COVID-19 subject UPHS-1665

2021-06-03

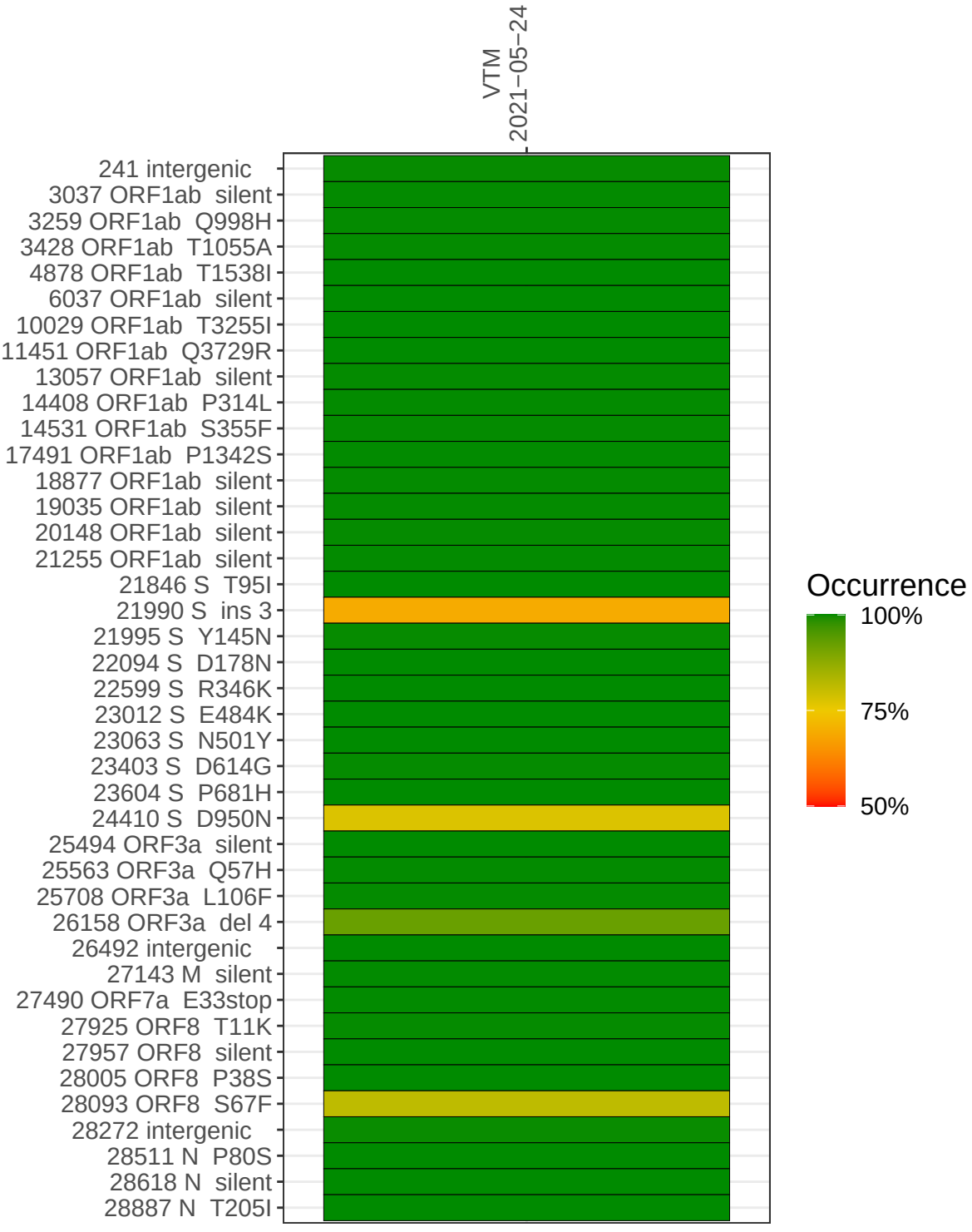
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

