COVID-19 subject HUP Q-0169

2021-06-23

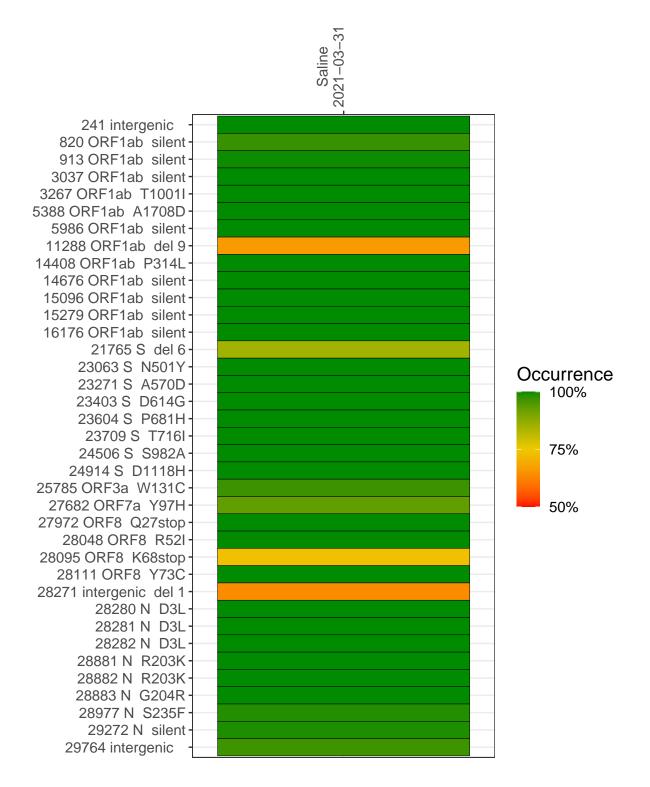
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1509-1	single experiment	NA	Saline	2021-03-31	22.32	B.1.1.7	99.3%	99.2%

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 2021-03-31

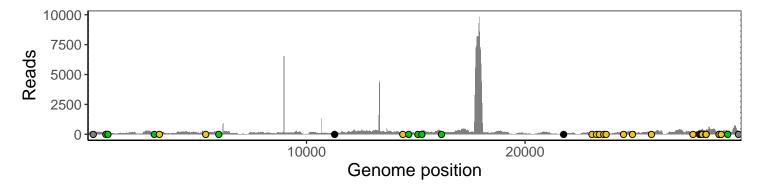
	2021-03-31
241 intergenic	154
820 ORF1ab silent	293
913 ORF1ab silent	297
3037 ORF1ab silent	78
3267 ORF1ab T1001I	200
5388 ORF1ab A1708D	171
5986 ORF1ab silent	67
11288 ORF1ab del 9	51
14408 ORF1ab P314L	138
14676 ORF1ab silent	112
15096 ORF1ab silent	97
15279 ORF1ab silent	309
16176 ORF1ab silent	206
21765 S del 6	100
23063 S N501Y	139
23271 S A570D	230
23403 S D614G	230
23604 S P681H	161
23709 S T716I	165
24506 S S982A	163
24914 S D1118H	270
25785 ORF3a W131C	163
27682 ORF7a Y97H	168
27972 ORF8 Q27stop	361
28048 ORF8 R52I	345
28095 ORF8 K68stop	406
28111 ORF8 Y73C	398
28271 intergenic del 1	258
28280 N D3L	159
28281 N D3L	159
28282 N D3L	169
28881 N R203K	61
28882 N R203K	61
28883 N G204R	61
28977 N S235F	84
29272 N silent	311
29764 intergenic	283
3,-	
	VSP1509-1
	2
	/SF



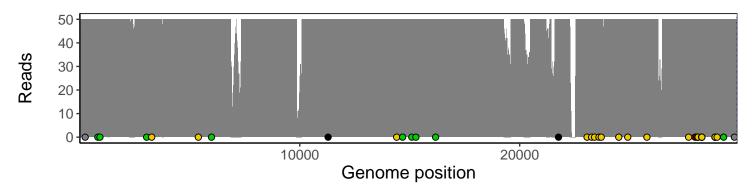
Analyses of individual experiments and composite results

VSP1509-1 | 2021-03-31 | Saline | HUP Q-0169 | genomes | single experiment

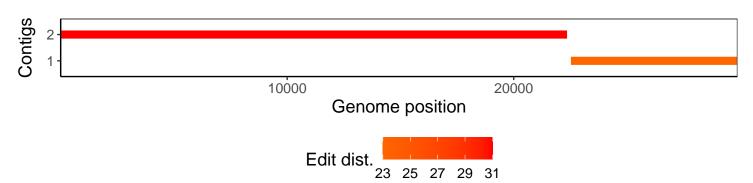
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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				