COVID-19 subject UPHS-0055

2021-06-23

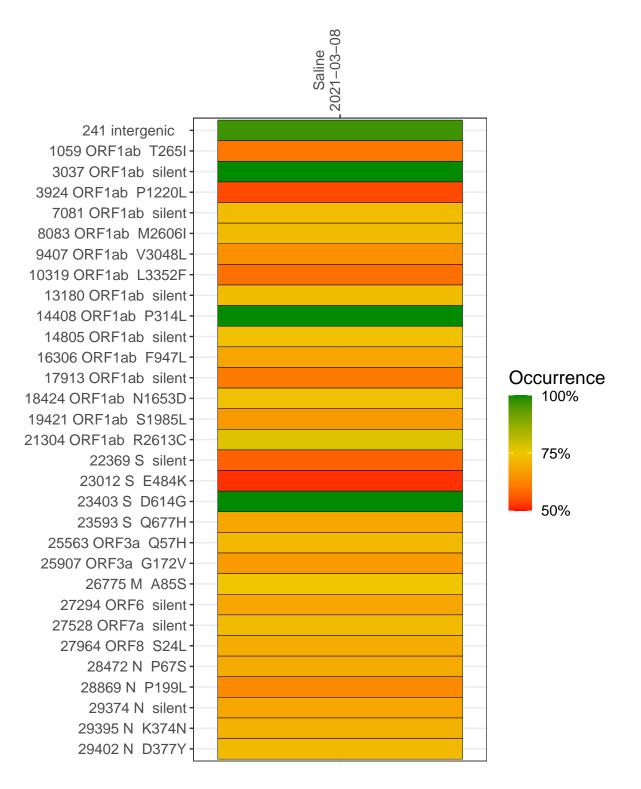
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP0987-1	single experiment	NA	Saline	2021-03-08	29.74	B.1.2	99.9%	99.8%

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.



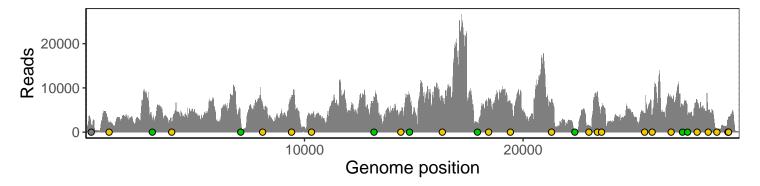
Saline 2021-03-08

	2021-03-00
241 intergenic	1634
1059 ORF1ab T265I	2063
3037 ORF1ab silent	2881
3924 ORF1ab P1220L	2290
7081 ORF1ab silent	2576
8083 ORF1ab M2606I	6339
9407 ORF1ab V3048L	7914
10319 ORF1ab L3352F	3960
13180 ORF1ab silent	7887
14408 ORF1ab P314L	4832
14805 ORF1ab silent	8534
16306 ORF1ab F947L	7708
17913 ORF1ab silent	2131
18424 ORF1ab N1653D	7299
19421 ORF1ab S1985L	6713
21304 ORF1ab R2613C	7329
22369 S silent	42
23012 S E484K	1420
23403 S D614G	8980
23593 S Q677H	5646
25563 ORF3a Q57H	4344
25907 ORF3a G172V	2925
26775 M A85S	8031
27294 ORF6 silent	6050
27528 ORF7a silent	3661
27964 ORF8 S24L	7191
28472 N P67S	4873
28869 N P199L	760
29374 N silent	2755
29395 N K374N	3203
29402 N D377Y	3333
	87–1
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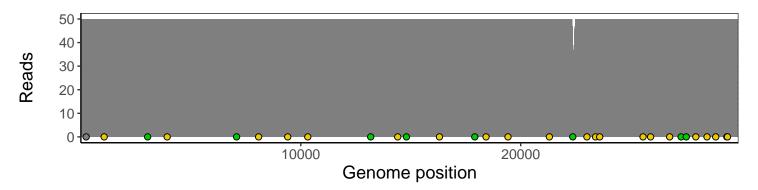
Analyses of individual experiments and composite results

$VSP0987\text{-}1 \mid 2021\text{-}03\text{-}08 \mid Saline \mid UPHS\text{-}0055 \mid genomes \mid single \ experiment$

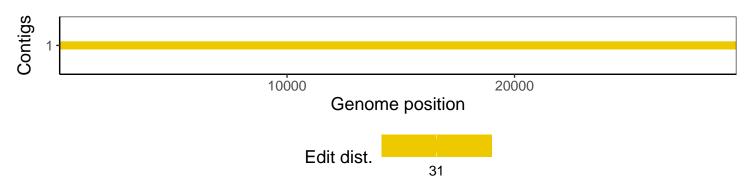
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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