COVID-19 subject UPHS-1234

2021-06-23

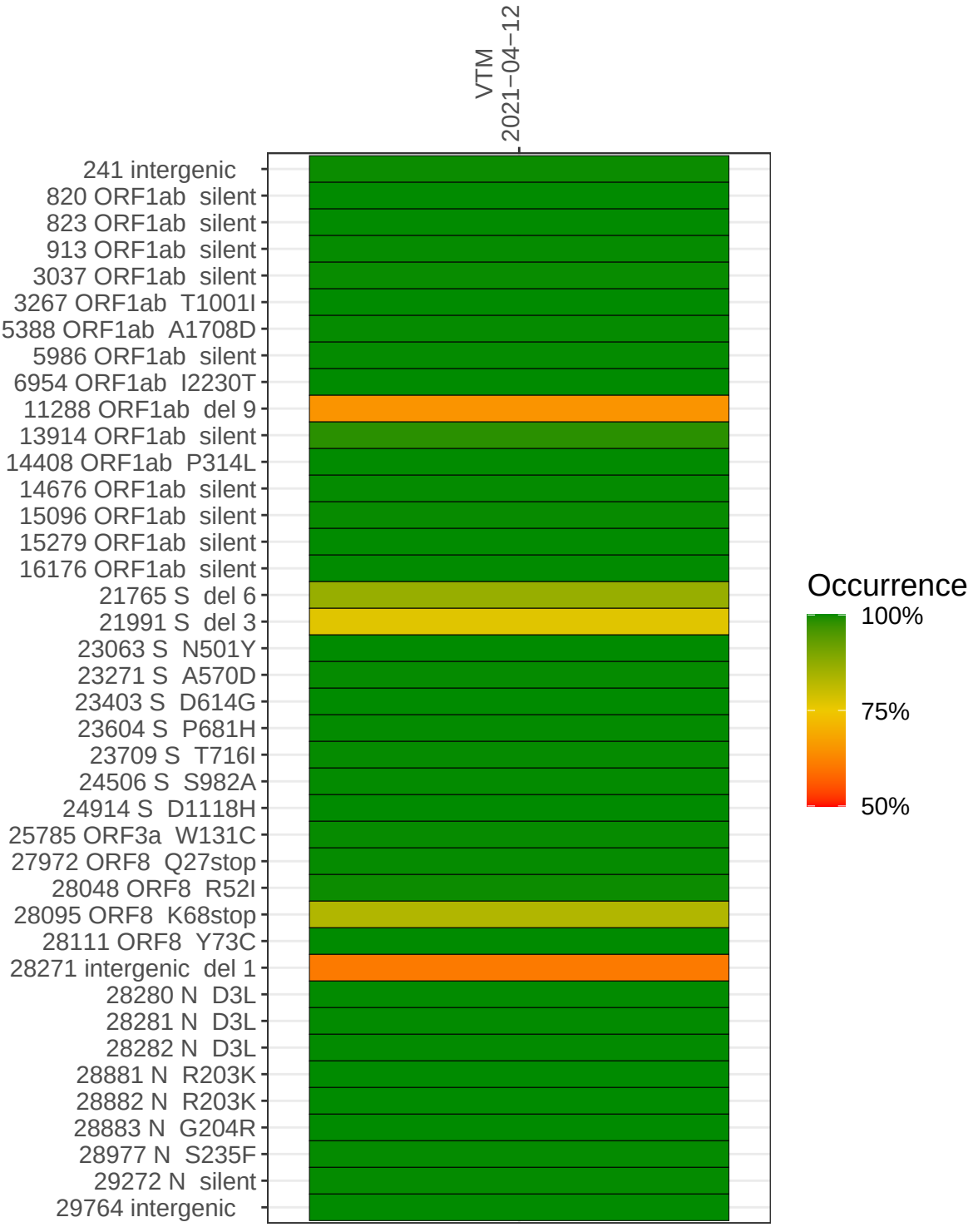
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

