COVID-19 subject UPHS-0818

2021-05-21

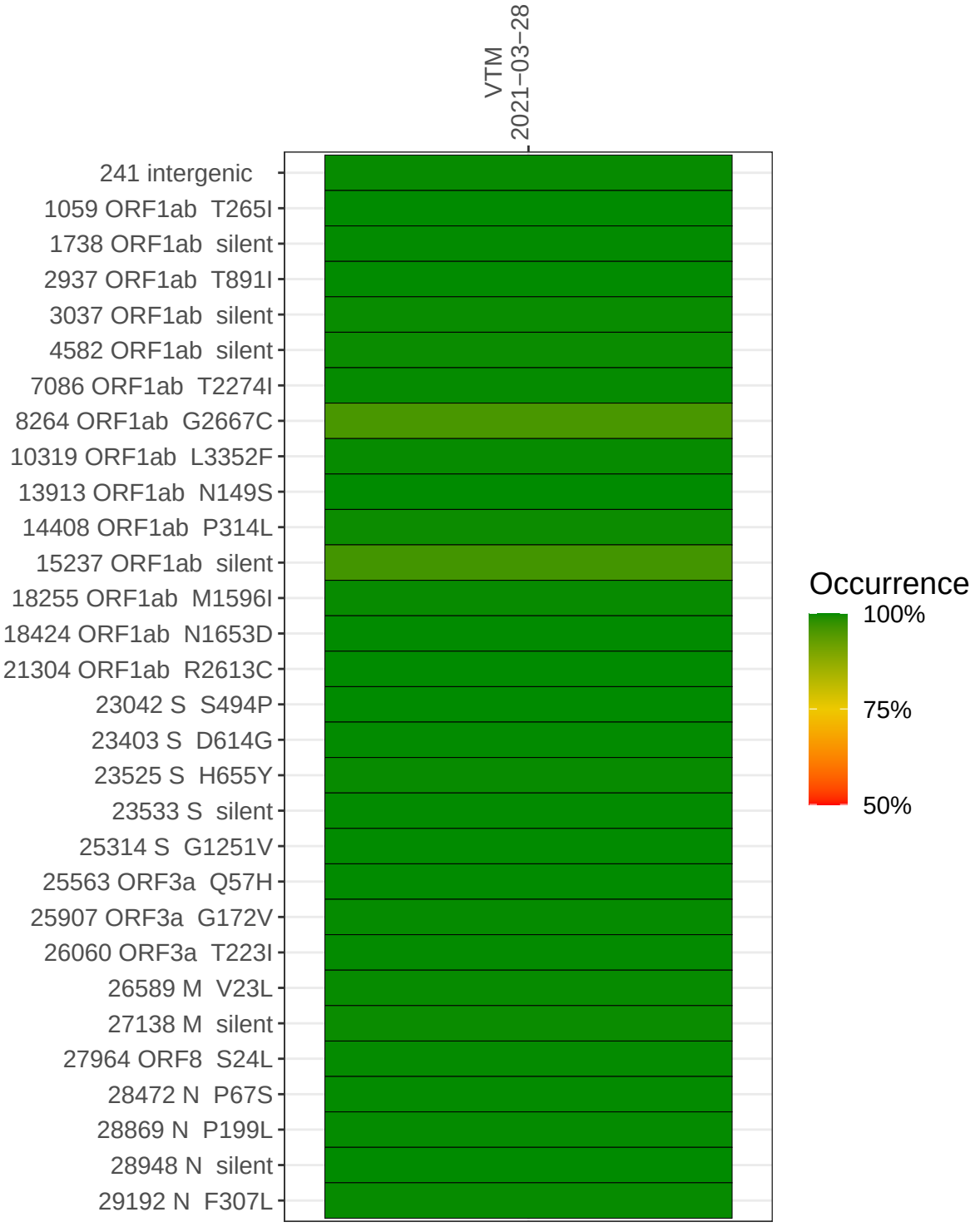
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

