# COVID-19 subject S-210226-01457

*2021-03-31*

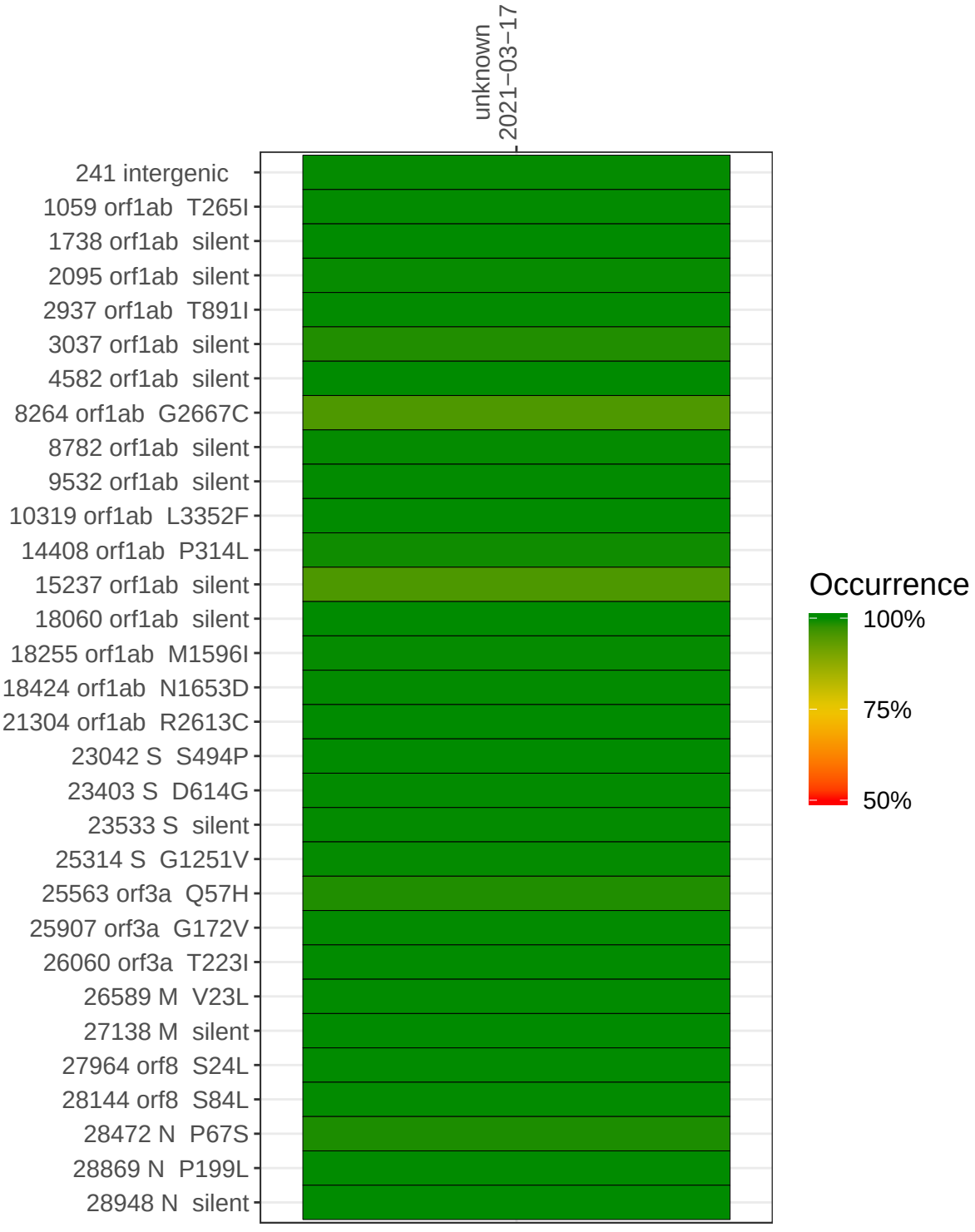
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