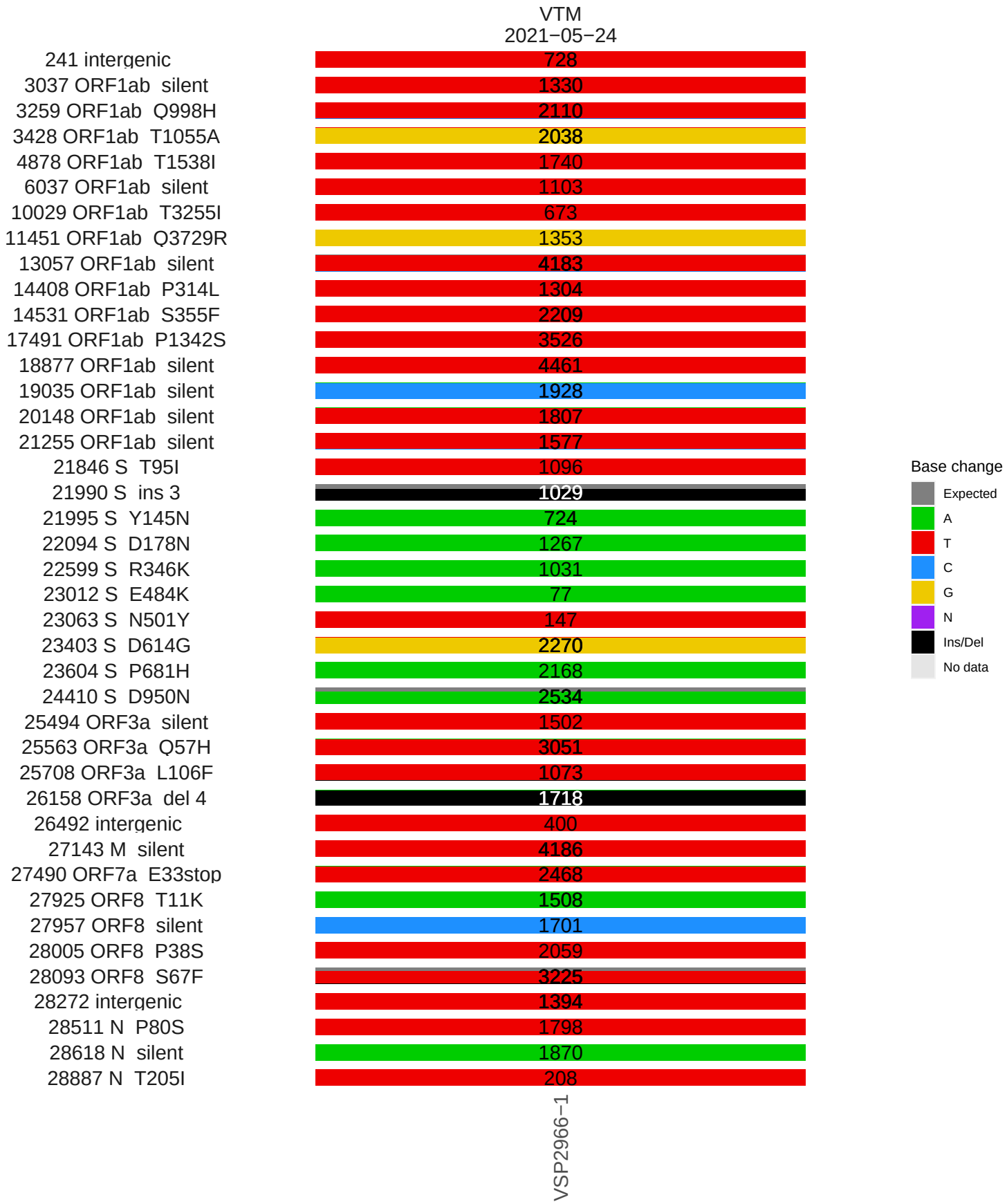
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2966-1	single experiment	NA	VTM	2021-05-24	29.86	B.1	99.8%	99.7%

