

# COVID-19 subject WA strain SARS-CoV-2

*2021-05-21*

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.

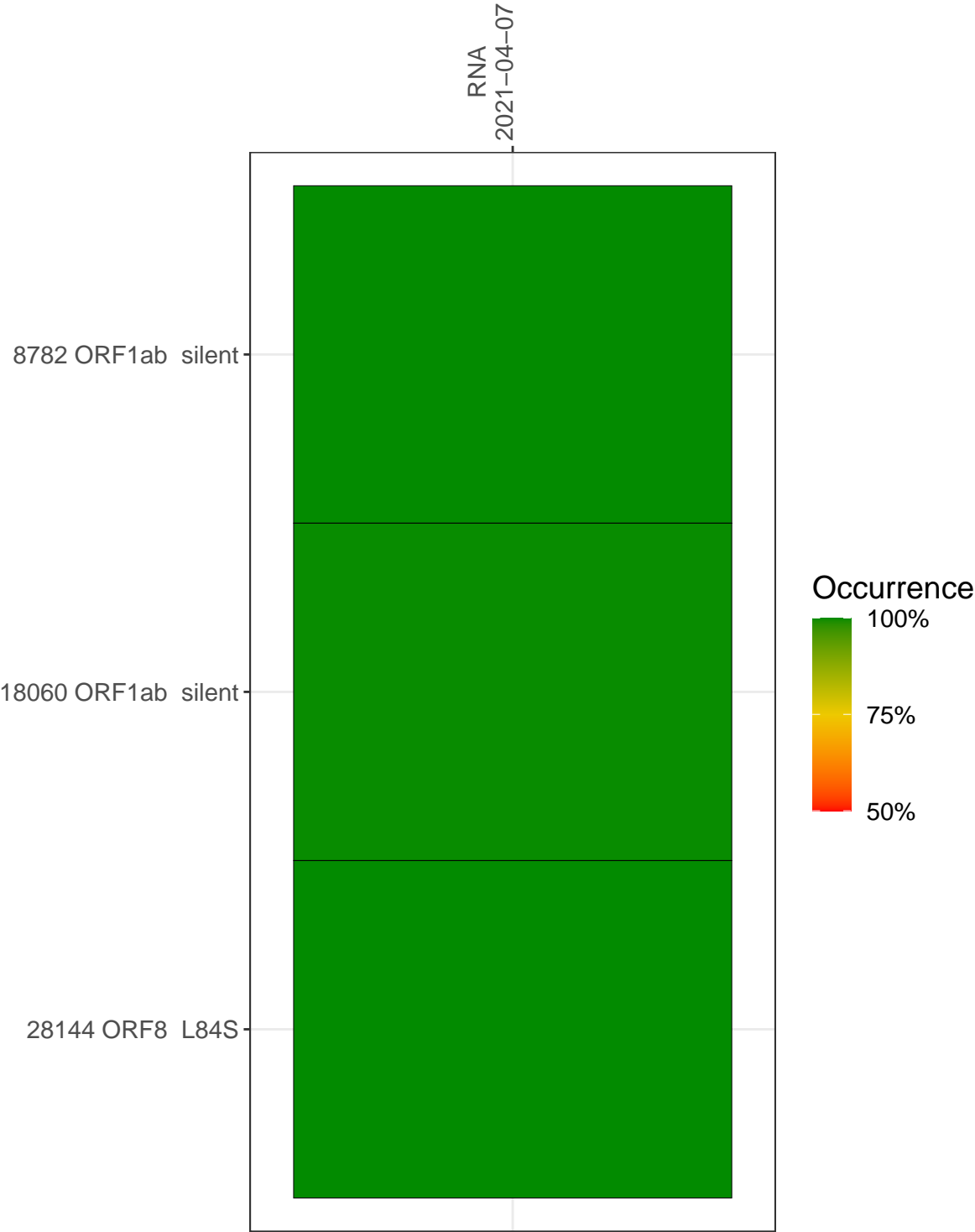
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with > 90% sequence coverage.

Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP1973	composite	NA	RNA	2021-04-07	29.96	A	100.0%	100.0%
VSP1973-1	single experiment	NA	RNA	2021-04-07	29.85	A	100.0%	99.8%
VSP1973-2	single experiment	NA	RNA	2021-04-07	29.83	A	99.8%	99.7%
VSP1973-3	single experiment	NA	RNA	2021-04-07	29.89	A	100.0%	99.9%
VSP1973-4	single experiment	NA	RNA	2021-04-07	29.85	A	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.



