# COVID-19 subject HUP Q-0135

*2021-05-05*

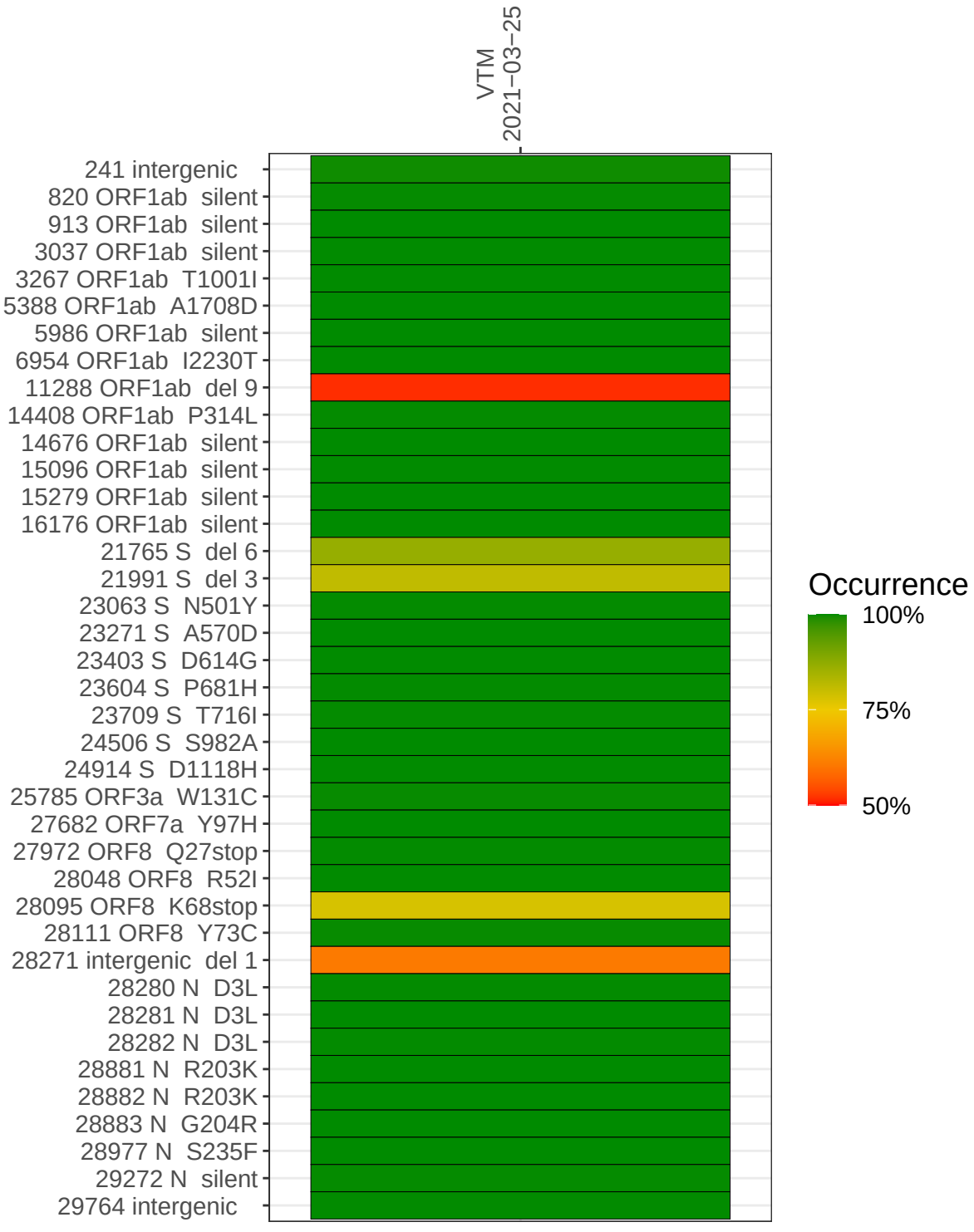
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

