COVID-19 subject UPHS-0136

2021-03-31

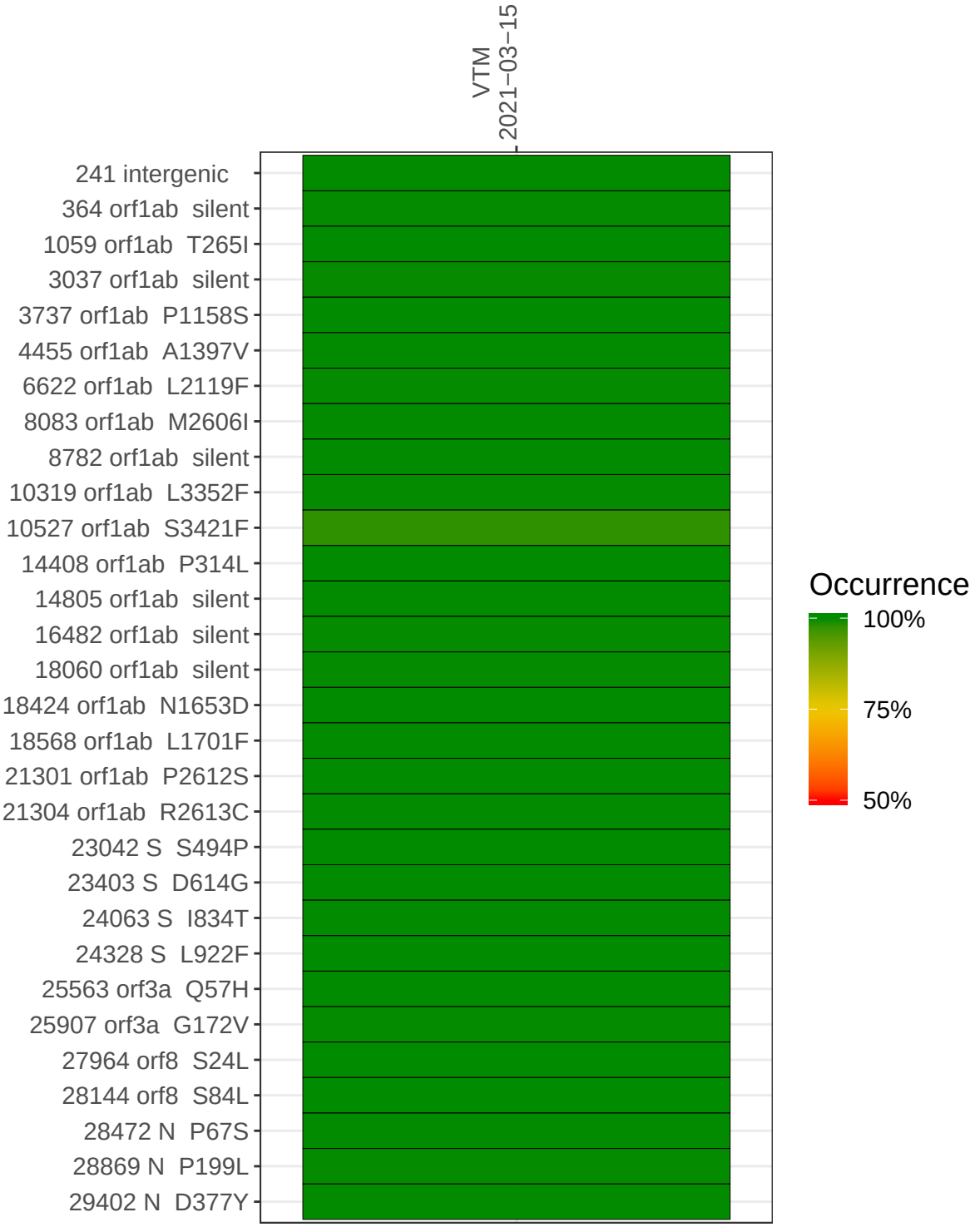
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

