COVID-19 subject HUP Q-0091

2021-05-05

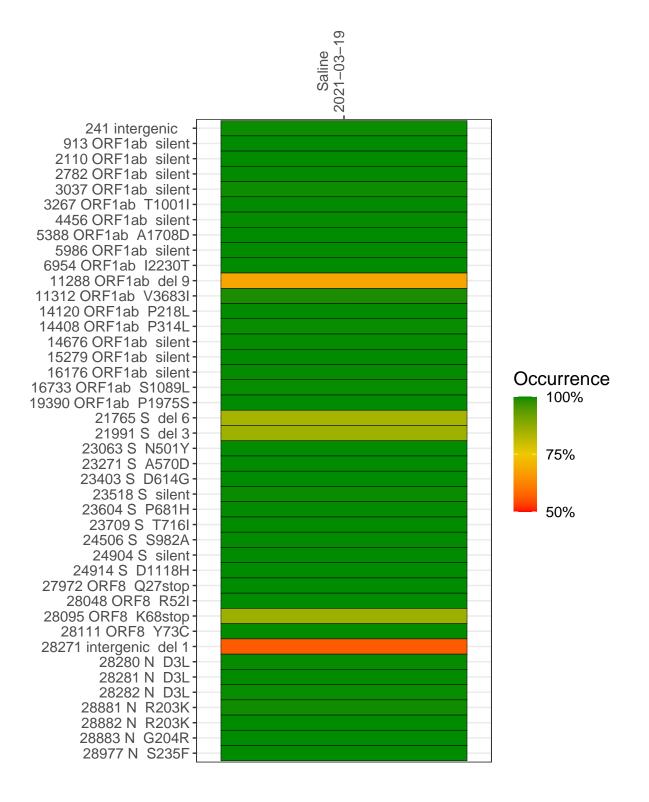
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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/everett/projects/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

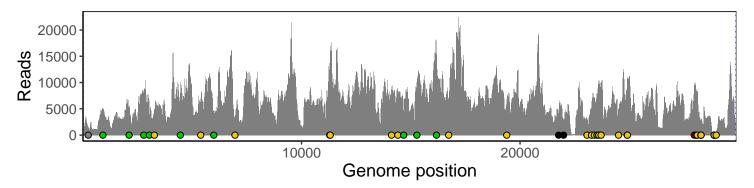
241 intercenic 913 ORF1ab silent 2110 ORF1ab silent 5050		2021-03-19
2110 ORF1ab silent 2782 ORF1ab silent 2782 ORF1ab silent 3037 ORF1ab silent 3037 ORF1ab silent 3267 ORF1ab T10011 4456 ORF1ab silent 5388 ORF1ab silent 5388 ORF1ab silent 6954 ORF1ab 12230T 11288 ORF1ab del 9 1312 ORF1ab v3683I 14120 ORF1ab v3683I 14120 ORF1ab v3683I 14120 ORF1ab P218L 14408 ORF1ab P218L 14676 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 28018 ORF8 R52I 28281 N D3L 28281 N D3L 28281 N D3L 28281 N D3L 28282 N R203K 28883 N G204R 28877 N S235F	241 intergenic	1326
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4456 ORF1ab silent 5388 ORF1ab A1708D 5986 ORF1ab silent 6954 ORF1ab silent 1230T 11288 ORF1ab del 9 11312 ORF1ab V3683I 14120 ORF1ab P218L 14408 ORF1ab P314L 14676 ORF1ab silent 15279 ORF1ab silent 16176 ORF1ab silent 16176 ORF1ab silent 16176 ORF1ab silent 16173 ORF1ab Silent 16733 ORF1ab SI089L 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 28280 N D3L 28281 N D3L 28281 N P30L 28881 N R203K 28883 N G204R 28877 N S235F 362	3037 ORF1ab silent	4536
5388 ORF1ab A1708D 5986 ORF1ab silent 6954 ORF1ab silent 6954 ORF1ab l2230T 11288 ORF1ab del 9 11312 ORF1ab V3683I 13413 14120 ORF1ab P218L 1408 ORF1ab P314L 15279 ORF1ab silent 15279 ORF1ab silent 15279 ORF1ab silent 15155 16733 ORF1ab S1089L 19390 ORF1ab S1089L 19390 ORF1ab S1089L 21765 S del 6 21991 S del 3 23063 S N501Y 23271 S A570D 23403 S D614G 23518 S silent 23709 S T716I 24506 S S982A 24904 S silent 24914 S D1118H 27972 ORF8 K68stop 28014 ORF8 R52I 28081 N D3L 28281 N D3L 28282 N D3L 28282 N D3L 28881 N R203K 28883 N G204R 28977 N S235F	3267 ORF1ab T1001I	5011
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11312 ORF1ab V3683I 14120 ORF1ab P218L 14408 ORF1ab P314L 14676 ORF1ab silent 15279 ORF1ab silent 16176 ORF1ab silent 16176 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 23709 S T716I 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 28281 N D3L 28282 N D3L 28881 N R203K 28882 N R203K 28977 N S235F	6954 ORF1ab I2230T	3247
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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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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		
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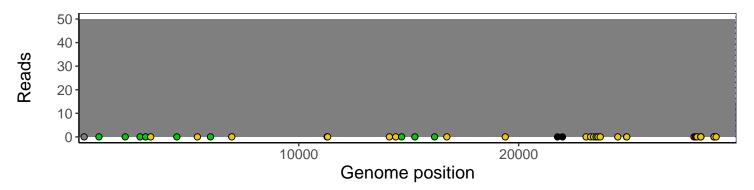
Analyses of individual experiments and composite results

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

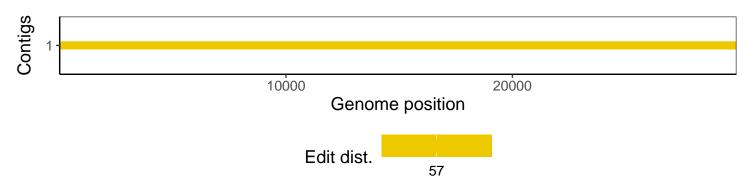
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.8
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	3.0.0
tidyverse	1.2.1
ShortRead	1.34.2
${\it Genomic Alignments}$	1.12.2
SummarizedExperiment	1.6.5
DelayedArray	0.2.7
matrixStats	0.54.0
Biobase	2.36.2
Rsamtools	1.28.0
GenomicRanges	1.28.6
$\operatorname{GenomeInfoDb}$	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