COVID-19 subject UPHS-1657

2021-06-23

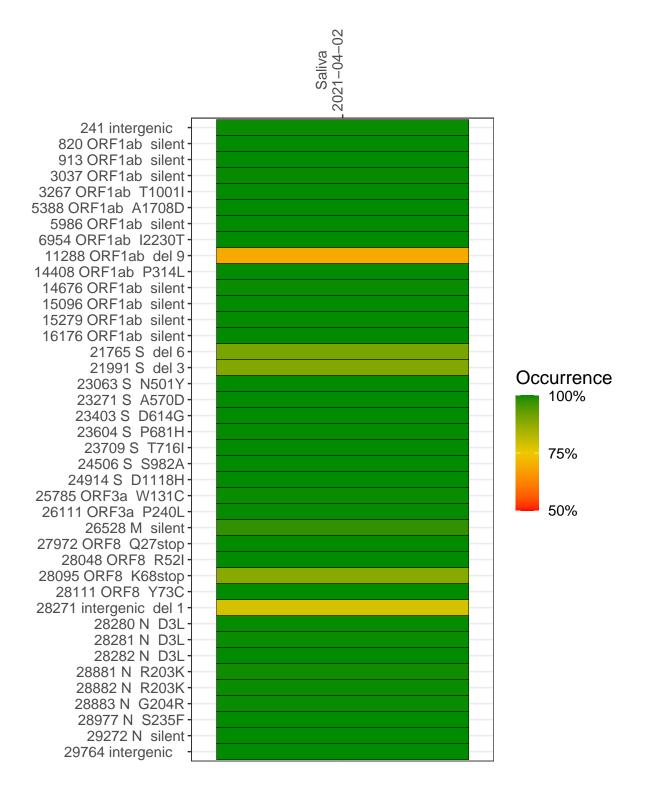
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP2958-1	single experiment	NA	Saliva	2021-04-02	29.82	B.1.1.7	99.9%	99.8%

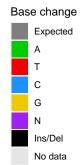
Variants shared across samples

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 2021-04-02

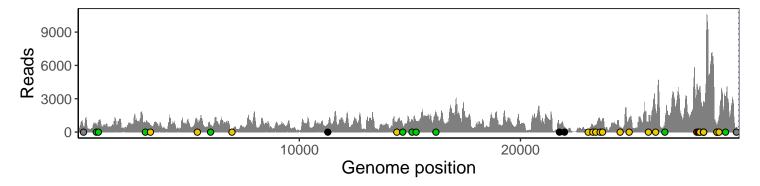
	2021-04-02
241 intergenic	460
820 ORF1ab silent	789
913 ORF1ab silent	849
3037 ORF1ab silent	750
3267 ORF1ab T1001I	663
5388 ORF1ab A1708D	886
5986 ORF1ab silent	549
6954 ORF1ab I2230T	92
11288 ORF1ab del 9	401
14408 ORF1ab P314L	781
14676 ORF1ab silent	515
15096 ORF1ab silent	1075
15279 ORF1ab silent	916
16176 ORF1ab silent	1744
21765 S del 6	586
21991 S del 3	389
23063 S N501Y	225
23271 S A570D	626
23403 S D614G	608
23604 S P681H	1087
23709 S T716I	1132
24506 S S982A	477
24914 S D1118H	1204
25785 ORF3a W131C	859
26111 ORF3a P240L	2028
26528 M silent	550
27972 ORF8 Q27stop	4156
28048 ORF8 R52I	3225
28095 ORF8 K68stop	4000
28111 ORF8 Y73C	3893
28271 intergenic del 1	2072
28280 N D3L	1576
28281 N D3L	1576
28282 N D3L	1660
28881 N R203K	458
28882 N R203K	454
28883 N G204R	456
28977 N S235F	1295
29272 N silent	3217
29764 intergenic	440
	-
	VSP2958-1
	26
	/SF
	>



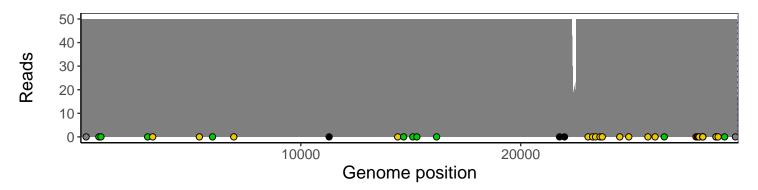
Analyses of individual experiments and composite results

$VSP2958-1 \mid 2021-04-02 \mid Saliva \mid UPHS-1657 \mid genomes \mid single \; experiment$

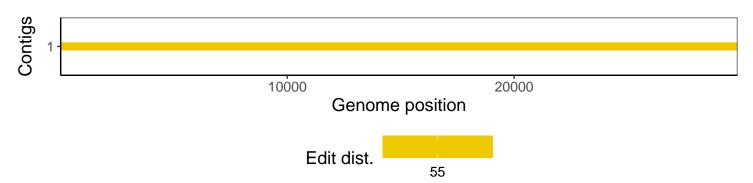
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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