# COVID-19 subject UPHS-0825

*2021-05-21*

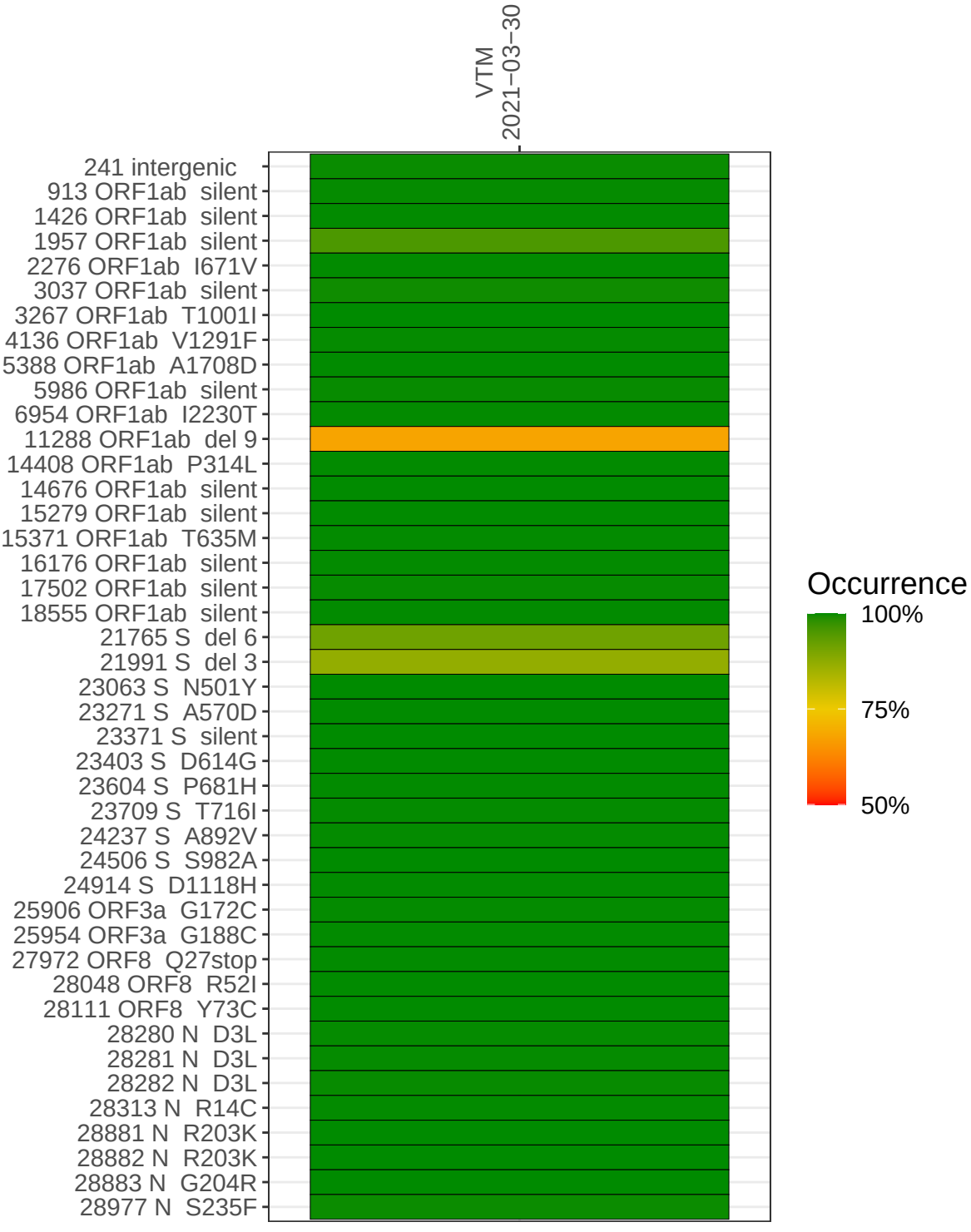
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

