# COVID-19 subject UPHS-0158

2021-06-23

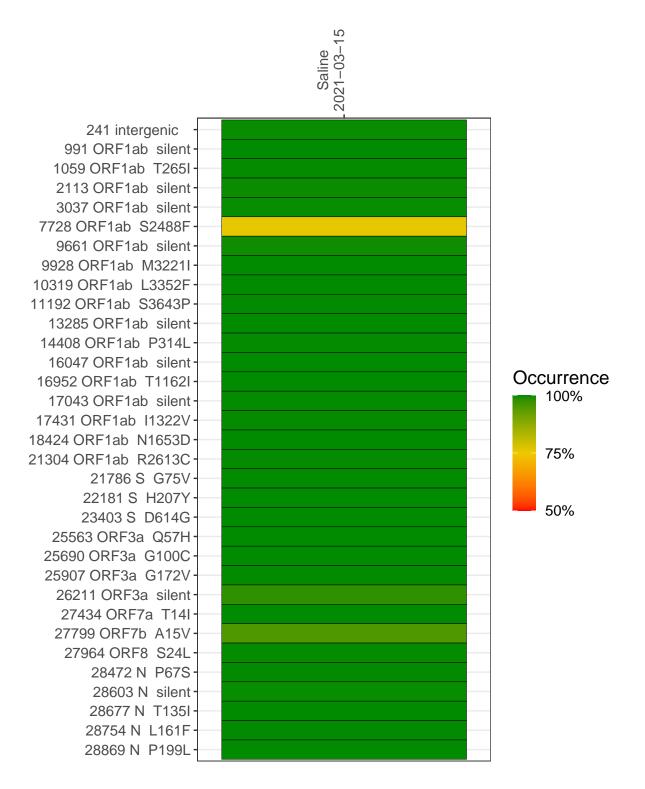
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1143-1	single experiment	NA	Saline	2021 - 03 - 15	29.86	B.1.2	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.



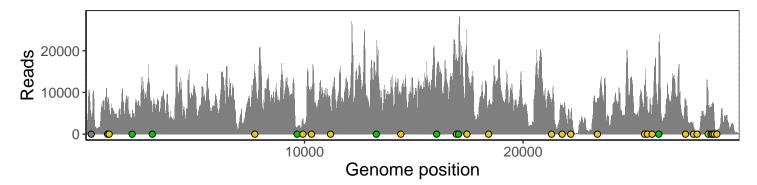
#### Saline 2021-03-15

	2021-03-13
241 intergenic	4073
991 ORF1ab silent	8636
1059 ORF1ab T265I	6307
2113 ORF1ab silent	5425
3037 ORF1ab silent	5491
7728 ORF1ab S2488F	13304
9661 ORF1ab silent	1595
9928 ORF1ab M3221I	3517
10319 ORF1ab L3352F	10671
11192 ORF1ab S3643P	6610
13285 ORF1ab silent	14047
14408 ORF1ab P314L	8079
16047 ORF1ab silent	13739
16952 ORF1ab T1162I	19135
17043 ORF1ab silent	18024
17431 ORF1ab I1322V	20747
18424 ORF1ab N1653D	7233
21304 ORF1ab R2613C	7177
21786 S G75V	6891
22181 S H207Y	4048
23403 S D614G	8547
25563 ORF3a Q57H	11626
25690 ORF3a G100C	6113
25907 ORF3a G172V	4660
26211 ORF3a silent	17614
27434 ORF7a T14I	7417
27799 ORF7b A15V	1846
27964 ORF8 S24L	791
28472 N P67S	10472
28603 N silent	6498
28677 N T135I	7108
28754 N L161F	3768
28869 N P199L	942
	43–1
	4,

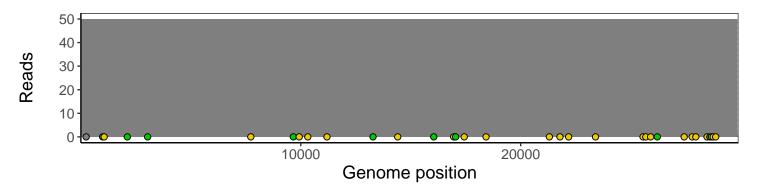
### Analyses of individual experiments and composite results

#### $VSP1143-1 \mid 2021-03-15 \mid Saline \mid UPHS-0158 \mid genomes \mid single \; experiment$

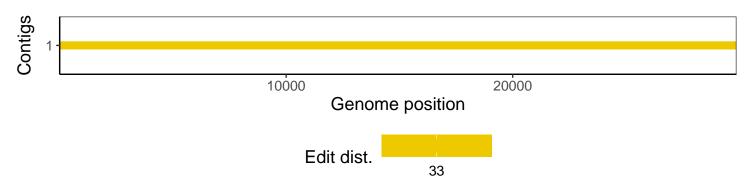
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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