COVID-19 subject UPHS-0131

2021-03-29

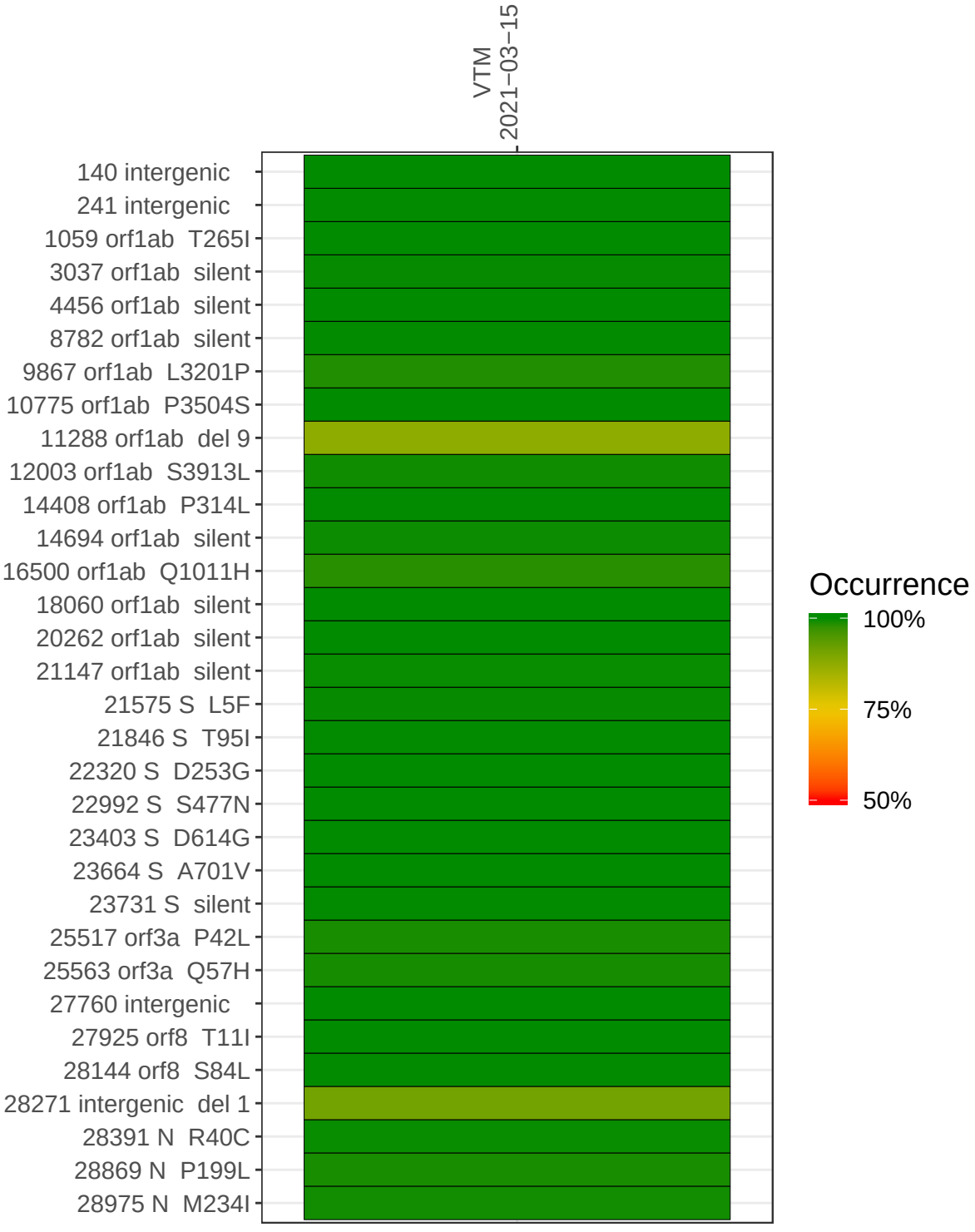
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