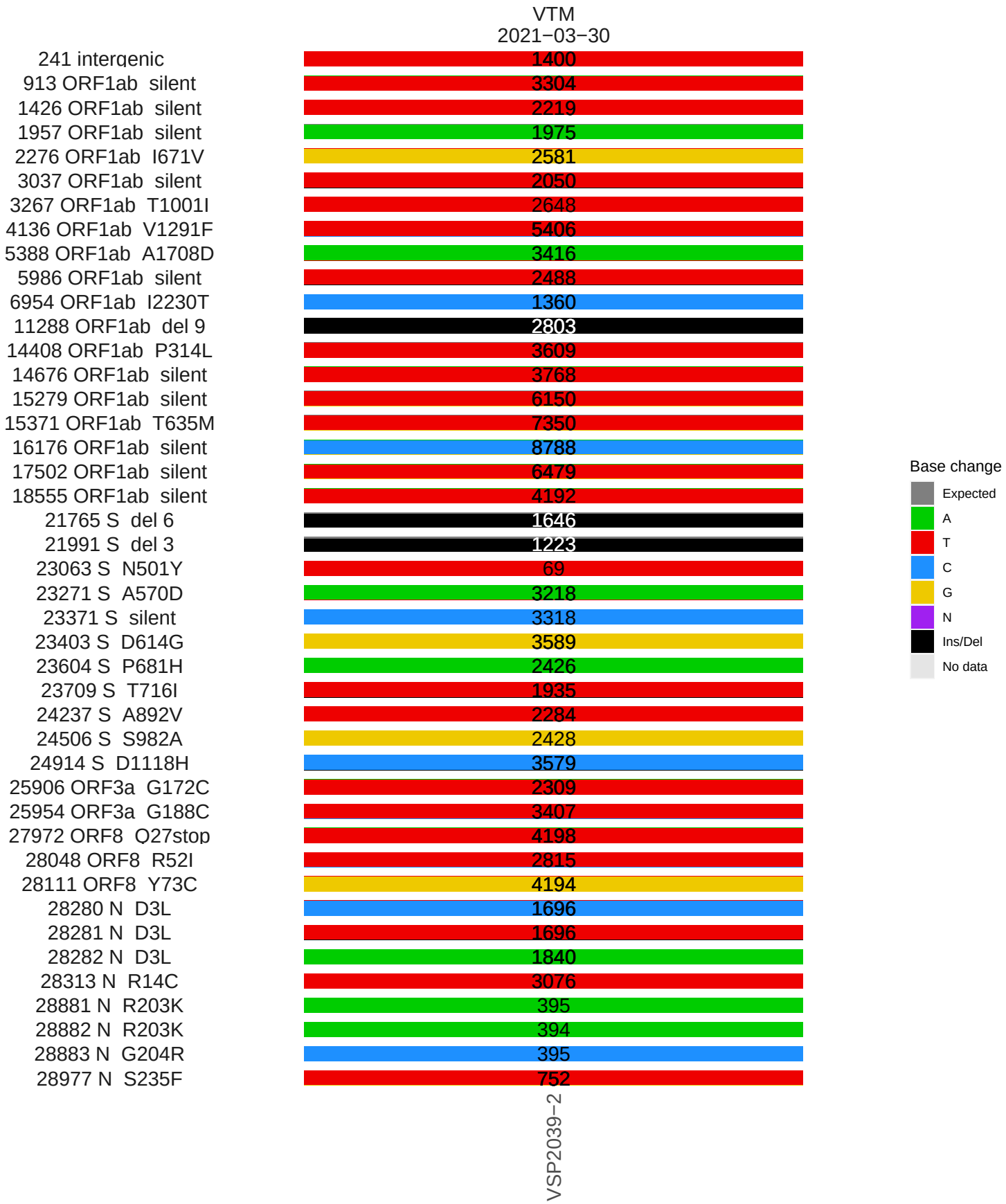
Table 1. Sample summary.

| Experiment | Type | Genomes | Sample type | Sample date | Largest contig (KD) | Lineage | Reference read coverage | Reference read coverage (>= 5 reads) |
|---|---|---|---|---|---|---|---|---|
| VSP2039-2 | single experiment | NA | VTM | 2021-03-30 | 29.80 | B.1.1.7 | 99.7% | 99.7% |

**Variants shared across samples**

The heat map below shows how variants (reference genome /home/everett/projects/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.

