COVID-19 subject UPHS-0804

2021-06-23

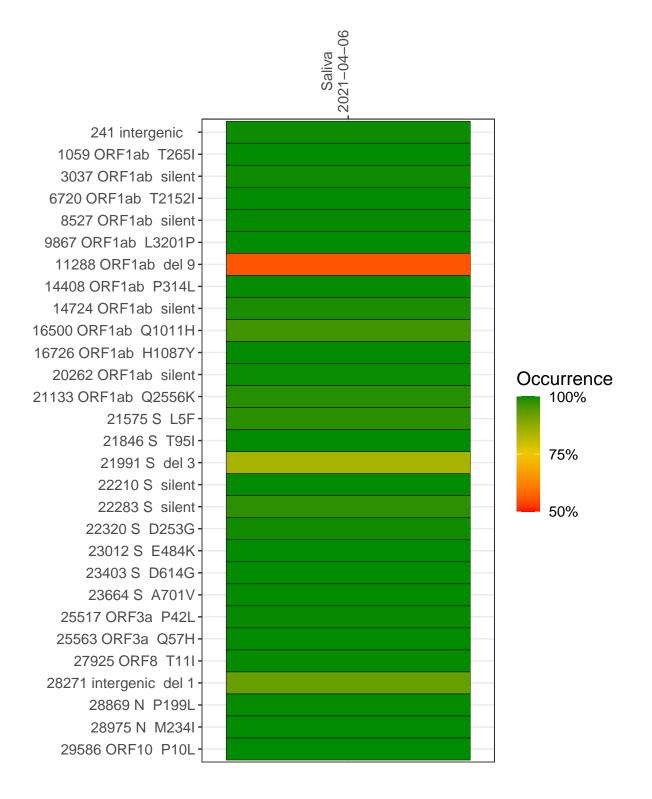
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP2018-2	single experiment	NA	Saliva	2021-04-06	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.



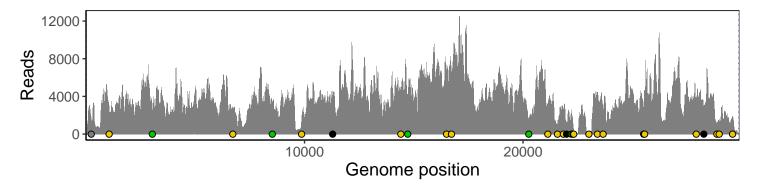
Saliva 2021–04–06

	2021-04-06
241 intergenic	1559
1059 ORF1ab T265I	2703
3037 ORF1ab silent	2664
6720 ORF1ab T2152I	2877
8527 ORF1ab silent	3301
9867 ORF1ab L3201P	1336
11288 ORF1ab del 9	2134
14408 ORF1ab P314L	4064
14724 ORF1ab silent	3433
16500 ORF1ab Q1011H	6832
16726 ORF1ab H1087Y	6676
20262 ORF1ab silent	1516
21133 ORF1ab Q2556K	3074
21575 S L5F	1037
21846 S T95I	2394
21991 S del 3	1019
22210 S silent	2114
22283 S silent	1107
22320 S D253G	449
23012 S E484K	177
23403 S D614G	4357
23664 S A701V	2599
25517 ORF3a P42L	2720
25563 ORF3a Q57H	4638
27925 ORF8 T11I	3548
28271 intergenic del 1	2926
28869 N P199L	1155
28975 N M234I	1538
29586 ORF10 P10L	1788
	}-2
	3103
	VSP2018-2
	>

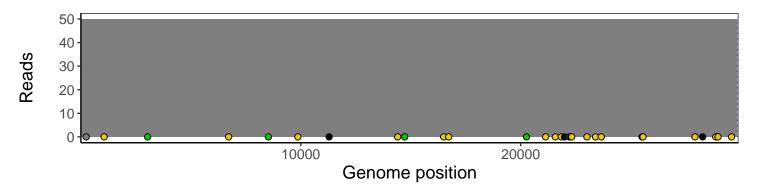
Analyses of individual experiments and composite results

$VSP2018-2\mid 2021-04-06\mid Saliva\mid UPHS-0804\mid genomes\mid single\ experiment$

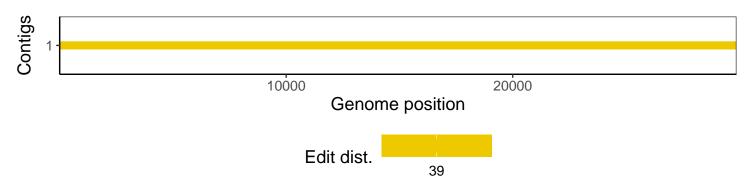
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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