

COVID-19 subject MPCluster2-Seq11

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	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0769-1	single experiment	NA	Swab	2021-02-01	29.82	B.1.234	99.8%	99.7%

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.



Swab
2021-02-01

241 intergenic	11704
1738 ORF1ab silent	10095
2258 ORF1ab V665I	2848
3037 ORF1ab silent	6166
4596 ORF1ab T1444N	11372
5812 ORF1ab silent	17716
6441 ORF1ab K2059R	15584
8140 ORF1ab silent	12264
9204 ORF1ab D2980G	6335
14408 ORF1ab P314L	12669
20268 ORF1ab silent	1936
21575 S L5F	1891
23202 S T547K	7900
23403 S D614G	17692
28854 N S194L	1761
29384 N D371Y	1697
29445 N T391I	2357

Base change

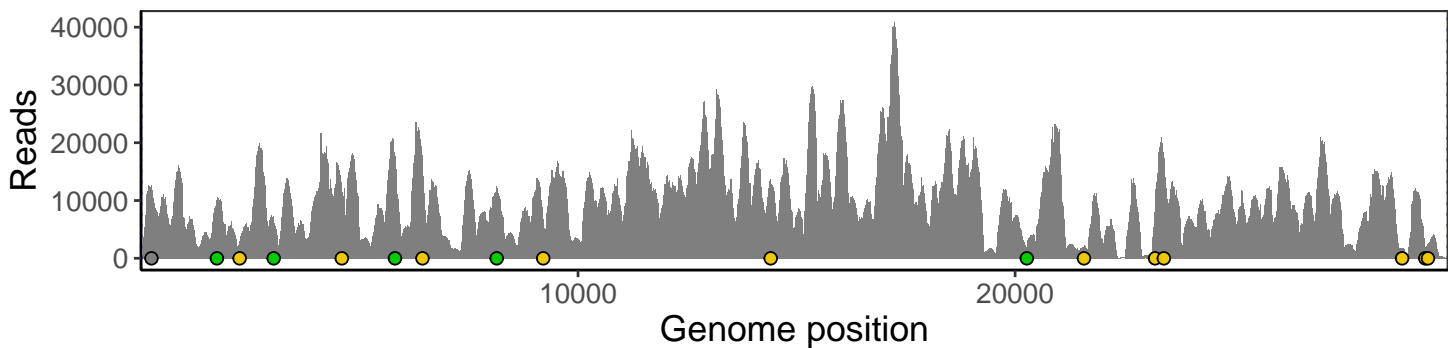


VSP0769-1

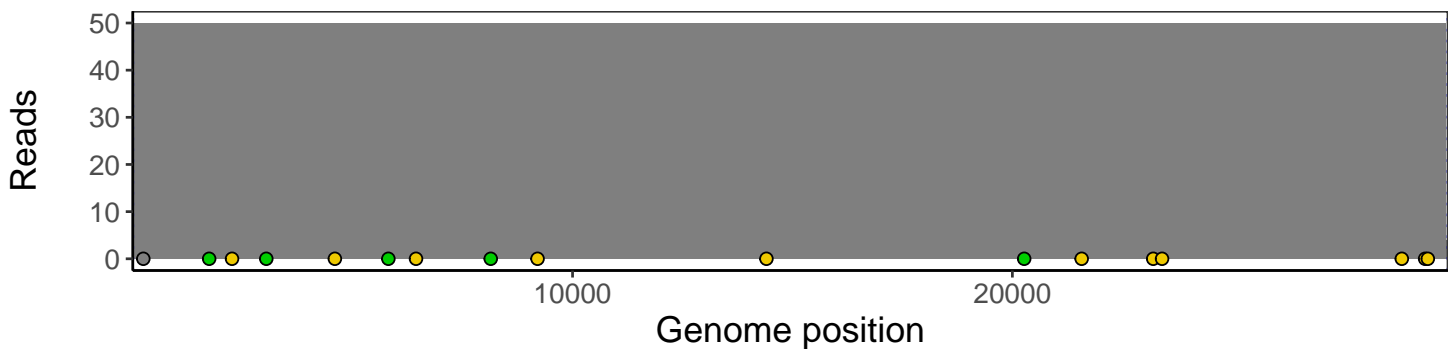
Analyses of individual experiments and composite results

VSP0769-1 | 2021-02-01 | Swab | MPCluster2-Seq11 | genomes | single experiment

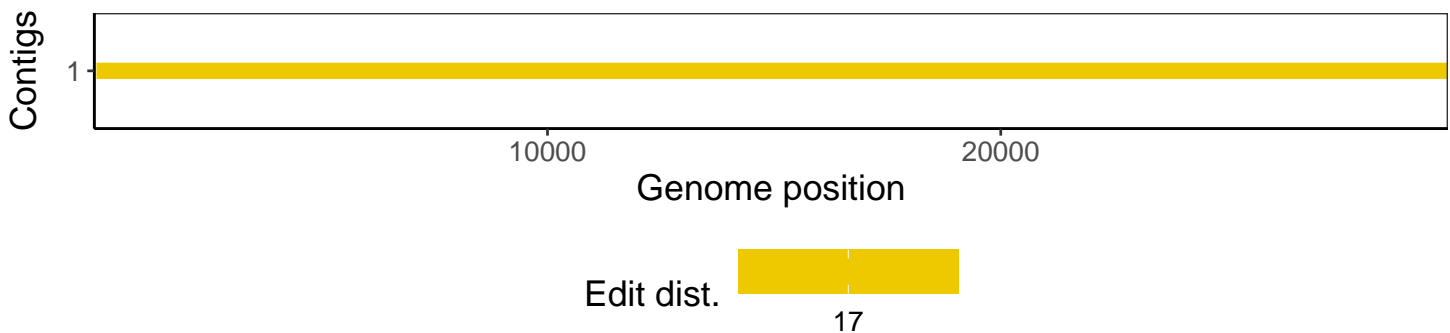
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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 htlib 1.10
bcftools	1.10.2-34-g1a12af0-dirty Using htlib 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
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
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