

COVID-19 subject molpath-seq1

2021-02-02

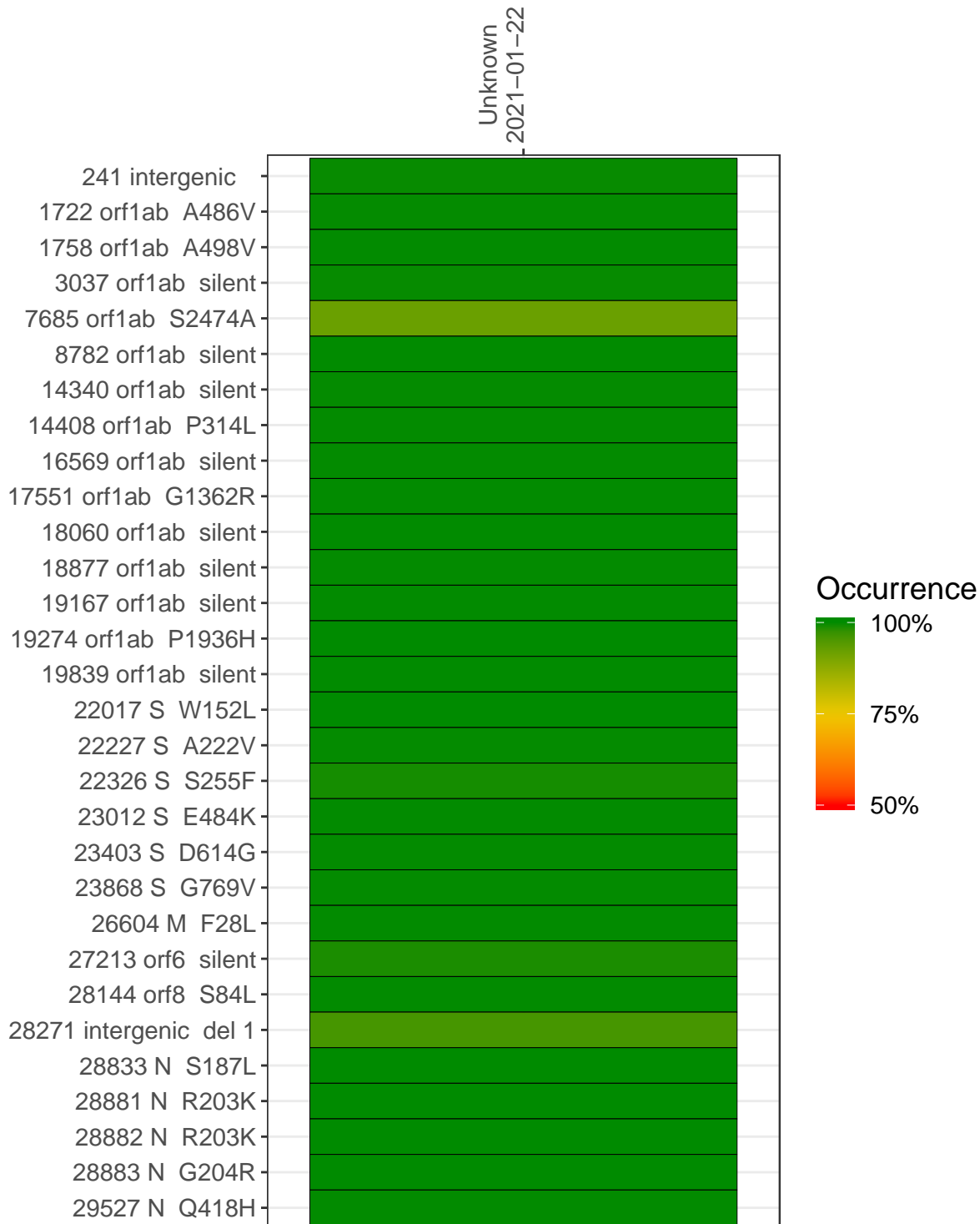
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP0626	composite	NA	Unknown	2021-01-22	20.39	B.1.1	99.7%	99.1%
VSP0626-1	single experiment	NA	Unknown	2021-01-22	21.48	B.1.1	99.0%	99.0%
VSP0626-2	single experiment	NA	Unknown	2021-01-22	20.65	B.1.1	99.7%	99.1%

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.



