

# COVID-19 subject TWIST RNA

2021-06-23

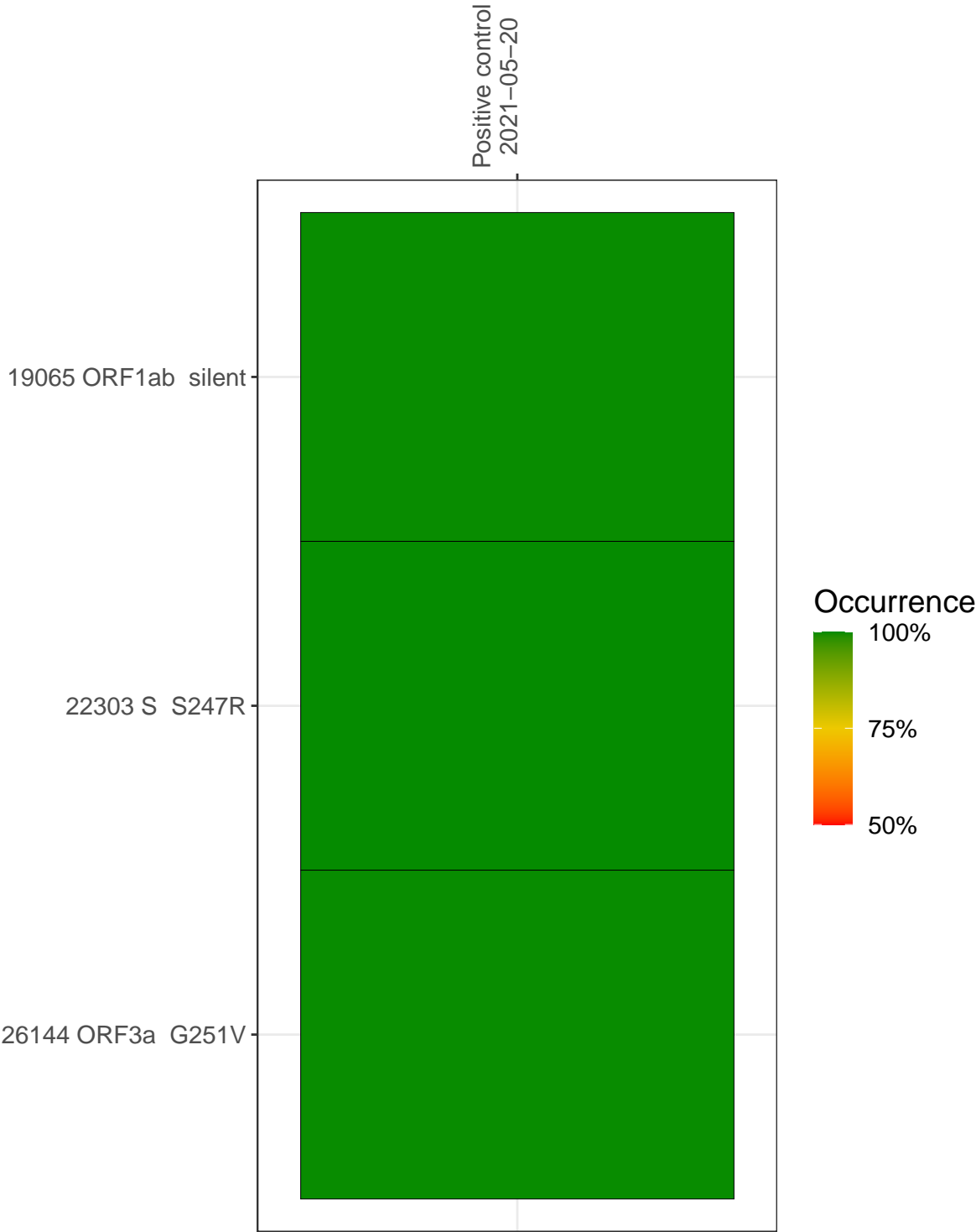
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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 ( $\geq 5$ reads)
VSP3000	composite	NA	Positive control	2021-05-20	5.11	B	99.9%	99.0%
VSP3000-1	single experiment	NA	Positive control	2021-05-20	4.99	B	98.2%	96.2%
VSP3000-10	single experiment	NA	Positive control	2021-05-20	4.85	NA	94.8%	92.1%
VSP3000-11	single experiment	NA	Positive control	2021-05-20	4.96	NA	97.9%	94.4%
VSP3000-12	single experiment	NA	Positive control	2021-05-20	4.89	B	98.0%	95.0%
VSP3000-2	single experiment	NA	Positive control	2021-05-20	5.07	B	99.2%	97.5%
VSP3000-3	single experiment	NA	Positive control	2021-05-20	5.01	NA	97.8%	94.9%
VSP3000-4	single experiment	NA	Positive control	2021-05-20	4.88	NA	96.1%	93.5%
VSP3000-7	single experiment	NA	Positive control	2021-05-20	4.89	NA	96.1%	94.0%
VSP3000-8	single experiment	NA	Positive control	2021-05-20	5.03	B	99.0%	96.5%

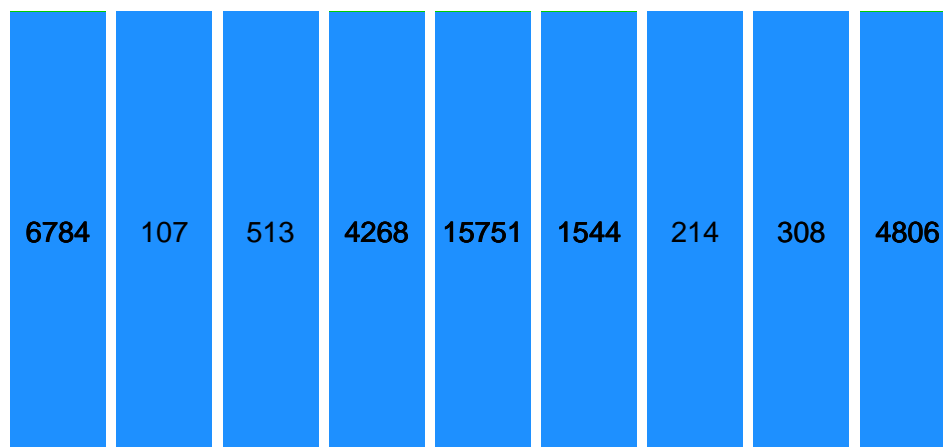
**Variants shared across samples**

The heat map below shows how variants (reference genome `/home/common/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.

