# COVID-19 subject UPHS-0124

*2021-04-01*

The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of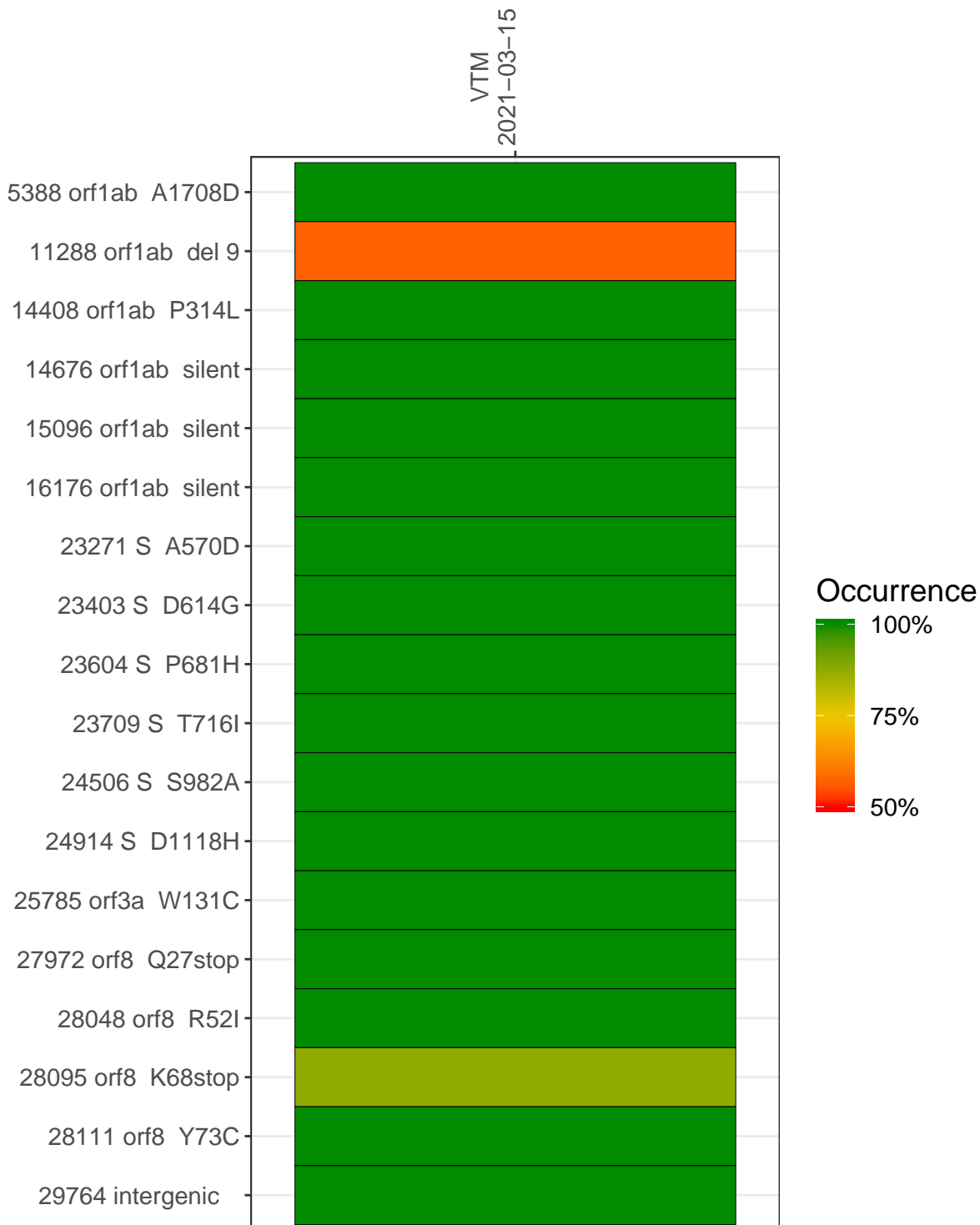 sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with > 90% sequence coverage.
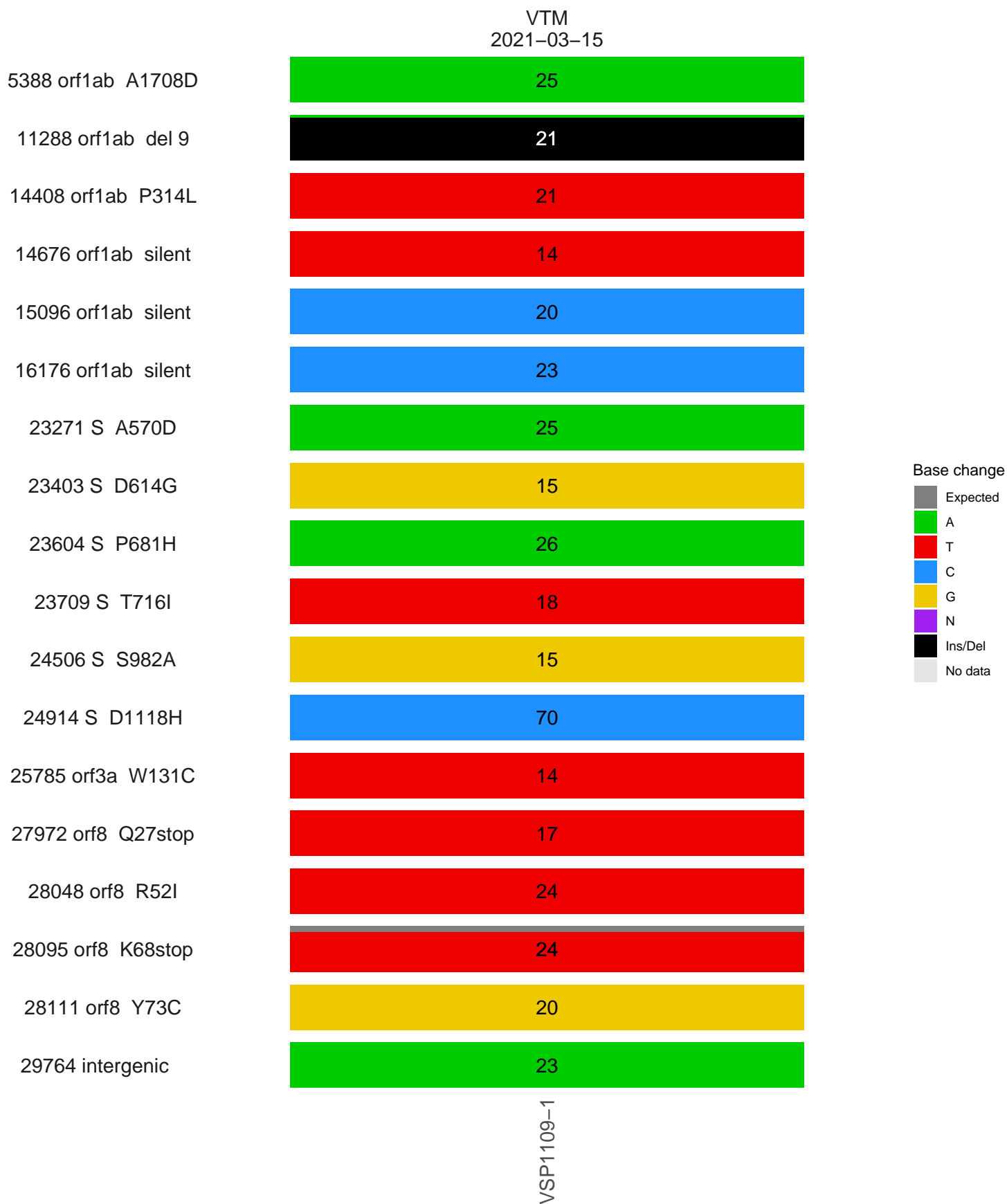
Table 1. Sample summary.

