COVID-19 subject UPHS-1616

2021-06-23

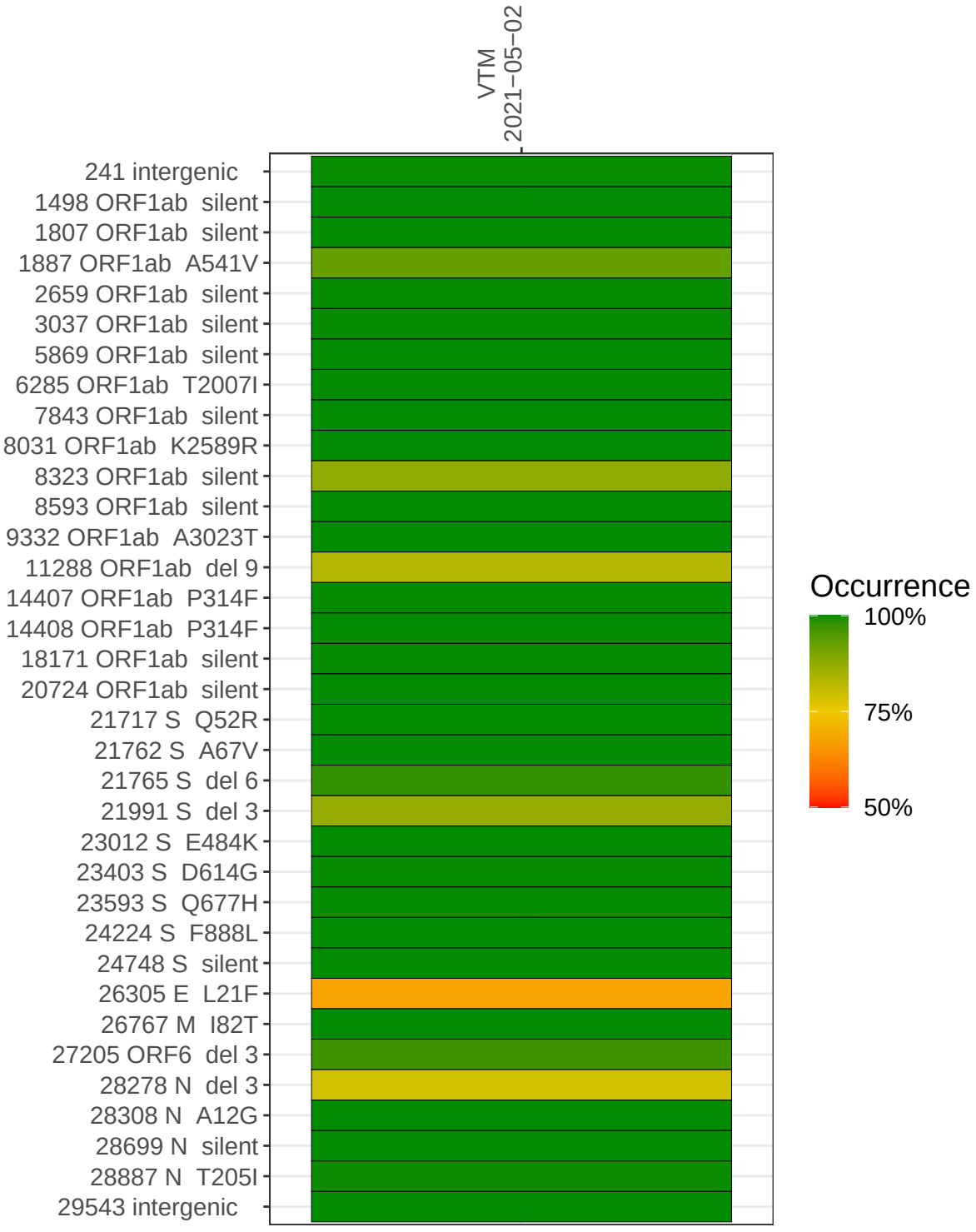
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

