COVID-19 subject UPHS-0177

2021-03-31

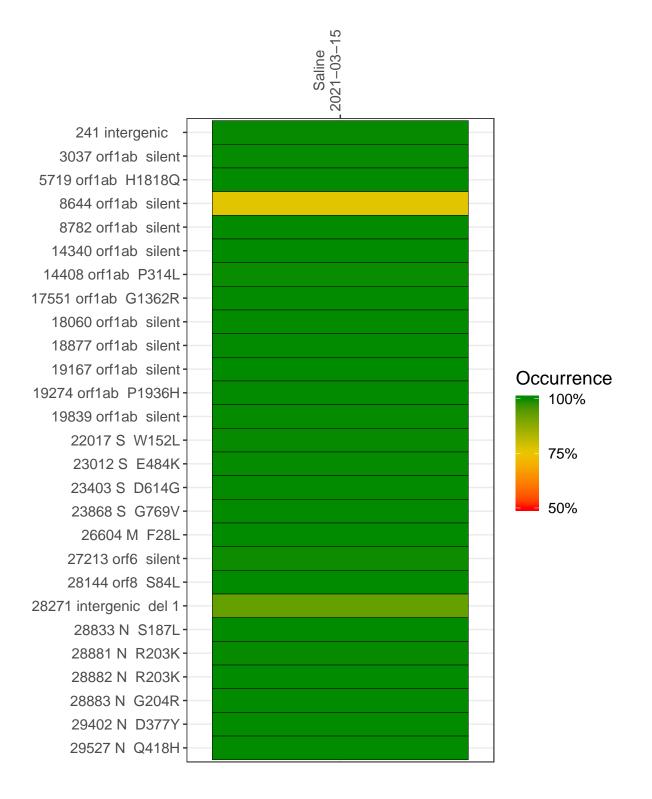
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1161-1	single experiment	NA	Saline	2021-03-15	29.83	R.1	99.8%	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 2021-03-15

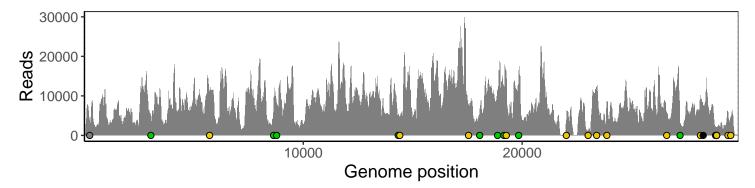
	2021-03-13
241 intergenic	3507
3037 orf1ab silent	3807
5719 orf1ab H1818Q	10516
8644 orf1ab silent	8287
8782 orf1ab silent	8081
14340 orf1ab silent	4949
14408 orf1ab P314L	4042
17551 orf1ab G1362R	7320
18060 orf1ab silent	6452
18877 orf1ab silent	11040
19167 orf1ab silent	11928
19274 orf1ab P1936H	13930
19839 orf1ab silent	14538
22017 S W152L	3720
23012 S E484K	915
23403 S D614G	12091
23868 S G769V	8664
26604 M F28L	6021
27213 orf6 silent	3017
28144 orf8 S84L	9078
28271 intergenic del 1	7200
28833 N S187L	2186
28881 N R203K	1413
28882 N R203K	1407
28883 N G204R	1413
29402 N D377Y	6102
29527 N Q418H	3950
	1161–1
	116



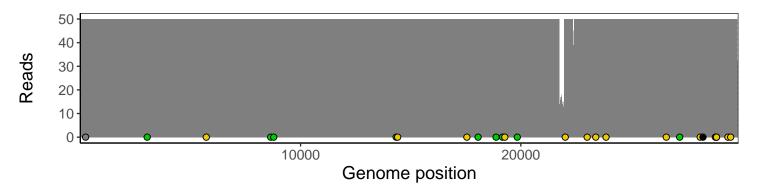
Analyses of individual experiments and composite results

VSP1161-1 | 2021-03-15 | Saline | UPHS-0177 | genomes | single experiment

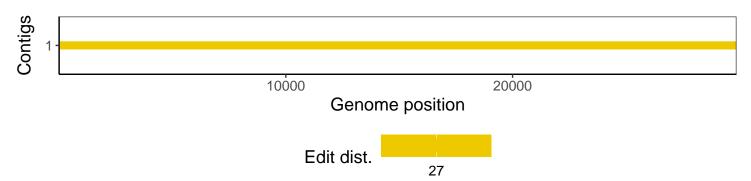
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	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
${\bf Summarized Experiment}$	1.6.5
DelayedArray	0.2.7
matrixStats	0.54.0
Biobase	2.36.2
Rsamtools	1.28.0
GenomicRanges	1.28.6
$\operatorname{GenomeInfoDb}$	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