COVID-19 subject UPHS-1537

2021-06-23

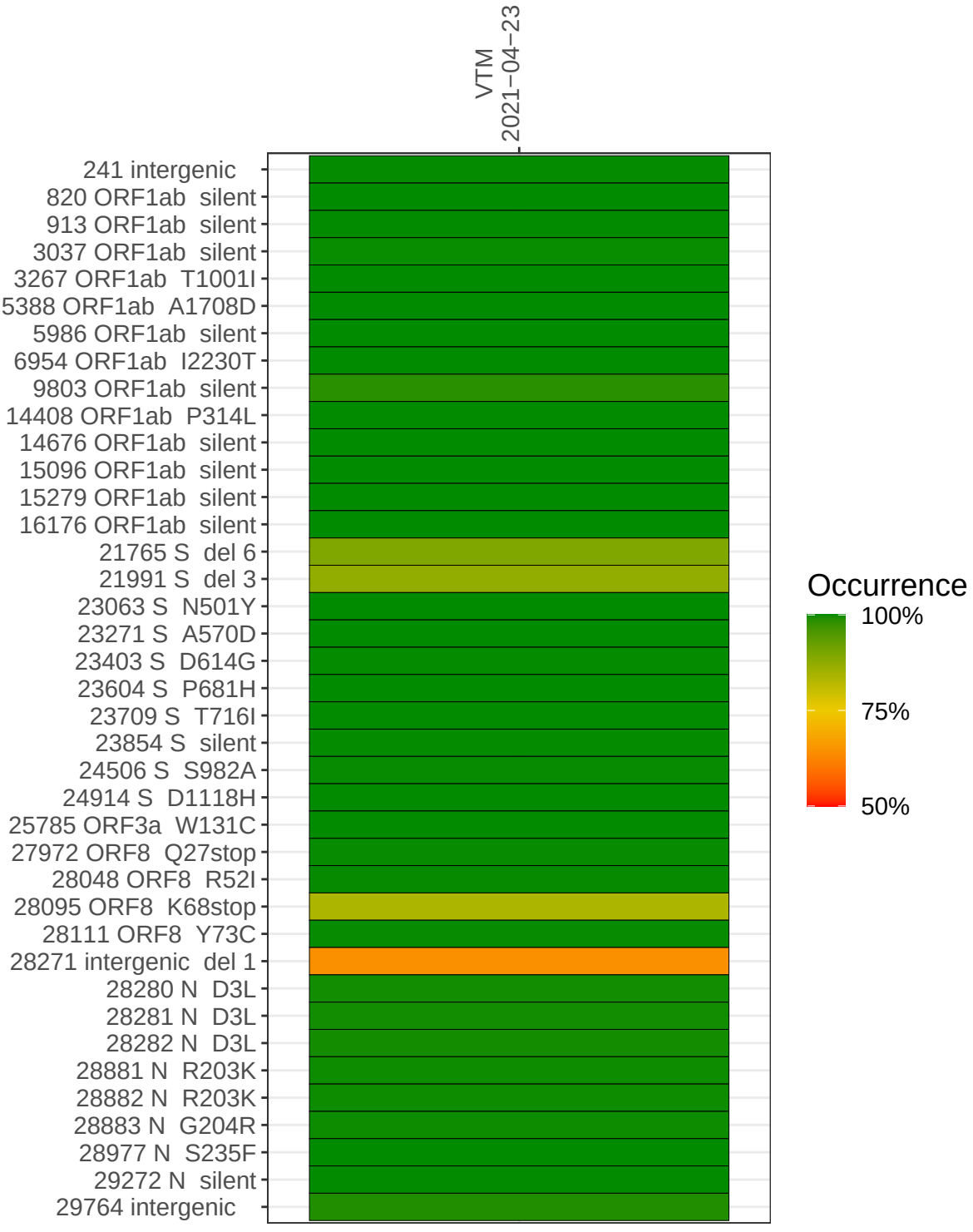
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

