

COVID-19 subject SARS_CoV_76

2021-06-29

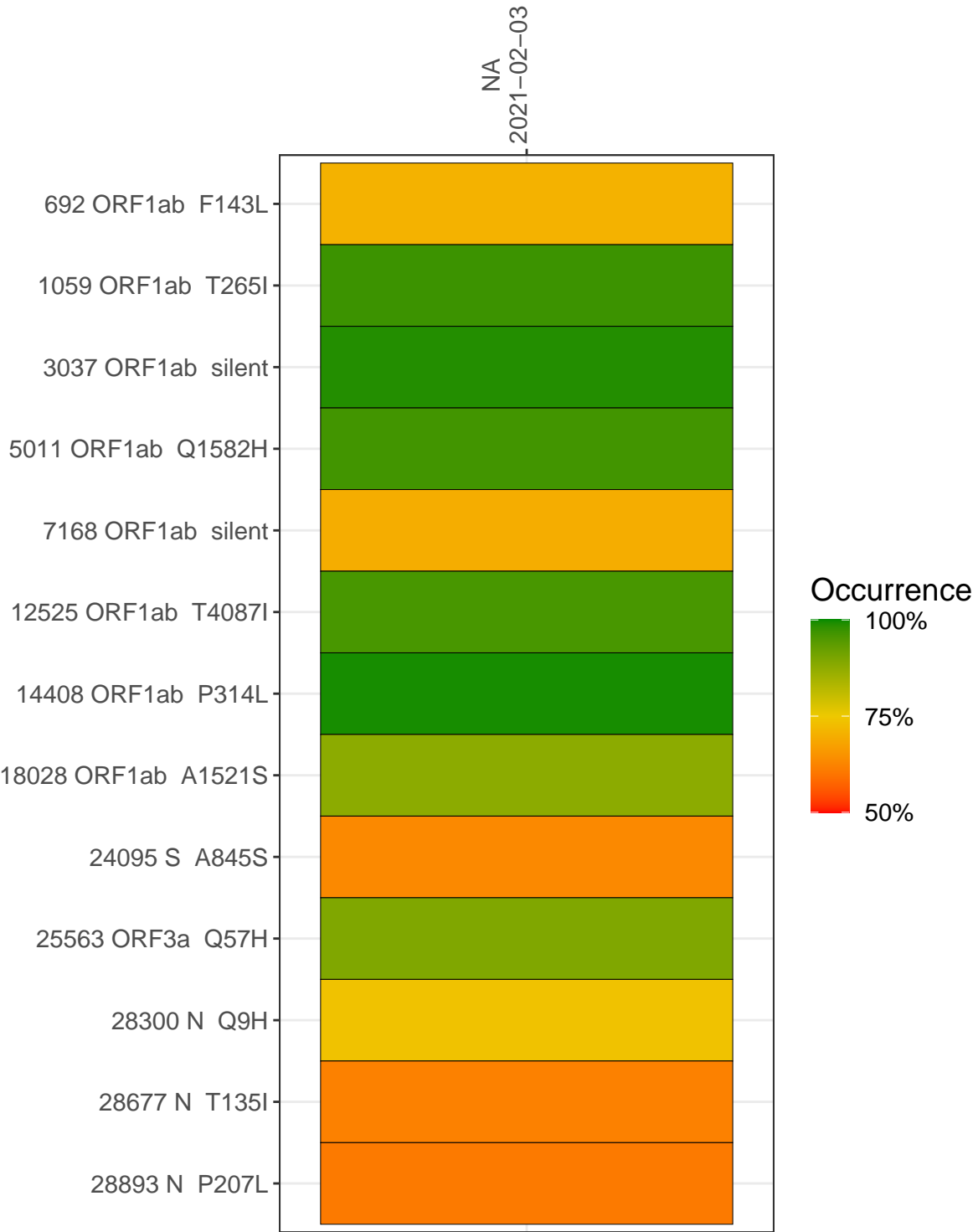
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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) |
|------------|-------------------|---------|-------------|-------------|---------------------|---------|-------------------------|--------------------------------------|
| VSP3001-1 | single experiment | NA | NA | 2021-02-03 | 2.11 | B.1.311 | 99.8% | 99.5% |

Variants shared across samples

The heat map below shows how variants (reference genome `/home/common/SARS-CoV-2-Philadelphia/NC_045512`) 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
2021-02-03

