# COVID-19 subject UPHS-0834

2021-05-21

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 | Туре              | Genomes | Sample type | Sample date | Largest contig<br>(KD) | Lineage | Reference read<br>coverage | Reference read coverage (>= 5 reads) |
|------------|-------------------|---------|-------------|-------------|------------------------|---------|----------------------------|--------------------------------------|
| VSP2048-2  | single experiment | NA      | Saline      | 2021-04-02  | 29.82                  | B.1.2   | 99.8%                      | 99.8%                                |

#### Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/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 2021-04-02

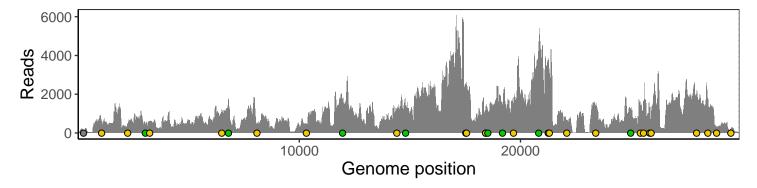
|                     | 2021-04-02 |
|---------------------|------------|
| 241 intergenic      | 142        |
| 1059 ORF1ab T265I   | 477        |
| 2238 ORF1ab E658G   | 453        |
| 3037 ORF1ab silent  | 446        |
| 3234 ORF1ab Q990L   | 583        |
| 6492 ORF1ab I2076T  | 1181       |
| 6796 ORF1ab silent  | 1707       |
| 8083 ORF1ab M2606I  | 433        |
| 10319 ORF1ab L3352F | 453        |
| 11956 ORF1ab silent | 1412       |
| 14408 ORF1ab P314L  | 1106       |
| 14805 ORF1ab silent | 1340       |
| 17528 ORF1ab T1354I | 2270       |
| 17561 ORF1ab R1365Q | 2402       |
| 18424 ORF1ab N1653D | 1094       |
| 18426 ORF1ab N1653D | 1120       |
| 18525 ORF1ab silent | 1046       |
| 19186 ORF1ab silent | 1473       |
| 19684 ORF1ab V2073L | 1436       |
| 20823 ORF1ab silent | 3629       |
| 21255 ORF1ab silent | 3823       |
| 21304 ORF1ab R2613C | 2976       |
| 22094 S D178N       | 634        |
| 23403 S D614G       | 1380       |
| 24983 S silent      | 987        |
| 25420 ORF3a I10L    | 1567       |
| 25563 ORF3a Q57H    | 1599       |
| 25844 ORF3a T151I   | 1290       |
| 25907 ORF3a G172V   | 705        |
| 27964 ORF8 S24L     | 2091       |
| 28472 N P67S        | 1733       |
| 28869 N P199L       | 287        |
| 29513 N A414S       | 210        |
|                     | 2048-2     |
|                     | 2044       |
|                     |            |



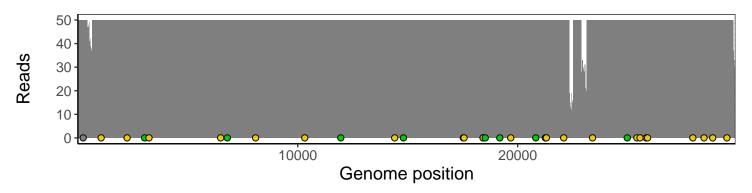
### Analyses of individual experiments and composite results

#### VSP2048-2 | 2021-04-02 | Saline | UPHS-0834 | genomes | single experiment

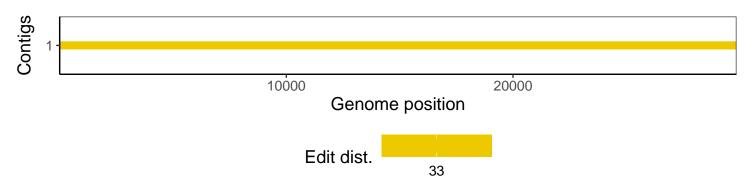
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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                      | 2.3.8  |
| 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   |
| ${\it Genomic Alignments}$    | 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   |
| $\operatorname{GenomeInfoDb}$ | 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   |