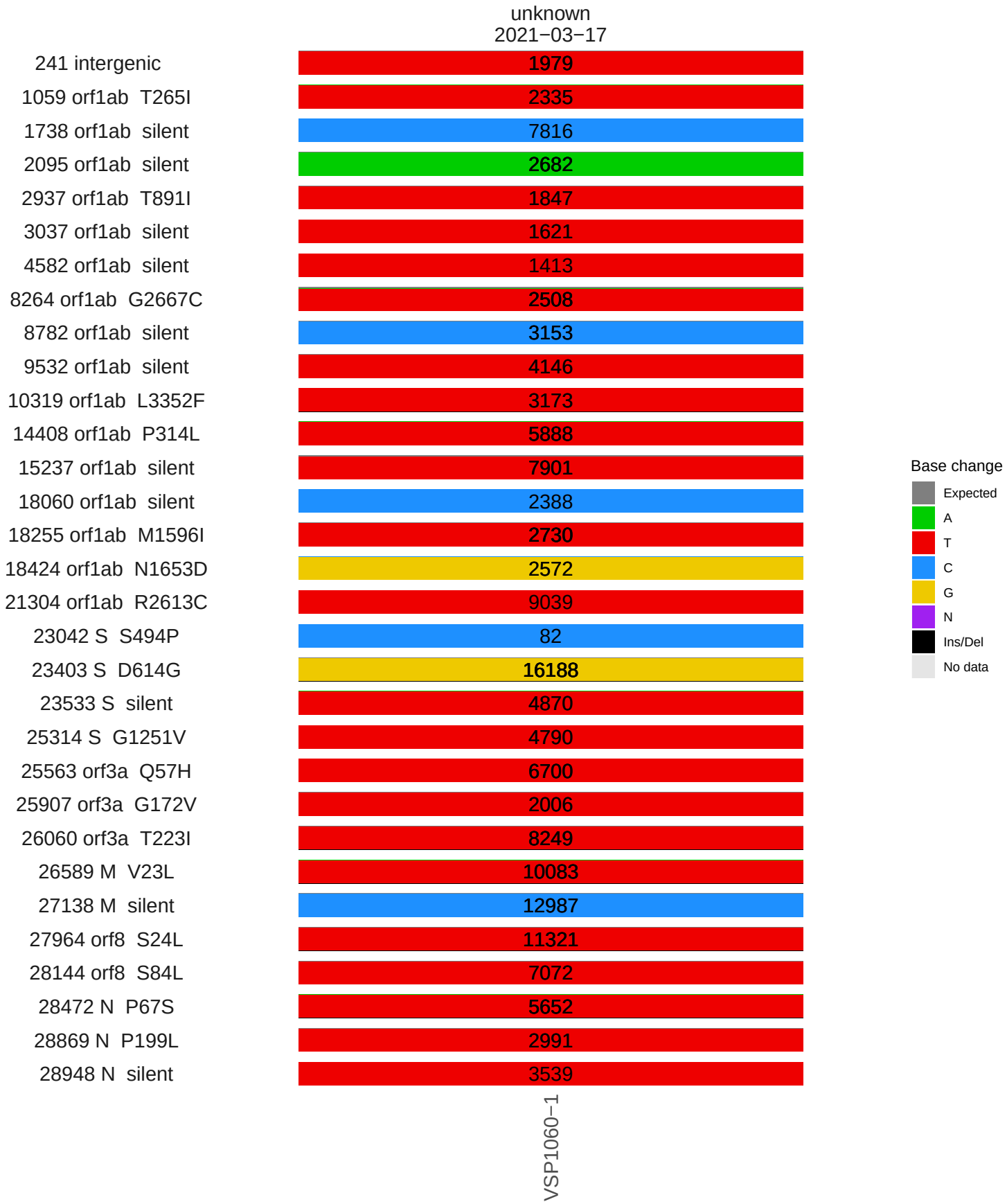
Table 1. Sample summary.

| Experiment | Type | Genomes | Sample type | Sample date | Largest contig (KD) | Lineage | Reference read coverage | Reference read coverage (>= 5 reads) |
|---|---|---|---|---|---|---|---|---|
| VSP1060-1 | single experiment | NA | unknown | 2021-03-17 | 29.84 | B.1.2 | 99.9% | 99.8% |

**Variants shared across samples**

The heat map below shows how variants (reference genome USA-WA1-2020) 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.

