COVID-19 subject UPHS-0679

2021-06-23

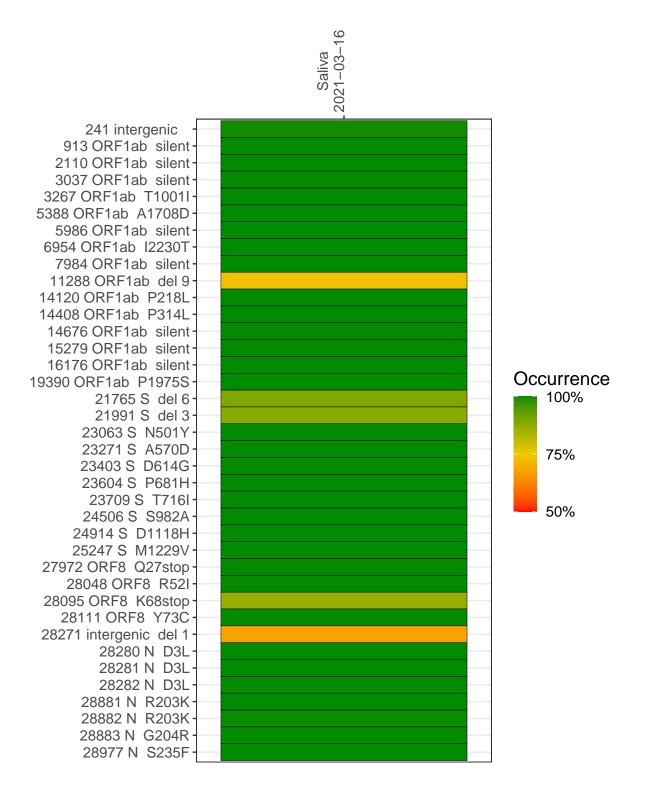
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1897-1	single experiment	NA	Saliva	2021-03-16	29.82	B.1.1.7	99.8%	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 2021-03-16

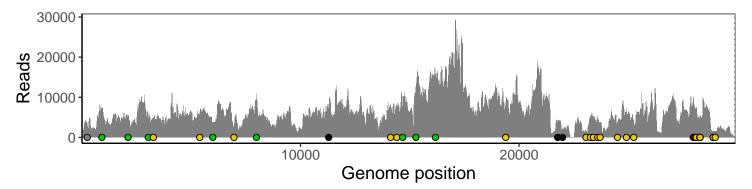
	202. 00 .0
241 intergenic	2982
913 ORF1ab silent	6639
2110 ORF1ab silent	4918
3037 ORF1ab silent	4806
3267 ORF1ab T1001I	4958
5388 ORF1ab A1708D	5536
5986 ORF1ab silent	3595
6954 ORF1ab I2230T	2426
7984 ORF1ab silent	10062
11288 ORF1ab del 9	4667
14120 ORF1ab P218L	7624
14408 ORF1ab P314L	7197
14676 ORF1ab silent	7153
15279 ORF1ab silent	10912
16176 ORF1ab silent	15365
19390 ORF1ab P1975S	8504
21765 S del 6	3025
21991 S del 3	1887
23063 S N501Y	1635
23271 S A570D	4700
23403 S D614G	5089
23604 S P681H	4653
23709 S T716I	3644
24506 S S982A	3921
24914 S D1118H	6848
25247 S M1229V	4519
27972 ORF8 Q27stop	9745
28048 ORF8 R52I	6480
28095 ORF8 K68stop	7215
28111 ORF8 Y73C	6967
28271 intergenic del 1	4254
28280 N D3L	2771
28281 N D3L	2771
28282 N D3L	2983
28881 N R203K	1035
28882 N R203K	1032
28883 N G204R	1037
28977 N S235F	1522
	7
	<u> </u>

Base change

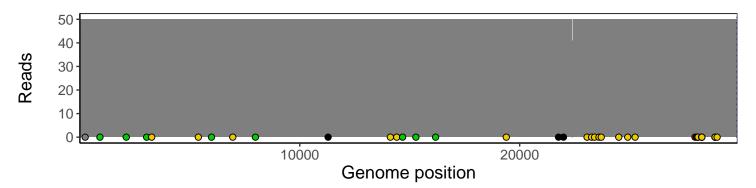
Analyses of individual experiments and composite results

VSP1897-1 | 2021-03-16 | Saliva | UPHS-0679 | genomes | single experiment

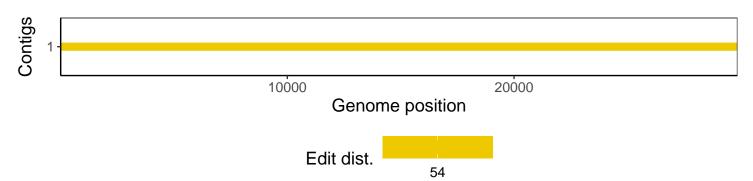
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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				