COVID-19 subject UPHS-0744

2021-05-05

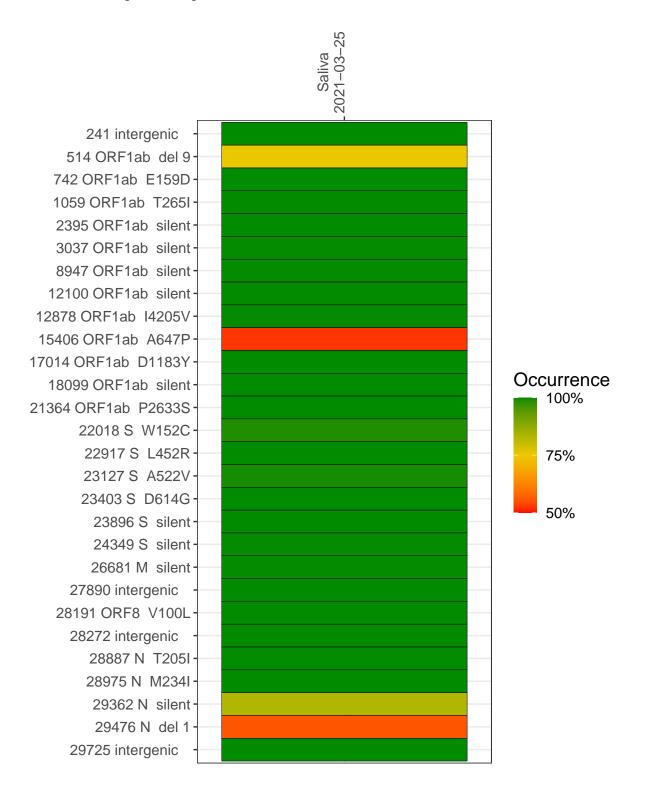
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1962-1	single experiment	NA	Saliva	2021-03-25	4.26	NA	84.7%	84.0%

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.



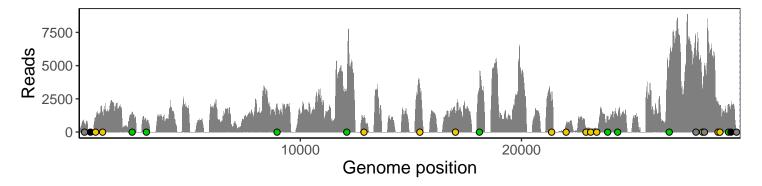
Saliva 2021-03-25

	2021-03-23
241 intergenic	594
514 ORF1ab del 9	125
742 ORF1ab E159D	820
1059 ORF1ab T265I	1250
2395 ORF1ab silent	1383
3037 ORF1ab silent	789
8947 ORF1ab silent	2130
12100 ORF1ab silent	2918
12878 ORF1ab I4205V	1122
15406 ORF1ab A647P	3324
17014 ORF1ab D1183Y	1403
18099 ORF1ab silent	3241
21364 ORF1ab P2633S	2479
22018 S W152C	564
22917 S L452R	264
23127 S A522V	181
23403 S D614G	241
23896 S silent	1126
24349 S silent	1009
26681 M silent	4392
27890 intergenic	5566
28191 ORF8 V100L	3540
28272 intergenic	4768
28887 N T205I	2234
28975 N M234I	1965
29362 N silent	2013
29476 N del 1	1867
29725 intergenic	16
	22-7
	SP1962-1
	R. A. C.

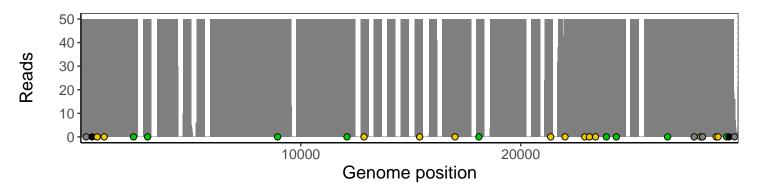
Analyses of individual experiments and composite results

VSP1962-1 | 2021-03-25 | Saliva | UPHS-0744 | genomes | single experiment

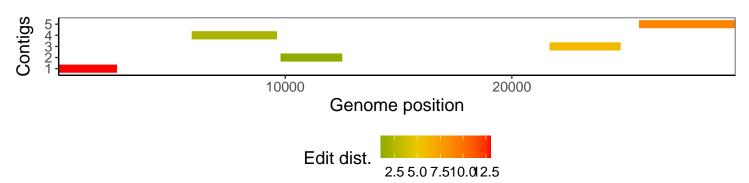
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.0.0
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