

COVID-19 subject 266

2021-01-31

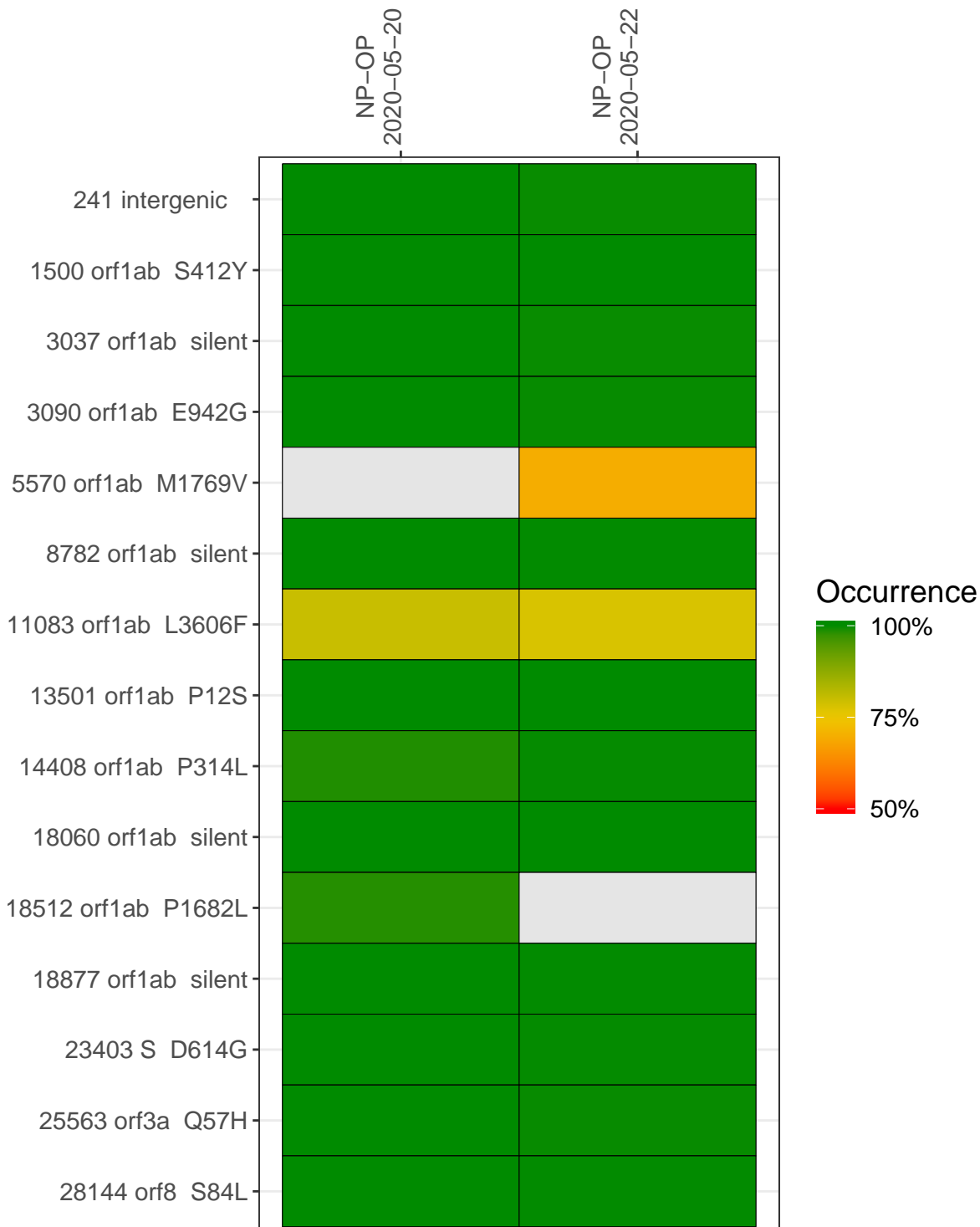
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP0155	composite	NA	NP-OP	2020-05-20	22.33	B.1.255	99.8%	99.3%
VSP0163	composite	NA	NP-OP	2020-05-22	29.75	B.1.255	99.9%	99.8%
VSP0155-1	single experiment	17000	NP-OP	2020-05-20	21.43	B.1.255	99.4%	98.8%
VSP0155-2	single experiment	85000	NP-OP	2020-05-20	22.33	B.1.255	99.7%	98.8%
VSP0163-1	single experiment	1530000	NP-OP	2020-05-22	29.75	B.1.255	99.9%	99.8%
VSP0163-2	single experiment	7650000	NP-OP	2020-05-22	29.84	B.1.255	99.9%	99.8%
VSP0319-1	single experiment	143500	NP-OP	2020-05-20	22.25	B.1.255	99.3%	98.7%
VSP0320-1	single experiment	5750000	NP-OP	2020-05-22	29.86	B.1.255	99.8%	99.8%

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.