RNA  
2021-04-07

8782 ORF1ab silent

2585

780

9381

805

18060 ORF1ab silent

910

389

7714

529

28144 ORF8 L84S

1114

481

8675

563

Base change



VSP1973-1

VSP1973-2

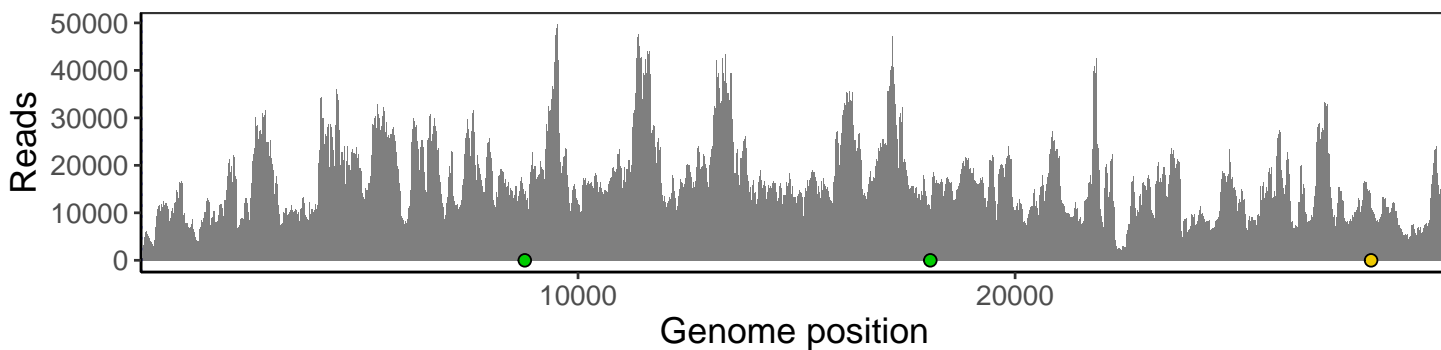
VSP1973-3

VSP1973-4

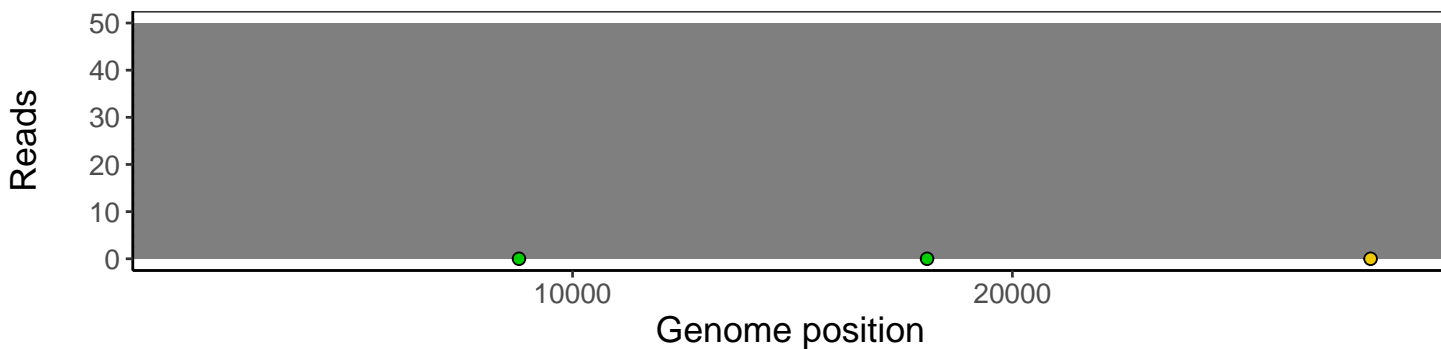
## Analyses of individual experiments and composite results

