COVID-19 subject UPHS-1577

2021-06-23

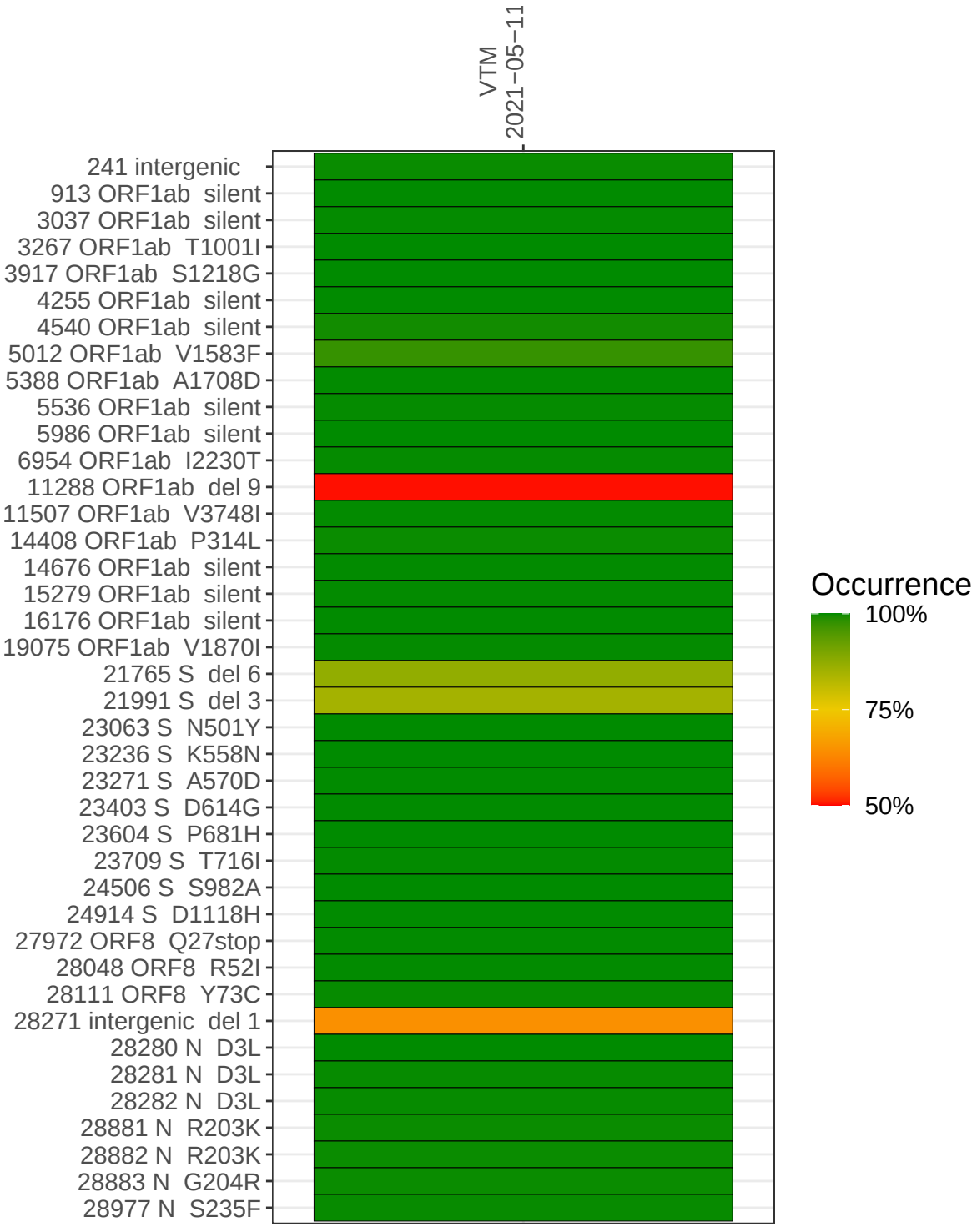
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

