COVID-19 subject UPHS-0224

2021-06-23

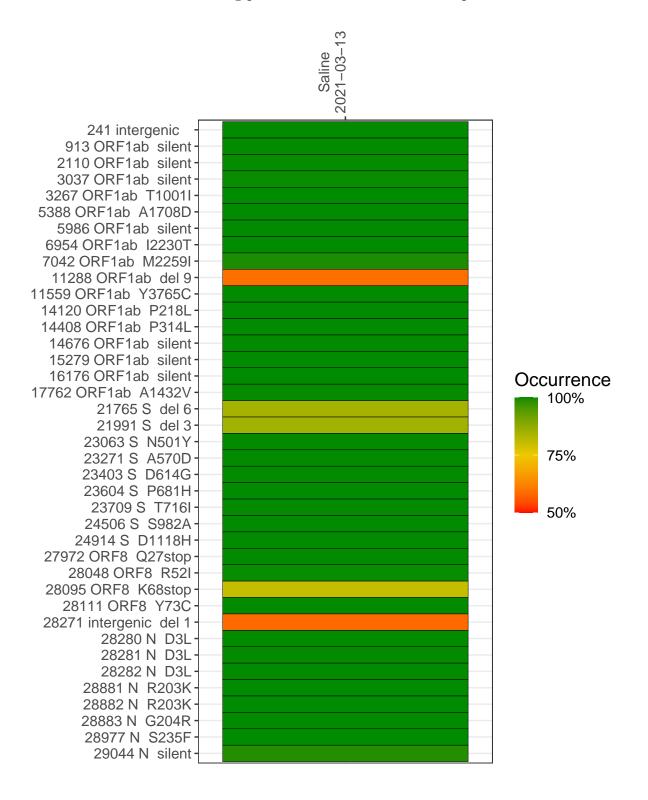
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1271-1	single experiment	NA	Saline	2021-03-13	29.82	B.1.1.7	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 2021-03-13

	2021-03-13
241 intergenic	1705
913 ORF1ab silent	5552
2110 ORF1ab silent	5273
3037 ORF1ab silent	4207
3267 ORF1ab T1001I	5125
5388 ORF1ab A1708D	7831
5986 ORF1ab silent	3744
6954 ORF1ab I2230T	2984
7042 ORF1ab M2259I	4626
11288 ORF1ab del 9	6301
11559 ORF1ab Y3765C	7348
14120 ORF1ab P218L	7932
14408 ORF1ab P314L	5732
14676 ORF1ab silent	3147
15279 ORF1ab silent	8425
16176 ORF1ab silent	13993
17762 ORF1ab A1432V	1897
21765 S del 6	3110
21991 S del 3	2127
23063 S N501Y	3247
23271 S A570D	5298
23403 S D614G	7104
23604 S P681H	7476
23709 S T716I	6945
24506 S S982A	4195
24914 S D1118H	11620
27972 ORF8 Q27stop	7893
28048 ORF8 R52I	8603
28095 ORF8 K68stop	8282
28111 ORF8 Y73C	6910
28271 intergenic del 1	2605
28280 N D3L	1451
28281 N D3L	1451
28282 N D3L	1562
28881 N R203K	46
28882 N R203K	46
28883 N G204R	48
28977 N S235F	104
29044 N silent	1165
	<u>\</u>
	271

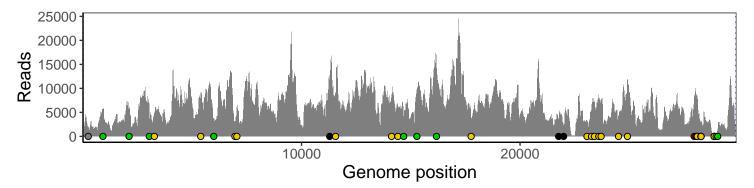
No data

Base change

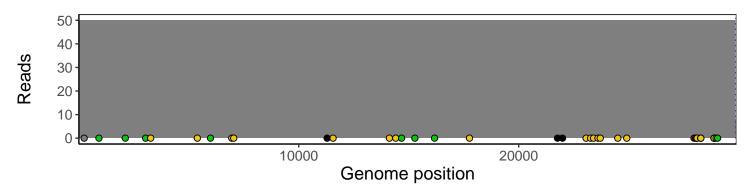
Analyses of individual experiments and composite results

$VSP1271\text{-}1 \mid 2021\text{-}03\text{-}13 \mid Saline \mid UPHS\text{-}0224 \mid genomes \mid single \ experiment$

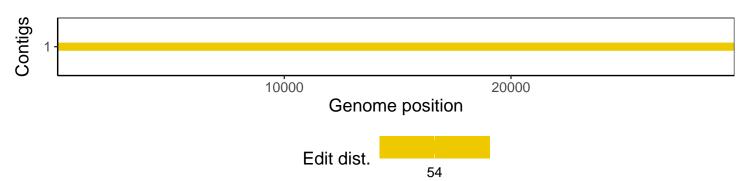
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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