# COVID-19 subject UPHS-0534

*2021-06-03*

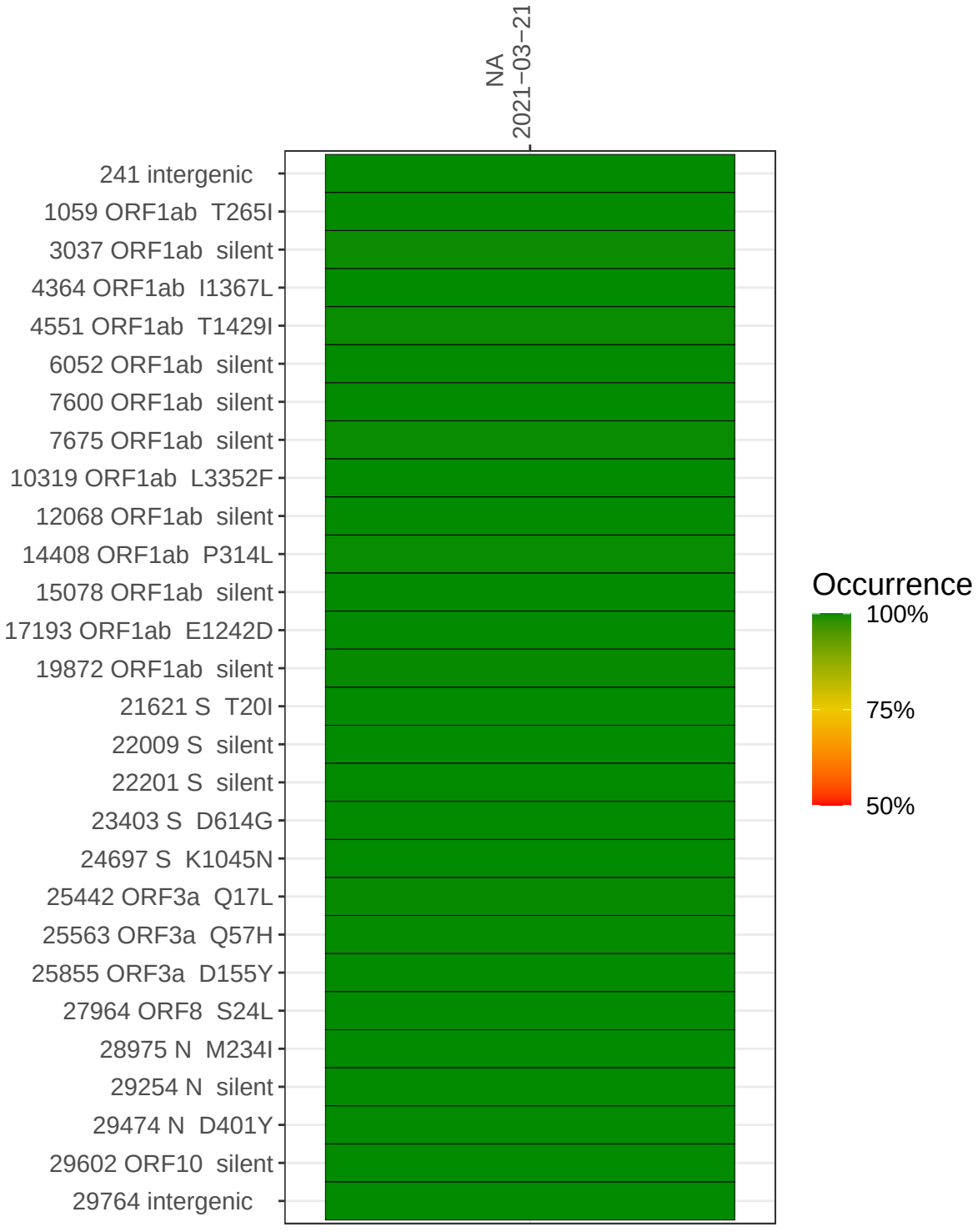
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