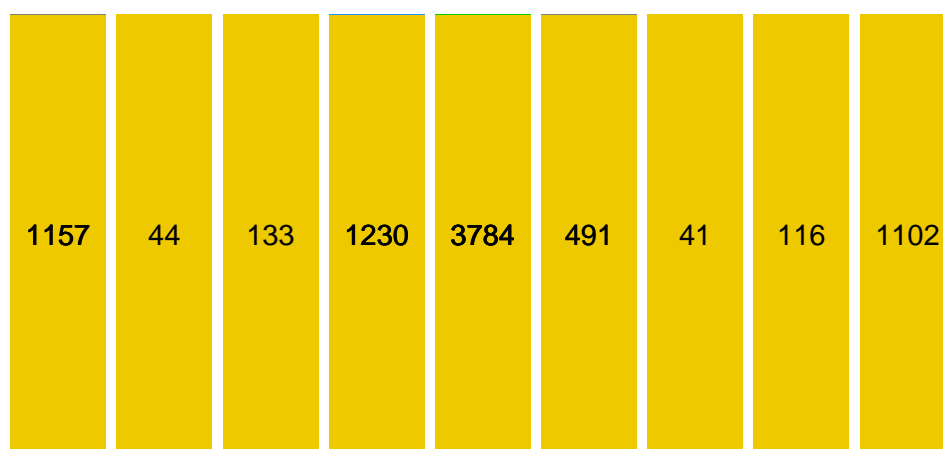


Positive control  
2021-05-20

19065 ORF1ab silent



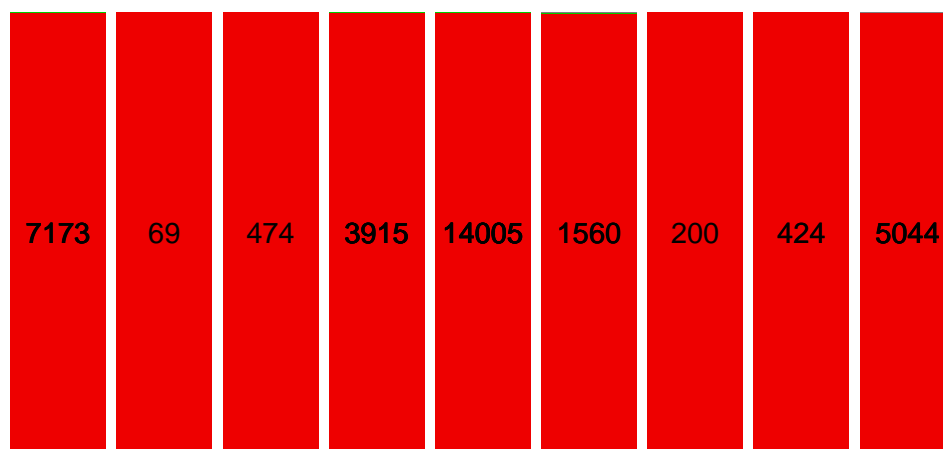
22303 S S247R



Base change



26144 ORF3a G251V



VSP3000-1

VSP3000-10

VSP3000-11

VSP3000-12

VSP3000-2

VSP3000-3

VSP3000-4

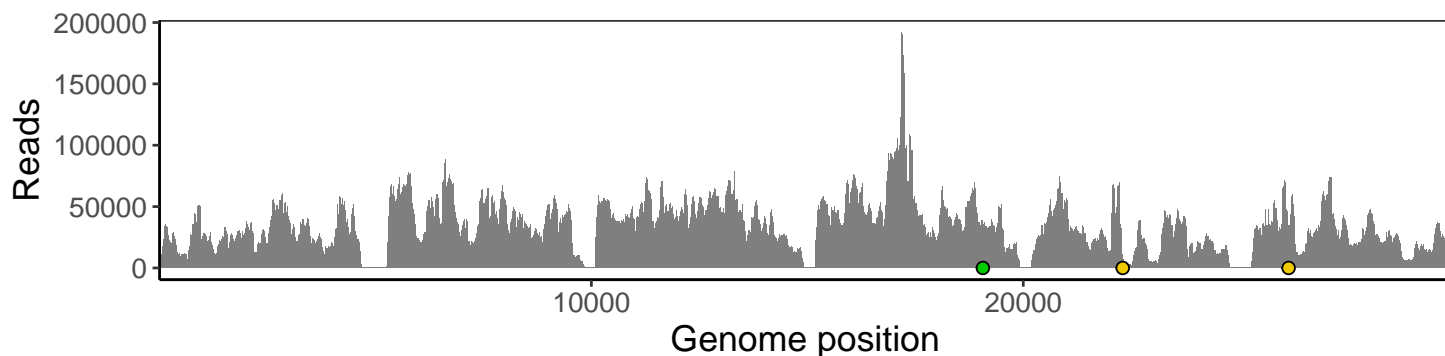
VSP3000-7

VSP3000-8

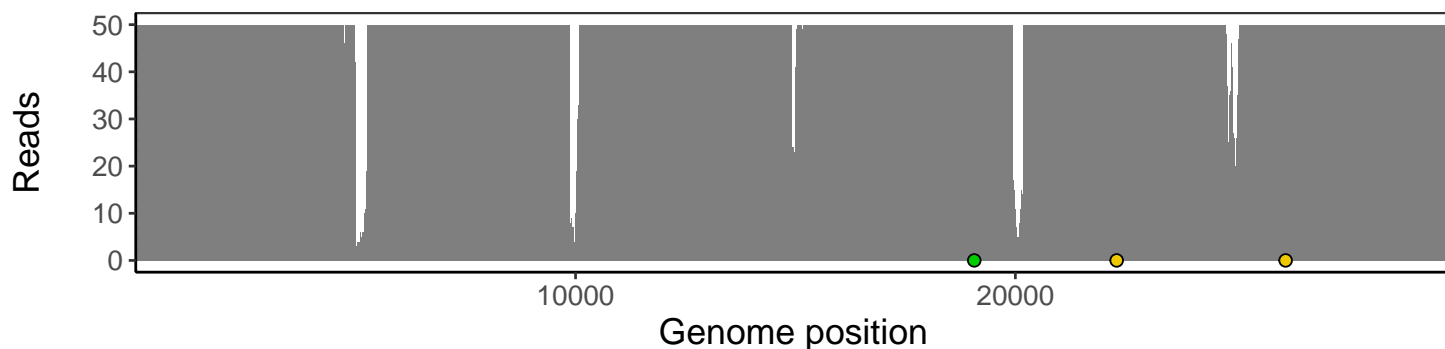
## Analyses of individual experiments and composite results

VSP3000 | 2021-05-20 | Positive control | TWIST RNA | composite result

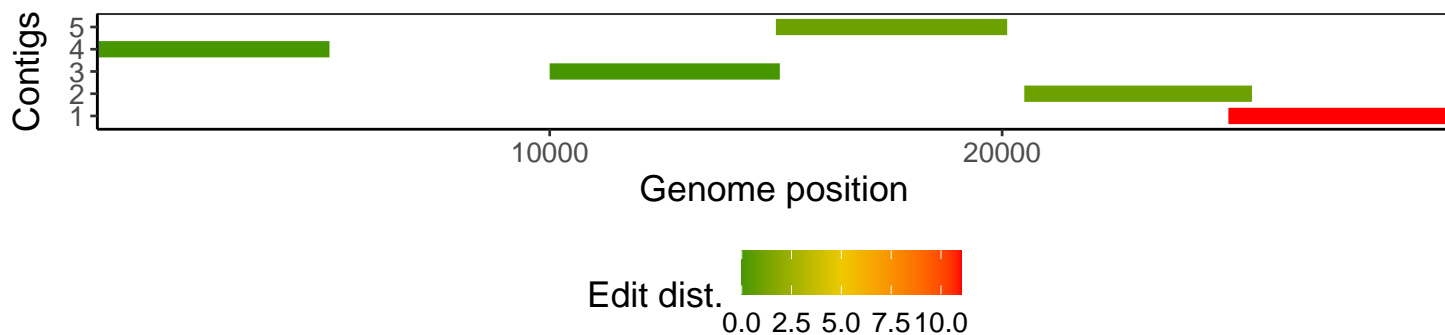
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