	NP-OP 2020-05-20			NP-OP 2020-05-22		
241 intergenic	71	658	569	5193	2763	4882
1500 orf1ab S412Y	246	60	63	754	1881	2905
3037 orf1ab silent	68	613	536	3684	2609	3284
3090 orf1ab E942G	79	842	657	4173	2180	2702
5570 orf1ab M1769V	59	116	146	1387	2625	3629
8782 orf1ab silent	33	179	210	1458	2932	4598
11083 orf1ab L3606F	131	268	260	1133	1645	1308
13501 orf1ab P12S	63	172	145	1225	3581	5258
14408 orf1ab P314L	100	154	183	2018	3763	4215
18060 orf1ab silent	55	143	100	1366	1898	2185
18512 orf1ab P1682L	125	469	443	1867	5306	6616
18877 orf1ab silent	97	766	745	3292	3404	3940
23403 S D614G	149	1210	1351	5798	4166	5545
25563 orf3a Q57H	76	538	507	4838	2378	3408
28144 orf8 S84L	137	473	552	3547	1656	2149
	VSP0155-1	VSP0155-2	VSP0319-1	VSP0163-1	VSP0163-2	VSP0320-1

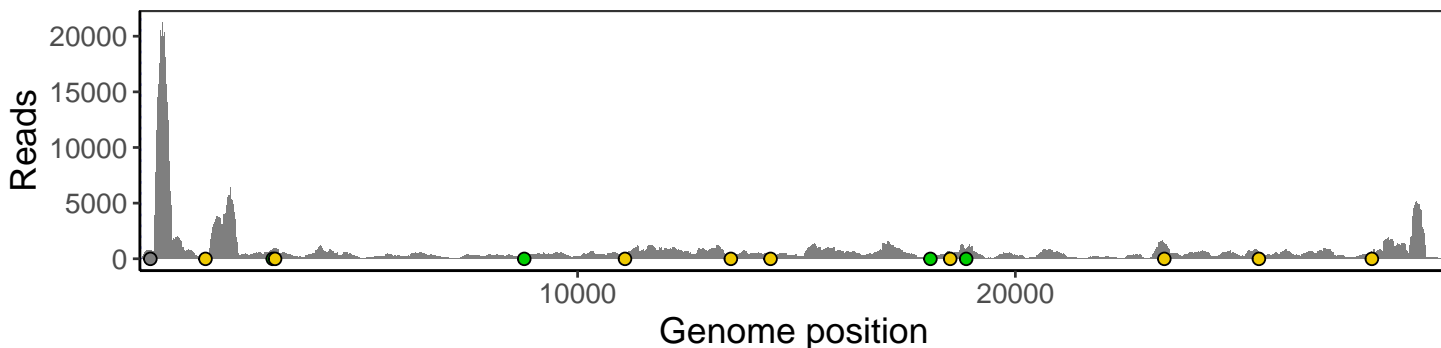
Base change

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

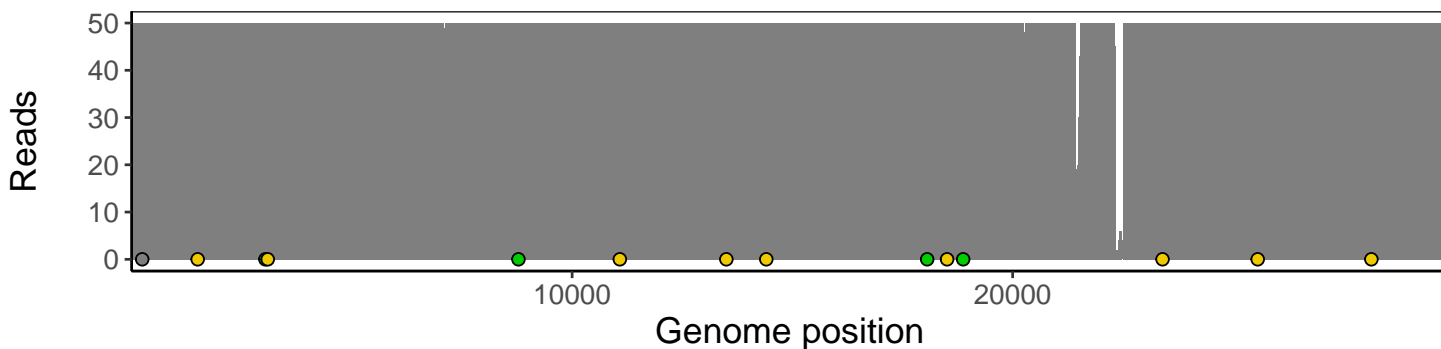
