COVID-19 subject UPHS-0602

2021-06-01

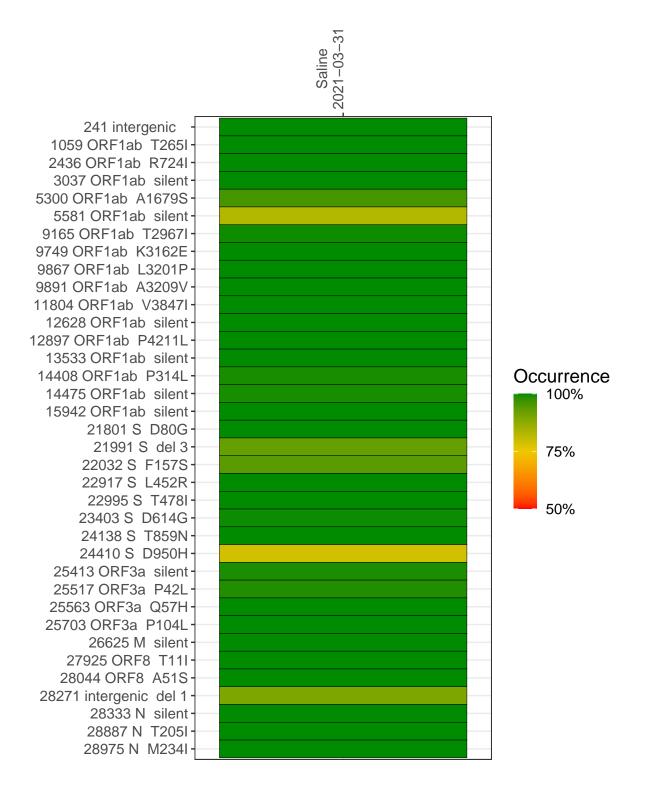
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1787-1	single experiment	NA	Saline	2021-03-31	29.80	B.1.413	99.7%	99.6%

Variants shared across samples

The heat map below shows how variants (reference genome /home/common/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 2021-03-31

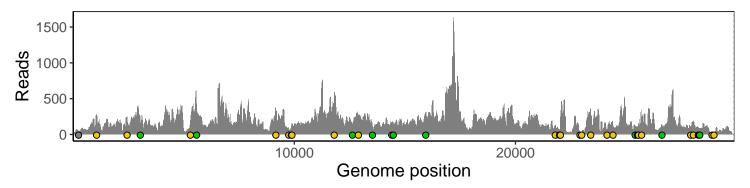
	2021 00 01
241 intergenic	41
1059 ORF1ab T265I	259
2436 ORF1ab R724I	240
3037 ORF1ab silent	166
5300 ORF1ab A1679S	176
5581 ORF1ab silent	415
9165 ORF1ab T2967I	317
9749 ORF1ab K3162E	85
9867 ORF1ab L3201P	112
9891 ORF1ab A3209V	154
11804 ORF1ab V3847I	447
12628 ORF1ab silent	136
12897 ORF1ab P4211L	248
13533 ORF1ab silent	116
14408 ORF1ab P314L	142
14475 ORF1ab silent	153
15942 ORF1ab silent	294
21801 S D80G	115
21991 S del 3	54
22032 S F157S	101
22917 S L452R	30
22995 S T478I	32
23403 S D614G	348
24138 S T859N	70
24410 S D950H	104
25413 ORF3a silent	118
25517 ORF3a P42L	88
25563 ORF3a Q57H	148
25703 ORF3a P104L	237
26625 M silent	111
27925 ORF8 T11I	106
28044 ORF8 A51S	173
28271 intergenic del 1	84
28333 N silent	74
28887 N T205I	21
28975 N M234I	25
	7
	VSP1787-1
	7
	S>



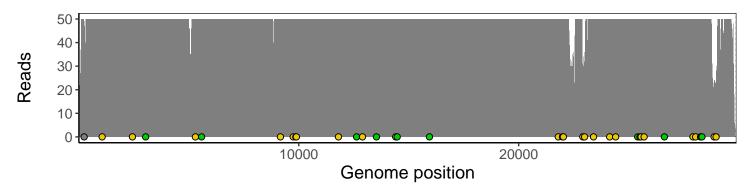
Analyses of individual experiments and composite results

$VSP1787-1 \mid 2021-03-31 \mid Saline \mid UPHS-0602 \mid genomes \mid single \; experiment$

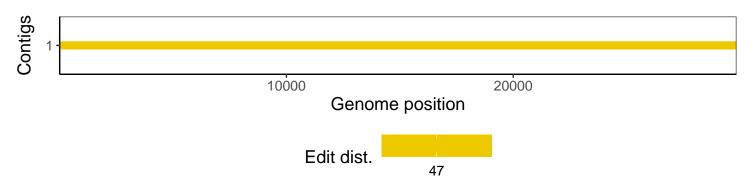
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.8
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	3.3.3
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