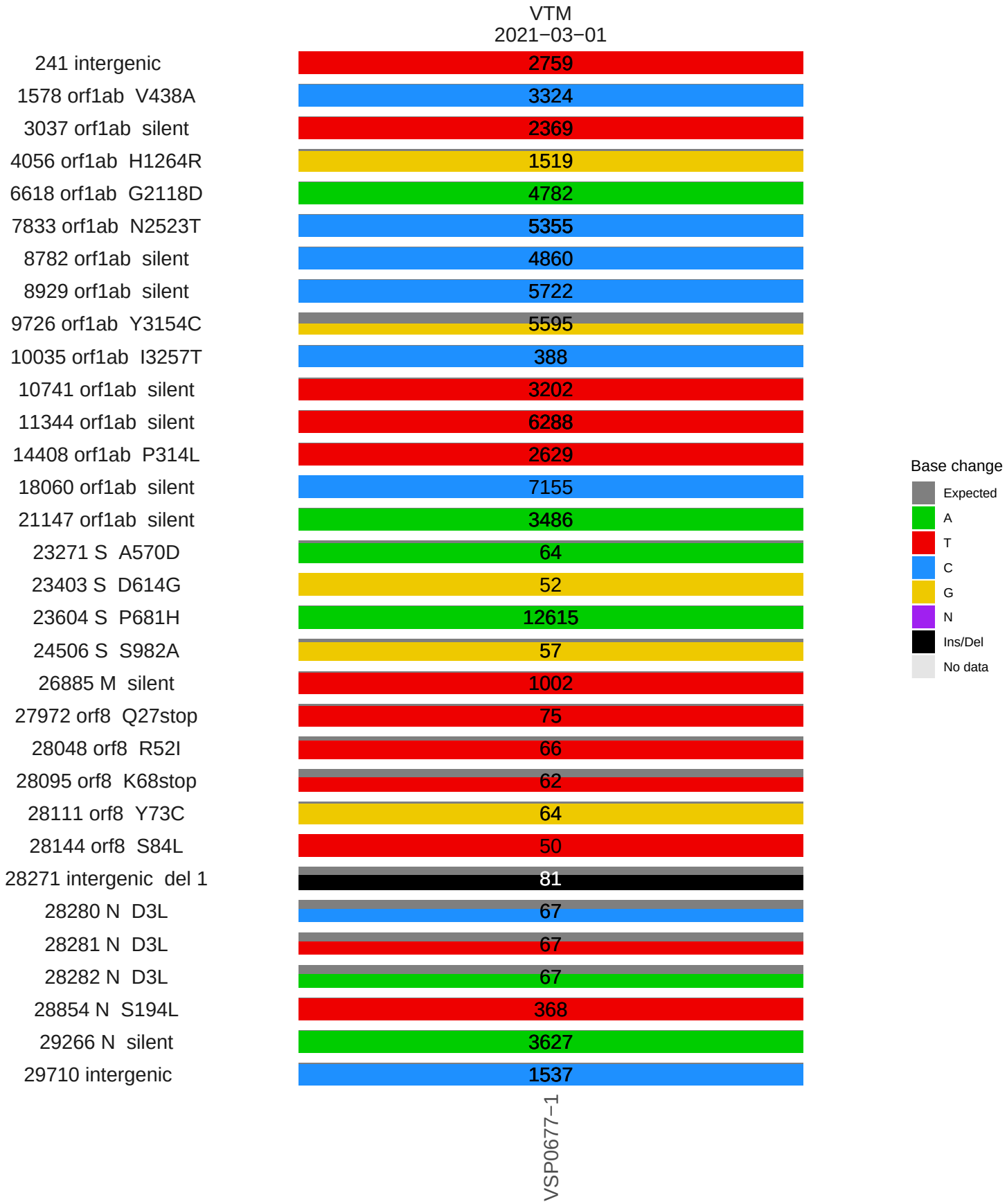
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0677-1	single experiment	NA	VTM	2021-03-01	29.83	B.1	99.8%	99.4%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/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.

