COVID-19 subject HUP PH-0018

2021-03-05

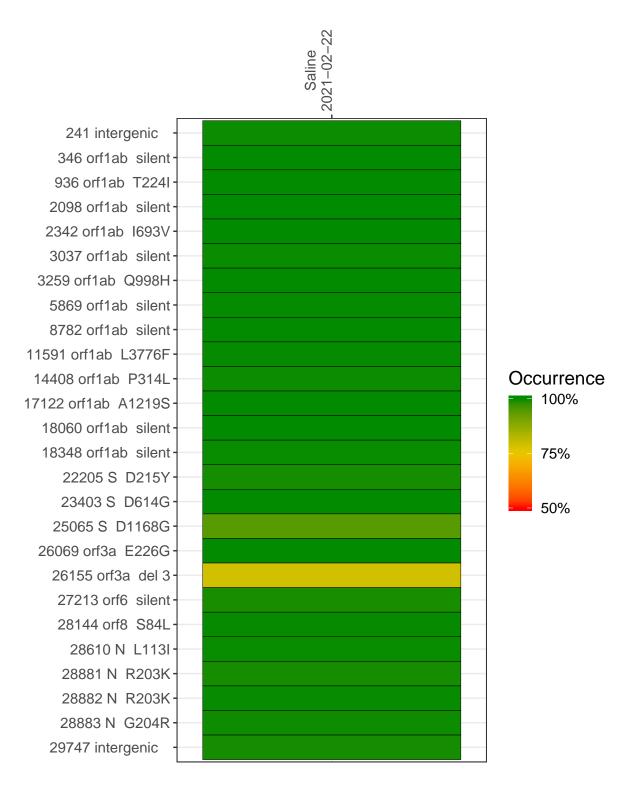
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with > 90% sequence coverage.

Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0862-1	single experiment	NA	Saline	2021-02-22	29.86	B.1.1.304	99.9%	99.9%

Variants shared across samples

The heat map below shows how variants (reference genome USA-WA1-2020) 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 2021-02-22

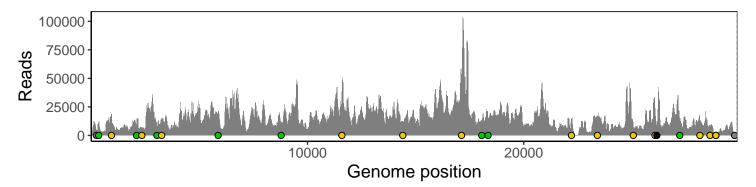
	2021-02-22
241 intergenic	4692
346 orf1ab silent	11545
936 orf1ab T224I	18737
2098 orf1ab silent	8073
2342 orf1ab I693V	5184
3037 orf1ab silent	8139
3259 orf1ab Q998H	15139
5869 orf1ab silent	18435
8782 orf1ab silent	10615
11591 orf1ab L3776F	36793
14408 orf1ab P314L	10523
17122 orf1ab A1219S	55017
18060 orf1ab silent	13233
18348 orf1ab silent	14361
22205 S D215Y	13721
23403 S D614G	16456
25065 S D1168G	9716
26069 orf3a E226G	23723
26155 orf3a del 3	8057
27213 orf6 silent	13316
28144 orf8 S84L	14791
28610 N L113I	8165
28881 N R203K	1121
28882 N R203K	1116
28883 N G204R	1119
29747 intergenic	1943
	862–1
	<u>Θ</u>



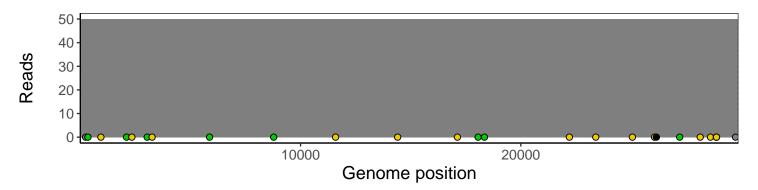
Analyses of individual experiments and composite results

$VSP0862\text{-}1 \mid 2021\text{-}02\text{-}22 \mid Saline \mid HUP\text{-}PH\text{-}0018 \mid genomes \mid single \ experiment}$

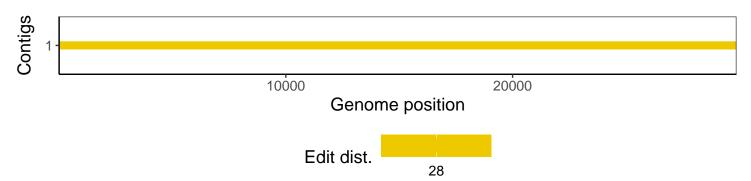
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.3
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	3.0.0
tidyverse	1.2.1
ShortRead	1.34.2
$\operatorname{GenomicAlignments}$	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