COVID-19 subject UPHS-1575

2021-06-23

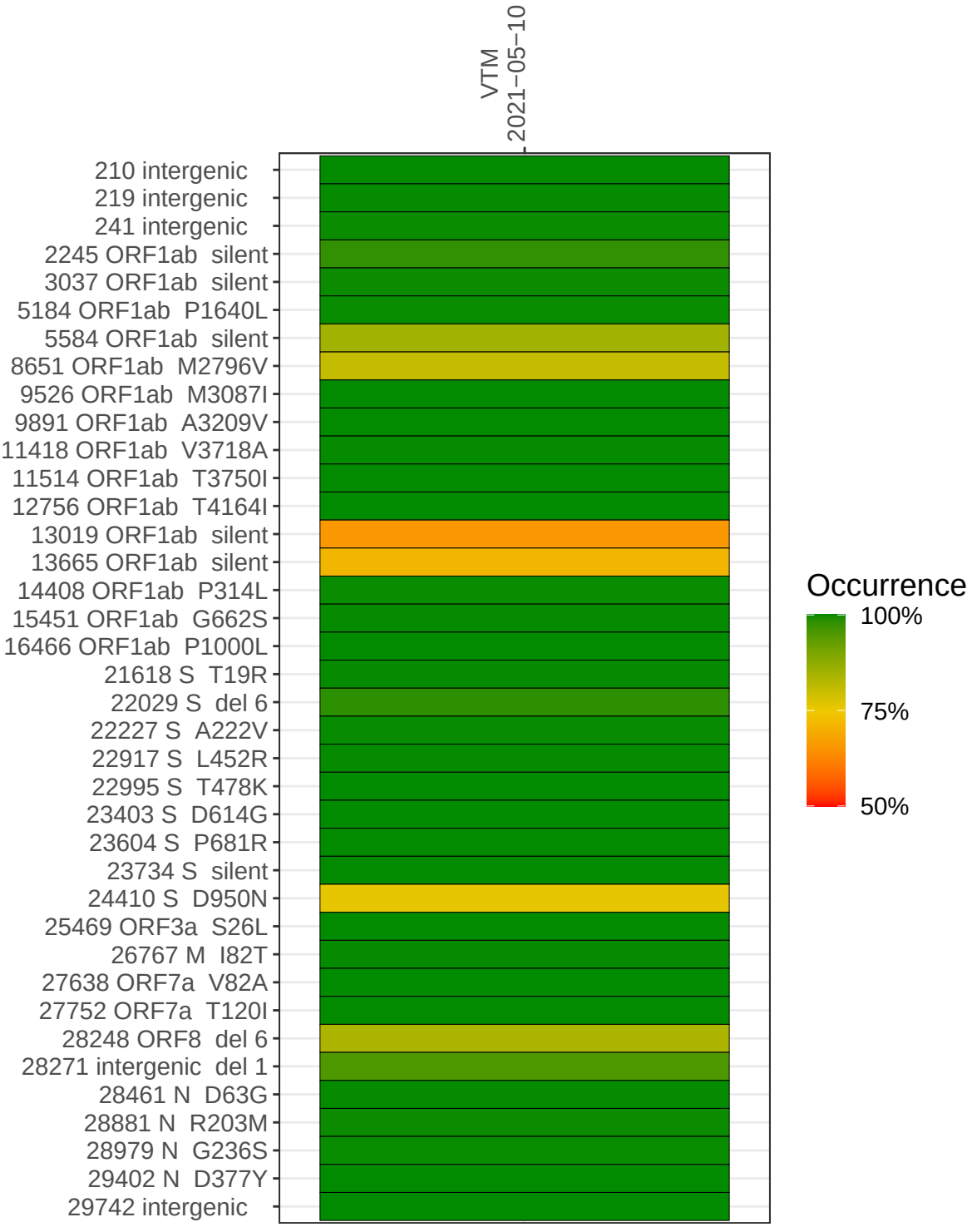
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

