COVID-19 subject UPHS-1534

2021-06-23

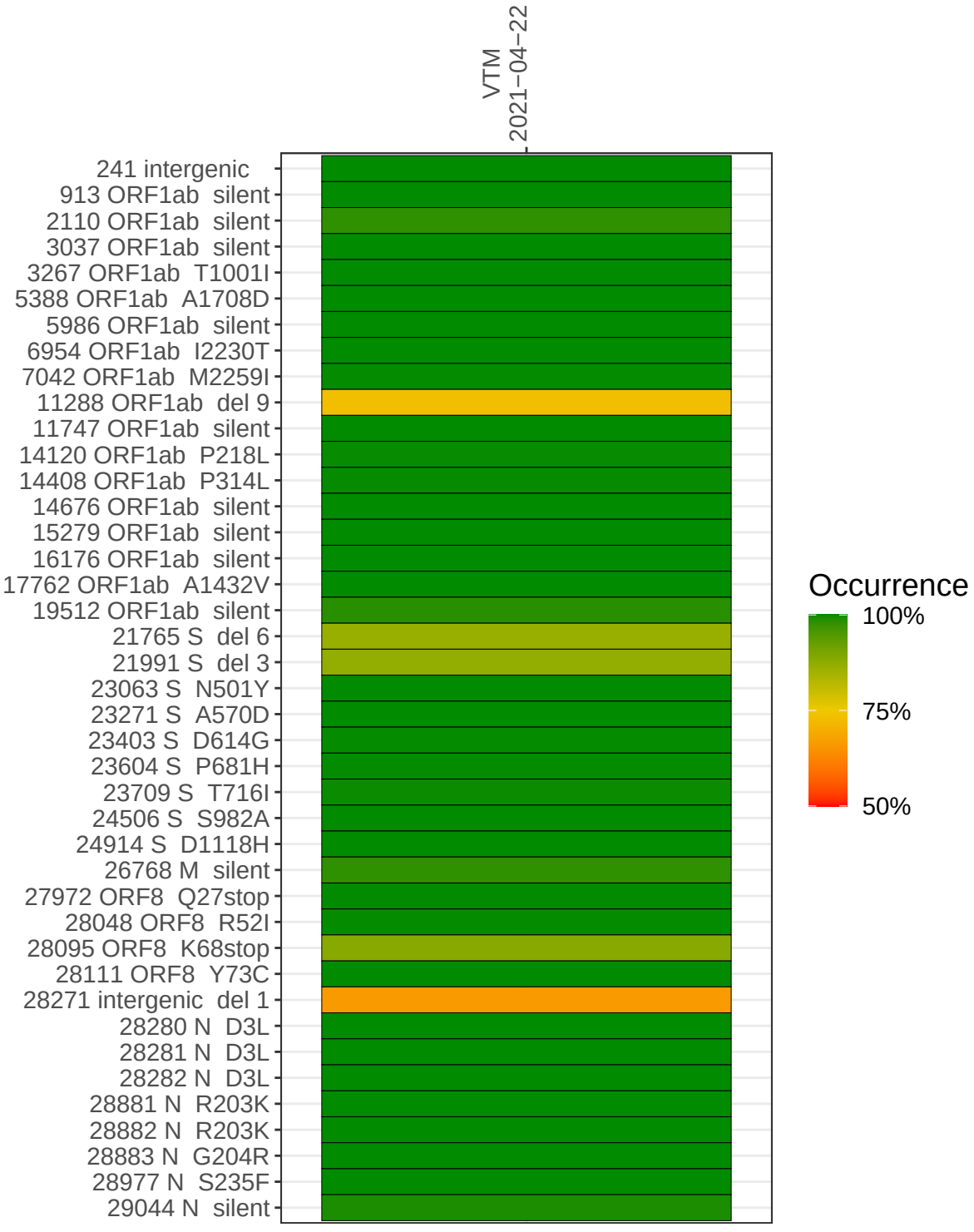
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