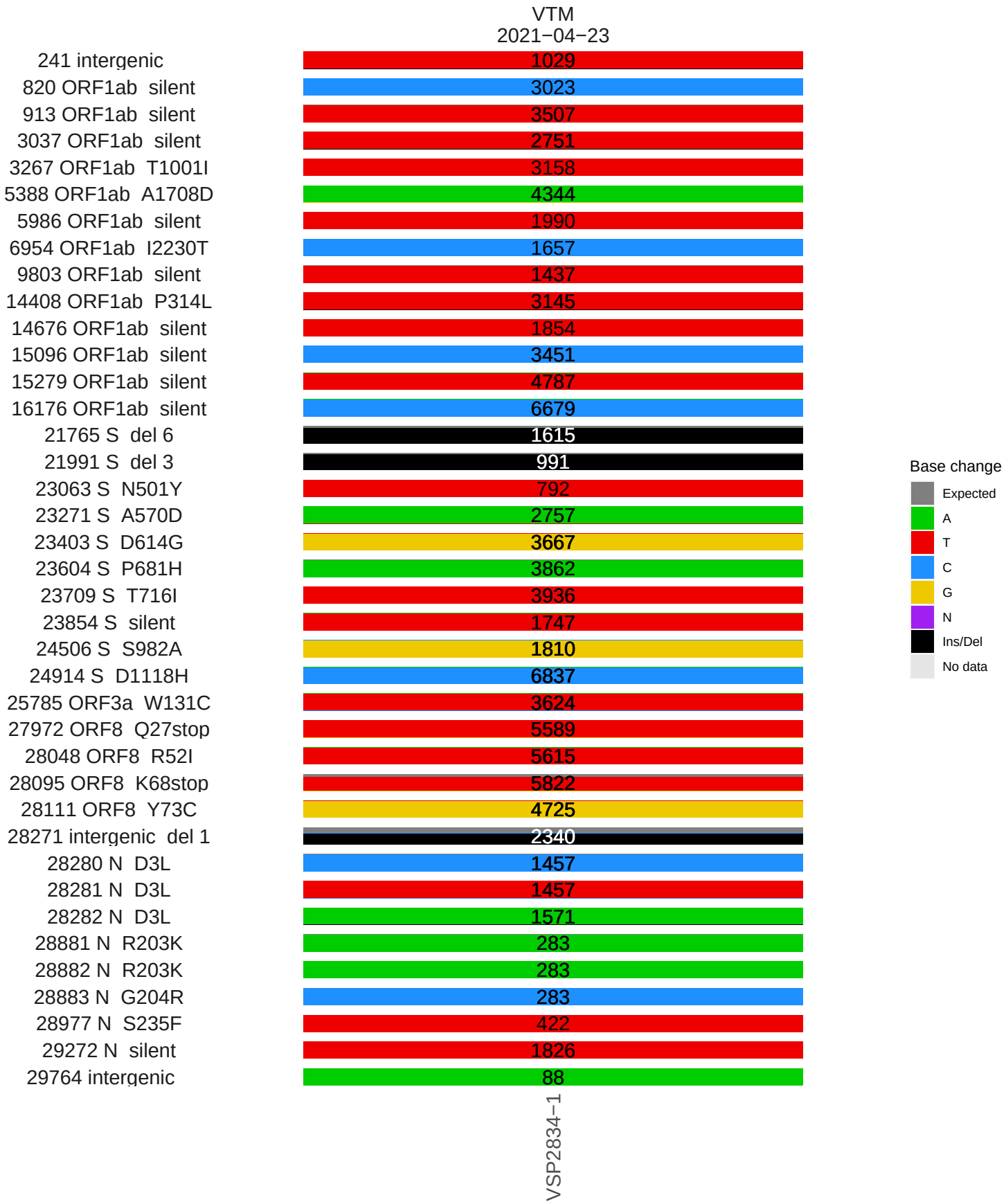
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2834-1	single experiment	NA	VTM	2021-04-23	29.84	B.1.1.7	99.8%	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.

