# COVID-19 subject UPHS-1120

*2021-06-23*

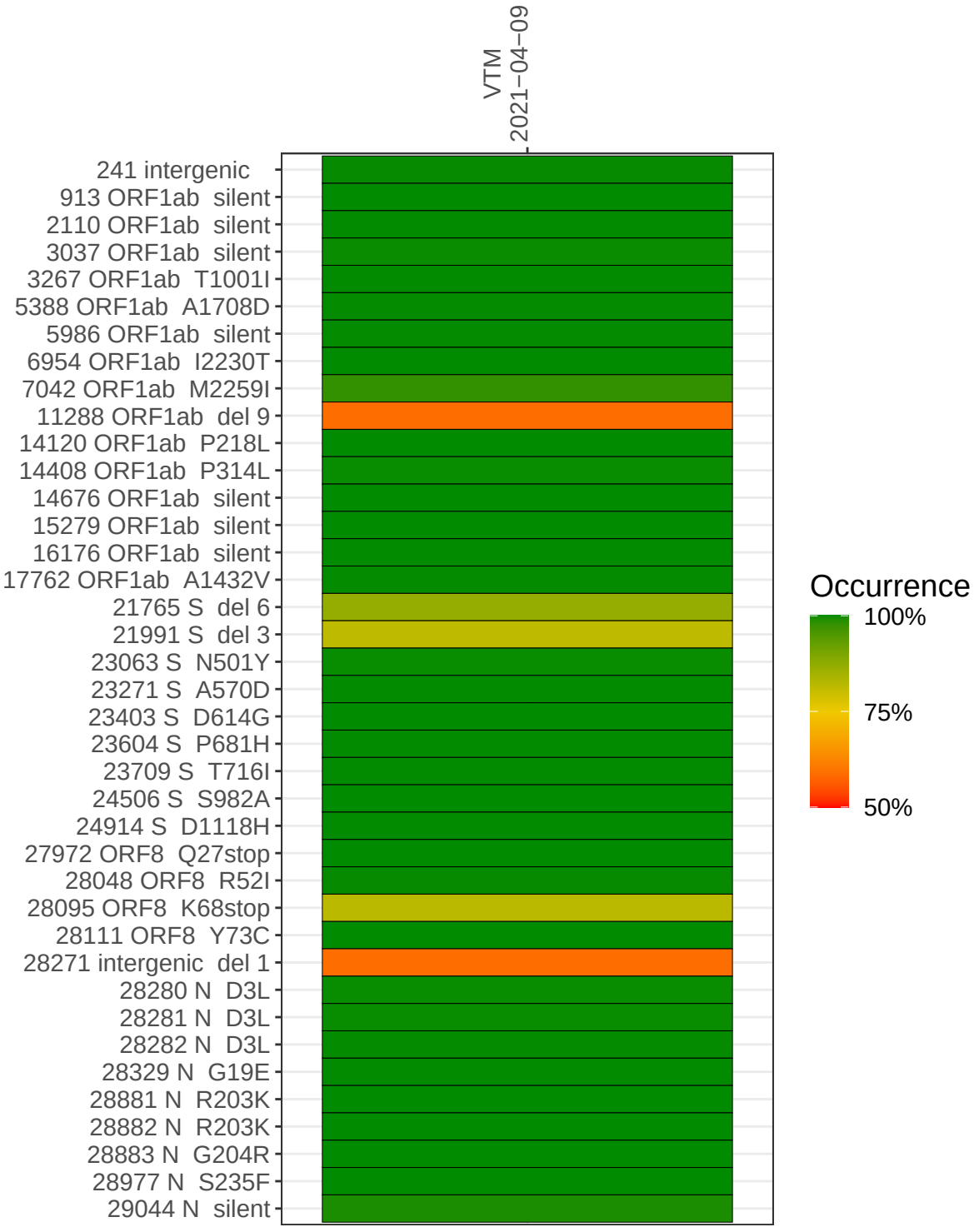
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

