COVID-19 subject UPHS-0077

2021-05-05

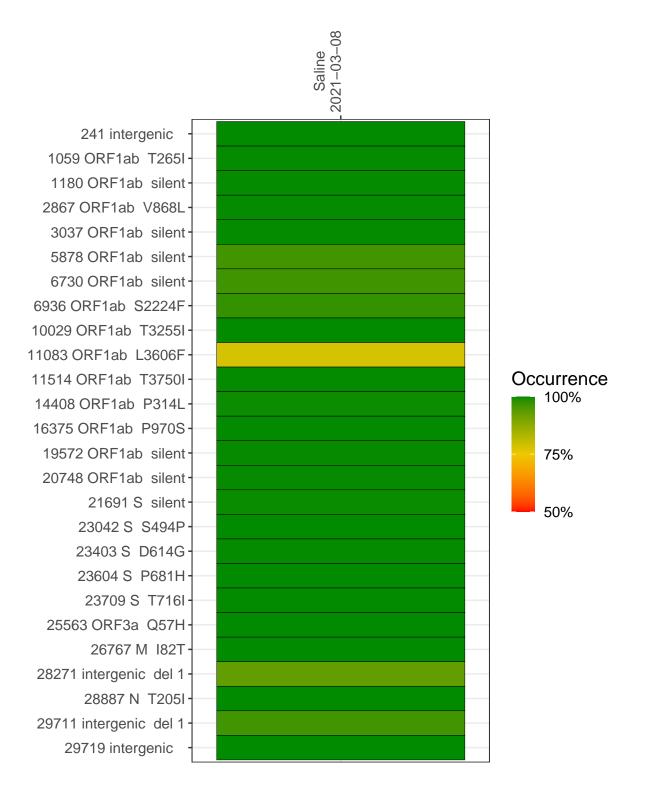
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1009-1	single experiment	NA	Saline	2021-03-08	29.89	B.1.575	99.8%	99.7%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/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 2021-03-08

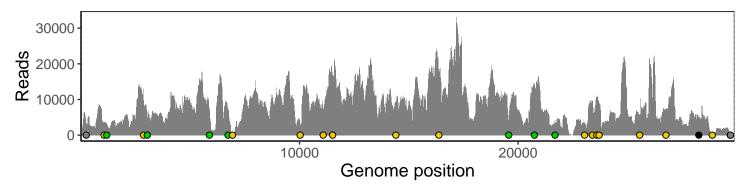
	202: 00 00
241 intergenic	2995
1059 ORF1ab T265I	3465
1180 ORF1ab silent	3026
2867 ORF1ab V868L	9676
3037 ORF1ab silent	5125
5878 ORF1ab silent	7299
6730 ORF1ab silent	7146
6936 ORF1ab S2224F	165
10029 ORF1ab T3255I	3233
11083 ORF1ab L3606F	6444
11514 ORF1ab T3750I	16541
14408 ORF1ab P314L	9452
16375 ORF1ab P970S	18261
19572 ORF1ab silent	3720
20748 ORF1ab silent	14021
21691 S silent	3567
23042 S S494P	3457
23403 S D614G	9464
23604 S P681H	10542
23709 S T716I	8766
25563 ORF3a Q57H	5772
26767 M 182T	7295
28271 intergenic del 1	4836
28887 N T205I	572
29711 intergenic del 1	286
29719 intergenic	277
	1009–1
	100



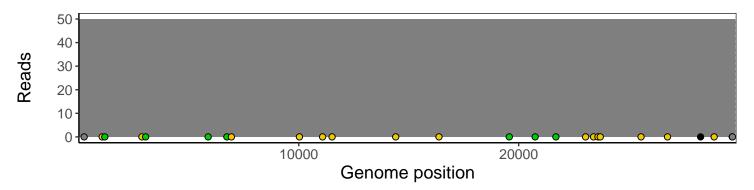
Analyses of individual experiments and composite results

VSP1009-1 | 2021-03-08 | Saline | UPHS-0077 | genomes | single experiment

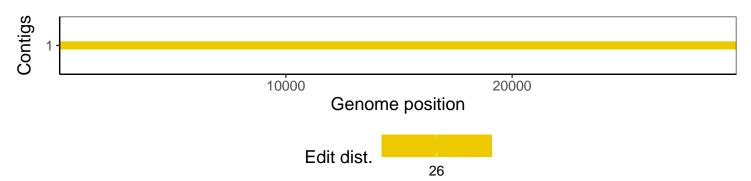
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.8
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
${\it Genomic Alignments}$	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