Unknown
2021-01-22

241 intergenic	4295	13592
1722 orf1ab A486V	4756	7711
1758 orf1ab A498V	4963	8456
3037 orf1ab silent	3048	10175
7685 orf1ab S2474A	854	4613
8782 orf1ab silent	2119	6693
14340 orf1ab silent	4275	11546
14408 orf1ab P314L	5238	15444
16569 orf1ab silent	560	3808
17551 orf1ab G1362R	7597	22681
18060 orf1ab silent	2556	6706
18877 orf1ab silent	6310	25467
19167 orf1ab silent	4156	20668
19274 orf1ab P1936H	1436	7513
19839 orf1ab silent	1775	7250
22017 S W152L	619	752
22227 S A222V	1403	2339
22326 S S255F	153	351
23012 S E484K	2064	6336
23403 S D614G	6662	19780
23868 S G769V	2114	4865
26604 M F28L	4322	9342
27213 orf6 silent	1889	8842
28144 orf8 S84L	3458	8155
28271 intergenic del 1	4332	13296
28833 N S187L	519	2116
28881 N R203K	449	1886
28882 N R203K	446	1884
28883 N G204R	448	1885
29527 N Q418H	485	4825

Base change

- Expected
- A
- T
- C
- G
- N
- Ins/Del
- No data

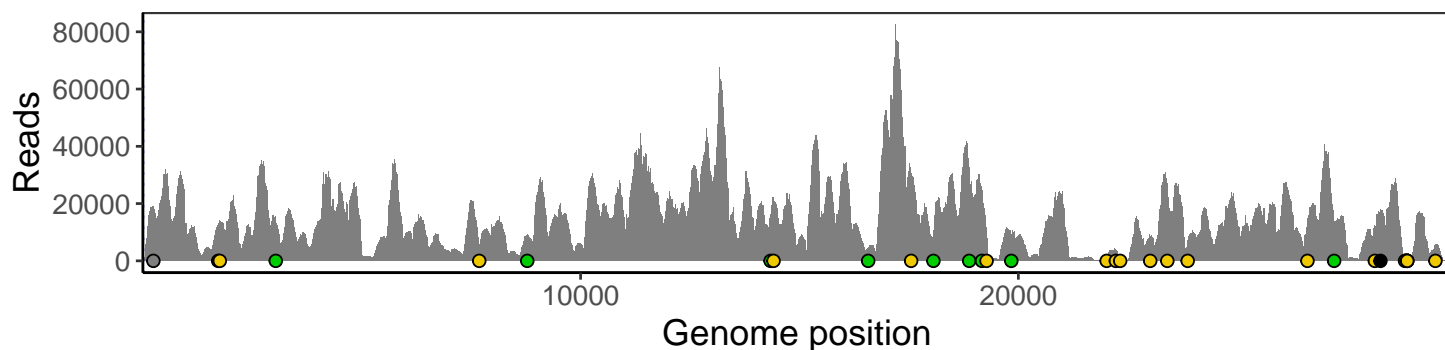
VSP0626-1

VSP0626-2

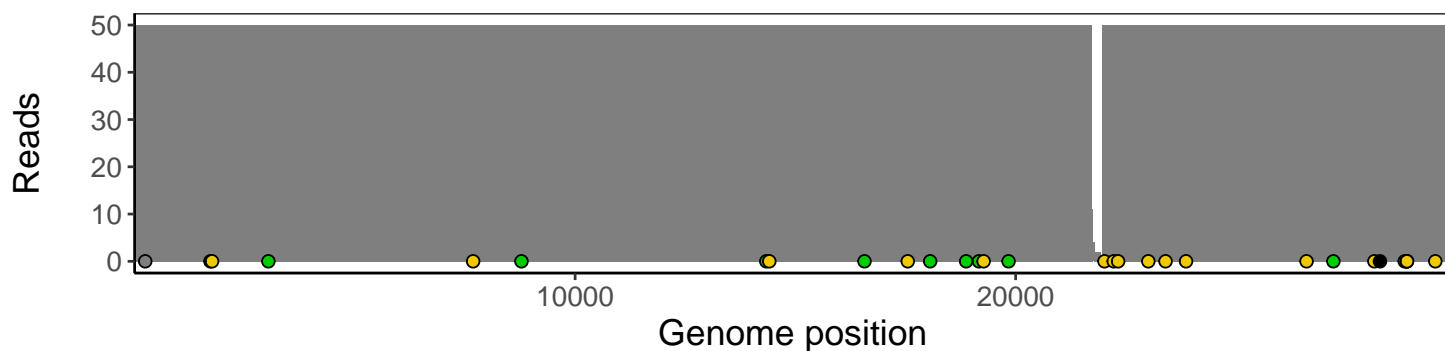
Analyses of individual experiments and composite results