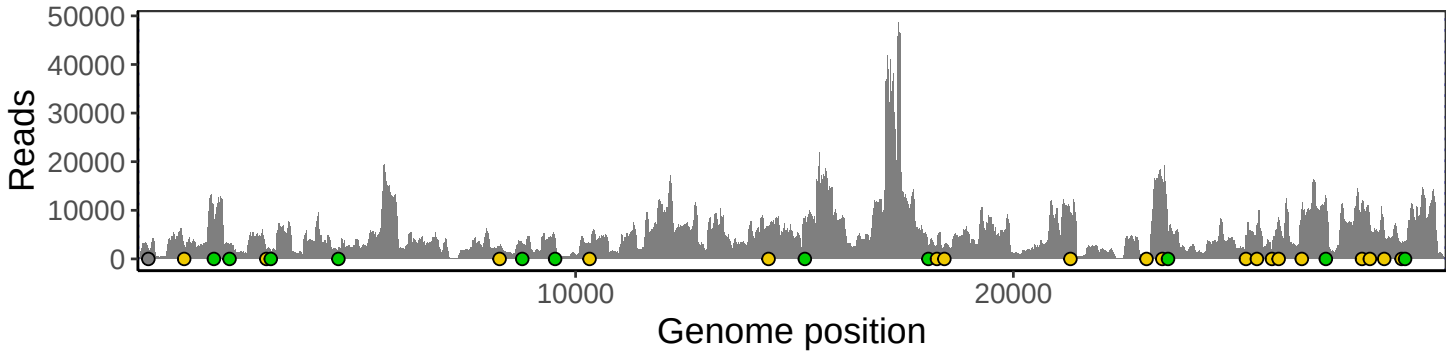



unknown
2021−03−17
241 intergenic
1059 orf1ab T265I
1738 orf1ab silent
2095 orf1ab silent
2937 orf1ab T891I
3037 orf1ab silent
4582 orf1ab silent
8264 orf1ab G2667C
8782 orf1ab silent
9532 orf1ab silent
10319 orf1ab L3352F
14408 orf1ab P314L
15237 orf1ab silent
18060 orf1ab silent
18255 orf1ab M1596I
18424 orf1ab N1653D
21304 orf1ab R2613C
23042 S S494P
23403 S D614G
23533 S silent
25314 S G1251V
25563 orf3a Q57H
25907 orf3a G172V
26060 orf3a T223I
26589 M V23L
27138 M silent
27964 orf8 S24L
28144 orf8 S84L
28472 N P67S
28869 N P199L
28948 N silent
1979
2335
7816
2682
1847
1621
1413
2508
3153
4146
3173
5888
7901
2388
2730
2572
9039
82
16188
4870
4790
6700
2006
8249
10083
12987
11321
7072
5652
2991
3539
VSP1060−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

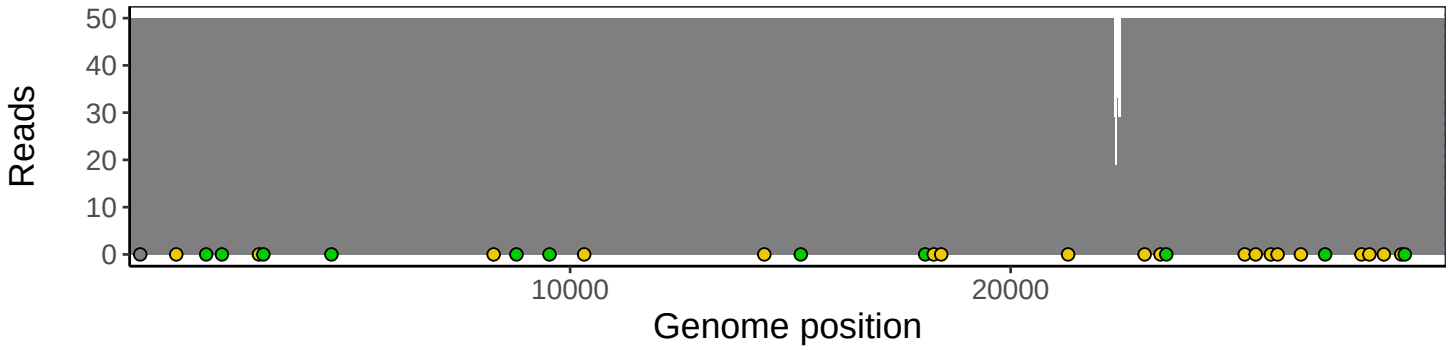
## Analyses of individual experiments and composite results

### VSP1060-1 | 2021-03-17 | unknown | S-210226-01457 | genomes | single experiment

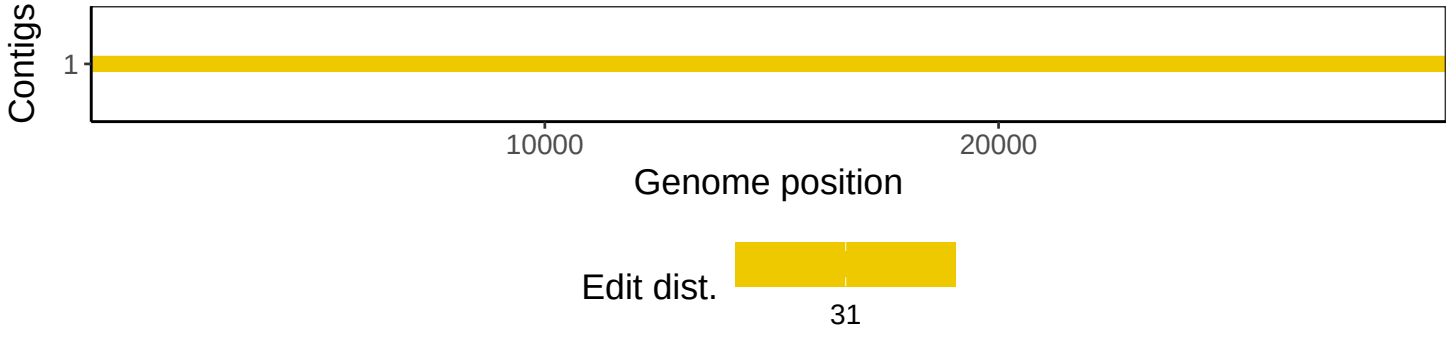
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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 | 2.3.3 |
| 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 | 3.0.0 |
| 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 |