COVID-19 subject HUP Q-0033

2021-06-23

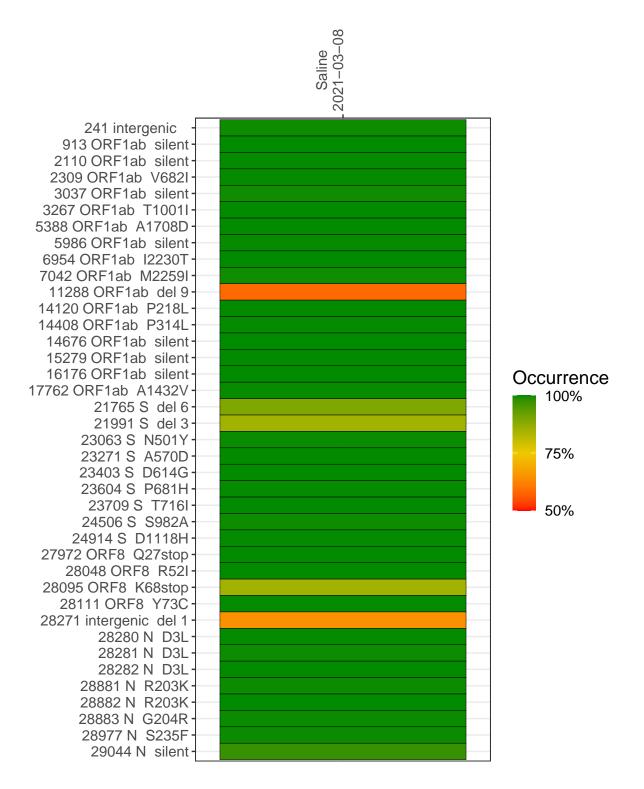
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1035-1	single experiment	NA	Saline	2021-03-08	29.87	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.



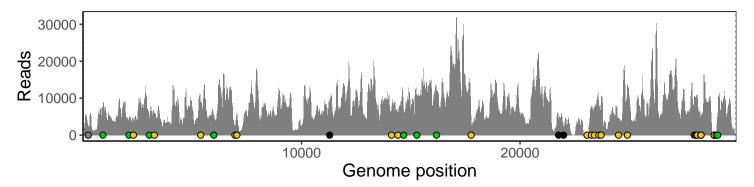
Saline 2021-03-08

	2021-00-00
241 intergenic	2244
913 ORF1ab silent	7365
2110 ORF1ab silent	3894
2309 ORF1ab V682I	4182
3037 ORF1ab silent	4486
3267 ORF1ab T1001I	6124
5388 ORF1ab A1708D	8515
5986 ORF1ab silent	5427
6954 ORF1ab I2230T	2092
7042 ORF1ab M2259I	5743
11288 ORF1ab del 9	4871
14120 ORF1ab P218L	6170
14408 ORF1ab P314L	5346
14676 ORF1ab silent	5482
15279 ORF1ab silent	9883
16176 ORF1ab silent	11823
17762 ORF1ab A1432V	3564
21765 S del 6	3836
21991 S del 3	2403
23063 S N501Y	406
23271 S A570D	7169
23403 S D614G	7430
23604 S P681H	8775
23709 S T716I	8115
24506 S S982A	4660
24914 S D1118H	13471
27972 ORF8 Q27stop	10364
28048 ORF8 R52I	9148
28095 ORF8 K68stop	10751
28111 ORF8 Y73C	9760
28271 intergenic del 1	4494
28280 N D3L	2793
28281 N D3L	2793
28282 N D3L	3084
28881 N R203K	393
28882 N R203K	390
28883 N G204R	390
28977 N S235F	749
29044 N silent	5325
	T
	035

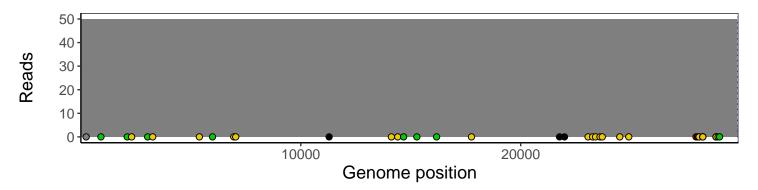
Analyses of individual experiments and composite results

VSP1035-1 | 2021-03-08 | Saline | HUP Q-0033 | genomes | single experiment

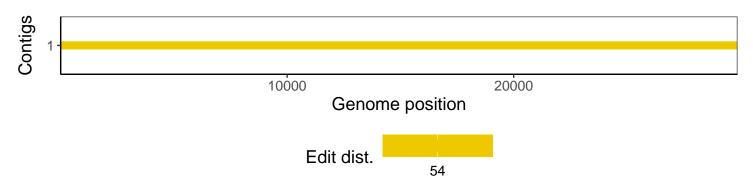
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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