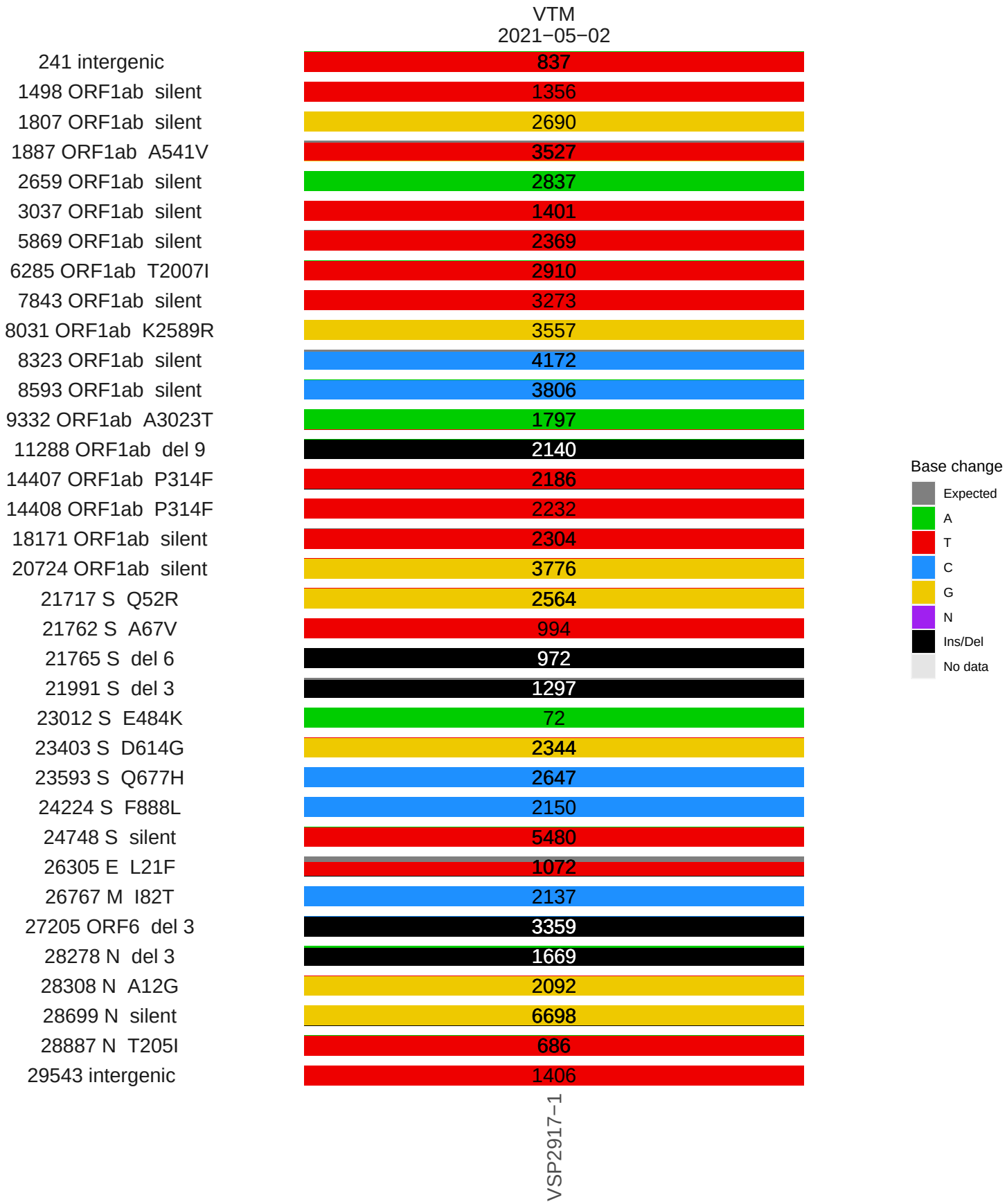
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2917-1	single experiment	NA	VTM	2021-05-02	29.75	B.1.525	99.7%	99.5%

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.

