COVID-19 subject UPHS-0050

2021-06-23

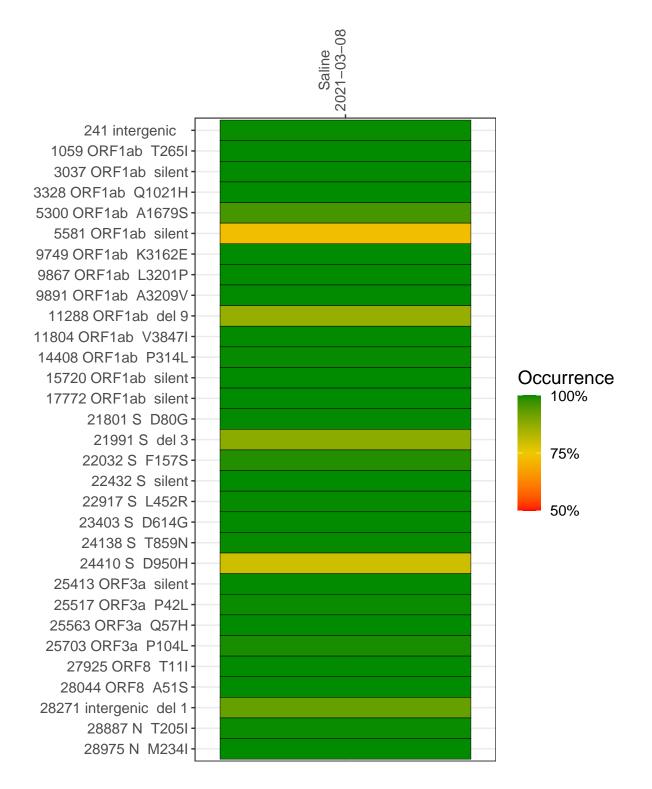
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP0982-1	single experiment	NA	Saline	2021-03-08	29.89	B.1.526	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 2021-03-08

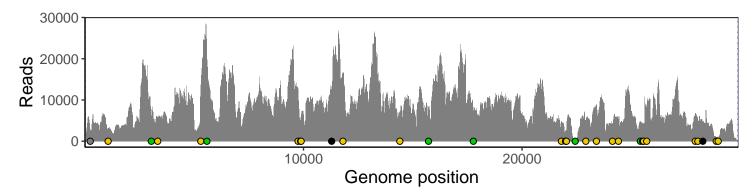
	2021-03-00
241 intergenic	2621
1059 ORF1ab T265I	3045
3037 ORF1ab silent	6526
3328 ORF1ab Q1021H	5833
5300 ORF1ab A1679S	11860
5581 ORF1ab silent	19623
9749 ORF1ab K3162E	12711
9867 ORF1ab L3201P	4068
9891 ORF1ab A3209V	6077
11288 ORF1ab del 9	10604
11804 ORF1ab V3847I	16473
14408 ORF1ab P314L	7212
15720 ORF1ab silent	8164
17772 ORF1ab silent	7170
21801 S D80G	4522
21991 S del 3	2187
22032 S F157S	2500
22432 S silent	195
22917 S L452R	4702
23403 S D614G	8775
24138 S T859N	4327
24410 S D950H	5443
25413 ORF3a silent	4743
25517 ORF3a P42L	4221
25563 ORF3a Q57H	4391
25703 ORF3a P104L	7306
27925 ORF8 T11I	6692
28044 ORF8 A51S	4970
28271 intergenic del 1	4584
28887 N T205I	974
28975 N M234I	814
	982-1
	80



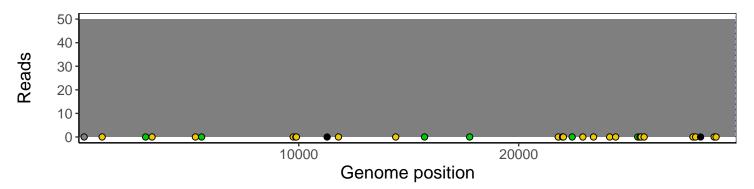
Analyses of individual experiments and composite results

$VSP0982\text{-}1 \mid 2021\text{-}03\text{-}08 \mid Saline \mid UPHS\text{-}0050 \mid genomes \mid single \ experiment$

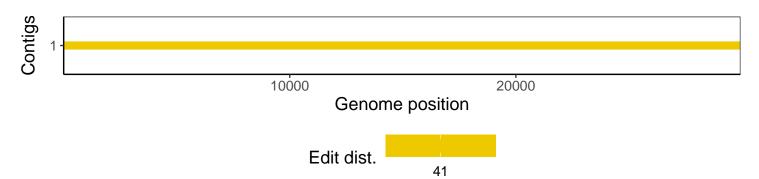
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	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				