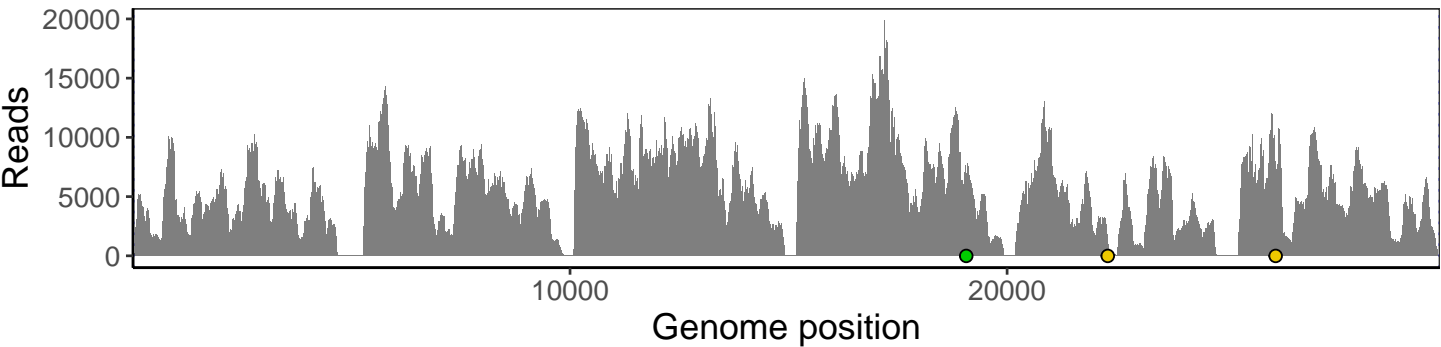
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



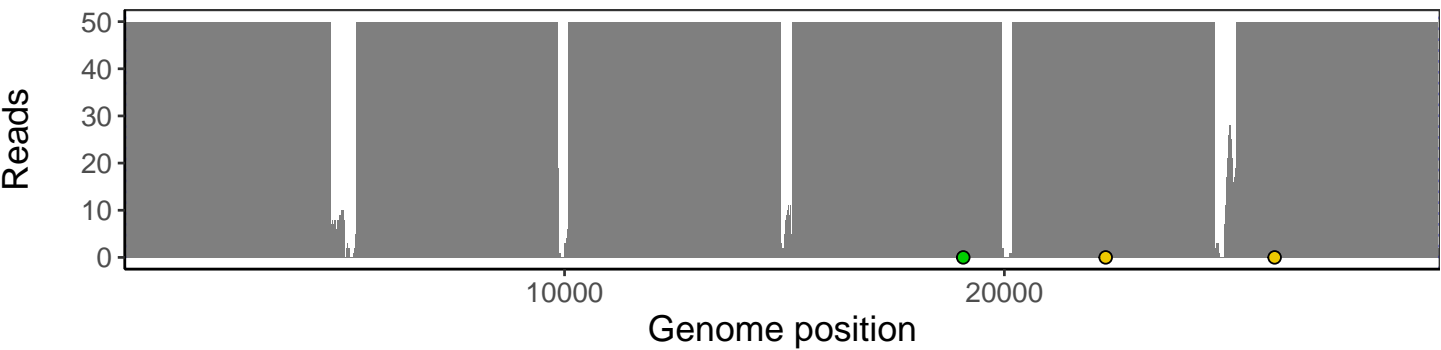
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



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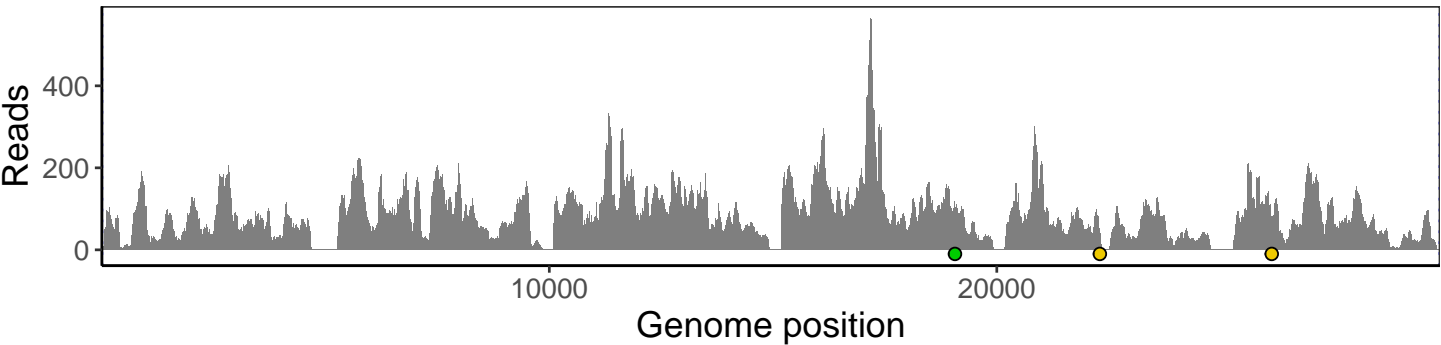
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