VSP1973 | 2021-04-07 | RNA | WA strain SARS-CoV-2 | composite result

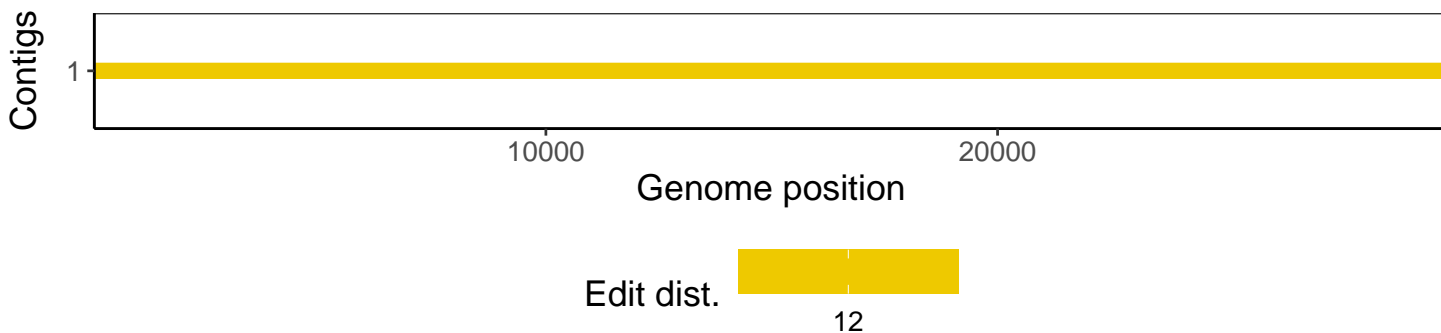
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



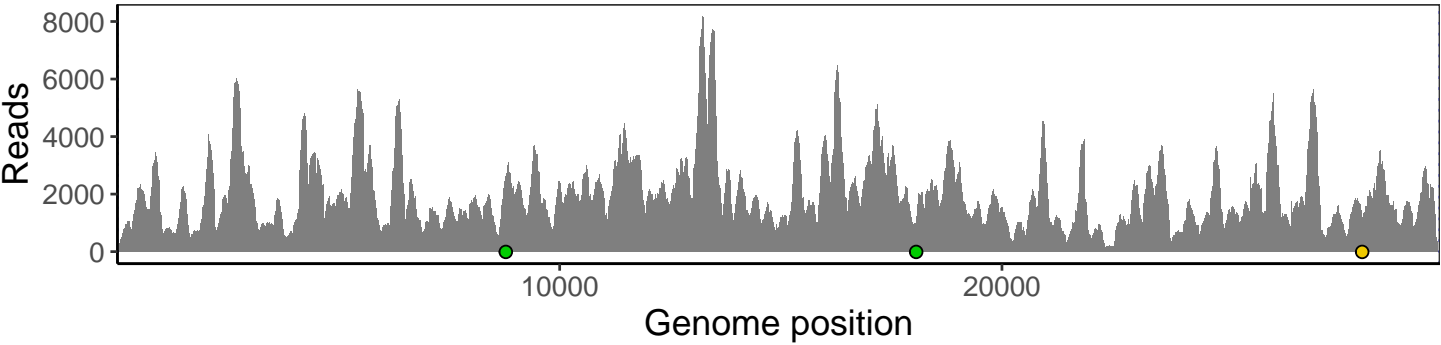
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



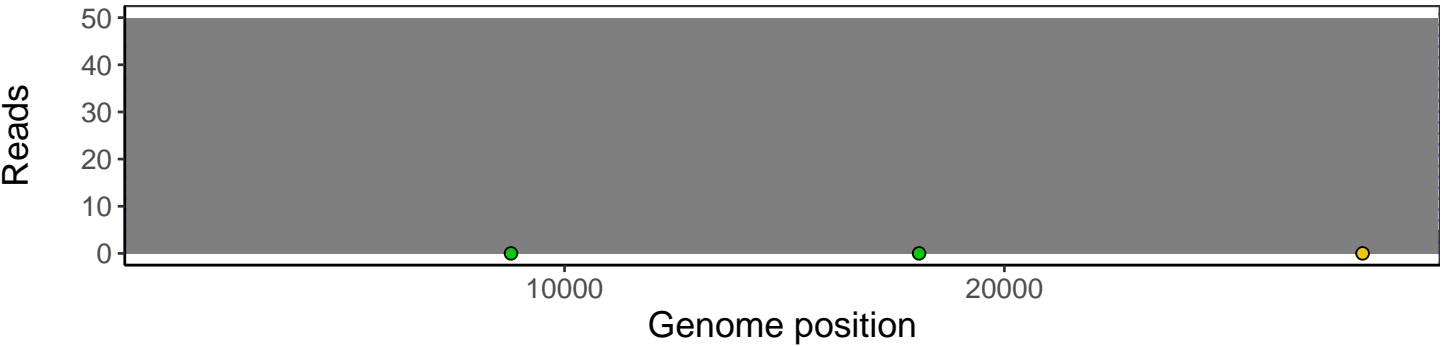
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