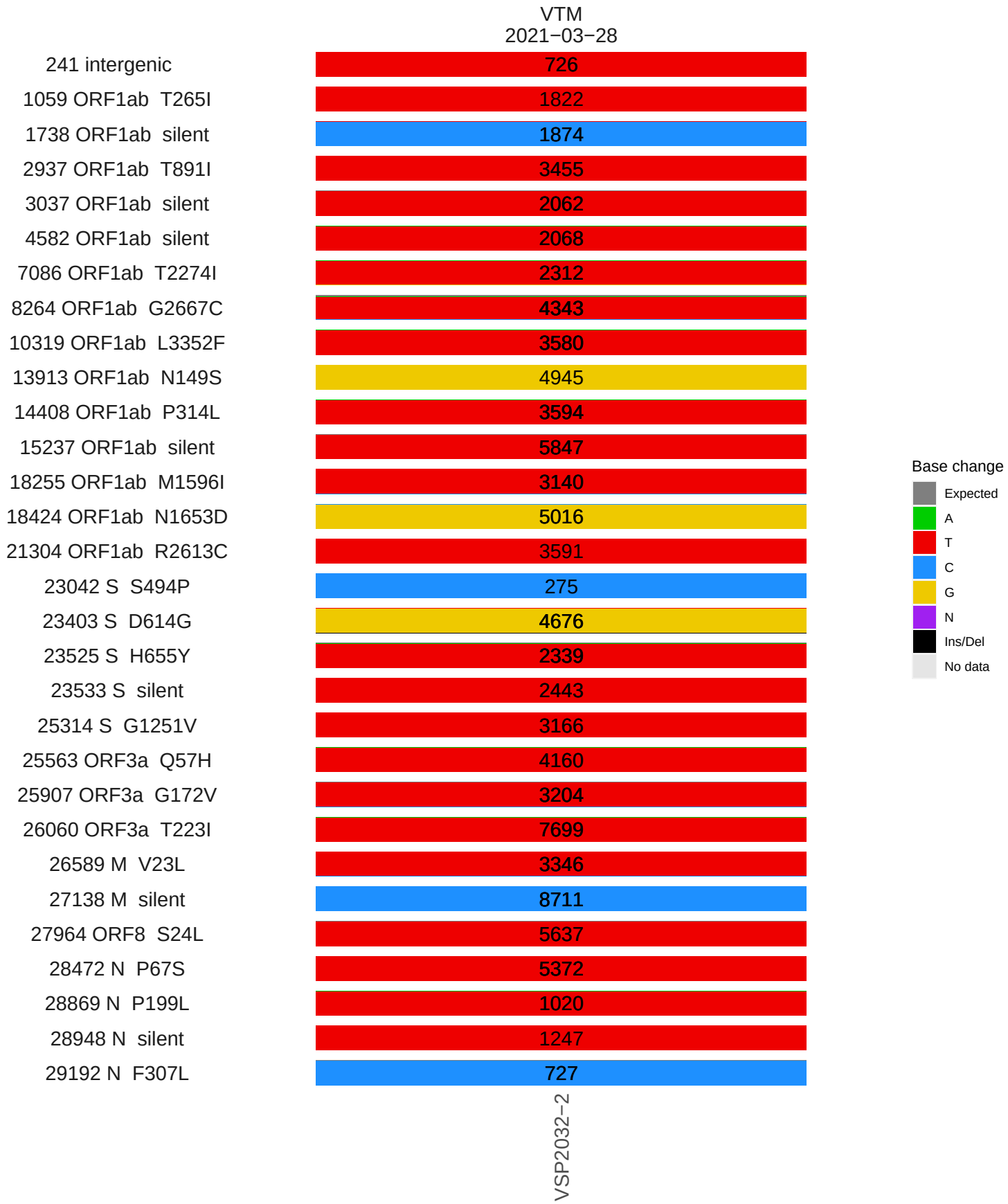
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2032-2	single experiment	NA	VTM	2021-03-28	29.84	B.1.2	99.8%	99.7%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/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.