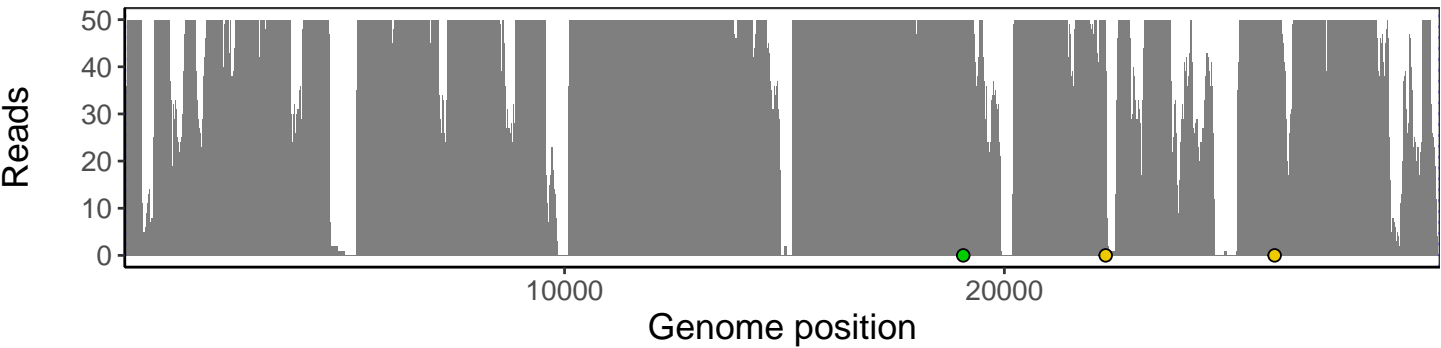
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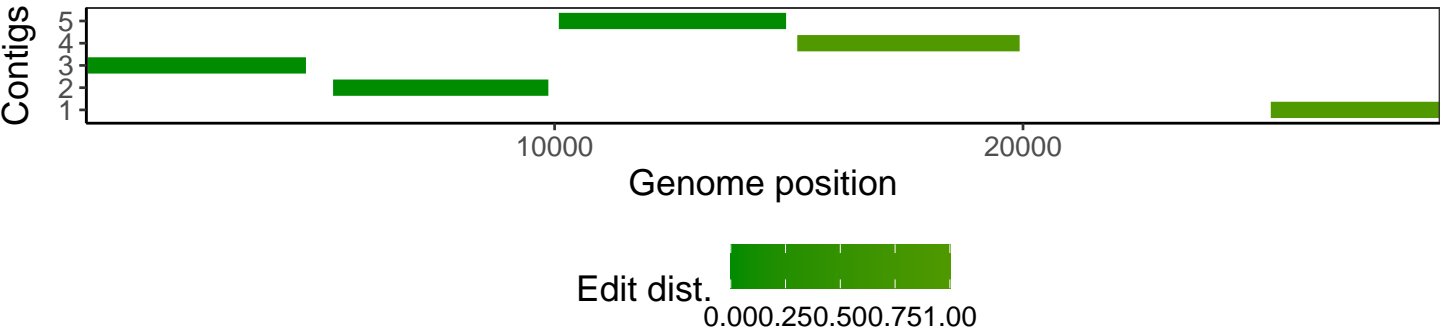
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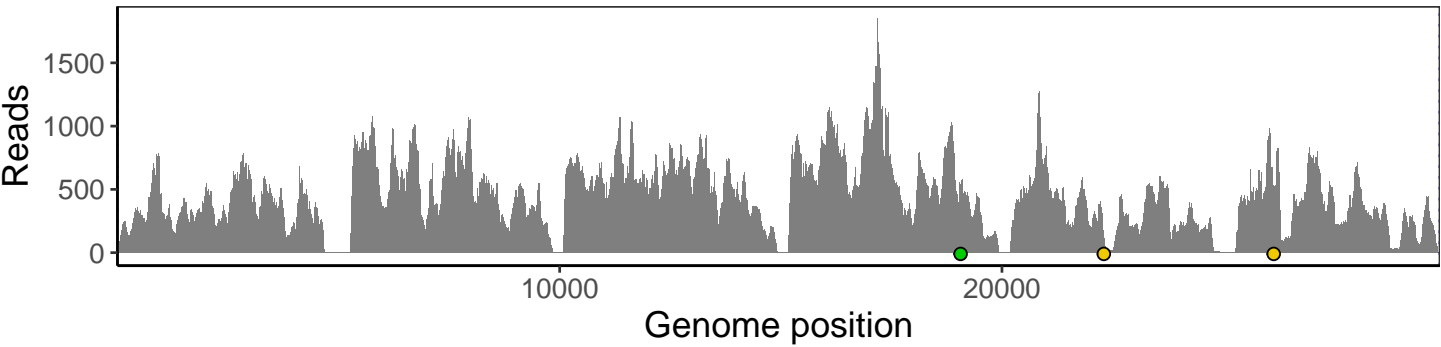
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



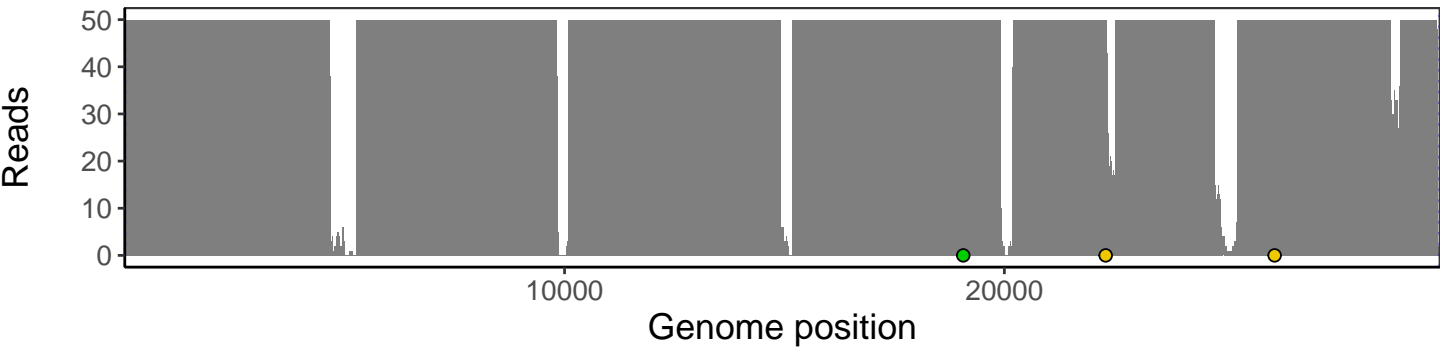
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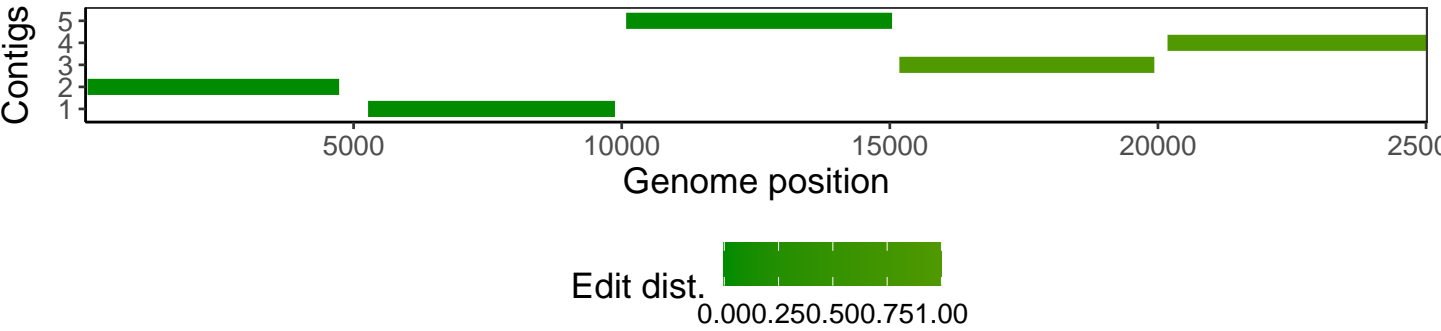
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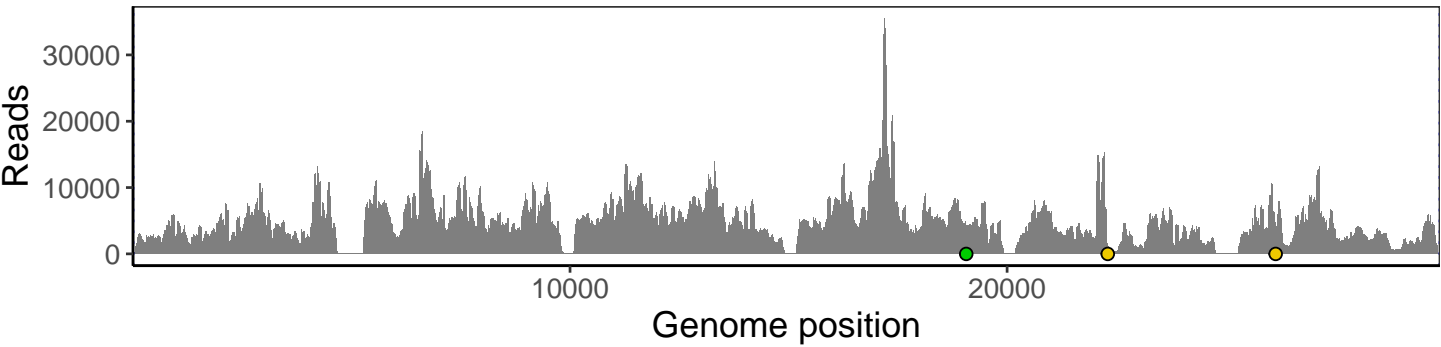
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



