COVID-19 subject UPHS-0039

2021-06-23

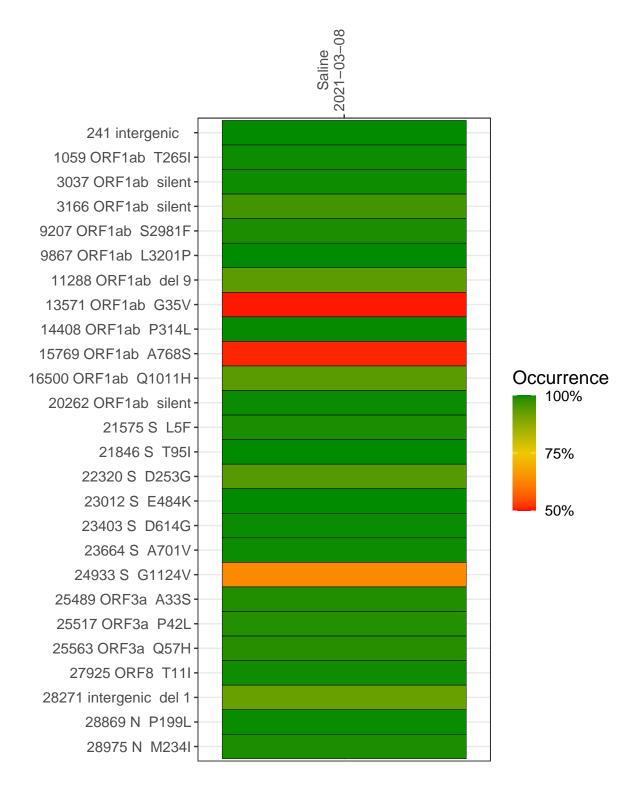
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP0971-1	single experiment	NA	Saline	2021-03-08	18.27	B.1.526	99.7%	99.6%

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

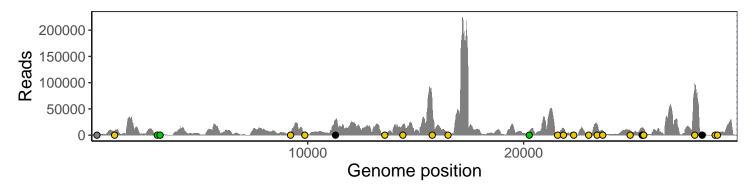
	202. 00 00
241 intergenic	1899
1059 ORF1ab T265I	7907
3037 ORF1ab silent	898
3166 ORF1ab silent	423
9207 ORF1ab S2981F	1826
9867 ORF1ab L3201P	316
11288 ORF1ab del 9	25423
13571 ORF1ab G35V	1553
14408 ORF1ab P314L	19609
15769 ORF1ab A768S	65692
16500 ORF1ab Q1011H	1696
20262 ORF1ab silent	5969
21575 S L5F	1485
21846 S T95I	13020
22320 S D253G	1411
23012 S E484K	269
23403 S D614G	21866
23664 S A701V	8003
24933 S G1124V	8559
25489 ORF3a A33S	14823
25517 ORF3a P42L	14057
25563 ORF3a Q57H	12503
27925 ORF8 T11I	95724
28271 intergenic del 1	6425
28869 N P199L	520
28975 N M234I	451
	VSP0971-1
	>



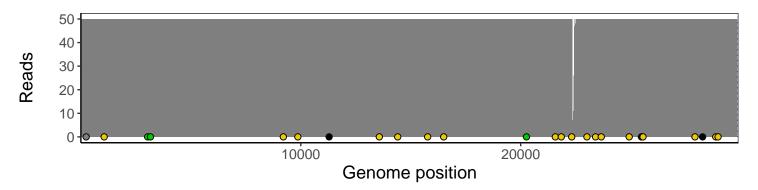
Analyses of individual experiments and composite results

VSP0971-1 | 2021-03-08 | Saline | UPHS-0039 | genomes | single experiment

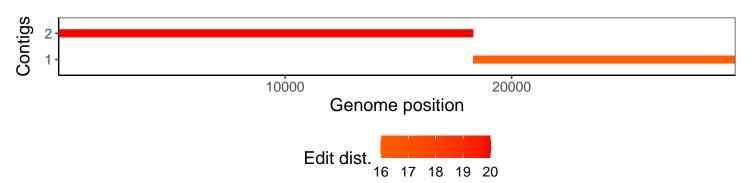
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	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