692 ORF1ab F143L

2265

1059 ORF1ab T265I

1787

3037 ORF1ab silent

2343

5011 ORF1ab Q1582H

1403

7168 ORF1ab silent

66

12525 ORF1ab T4087I

1229

14408 ORF1ab P314L

3370

18028 ORF1ab A1521S

3774

24095 S A845S

38

25563 ORF3a Q57H

2009

28300 N Q9H

114

28677 N T135I

5856

28893 N P207L

5124

VSP3001-1

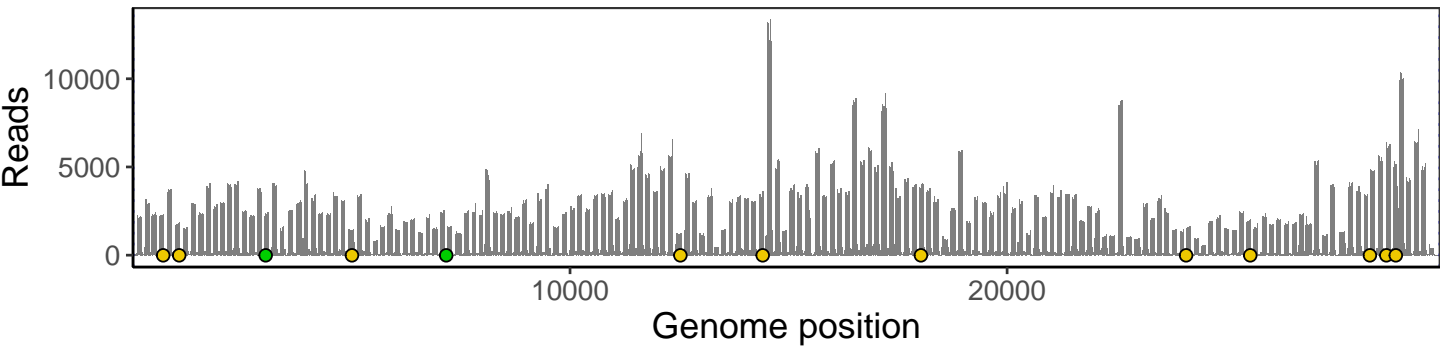
Base change



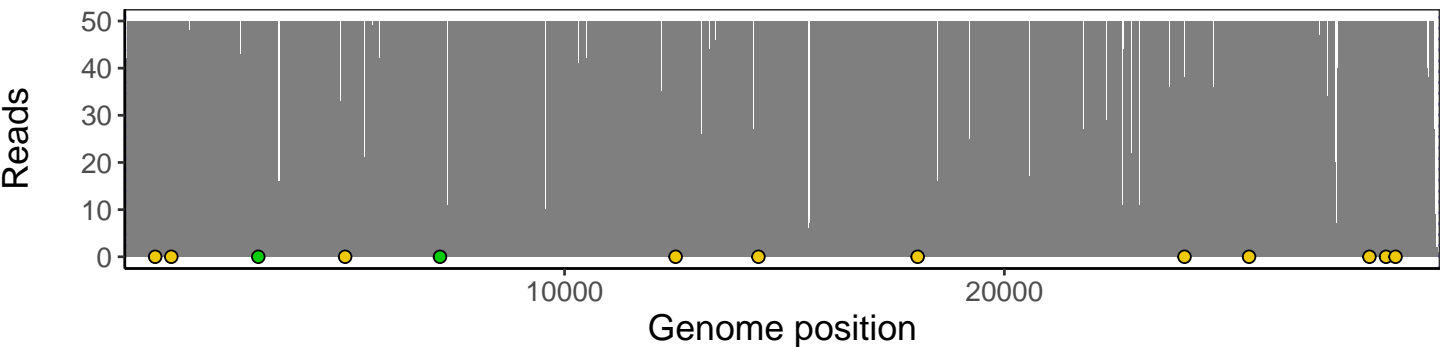
Analyses of individual experiments and composite results

VSP3001-1 | 2021-02-03 | NA | SARS_CoV_76 | genomes | single experiment

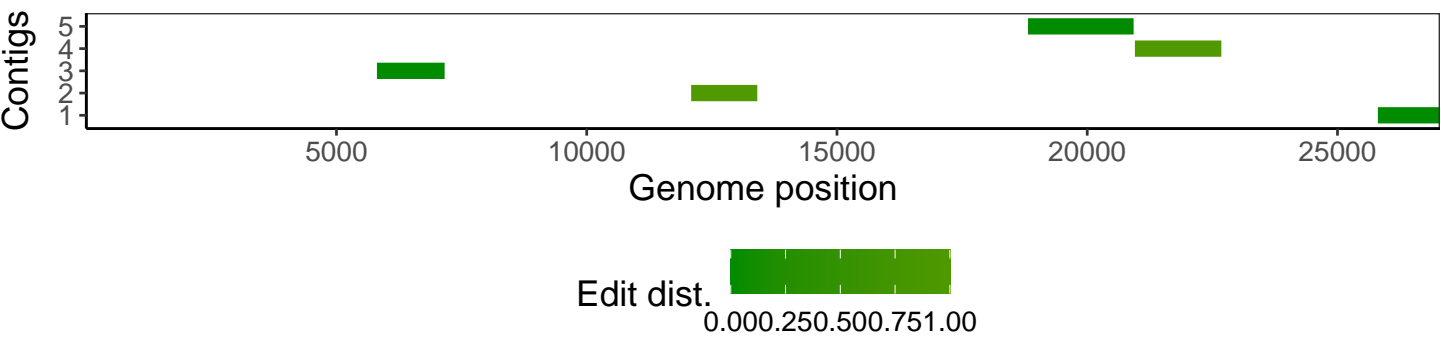
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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 htlib 1.10 |
| bcftools | 1.10.2-34-g1a12af0-dirty Using htlib 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 |