COVID-19 subject UPHS-0108

2021-04-01

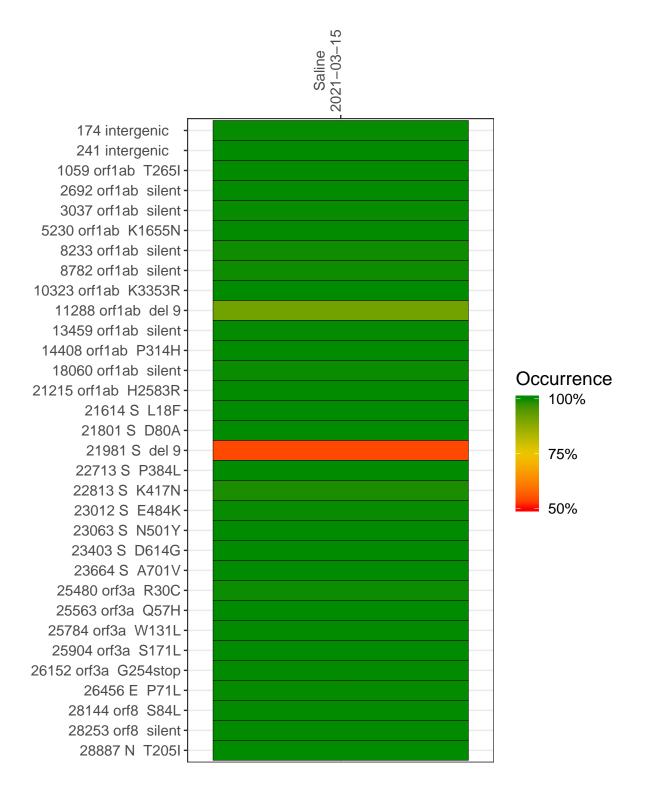
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1093-1	single experiment	NA	Saline	2021-03-15	21.97	B.1.351	99.1%	98.8%

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 2021-03-15

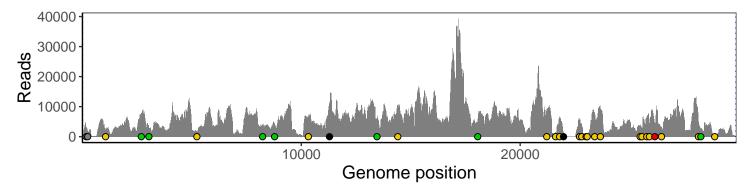
	2021-03-13
174 intergenic	3096
241 intergenic	1789
1059 orf1ab T265I	2357
2692 orf1ab silent	7538
3037 orf1ab silent	3008
5230 orf1ab K1655N	1652
8233 orf1ab silent	4052
8782 orf1ab silent	4256
10323 orf1ab K3353R	6442
11288 orf1ab del 9	9314
13459 orf1ab silent	5550
14408 orf1ab P314H	9978
18060 orf1ab silent	5542
21215 orf1ab H2583R	8546
21614 S L18F	1255
21801 S D80A	6329
21981 S del 9	1351
22713 S P384L	5671
22813 S K417N	3796
23012 S E484K	592
23063 S N501Y	609
23403 S D614G	8040
23664 S A701V	8501
25480 orf3a R30C	3619
25563 orf3a Q57H	2948
25784 orf3a W131L	6613
25904 orf3a S171L	4344
26152 orf3a G254stop	4707
26456 E P71L	3036
28144 orf8 S84L	5159
28253 orf8 silent	2360
28887 N T205I	376
	\sum_{i}



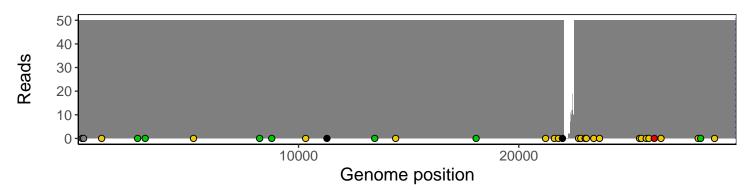
Analyses of individual experiments and composite results

$VSP1093\text{-}1 \mid 2021\text{-}03\text{-}15 \mid Saline \mid UPHS\text{-}0108 \mid genomes \mid single \ experiment$

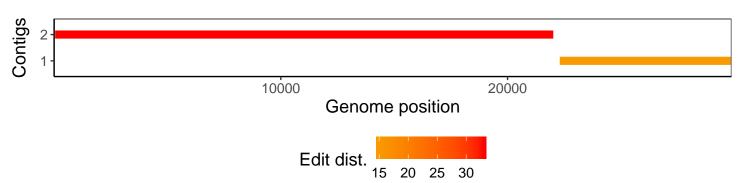
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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