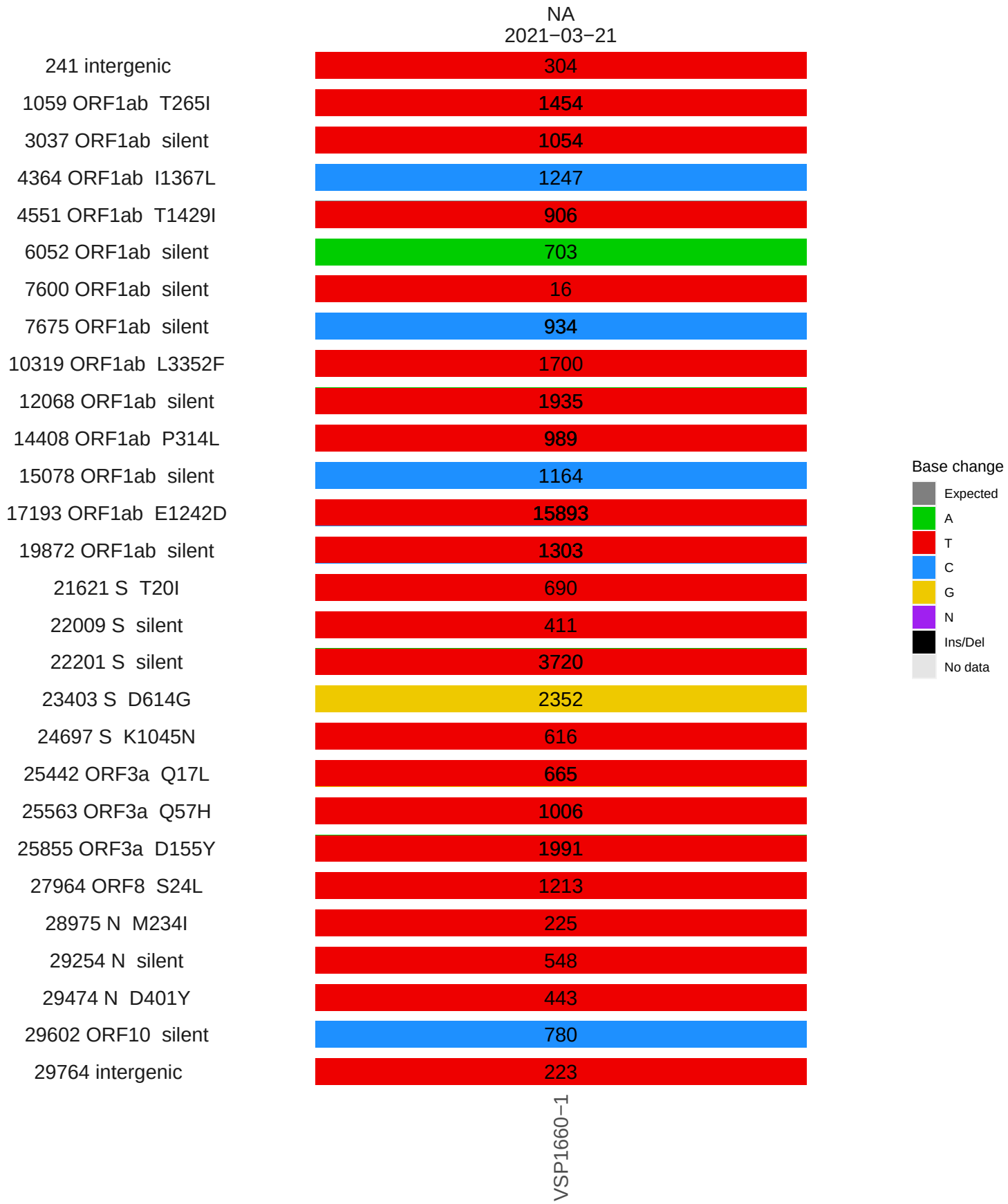
Table 1. Sample summary.

| Experiment | Type | Genomes | Sample type | Sample date | Largest contig (KD) | Lineage | Reference read coverage | Reference read coverage (>= 5 reads) |
|---|---|---|---|---|---|---|---|---|
| VSP1660-1 | single experiment | NA | NA | 2021-03-21 | 29.82 | B.1.588 | 99.7% | 99.6% |

