COVID-19 subject UPHS-0121

2021-03-29

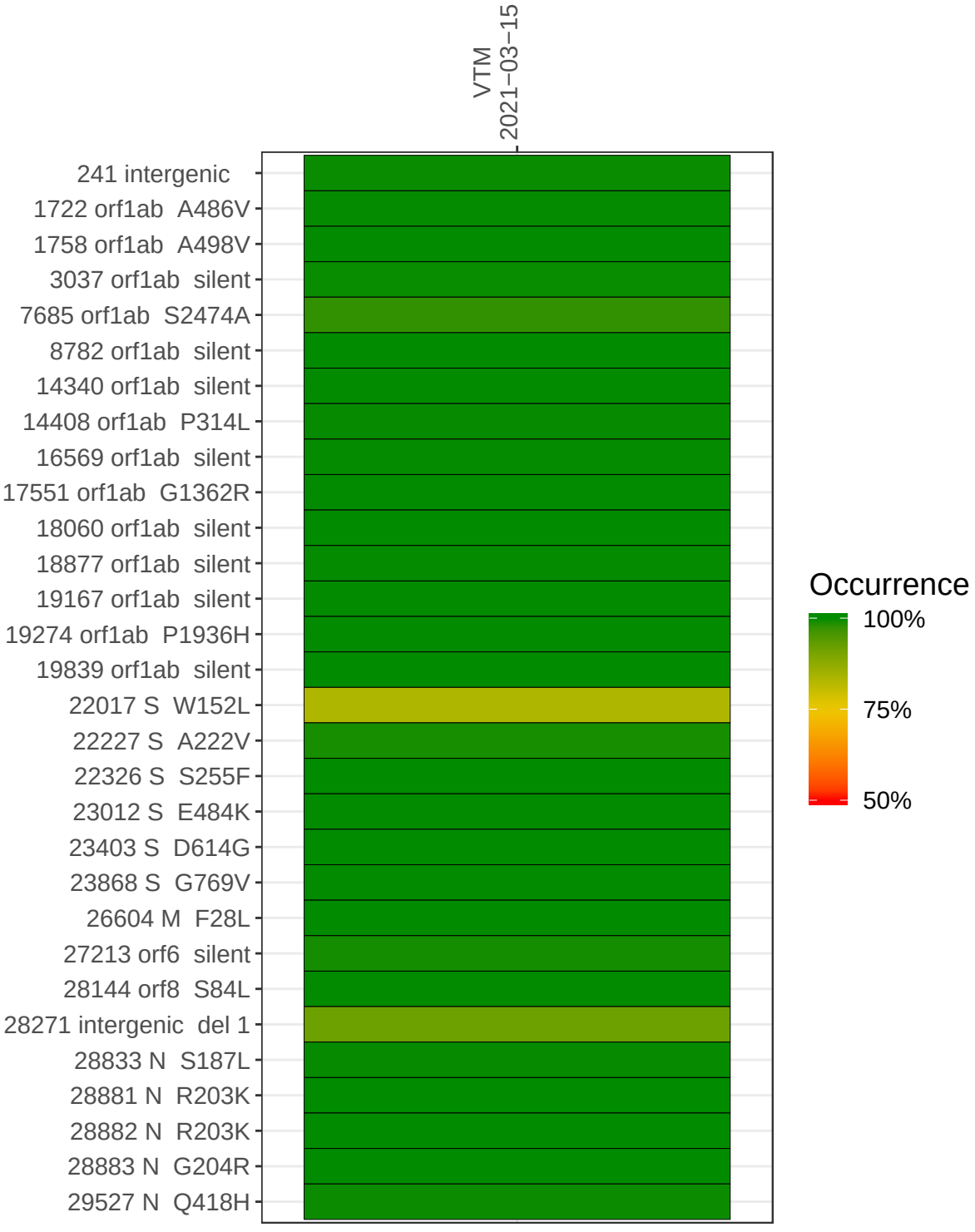
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

