# COVID-19 subject HUP Q-0091

2021-06-23

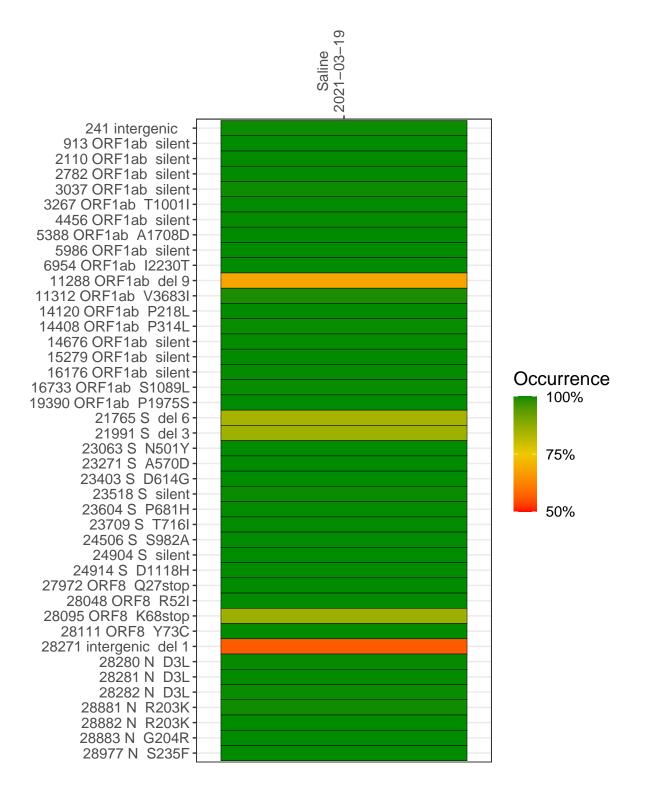
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1258-1	single experiment	NA	Saline	2021-03-19	29.86	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 2021-03-19

