

COVID-19 subject H2102200033

2021-03-29

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) |
|------------|-------------------|---------|-------------|-------------|---------------------|---------|-------------------------|---|
| VSP0679-1 | single experiment | NA | VTM | 2021-03-01 | 29.93 | 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.



VTM

| | |
|---------------------|-------|
| 241 intergenic | 3177 |
| 875 orf1ab L204I | 11116 |
| 1059 orf1ab T265I | 4885 |
| 3037 orf1ab silent | 5981 |
| 4999 orf1ab silent | 4816 |
| 8083 orf1ab M2606I | 7288 |
| 8782 orf1ab silent | 8892 |
| 9085 orf1ab silent | 13354 |
| 10319 orf1ab L3352F | 12195 |
| 14408 orf1ab P314L | 10196 |
| 14805 orf1ab silent | 8058 |
| 16456 orf1ab S997A | 14632 |
| 18060 orf1ab silent | 10311 |
| 18424 orf1ab N1653D | 10109 |
| 18555 orf1ab silent | 8405 |
| 21304 orf1ab R2613C | 5592 |
| 23403 S D614G | 12316 |
| 23593 S Q677H | 11697 |
| 25563 orf3a Q57H | 4462 |
| 25907 orf3a G172V | 4961 |
| 26148 orf3a silent | 7580 |
| 27964 orf8 S24L | 16669 |
| 28057 orf8 A55V | 14343 |
| 28144 orf8 S84L | 8032 |
| 28472 N P67S | 7380 |
| 28869 N P199L | 1225 |
| 29402 N D377Y | 5226 |

Base change

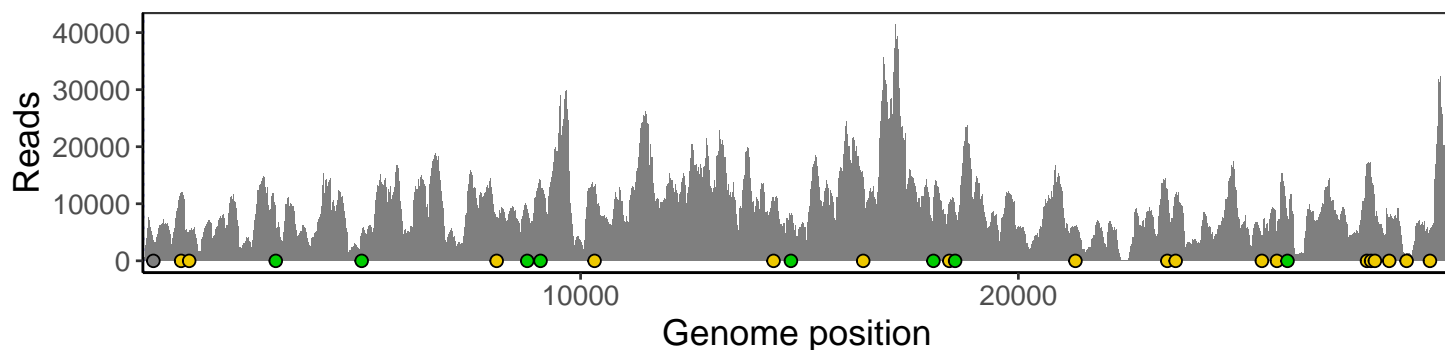


VSP0679-1

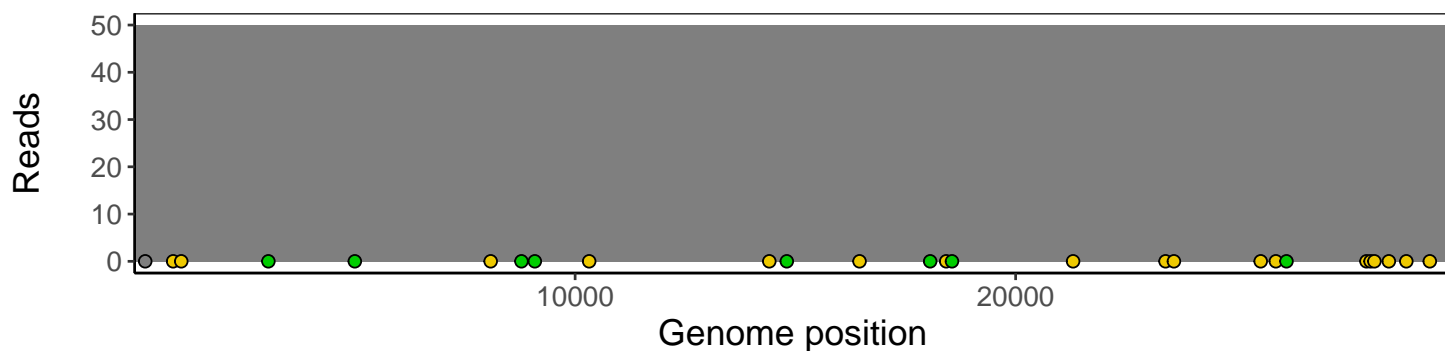
Analyses of individual experiments and composite results

VSP0679-1 | 2021-03-01 | VTM | H2102200033 | genomes | single experiment

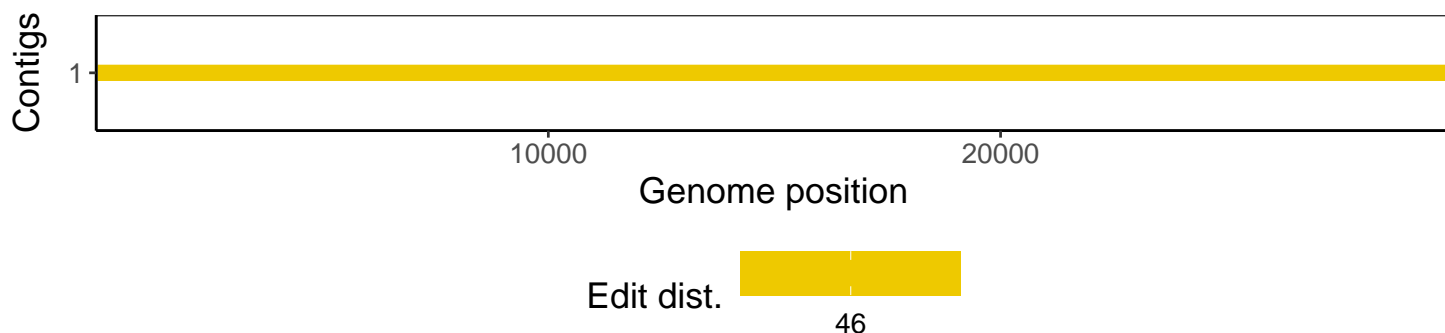
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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 | 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 |