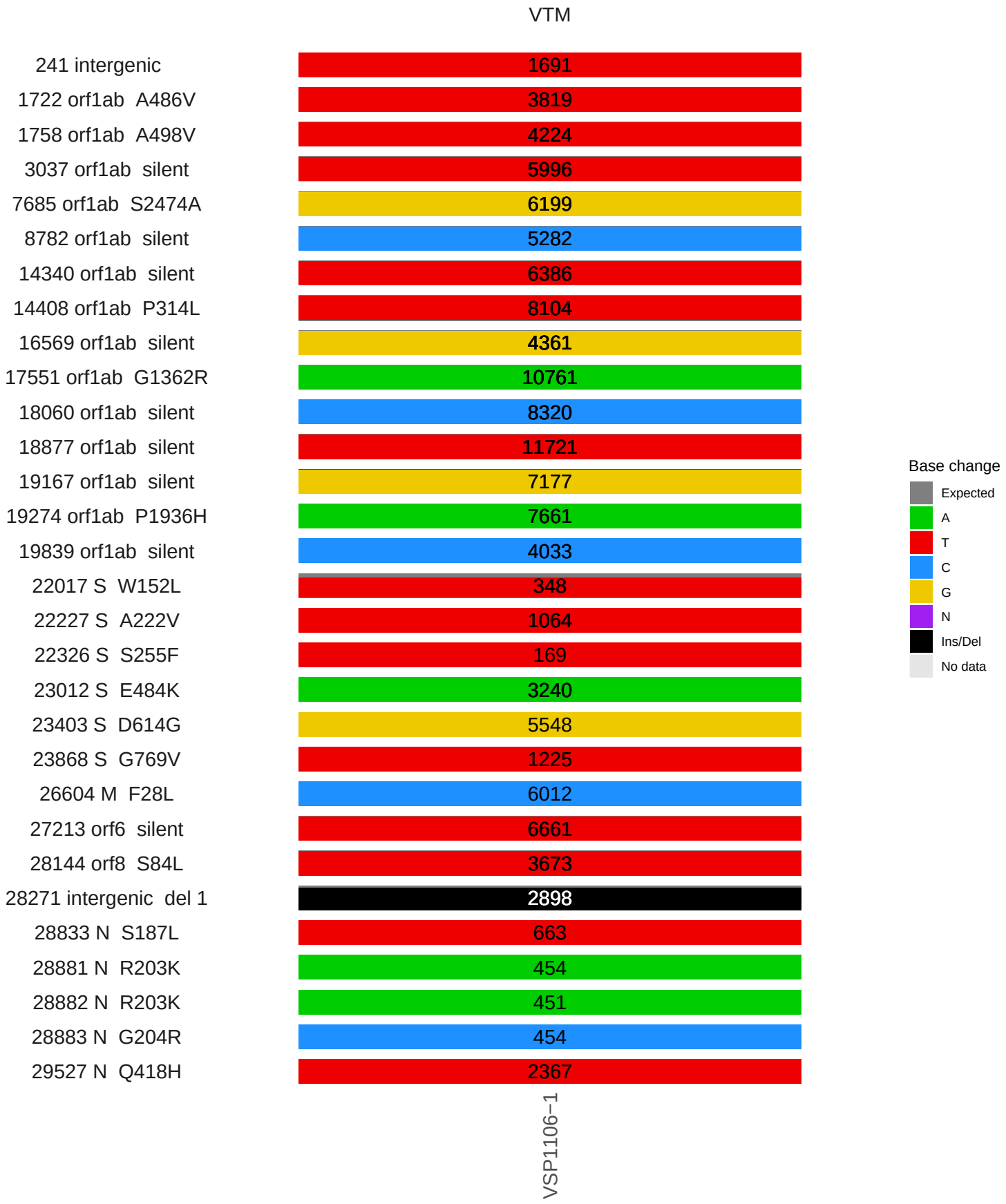
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1106-1	single experiment	NA	VTM	2021-03-15	29.83	R.1	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.