VSP0626 | 2021-01-22 | Unknown | molpath-seq1 | composite result

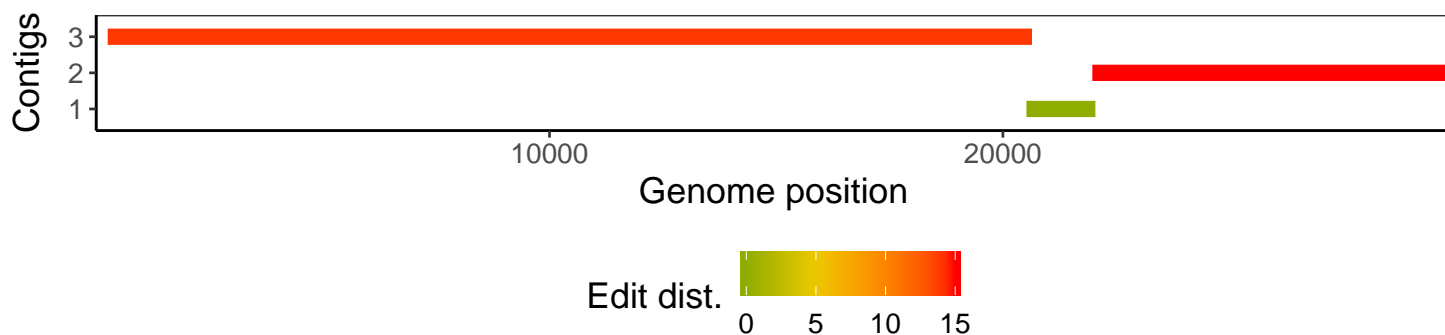
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



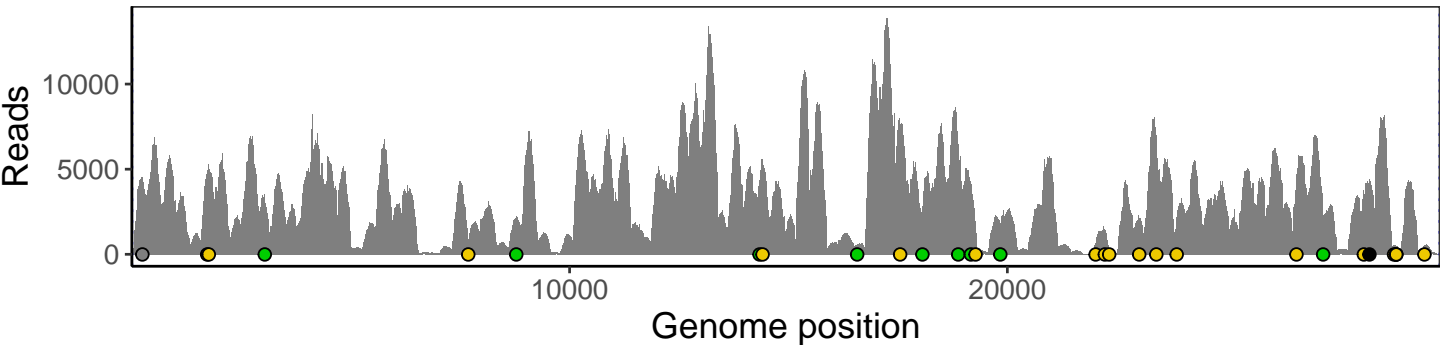
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