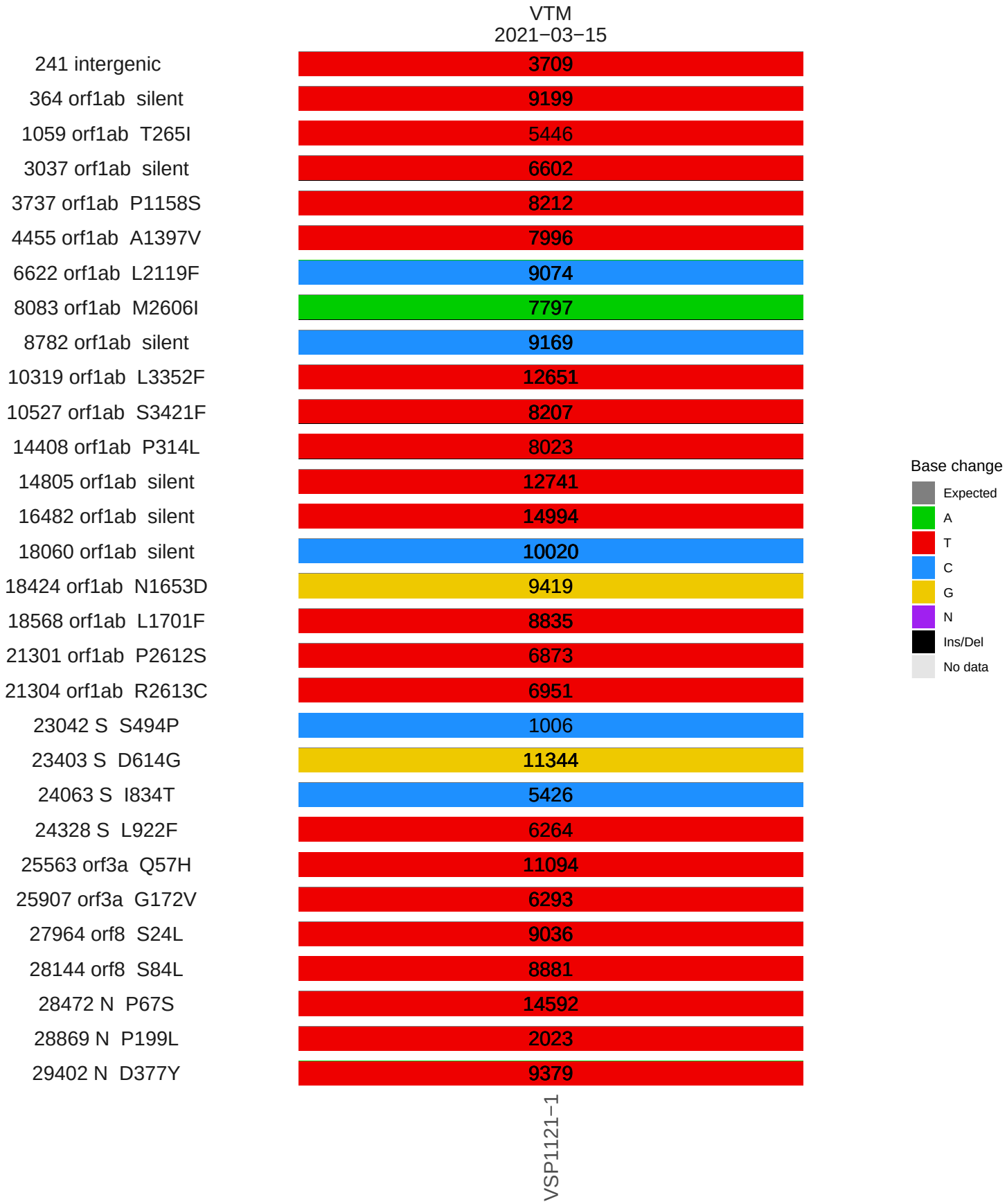
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1121-1	single experiment	NA	VTM	2021-03-15	29.90	B.1.2	99.9%	99.9%

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.

