COVID-19 subject UPHS- 0788

2021-06-23

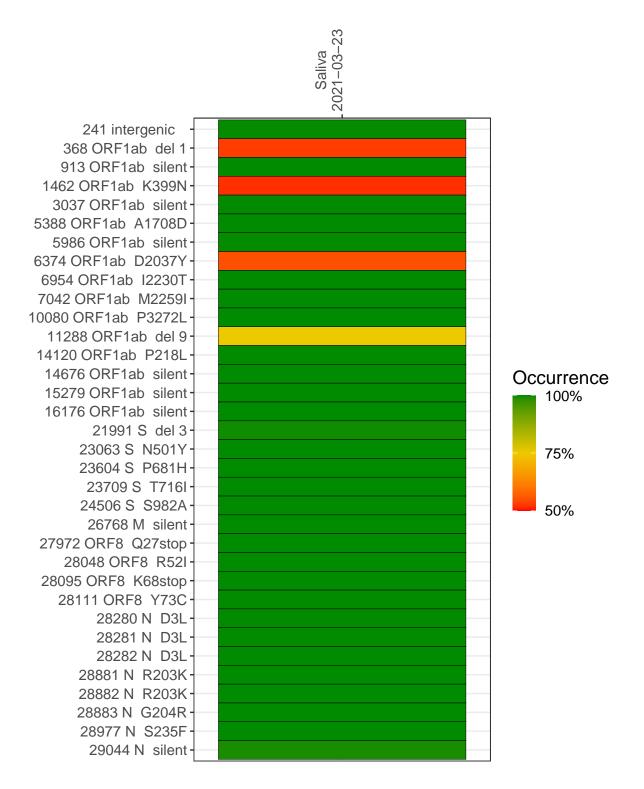
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP1905-1	single experiment	NA	Saliva	2021-03-23	1.95	NA	69.2%	68.0%

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.



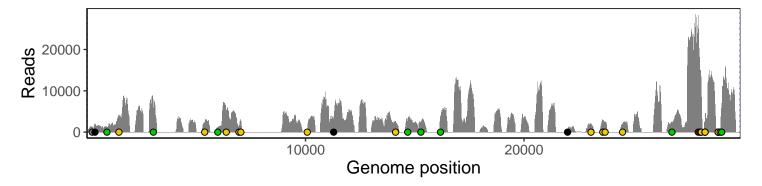
Saliva 2021-03-23

	2021-03-23
241 intergenic	1129
368 ORF1ab del 1	1992
913 ORF1ab silent	1142
1462 ORF1ab K399N	4237
3037 ORF1ab silent	6444
5388 ORF1ab A1708D	2240
5986 ORF1ab silent	990
6374 ORF1ab D2037Y	5305
6954 ORF1ab I2230T	1250
7042 ORF1ab M2259I	2866
10080 ORF1ab P3272L	162
11288 ORF1ab del 9	2142
14120 ORF1ab P218L	2479
14676 ORF1ab silent	2402
15279 ORF1ab silent	2133
16176 ORF1ab silent	3744
21991 S del 3	544
23063 S N501Y	2070
23604 S P681H	2845
23709 S T716I	2463
24506 S S982A	2017
26768 M silent	2363
27972 ORF8 Q27stop	26422
28048 ORF8 R52I	13709
28095 ORF8 K68stop	13325
28111 ORF8 Y73C	9809
28280 N D3L	2430
28281 N D3L	2430
28282 N D3L	2539
28881 N R203K	451
28882 N R203K	449
28883 N G204R	451
28977 N S235F	613
29044 N silent	6505
	1905–1
	190

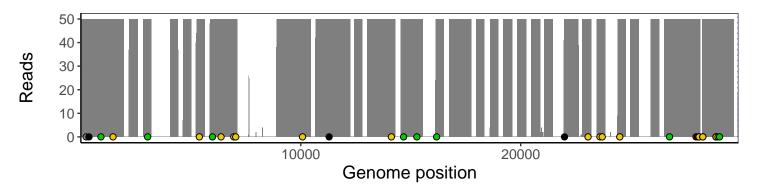
Analyses of individual experiments and composite results

VSP1905-1 | 2021-03-23 | Saliva | UPHS-0788 | genomes | single experiment

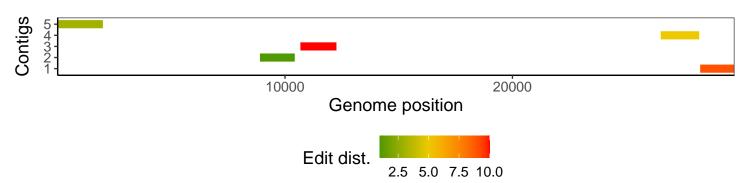
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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