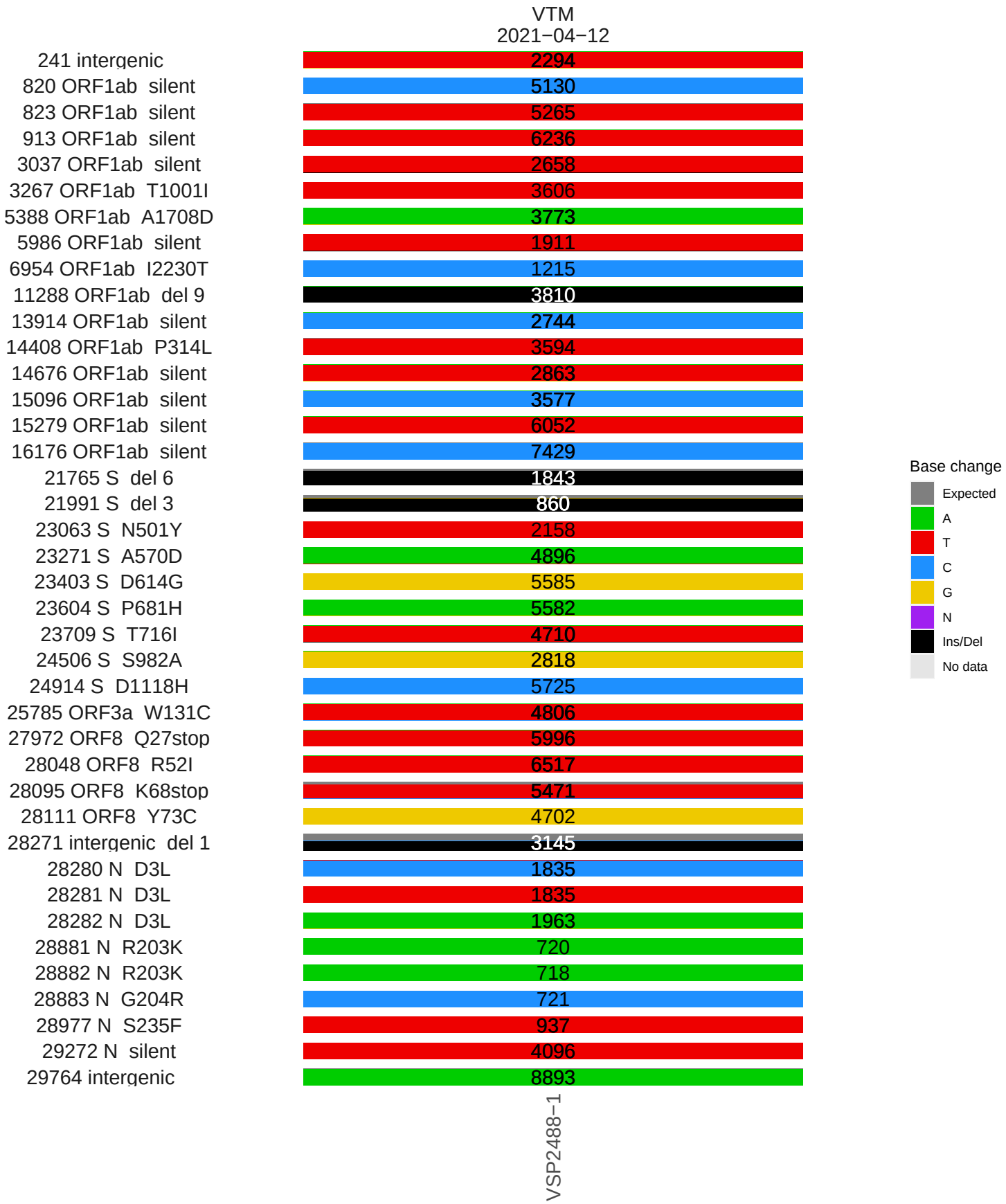
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2488-1	single experiment	NA	VTM	2021-04-12	29.91	B.1.1.7	99.9%	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.