**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.

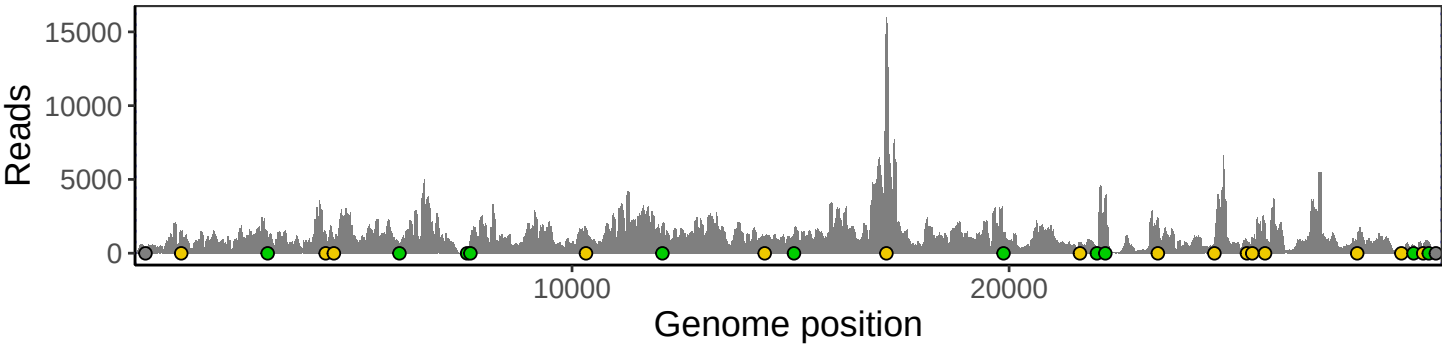



NA
2021−03−21
241 intergenic
304
1059 ORF1ab T265I
1454
3037 ORF1ab silent
1054
4364 ORF1ab I1367L
1247
4551 ORF1ab T1429I
906
6052 ORF1ab silent
703
7600 ORF1ab silent
16
7675 ORF1ab silent
934
10319 ORF1ab L3352F
1700
12068 ORF1ab silent
1935
14408 ORF1ab P314L
989
15078 ORF1ab silent
1164
17193 ORF1ab E1242D
15893
19872 ORF1ab silent
1303
21621 S T20I
690
22009 S silent
411
22201 S silent
3720
23403 S D614G
2352
24697 S K1045N
616
25442 ORF3a Q17L
665
25563 ORF3a Q57H
1006
25855 ORF3a D155Y
1991
27964 ORF8 S24L
1213
28975 N M234I
225
29254 N silent
548
29474 N D401Y
443
29602 ORF10 silent
780
29764 intergenic
223
VSP1660−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

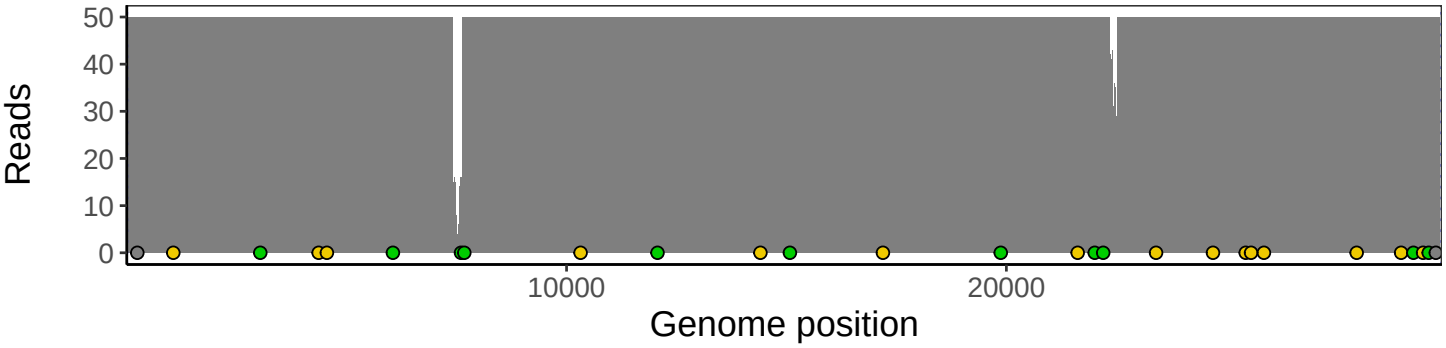
## Analyses of individual experiments and composite results

### VSP1660-1 | 2021-03-21 | NA | UPHS-0534 | genomes | single experiment

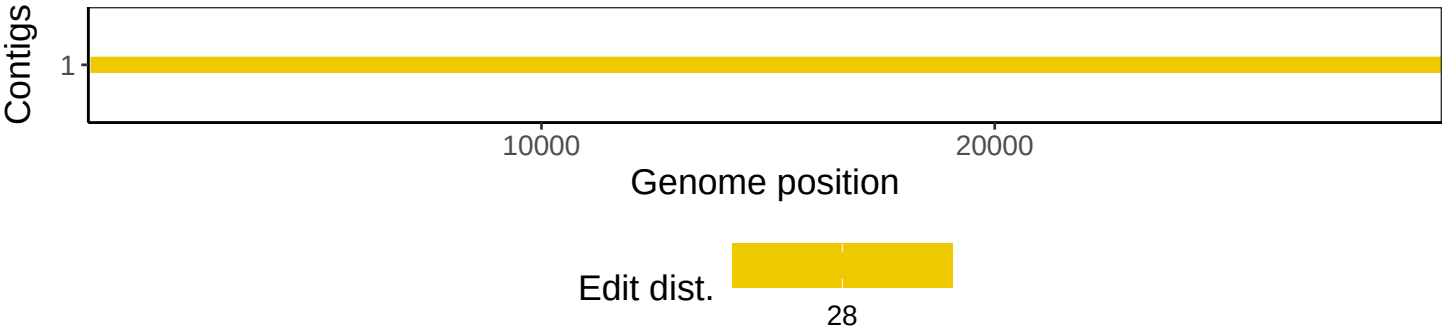
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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 |