

COVID-19 subject 228

2021-01-10

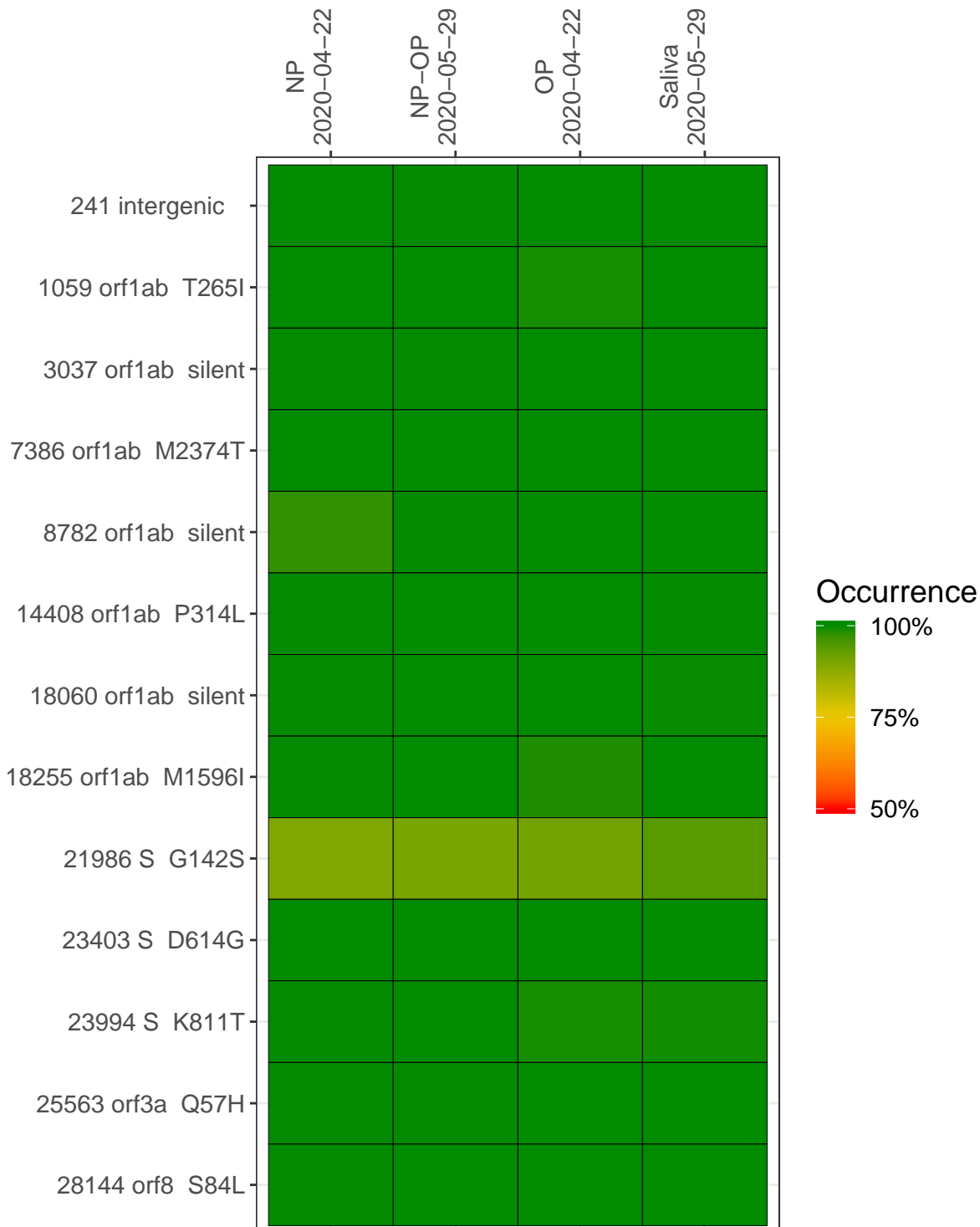
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found ([here](#)).

Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0021	composite	NA	NP	2020-04-22	29.82	99.8%	99.8%
VSP0022	composite	NA	OP	2020-04-22	29.68	99.8%	98.8%
VSP0187	composite	NA	ETA	2020-05-29	0.30	14.0%	0.0%
VSP0188	composite	NA	NP-OP	2020-05-29	29.90	99.8%	99.8%
VSP0021-1m	single experiment	NA	NP	2020-04-22	29.82	99.8%	99.7%
VSP0021-2	single experiment	1.10e+04	NP	2020-04-22	29.82	99.8%	99.8%
VSP0022-1a	single experiment	2.68e+05	OP	2020-04-22	1.80	81.4%	44.7%
VSP0022-2	single experiment	1.34e+06	OP	2020-04-22	0.24	6.2%	0.0%
VSP0022-3	single experiment	1.34e+06	OP	2020-04-22	29.68	99.8%	98.8%
VSP0187-1	single experiment	6.02e+01	ETA	2020-05-29	0.30	12.0%	0.0%
VSP0187-2	single experiment	3.01e+02	ETA	2020-05-29	NA	2.3%	0.0%
VSP0188-1	single experiment	2.04e+03	NP-OP	2020-05-29	9.60	93.7%	93.5%
VSP0188-2	single experiment	1.02e+04	NP-OP	2020-05-29	22.61	99.1%	99.1%
VSP0188-3	single experiment	1.02e+04	NP-OP	2020-05-29	29.87	99.8%	99.8%
VSP0189-1	single experiment	8.51e+04	Saliva	2020-05-29	29.82	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 for 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 2020-04-22		NP-OP 2020-05-29			OP 2020-04-22		Saliva 2020-05-29	
241 intergenic	715	3376	952	2393	2054	10		429	525
1059 orf1ab T265I	526	1367	1084	967	1267	2		159	300
3037 orf1ab silent	761	2478	808	1092	2805			526	718
7386 orf1ab M2374T	399	1272	1422	171	561	4		259	320
8782 orf1ab silent	358	2690	927	727	3339			244	338
14408 orf1ab P314L	1126	5107	1254	3384	3087	4		165	1362
18060 orf1ab silent	687	2681	1451	1013	2892			200	493
18255 orf1ab M1596I	597	3806	1484	1056	3890			203	579
21986 S G142S	285	583	225	374	521			56	260
23403 S D614G	683	4556	5997	8078	11471	43		516	1428
23994 S K811T	732	1981	1462	1130	843	11	1	305	270
25563 orf3a Q57H	470	3550	1782	2110	3106	5		324	1016
28144 orf8 S84L	714	4499	1899	2377	1800	23		355	572
	VSP0021-1m	VSP0021-2	VSP0188-1	VSP0188-2	VSP0188-3	VSP0022-1a	VSP0022-2	VSP0022-3	VSP0189-1

