# COVID-19 subject UPHS-0363

*2021-06-23*

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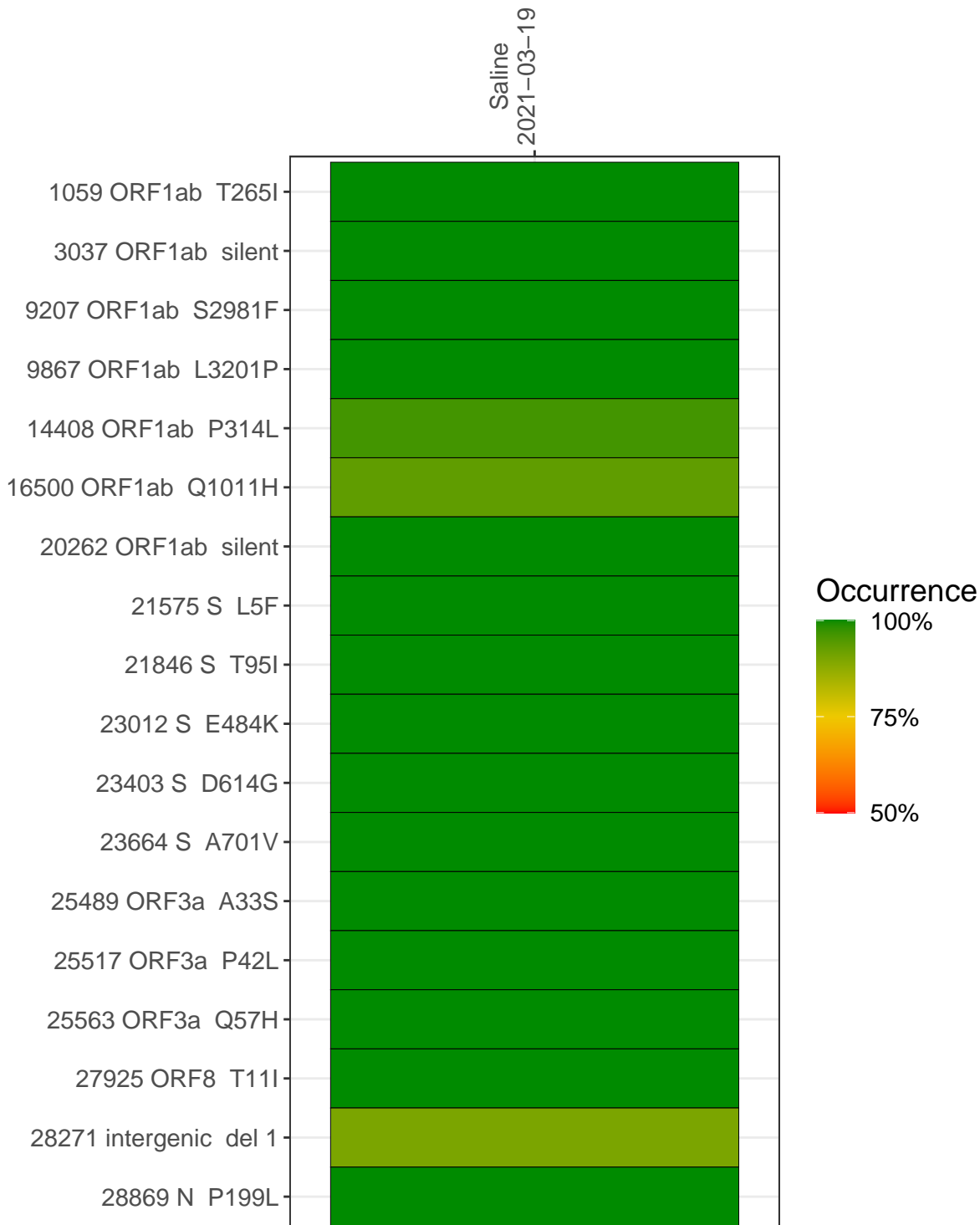 sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with > 90% sequence coverage.
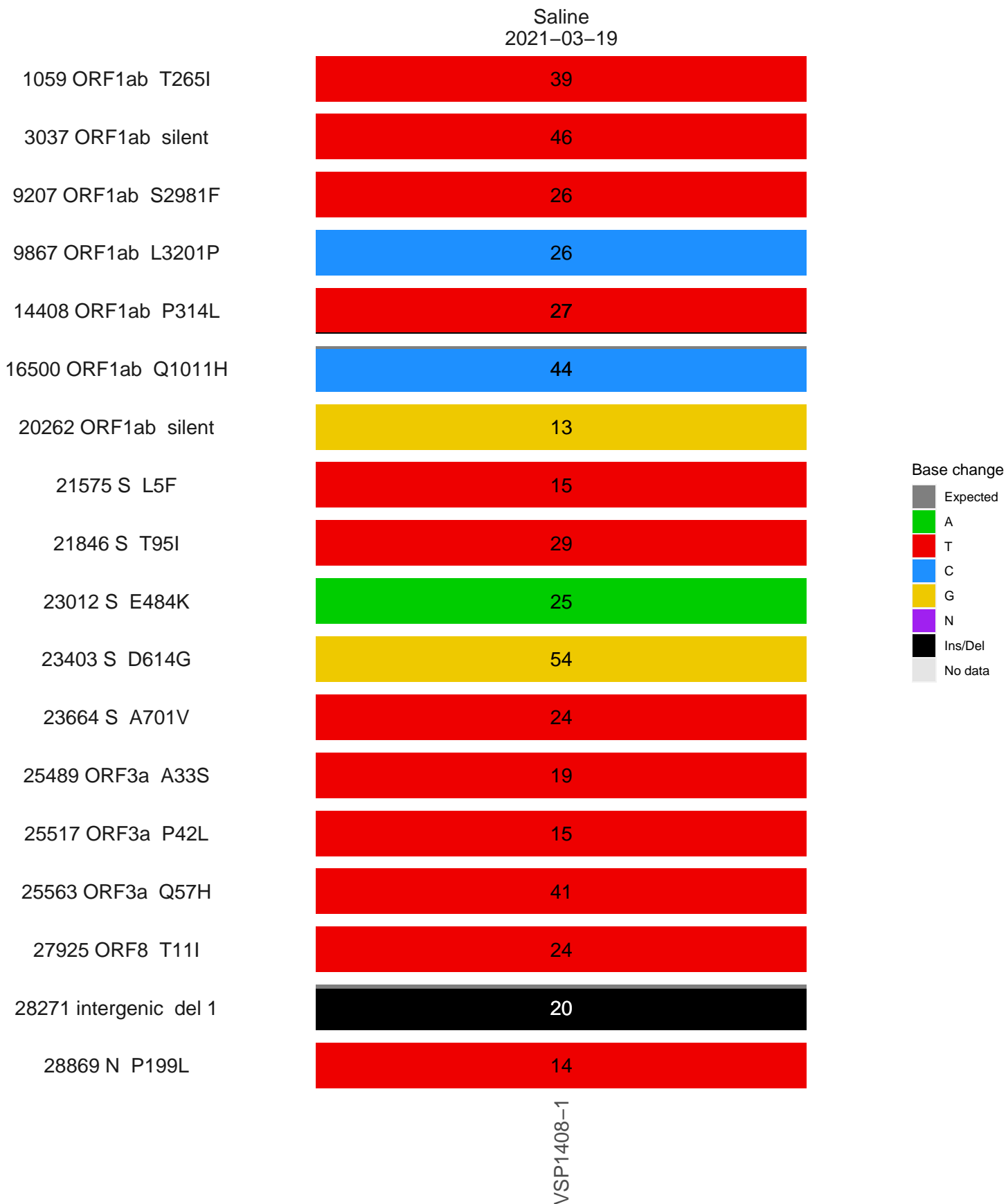
Table 1. Sample summary.