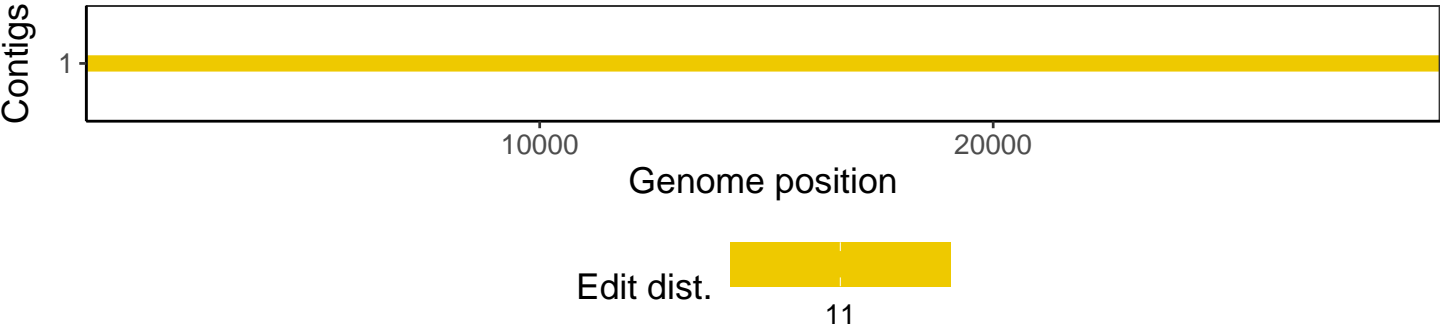
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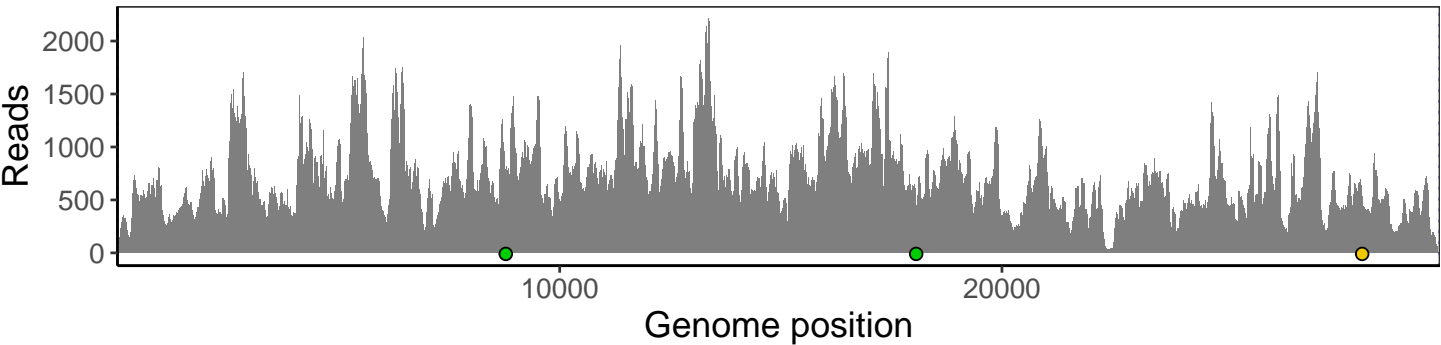
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