Analyses of individual experiments and composite results

VSP0155 | 2020-05-20 | NP-OP | 266no-q | composite result

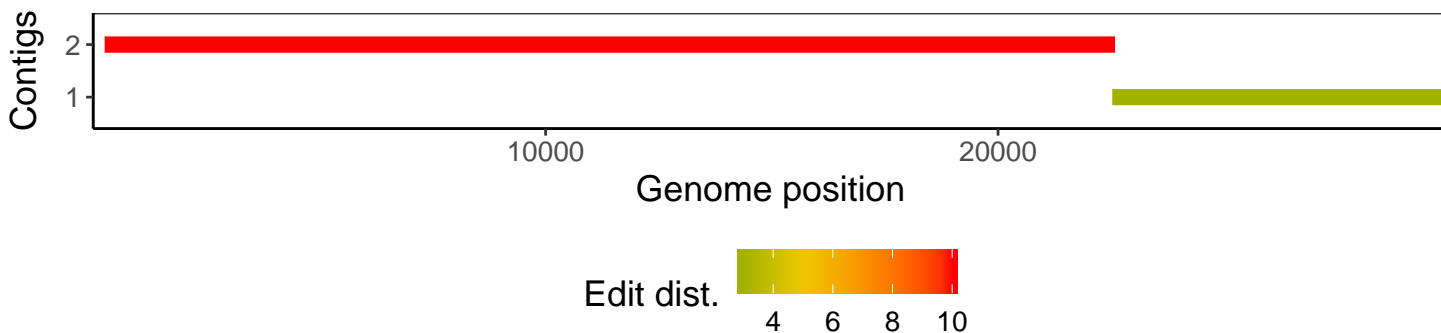
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



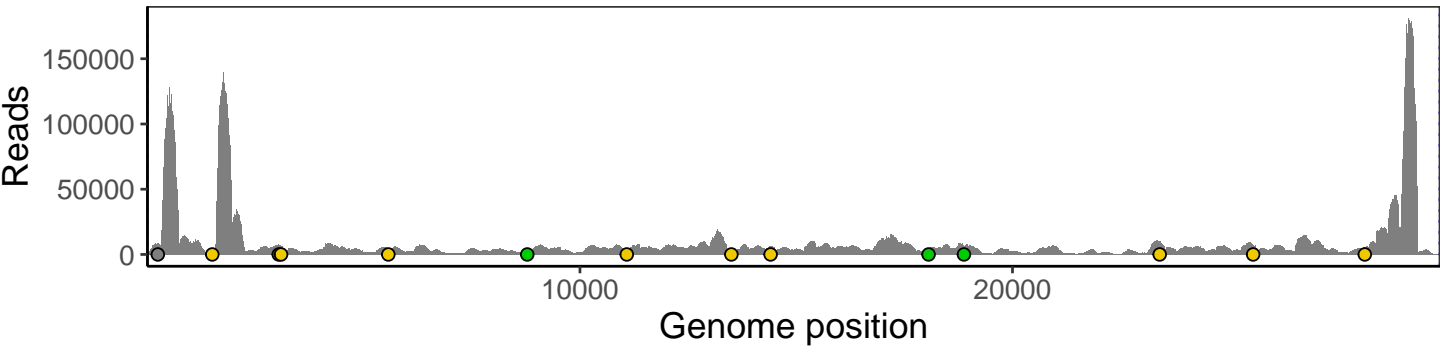
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



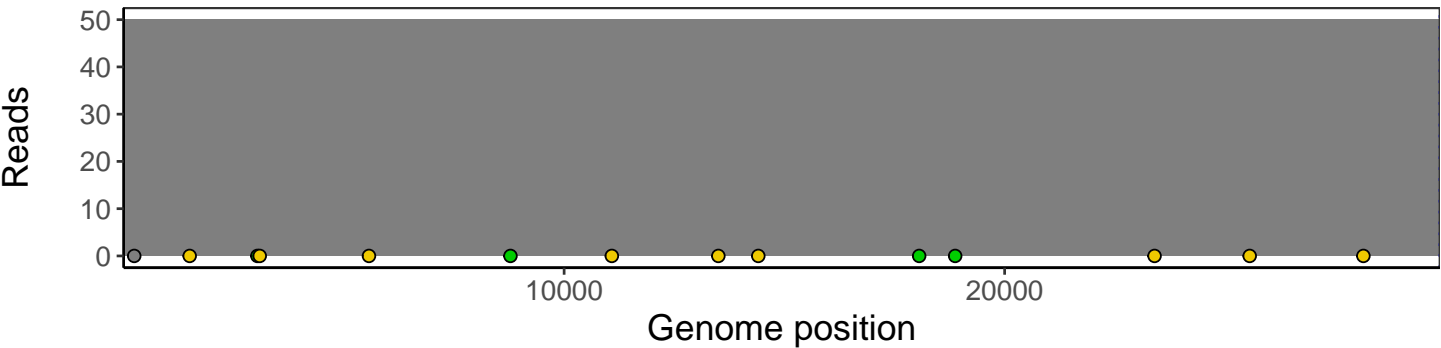
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



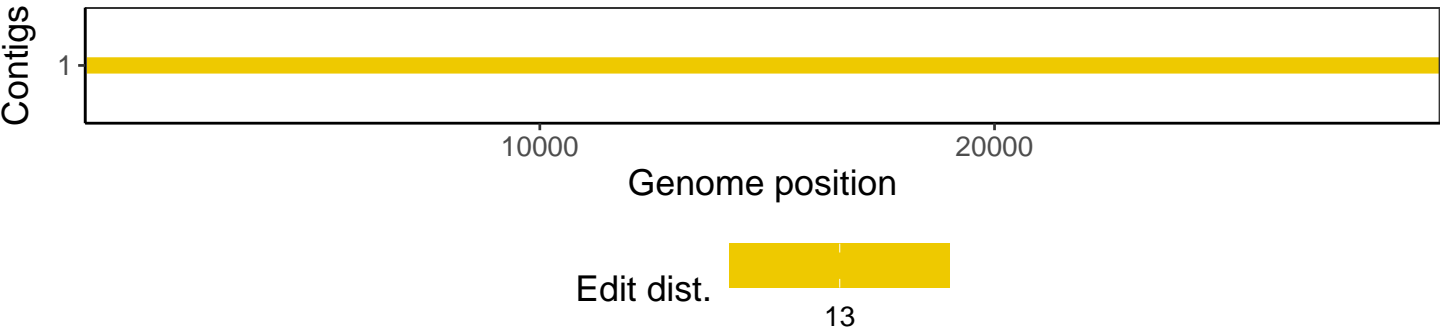
