COVID-19 subject UPHS-0333

2021-06-23

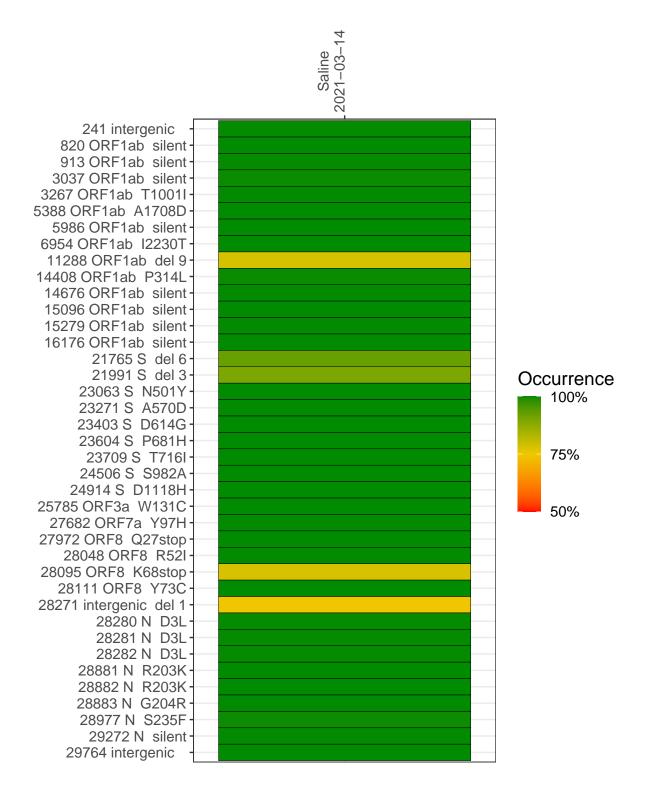
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1378-1	single experiment	NA	Saline	2021-03-14	29.85	B.1.1.7	99.9%	99.8%

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.



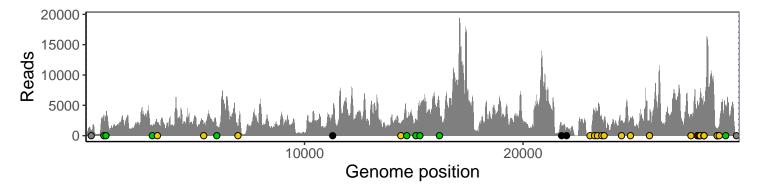
Saline 2021-03-14

	2021-03-14
241 intergenic	816
820 ORF1ab silent	3354
913 ORF1ab silent	3032
3037 ORF1ab silent	1403
3267 ORF1ab T1001I	2257
5388 ORF1ab A1708D	1858
5986 ORF1ab silent	1529
6954 ORF1ab I2230T	1041
11288 ORF1ab del 9	2101
14408 ORF1ab P314L	1715
14676 ORF1ab silent	2634
15096 ORF1ab silent	2653
15279 ORF1ab silent	4454
16176 ORF1ab silent	4554
21765 S del 6	1375
21991 S del 3	1165
23063 S N501Y	73
23271 S A570D	3810
23403 S D614G	3988
23604 S P681H	2979
23709 S T716I	2734
24506 S S982A	2523
24914 S D1118H	2988
25785 ORF3a W131C	2366
27682 ORF7a Y97H	3454
27972 ORF8 Q27stop	5592
28048 ORF8 R52I	4435
28095 ORF8 K68stop	6375
28111 ORF8 Y73C	6943
28271 intergenic del 1	4417
28280 N D3L	3130
28281 N D3L	3130
28282 N D3L	3359
28881 N R203K	768
28882 N R203K	765
28883 N G204R	766
28977 N S235F	1770
29272 N silent	4872
29764 intergenic	261
	<u> </u>
	378
	VSP1378-1
	/SF

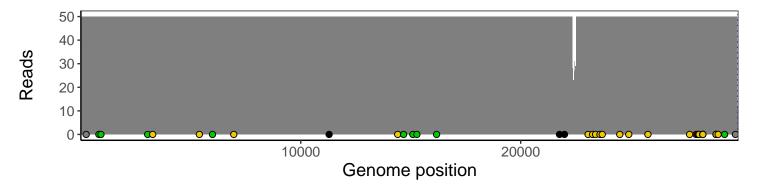
Analyses of individual experiments and composite results

$VSP1378-1 \mid 2021-03-14 \mid Saline \mid UPHS-0333 \mid genomes \mid single \; experiment$

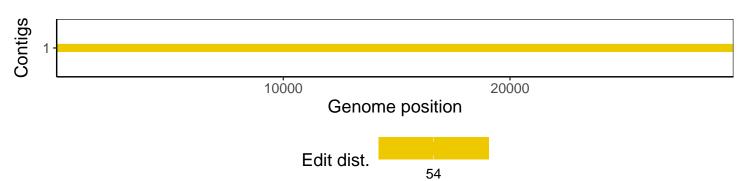
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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				