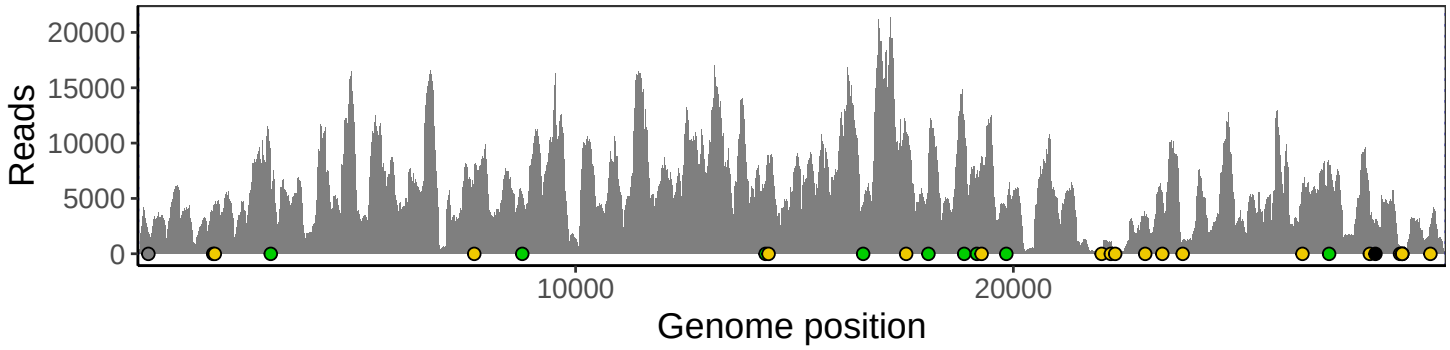



VTM
241 intergenic
1722 orf1ab A486V
1758 orf1ab A498V
3037 orf1ab silent
7685 orf1ab S2474A
8782 orf1ab silent
14340 orf1ab silent
14408 orf1ab P314L
16569 orf1ab silent
17551 orf1ab G1362R
18060 orf1ab silent
18877 orf1ab silent
19167 orf1ab silent
19274 orf1ab P1936H
19839 orf1ab silent
22017 S W152L
22227 S A222V
22326 S S255F
23012 S E484K
23403 S D614G
23868 S G769V
26604 M F28L
27213 orf6 silent
28144 orf8 S84L
28271 intergenic del 1
28833 N S187L
28881 N R203K
28882 N R203K
28883 N G204R
29527 N Q418H
1691
3819
4224
5996
6199
5282
6386
8104
4361
10761
8320
11721
7177
7661
4033
348
1064
169
3240
5548
1225
6012
6661
3673
2898
663
454
451
454
2367
VSP1106−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

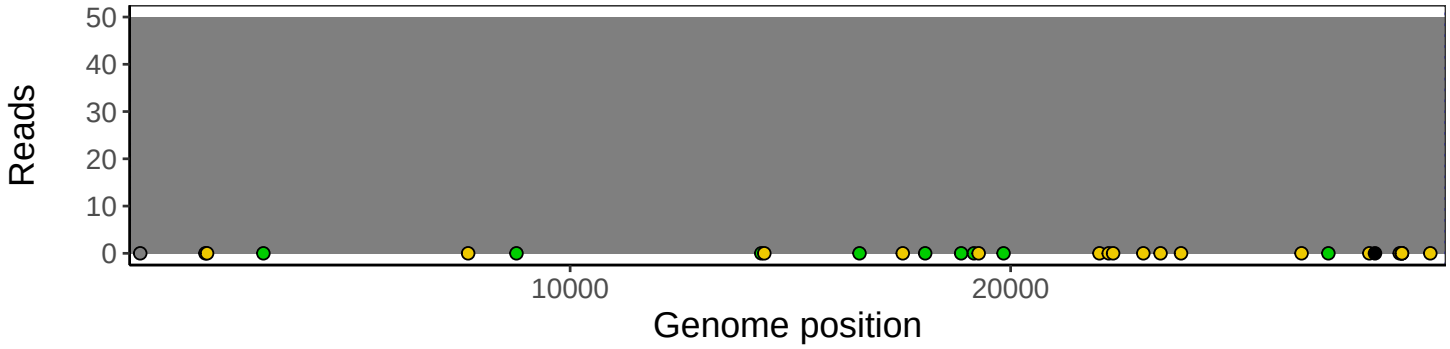
Analyses of individual experiments and composite results

VSP1106-1 | 2021-03-15 | VTM | UPHS-0121 | genomes | single experiment

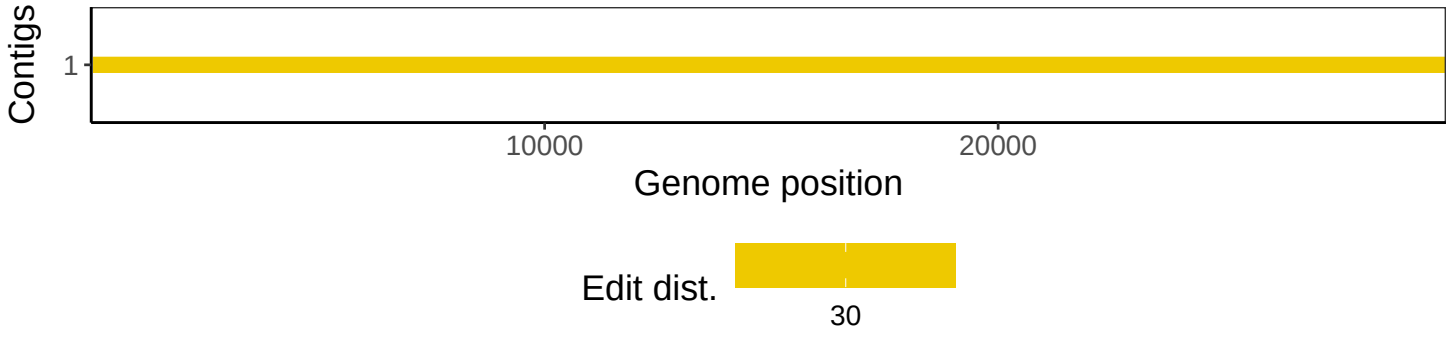
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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