

# COVID-19 subject 235

*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.

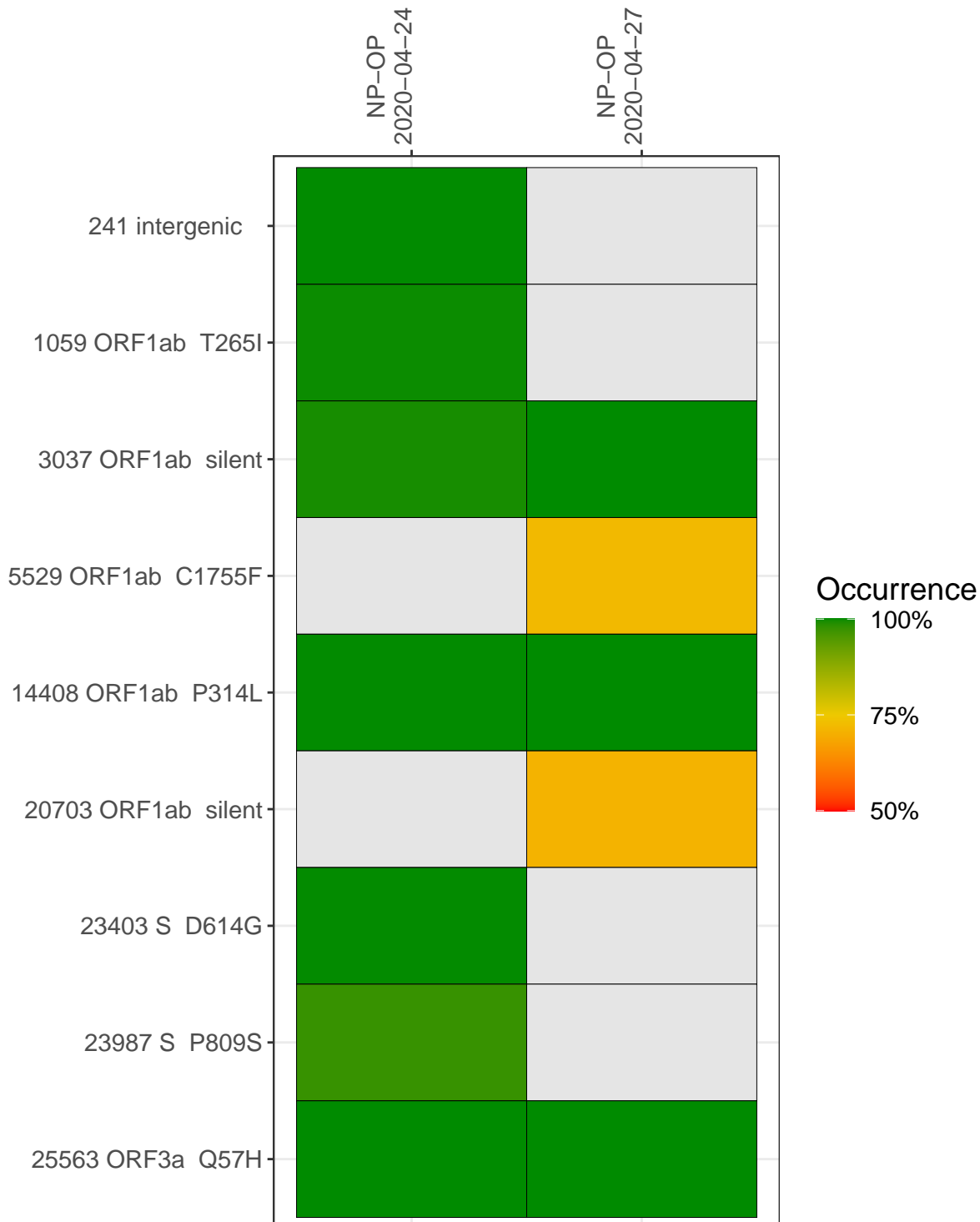
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with > 90% sequence coverage.

Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0030	composite	NA	NP-OP	2020-04-27	2.47	NA	76.8%	57.1%
VSP0029-1m	single experiment	NA	NP-OP	2020-04-27	0.50	NA	17.5%	12.5%
VSP0030-1m	single experiment	NA	NP-OP	2020-04-27	1.05	NA	51.2%	23.5%
VSP0030-2	single experiment	NA	NP-OP	2020-04-27	1.96	NA	55.1%	53.1%
VSP0080-1	single experiment	176000	NP-OP	2020-04-24	29.87	B.1	99.8%	99.8%

## 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.



	NP-OP 2020-04-24		NP-OP 2020-04-27	
241 intergenic	6340	0	2	0
1059 ORF1ab T265I	1896	0	0	0
3037 ORF1ab silent	3625	1	0	476
5529 ORF1ab C1755F	5878	0	0	808
14408 ORF1ab P314L	6876	0	505	1170
20703 ORF1ab silent	7221	363	501	1210
23403 S D614G	14214	0	2	0
23987 S P809S	1622	0	0	0
25563 ORF3a Q57H	3637	0	0	945
	VSP0080-1	VSP0029-1m	VSP0030-1m	VSP0030-2

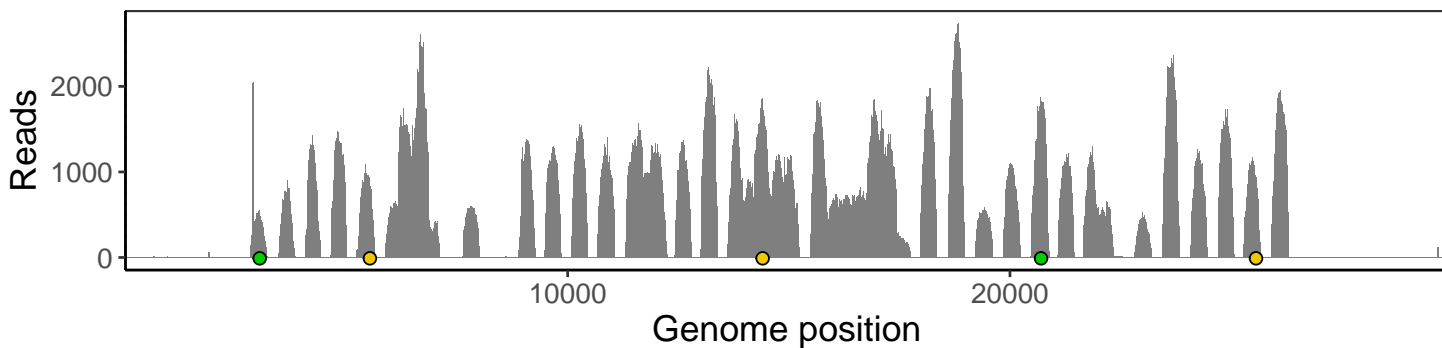
Base change



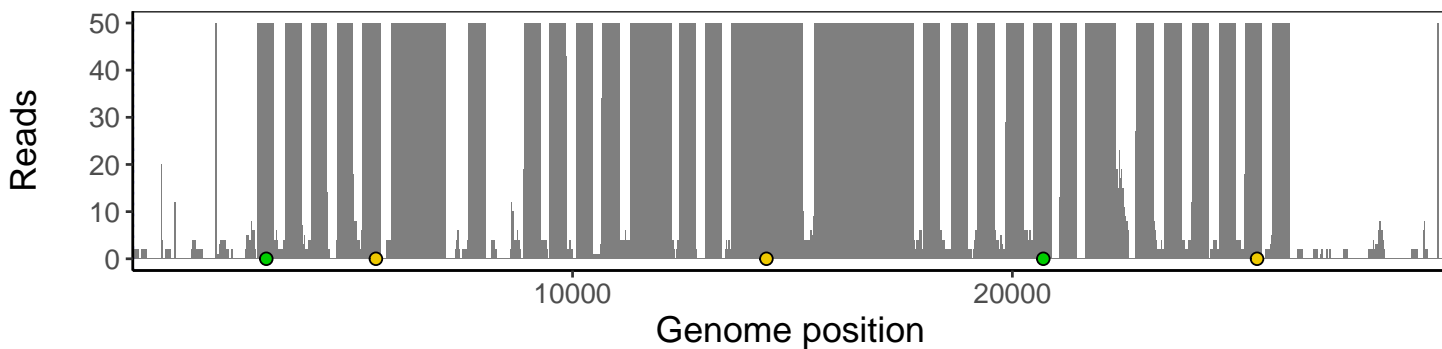
## Analyses of individual experiments and composite results

