COVID-19 subject UPHS-0090

2021-03-25

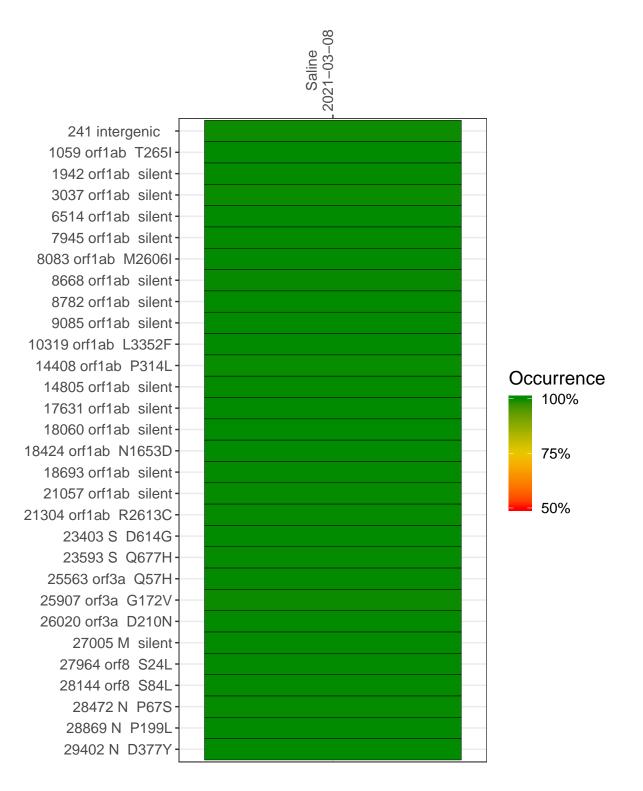
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1021-1	single experiment	NA	Saline	2021-03-08	29.93	B.1.2	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

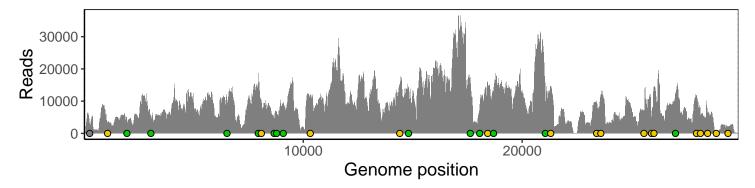
	2021-03-06
241 intergenic	2871
1059 orf1ab T265I	3326
1942 orf1ab silent	3269
3037 orf1ab silent	4636
6514 orf1ab silent	9205
7945 orf1ab silent	15643
8083 orf1ab M2606l	9891
8668 orf1ab silent	4298
8782 orf1ab silent	6321
9085 orf1ab silent	9298
10319 orf1ab L3352F	11240
14408 orf1ab P314L	14931
14805 orf1ab silent	14210
17631 orf1ab silent	16687
18060 orf1ab silent	8121
18424 orf1ab N1653D	14833
18693 orf1ab silent	13133
21057 orf1ab silent	11466
21304 orf1ab R2613C	14386
23403 S D614G	9821
23593 S Q677H	11793
25563 orf3a Q57H	7094
25907 orf3a G172V	4694
26020 orf3a D210N	14067
27005 M silent	11871
27964 orf8 S24L	11679
28144 orf8 S84L	5844
28472 N P67S	6276
28869 N P199L	645
29402 N D377Y	2135
	



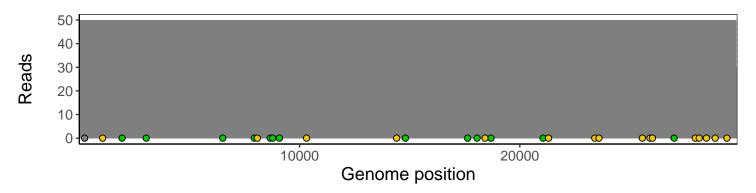
Analyses of individual experiments and composite results

$VSP1021\text{-}1 \mid 2021\text{-}03\text{-}08 \mid Saline \mid UPHS\text{-}0090 \mid genomes \mid single \ experiment$

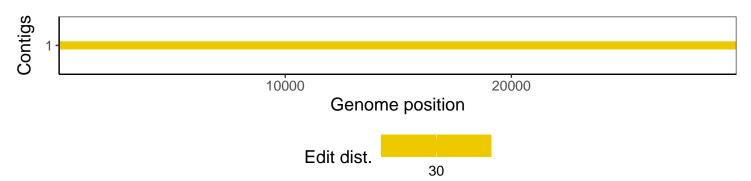
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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