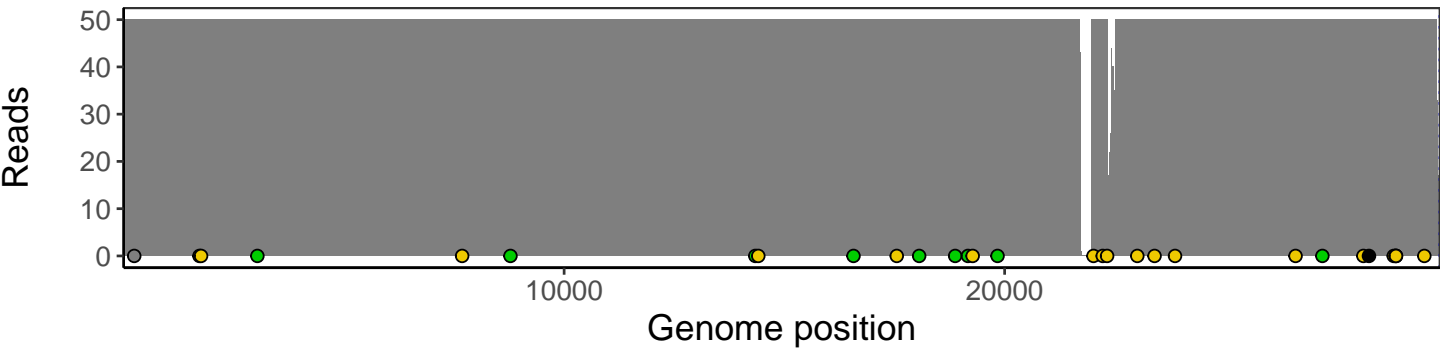
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



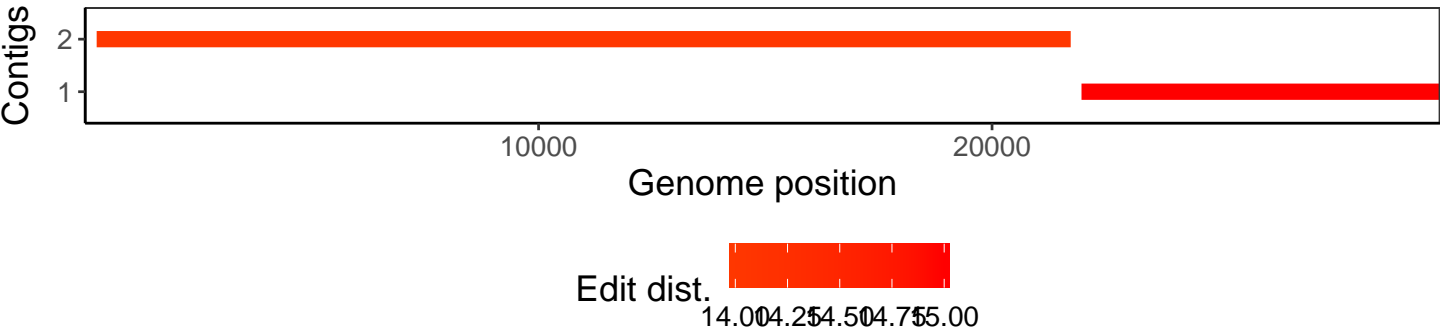
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



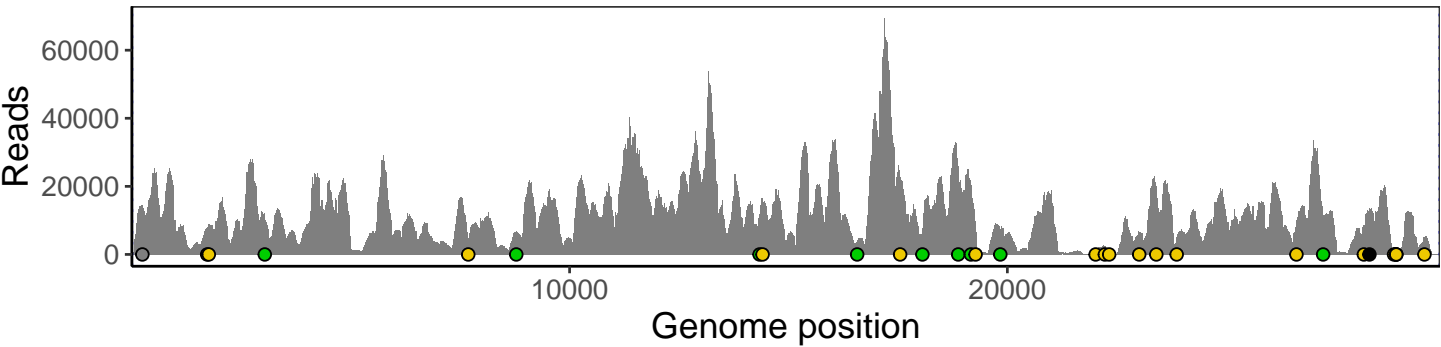
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