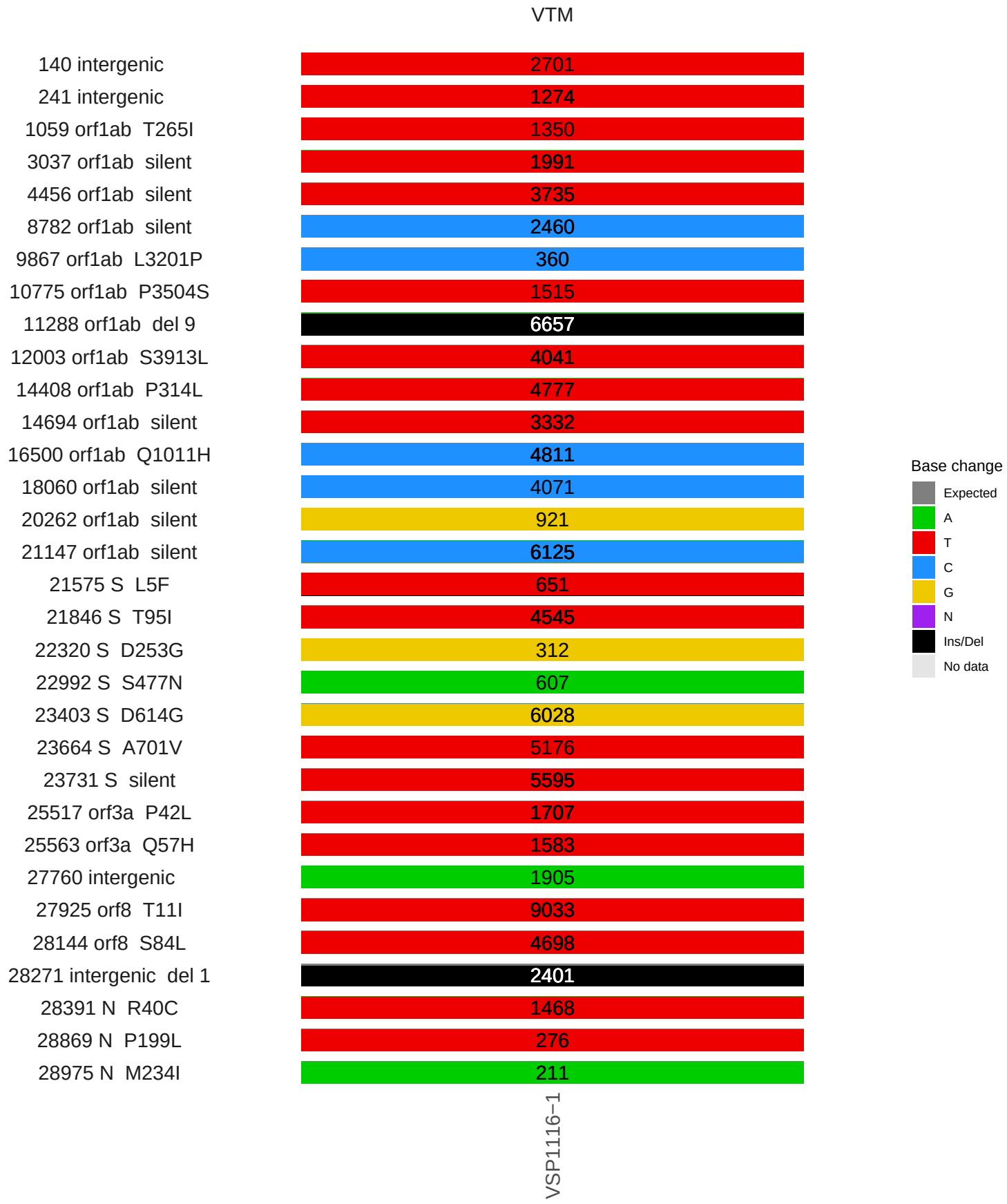
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1116-1	single experiment	NA	VTM	2021-03-15	29.88	B.1.526	99.9%	99.8%

Variants shared across samples

The heat map below shows how variants (reference genome 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.

