COVID-19 subject UPHS-1588

2021-06-03

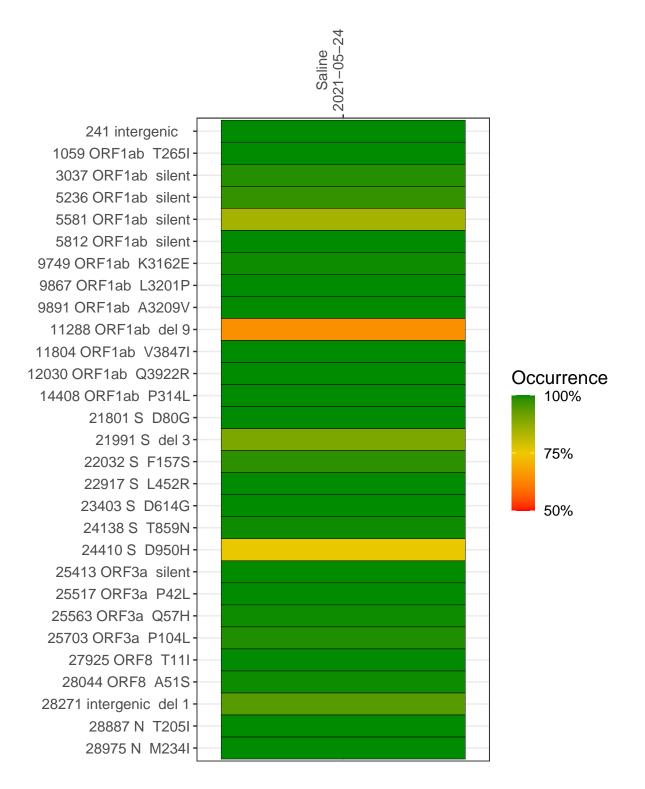
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP2889-1	single experiment	NA	Saline	2021-05-24	29.80	B.1.526.1	99.7%	99.6%

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.



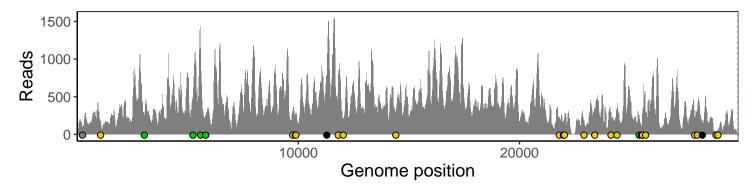
Saline 2021-05-24

	2021-05-24
241 intergenic	92
1059 ORF1ab T265I	154
3037 ORF1ab silent	229
5236 ORF1ab silent	491
5581 ORF1ab silent	1075
5812 ORF1ab silent	237
9749 ORF1ab K3162E	322
9867 ORF1ab L3201P	243
9891 ORF1ab A3209V	288
11288 ORF1ab del 9	449
11804 ORF1ab V3847I	552
12030 ORF1ab Q3922R	140
14408 ORF1ab P314L	252
21801 S D80G	212
21991 S del 3	147
22032 S F157S	160
22917 S L452R	172
23403 S D614G	353
24138 S T859N	289
24410 S D950H	341
25413 ORF3a silent	250
25517 ORF3a P42L	109
25563 ORF3a Q57H	277
25703 ORF3a P104L	286
27925 ORF8 T11I	205
28044 ORF8 A51S	308
28271 intergenic del 1	153
28887 N T205I	32
28975 N M234I	63
	9–7
	VSP2889–1
	/SP

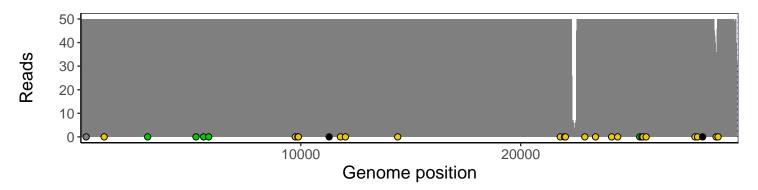
Analyses of individual experiments and composite results

$VSP2889\text{-}1 \mid 2021\text{-}05\text{-}24 \mid Saline \mid UPHS\text{-}1588 \mid genomes \mid single \ experiment$

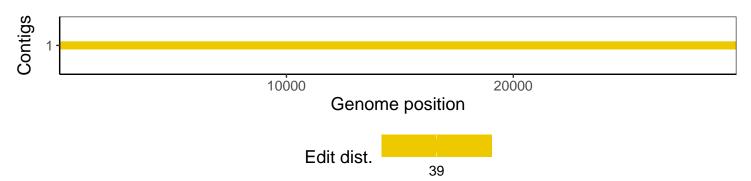
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.8
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	3.3.3
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