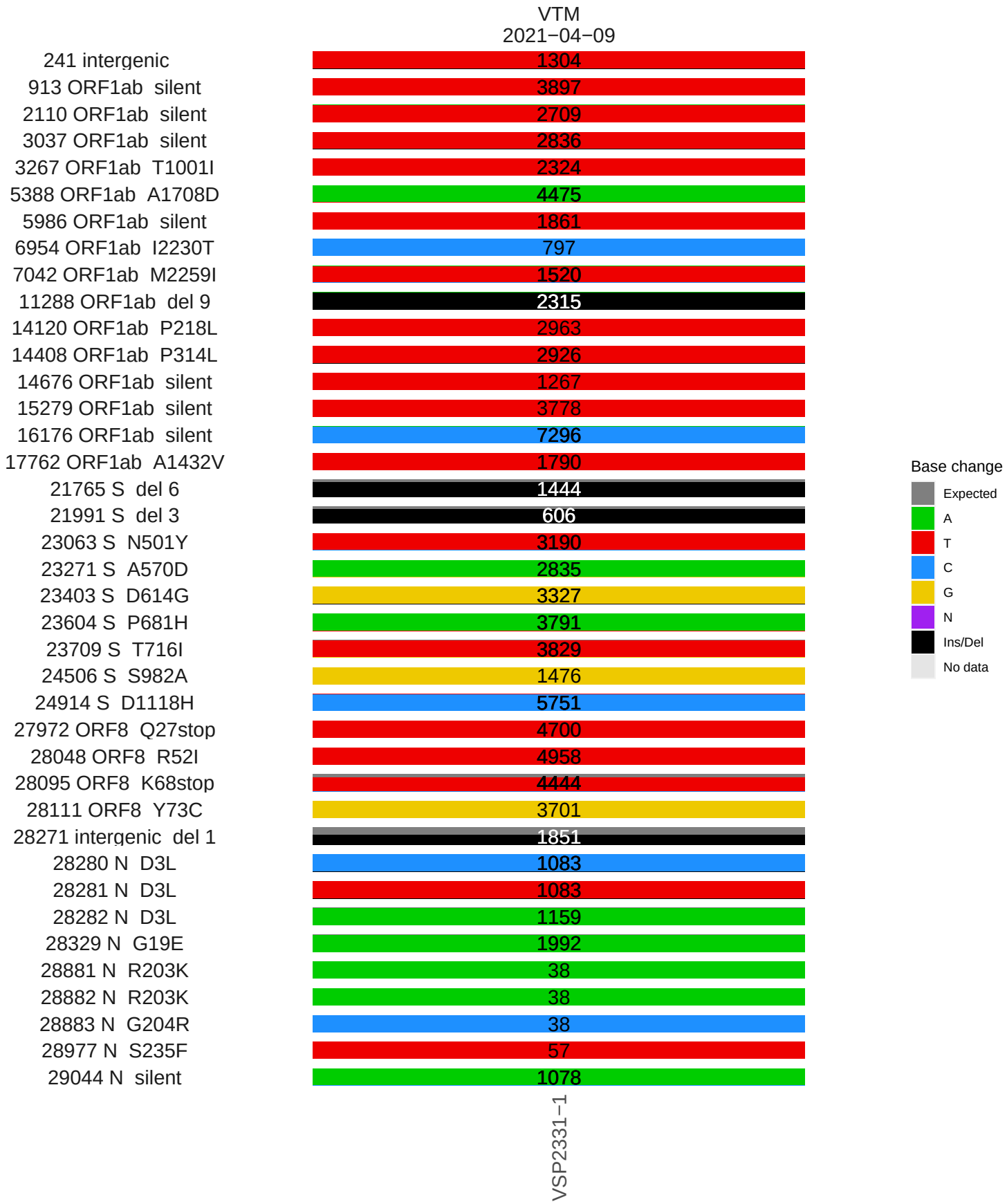
Table 1. Sample summary.

| Experiment | Type | Genomes | Sample type | Sample date | Largest contig (KD) | Lineage | Reference read coverage | Reference read coverage (>= 5 reads) |
|---|---|---|---|---|---|---|---|---|
| VSP2331-1 | single experiment | NA | VTM | 2021-04-09 | 29.92 | B.1.1.7 | 99.8% | 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.