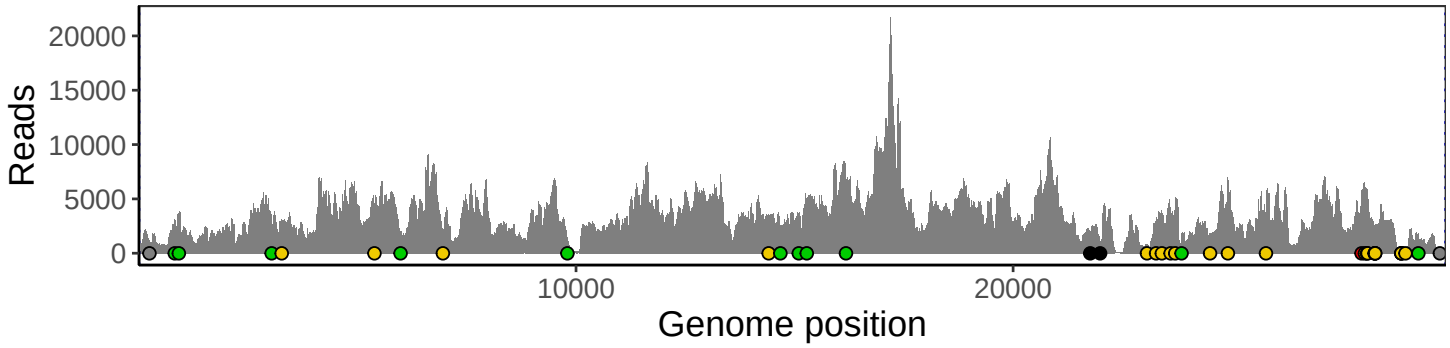



VTM
2021−04−23
241 intergenic 1029
820 ORF1ab silent 3023
913 ORF1ab silent 3507
3037 ORF1ab silent 2751
3267 ORF1ab T1001I 3158
5388 ORF1ab A1708D 4344
5986 ORF1ab silent 1990
6954 ORF1ab I2230T 1657
9803 ORF1ab silent 1437
14408 ORF1ab P314L 3145
14676 ORF1ab silent 1854
15096 ORF1ab silent 3451
15279 ORF1ab silent 4787
16176 ORF1ab silent 6679
21765 S del 6 1615
21991 S del 3 991
23063 S N501Y 792
23271 S A570D 2757
23403 S D614G 3667
23604 S P681H 3862
23709 S T716I 3936
23854 S silent 1747
24506 S S982A 1810
24914 S D1118H 6837
25785 ORF3a W131C 3624
27972 ORF8 Q27stop 5589
28048 ORF8 R52I 5615
28095 ORF8 K68stop 5822
28111 ORF8 Y73C 4725
28271 intergenic del 1 2340
28280 N D3L 1457
28281 N D3L 1457
28282 N D3L 1571
28881 N R203K 283
28882 N R203K 283
28883 N G204R 283
28977 N S235F 422
29272 N silent 1826
29764 intergenic 88
VSP2834−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

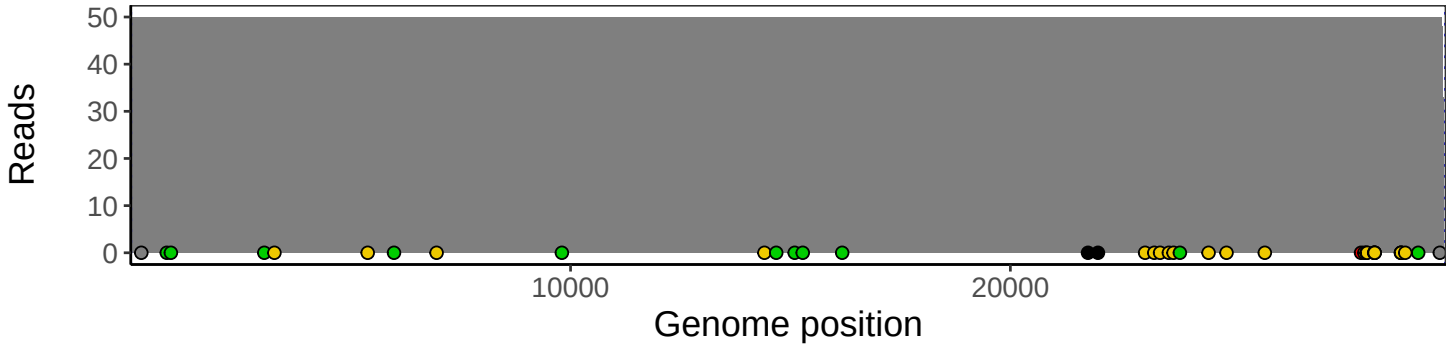
Analyses of individual experiments and composite results

VSP2834-1 | 2021-04-23 | VTM | UPHS-1537 | genomes | single experiment

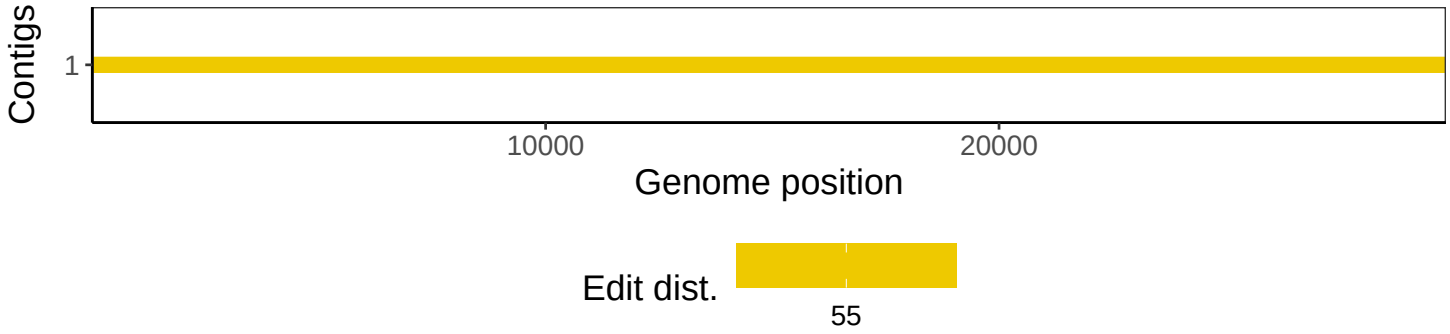
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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