Variants shared across samples

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

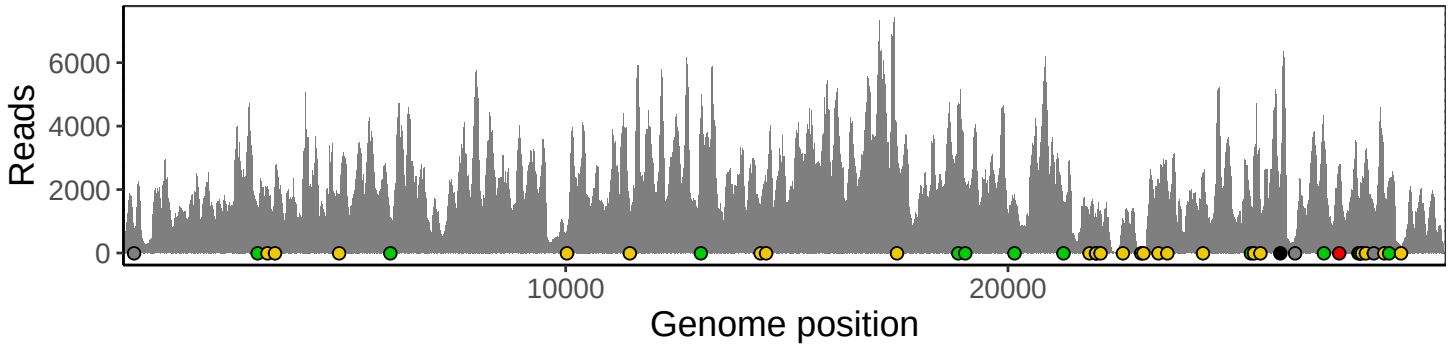



VTM
2021−05−24
241 intergenic
3037 ORF1ab silent
3259 ORF1ab Q998H
3428 ORF1ab T1055A
4878 ORF1ab T1538I
6037 ORF1ab silent
10029 ORF1ab T3255I
11451 ORF1ab Q3729R
13057 ORF1ab silent
14408 ORF1ab P314L
14531 ORF1ab S355F
17491 ORF1ab P1342S
18877 ORF1ab silent
19035 ORF1ab silent
20148 ORF1ab silent
21255 ORF1ab silent
21846 S T95I
21990 S ins 3
21995 S Y145N
22094 S D178N
22599 S R346K
23012 S E484K
23063 S N501Y
23403 S D614G
23604 S P681H
24410 S D950N
25494 ORF3a silent
25563 ORF3a Q57H
25708 ORF3a L106F
26158 ORF3a del 4
26492 intergenic
27143 M silent
27490 ORF7a E33stop
27925 ORF8 T11K
27957 ORF8 silent
28005 ORF8 P38S
28093 ORF8 S67F
28272 intergenic
28511 N P80S
28618 N silent
28887 N T205I
728
1330
2110
2038
1740
1103
673
1353
4183
1304
2209
3526
4461
1928
1807
1577
1096
1029
724
1267
1031
77
147
2270
2168
2534
1502
3051
1073
1718
400
4186
2468
1508
1701
2059
3225
1394
1798
1870
208
VSP2966−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

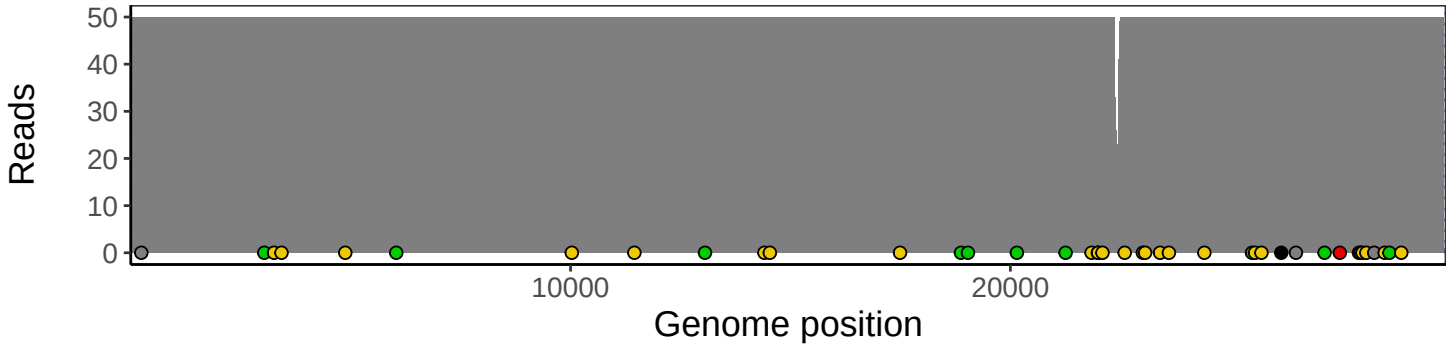
Analyses of individual experiments and composite results

VSP2966-1 | 2021-05-24 | VTM | UPHS-1665 | genomes | single experiment

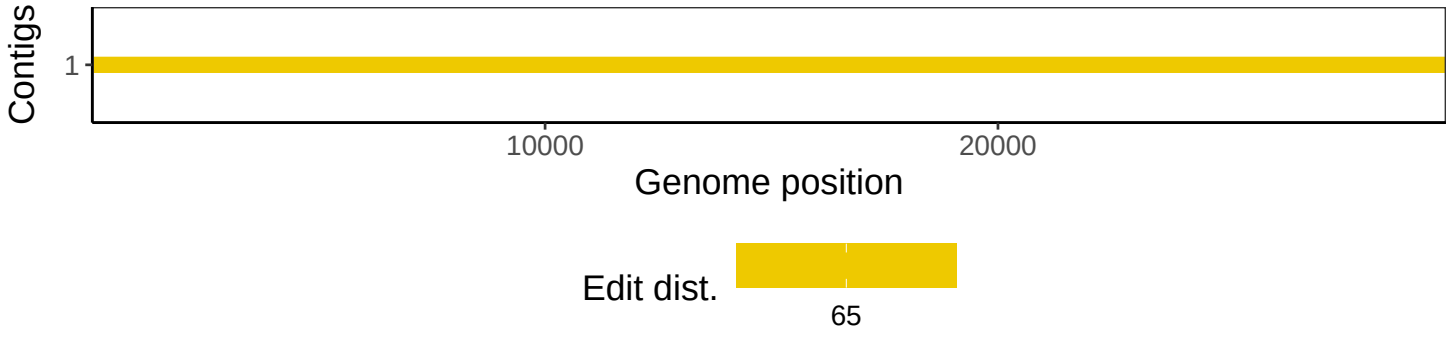
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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