COVID-19 subject UPHS-0625

2021-06-01

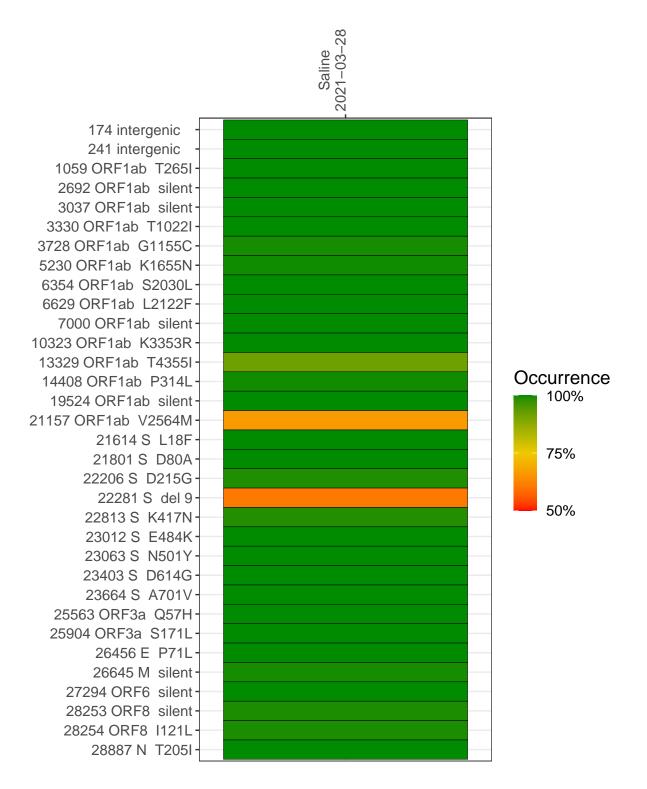
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1810-1	single experiment	NA	Saline	2021-03-28	22.28	B.1.351	99.5%	99.0%

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 2021-03-28

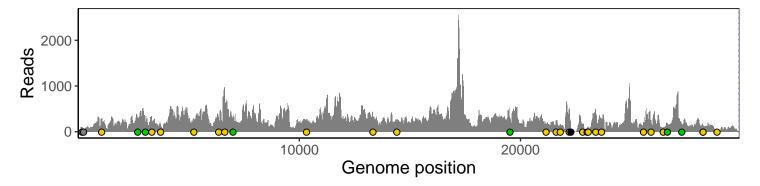
	2021-03-20
174 intergenic	98
241 intergenic	55
1059 ORF1ab T265I	274
2692 ORF1ab silent	307
3037 ORF1ab silent	223
3330 ORF1ab T1022I	292
3728 ORF1ab G1155C	164
5230 ORF1ab K1655N	269
6354 ORF1ab S2030L	309
6629 ORF1ab L2122F	521
7000 ORF1ab silent	298
10323 ORF1ab K3353R	237
13329 ORF1ab T4355I	292
14408 ORF1ab P314L	220
19524 ORF1ab silent	304
21157 ORF1ab V2564M	157
21614 S L18F	223
21801 S D80A	158
22206 S D215G	484
22281 S del 9	66
22813 S K417N	162
23012 S E484K	64
23063 S N501Y	102
23403 S D614G	484
23664 S A701V	245
25563 ORF3a Q57H	209
25904 ORF3a S171L	254
26456 E P71L	76
26645 M silent	165
27294 ORF6 silent	191
28253 ORF8 silent	115
28254 ORF8 I121L	117
28887 N T205I	22
	7
	810
	VSP1810-1
	>



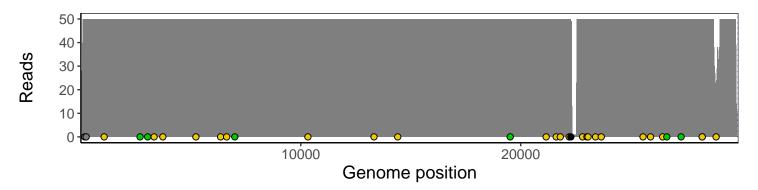
Analyses of individual experiments and composite results

VSP1810-1 | 2021-03-28 | Saline | UPHS-0625 | genomes | single experiment

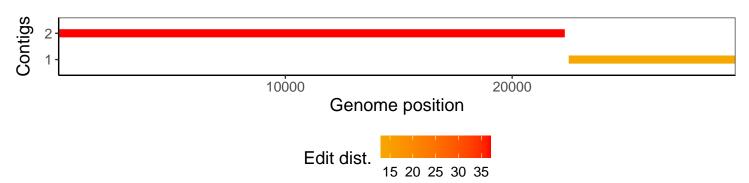
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	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