COVID-19 subject UPHS-0130

2021-04-17

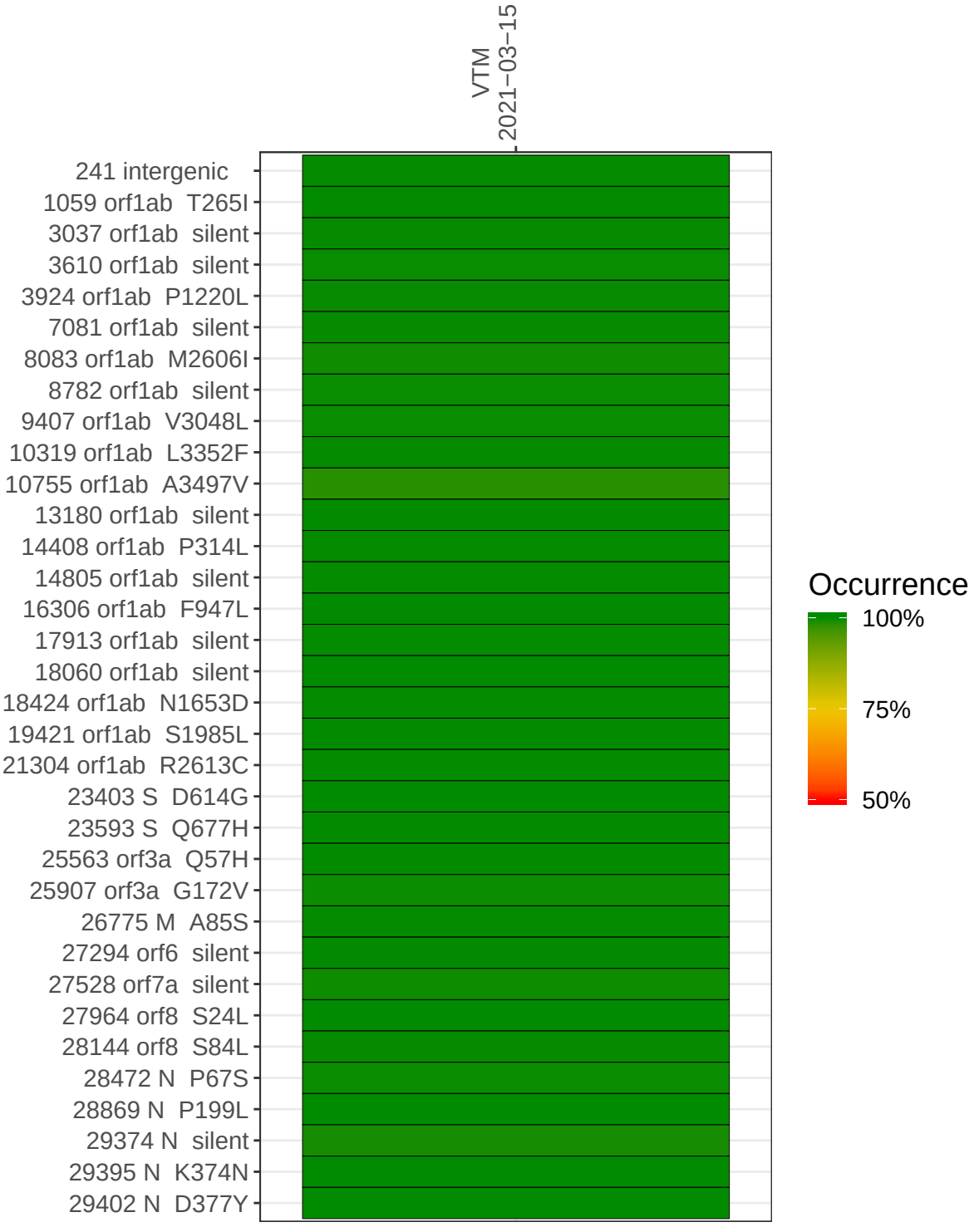
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