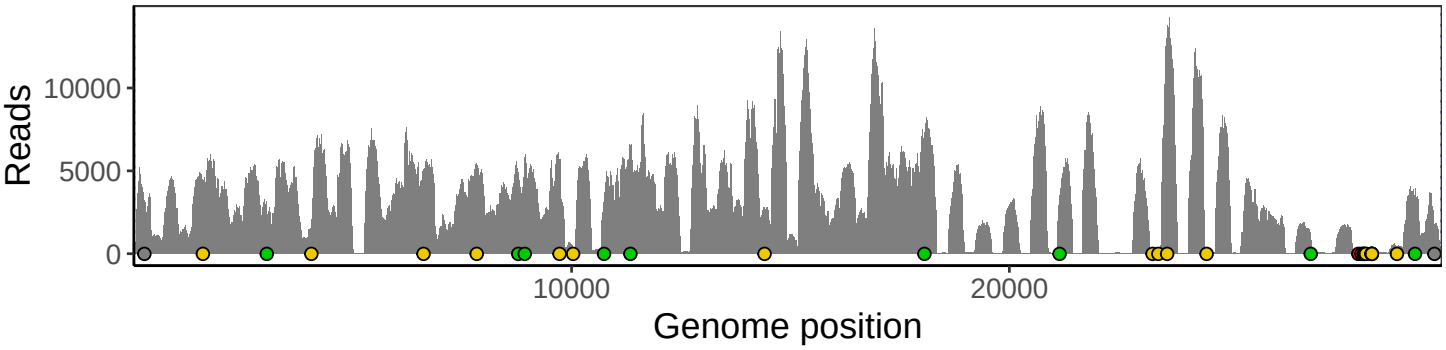



VTM
2021−03−01
241 intergenic
1578 orf1ab V438A
3037 orf1ab silent
4056 orf1ab H1264R
6618 orf1ab G2118D
7833 orf1ab N2523T
8782 orf1ab silent
8929 orf1ab silent
9726 orf1ab Y3154C
10035 orf1ab I3257T
10741 orf1ab silent
11344 orf1ab silent
14408 orf1ab P314L
18060 orf1ab silent
21147 orf1ab silent
23271 S A570D
23403 S D614G
23604 S P681H
24506 S S982A
26885 M silent
27972 orf8 Q27stop
28048 orf8 R52I
28095 orf8 K68stop
28111 orf8 Y73C
28144 orf8 S84L
28271 intergenic del 1
28280 N D3L
28281 N D3L
28282 N D3L
28854 N S194L
29266 N silent
29710 intergenic
2759
3324
2369
1519
4782
5355
4860
5722
5595
388
3202
6288
2629
7155
3486
64
52
12615
57
1002
75
66
62
64
50
81
67
67
67
368
3627
1537
VSP0677−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

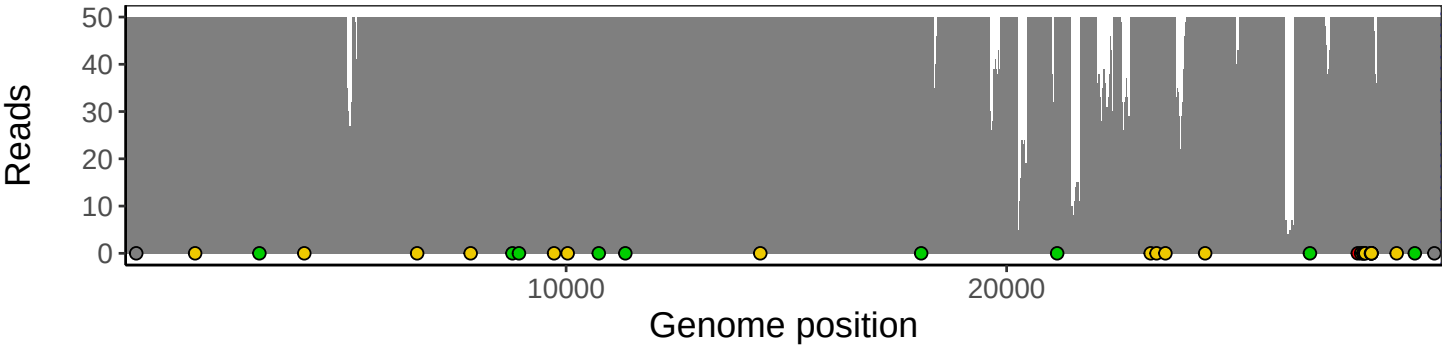
Analyses of individual experiments and composite results

VSP0677-1 | 2021-03-01 | VTM | H2102170736 | genomes | single experiment

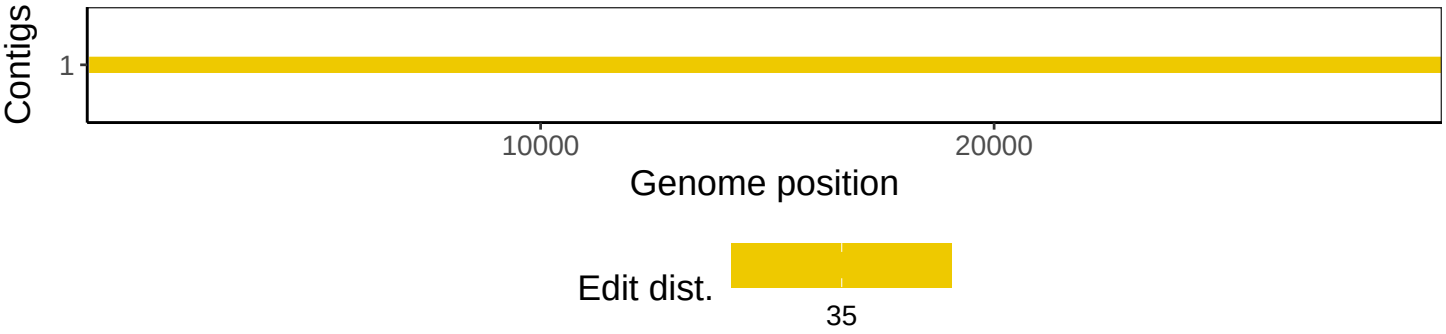
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.3
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