VSP0030 | 2020-04-27 | NP-OP | 235-qia | composite result

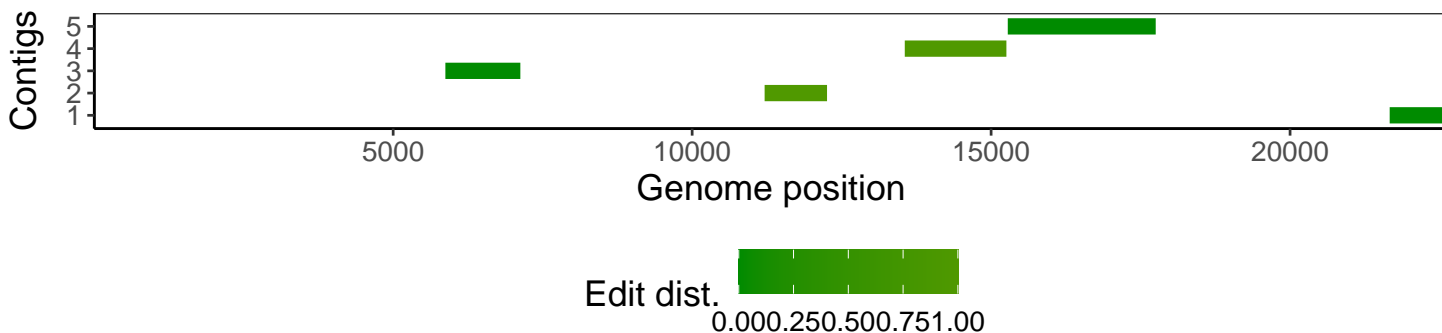
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



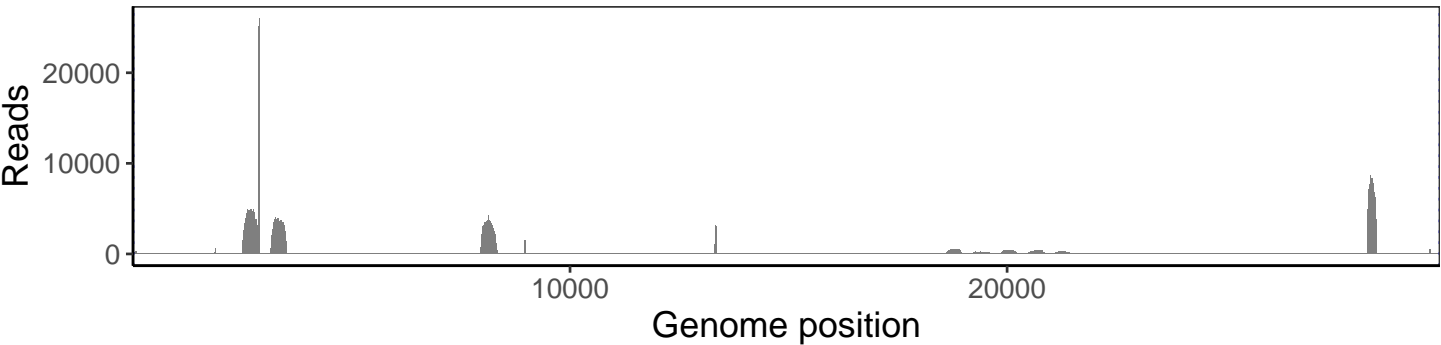
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



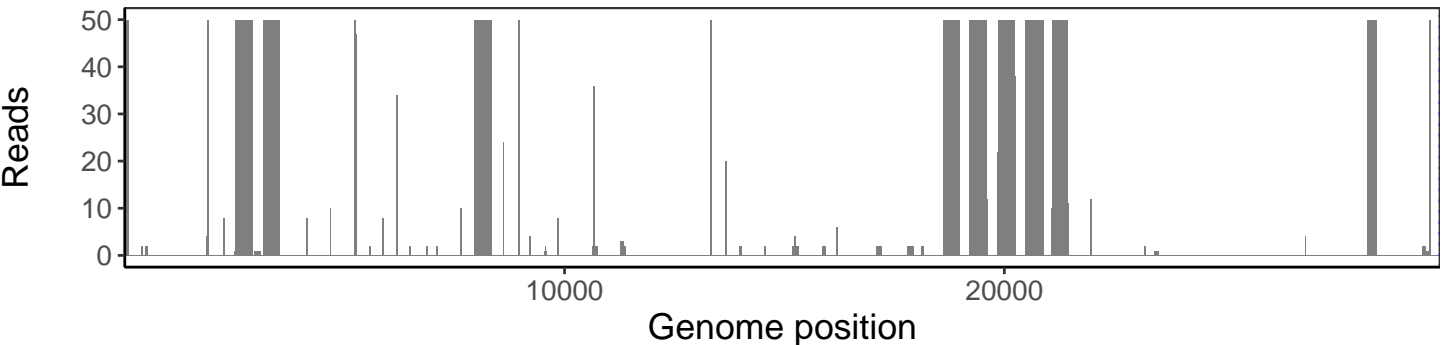
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