| Experiment | Type | Genomes | Sample type | Sample date | Largest contig (KD) | Lineage | Reference read coverage | Reference read coverage (>= 5 reads) |
|---|---|---|---|---|---|---|---|---|
| VSP1109-1 | single experiment | NA | VTM | 2021-03-15 | 11.56 | B.1.166 | 98.5% | 90.1% |

**Variants shared across samples**

The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/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
2021−03−15

| Mutation | VSP1109−1 |
|---|---|
| 5388 orf1ab A1708D | 25 |
| 11288 orf1ab del 9 | 21 |
| 14408 orf1ab P314L | 21 |
| 14676 orf1ab silent | 14 |
| 15096 orf1ab silent | 20 |
| 16176 orf1ab silent | 23 |
| 23271 S A570D | 25 |
| 23403 S D614G | 15 |
| 23604 S P681H | 26 |
| 23709 S T716I | 18 |
| 24506 S S982A | 15 |
| 24914 S D1118H | 70 |
| 25785 orf3a W131C | 14 |
| 27972 orf8 Q27stop | 17 |
| 28048 orf8 R52I | 24 |
| 28095 orf8 K68stop | 24 |
| 28111 orf8 Y73C | 20 |
| 29764 intergenic | 23 |

Base change

- Expected
- A
- T
- C
- G
- N
- Ins/Del
- No data

# Analyses of individual experiments and composite results

## VSP1109-1 | 2021-03-15 | VTM | UPHS-0124 | 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.
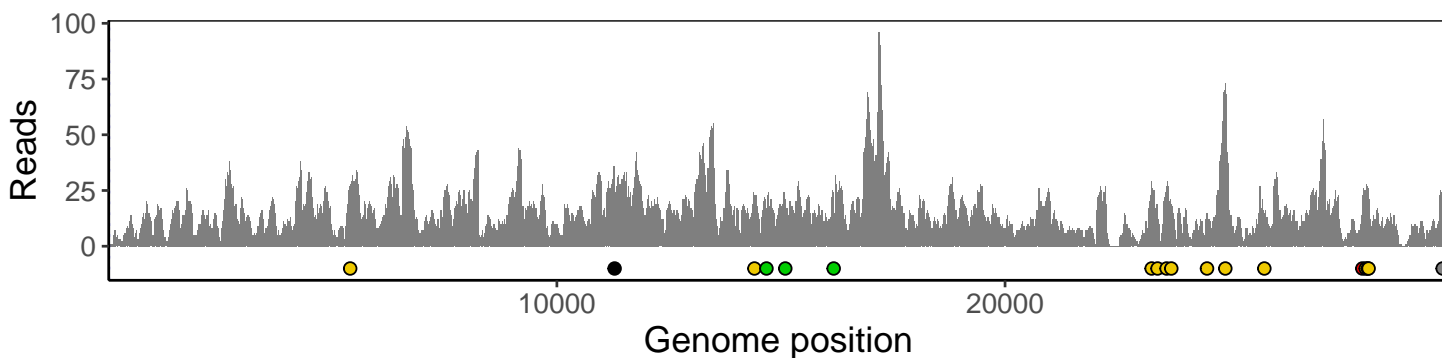


Excerpt from plot above focusing on reads coverage from 0 to 50 NT.
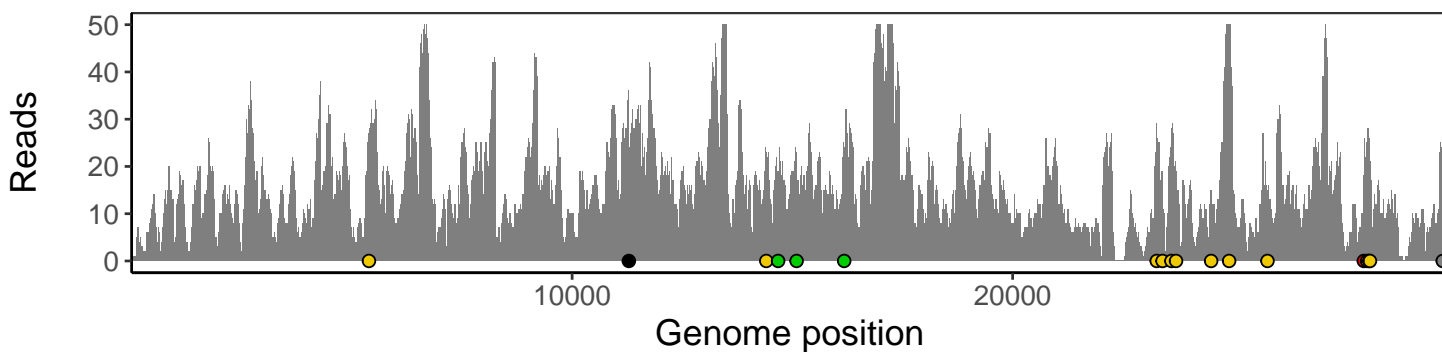


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.
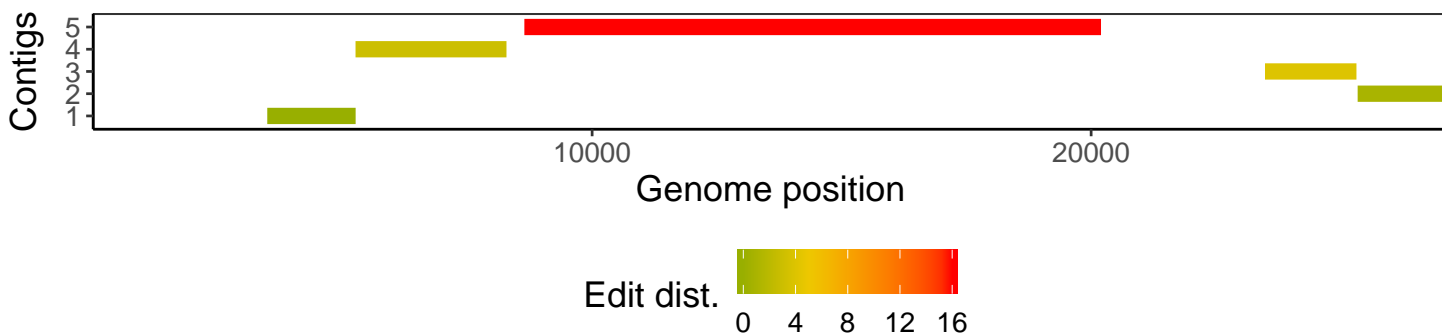
## Software environment

| 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 |