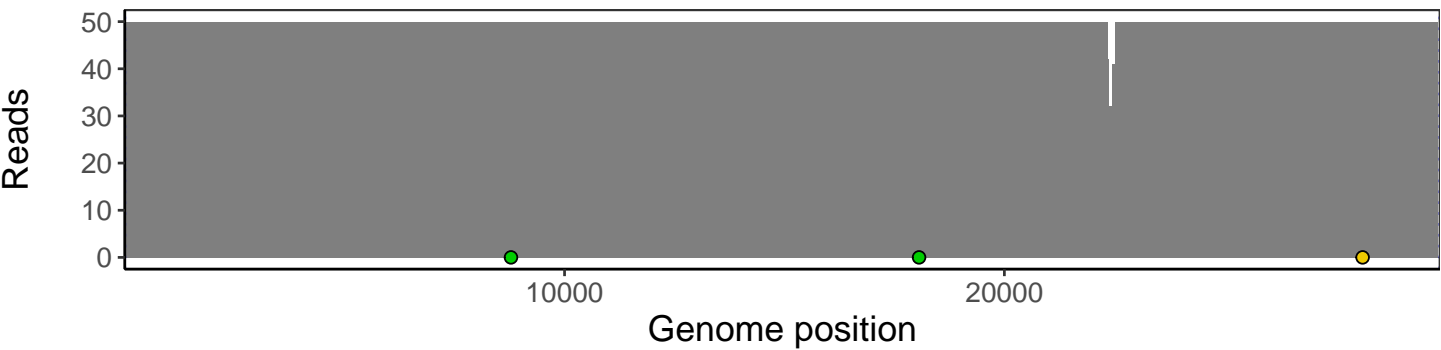
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