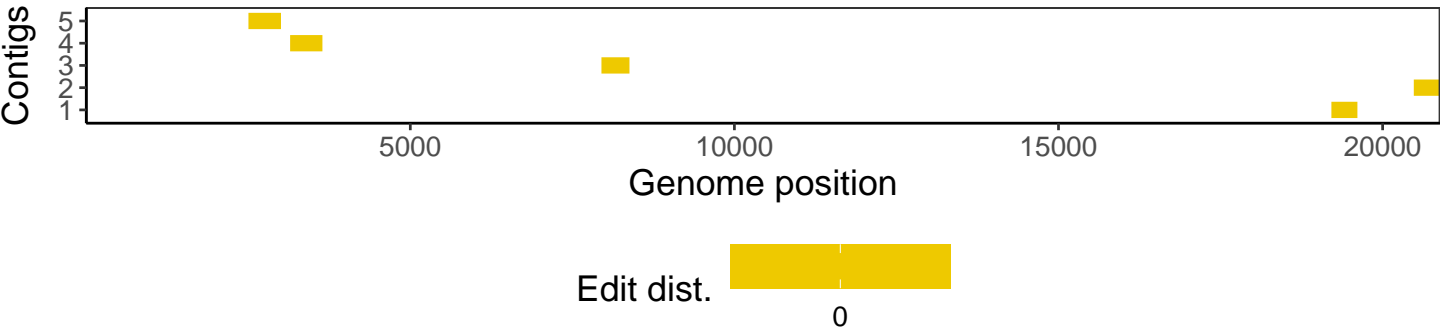
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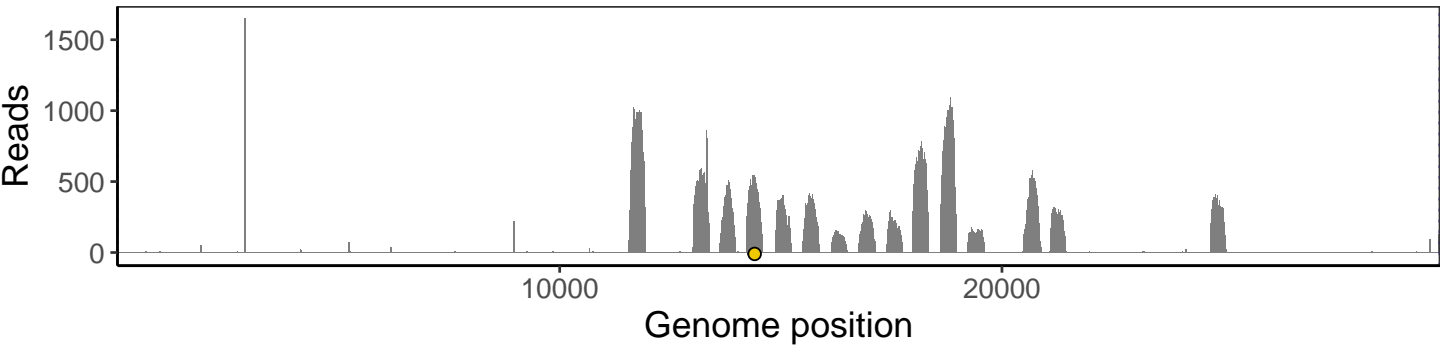
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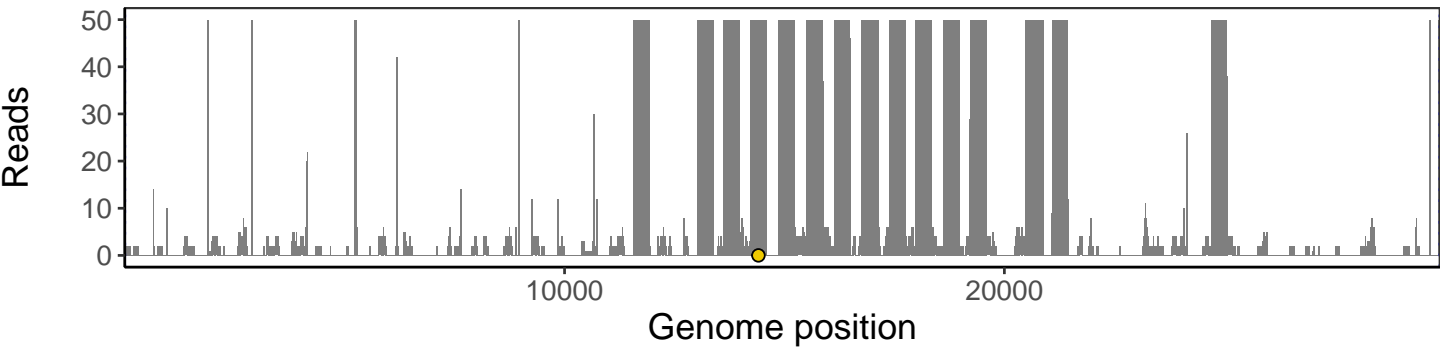
