# COVID-19 subject UPHS-0022

2021-03-25

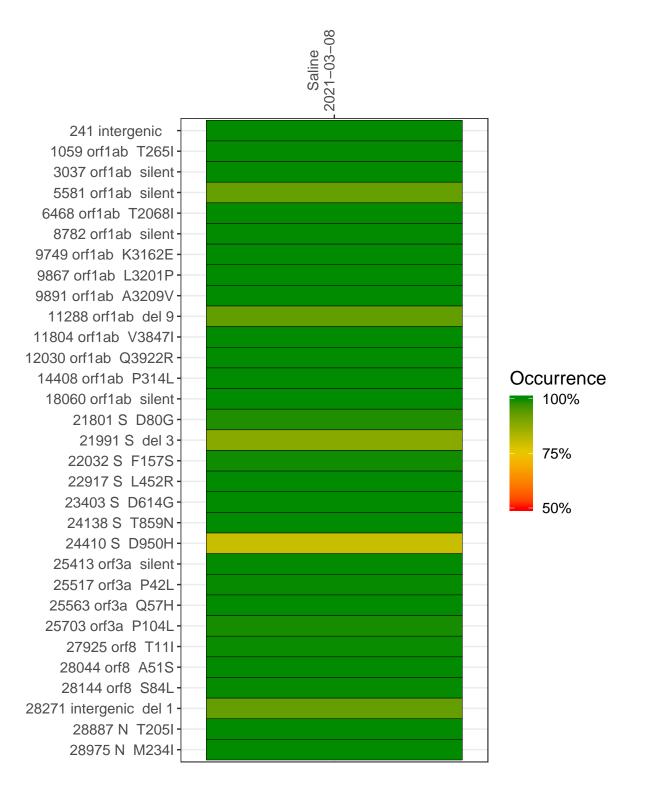
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP0954-1	single experiment	NA	Saline	2021-03-08	29.81	B.1	99.8%	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.



#### Saline 2021-03-08

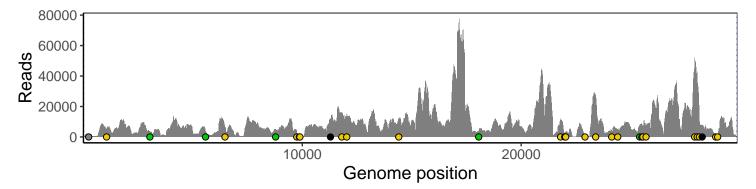
	2021-03-08
241 intergenic	1388
1059 orf1ab T265I	5105
3037 orf1ab silent	3229
5581 orf1ab silent	3378
6468 orf1ab T2068I	6200
8782 orf1ab silent	4814
9749 orf1ab K3162E	4060
9867 orf1ab L3201P	266
9891 orf1ab A3209V	283
11288 orf1ab del 9	10331
11804 orf1ab V3847I	15937
12030 orf1ab Q3922R	13399
14408 orf1ab P314L	11478
18060 orf1ab silent	3903
21801 S D80G	10857
21991 S del 3	2645
22032 S F157S	2681
22917 S L452R	329
23403 S D614G	27767
24138 S T859N	4460
24410 S D950H	5018
25413 orf3a silent	7319
25517 orf3a P42L	8131
25563 orf3a Q57H	7494
25703 orf3a P104L	7170
27925 orf8 T11I	50091
28044 orf8 A51S	36337
28144 orf8 S84L	10931
28271 intergenic del 1	7247
28887 N T205I	1866
28975 N M234I	1449
	1-4



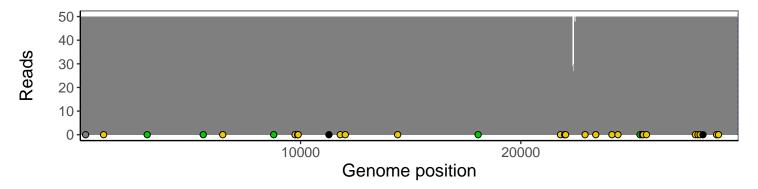
### Analyses of individual experiments and composite results

#### $VSP0954\text{-}1 \mid 2021\text{-}03\text{-}08 \mid Saline \mid UPHS\text{-}0022 \mid genomes \mid single \ experiment$

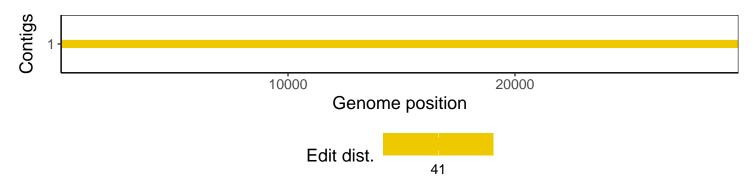
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	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
$\operatorname{GenomicAlignments}$	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
$\operatorname{GenomeInfoDb}$	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