Base change

Expected

A

T

C

G

N

Ins/Del

No data

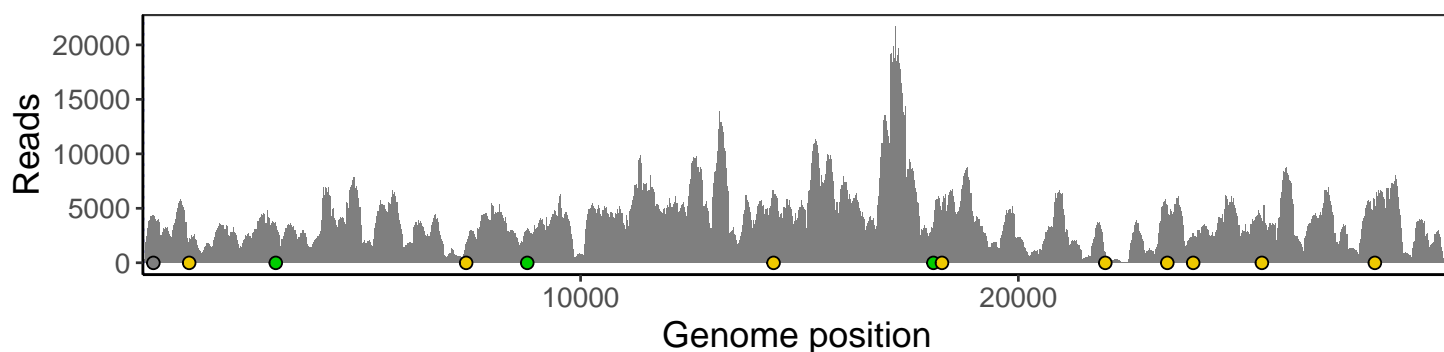
Base change

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

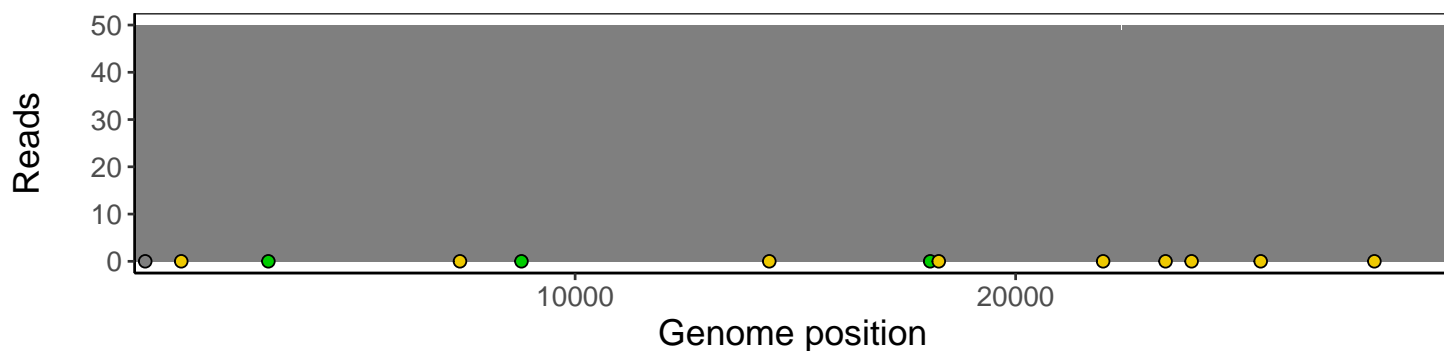
Analyses of individual experiments and composite results.

VSP0021 | 2020-04-22 | NP | 228n | composite result

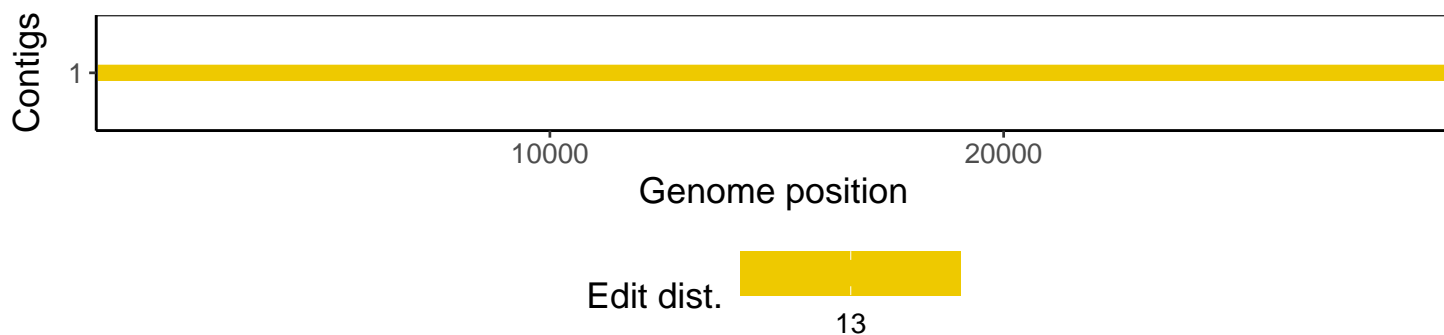
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



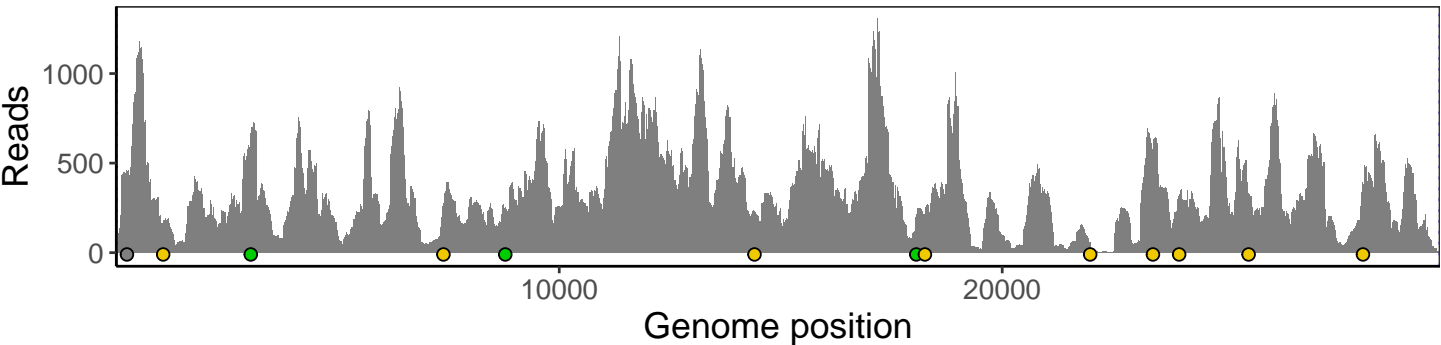
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



