COVID-19 subject UPHS-0379

2021-04-17

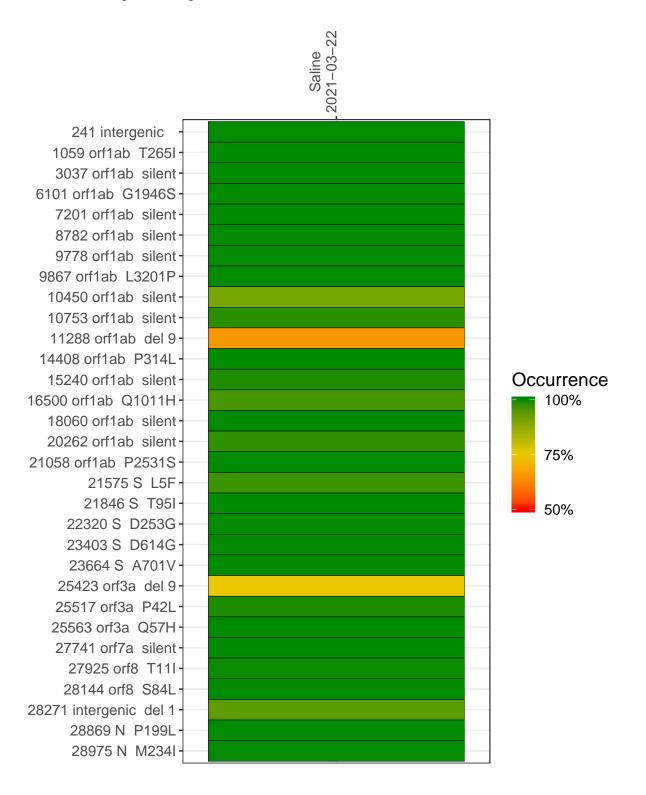
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1424-1	single experiment	NA	Saline	2021-03-22	29.79	B.1.526	99.8%	99.5%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/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 2021-03-22

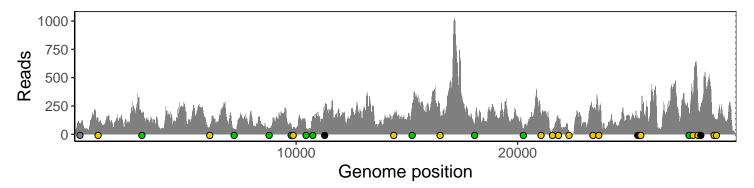
	2021-03-22
241 intergenic	84
1059 orf1ab T265I	130
3037 orf1ab silent	167
6101 orf1ab G1946S	65
7201 orf1ab silent	41
8782 orf1ab silent	53
9778 orf1ab silent	77
9867 orf1ab L3201P	46
10450 orf1ab silent	52
10753 orf1ab silent	126
11288 orf1ab del 9	133
14408 orf1ab P314L	166
15240 orf1ab silent	218
16500 orf1ab Q1011H	175
18060 orf1ab silent	83
20262 orf1ab silent	48
21058 orf1ab P2531S	157
21575 S L5F	34
21846 S T95I	123
22320 S D253G	24
23403 S D614G	216
23664 S A701V	176
25423 orf3a del 9	103
25517 orf3a P42L	120
25563 orf3a Q57H	193
27741 orf7a silent	178
27925 orf8 T11I	362
28144 orf8 S84L	284
28271 intergenic del 1	224
28869 N P199L	145
28975 N M234I	134
	
	VSP1424-1
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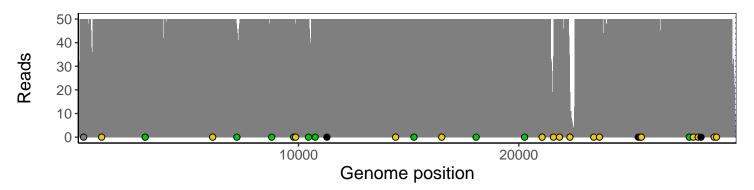
Analyses of individual experiments and composite results

VSP1424-1 | 2021-03-22 | Saline | UPHS-0379 | genomes | single experiment

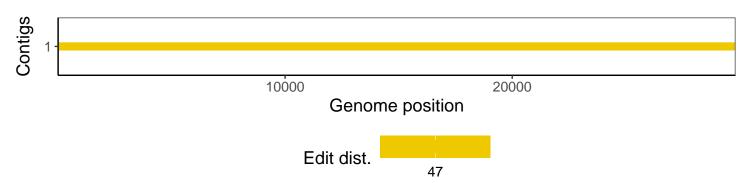
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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