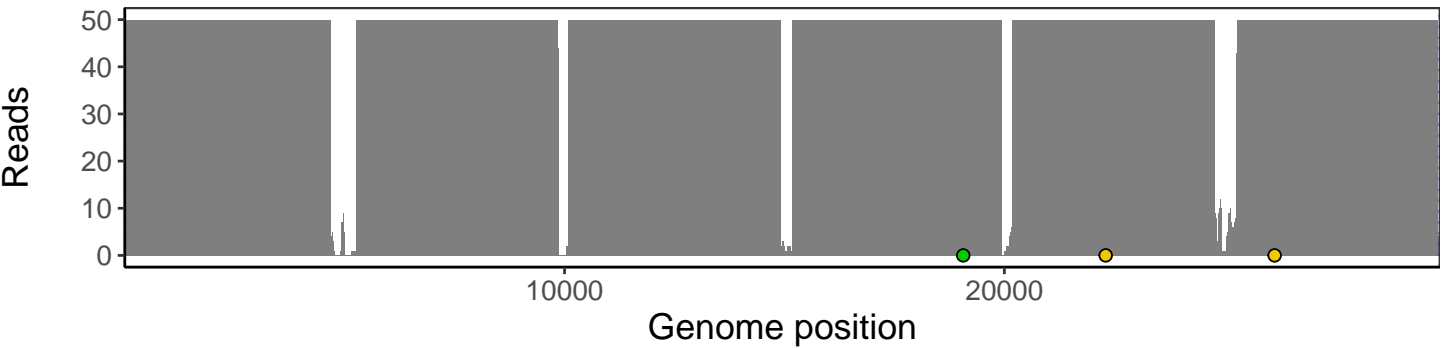
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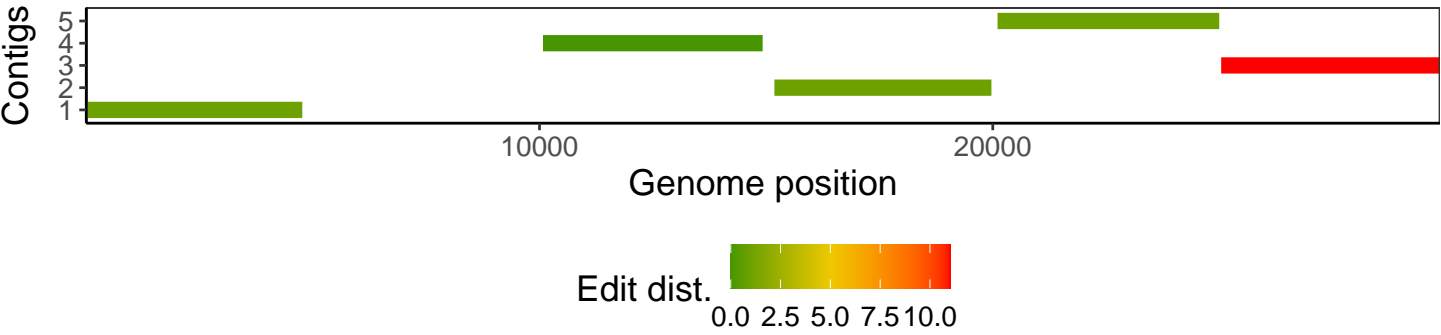
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Excerpt from plot above focusing on reads coverage from 0 to 50 NT.