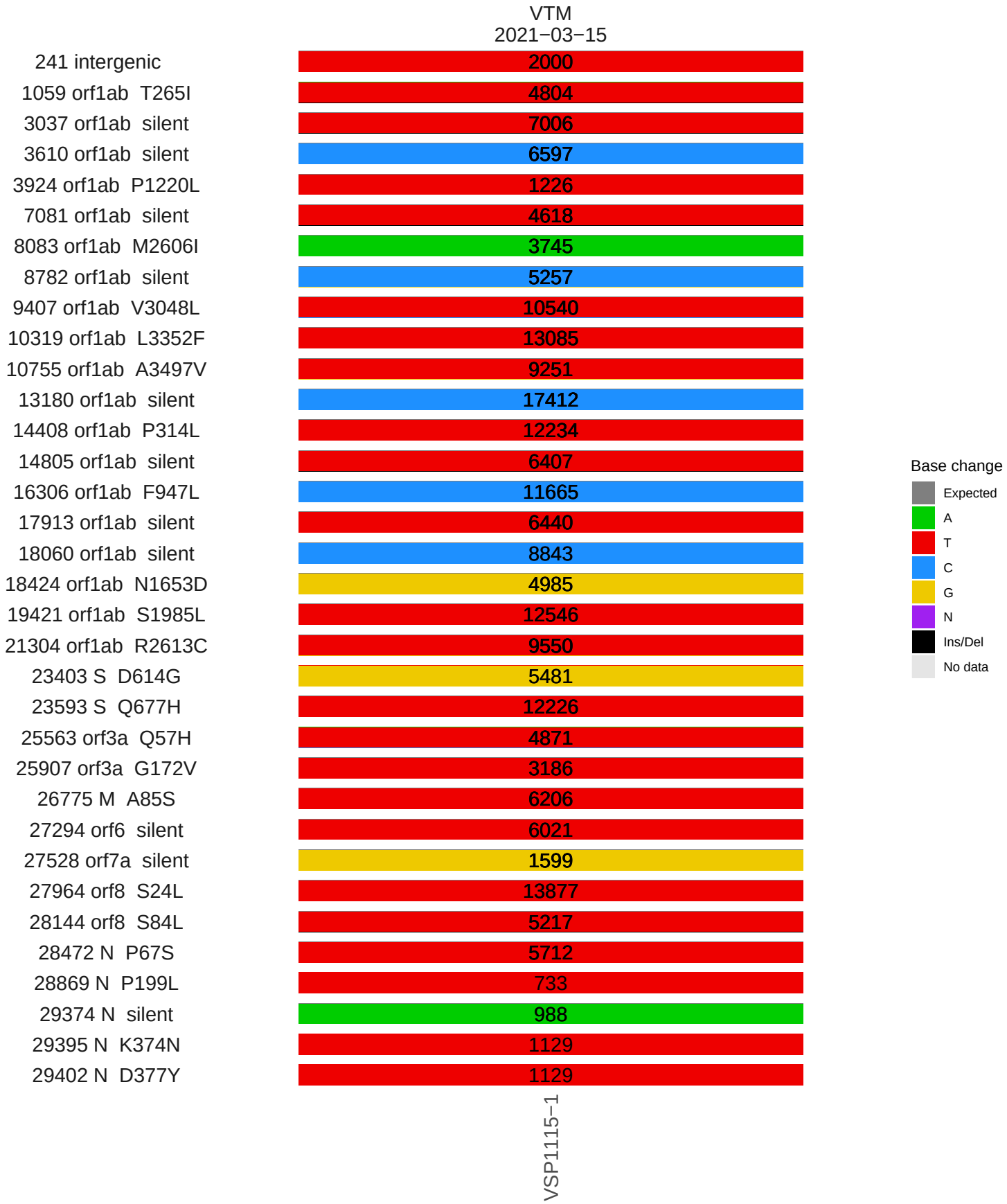
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1115-1	single experiment	NA	VTM	2021-03-15	29.83	B.1.2	99.9%	99.8%

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.