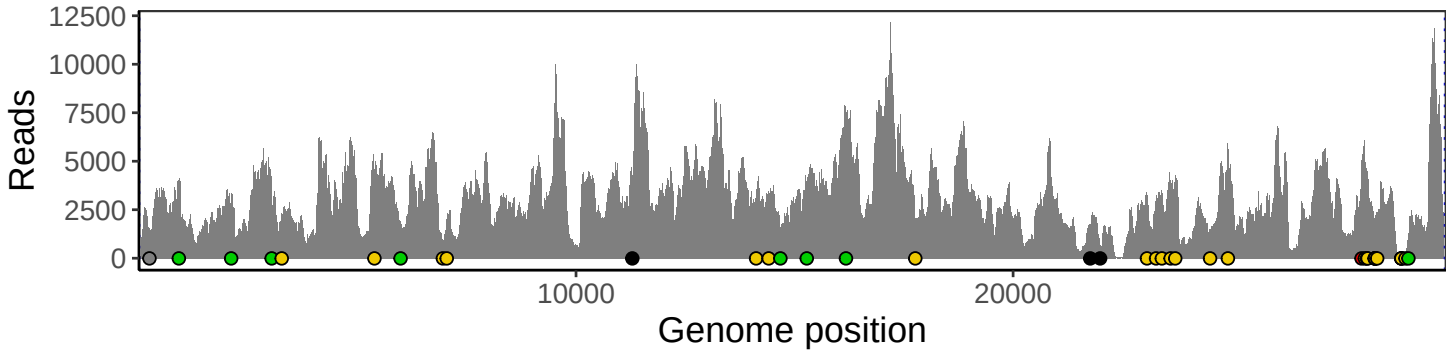



VTM
2021−04−09
241 intergenic 1304
913 ORF1ab silent 3897
2110 ORF1ab silent 2709
3037 ORF1ab silent 2836
3267 ORF1ab T1001I 2324
5388 ORF1ab A1708D 4475
5986 ORF1ab silent 1861
6954 ORF1ab I2230T 797
7042 ORF1ab M2259I 1520
11288 ORF1ab del 9 2315
14120 ORF1ab P218L 2963
14408 ORF1ab P314L 2926
14676 ORF1ab silent 1267
15279 ORF1ab silent 3778
16176 ORF1ab silent 7296
17762 ORF1ab A1432V 1790
21765 S del 6 1444
21991 S del 3 606
23063 S N501Y 3190
23271 S A570D 2835
23403 S D614G 3327
23604 S P681H 3791
23709 S T716I 3829
24506 S S982A 1476
24914 S D1118H 5751
27972 ORF8 Q27stop 4700
28048 ORF8 R52I 4958
28095 ORF8 K68stop 4444
28111 ORF8 Y73C 3701
28271 intergenic del 1 1851
28280 N D3L 1083
28281 N D3L 1083
28282 N D3L 1159
28329 N G19E 1992
28881 N R203K 38
28882 N R203K 38
28883 N G204R 38
28977 N S235F 57
29044 N silent 1078
VSP2331−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

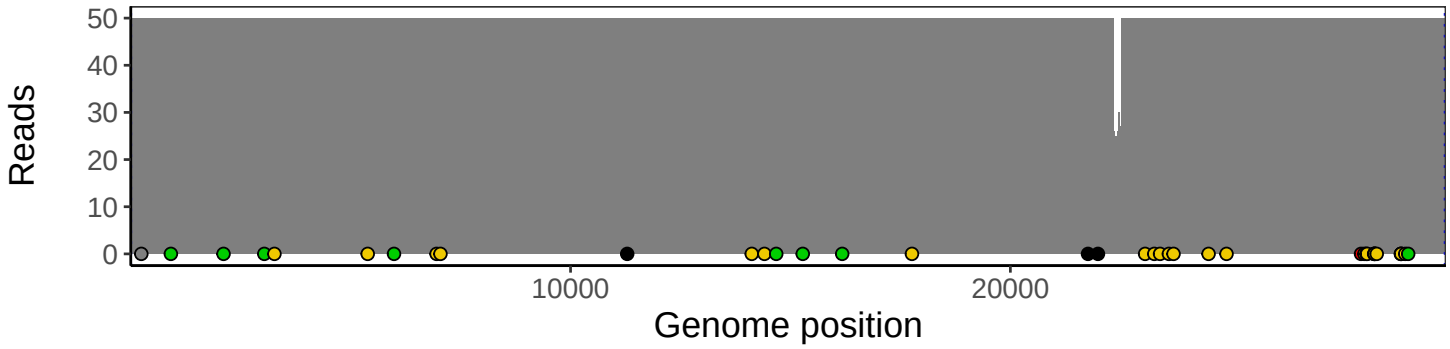
## Analyses of individual experiments and composite results

### VSP2331-1 | 2021-04-09 | VTM | UPHS-1120 | genomes | single experiment

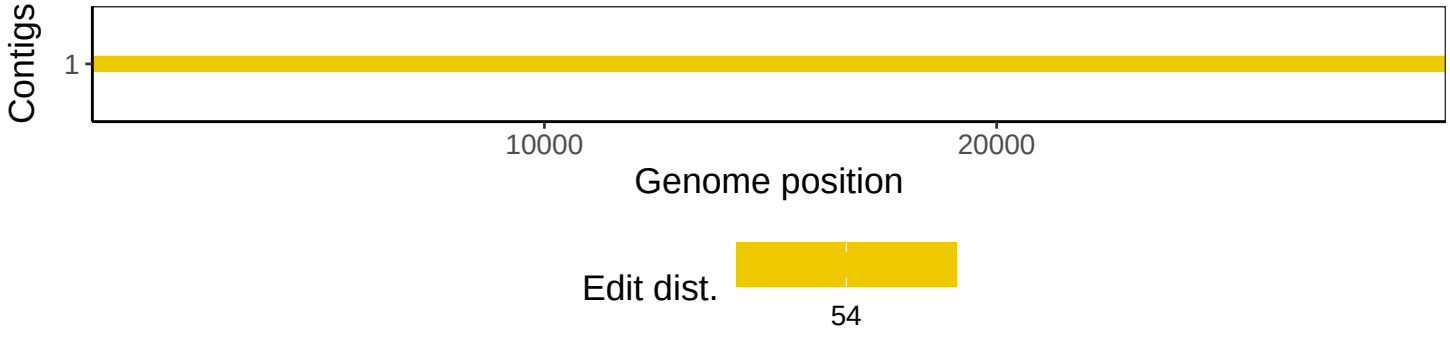
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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 |