COVID-19 subject UPHS-0688

2021-06-23

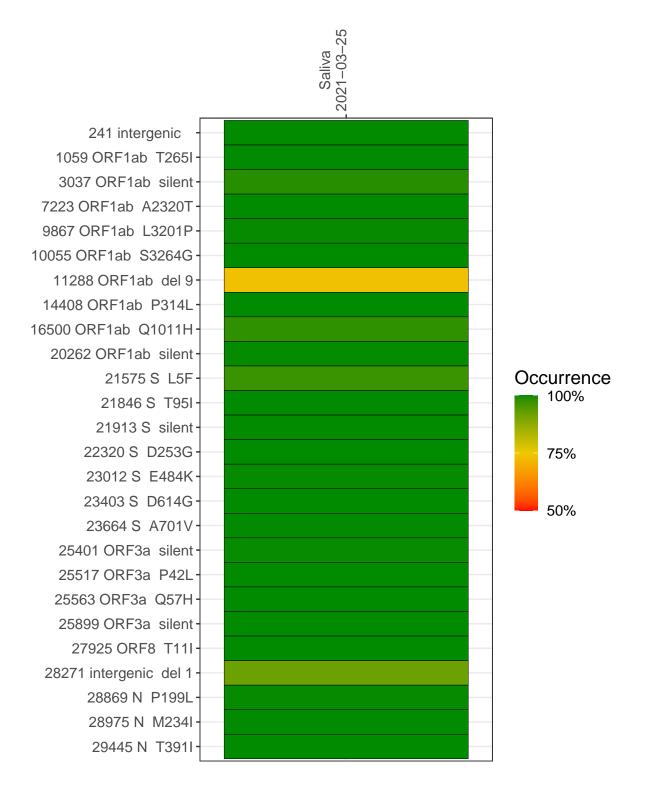
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1906-1	single experiment	NA	Saliva	2021-03-25	29.87	B.1.526	99.8%	99.7%

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.



Saliva 2021-03-25

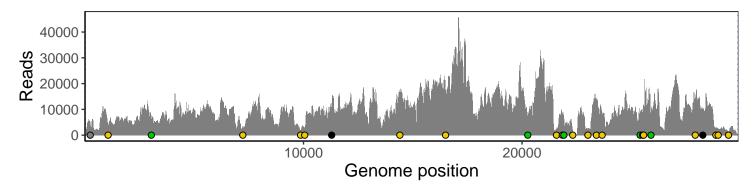
	2021-03-23
241 intergenic	4118
1059 ORF1ab T265I	3798
3037 ORF1ab silent	6423
7223 ORF1ab A2320T	3206
9867 ORF1ab L3201P	1395
10055 ORF1ab S3264G	2732
11288 ORF1ab del 9	6943
14408 ORF1ab P314L	15629
16500 ORF1ab Q1011H	15870
20262 ORF1ab silent	6717
21575 S L5F	2345
21846 S T95I	7750
21913 S silent	6645
22320 S D253G	1664
23012 S E484K	2023
23403 S D614G	13638
23664 S A701V	7824
25401 ORF3a silent	9049
25517 ORF3a P42L	8472
25563 ORF3a Q57H	11002
25899 ORF3a silent	8511
27925 ORF8 T11I	14221
28271 intergenic del 1	9627
28869 N P199L	2708
28975 N M234I	2460
29445 N T391I	1321
	VSP1906-1



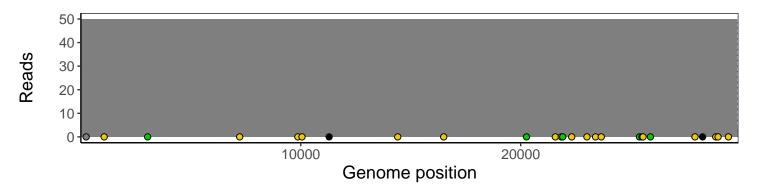
Analyses of individual experiments and composite results

$VSP1906\text{-}1 \mid 2021\text{-}03\text{-}25 \mid Saliva \mid UPHS\text{-}0688 \mid genomes \mid single \ experiment$

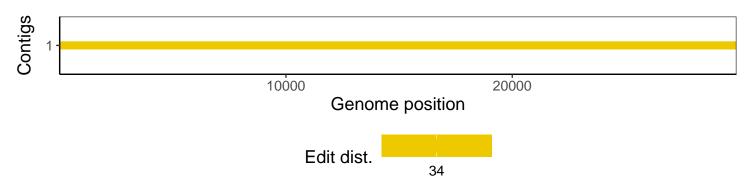
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	3.1.3
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	3.3.3
tidyverse	1.2.1
ShortRead	1.34.2
GenomicAlignments	1.12.2
${\bf Summarized Experiment}$	1.6.5
DelayedArray	0.2.7
matrixStats	0.54.0
Biobase	2.36.2
Rsamtools	1.28.0
GenomicRanges	1.28.6
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