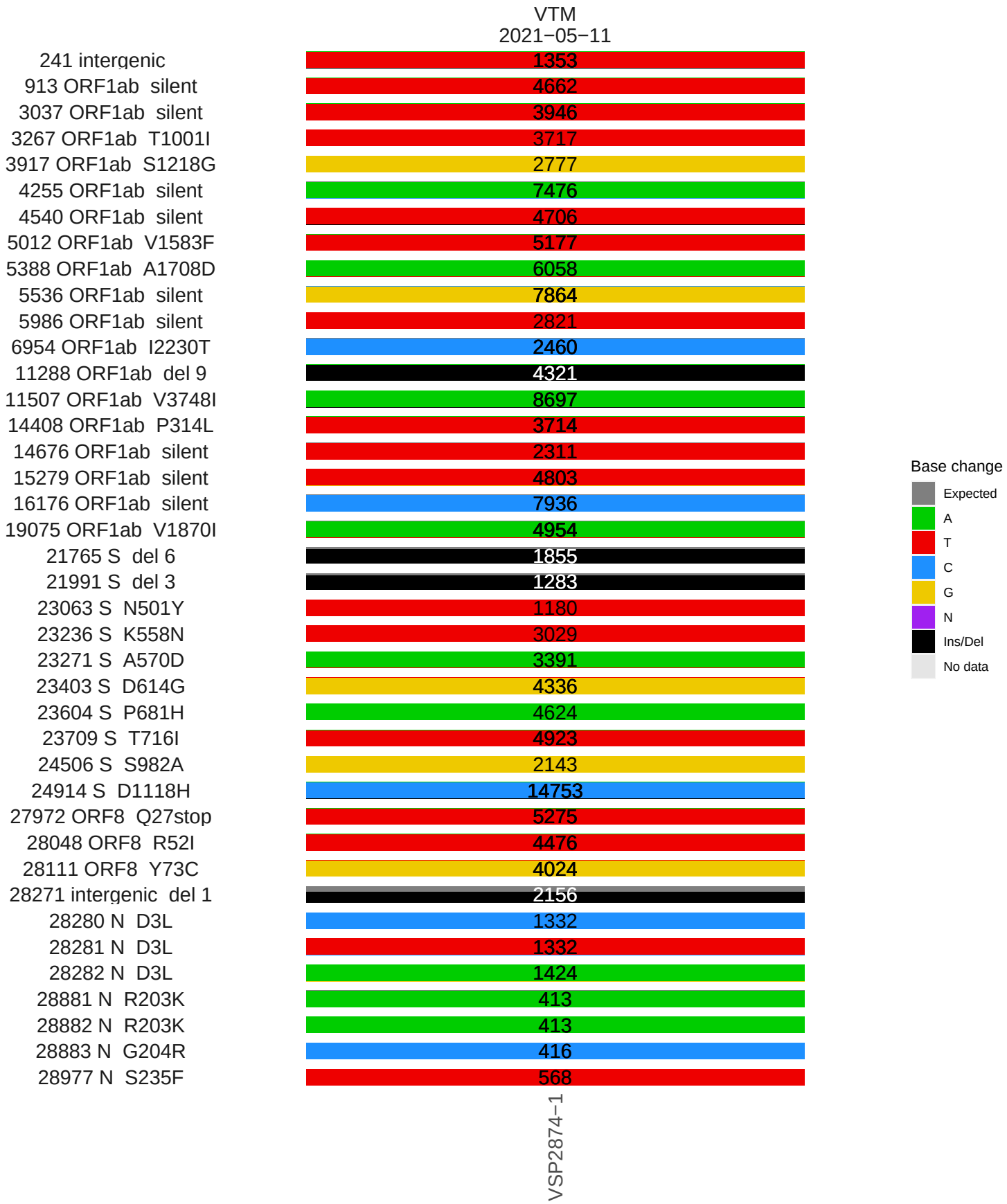
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP2874-1	single experiment	NA	VTM	2021-05-11	29.85	B.1.1.7	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.