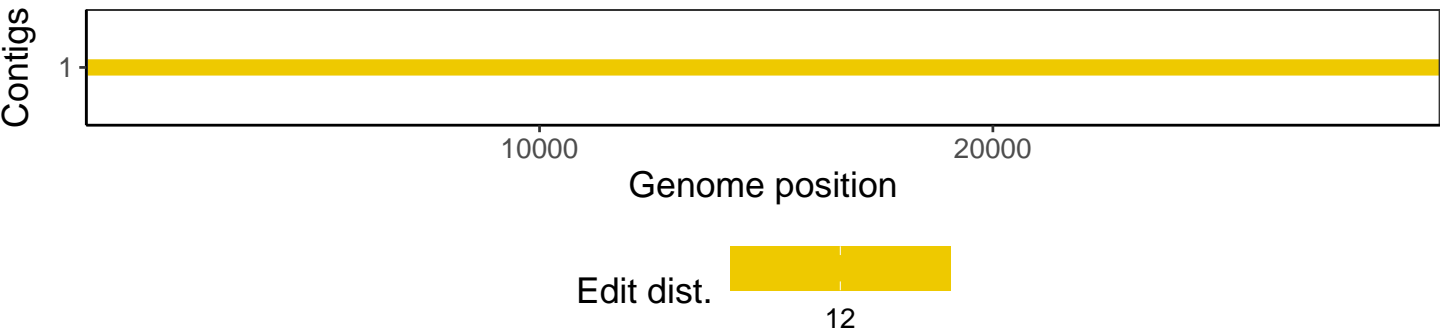
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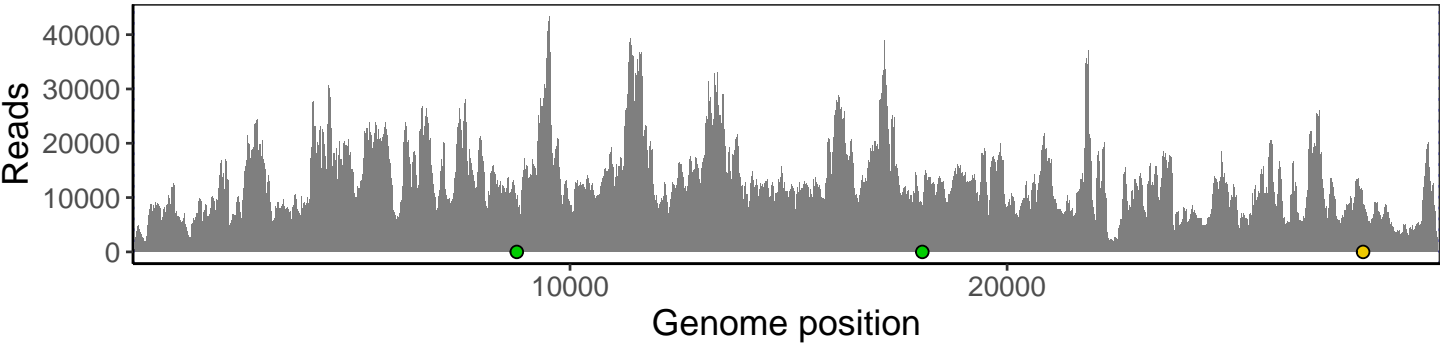
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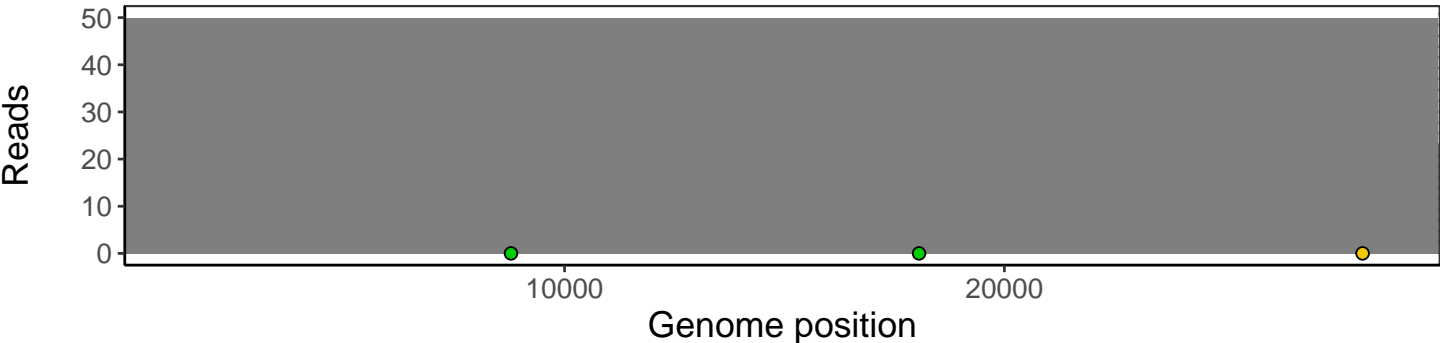
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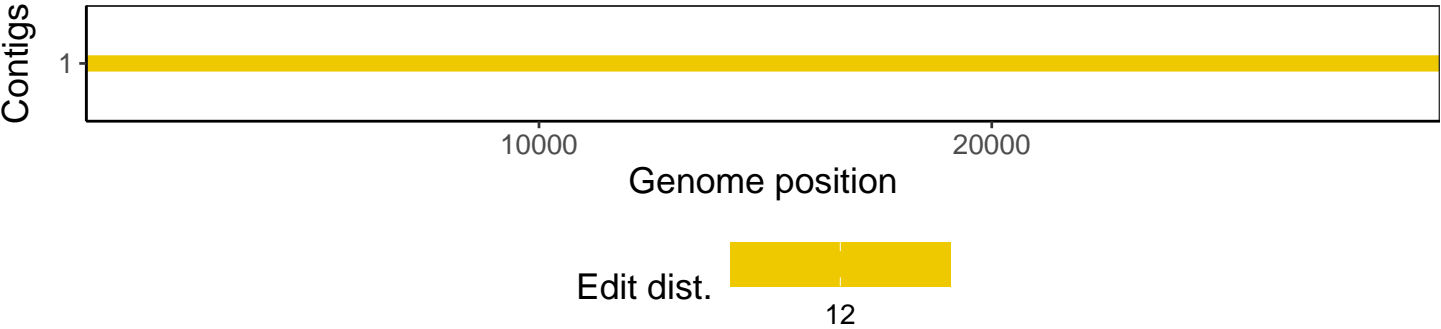
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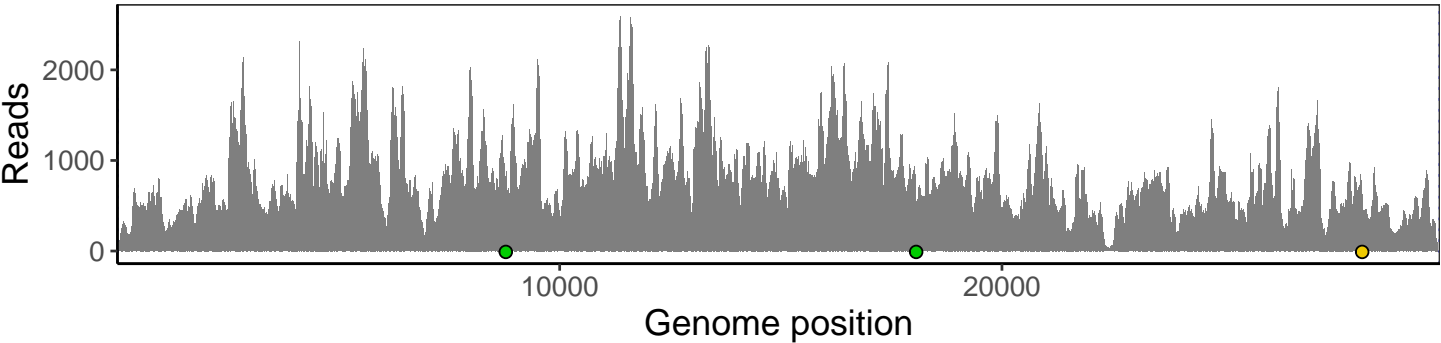
