COVID-19 subject HUP Q-0086

2021-06-23

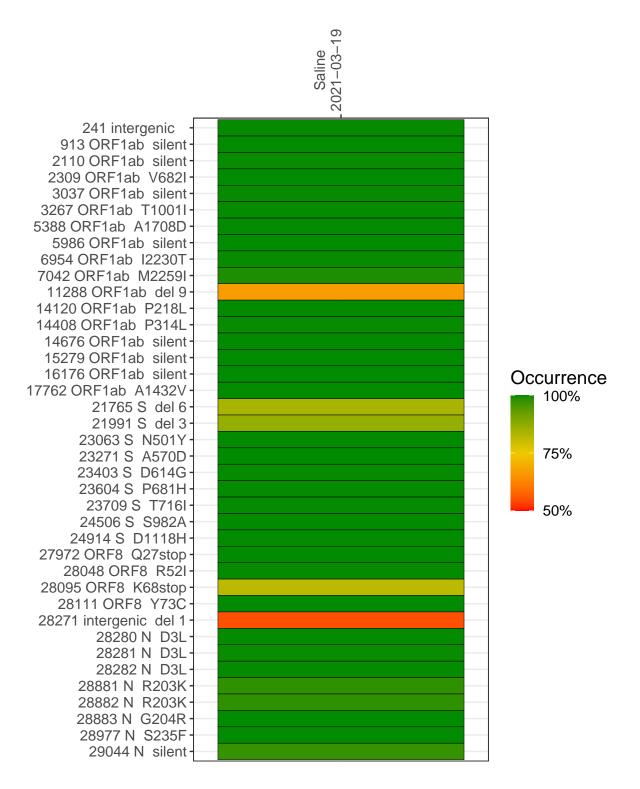
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1253-1	single experiment	NA	Saline	2021-03-19	29.89	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.



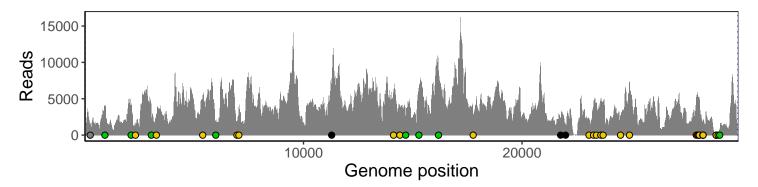
Saline 2021-03-19

	2021-03-19
241 intergenic	1351
913 ORF1ab silent	3962
2110 ORF1ab silent	3786
2309 ORF1ab V682I	1485
3037 ORF1ab silent	2622
3267 ORF1ab T1001I	2910
5388 ORF1ab A1708D	4914
5986 ORF1ab silent	1953
6954 ORF1ab I2230T	1789
7042 ORF1ab M2259I	2840
11288 ORF1ab del 9	4207
14120 ORF1ab P218L	5641
14408 ORF1ab P314L	3664
14676 ORF1ab silent	2088
15279 ORF1ab silent	5873
16176 ORF1ab silent	8764
17762 ORF1ab A1432V	1509
21765 S del 6	2000
21991 S del 3	1272
23063 S N501Y	2231
23271 S A570D	3849
23403 S D614G	4401
23604 S P681H	4496
23709 S T716I	4233
24506 S S982A	2636
24914 S D1118H	7235
27972 ORF8 Q27stop	5019
28048 ORF8 R52I	5037
28095 ORF8 K68stop	5143
28111 ORF8 Y73C	4461
28271 intergenic del 1	1674
28280 N D3L	892
28281 N D3L	892
28282 N D3L	955
28881 N R203K	49
28882 N R203K	49
28883 N G204R	49
28977 N S235F	73
29044 N silent	795
	<u></u>
	253
	VSP1253–1
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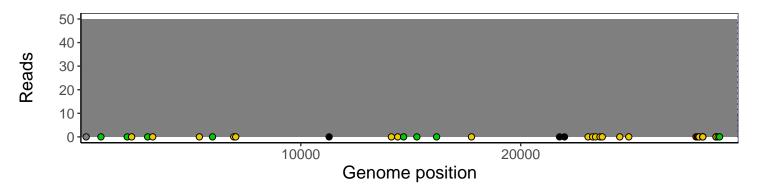
Analyses of individual experiments and composite results

VSP1253-1 | 2021-03-19 | Saline | HUP Q-0086 | genomes | single experiment

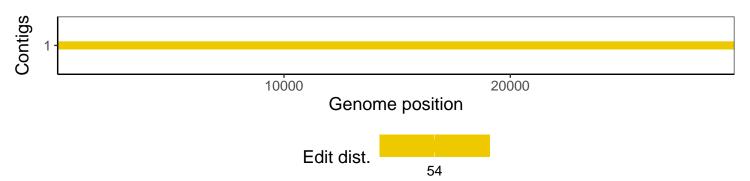
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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				