COVID-19 subject UPHS-0111

2021-06-23

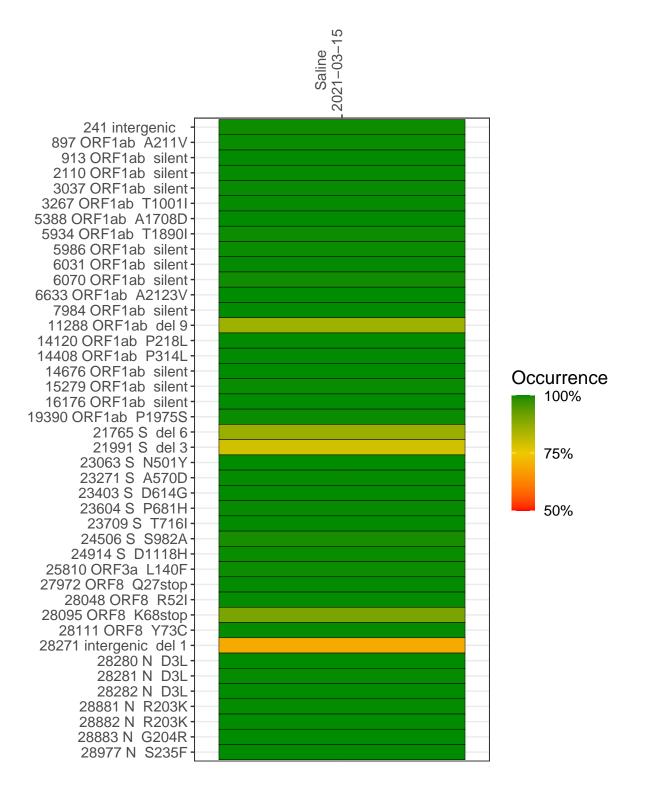
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1096-1	single experiment	NA	Saline	2021-03-15	20.28	B.1.1.7	99.7%	98.8%

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 2021-03-15

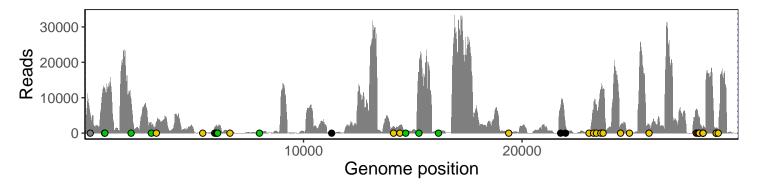
	2021-03-13
241 intergenic	4780
897 ORF1ab A211V	12601
913 ORF1ab silent	12357
2110 ORF1ab silent	9171
3037 ORF1ab silent	2261
3267 ORF1ab T1001I	3334
5388 ORF1ab A1708D	114
5934 ORF1ab T1890I	1697
5986 ORF1ab silent	2103
6031 ORF1ab silent	2118
6070 ORF1ab silent	1732
6633 ORF1ab A2123V	366
7984 ORF1ab silent	301
11288 ORF1ab del 9	234
14120 ORF1ab P218L	1841
14408 ORF1ab P314L	2130
14676 ORF1ab silent	352
15279 ORF1ab silent	17085
16176 ORF1ab silent	643
19390 ORF1ab P1975S	370
21765 S del 6	6678
21991 S del 3	1934
23063 S N501Y	104
23271 S A570D	6704
23403 S D614G	8046
23604 S P681H	11878
23709 S T716I	11627
24506 S S982A	2288
24914 S D1118H	493
25810 ORF3a L140F	2474
27972 ORF8 Q27stop	6517
28048 ORF8 R52I	5380
28095 ORF8 K68stop	4543
28111 ORF8 Y73C	4251
28271 intergenic del 1	1465
28280 N D3L	1018
28281 N D3L	1018
28282 N D3L	1052
28881 N R203K	1094
28882 N R203K	1090
28883 N G204R	1097
28977 N S235F	1044
	096-1
	3C



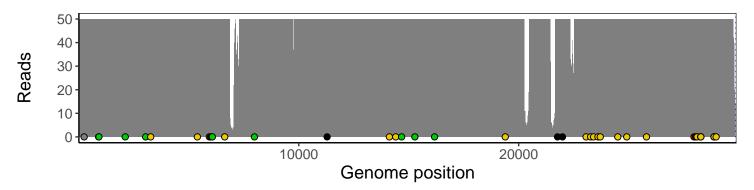
Analyses of individual experiments and composite results

$VSP1096\text{-}1 \mid 2021\text{-}03\text{-}15 \mid Saline \mid UPHS\text{-}0111 \mid genomes \mid single \ experiment$

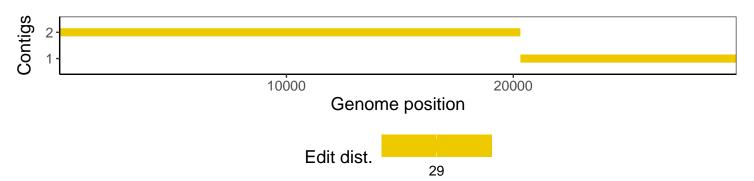
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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