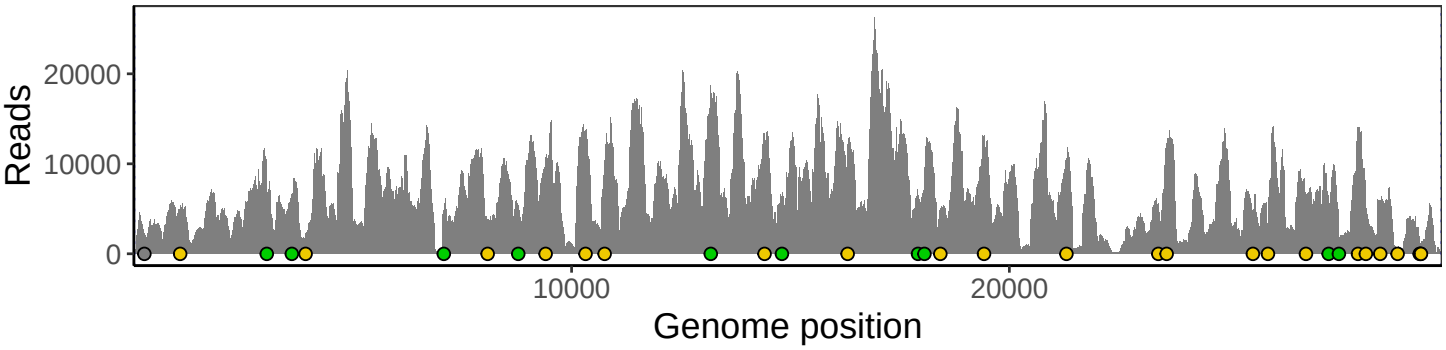



VTM
2021−03−15
241 intergenic
1059 orf1ab T265I
3037 orf1ab silent
3610 orf1ab silent
3924 orf1ab P1220L
7081 orf1ab silent
8083 orf1ab M2606I
8782 orf1ab silent
9407 orf1ab V3048L
10319 orf1ab L3352F
10755 orf1ab A3497V
13180 orf1ab silent
14408 orf1ab P314L
14805 orf1ab silent
16306 orf1ab F947L
17913 orf1ab silent
18060 orf1ab silent
18424 orf1ab N1653D
19421 orf1ab S1985L
21304 orf1ab R2613C
23403 S D614G
23593 S Q677H
25563 orf3a Q57H
25907 orf3a G172V
26775 M A85S
27294 orf6 silent
27528 orf7a silent
27964 orf8 S24L
28144 orf8 S84L
28472 N P67S
28869 N P199L
29374 N silent
29395 N K374N
29402 N D377Y
2000
4804
7006
6597
1226
4618
3745
5257
10540
13085
9251
17412
12234
6407
11665
6440
8843
4985
12546
9550
5481
12226
4871
3186
6206
6021
1599
13877
5217
5712
733
988
1129
1129
VSP1115−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

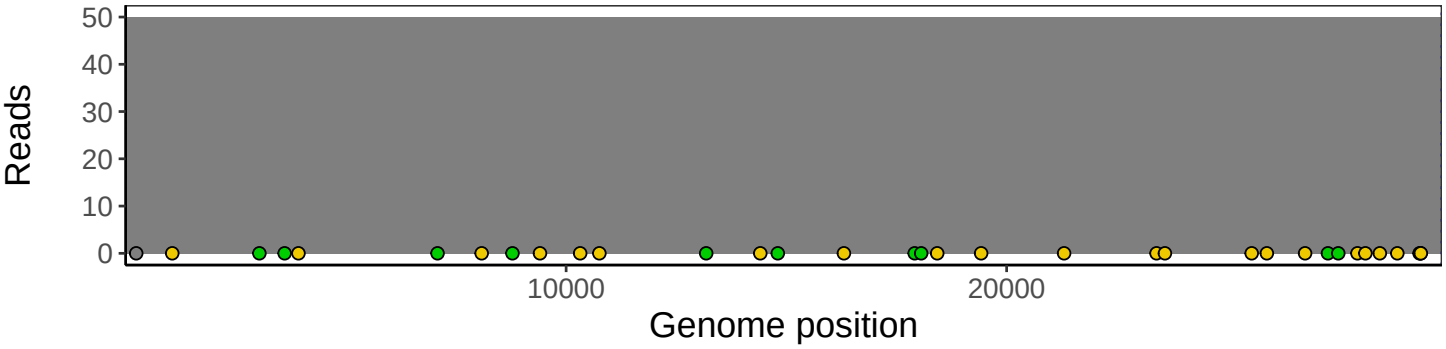
Analyses of individual experiments and composite results

VSP1115-1 | 2021-03-15 | VTM | UPHS-0130 | genomes | single experiment

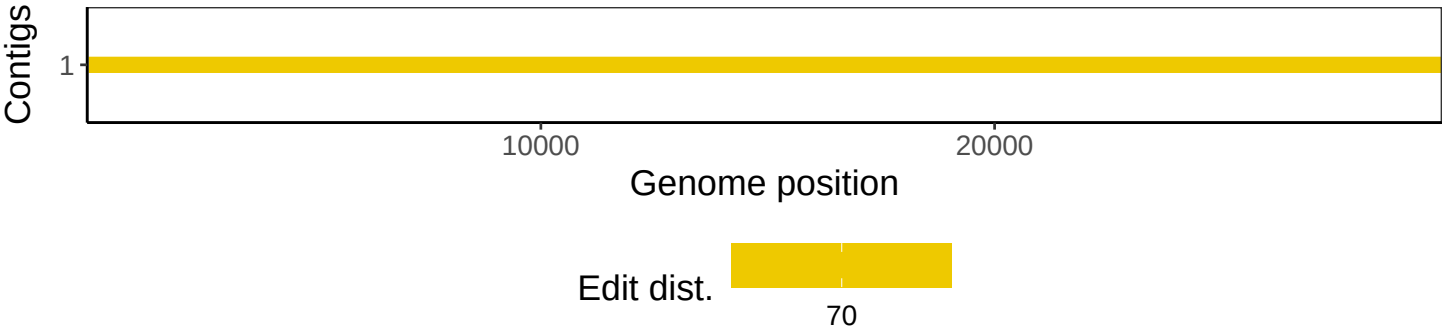
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.0.0
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