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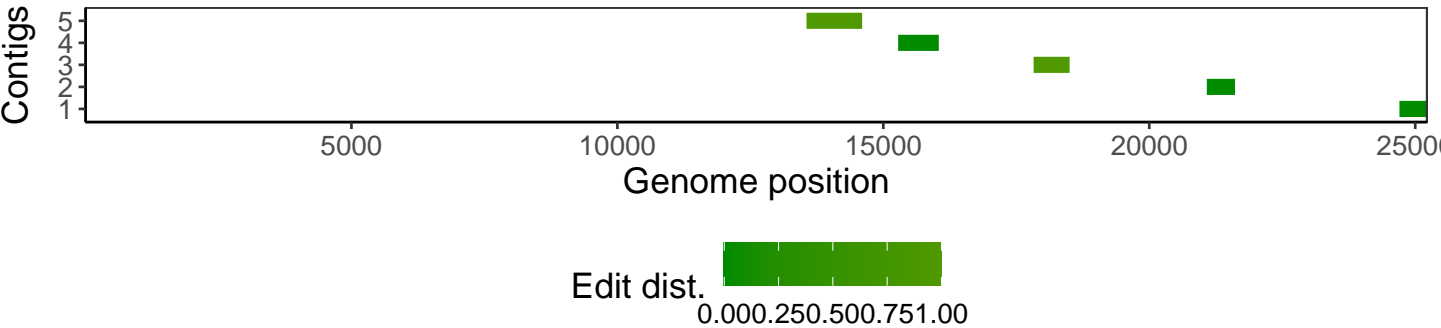
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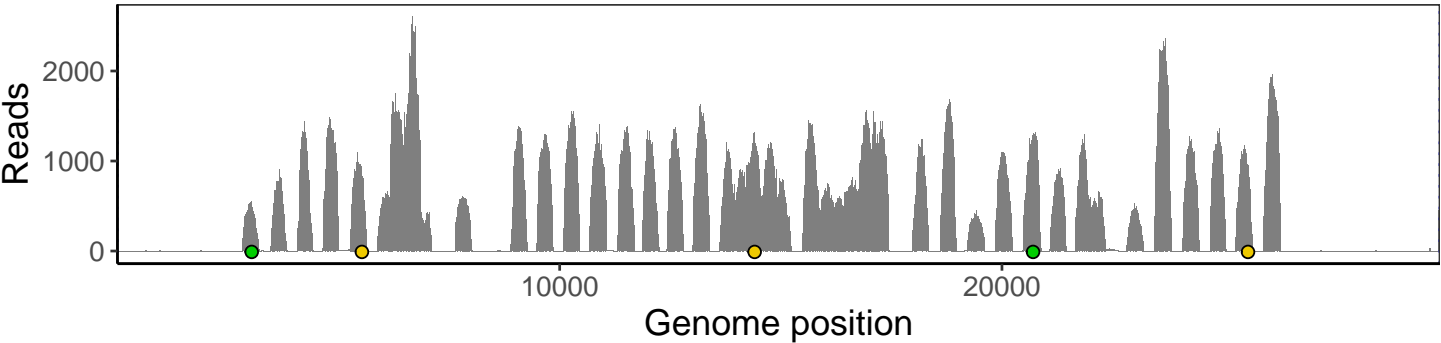
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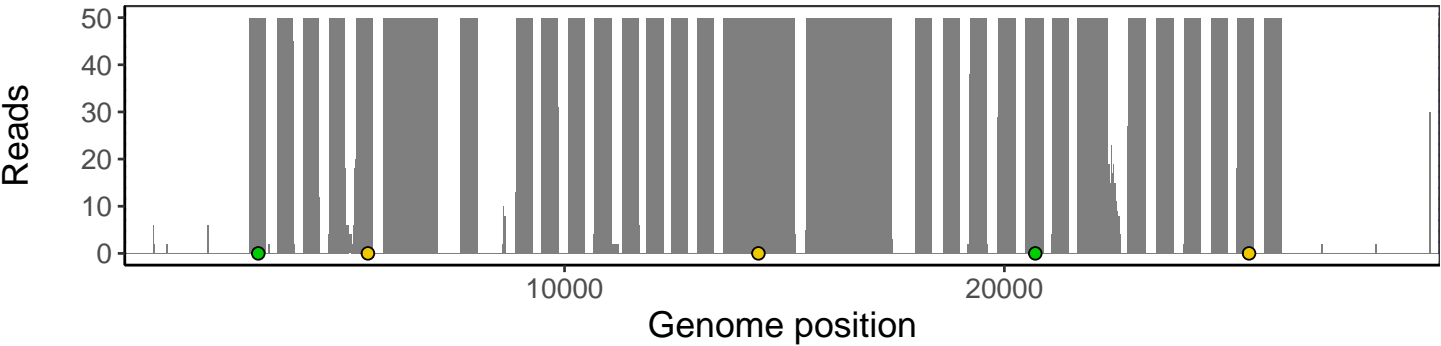