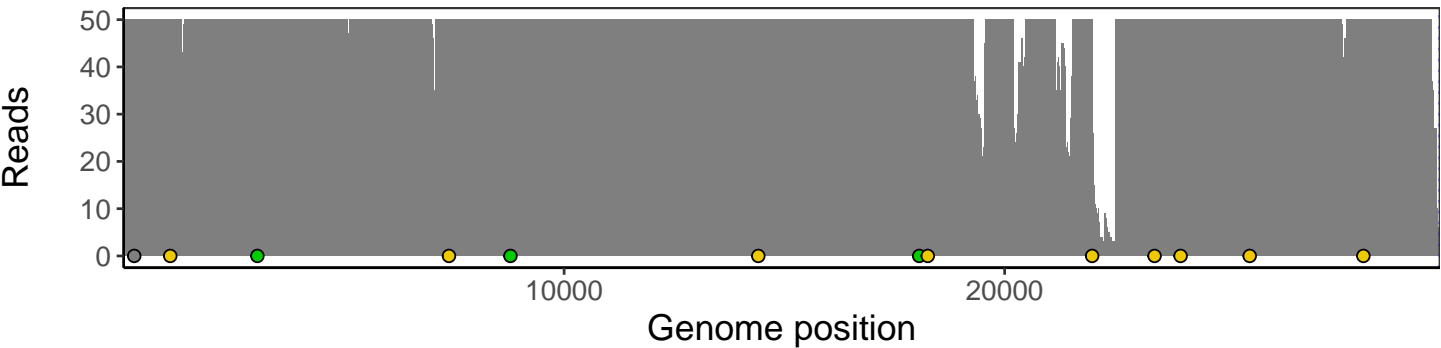
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



