COVID-19 subject UPHS-0699

2021-04-20

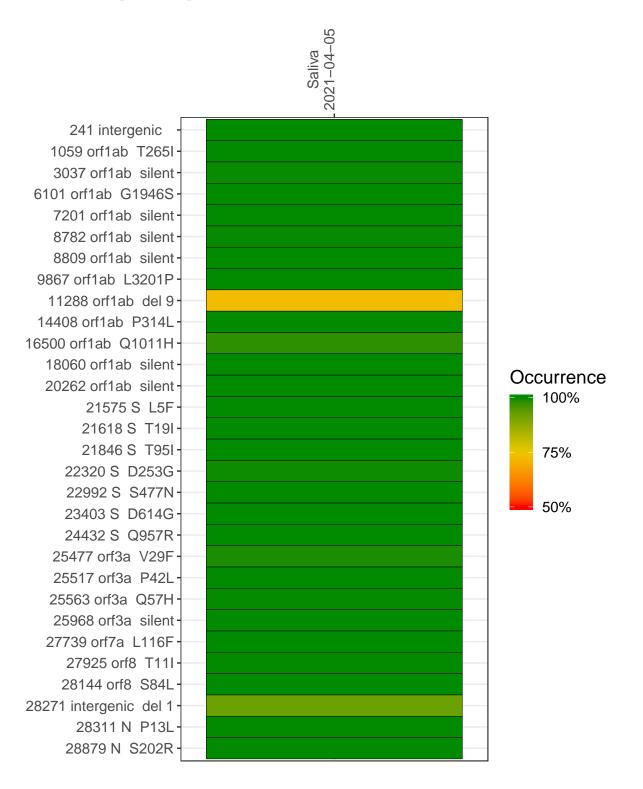
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with > 90% sequence coverage.

Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1917-1	single experiment	NA	Saliva	2021-04-05	15.76	B.1.526.2	96.9%	96.8%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/USA-WA1-2020) 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 2021-04-05

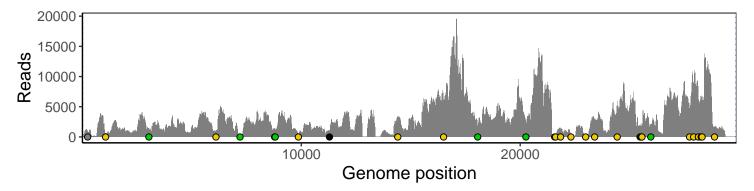
	2021 01 00
241 intergenic	851
1059 orf1ab T265I	505
3037 orf1ab silent	1202
6101 orf1ab G1946S	942
7201 orf1ab silent	400
8782 orf1ab silent	1355
8809 orf1ab silent	1096
9867 orf1ab L3201P	316
11288 orf1ab del 9	617
14408 orf1ab P314L	3009
16500 orf1ab Q1011H	5650
18060 orf1ab silent	1828
20262 orf1ab silent	2371
21575 S L5F	141
21618 S T19I	164
21846 S T95I	1242
22320 S D253G	310
22992 S S477N	357
23403 S D614G	2968
24432 S Q957R	4793
25477 orf3a V29F	1785
25517 orf3a P42L	1670
25563 orf3a Q57H	2114
25968 orf3a silent	1766
27739 orf7a L116F	4099
27925 orf8 T11I	8923
28144 orf8 S84L	6339
28271 intergenic del 1	6122
28311 N P13L	6404
28879 N S202R	1727
	<u>\</u>



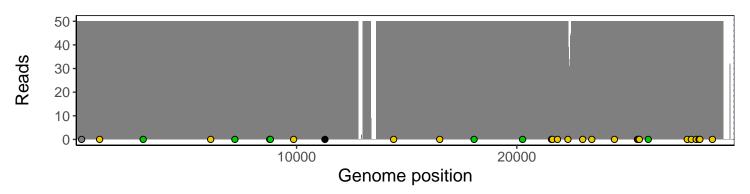
Analyses of individual experiments and composite results

VSP1917-1 | 2021-04-05 | Saliva | UPHS-0699 | genomes | single experiment

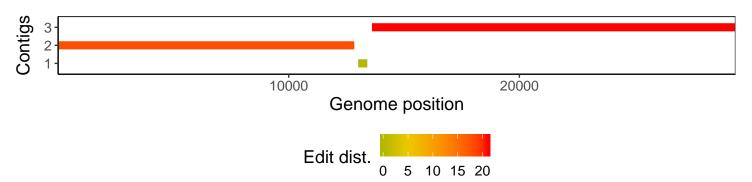
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.8
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	3.0.0
tidyverse	1.2.1
ShortRead	1.34.2
${\it Genomic Alignments}$	1.12.2
SummarizedExperiment	1.6.5
DelayedArray	0.2.7
matrixStats	0.54.0
Biobase	2.36.2
Rsamtools	1.28.0
GenomicRanges	1.28.6
$\operatorname{GenomeInfoDb}$	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