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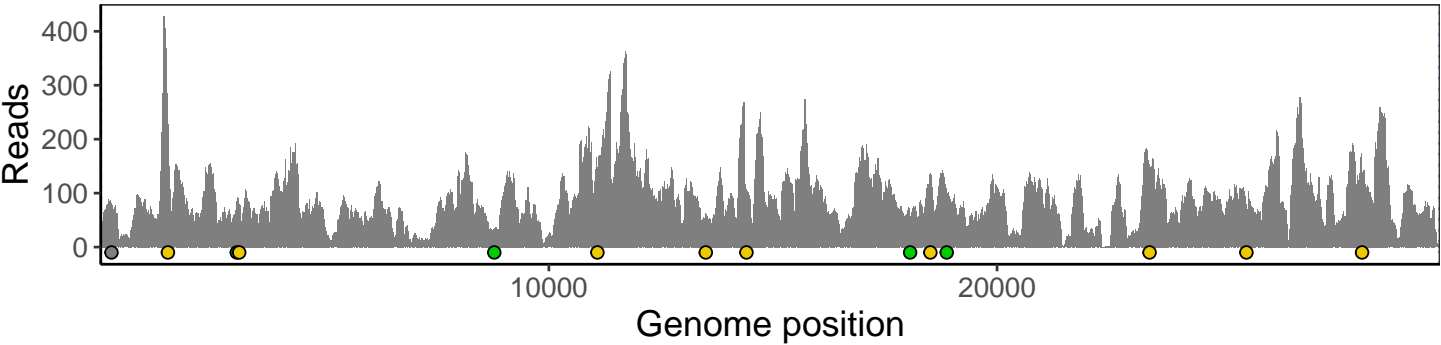
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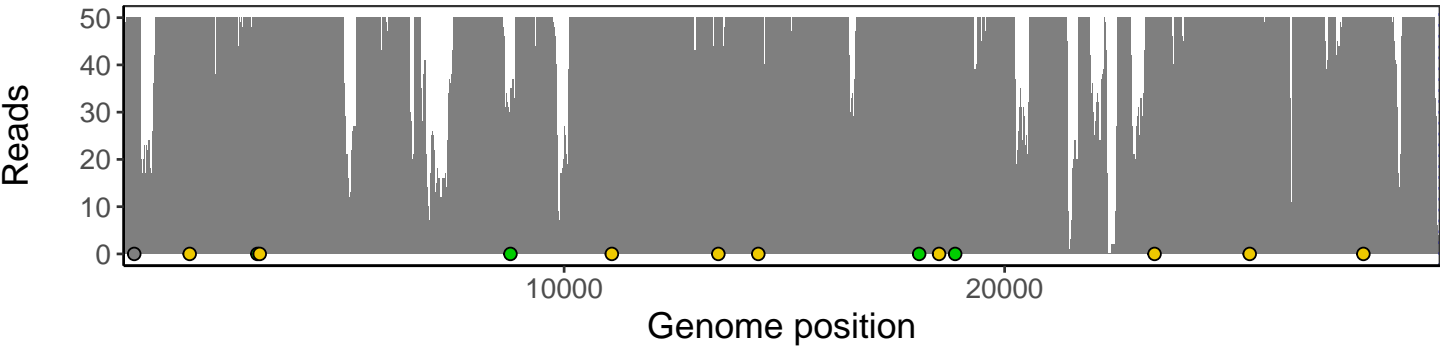
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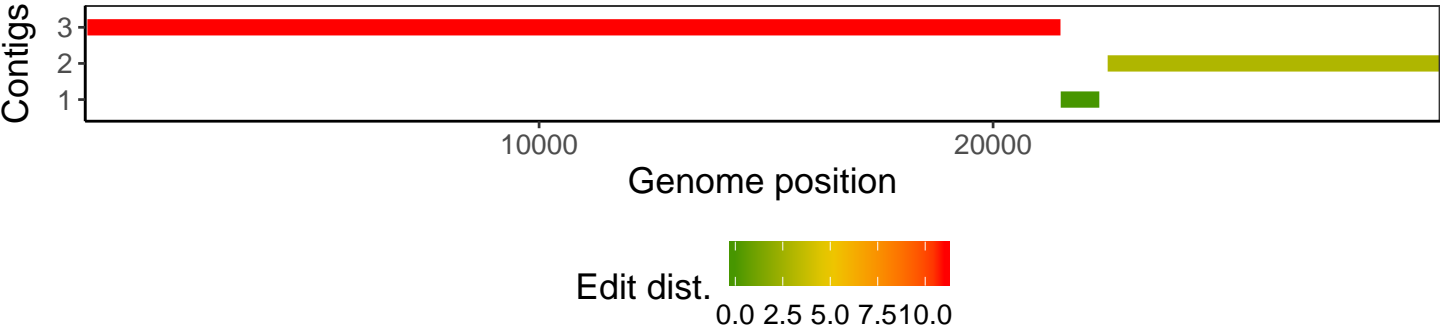
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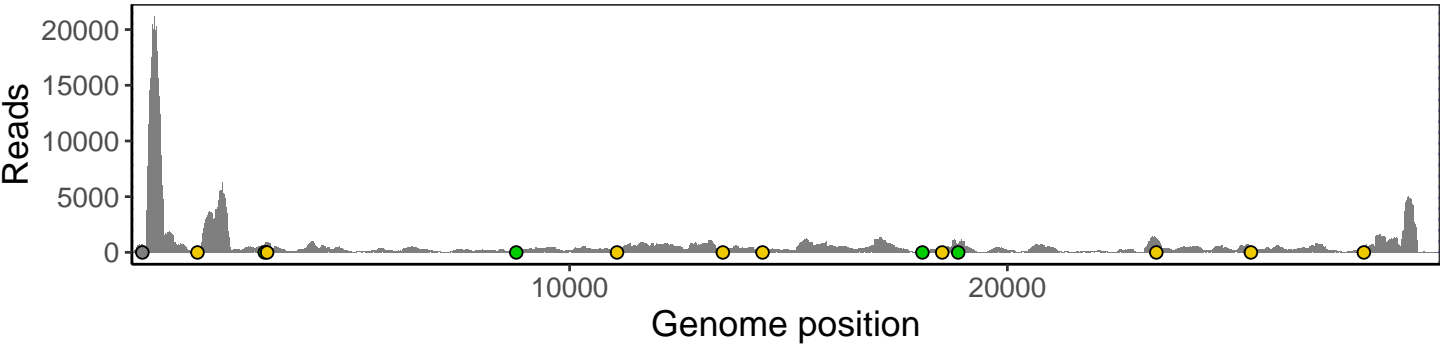
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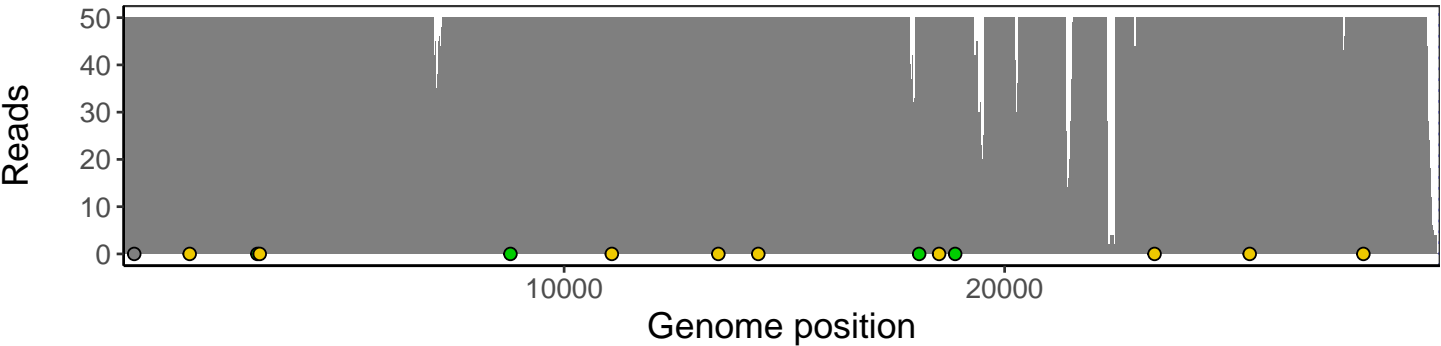