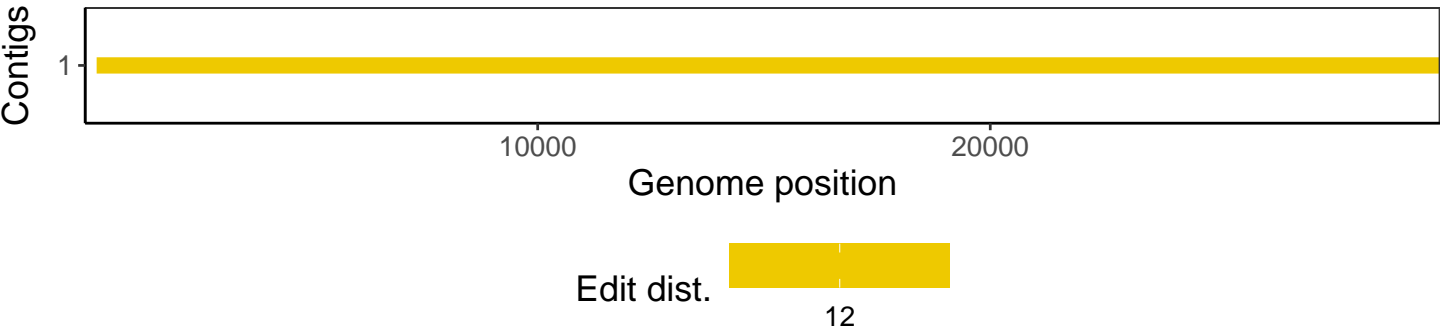
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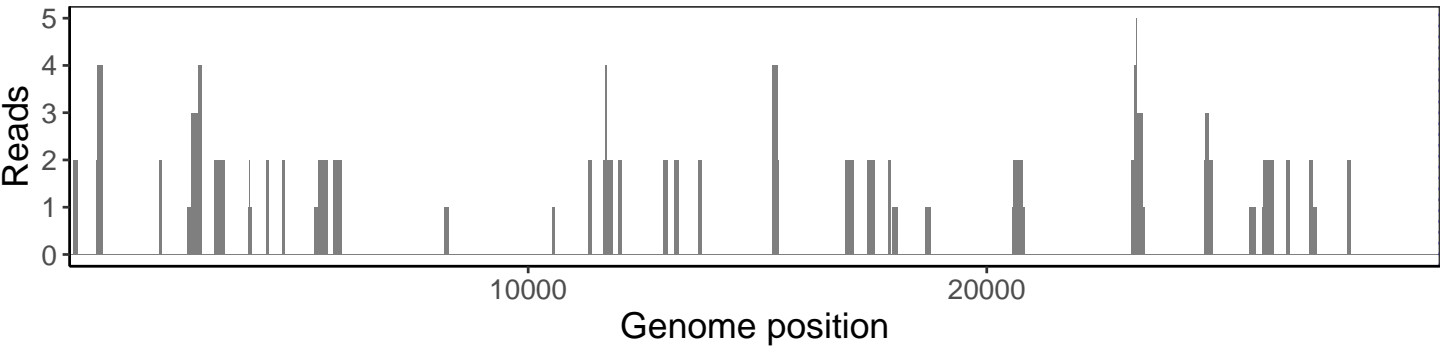
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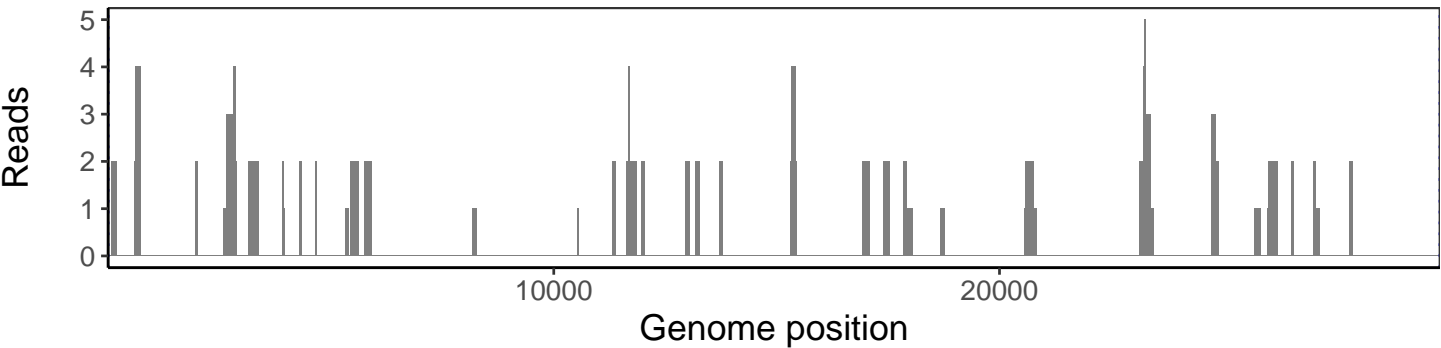
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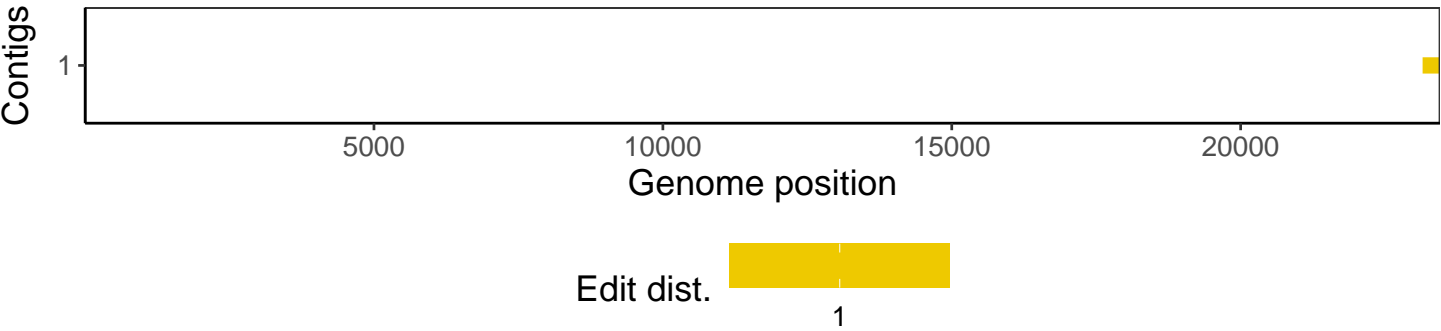
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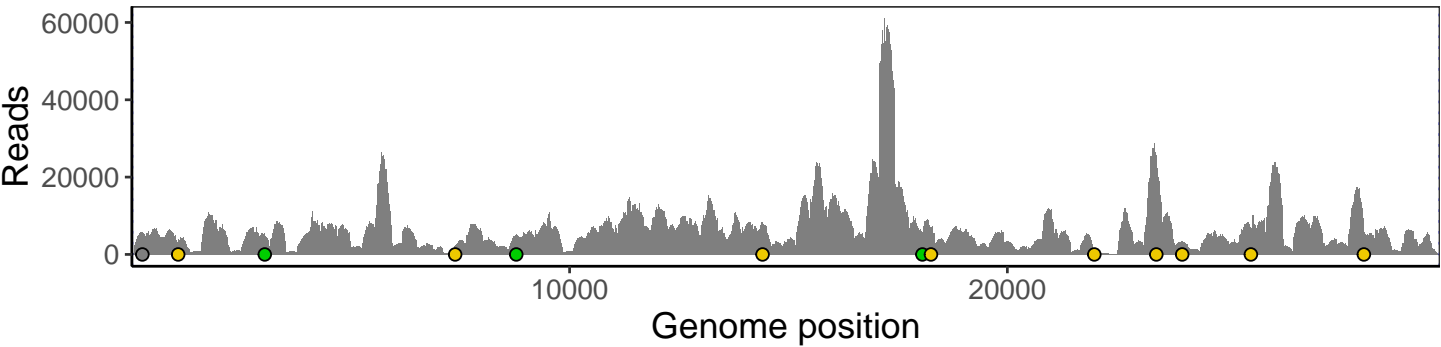
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



