COVID-19 subject HUP Q-0104

2021-06-23

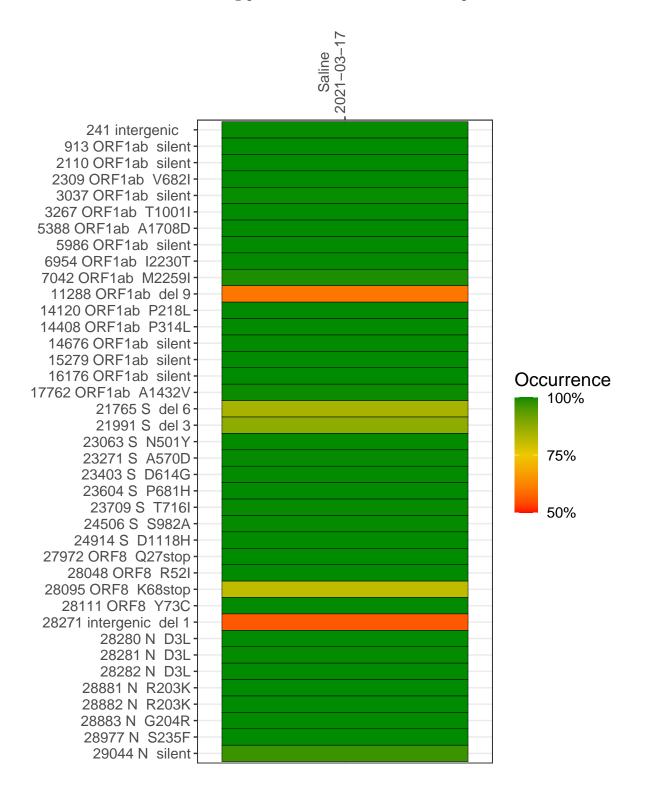
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1227-1	single experiment	NA	Saline	2021-03-17	29.85	B.1.1.7	99.8%	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.



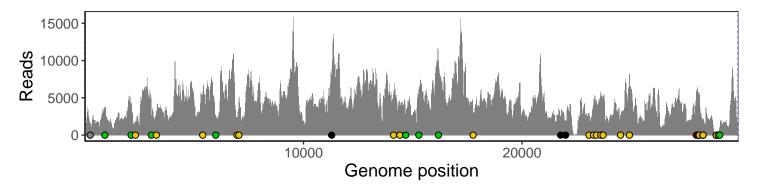
Saline 2021-03-17

	2021-03-17
241 intergenic	1371
913 ORF1ab silent	3597
2110 ORF1ab silent	3969
2309 ORF1ab V682I	1744
3037 ORF1ab silent	3045
3267 ORF1ab T1001I	3228
5388 ORF1ab A1708D	5338
5986 ORF1ab silent	2570
6954 ORF1ab I2230T	2261
7042 ORF1ab M2259I	3755
11288 ORF1ab del 9	4397
14120 ORF1ab P218L	5265
14408 ORF1ab P314L	3871
14676 ORF1ab silent	2148
15279 ORF1ab silent	5245
16176 ORF1ab silent	9757
17762 ORF1ab A1432V	1532
21765 S del 6	2053
21991 S del 3	1643
23063 S N501Y	2836
23271 S A570D	3863
23403 S D614G	4583
23604 S P681H	5101
23709 S T716I	4873
24506 S S982A	2645
24914 S D1118H	8145
27972 ORF8 Q27stop	5634
28048 ORF8 R52I	5482
28095 ORF8 K68stop	5594
28111 ORF8 Y73C	4810
28271 intergenic del 1	1866
28280 N D3L	1004
28281 N D3L	1004
28282 N D3L	1078
28881 N R203K	82
28882 N R203K	81
28883 N G204R	81
28977 N S235F	93
29044 N silent	958
	T
	1227-1
	27

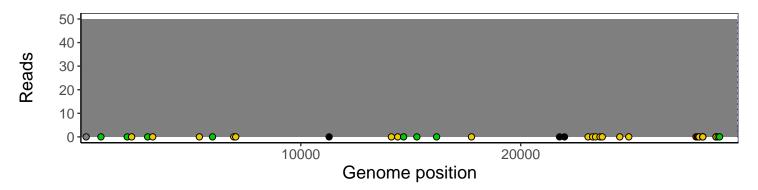
Analyses of individual experiments and composite results

VSP1227-1 | 2021-03-17 | Saline | HUP Q-0104 | genomes | single experiment

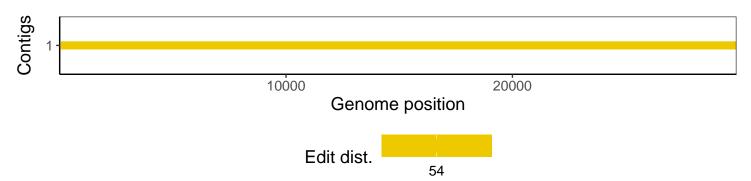
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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