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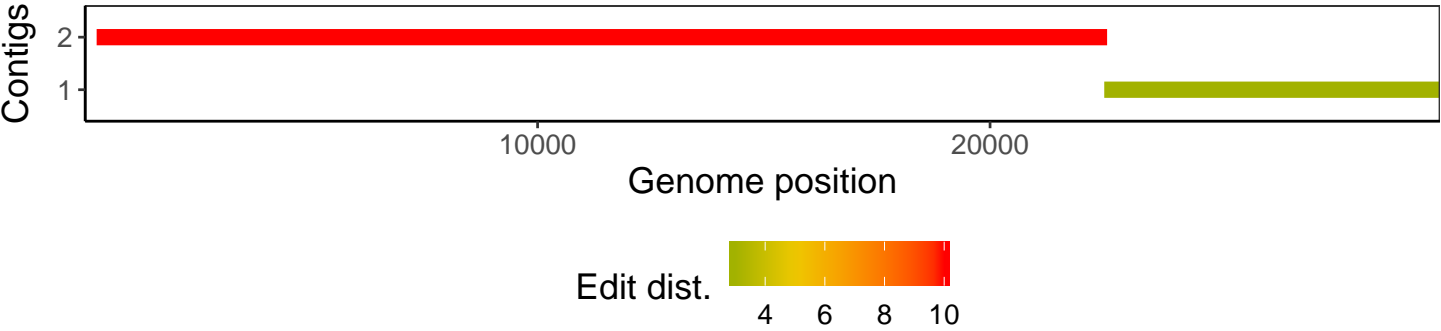
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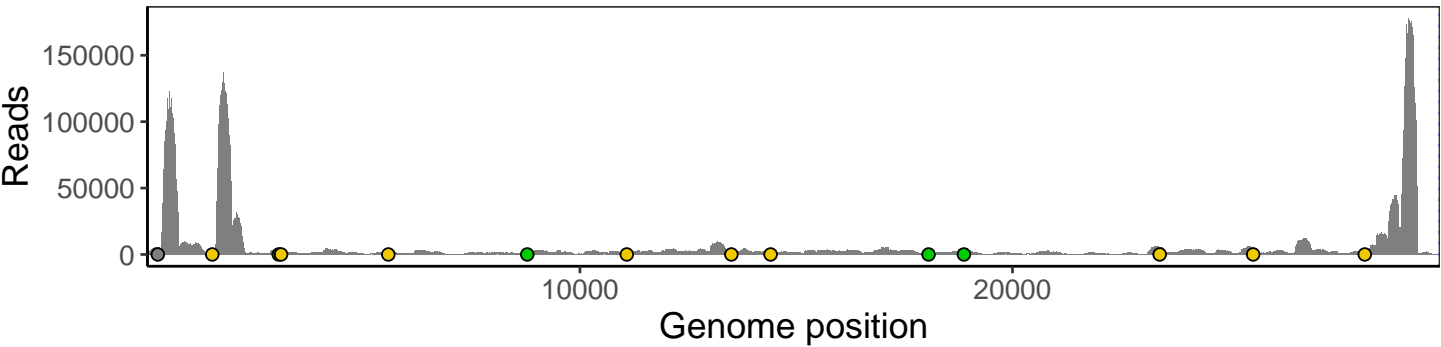
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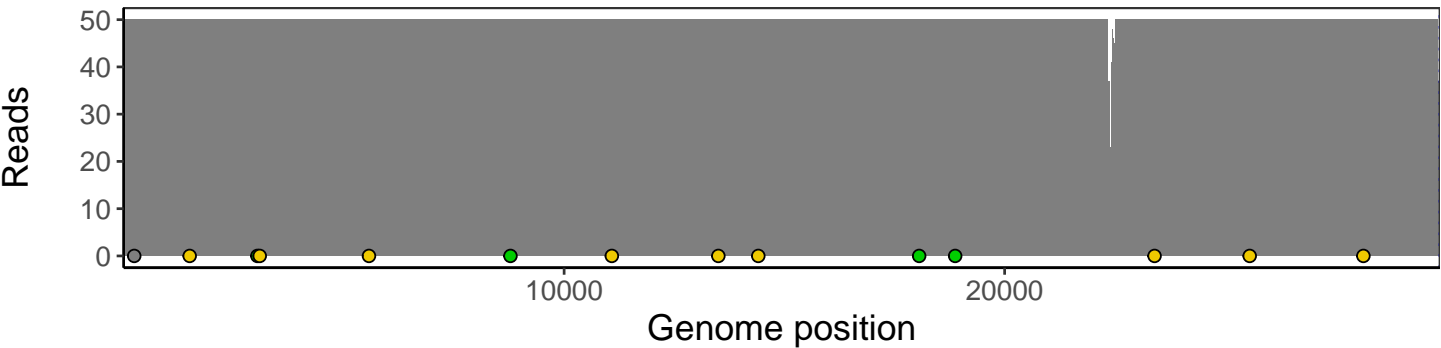
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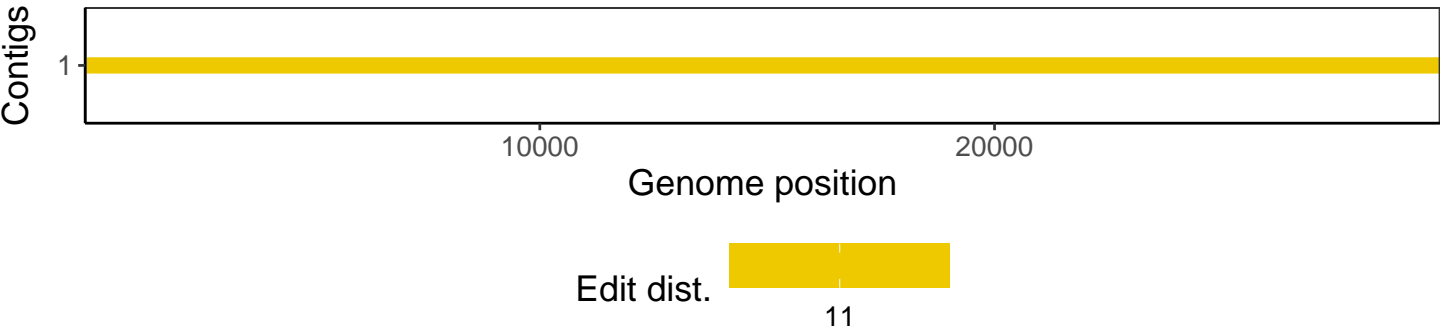
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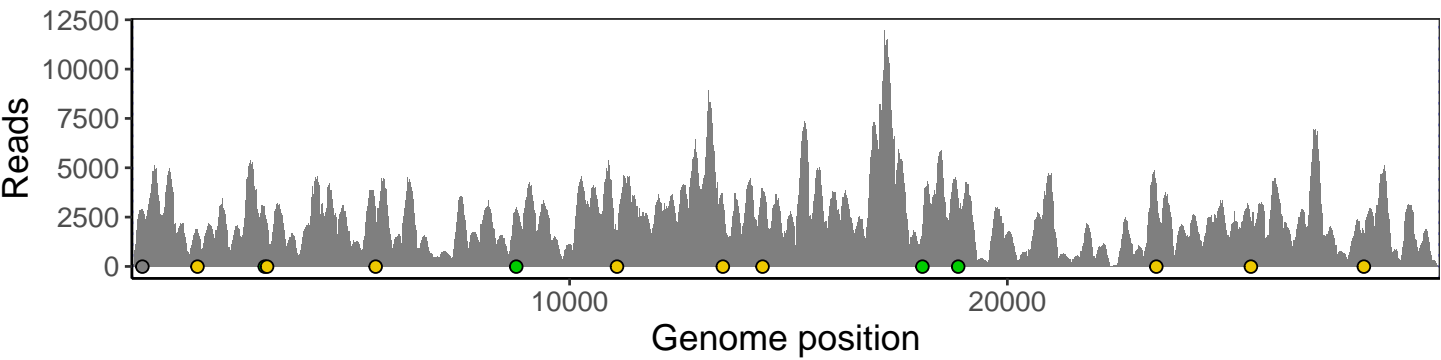