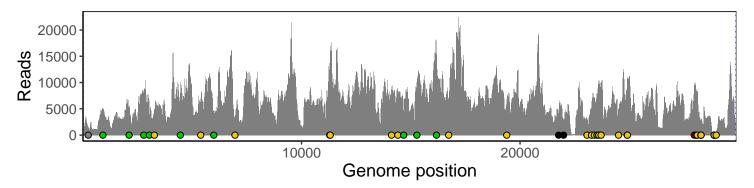
241 intercenic 913 ORF1ab silent 2110 ORF1ab silent 5050		2021-03-19
2110 ORF1ab silent 2782 ORF1ab silent 2782 ORF1ab silent 3037 ORF1ab silent 3037 ORF1ab silent 3267 ORF1ab T10011 4456 ORF1ab silent 5388 ORF1ab silent 6958 ORF1ab silent 6954 ORF1ab 12230T 11288 ORF1ab del 9 1312 ORF1ab v3683I 14120 ORF1ab v3683I 14120 ORF1ab v3683I 14120 ORF1ab v3683I 14120 ORF1ab silent 16176 ORF1ab S1089L 19390 ORF1ab P1975S 21765 S del 6 21991 S del 3 23063 S N501Y 23271 S A570D 23403 S D614G 23518 S silent 23604 S P681H 23709 S T716I 24506 S S982A 24904 S silent 24914 S D1118H 27972 ORF8 Q27stop 28048 ORF8 R52I 2808 O D3L 28281 N D3L 28281 N D3L 28281 N D3L 28281 N D3L 28282 N R203K 28883 N G204R 28977 N S235F	241 intergenic	1326
2782 ORF1ab silent 3037 ORF1ab silent 3037 ORF1ab silent 3267 ORF1ab silent 4536 3267 ORF1ab T1001I 4456 ORF1ab silent 57720 5388 ORF1ab A1708D 5986 ORF1ab silent 6954 ORF1ab silent 1288 ORF1ab del 9 11312 ORF1ab del 9 11312 ORF1ab V3683I 14120 ORF1ab P218L 14408 ORF1ab P314L 14676 ORF1ab silent 15279 ORF1ab silent 16176 ORF1ab S1089L 19390 ORF1ab P1975S 21765 S del 6 21991 S del 3 23063 S N501Y 23271 S A570D 23403 S D614G 23518 S silent 23604 S P681H 23709 S T716I 24506 S S982A 24904 S silent 24914 S D1118H 27972 ORF8 Q27stop 28048 ORF8 R52I 28095 ORF8 K68stop 28111 ORF8 Y73C 28271 intercenic del 1 28282 N D3L 28881 N R203K 28882 N R203K 28883 N G204R 28877 N S235F	913 ORF1ab silent	4814
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3267 ORF1ab T10011 4456 ORF1ab silent 5388 ORF1ab A1708D 5986 ORF1ab silent 6954 ORF1ab l2230T 11288 ORF1ab del 9 11312 ORF1ab v3683I 14120 ORF1ab P218L 14408 ORF1ab P218L 14676 ORF1ab silent 15279 ORF1ab silent 16176 ORF1ab s	2782 ORF1ab silent	7811
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16176 ORF1ab silent 16733 ORF1ab S1089L 19390 ORF1ab P1975S 21765 S del 6 21991 S del 3 23063 S N501Y 23271 S A570D 23403 S D614G 23518 S silent 23604 S P681H 23709 S T716l 24506 S S982A 24904 S silent 24914 S D1118H 27972 ORF8 Q27stop 28048 ORF8 R52l 28048 ORF8 R52l 28071 N D3L 28281 N D3L 28281 N D3L 28282 N D3L 28881 N R203K 28883 N G204R 28977 N S235F 362	14676 ORF1ab silent	3762
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24904 S silent       9206         24914 S D1118H       10437         27972 ORF8 Q27stop       9158         28048 ORF8 R52I       8484         28095 ORF8 K68stop       8219         28111 ORF8 Y73C       7584         28271 intergenic del 1       2524         28280 N D3L       1375         28281 N D3L       1375         28282 N D3L       1475         28881 N R203K       251         28882 N R203K       249         28883 N G204R       253         28977 N S235F       362		
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28095 ORF8 K68stop 28111 ORF8 Y73C  28271 intergenic del 1  28280 N D3L 28281 N D3L 28282 N D3L 28282 N D3L 28881 N R203K 28882 N R203K 28883 N G204R 28977 N S235F  362		
28111 ORF8 Y73C  28271 intergenic del 1  28280 N D3L  28281 N D3L  28282 N R203K  28882 N R203K  28882 N R203K  28883 N G204R  28883 N G204R  28977 N S235F  362		
28271 intergenic del 1  28280 N D3L  28281 N D3L  28282 N D3L  28282 N D3L  28282 N D3L  28881 N R203K  28882 N R203K  28882 N R203K  28883 N G204R  28883 N G204R  28977 N S235F  362		
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28883 N G204R 28977 N S235F 28977 N S235F 253 362		
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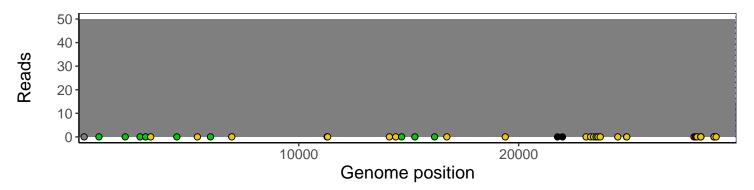
### Analyses of individual experiments and composite results

#### VSP1258-1 | 2021-03-19 | Saline | HUP Q-0091 | genomes | single experiment

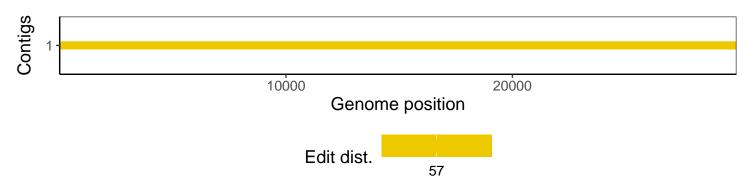
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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