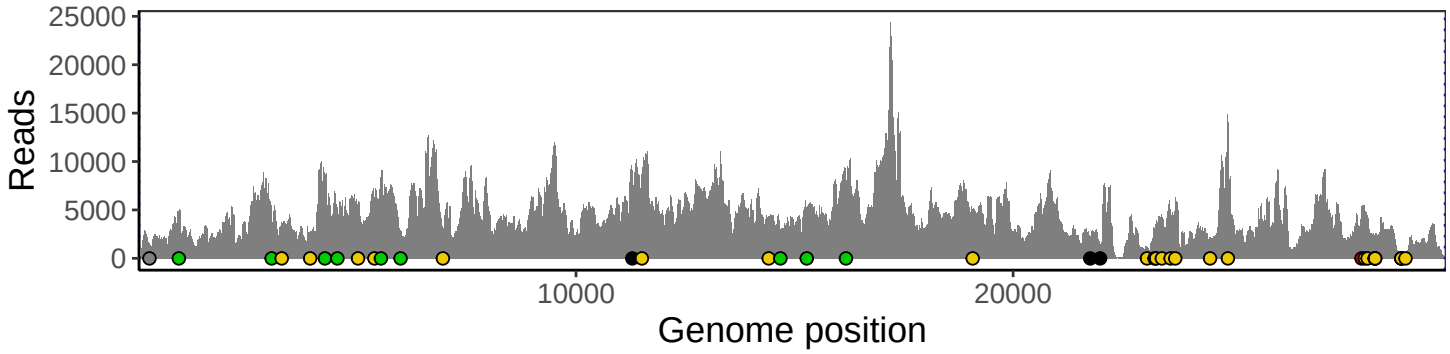



VTM
2021−05−11
241 intergenic 1353
913 ORF1ab silent 4662
3037 ORF1ab silent 3946
3267 ORF1ab T1001I 3717
3917 ORF1ab S1218G 2777
4255 ORF1ab silent 7476
4540 ORF1ab silent 4706
5012 ORF1ab V1583F 5177
5388 ORF1ab A1708D 6058
5536 ORF1ab silent 7864
5986 ORF1ab silent 2821
6954 ORF1ab I2230T 2460
11288 ORF1ab del 9 4321
11507 ORF1ab V3748I 8697
14408 ORF1ab P314L 3714
14676 ORF1ab silent 2311
15279 ORF1ab silent 4803
16176 ORF1ab silent 7936
19075 ORF1ab V1870I 4954
21765 S del 6 1855
21991 S del 3 1283
23063 S N501Y 1180
23236 S K558N 3029
23271 S A570D 3391
23403 S D614G 4336
23604 S P681H 4624
23709 S T716I 4923
24506 S S982A 2143
24914 S D1118H 14753
27972 ORF8 Q27stop 5275
28048 ORF8 R52I 4476
28111 ORF8 Y73C 4024
28271 intergenic del 1 2156
28280 N D3L 1332
28281 N D3L 1332
28282 N D3L 1424
28881 N R203K 413
28882 N R203K 413
28883 N G204R 416
28977 N S235F 568
VSP2874−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

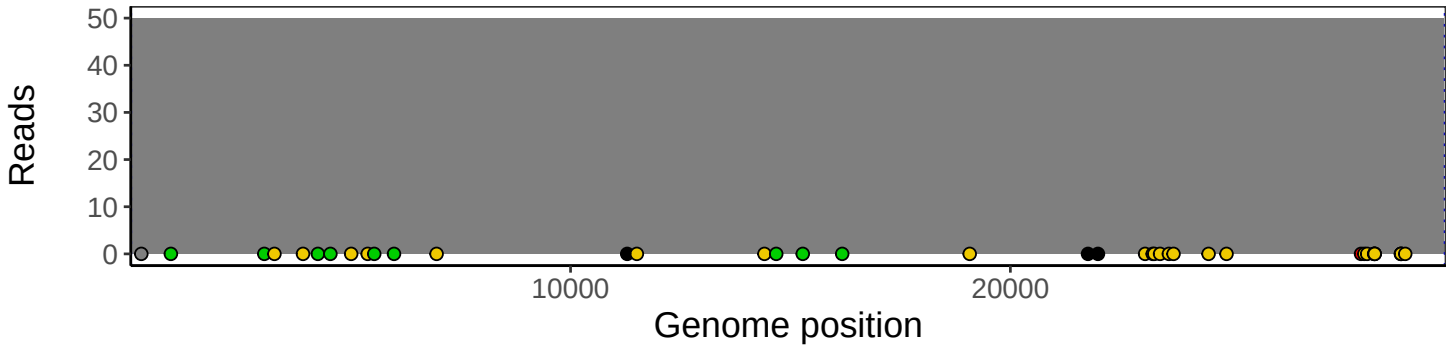
Analyses of individual experiments and composite results

VSP2874-1 | 2021-05-11 | VTM | UPHS-1577 | genomes | single experiment

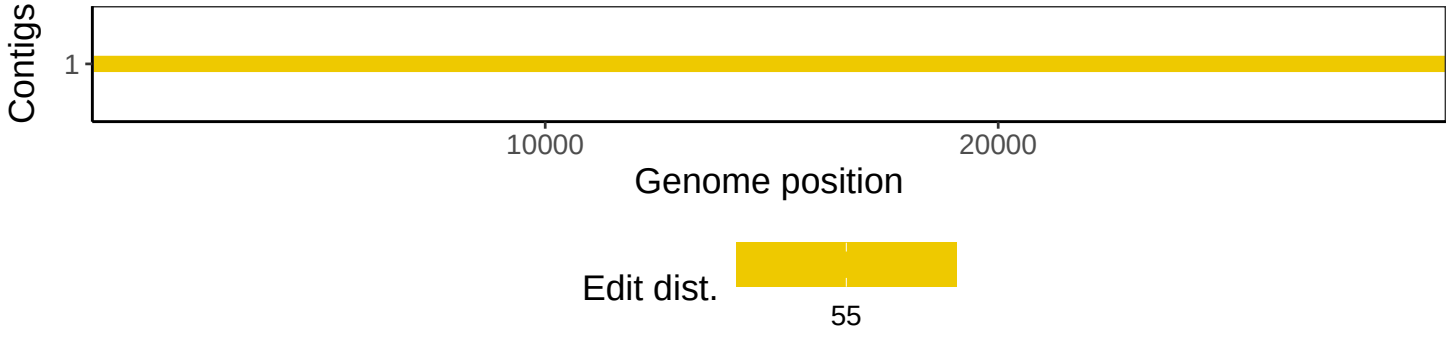
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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