COVID-19 subject UPHS-0085

2021-04-17

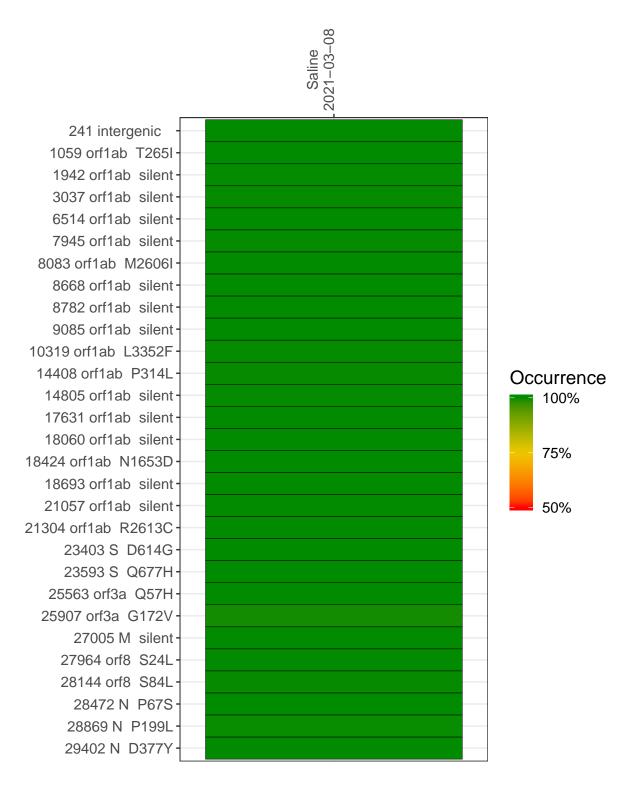
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1017-1	single experiment	NA	Saline	2021-03-08	29.87	B.1.2	99.9%	99.8%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/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 2021-03-08

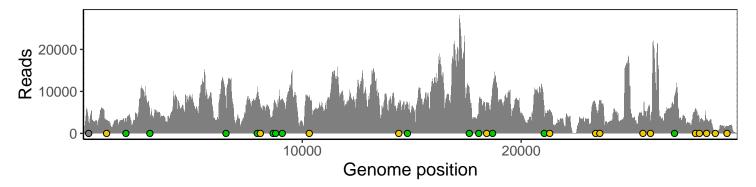
241 intergenic	2481
1059 orf1ab T265I	3083
1942 orf1ab silent	2331
3037 orf1ab silent	4399
6514 orf1ab silent	5745
7945 orf1ab silent	9703
8083 orf1ab M2606I	6616
8668 orf1ab silent	5278
8782 orf1ab silent	7023
9085 orf1ab silent	8127
10319 orf1ab L3352F	7921
14408 orf1ab P314L	7077
14805 orf1ab silent	7312
17631 orf1ab silent	10630
18060 orf1ab silent	6481
18424 orf1ab N1653D	7145
18693 orf1ab silent	10547
21057 orf1ab silent	4675
21304 orf1ab R2613C	5407
23403 S D614G	7130
23593 S Q677H	7807
25563 orf3a Q57H	4153
25907 orf3a G172V	2760
27005 M silent	8592
27964 orf8 S24L	5975
28144 orf8 S84L	2735
28472 N P67S	3212
28869 N P199L	522
29402 N D377Y	1802
	$\overline{}$



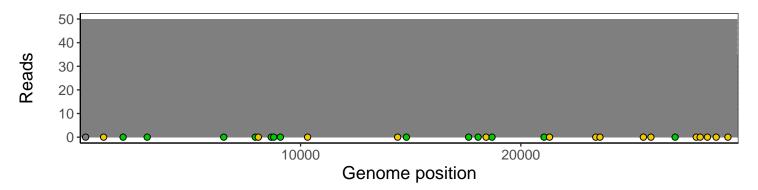
Analyses of individual experiments and composite results

$VSP1017\text{-}1 \mid 2021\text{-}03\text{-}08 \mid Saline \mid UPHS\text{-}0085 \mid genomes \mid single \ experiment$

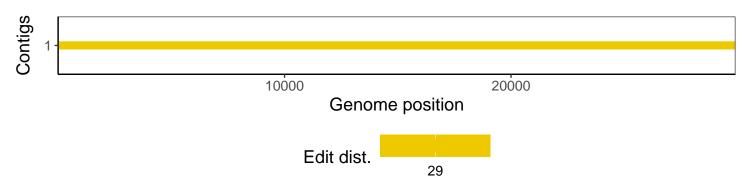
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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