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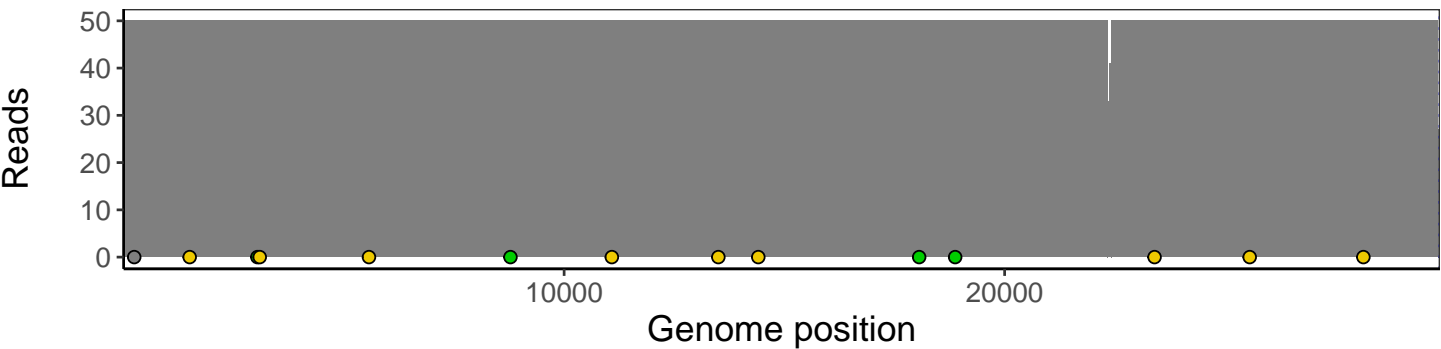
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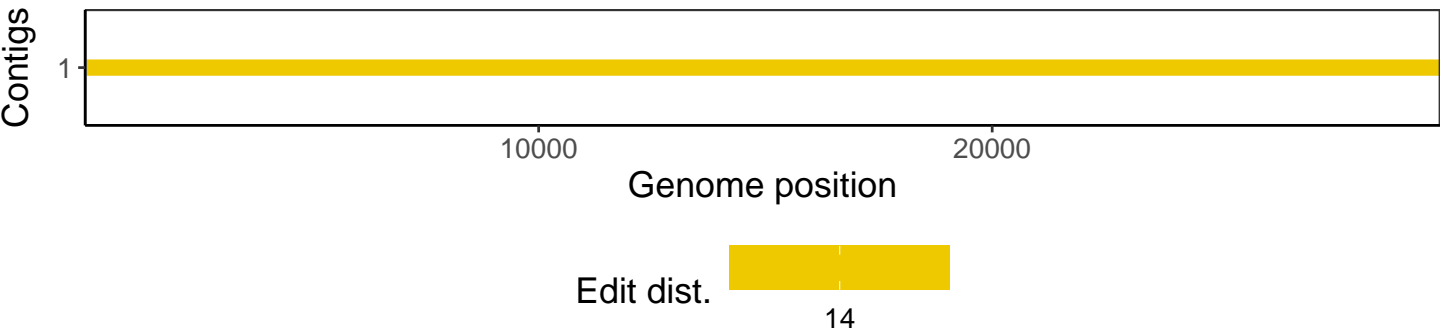
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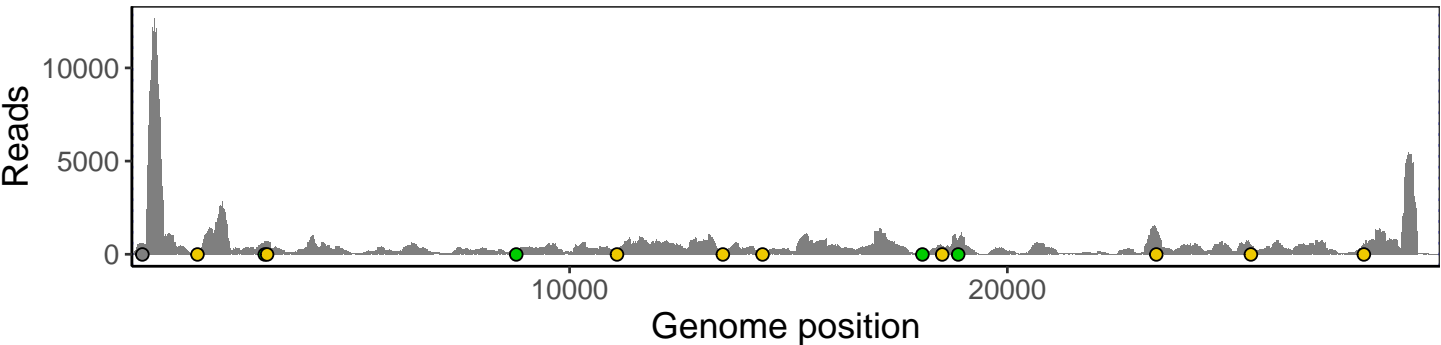
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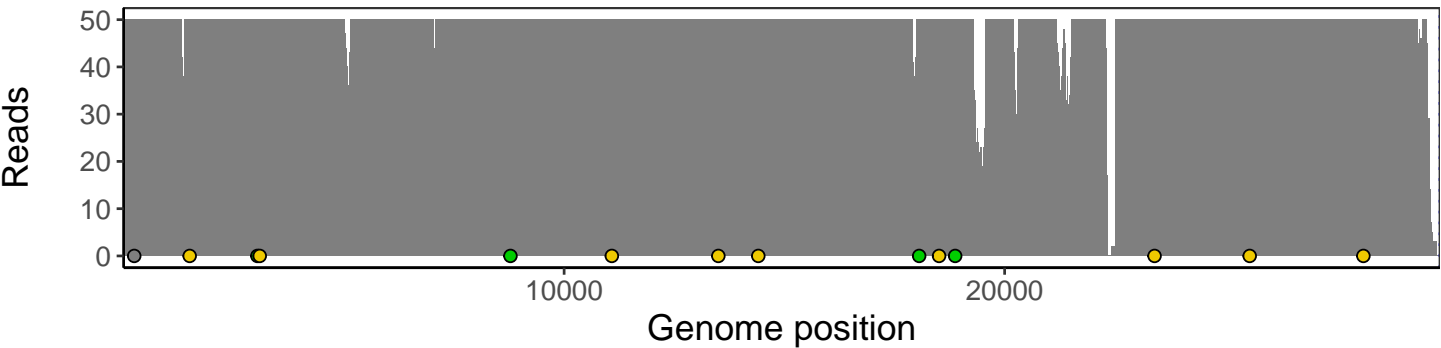
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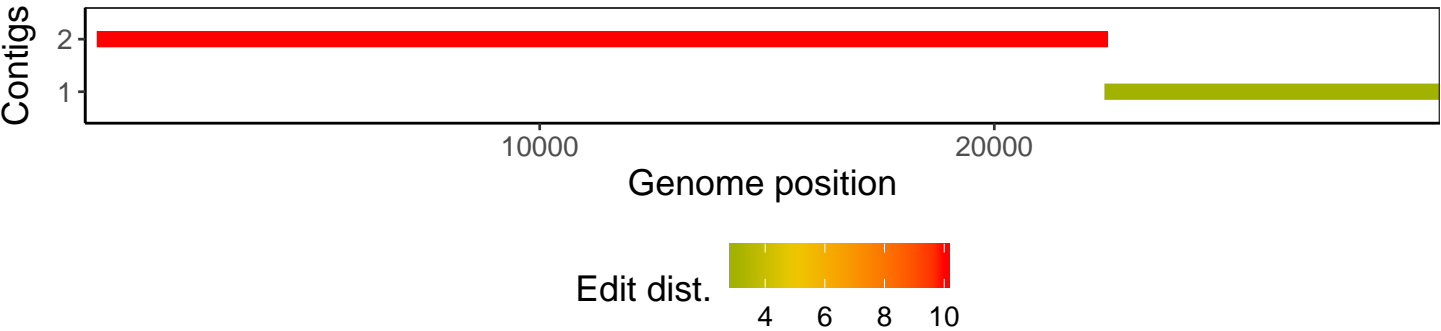