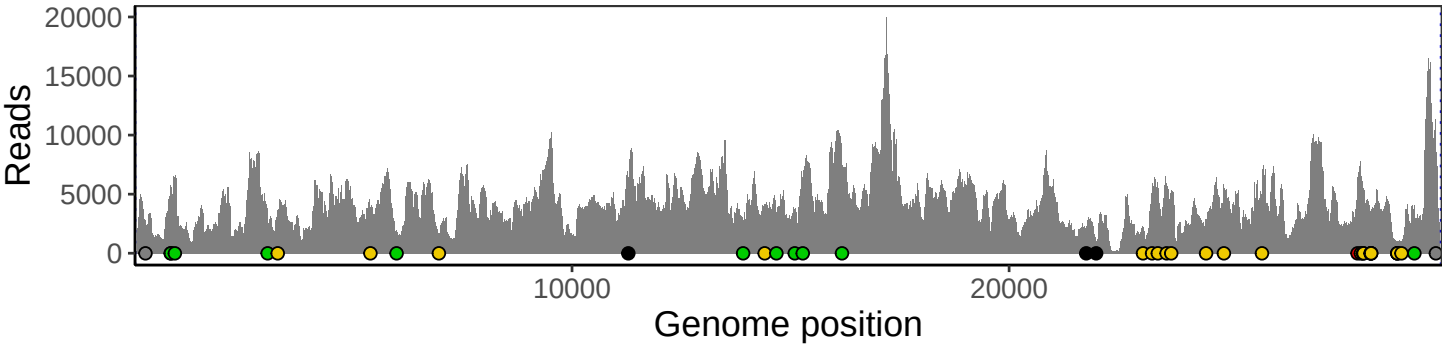



VTM
2021−04−12
241 intergenic 2294
820 ORF1ab silent 5130
823 ORF1ab silent 5265
913 ORF1ab silent 6236
3037 ORF1ab silent 2658
3267 ORF1ab T1001I 3606
5388 ORF1ab A1708D 3773
5986 ORF1ab silent 1911
6954 ORF1ab I2230T 1215
11288 ORF1ab del 9 3810
13914 ORF1ab silent 2744
14408 ORF1ab P314L 3594
14676 ORF1ab silent 2863
15096 ORF1ab silent 3577
15279 ORF1ab silent 6052
16176 ORF1ab silent 7429
21765 S del 6 1843
21991 S del 3 860
23063 S N501Y 2158
23271 S A570D 4896
23403 S D614G 5585
23604 S P681H 5582
23709 S T716I 4710
24506 S S982A 2818
24914 S D1118H 5725
25785 ORF3a W131C 4806
27972 ORF8 Q27stop 5996
28048 ORF8 R52I 6517
28095 ORF8 K68stop 5471
28111 ORF8 Y73C 4702
28271 intergenic del 1 3145
28280 N D3L 1835
28281 N D3L 1835
28282 N D3L 1963
28881 N R203K 720
28882 N R203K 718
28883 N G204R 721
28977 N S235F 937
29272 N silent 4096
29764 intergenic 8893
VSP2488−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

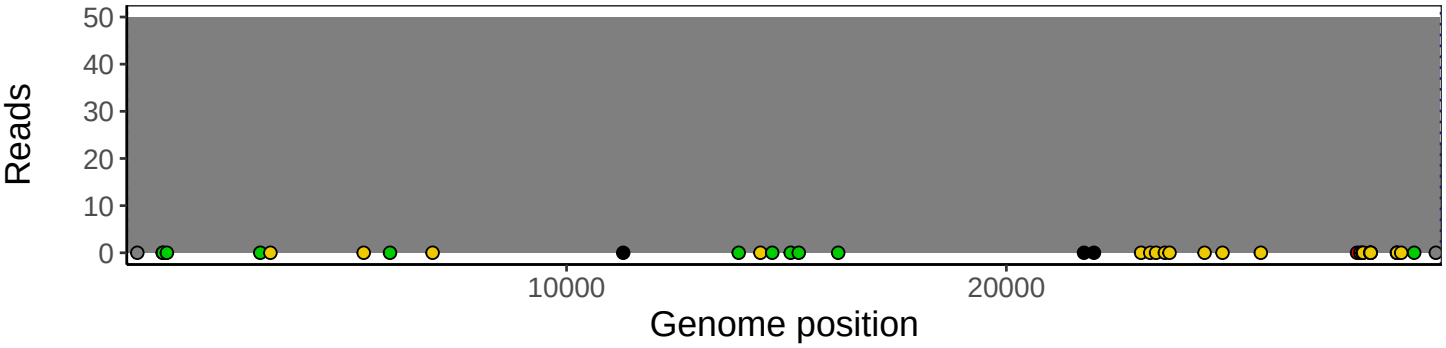
Analyses of individual experiments and composite results

VSP2488-1 | 2021-04-12 | VTM | UPHS-1234 | genomes | single experiment

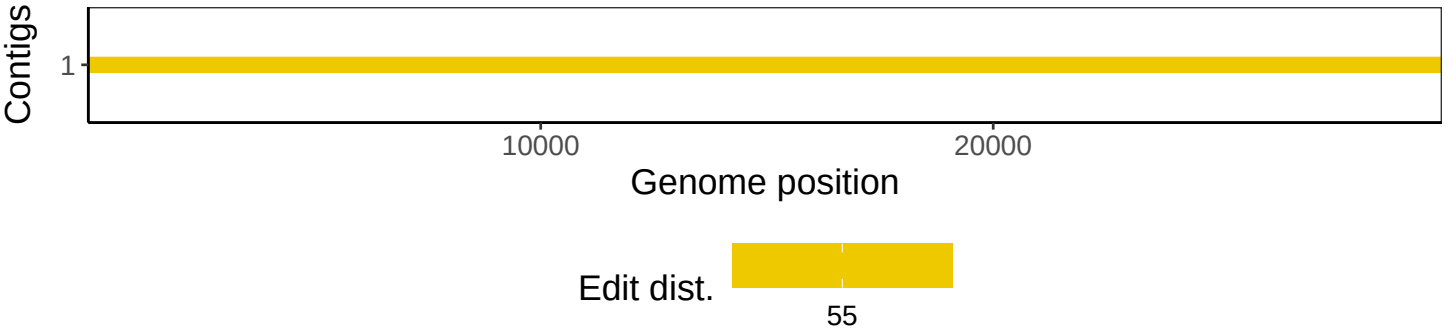
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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