| Experiment | Type | Genomes | Sample type | Sample date | Largest contig (KD) | Lineage | Reference read coverage | Reference read coverage (>= 5 reads) |
|---|---|---|---|---|---|---|---|---|
| VSP1408-1 | single experiment | NA | Saline | 2021-03-19 | 13.66 | B.1.526 | 99.3% | 98.3% |

**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.

Saline
2021−03−19

| | |
|---|---|
| 1059 ORF1ab T265I | 39 |
| 3037 ORF1ab silent | 46 |
| 9207 ORF1ab S2981F | 26 |
| 9867 ORF1ab L3201P | 26 |
| 14408 ORF1ab P314L | 27 |
| 16500 ORF1ab Q1011H | 44 |
| 20262 ORF1ab silent | 13 |
| 21575 S L5F | 15 |
| 21846 S T95I | 29 |
| 23012 S E484K | 25 |
| 23403 S D614G | 54 |
| 23664 S A701V | 24 |
| 25489 ORF3a A33S | 19 |
| 25517 ORF3a P42L | 15 |
| 25563 ORF3a Q57H | 41 |
| 27925 ORF8 T11I | 24 |
| 28271 intergenic del 1 | 20 |
| 28869 N P199L | 14 |

VSP1408−1

Base change

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

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# Analyses of individual experiments and composite results

