COVID-19 subject 459

2021-05-05

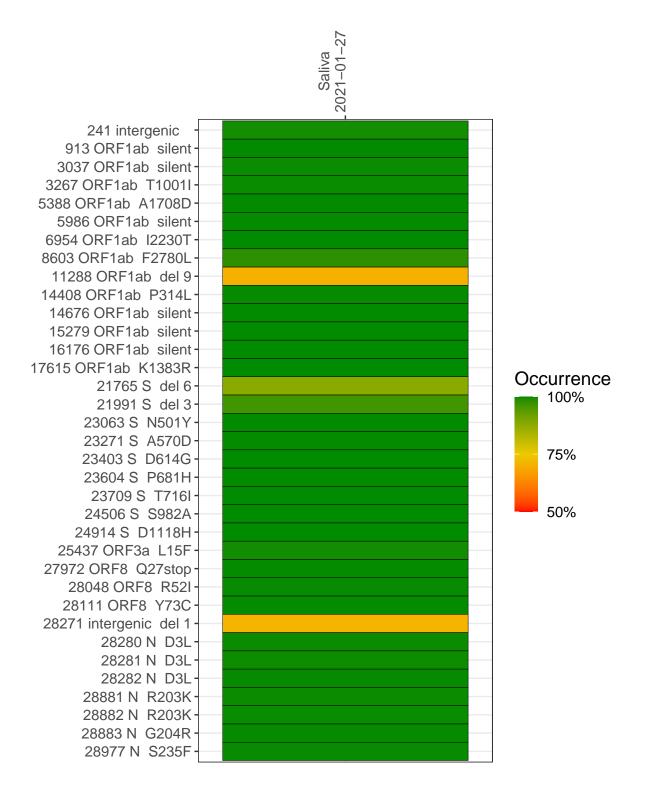
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP0654-1	single experiment	NA	Saliva	2021-01-27	29.86	B.1.1.7	100.0%	99.9%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/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 2021-01-27

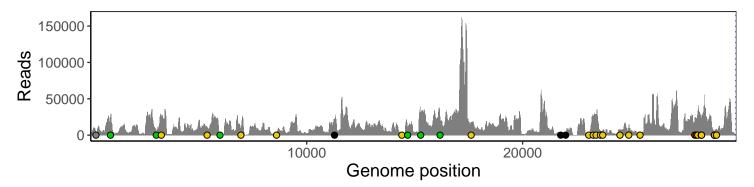
	2021-01-21
241 intergenic	5055
913 ORF1ab silent	24395
3037 ORF1ab silent	5755
3267 ORF1ab T1001I	28600
5388 ORF1ab A1708D	10365
5986 ORF1ab silent	1081
6954 ORF1ab I2230T	8948
8603 ORF1ab F2780L	1365
11288 ORF1ab del 9	13462
14408 ORF1ab P314L	1436
14676 ORF1ab silent	10356
15279 ORF1ab silent	29968
16176 ORF1ab silent	24112
17615 ORF1ab K1383R	16251
21765 S del 6	1183
21991 S del 3	3857
23063 S N501Y	1232
23271 S A570D	23194
23403 S D614G	27638
23604 S P681H	5795
23709 S T716I	5547
24506 S S982A	8408
24914 S D1118H	14446
25437 ORF3a L15F	4301
27972 ORF8 Q27stop	24242
28048 ORF8 R52I	18808
28111 ORF8 Y73C	33131
28271 intergenic del 1	22522
28280 N D3L	15320
28281 N D3L	15320
28282 N D3L	16582
28881 N R203K	4152
28882 N R203K	4129
28883 N G204R	4141
28977 N S235F	8185
	<u>T</u>
	4



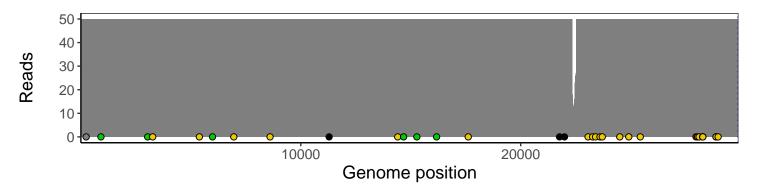
Analyses of individual experiments and composite results

VSP0654-1 | 2021-01-27 | Saliva | 459s | genomes | single experiment

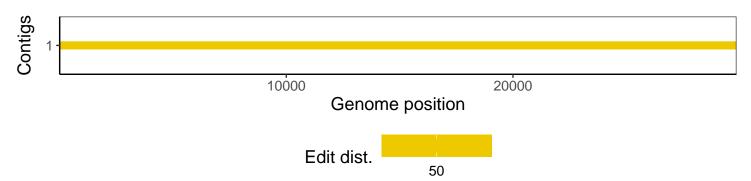
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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