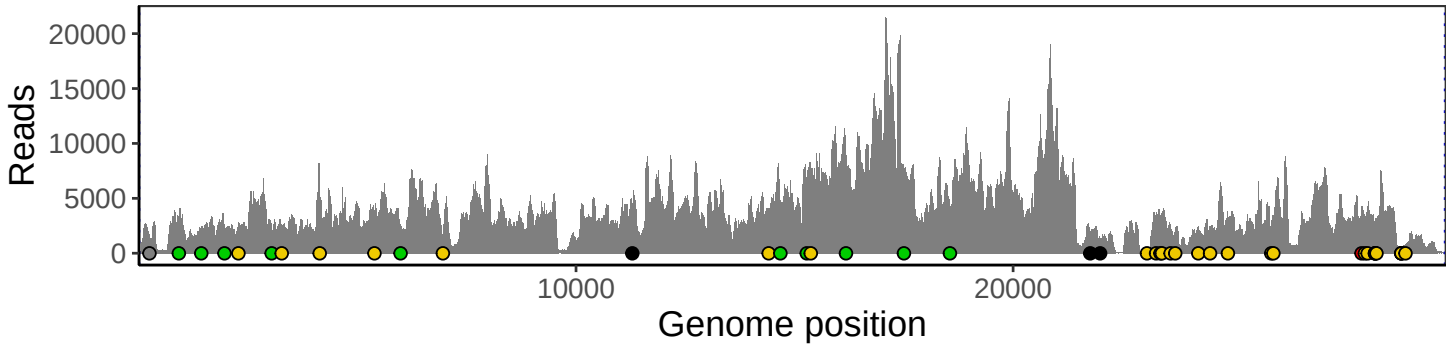



VTM
2021−03−30
241 intergenic
913 ORF1ab silent
1426 ORF1ab silent
1957 ORF1ab silent
2276 ORF1ab I671V
3037 ORF1ab silent
3267 ORF1ab T1001I
4136 ORF1ab V1291F
5388 ORF1ab A1708D
5986 ORF1ab silent
6954 ORF1ab I2230T
11288 ORF1ab del 9
14408 ORF1ab P314L
14676 ORF1ab silent
15279 ORF1ab silent
15371 ORF1ab T635M
16176 ORF1ab silent
17502 ORF1ab silent
18555 ORF1ab silent
21765 S del 6
21991 S del 3
23063 S N501Y
23271 S A570D
23371 S silent
23403 S D614G
23604 S P681H
23709 S T716I
24237 S A892V
24506 S S982A
24914 S D1118H
25906 ORF3a G172C
25954 ORF3a G188C
27972 ORF8 Q27stop
28048 ORF8 R52I
28111 ORF8 Y73C
28280 N D3L
28281 N D3L
28282 N D3L
28313 N R14C
28881 N R203K
28882 N R203K
28883 N G204R
28977 N S235F
1400
3304
2219
1975
2581
2050
2648
5406
3416
2488
1360
2803
3609
3768
6150
7350
8788
6479
4192
1646
1223
69
3218
3318
3589
2426
1935
2284
2428
3579
2309
3407
4198
2815
4194
1696
1696
1840
3076
395
394
395
752
VSP2039−2
Base change
Expected
A
T
C
G
N
Ins/Del
No data

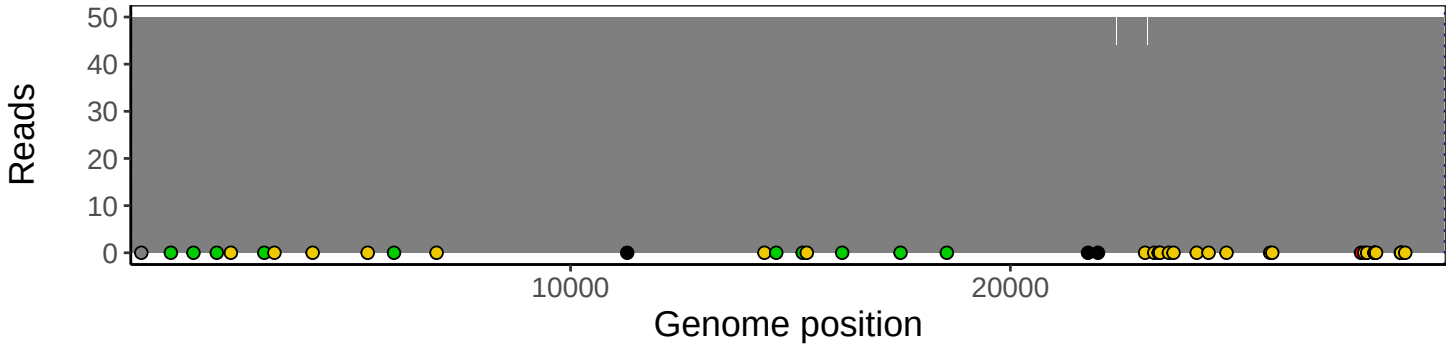
## Analyses of individual experiments and composite results

### VSP2039-2 | 2021-03-30 | VTM | UPHS-0825 | genomes | single experiment

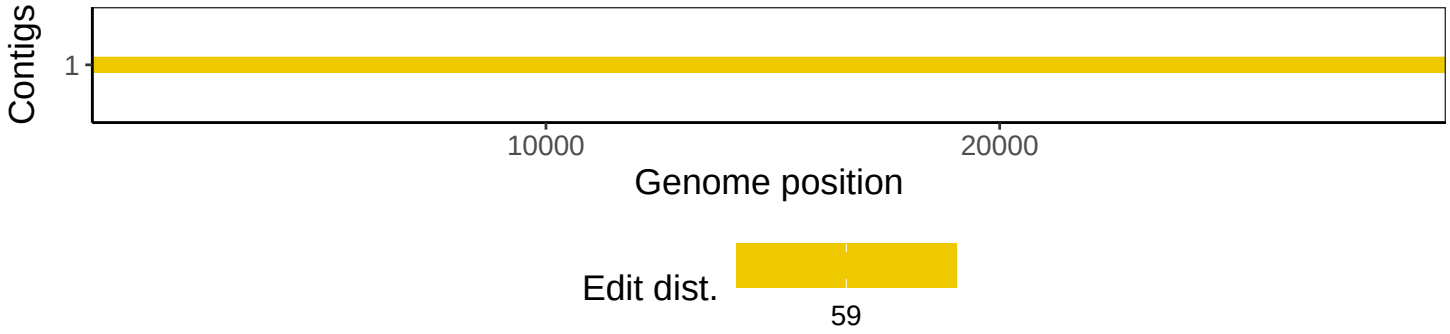
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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 | 2.3.8 |
| 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 |