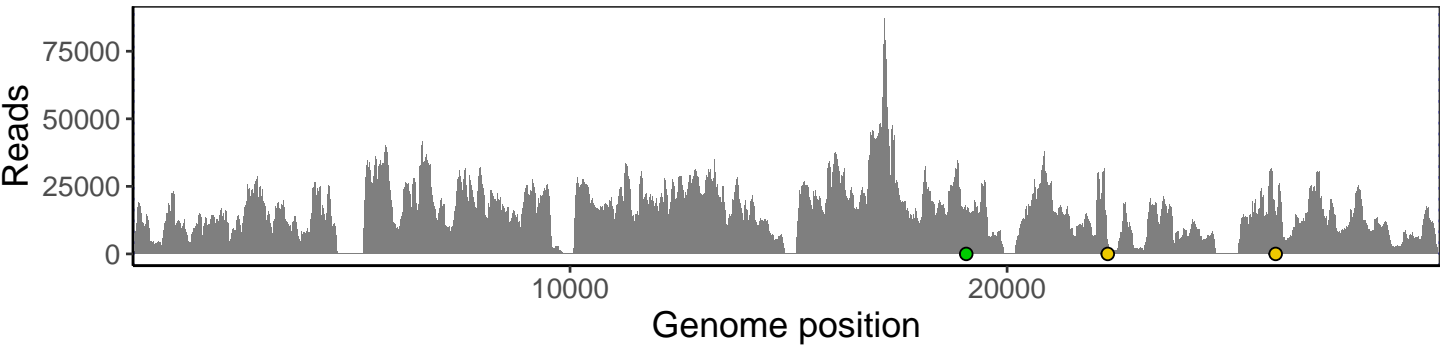


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

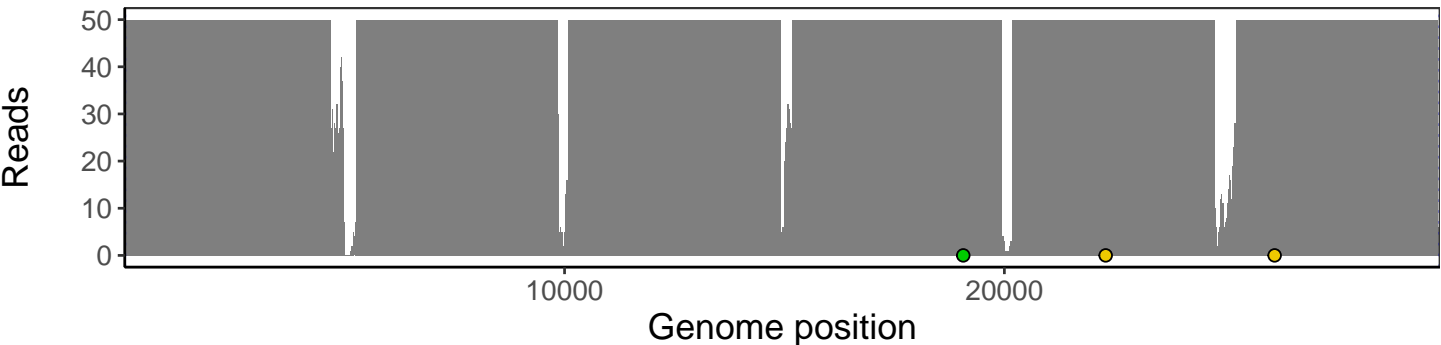




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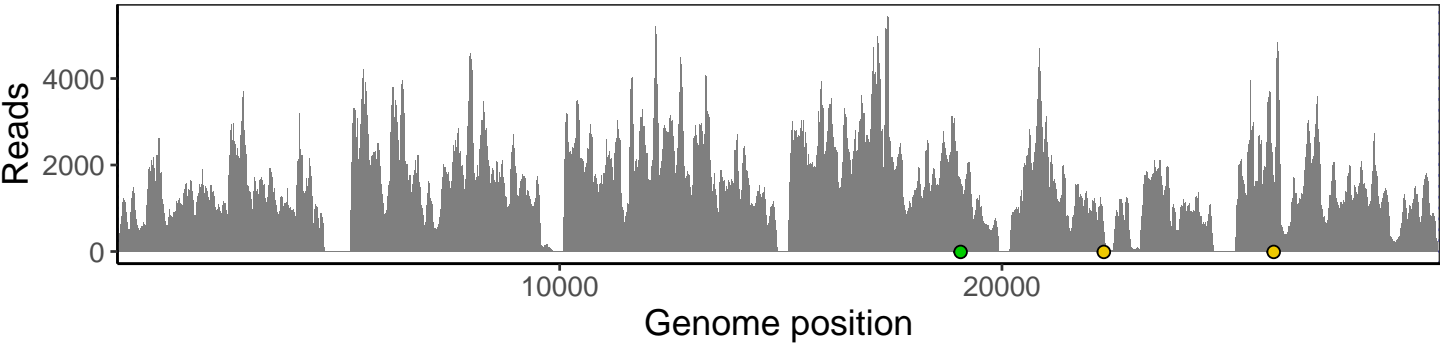
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



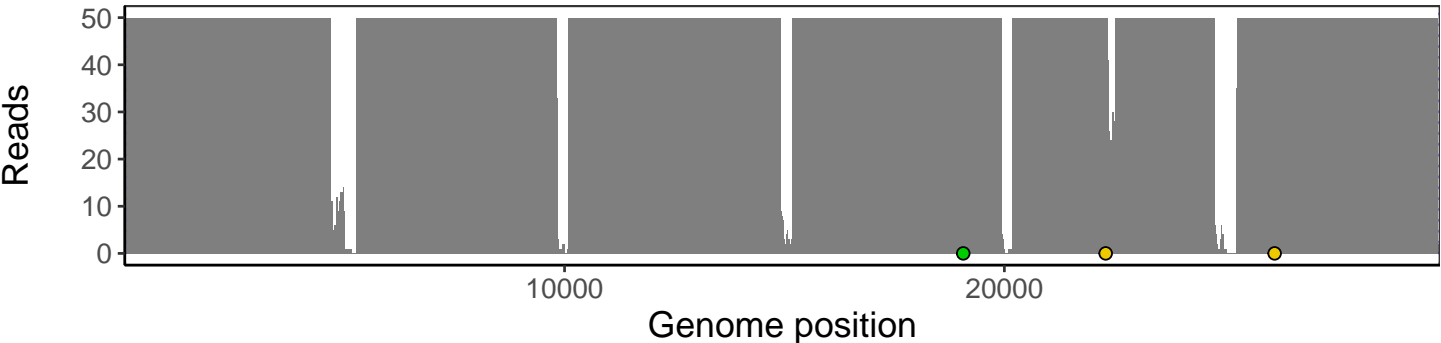
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



