COVID-19 subject UPHS-0798

2021-06-23

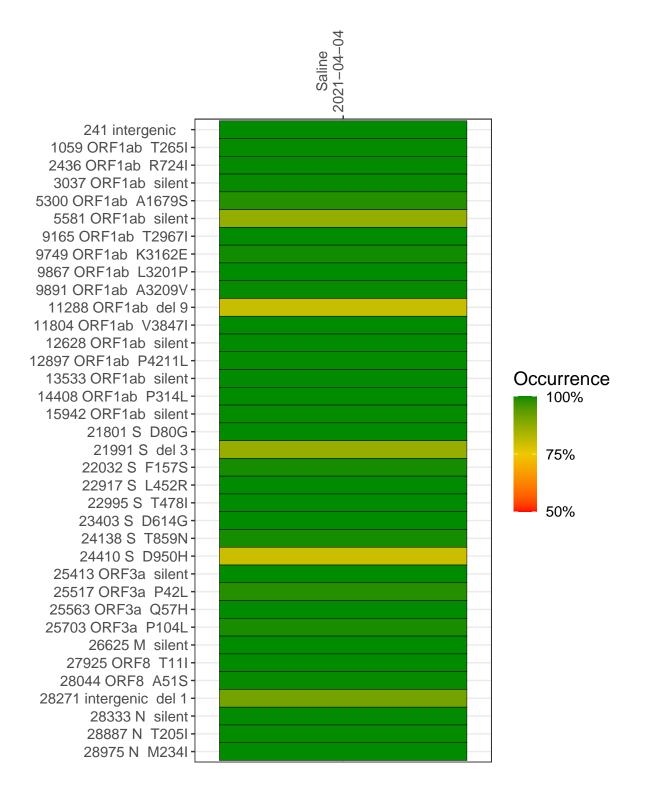
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP2012-2	single experiment	NA	Saline	2021-04-04	29.86	B.1.413	99.7%	99.7%

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 2021-04-04

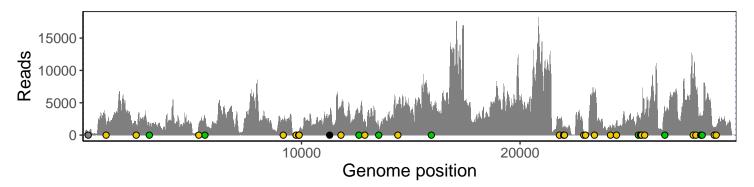
	2021-04
241 intergenic	432
1059 ORF1ab T265I	1695
2436 ORF1ab R724I	1542
3037 ORF1ab silent	1424
5300 ORF1ab A1679S	1404
5581 ORF1ab silent	2592
9165 ORF1ab T2967I	2230
9749 ORF1ab K3162E	232
9867 ORF1ab L3201P	462
9891 ORF1ab A3209V	641
11288 ORF1ab del 9	1881
11804 ORF1ab V3847I	4064
12628 ORF1ab silent	3143
12897 ORF1ab P4211L	2105
13533 ORF1ab silent	1441
14408 ORF1ab P314L	4162
15942 ORF1ab silent	4299
21801 S D80G	2495
21991 S del 3	1149
22032 S F157S	1155
22917 S L452R	161
22995 S T478I	116
23403 S D614G	6253
24138 S T859N	1471
24410 S D950H	2064
25413 ORF3a silent	3035
25517 ORF3a P42L	2252
25563 ORF3a Q57H	3298
25703 ORF3a P104L	2577
26625 M silent	3407
27925 ORF8 T11I	8024
28044 ORF8 A51S	6109
28271 intergenic del 1	2916
28333 N silent	2547
28887 N T205I	1146
28975 N M234I	1321
	7
	2012–2
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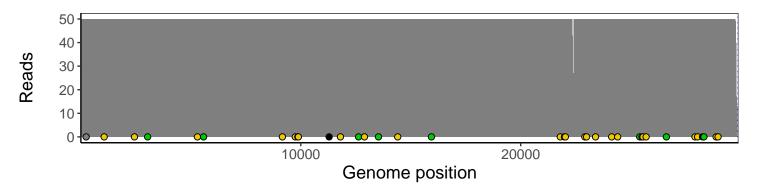
Analyses of individual experiments and composite results

VSP2012-2 | 2021-04-04 | Saline | UPHS-0798 | genomes | single experiment

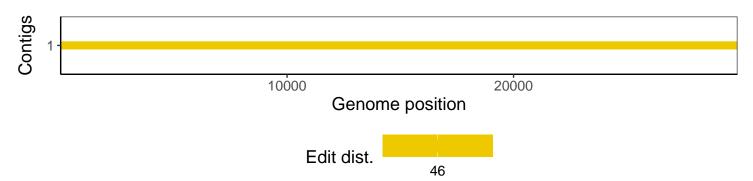
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.1.3				
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	3.3.3				
tidyverse	1.2.1				
ShortRead	1.34.2				
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				
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				