COVID-19 subject UPHS-0267

2021-05-05

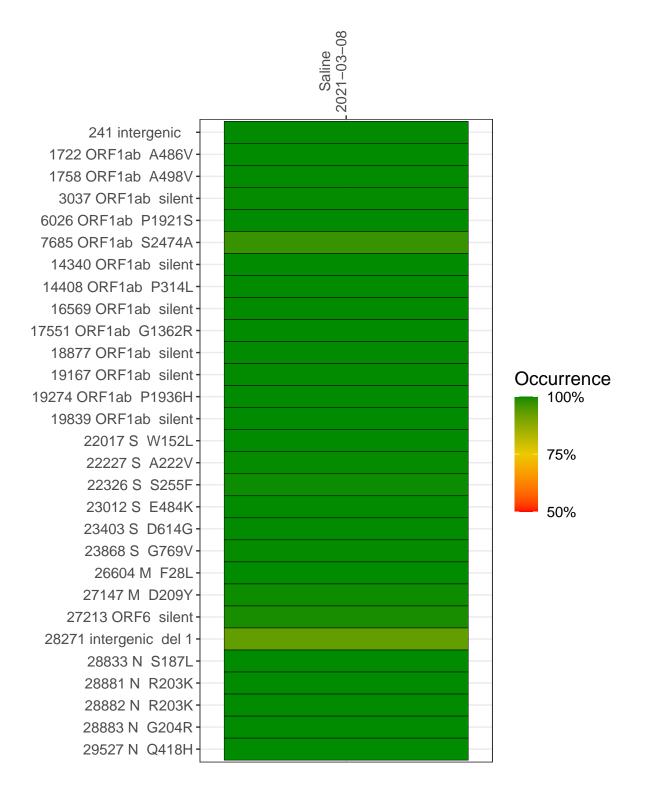
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

Table 1. Sample summary.

Experiment	Туре	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1312-1	single experiment	NA	Saline	2021-03-08	29.82	R.1	99.9%	99.7%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/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 2021-03-08

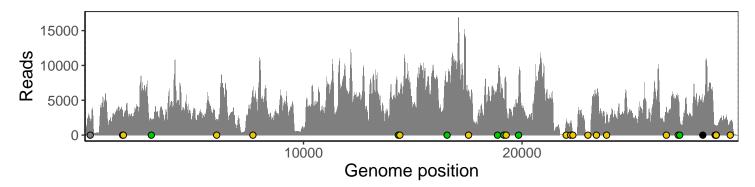
241 intergenic	2016
1722 ORF1ab A486V	3000
1758 ORF1ab A498V	2144
3037 ORF1ab silent	1917
6026 ORF1ab P1921S	2253
7685 ORF1ab S2474A	6186
14340 ORF1ab silent	5519
14408 ORF1ab P314L	5368
16569 ORF1ab silent	7286
17551 ORF1ab G1362R	5859
18877 ORF1ab silent	7149
19167 ORF1ab silent	4954
19274 ORF1ab P1936H	7140
19839 ORF1ab silent	6126
22017 S W152L	1682
22227 S A222V	1886
22326 S S255F	341
23012 S E484K	77
23403 S D614G	5657
23868 S G769V	3265
26604 M F28L	3762
27147 M D209Y	5126
27213 ORF6 silent	2403
28271 intergenic del 1	4616
28833 N S187L	1435
28881 N R203K	934
28882 N R203K	932
28883 N G204R	932
29527 N Q418H	1619
	1312–1
	131



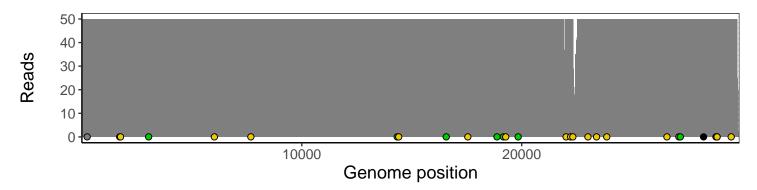
Analyses of individual experiments and composite results

$VSP1312\text{-}1 \mid 2021\text{-}03\text{-}08 \mid Saline \mid UPHS\text{-}0267 \mid genomes \mid single \ experiment$

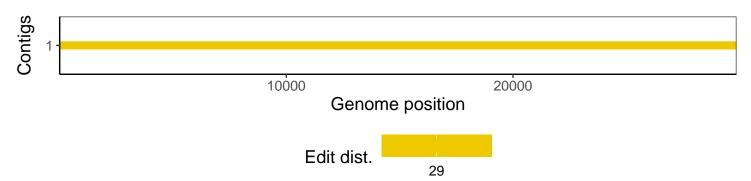
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.0.0
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