COVID-19 subject UPHS-0049

2021-03-25

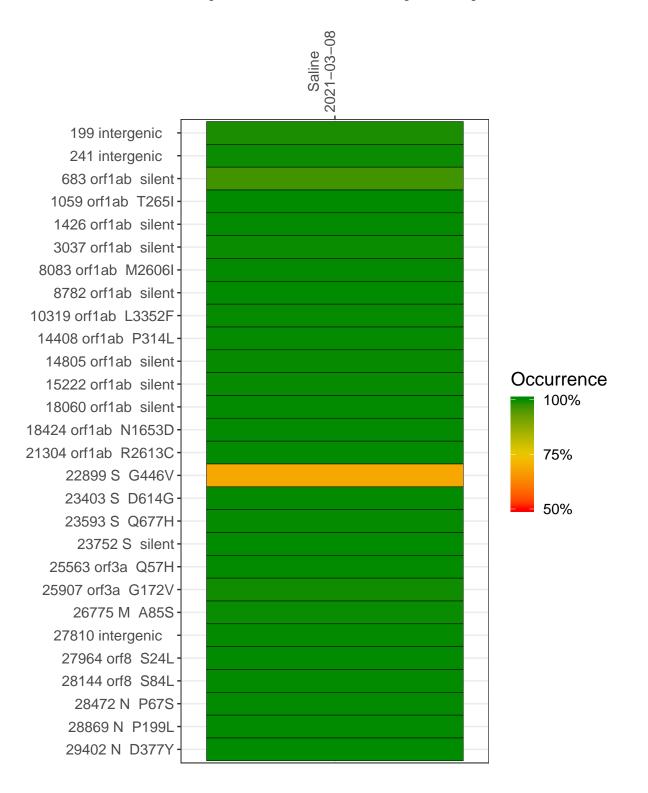
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP0981-1	single experiment	NA	Saline	2021-03-08	29.90	B.1.2	99.9%	99.9%

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

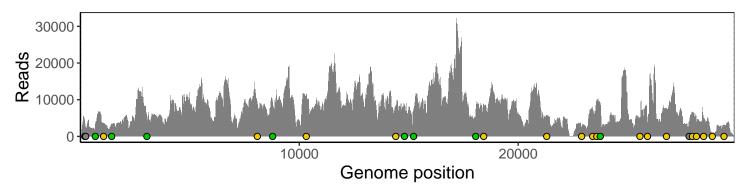
	2021-03-06
199 intergenic	3894
241 intergenic	2334
683 orf1ab silent	3055
1059 orf1ab T265I	3408
1426 orf1ab silent	3285
3037 orf1ab silent	4755
8083 orf1ab M2606l	9084
8782 orf1ab silent	9087
10319 orf1ab L3352F	10533
14408 orf1ab P314L	8343
14805 orf1ab silent	8594
15222 orf1ab silent	6954
18060 orf1ab silent	6824
18424 orf1ab N1653D	8406
21304 orf1ab R2613C	572 5
22899 S G446V	2283
23403 S D614G	7931
23593 S Q677H	9824
23752 S silent	8824
25563 orf3a Q57H	5155
25907 orf3a G172V	3588
26775 M A85S	7487
27810 intergenic	3923
27964 orf8 S24L	6734
28144 orf8 S84L	4119
28472 N P67S	5015
28869 N P199L	999
29402 N D377Y	3175
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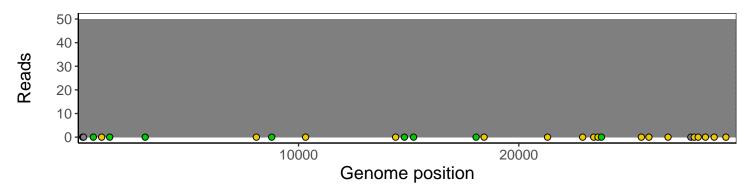
Analyses of individual experiments and composite results

$VSP0981\text{-}1 \mid 2021\text{-}03\text{-}08 \mid Saline \mid UPHS\text{-}0049 \mid genomes \mid single \ experiment$

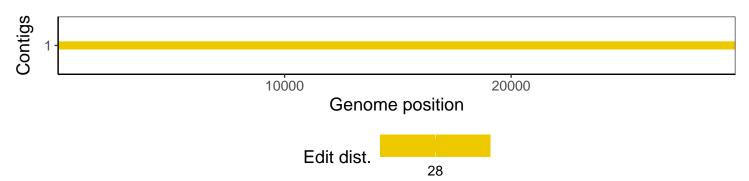
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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