# COVID-19 subject HUP Q-0074

2021-06-23

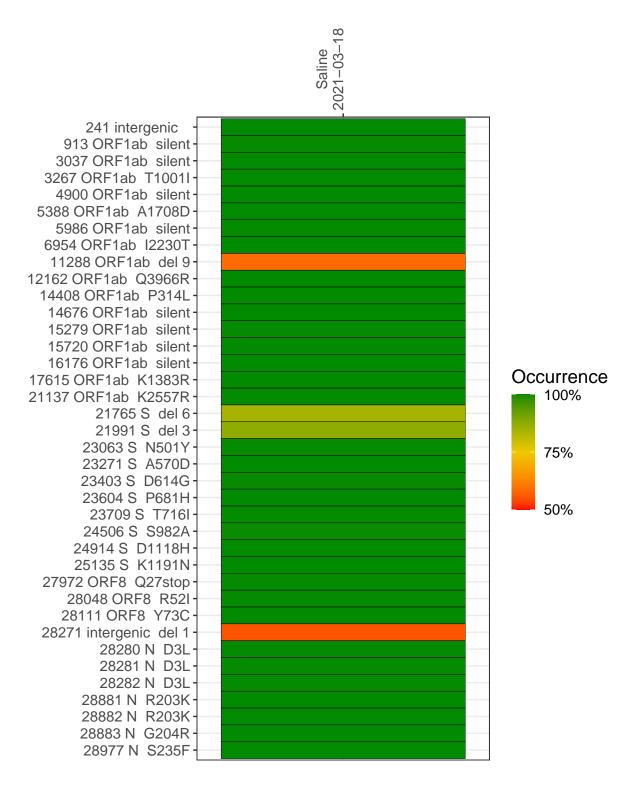
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1241-1	single experiment	NA	Saline	2021-03-18	29.88	B.1.1.7	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.



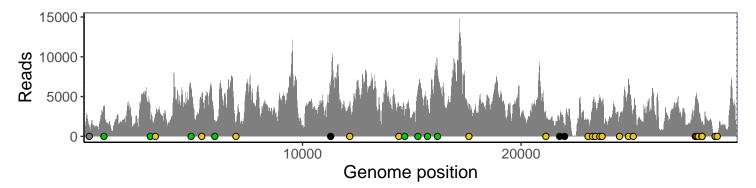
#### Saline 2021-03-18

	2021–03–18
241 intergenic	1110
913 ORF1ab silent	3706
3037 ORF1ab silent	2413
3267 ORF1ab T1001I	2852
4900 ORF1ab silent	5632
5388 ORF1ab A1708D	4683
5986 ORF1ab silent	1995
6954 ORF1ab I2230T	1669
11288 ORF1ab del 9	3349
12162 ORF1ab Q3966R	3772
14408 ORF1ab P314L	3619
14676 ORF1ab silent	1949
15279 ORF1ab silent	5272
15720 ORF1ab silent	4438
16176 ORF1ab silent	8109
17615 ORF1ab K1383R	3820
21137 ORF1ab K2557R	2580
21765 S del 6	1811
21991 S del 3	1197
23063 S N501Y	2128
23271 S A570D	3458
23403 S D614G	4198
23604 S P681H	4653
23709 S T716I	4039
24506 S S982A	2360
24914 S D1118H	7118
25135 S K1191N	3164
27972 ORF8 Q27stop	4645
28048 ORF8 R52I	4561
28111 ORF8 Y73C	3830
28271 intergenic del 1	1566
28280 N D3L	832
28281 N D3L	832
28282 N D3L	900
28881 N R203K	172
28882 N R203K	171
28883 N G204R	172
28977 N S235F	235
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	VSP1241-1
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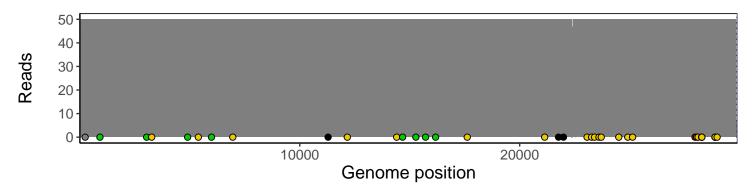
## Analyses of individual experiments and composite results

### VSP1241-1 | 2021-03-18 | Saline | HUP Q-0074 | genomes | single experiment

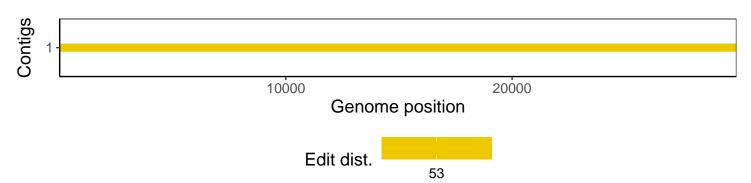
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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