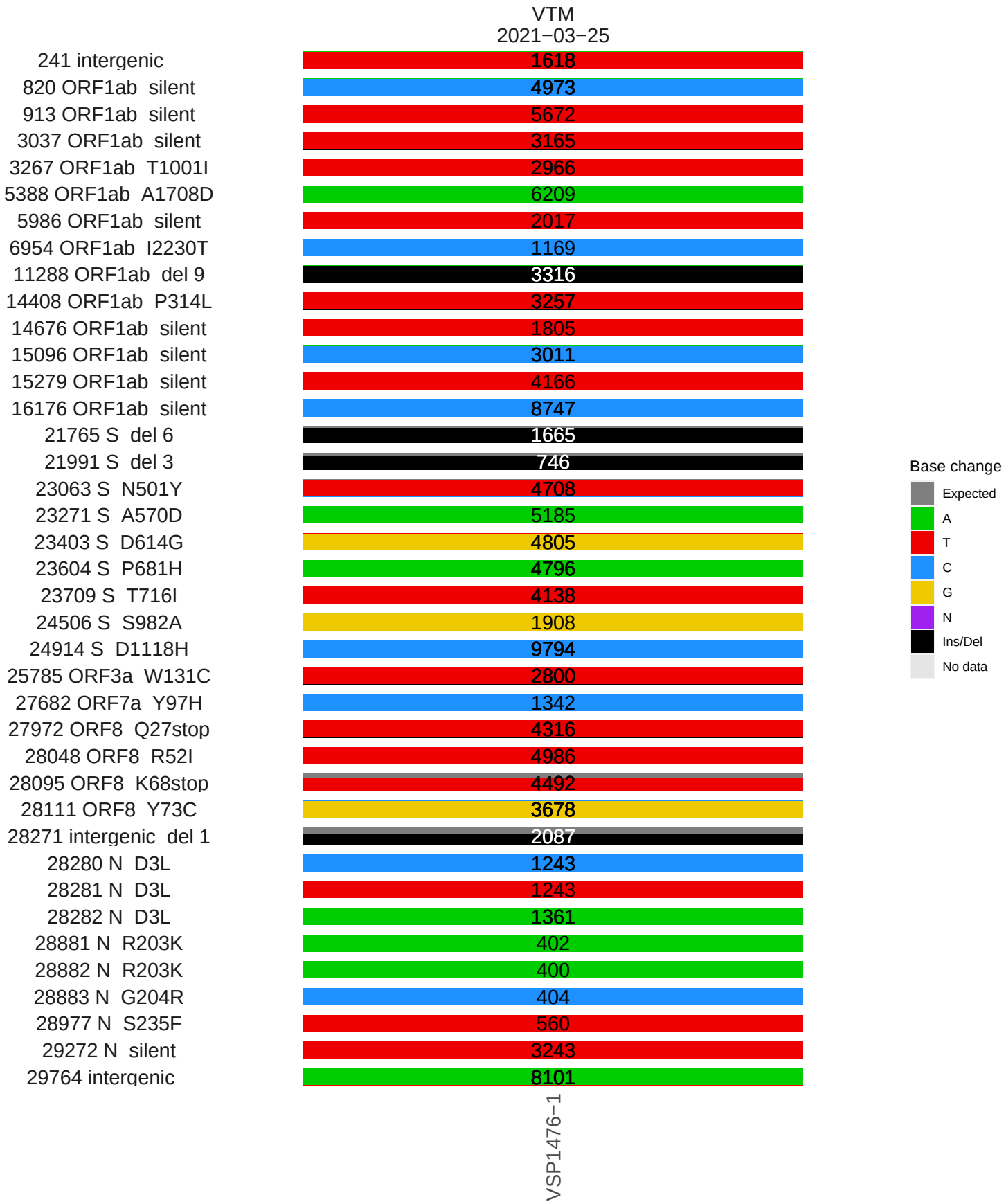
Table 1. Sample summary.

| Experiment | Type | Genomes | Sample type | Sample date | Largest contig (KD) | Lineage | Reference read coverage | Reference read coverage (>= 5 reads) |
|---|---|---|---|---|---|---|---|---|
| VSP1476-1 | single experiment | NA | VTM | 2021-03-25 | 29.87 | B.1.1.7 | 99.9% | 99.8% |