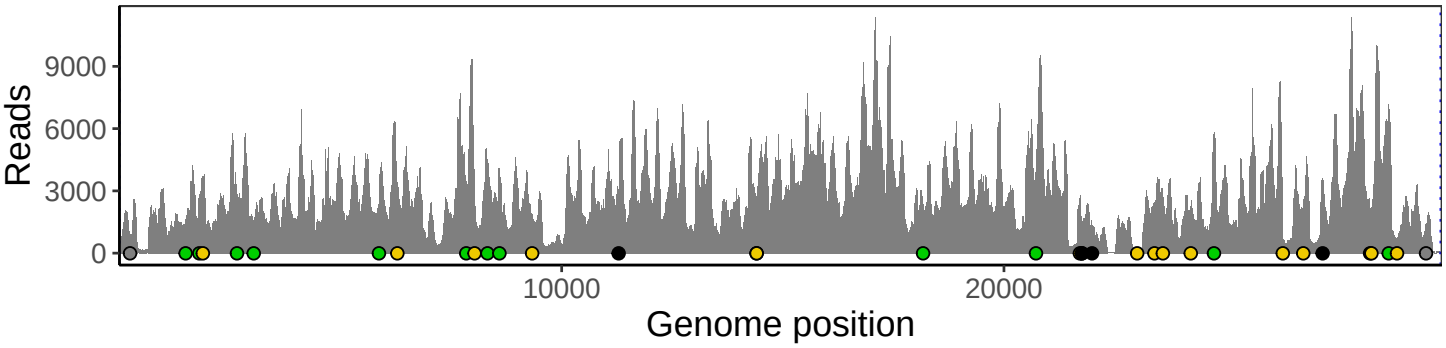



VTM
2021−05−02
241 intergenic
1498 ORF1ab silent
1807 ORF1ab silent
1887 ORF1ab A541V
2659 ORF1ab silent
3037 ORF1ab silent
5869 ORF1ab silent
6285 ORF1ab T2007I
7843 ORF1ab silent
8031 ORF1ab K2589R
8323 ORF1ab silent
8593 ORF1ab silent
9332 ORF1ab A3023T
11288 ORF1ab del 9
14407 ORF1ab P314F
14408 ORF1ab P314F
18171 ORF1ab silent
20724 ORF1ab silent
21717 S Q52R
21762 S A67V
21765 S del 6
21991 S del 3
23012 S E484K
23403 S D614G
23593 S Q677H
24224 S F888L
24748 S silent
26305 E L21F
26767 M I82T
27205 ORF6 del 3
28278 N del 3
28308 N A12G
28699 N silent
28887 N T205I
29543 intergenic
837
1356
2690
3527
2837
1401
2369
2910
3273
3557
4172
3806
1797
2140
2186
2232
2304
3776
2564
994
972
1297
72
2344
2647
2150
5480
1072
2137
3359
1669
2092
6698
686
1406
VSP2917−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

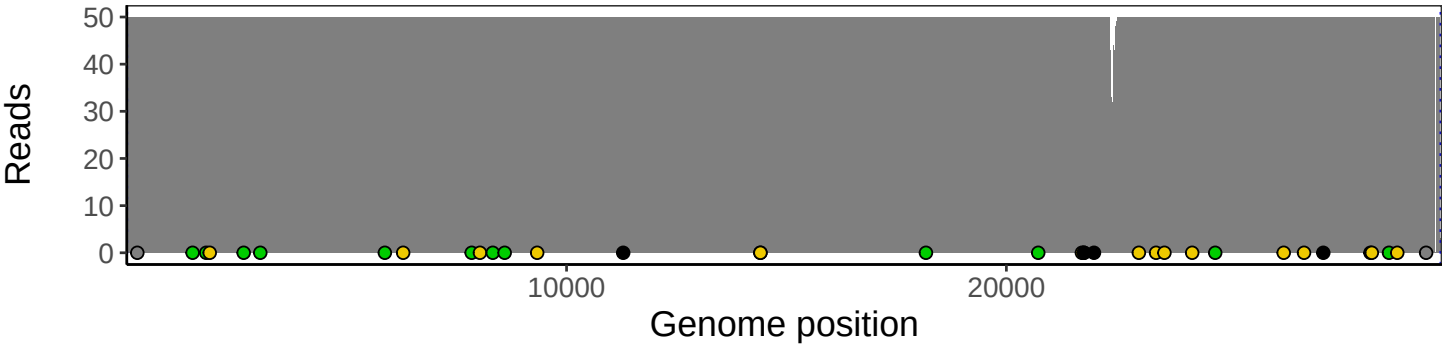
Analyses of individual experiments and composite results

VSP2917-1 | 2021-05-02 | VTM | UPHS-1616 | genomes | single experiment

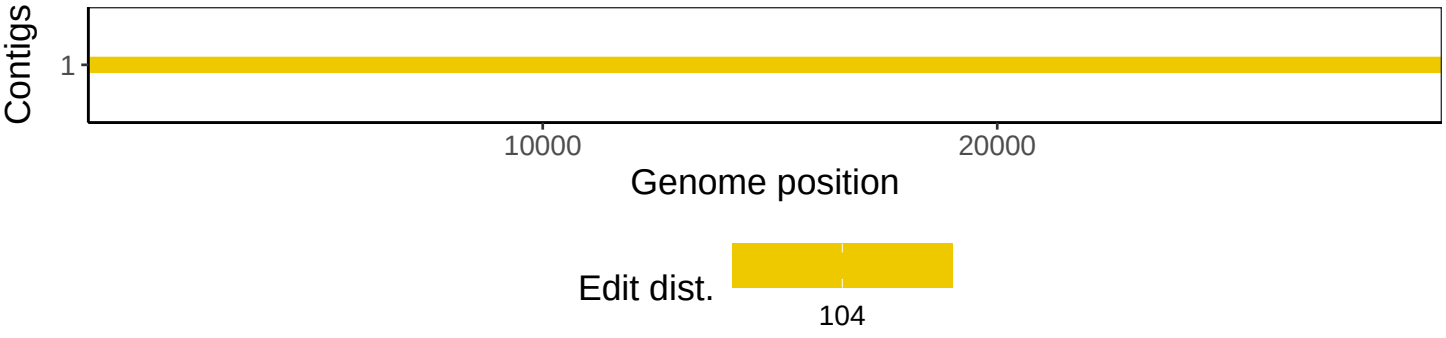
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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