COVID-19 subject UPHS-0025

2021-06-23

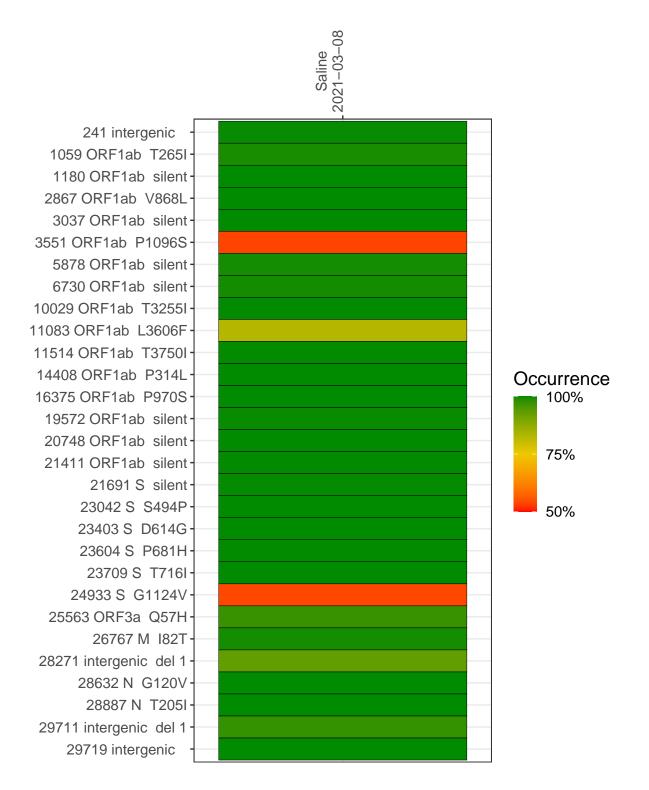
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP0957-1	single experiment	NA	Saline	2021-03-08	29.83	B.1.575	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.



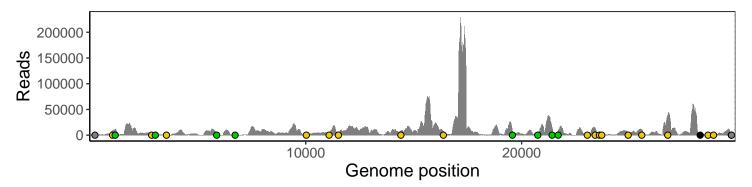
Saline 2021-03-08

	2021-03-00
241 intergenic	1855
1059 ORF1ab T265I	8193
1180 ORF1ab silent	12124
2867 ORF1ab V868L	1598
3037 ORF1ab silent	434
3551 ORF1ab P1096S	388
5878 ORF1ab silent	4580
6730 ORF1ab silent	190
10029 ORF1ab T3255I	811
11083 ORF1ab L3606F	3415
11514 ORF1ab T3750l	6472
14408 ORF1ab P314L	8647
16375 ORF1ab P970S	7684
19572 ORF1ab silent	9077
20748 ORF1ab silent	5307
21411 ORF1ab silent	13805
21691 S silent	8234
23042 S S494P	334
23403 S D614G	14958
23604 S P681H	5951
23709 S T716I	3300
24933 S G1124V	6184
25563 ORF3a Q57H	10787
26767 M 182T	38672
28271 intergenic del 1	4614
28632 N G120V	437
28887 N T205I	197
29711 intergenic del 1	1017
29719 intergenic	940
	1-7
	092
	VSP0957-1

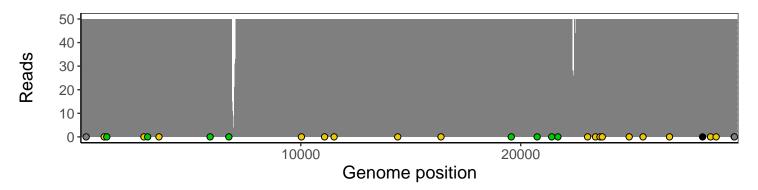
Analyses of individual experiments and composite results

VSP0957-1 | 2021-03-08 | Saline | UPHS-0025 | genomes | single experiment

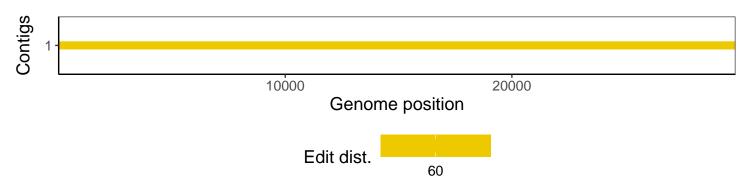
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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				