# COVID-19 subject UPHS-0021

2021-06-23

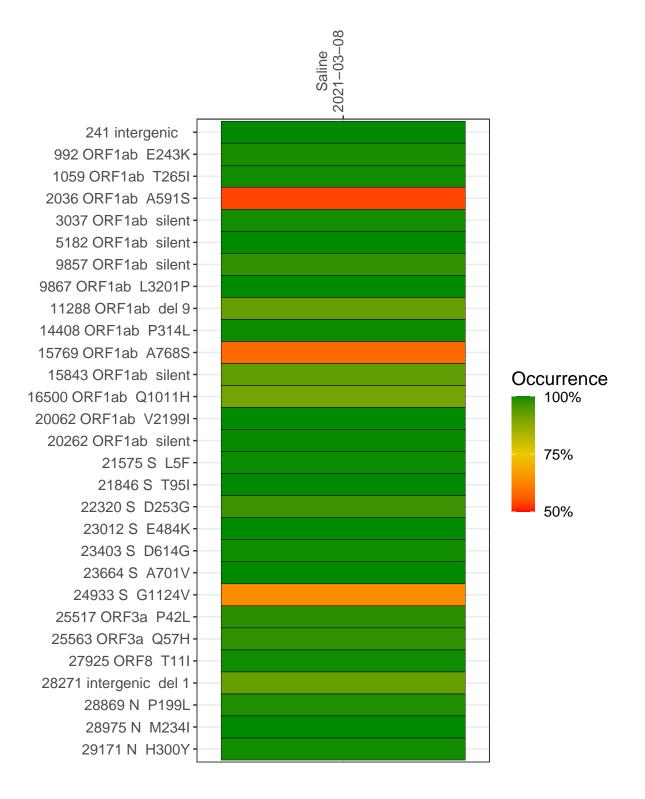
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

Table 1. Sample summary.

Experiment	Туре	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0953-1	single experiment	NA	Saline	2021-03-08	22.44	B.1.526	99.8%	99.7%

#### 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 2021-03-08

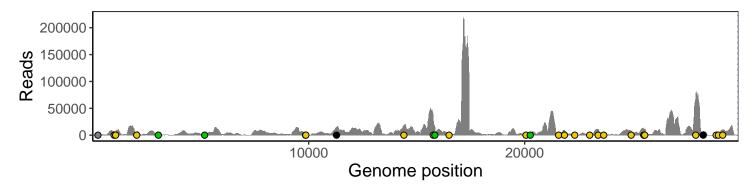
	2021-03-00
241 intergenic	1513
992 ORF1ab E243K	7228
1059 ORF1ab T265I	7141
2036 ORF1ab A591S	6649
3037 ORF1ab silent	1545
5182 ORF1ab silent	866
9857 ORF1ab silent	134
9867 ORF1ab L3201P	144
11288 ORF1ab del 9	12890
14408 ORF1ab P314L	18132
15769 ORF1ab A768S	37413
15843 ORF1ab silent	16279
16500 ORF1ab Q1011H	1076
20062 ORF1ab V2199I	1303
20262 ORF1ab silent	2940
21575 S L5F	1001
21846 S T95I	8953
22320 S D253G	1079
23012 S E484K	72
23403 S D614G	11177
23664 S A701V	4911
24933 S G1124V	7785
25517 ORF3a P42L	12336
25563 ORF3a Q57H	11267
27925 ORF8 T11I	75966
28271 intergenic del 1	6939
28869 N P199L	387
28975 N M234I	253
29171 N H300Y	10193
	53–1
	$\Omega$



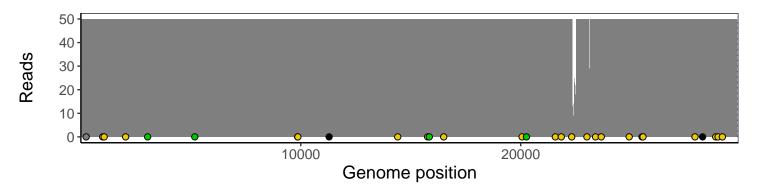
### Analyses of individual experiments and composite results

#### $VSP0953\text{-}1 \mid 2021\text{-}03\text{-}08 \mid Saline \mid UPHS\text{-}0021 \mid genomes \mid single \ experiment$

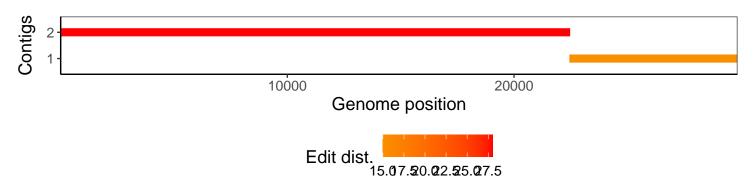
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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
${\bf Summarized Experiment}$	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