COVID-19 subject UPHS-0704

2021-06-23

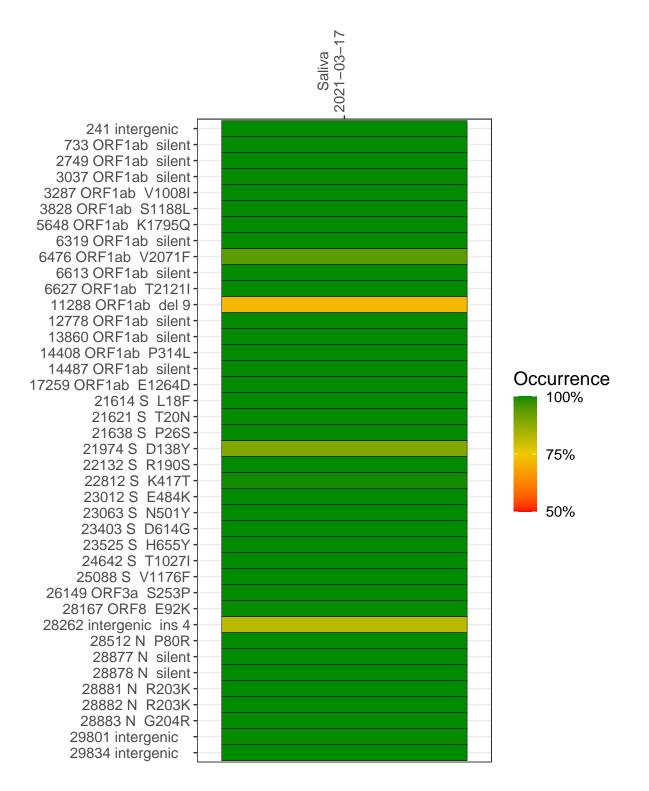
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1922-1	single experiment	NA	Saliva	2021-03-17	29.87	P.1	99.9%	99.8%

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 2021-03-17

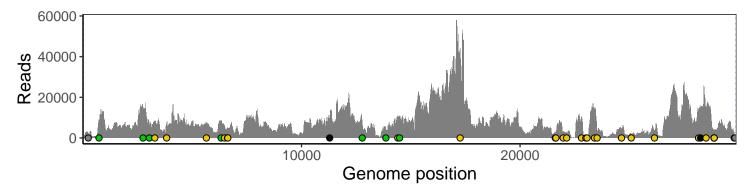
	2021-03-17
241 intergenic	2181
733 ORF1ab silent	8633
2749 ORF1ab silent	14184
3037 ORF1ab silent	6447
3287 ORF1ab V1008I	7534
3828 ORF1ab S1188L	7232
5648 ORF1ab K1795Q	6421
6319 ORF1ab silent	7872
6476 ORF1ab V2071F	5758
6613 ORF1ab silent	4913
6627 ORF1ab T2121I	4565
11288 ORF1ab del 9	6158
12778 ORF1ab silent	8252
13860 ORF1ab silent	4108
14408 ORF1ab P314L	9788
14487 ORF1ab silent	10406
17259 ORF1ab E1264D	40110
21614 S L18F	2692
21621 S T20N	2541
21638 S P26S	2712
21974 S D138Y 22132 S R190S	2448
22132 S K1903 22812 S K417T	2533 9529
23012 S K4171 23012 S E484K	773
23063 S N501Y	1103
23403 S D614G	14321
23525 S H655Y	2639
24642 S T1027I	4657
25088 S V1176F	1785
26149 ORF3a S253P	3682
28167 ORF8 E92K	11302
28262 intergenic ins 4	12415
28512 N P80R	14739
28877 N silent	1898
28878 N silent	1882
28881 N R203K	1882
28882 N R203K	1882
28883 N G204R	1907
29801 intergenic	1963
29834 intergenic	1024
	Ţ
	VSP1922-1
	27
	S/SI



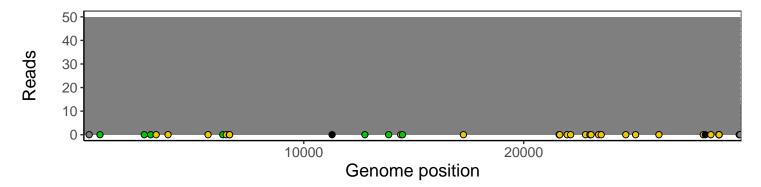
Analyses of individual experiments and composite results

VSP1922-1 | 2021-03-17 | Saliva | UPHS-0704 | genomes | single experiment

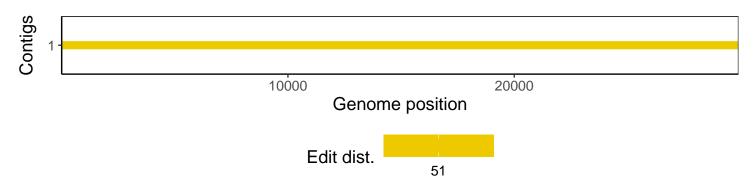
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	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