COVID-19 subject UPHS-0035

2021-06-23

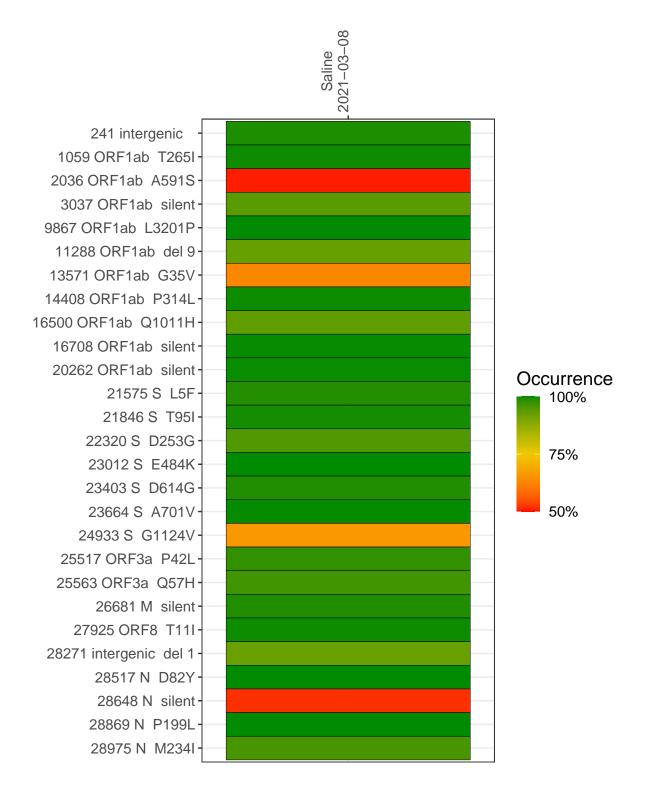
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP0967-1	single experiment	NA	Saline	2021-03-08	29.81	B.1.526	99.7%	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

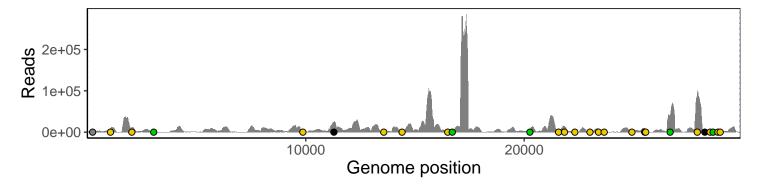
	202. 00 00
241 intergenic	3019
1059 ORF1ab T265I	8812
2036 ORF1ab A591S	10907
3037 ORF1ab silent	267
9867 ORF1ab L3201P	249
11288 ORF1ab del 9	20929
13571 ORF1ab G35V	492
14408 ORF1ab P314L	6343
16500 ORF1ab Q1011H	691
16708 ORF1ab silent	1189
20262 ORF1ab silent	6555
21575 S L5F	1505
21846 S T95I	14201
22320 S D253G	915
23012 S E484K	223
23403 S D614G	8804
23664 S A701V	1735
24933 S G1124V	4871
25517 ORF3a P42L	9359
25563 ORF3a Q57H	8083
26681 M silent	31655
27925 ORF8 T11I	97779
28271 intergenic del 1	7594
28517 N D82Y	52
28648 N silent	52
28869 N P199L	92
28975 N M234I	72
	7-7
	VSP0967-1
	> SF



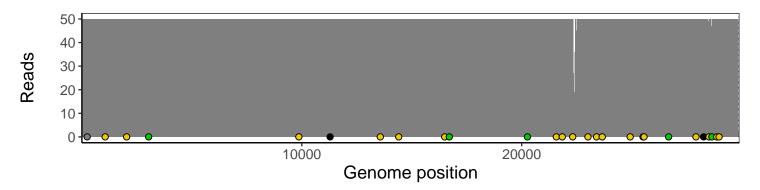
Analyses of individual experiments and composite results

VSP0967-1 | 2021-03-08 | Saline | UPHS-0035 | genomes | single experiment

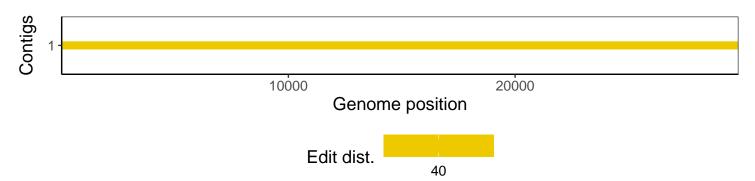
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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				