**VSP1408-1 | 2021-03-19 | Saline | UPHS-0363 | 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.
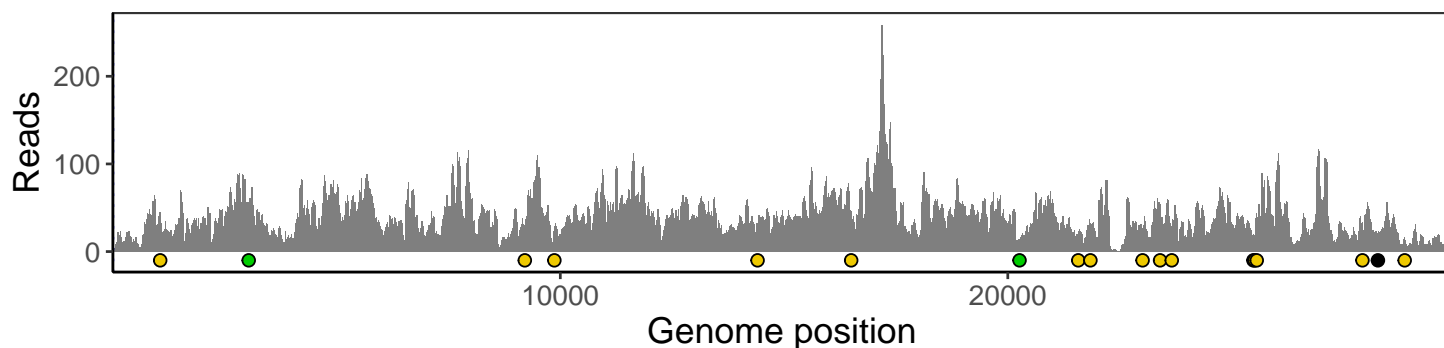


Excerpt from plot above focusing on reads coverage from 0 to 50 NT.
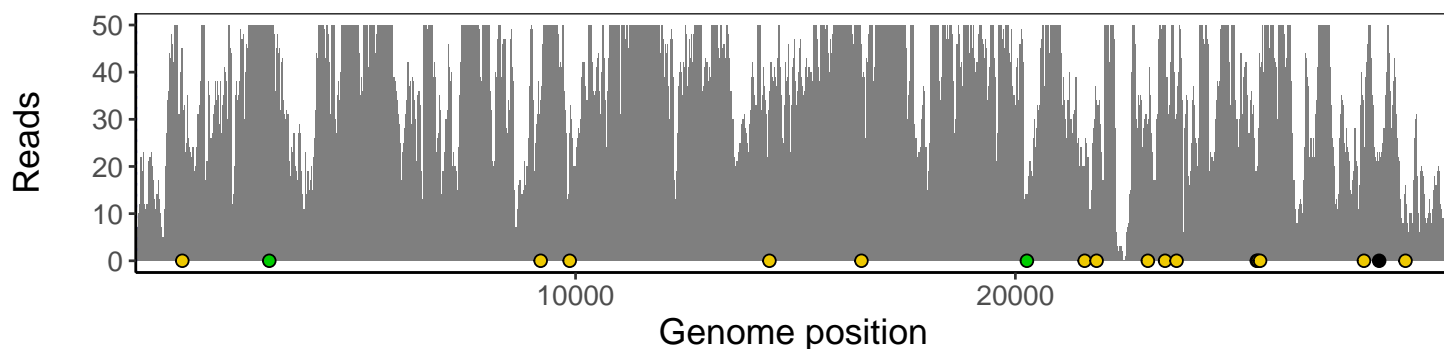


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.
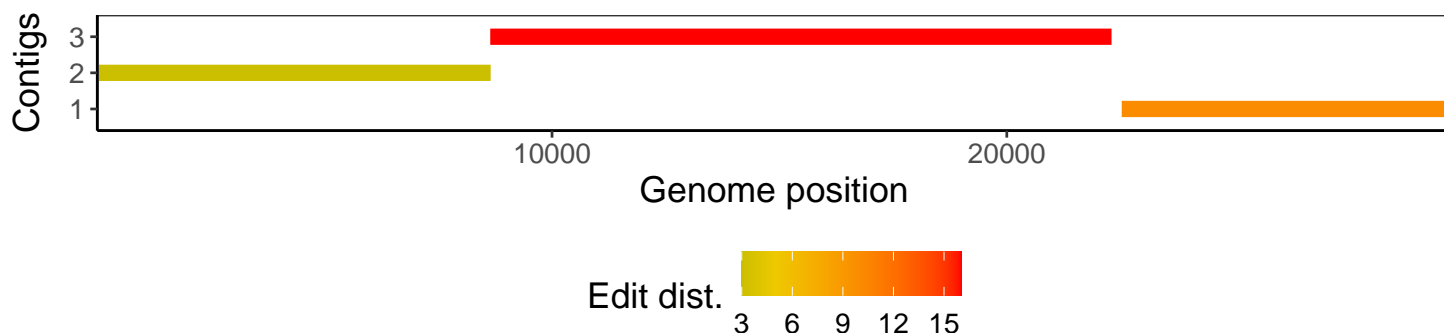
# Software environment

| 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 | 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 |