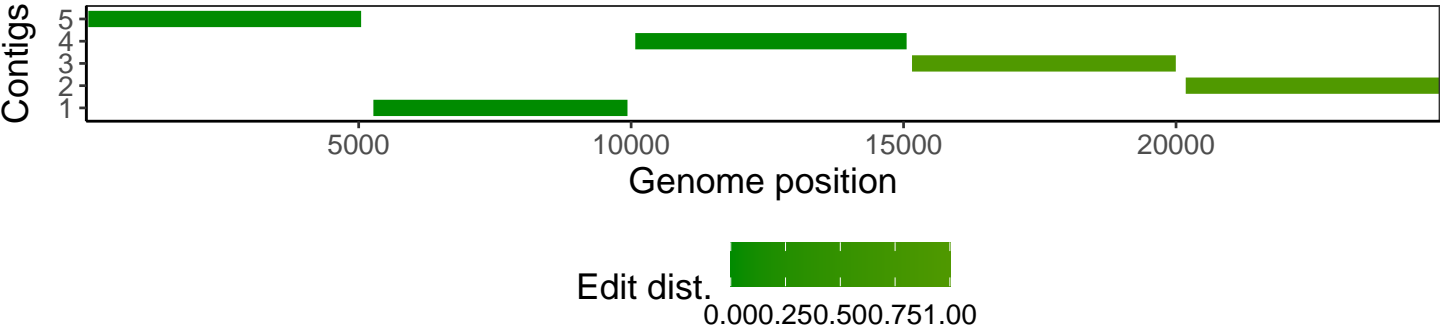
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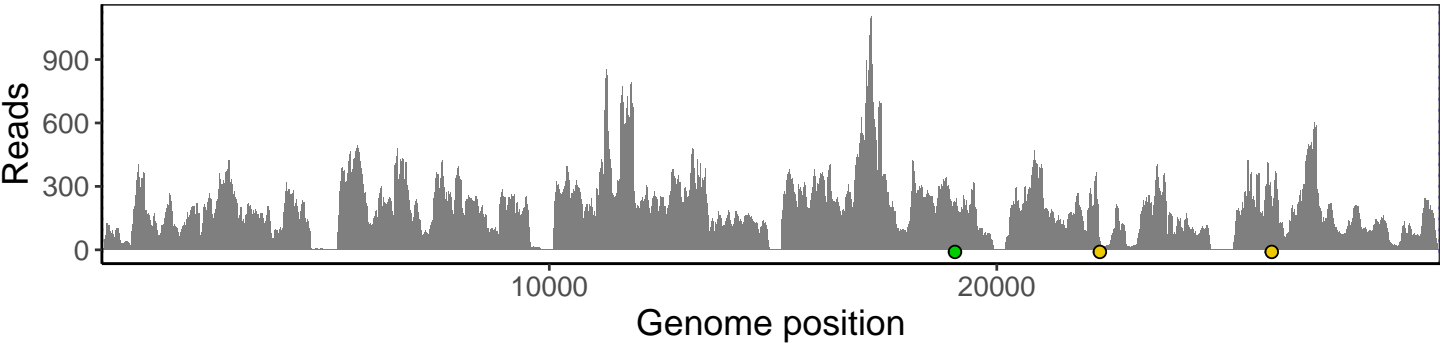
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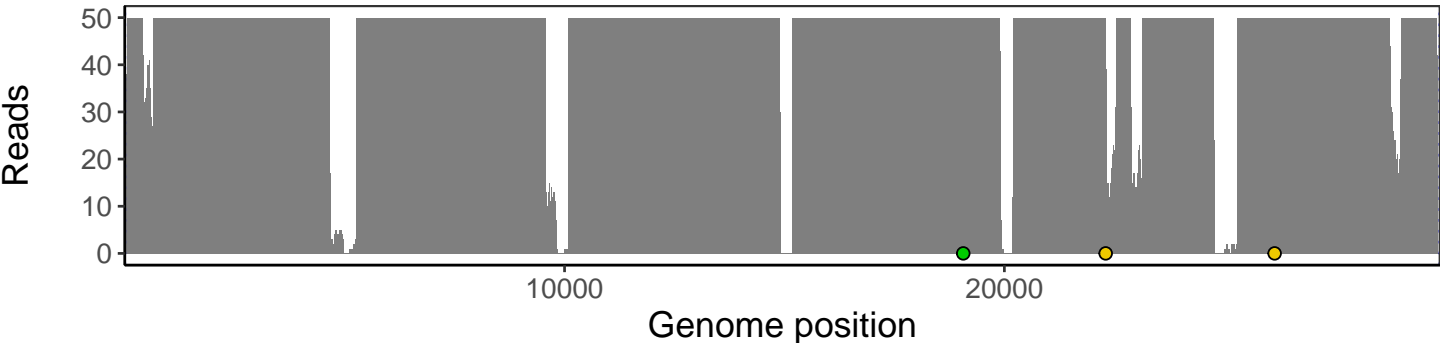
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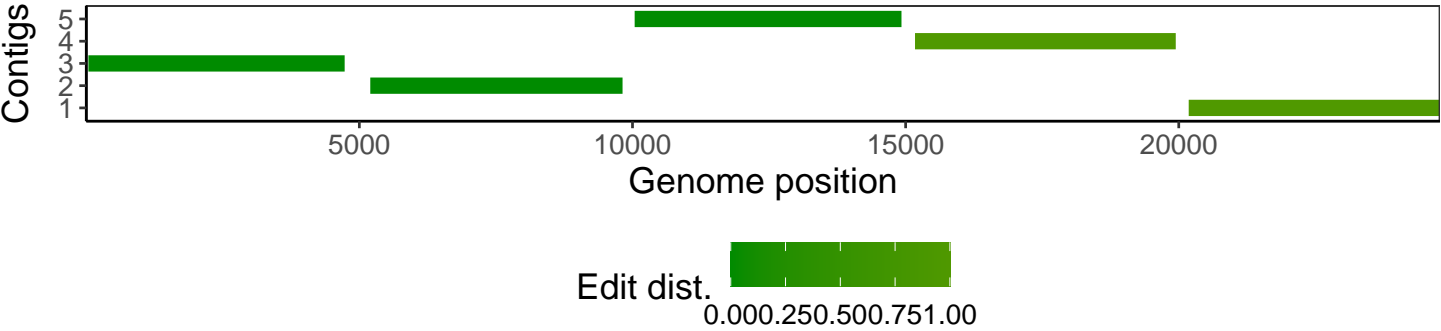
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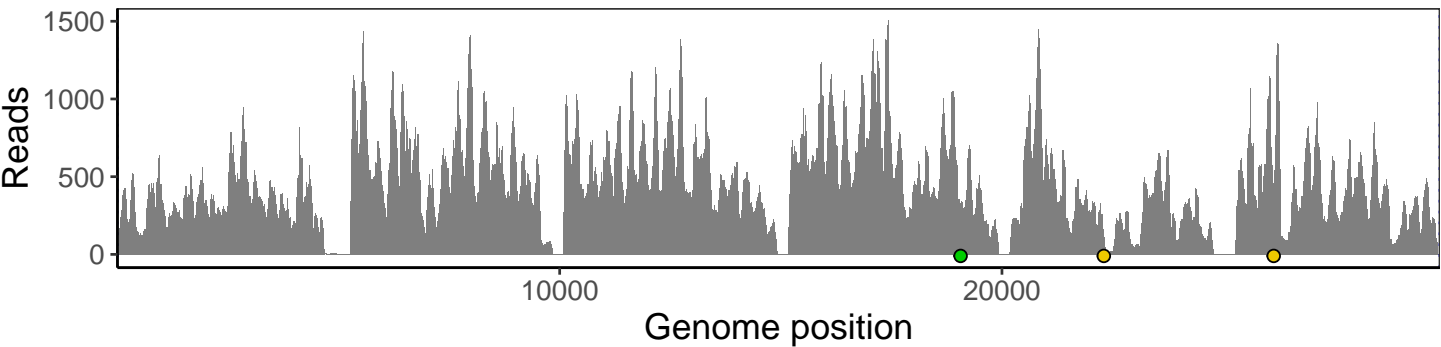
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