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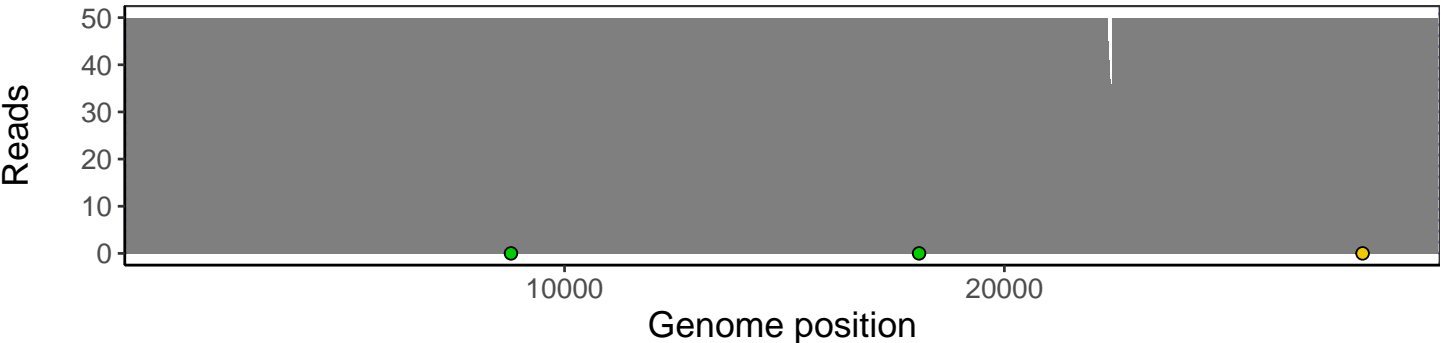
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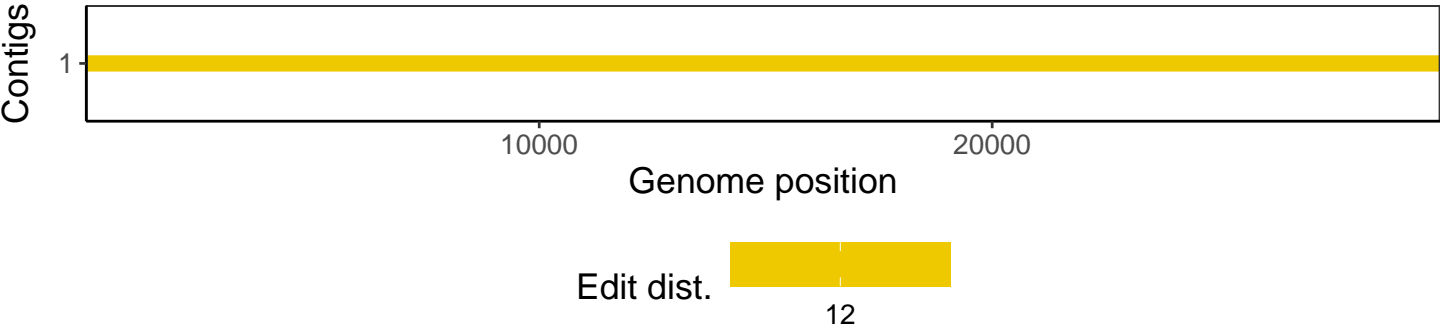
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Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



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	3.3.3
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