COVID-19 subject UPHS-0662

2021-06-23

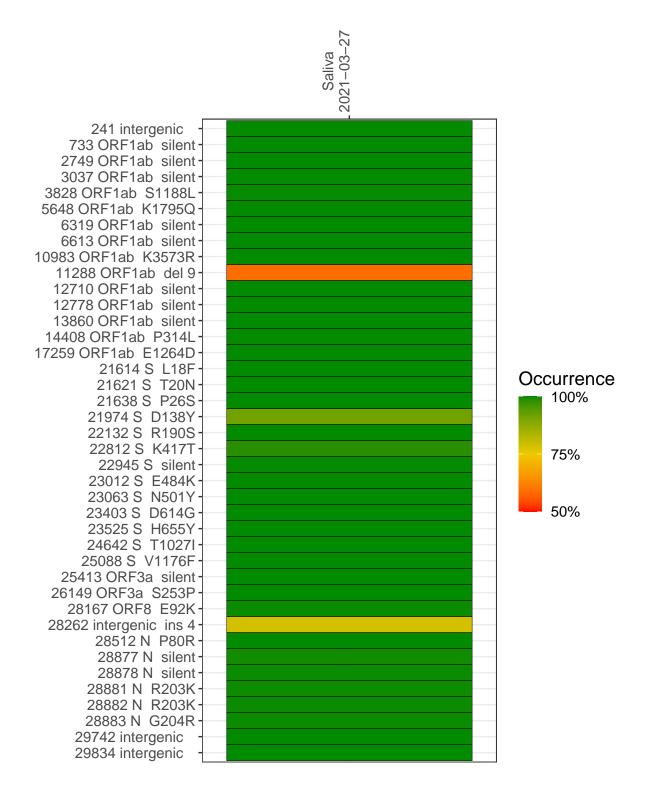
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1880-1	single experiment	NA	Saliva	2021-03-27	29.92	P.1	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 2021-03-27

	2021-03-27
241 intergenic	6440
733 ORF1ab silent	9204
2749 ORF1ab silent	15854
3037 ORF1ab silent	8567
3828 ORF1ab S1188L	5264
5648 ORF1ab K1795Q	14542
6319 ORF1ab silent	18887
6613 ORF1ab silent	15779
10983 ORF1ab K3573R	8505
11288 ORF1ab del 9	8087
12710 ORF1ab silent	17829
12778 ORF1ab silent	19775
13860 ORF1ab silent	11077
14408 ORF1ab P314L	10796
17259 ORF1ab E1264D	19553
21614 S L18F	5130
21621 S T20N	4967
21638 S P26S	5360
21974 S D138Y	2913
22132 S R190S	4409
22812 S K417T	7201
22945 S silent	1664
23012 S E484K	1432
23063 S N501Y	1912
23403 S D614G	12275
23525 S H655Y	9476
24642 S T1027I	7958
25088 S V1176F	7270
25413 ORF3a silent	9465
26149 ORF3a S253P	11061
28167 ORF8 E92K	6470
28262 intergenic ins 4	6616
28512 N P80R	10098
28877 N silent	1179
28878 N silent	1164
28881 N R203K	1164
28882 N R203K	1164
28883 N G204R	1182
29742 intergenic	3251
29834 intergenic	823
	0-1
	0

Base change

Expected

A

T

C

G

N

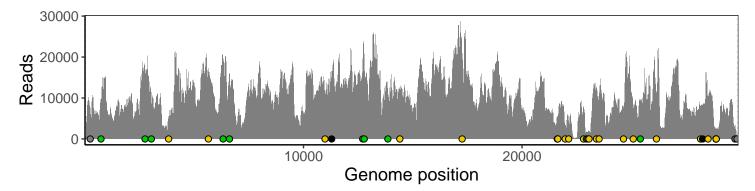
Ins/Del

No data

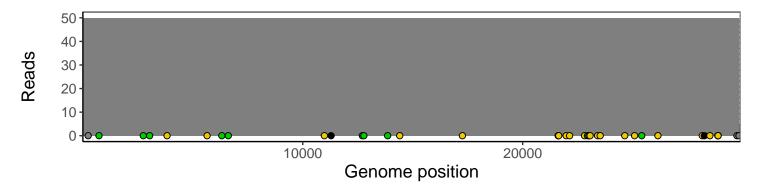
Analyses of individual experiments and composite results

VSP1880-1 | 2021-03-27 | Saliva | UPHS-0662 | genomes | single experiment

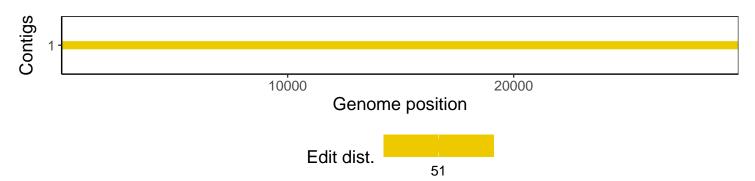
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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