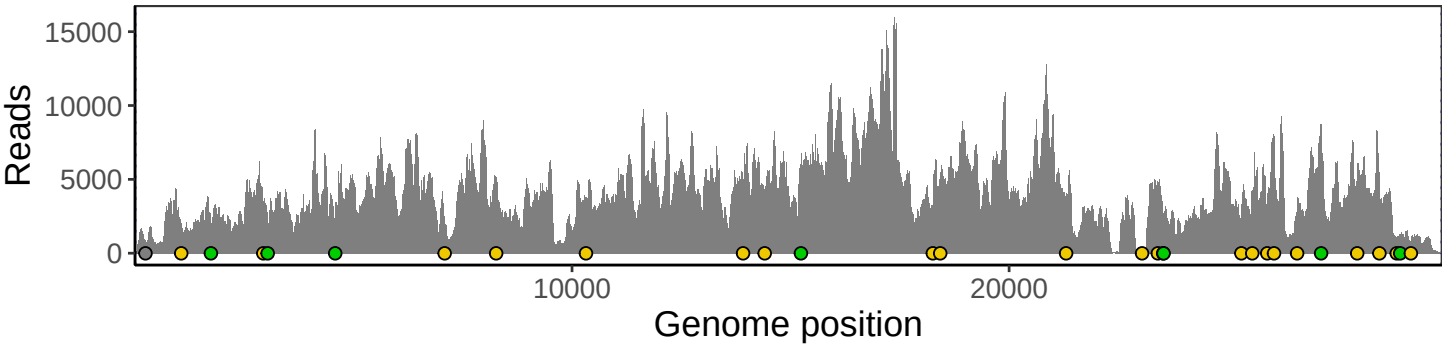



VTM
2021−03−28
241 intergenic
1059 ORF1ab T265I
1738 ORF1ab silent
2937 ORF1ab T891I
3037 ORF1ab silent
4582 ORF1ab silent
7086 ORF1ab T2274I
8264 ORF1ab G2667C
10319 ORF1ab L3352F
13913 ORF1ab N149S
14408 ORF1ab P314L
15237 ORF1ab silent
18255 ORF1ab M1596I
18424 ORF1ab N1653D
21304 ORF1ab R2613C
23042 S S494P
23403 S D614G
23525 S H655Y
23533 S silent
25314 S G1251V
25563 ORF3a Q57H
25907 ORF3a G172V
26060 ORF3a T223I
26589 M V23L
27138 M silent
27964 ORF8 S24L
28472 N P67S
28869 N P199L
28948 N silent
29192 N F307L
726
1822
1874
3455
2062
2068
2312
4343
3580
4945
3594
5847
3140
5016
3591
275
4676
2339
2443
3166
4160
3204
7699
3346
8711
5637
5372
1020
1247
727
VSP2032−2
Base change
Expected
A
T
C
G
N
Ins/Del
No data

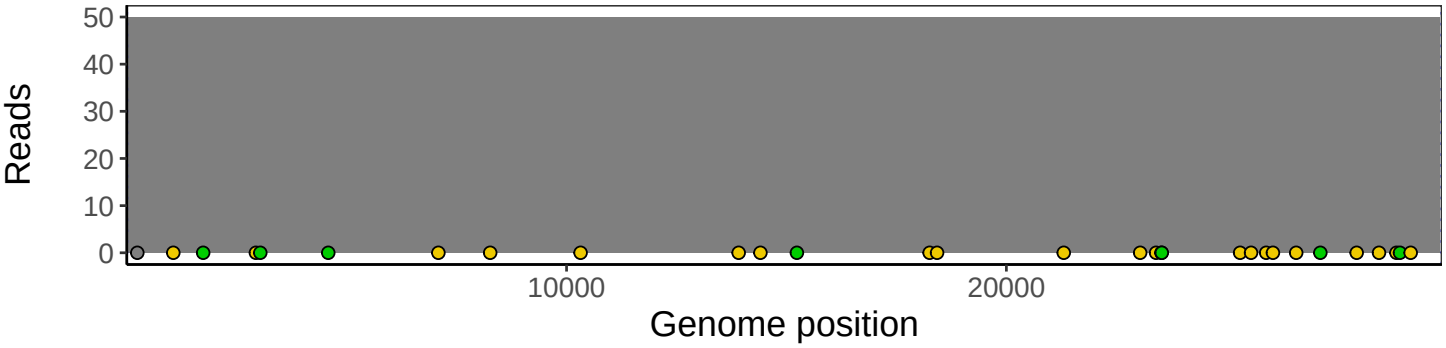
Analyses of individual experiments and composite results

VSP2032-2 | 2021-03-28 | VTM | UPHS-0818 | genomes | single experiment

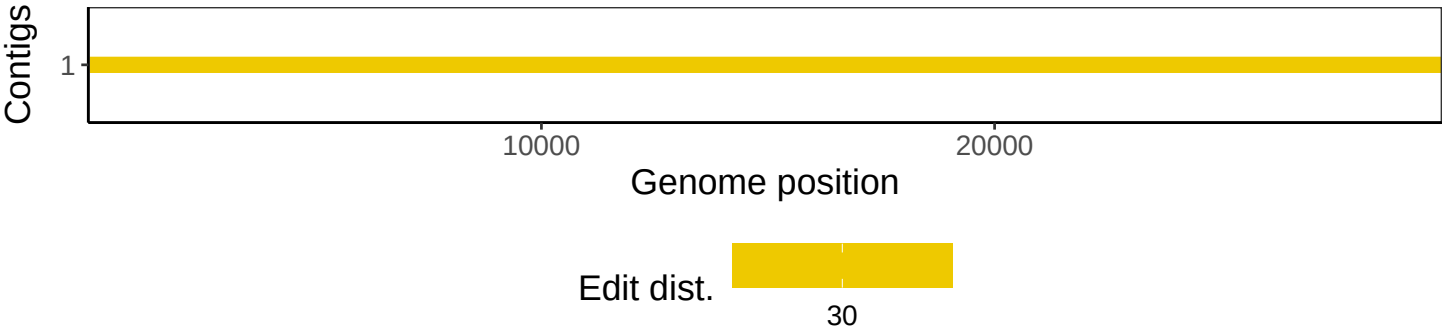
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.8
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