COVID-19 subject PQ-Seq19

2021-03-01

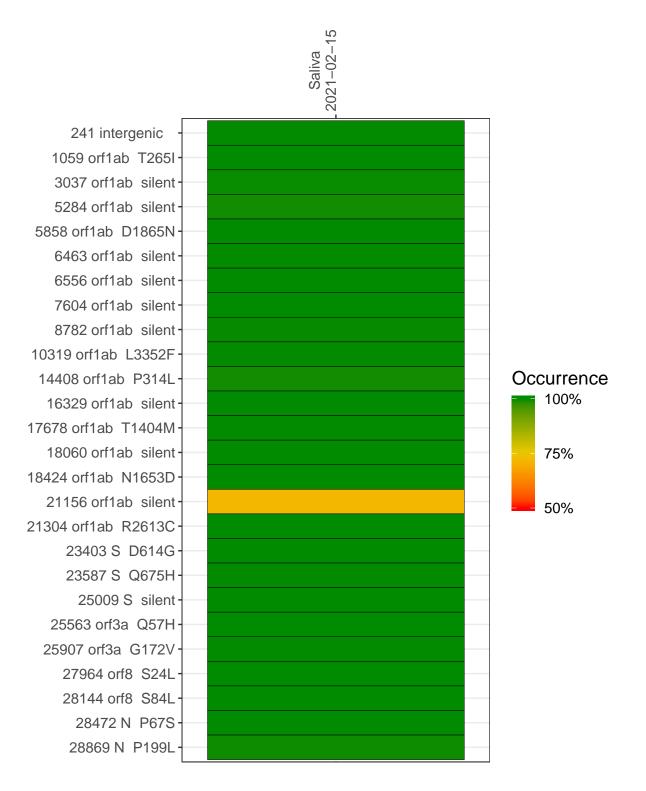
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP0846-1	single experiment	NA	Saliva	2021-02-15	29.76	B.1.2	99.8%	99.7%

Variants shared across samples

The heat map below shows how variants (reference genome 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 2021–02–15

	2021-02-13
241 intergenic	12626
1059 orf1ab T265I	3966
3037 orf1ab silent	4253
5284 orf1ab silent	2188
5858 orf1ab D1865N	14541
6463 orf1ab silent	9892
6556 orf1ab silent	8144
7604 orf1ab silent	6446
8782 orf1ab silent	8251
10319 orf1ab L3352F	14219
14408 orf1ab P314L	14056
16329 orf1ab silent	10247
17678 orf1ab T1404M	10252
18060 orf1ab silent	3818
18424 orf1ab N1653D	20741
21156 orf1ab silent	1116
21304 orf1ab R2613C	1742
23403 S D614G	13438
23587 S Q675H	10146
25009 S silent	5845
25563 orf3a Q57H	9478
25907 orf3a G172V	5100
27964 orf8 S24L	6505
28144 orf8 S84L	9115
28472 N P67S	15451
28869 N P199L	1906
	<u>\</u>

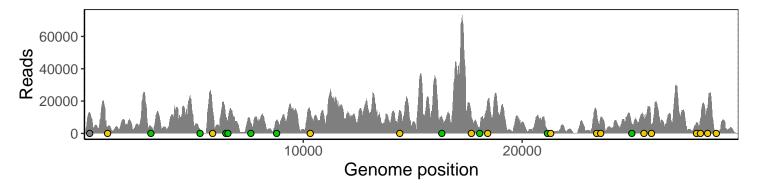


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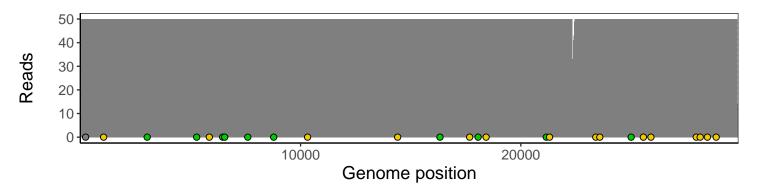
Analyses of individual experiments and composite results

$VSP0846\text{-}1 \mid 2021\text{-}02\text{-}15 \mid Saliva \mid PQ\text{-}Seq19 \mid genomes \mid single \ experiment$

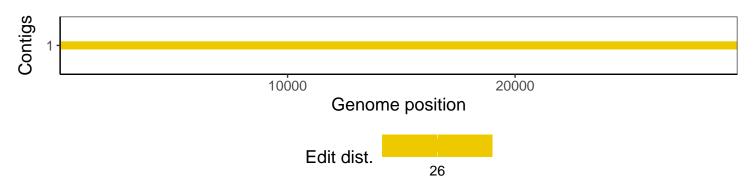
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.3
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	3.0.0
tidyverse	1.2.1
ShortRead	1.34.2
$\operatorname{GenomicAlignments}$	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