COVID-19 subject UPHS-0043

2021-06-23

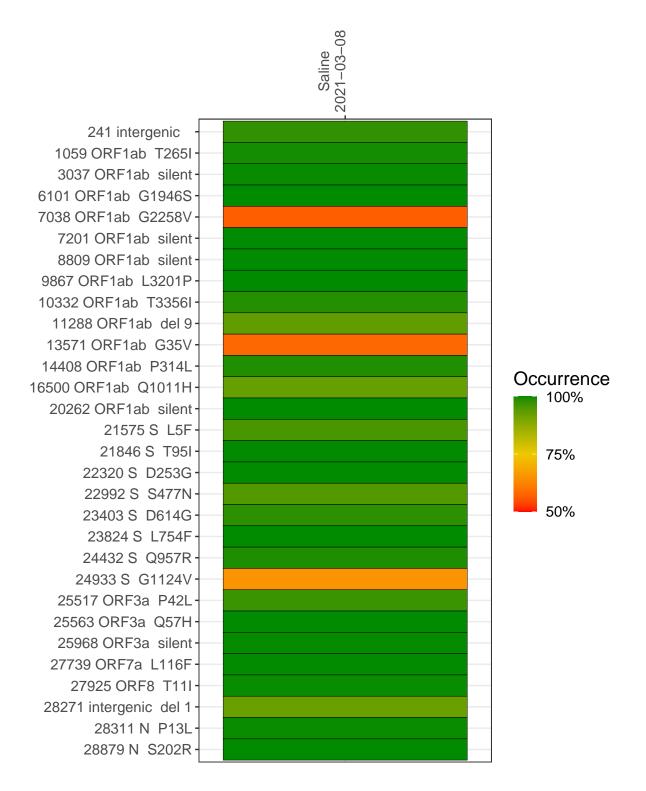
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP0975-1	single experiment	NA	Saline	2021-03-08	22.40	B.1.526	99.8%	99.2%

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

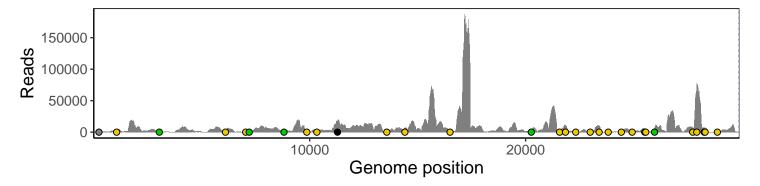
	2021 00 00
241 intergenic	1135
1059 ORF1ab T265I	3984
3037 ORF1ab silent	628
6101 ORF1ab G1946S	3041
7038 ORF1ab G2258V	573
7201 ORF1ab silent	268
8809 ORF1ab silent	2843
9867 ORF1ab L3201P	245
10332 ORF1ab T3356I	5090
11288 ORF1ab del 9	15898
13571 ORF1ab G35V	565
14408 ORF1ab P314L	6628
16500 ORF1ab Q1011H	959
20262 ORF1ab silent	3394
21575 S L5F	1182
21846 S T95I	10808
22320 S D253G	593
22992 S S477N	192
23403 S D614G	10560
23824 S L754F	226
24432 S Q957R	1482
24933 S G1124V	2922
25517 ORF3a P42L	5643
25563 ORF3a Q57H	5273
25968 ORF3a silent	6388
27739 ORF7a L116F	6813
27925 ORF8 T11I	74664
28271 intergenic del 1	7117
28311 N P13L	6904
28879 N S202R	251
	<u> </u>



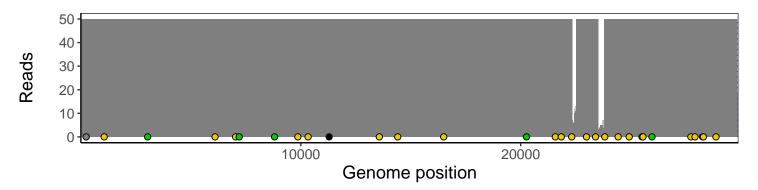
Analyses of individual experiments and composite results

VSP0975-1 | 2021-03-08 | Saline | UPHS-0043 | genomes | single experiment

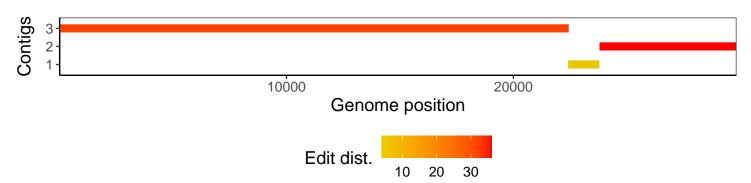
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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