COVID-19 subject HUP Q-0224

2021-06-23

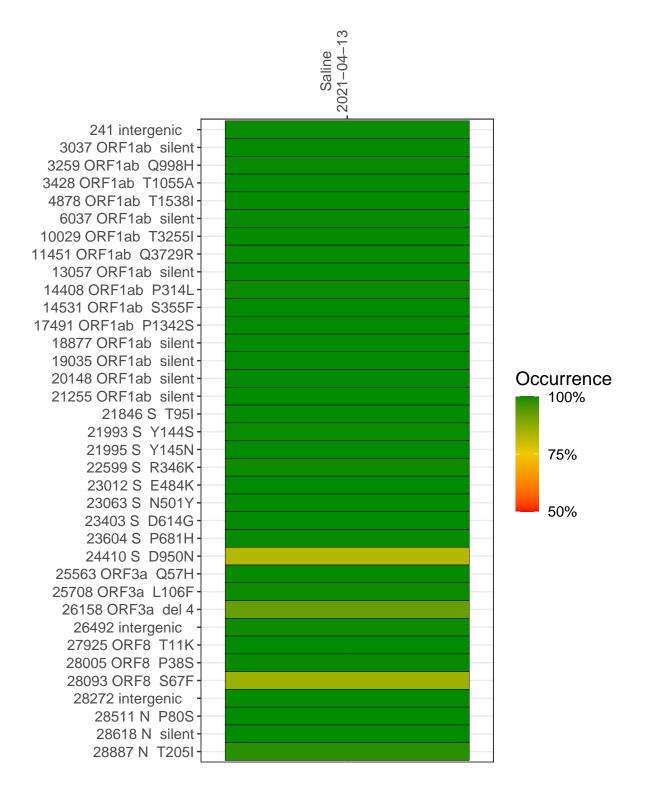
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP2405-1	single experiment	NA	Saline	2021-04-13	29.84	B.1.621	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.



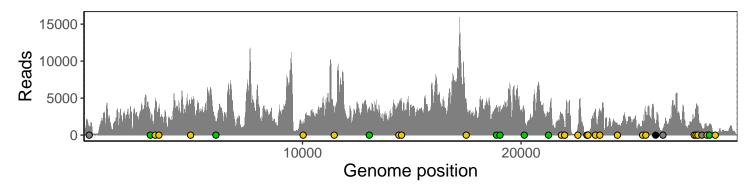
Saline 2021-04-13

	2021-04-13
241 intergenic	1030
3037 ORF1ab silent	2366
3259 ORF1ab Q998H	5028
3428 ORF1ab T1055A	3765
4878 ORF1ab T1538I	4100
6037 ORF1ab silent	1682
10029 ORF1ab T3255I	1849
11451 ORF1ab Q3729R	3032
13057 ORF1ab silent	3532
14408 ORF1ab P314L	3748
14531 ORF1ab S355F	4499
17491 ORF1ab P1342S	4612
18877 ORF1ab silent	3860
19035 ORF1ab silent	3501
20148 ORF1ab silent	3524
21255 ORF1ab silent	2799
21846 S T95I	2614
21993 S Y144S	418
21995 S Y145N	427
22599 S R346K	1208
23012 S E484K	253
23063 S N501Y	495
23403 S D614G	3425
23604 S P681H	3089
24410 S D950N	1280
25563 ORF3a Q57H	1838
25708 ORF3a L106F	2520
26158 ORF3a del 4	1275
26492 intergenic	892
27925 ORF8 T11K	2110
28005 ORF8 P38S	3528
28093 ORF8 S67F	3799
28272 intergenic	1161
28511 N P80S	1177
28618 N silent	1188
28887 N T205I	24 3
	10

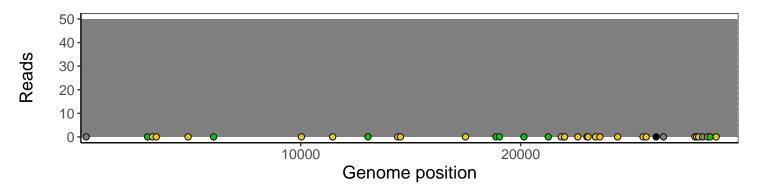
Analyses of individual experiments and composite results

$VSP2405\text{-}1 \mid 2021\text{-}04\text{-}13 \mid Saline \mid HUP \text{ Q-}0224 \mid genomes \mid single \text{ experiment}$

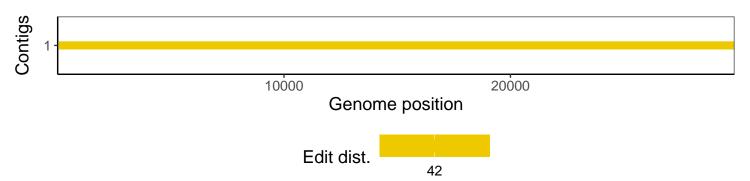
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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