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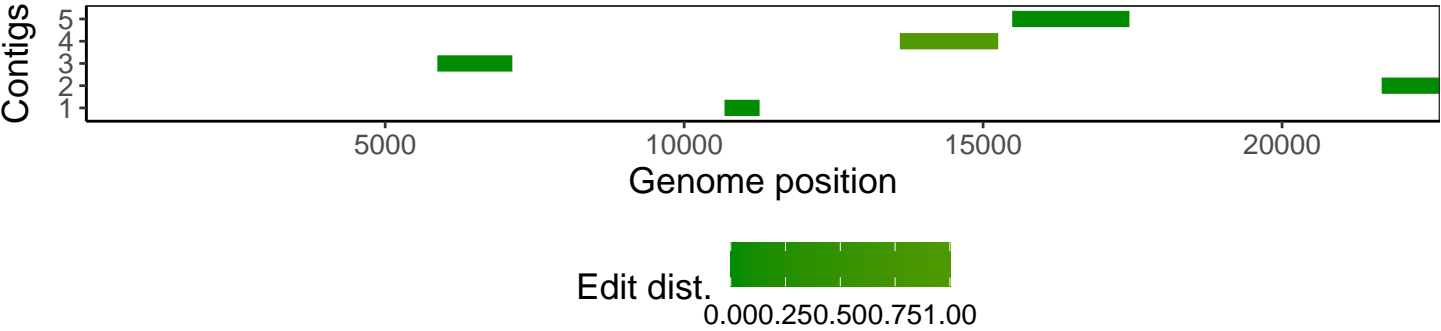
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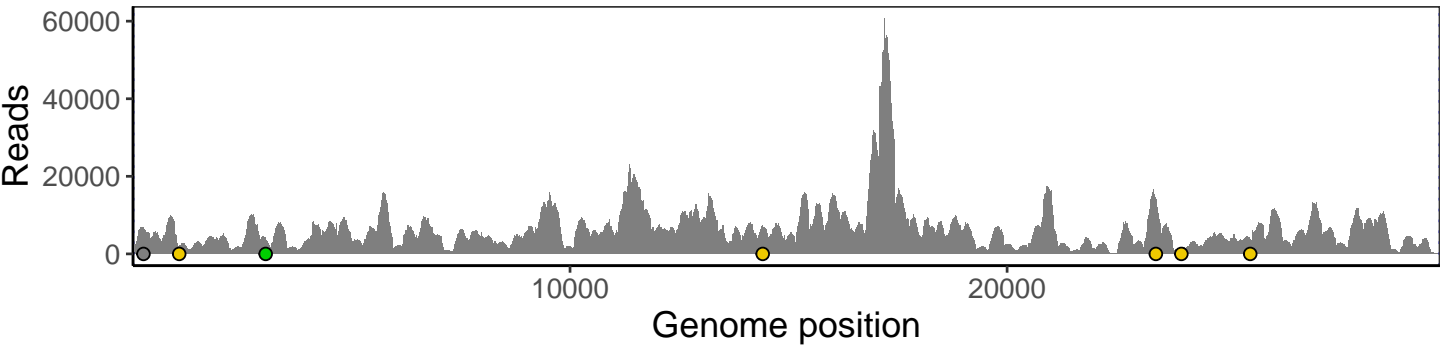
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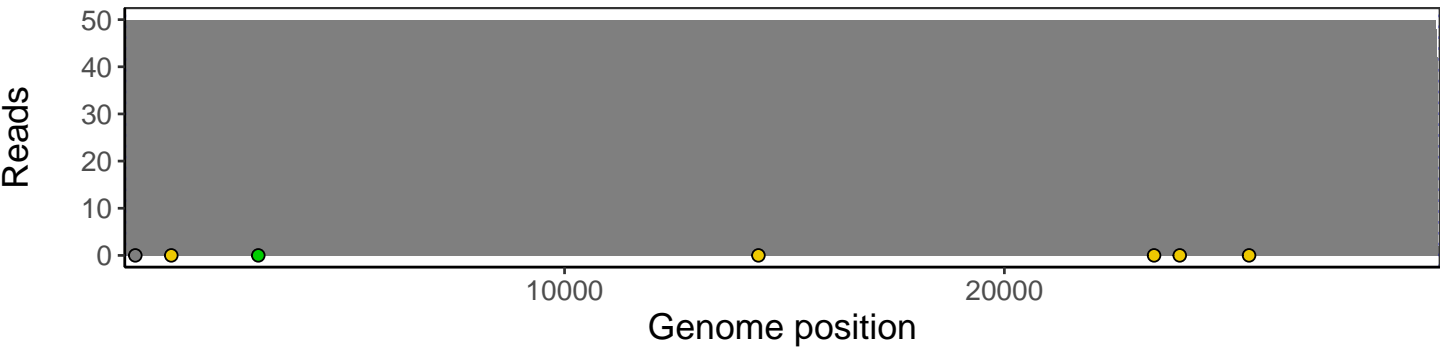