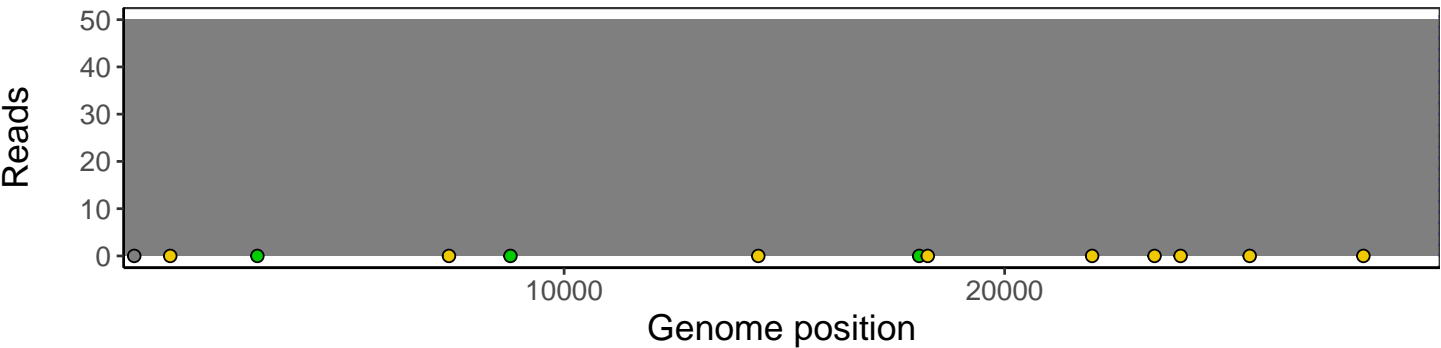
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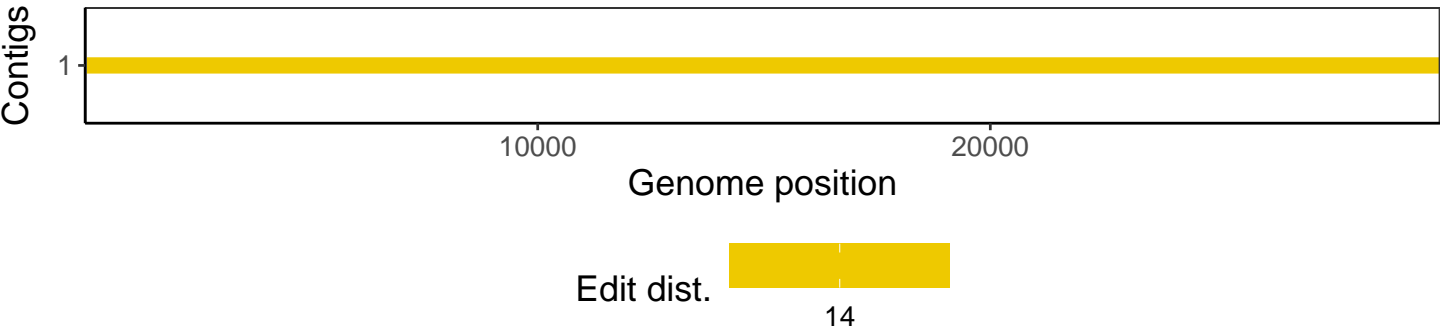
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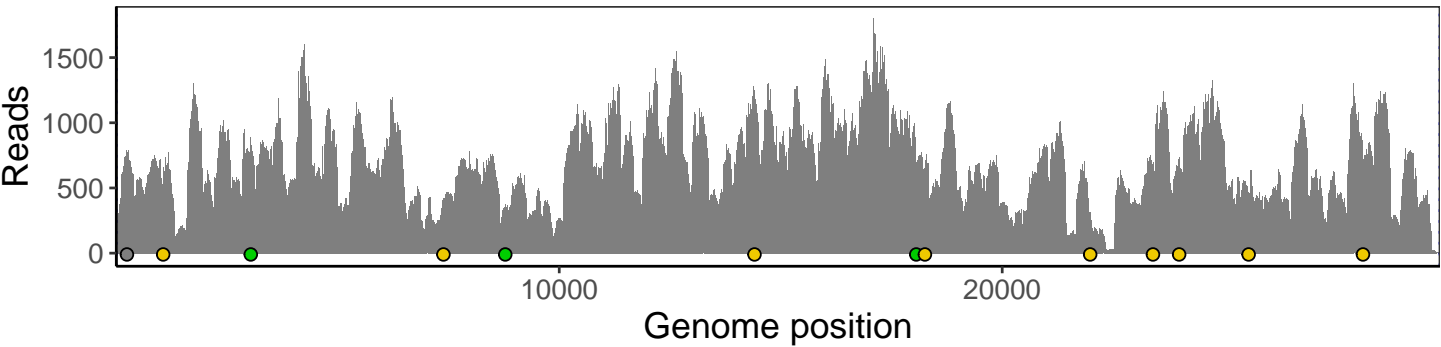
