COVID-19 subject UPHS-0229

2021-06-23

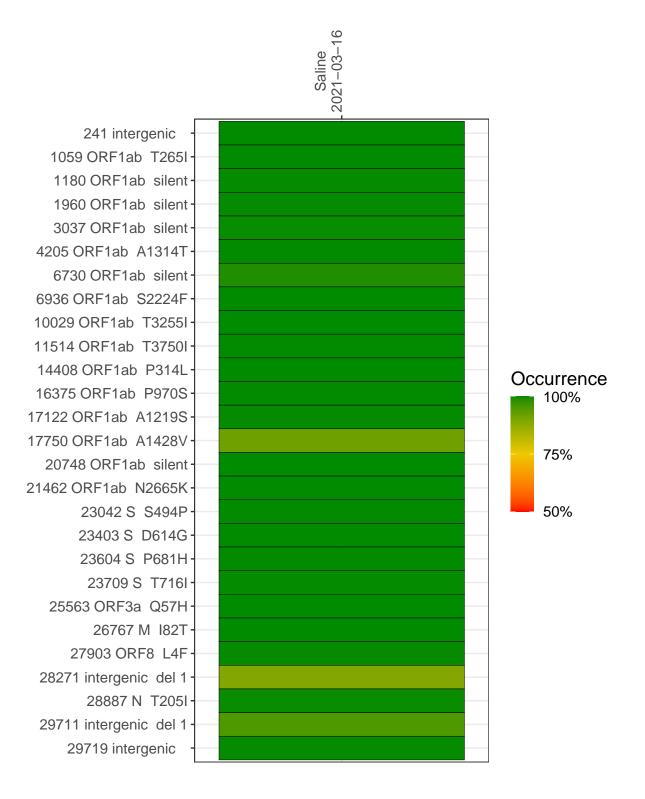
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1274-1	single experiment	NA	Saline	2021-03-16	29.87	B.1.575	99.8%	99.8%

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 2021-03-16

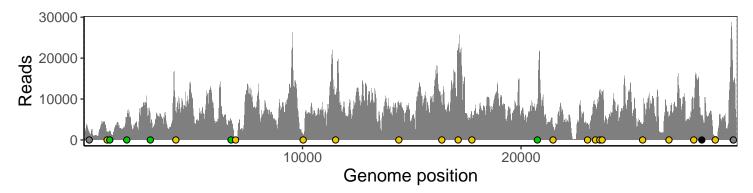
	2021-03-10
241 intergenic	1594
1059 ORF1ab T265I	1802
1180 ORF1ab silent	2155
1960 ORF1ab silent	4386
3037 ORF1ab silent	4559
4205 ORF1ab A1314T	6414
6730 ORF1ab silent	4706
6936 ORF1ab S2224F	108
10029 ORF1ab T3255I	1334
11514 ORF1ab T3750I	10585
14408 ORF1ab P314L	8269
16375 ORF1ab P970S	8303
17122 ORF1ab A1219S	22028
17750 ORF1ab A1428V	5771
20748 ORF1ab silent	8364
21462 ORF1ab N2665K	2886
23042 S S494P	4096
23403 S D614G	8443
23604 S P681H	11187
23709 S T716I	10825
25563 ORF3a Q57H	3821
26767 M 182T	5406
27903 ORF8 L4F	6570
28271 intergenic del 1	5770
28887 N T205I	888
29711 intergenic del 1	13853
29719 intergenic	11932
	274-1
	27



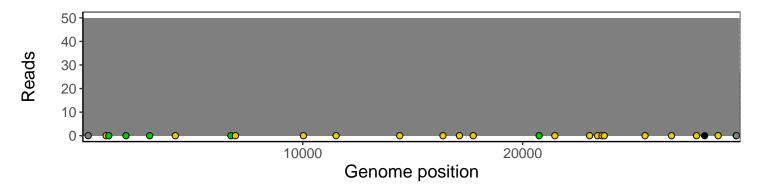
Analyses of individual experiments and composite results

VSP1274-1 | 2021-03-16 | Saline | UPHS-0229 | genomes | single experiment

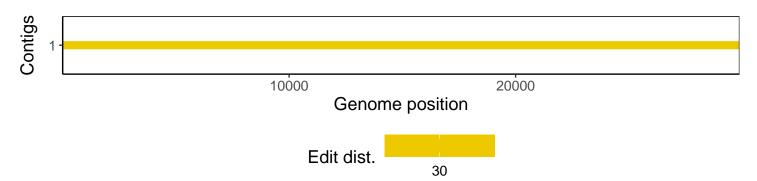
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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