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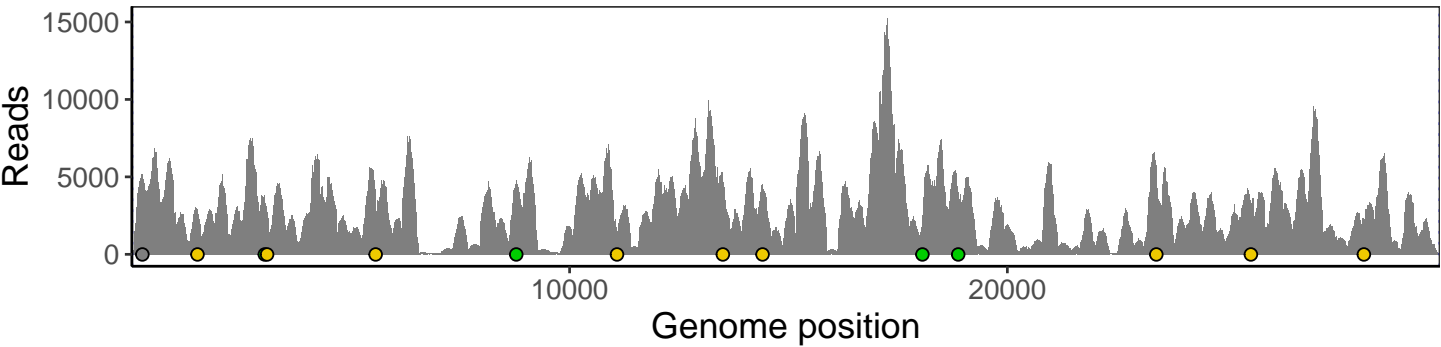
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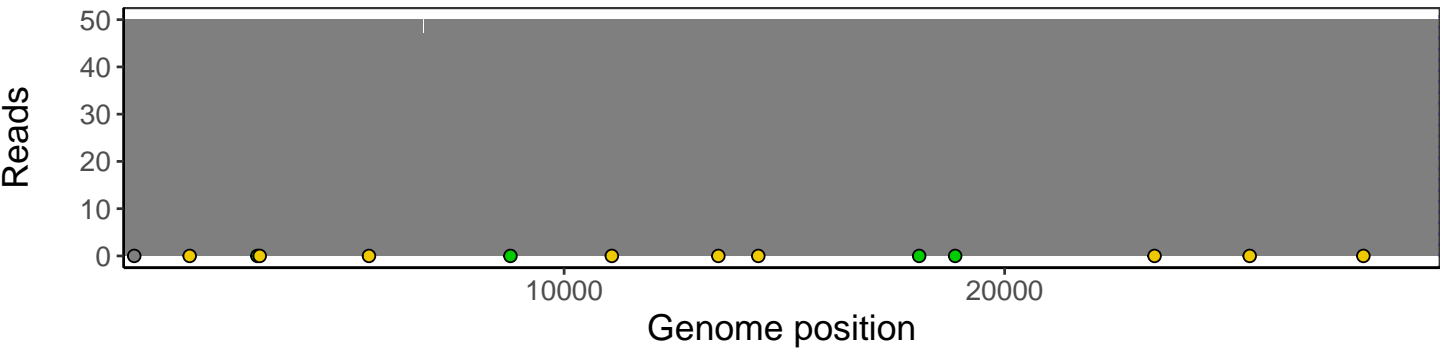
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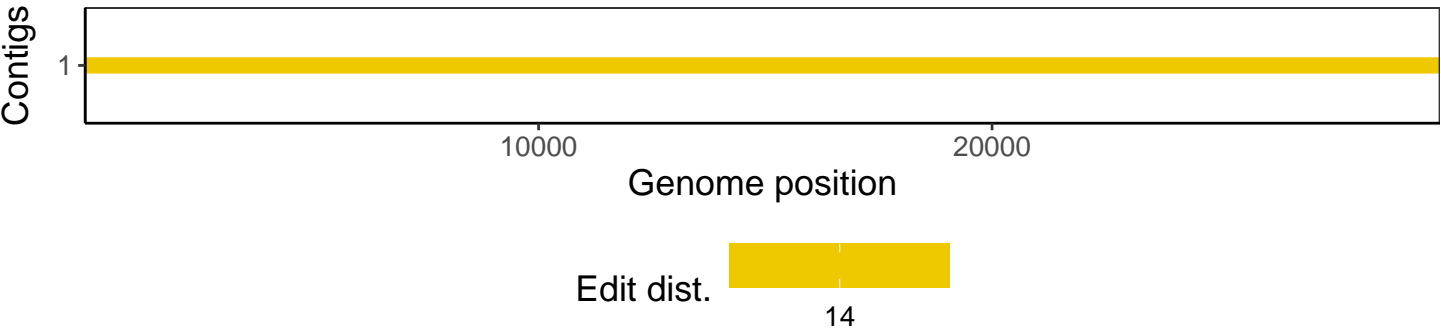
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Software environment

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	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