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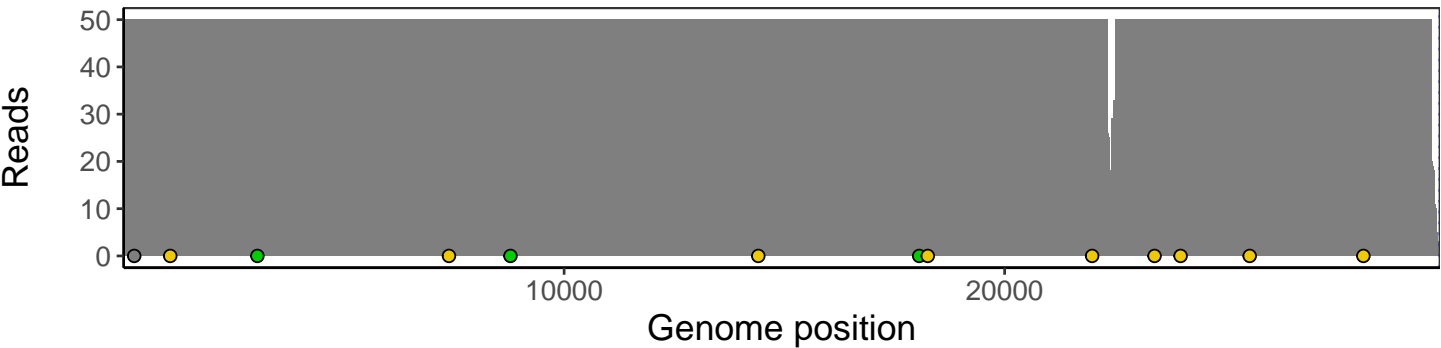
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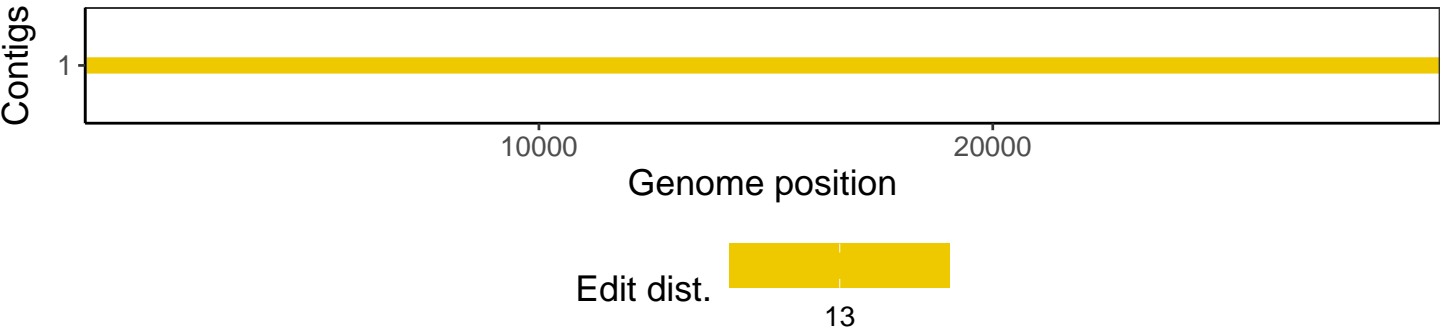
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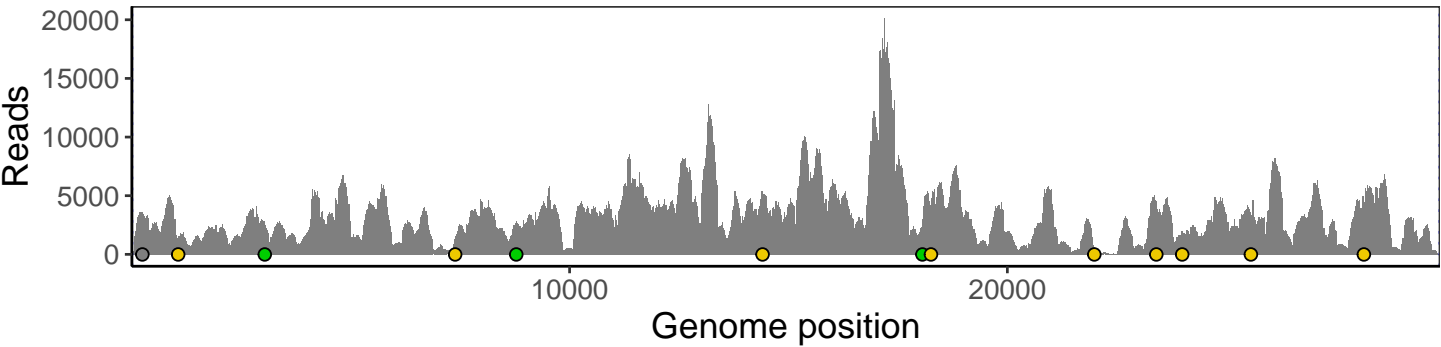