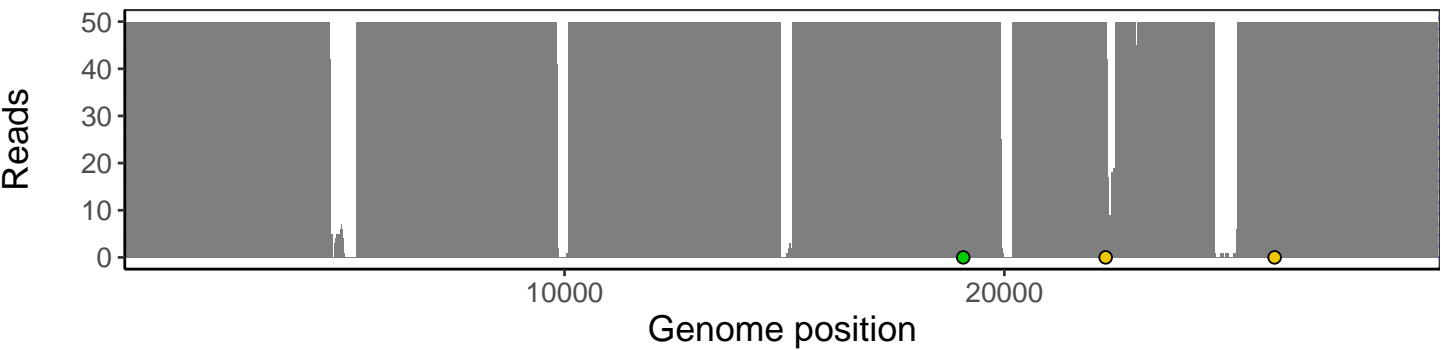
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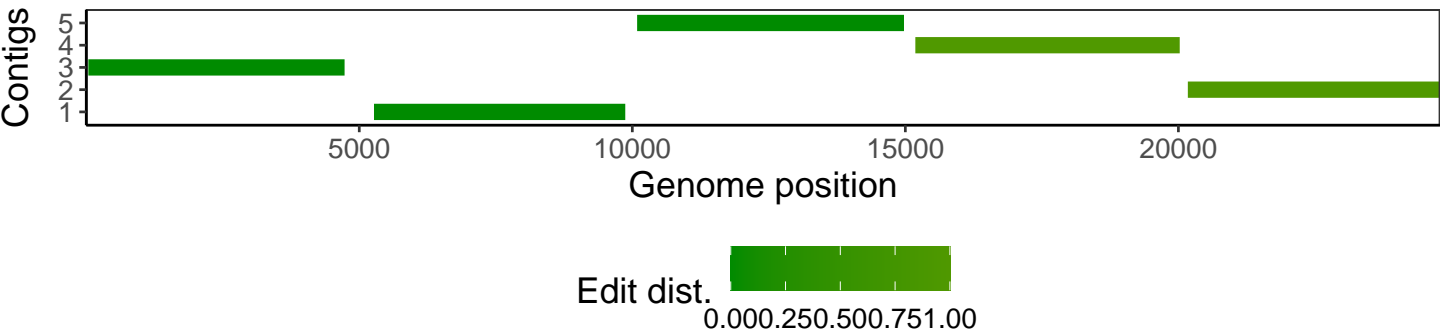
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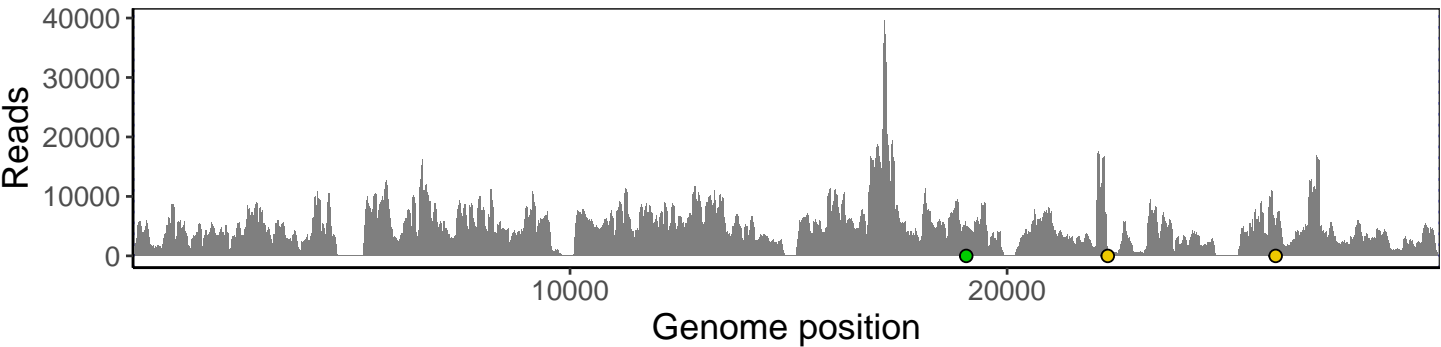
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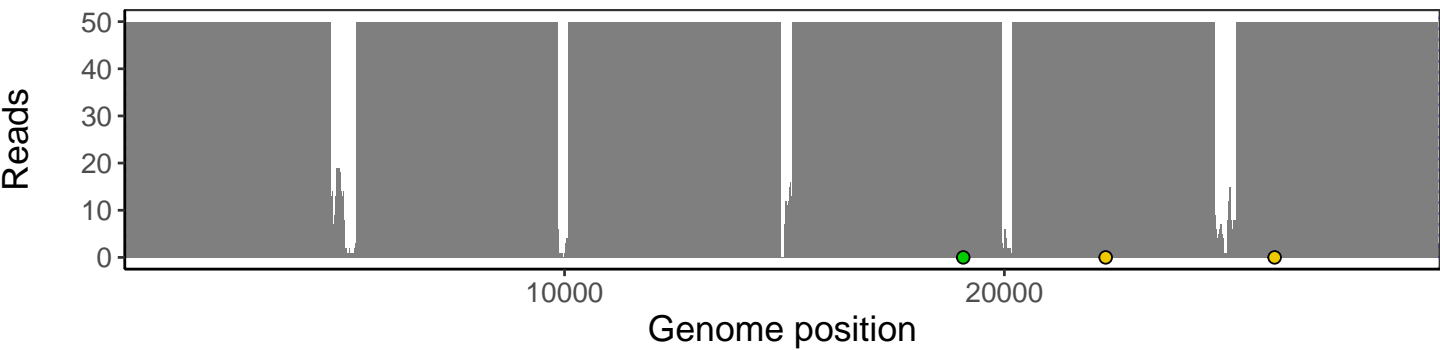
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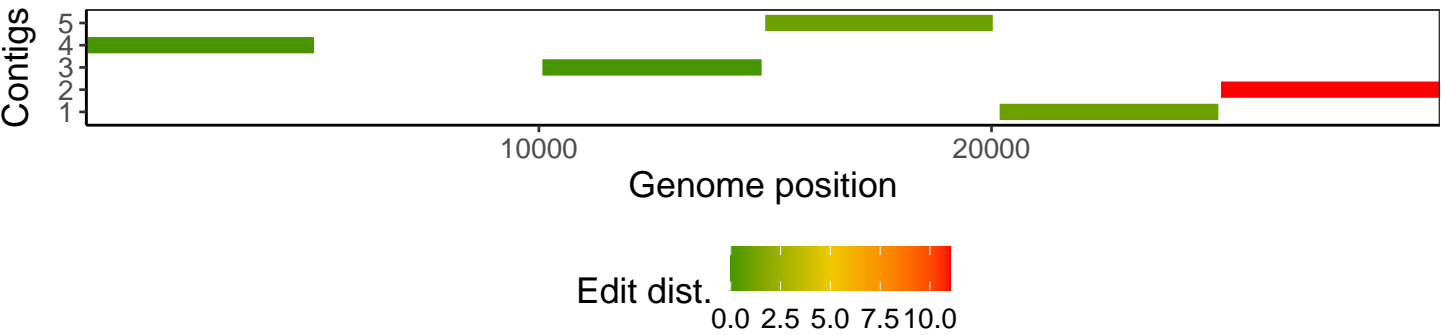
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## Software environment

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	3.1.3
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	3.3.3
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