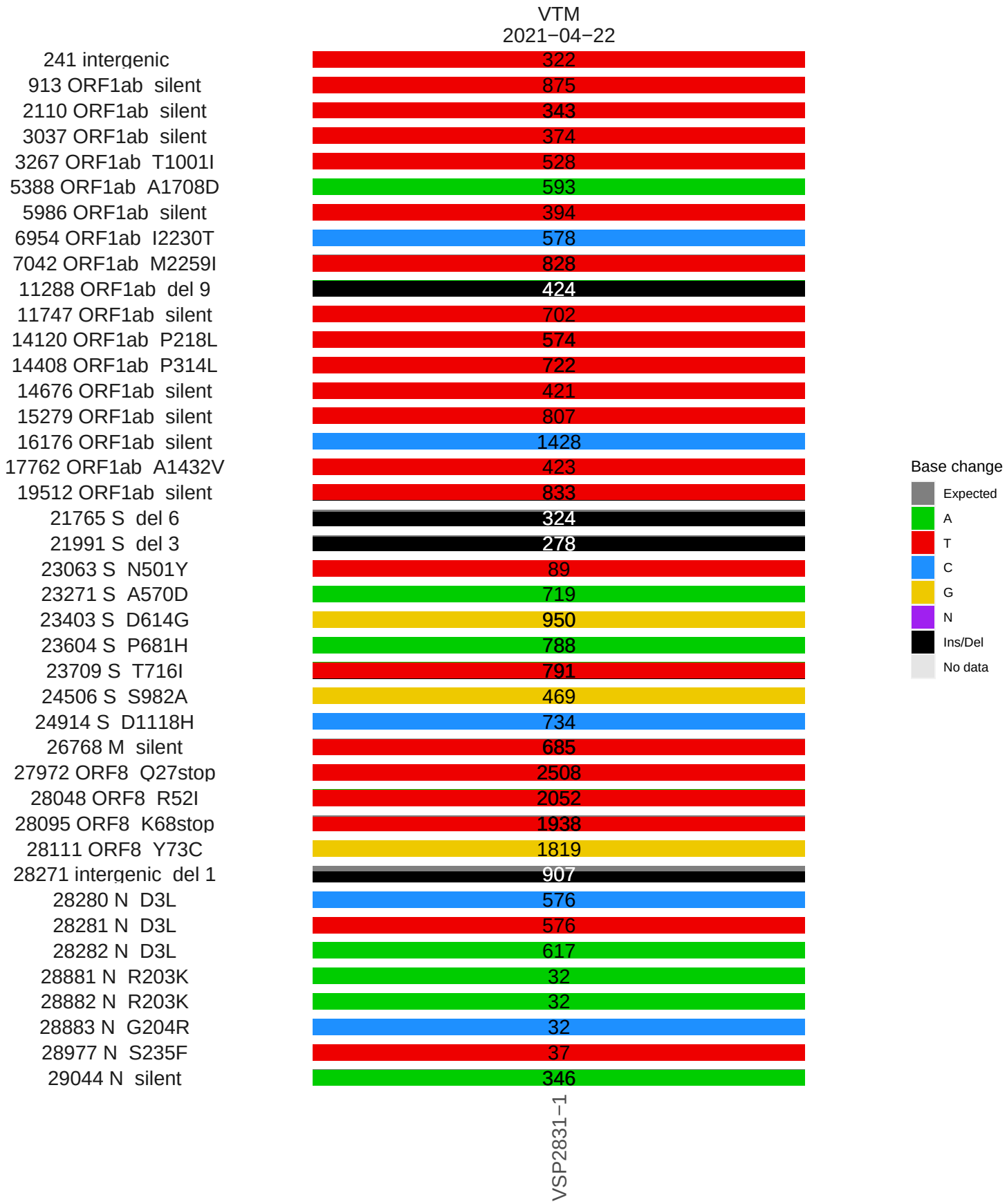
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2831-1	single experiment	NA	VTM	2021-04-22	29.63	B.1.1.7	99.3%	99.3%

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.