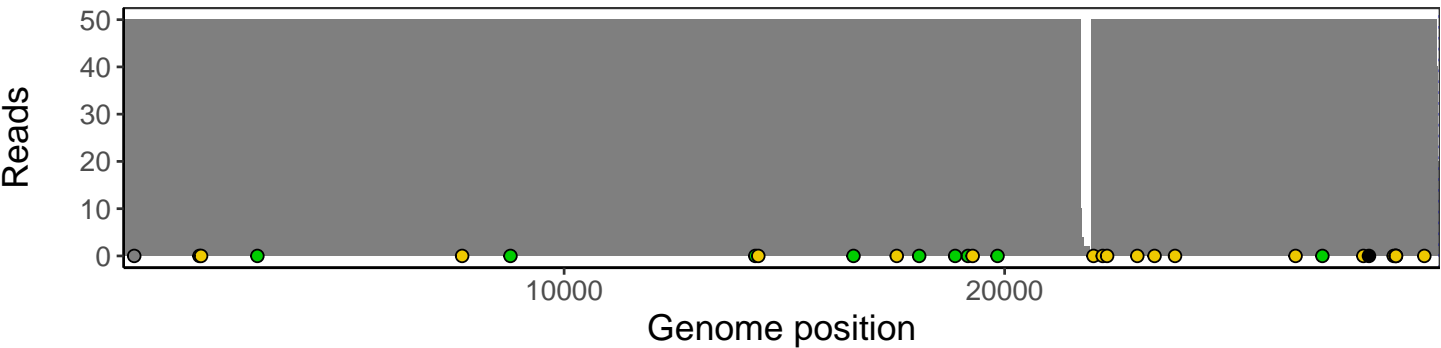
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



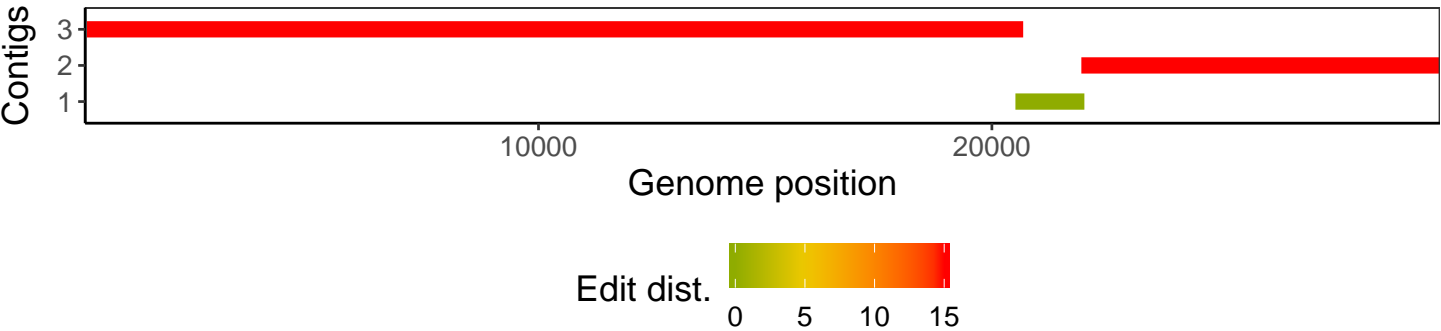
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



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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	2.1.7
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