COVID-19 subject MPCluster2-Seq15

2021-03-04

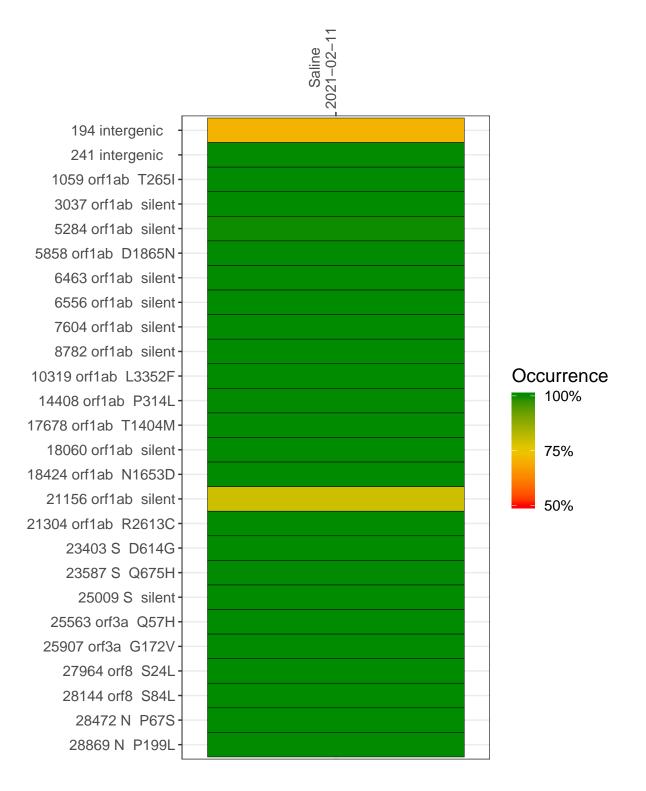
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP0807-1	single experiment	NA	Saline	2021-02-11	29.82	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.



Saline 2021–02–11

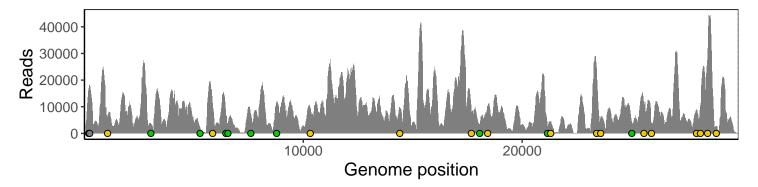
	2021-02-11
194 intergenic	16672
241 intergenic	17284
1059 orf1ab T265I	6263
3037 orf1ab silent	3530
5284 orf1ab silent	2210
5858 orf1ab D1865N	10425
6463 orf1ab silent	7353
6556 orf1ab silent	3736
7604 orf1ab silent	7005
8782 orf1ab silent	11545
10319 orf1ab L3352F	9579
14408 orf1ab P314L	9456
17678 orf1ab T1404M	8328
18060 orf1ab silent	3015
18424 orf1ab N1653D	10454
21156 orf1ab silent	2628
21304 orf1ab R2613C	4259
23403 S D614G	23924
23587 S Q675H	6072
25009 S silent	3876
25563 orf3a Q57H	11302
25907 orf3a G172V	3665
27964 orf8 S24L	8765
28144 orf8 S84L	10300
28472 N P67S	27871
28869 N P199L	2643
	<u></u>



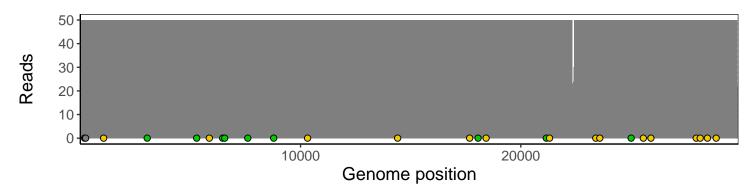
Analyses of individual experiments and composite results

$VSP0807\text{-}1 \mid 2021\text{-}02\text{-}11 \mid Saline \mid MPCluster2\text{-}Seq15 \mid genomes \mid single \ experiment$

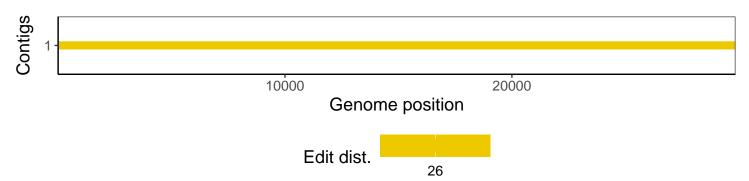
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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