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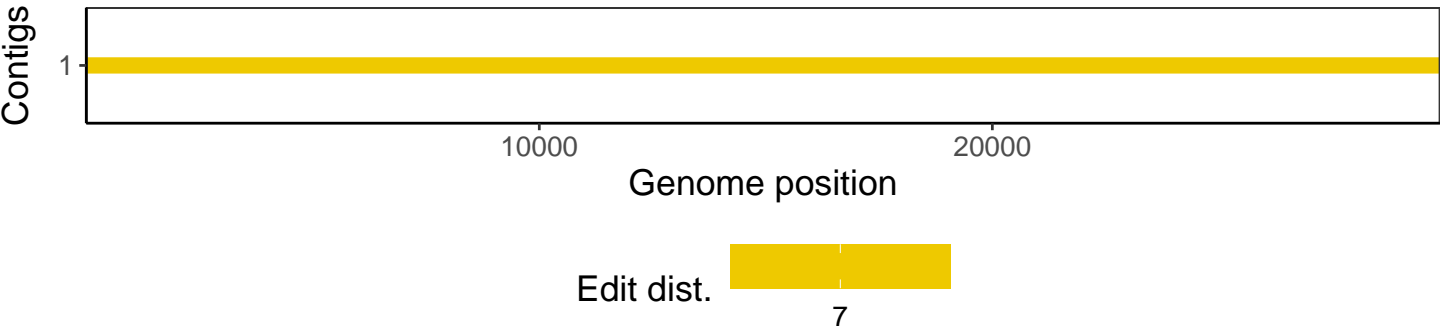
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## Software environment

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