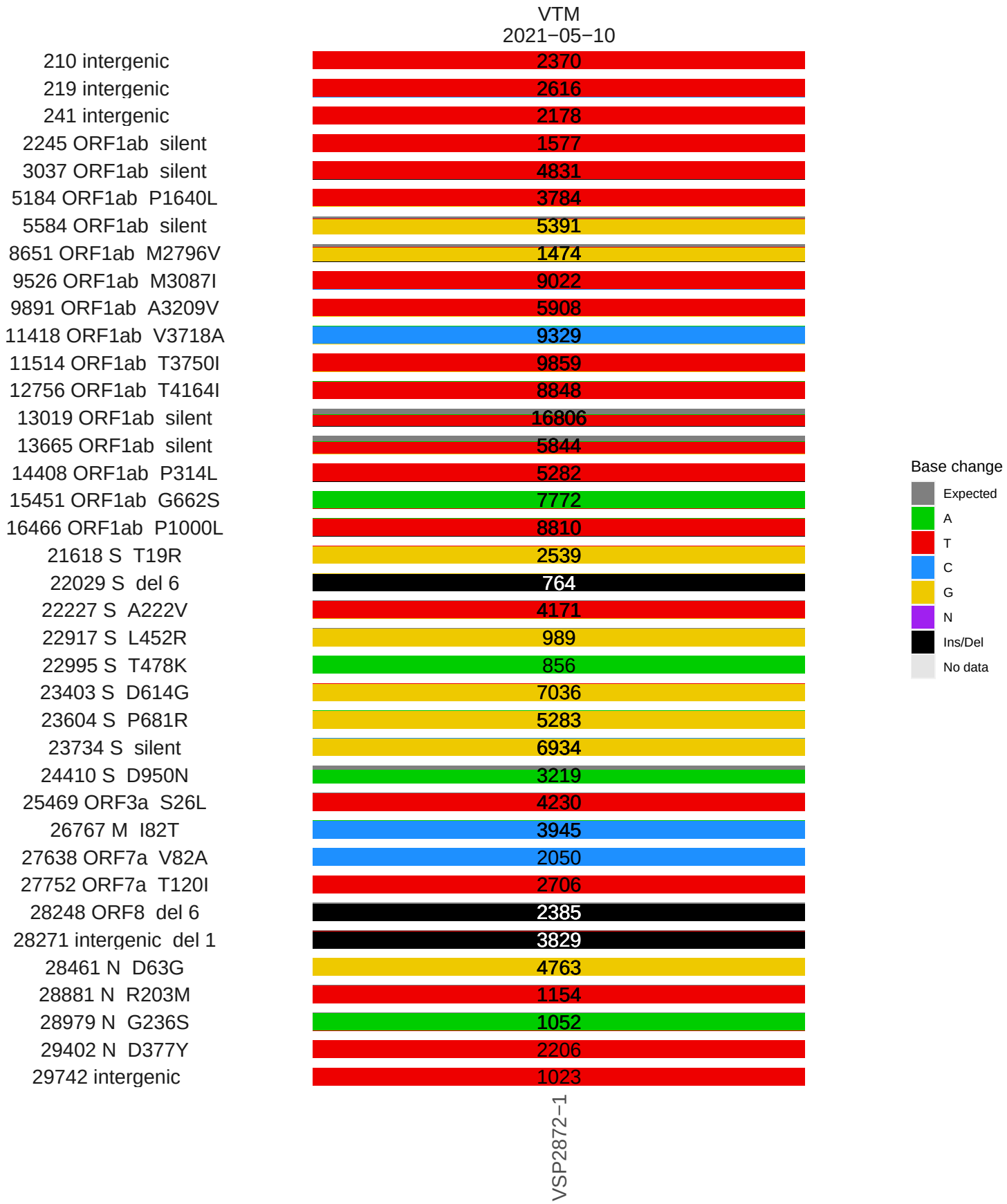
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2872-1	single experiment	NA	VTM	2021-05-10	29.88	B.1.617.2	99.9%	99.8%

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.

