COVID-19 subject UPHS-0071

2021-03-25

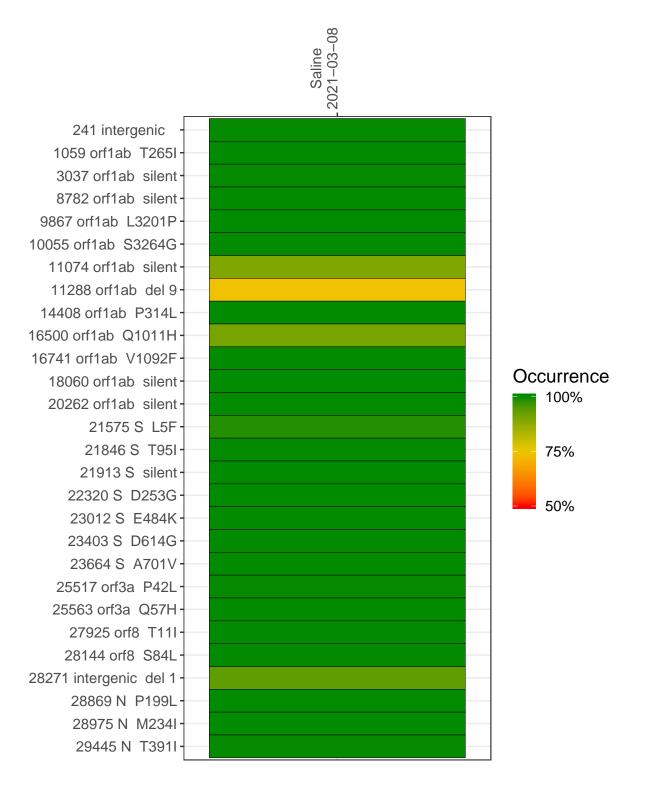
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1003-1	single experiment	NA	Saline	2021-03-08	29.90	B.1.526	99.9%	99.8%

Variants shared across samples

The heat map below shows how variants (reference genome USA-WA1-2020) 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

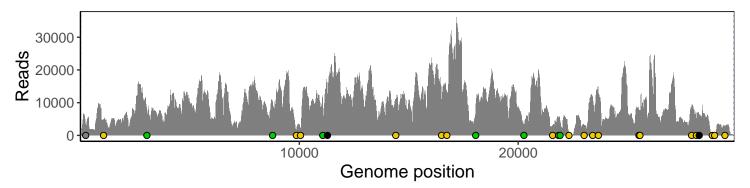
	2021-03-08
241 intergenic	3249
1059 orf1ab T265I	4730
3037 orf1ab silent	6872
8782 orf1ab silent	9872
9867 orf1ab L3201P	1756
10055 orf1ab S3264G	2264
11074 orf1ab silent	8942
11288 orf1ab del 9	11450
14408 orf1ab P314L	10969
16500 orf1ab Q1011H	10941
16741 orf1ab V1092F	13046
18060 orf1ab silent	8786
20262 orf1ab silent	3201
21575 S L5F	2924
21846 S T95I	5511
21913 S silent	4500
22320 S D253G	684
23012 S E484K	3011
23403 S D614G	12046
23664 S A701V	12925
25517 orf3a P42L	7719
25563 orf3a Q57H	7715
27925 orf8 T11I	9140
28144 orf8 S84L	5342
28271 intergenic del 1	6072
28869 N P199L	713
28975 N M234I	594
29445 N T391I	2762
	3–7



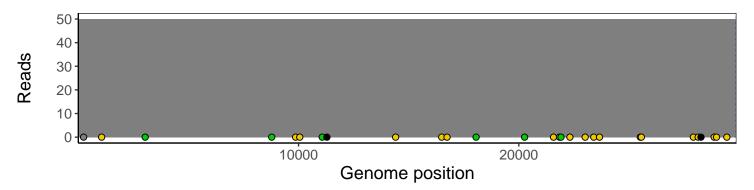
Analyses of individual experiments and composite results

$VSP1003\text{-}1 \mid 2021\text{-}03\text{-}08 \mid Saline \mid UPHS\text{-}0071 \mid genomes \mid single \ experiment$

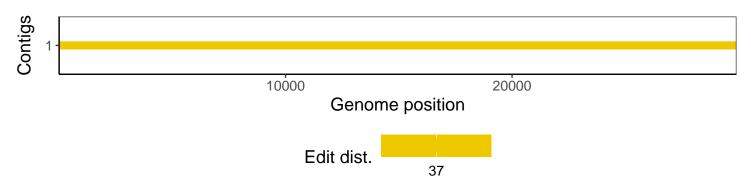
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.3
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	3.0.0
tidyverse	1.2.1
ShortRead	1.34.2
$\operatorname{GenomicAlignments}$	1.12.2
SummarizedExperiment	1.6.5
DelayedArray	0.2.7
matrixStats	0.54.0
Biobase	2.36.2
Rsamtools	1.28.0
GenomicRanges	1.28.6
$\operatorname{GenomeInfoDb}$	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