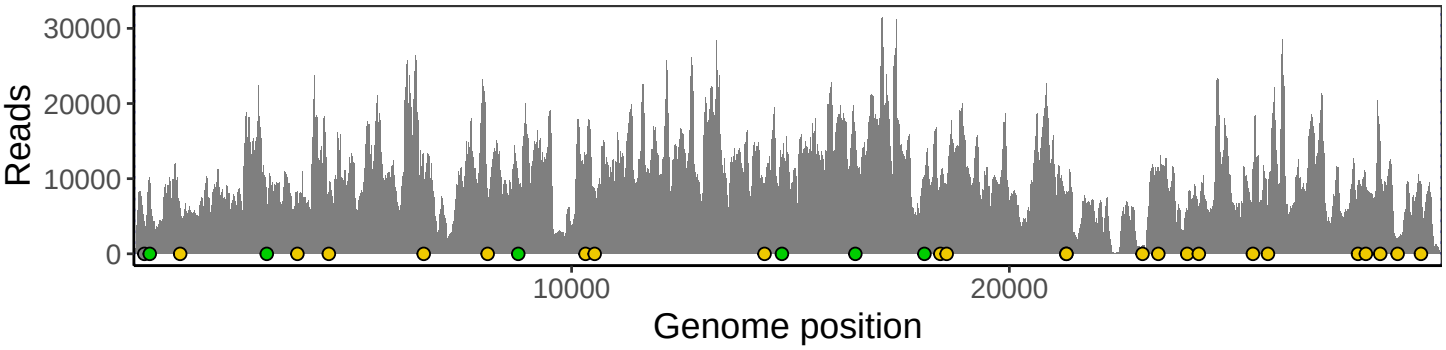



VTM
2021−03−15
241 intergenic
364 orf1ab silent
1059 orf1ab T265I
3037 orf1ab silent
3737 orf1ab P1158S
4455 orf1ab A1397V
6622 orf1ab L2119F
8083 orf1ab M2606I
8782 orf1ab silent
10319 orf1ab L3352F
10527 orf1ab S3421F
14408 orf1ab P314L
14805 orf1ab silent
16482 orf1ab silent
18060 orf1ab silent
18424 orf1ab N1653D
18568 orf1ab L1701F
21301 orf1ab P2612S
21304 orf1ab R2613C
23042 S S494P
23403 S D614G
24063 S I834T
24328 S L922F
25563 orf3a Q57H
25907 orf3a G172V
27964 orf8 S24L
28144 orf8 S84L
28472 N P67S
28869 N P199L
29402 N D377Y
3709
9199
5446
6602
8212
7996
9074
7797
9169
12651
8207
8023
12741
14994
10020
9419
8835
6873
6951
1006
11344
5426
6264
11094
6293
9036
8881
14592
2023
9379
VSP1121−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

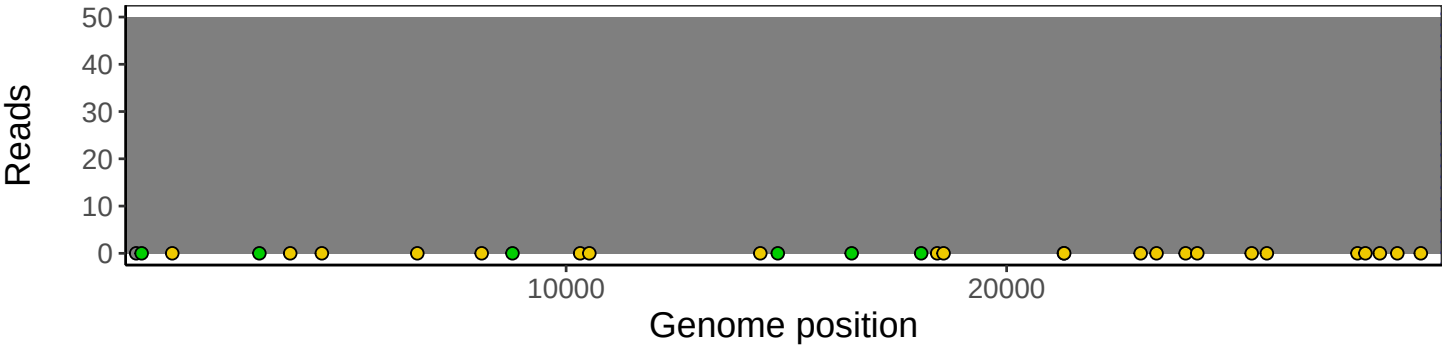
Analyses of individual experiments and composite results

VSP1121-1 | 2021-03-15 | VTM | UPHS-0136 | genomes | single experiment

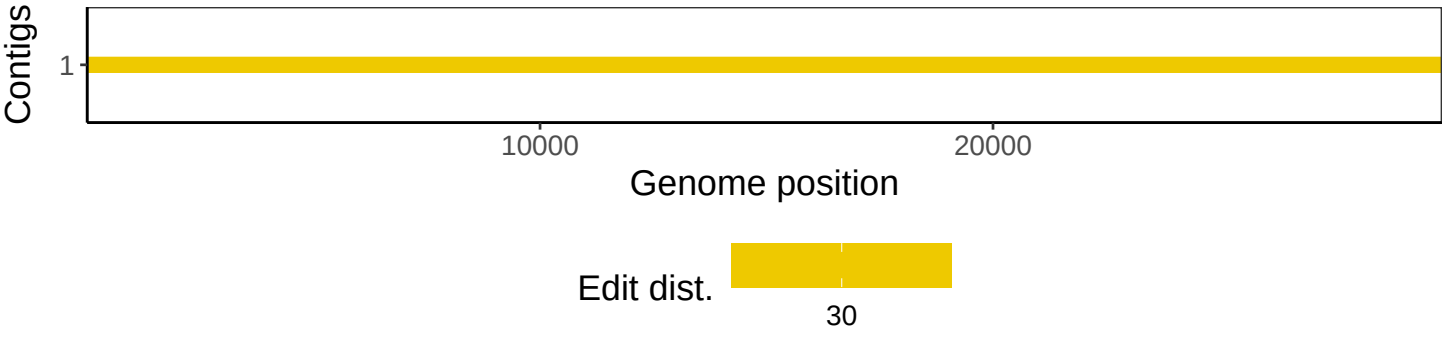
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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