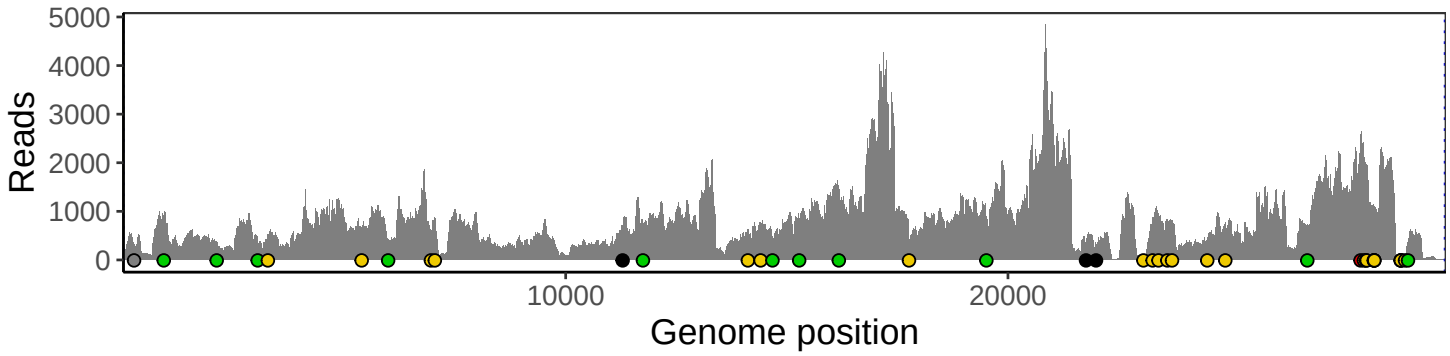



VTM
2021−04−22
241 intergenic 322
913 ORF1ab silent 875
2110 ORF1ab silent 343
3037 ORF1ab silent 374
3267 ORF1ab T1001I 528
5388 ORF1ab A1708D 593
5986 ORF1ab silent 394
6954 ORF1ab I2230T 578
7042 ORF1ab M2259I 828
11288 ORF1ab del 9 424
11747 ORF1ab silent 702
14120 ORF1ab P218L 574
14408 ORF1ab P314L 722
14676 ORF1ab silent 421
15279 ORF1ab silent 807
16176 ORF1ab silent 1428
17762 ORF1ab A1432V 423
19512 ORF1ab silent 833
21765 S del 6 324
21991 S del 3 278
23063 S N501Y 89
23271 S A570D 719
23403 S D614G 950
23604 S P681H 788
23709 S T716I 791
24506 S S982A 469
24914 S D1118H 734
26768 M silent 685
27972 ORF8 Q27stop 2508
28048 ORF8 R52I 2052
28095 ORF8 K68stop 1938
28111 ORF8 Y73C 1819
28271 intergenic del 1 907
28280 N D3L 576
28281 N D3L 576
28282 N D3L 617
28881 N R203K 32
28882 N R203K 32
28883 N G204R 32
28977 N S235F 37
29044 N silent 346
VSP2831−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

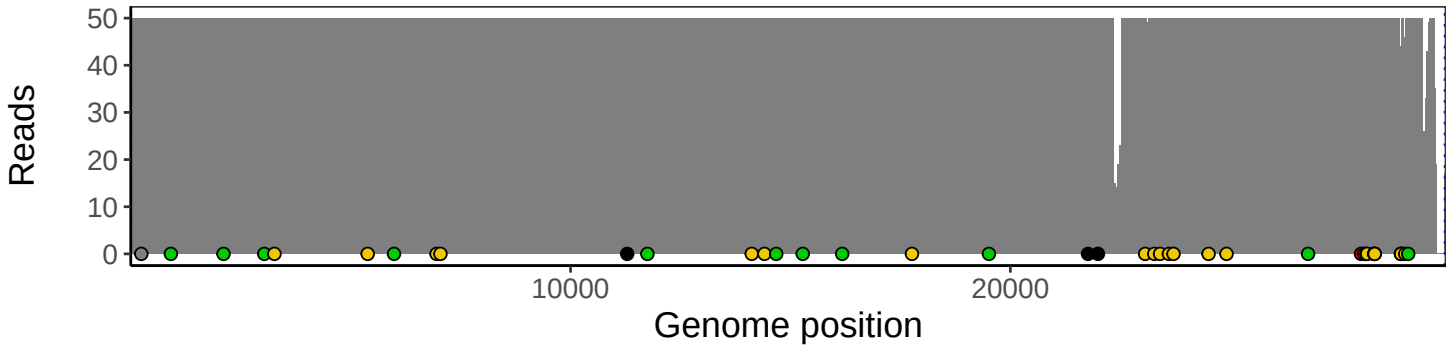
Analyses of individual experiments and composite results

VSP2831-1 | 2021-04-22 | VTM | UPHS-1534 | genomes | single experiment

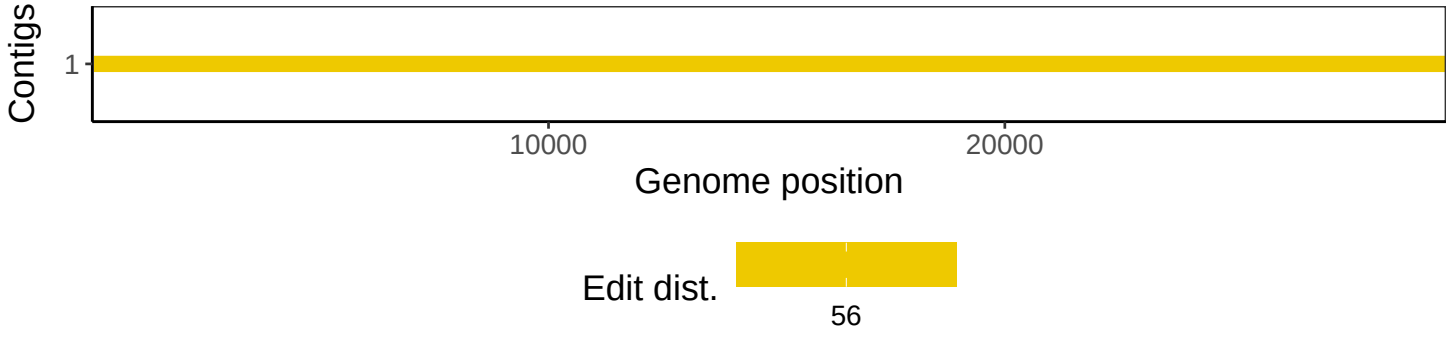
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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