COVID-19 subject UPHS-0727

2021-06-23

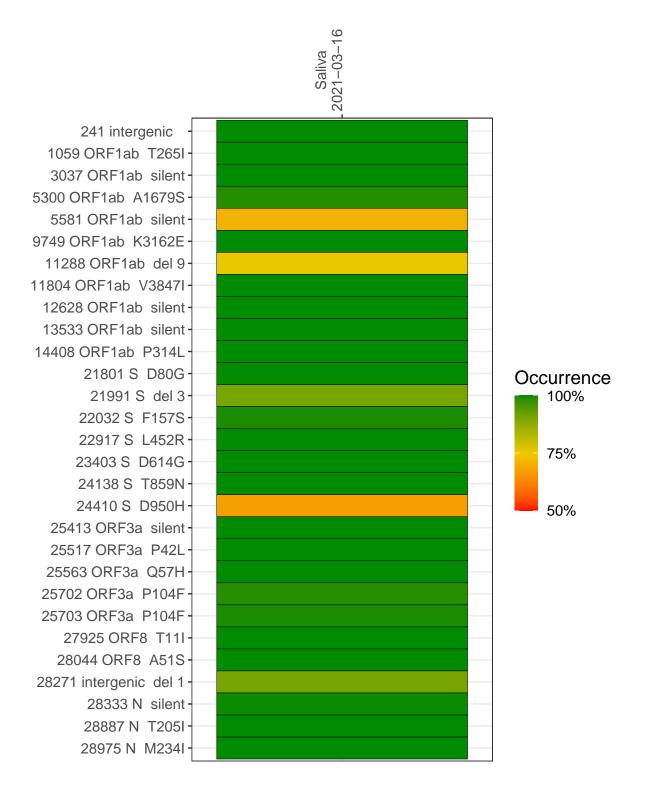
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1945-1	single experiment	NA	Saliva	2021-03-16	20.37	B.1	98.3%	98.2%

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

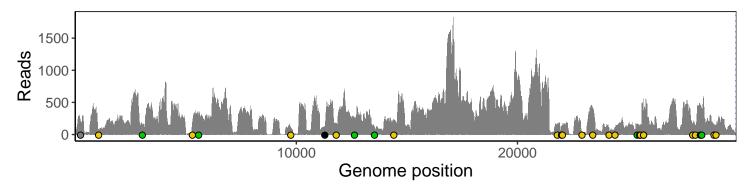
	2021-03-16
241 intergenic	207
1059 ORF1ab T265I	65
3037 ORF1ab silent	130
5300 ORF1ab A1679S	168
5581 ORF1ab silent	272
9749 ORF1ab K3162E	108
11288 ORF1ab del 9	68
11804 ORF1ab V3847I	147
12628 ORF1ab silent	255
13533 ORF1ab silent	110
14408 ORF1ab P314L	216
21801 S D80G	157
21991 S del 3	112
22032 S F157S	127
22917 S L452R	20
23403 S D614G	416
24138 S T859N	104
24410 S D950H	115
25413 ORF3a silent	149
25517 ORF3a P42L	133
25563 ORF3a Q57H	154
25702 ORF3a P104F	289
25703 ORF3a P104F	285
27925 ORF8 T11I	178
28044 ORF8 A51S	136
28271 intergenic del 1	431
28333 N silent	376
28887 N T205I	142
28975 N M234I	151
	7
	1945
	VSP1945-1
	>



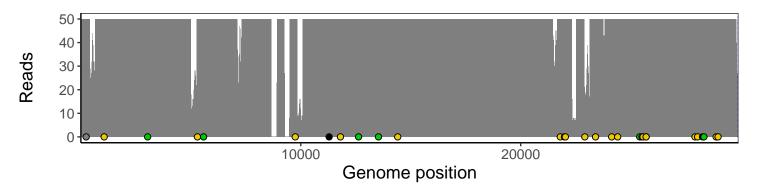
Analyses of individual experiments and composite results

VSP1945-1 | 2021-03-16 | Saliva | UPHS-0727 | genomes | single experiment

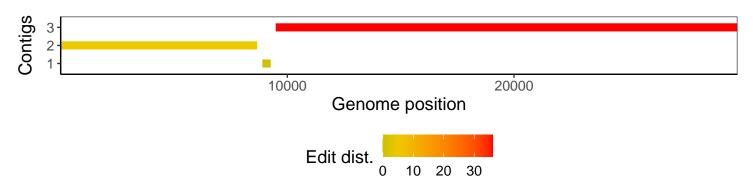
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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