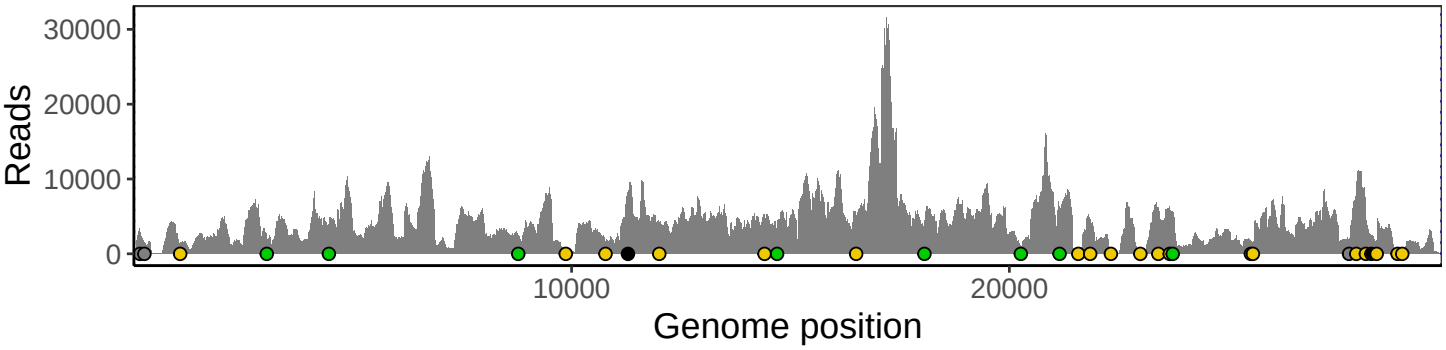



VTM
140 intergenic
241 intergenic
1059 orf1ab T265I
3037 orf1ab silent
4456 orf1ab silent
8782 orf1ab silent
9867 orf1ab L3201P
10775 orf1ab P3504S
11288 orf1ab del 9
12003 orf1ab S3913L
14408 orf1ab P314L
14694 orf1ab silent
16500 orf1ab Q1011H
18060 orf1ab silent
20262 orf1ab silent
21147 orf1ab silent
21575 S L5F
21846 S T95I
22320 S D253G
22992 S S477N
23403 S D614G
23664 S A701V
23731 S silent
25517 orf3a P42L
25563 orf3a Q57H
27760 intergenic
27925 orf8 T11I
28144 orf8 S84L
28271 intergenic del 1
28391 N R40C
28869 N P199L
28975 N M234I
2701
1274
1350
1991
3735
2460
360
1515
6657
4041
4777
3332
4811
4071
921
6125
651
4545
312
607
6028
5176
5595
1707
1583
1905
9033
4698
2401
1468
276
211
VSP1116−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

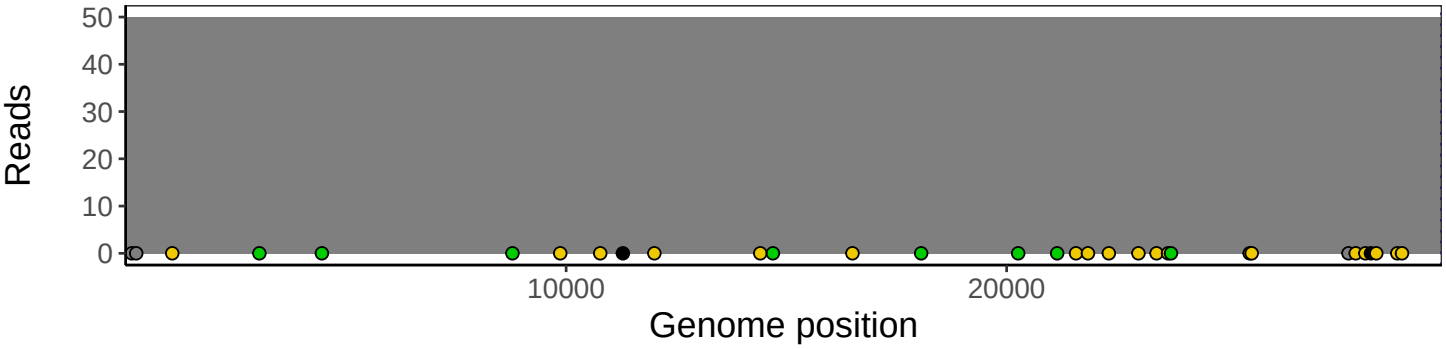
Analyses of individual experiments and composite results

VSP1116-1 | 2021-03-15 | VTM | UPHS-0131 | genomes | single experiment

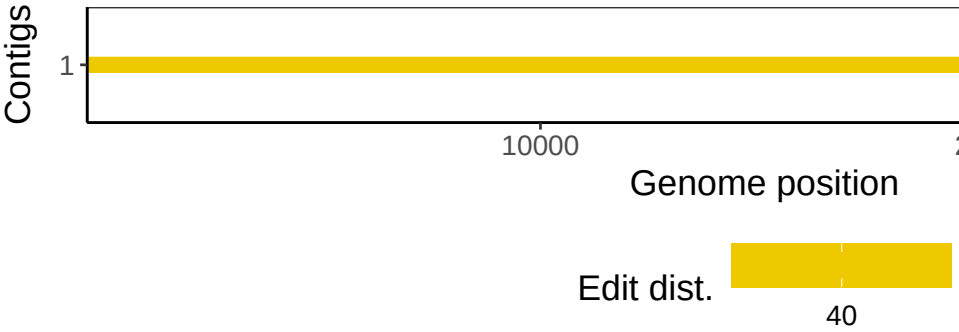
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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