**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.

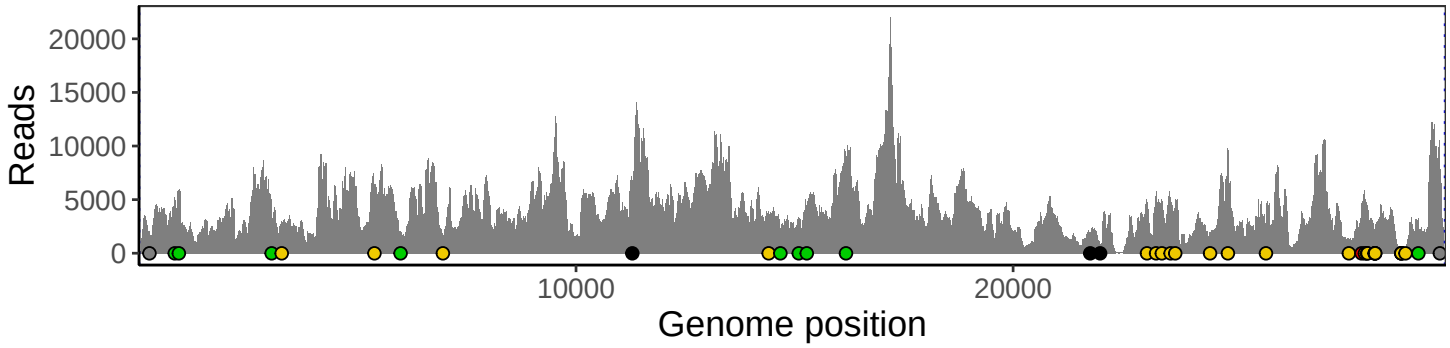



VTM
2021−03−25
241 intergenic 1618
820 ORF1ab silent 4973
913 ORF1ab silent 5672
3037 ORF1ab silent 3165
3267 ORF1ab T1001I 2966
5388 ORF1ab A1708D 6209
5986 ORF1ab silent 2017
6954 ORF1ab I2230T 1169
11288 ORF1ab del 9 3316
14408 ORF1ab P314L 3257
14676 ORF1ab silent 1805
15096 ORF1ab silent 3011
15279 ORF1ab silent 4166
16176 ORF1ab silent 8747
21765 S del 6 1665
21991 S del 3 746
23063 S N501Y 4708
23271 S A570D 5185
23403 S D614G 4805
23604 S P681H 4796
23709 S T716I 4138
24506 S S982A 1908
24914 S D1118H 9794
25785 ORF3a W131C 2800
27682 ORF7a Y97H 1342
27972 ORF8 Q27stop 4316
28048 ORF8 R52I 4986
28095 ORF8 K68stop 4492
28111 ORF8 Y73C 3678
28271 intergenic del 1 2087
28280 N D3L 1243
28281 N D3L 1243
28282 N D3L 1361
28881 N R203K 402
28882 N R203K 400
28883 N G204R 404
28977 N S235F 560
29272 N silent 3243
29764 intergenic 8101
VSP1476−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

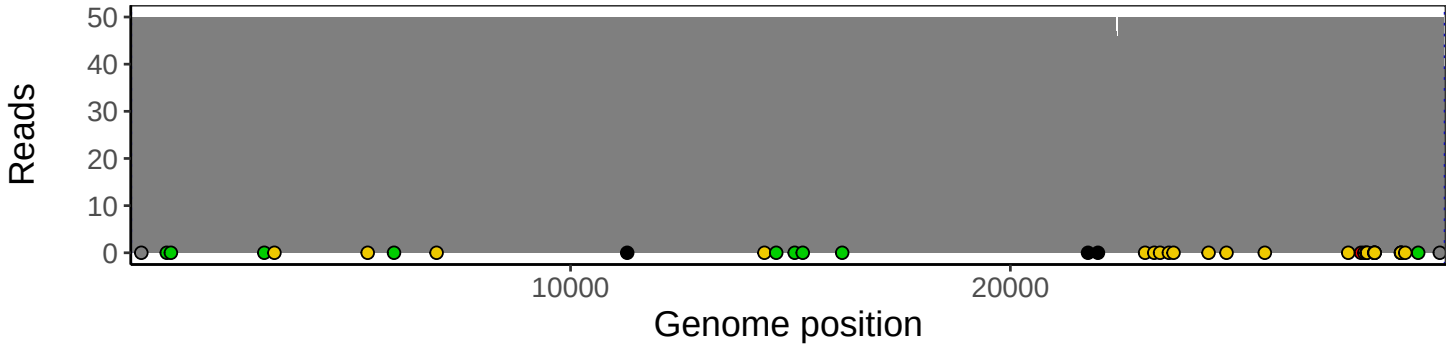
## Analyses of individual experiments and composite results

### VSP1476-1 | 2021-03-25 | VTM | HUP Q-0135 | genomes | single experiment

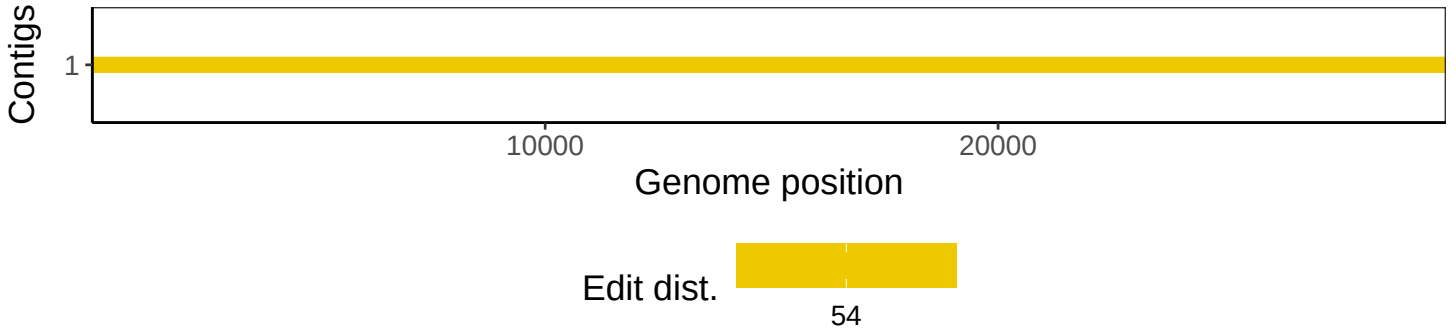
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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 |