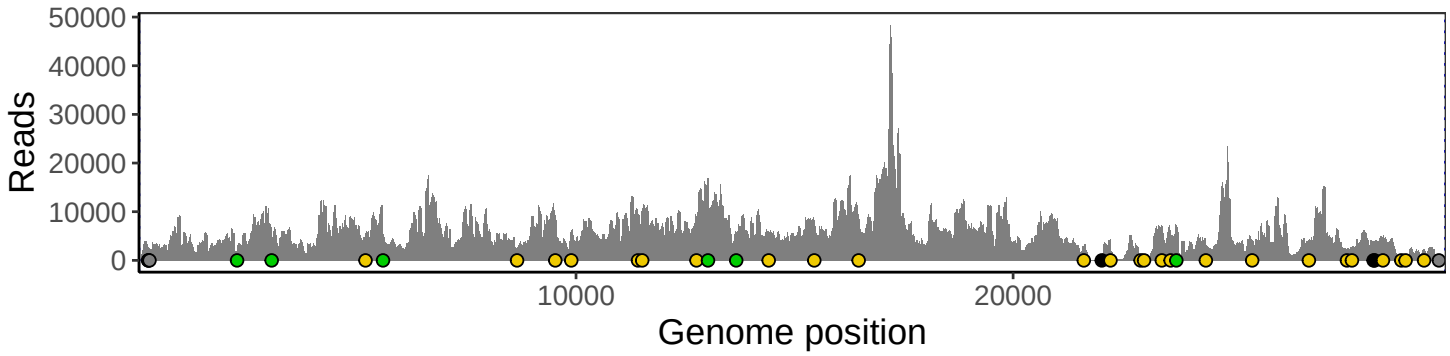



VTM
2021−05−10
210 intergenic
219 intergenic
241 intergenic
2245 ORF1ab silent
3037 ORF1ab silent
5184 ORF1ab P1640L
5584 ORF1ab silent
8651 ORF1ab M2796V
9526 ORF1ab M3087I
9891 ORF1ab A3209V
11418 ORF1ab V3718A
11514 ORF1ab T3750I
12756 ORF1ab T4164I
13019 ORF1ab silent
13665 ORF1ab silent
14408 ORF1ab P314L
15451 ORF1ab G662S
16466 ORF1ab P1000L
21618 S T19R
22029 S del 6
22227 S A222V
22917 S L452R
22995 S T478K
23403 S D614G
23604 S P681R
23734 S silent
24410 S D950N
25469 ORF3a S26L
26767 M I82T
27638 ORF7a V82A
27752 ORF7a T120I
28248 ORF8 del 6
28271 intergenic del 1
28461 N D63G
28881 N R203M
28979 N G236S
29402 N D377Y
29742 intergenic
2370
2616
2178
1577
4831
3784
5391
1474
9022
5908
9329
9859
8848
16806
5844
5282
7772
8810
2539
764
4171
989
856
7036
5283
6934
3219
4230
3945
2050
2706
2385
3829
4763
1154
1052
2206
1023
VSP2872−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

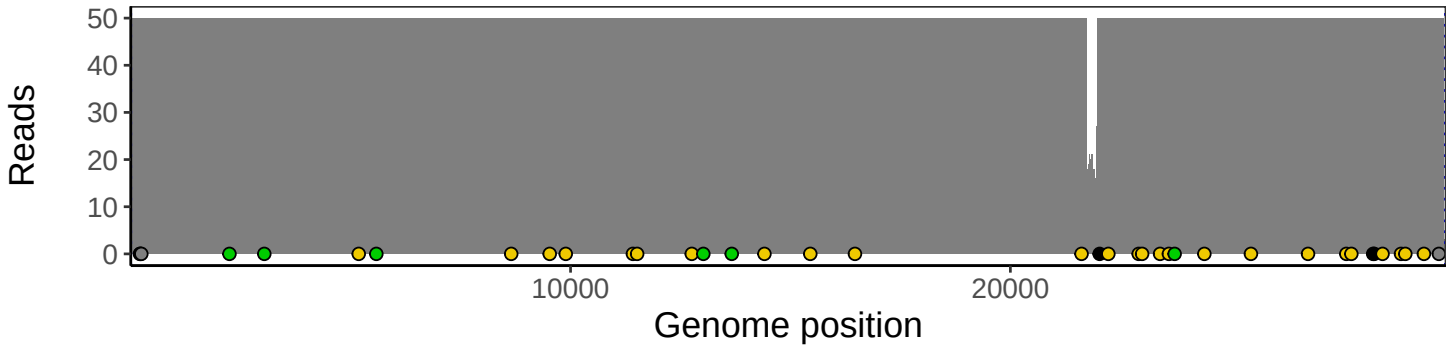
Analyses of individual experiments and composite results

VSP2872-1 | 2021-05-10 | VTM | UPHS-1575 | genomes | single experiment

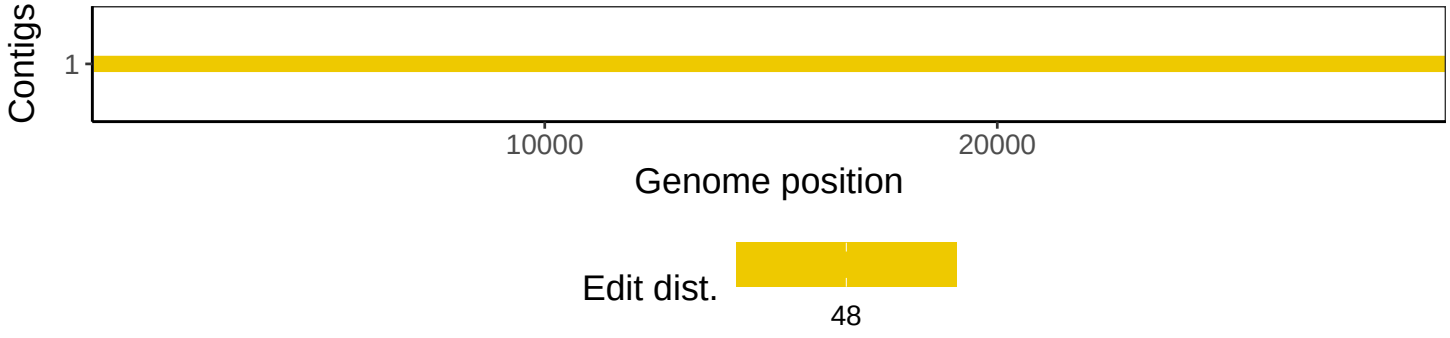
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.1.3
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	3.3.3
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