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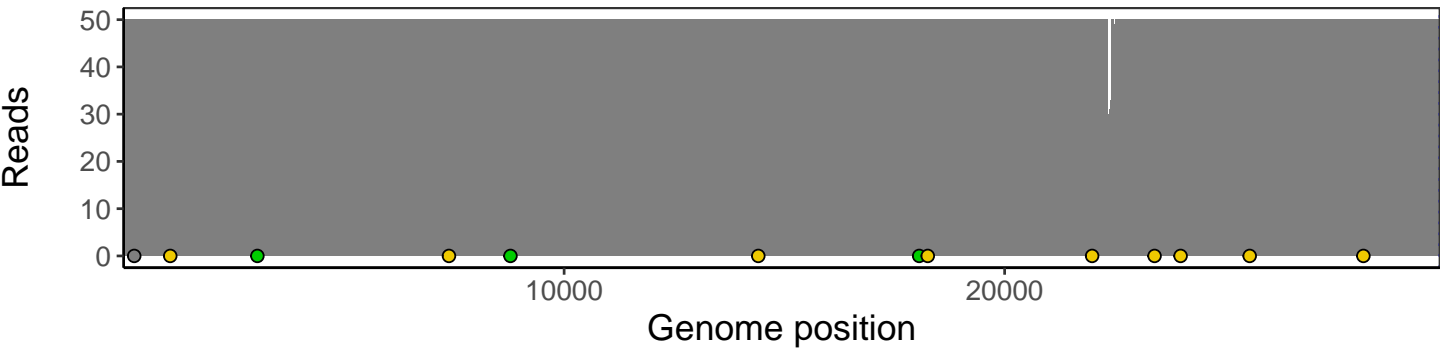
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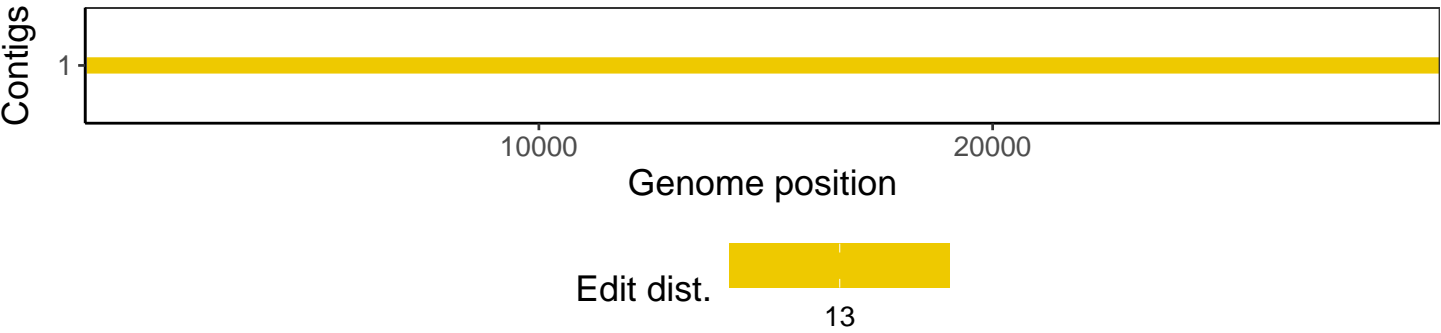
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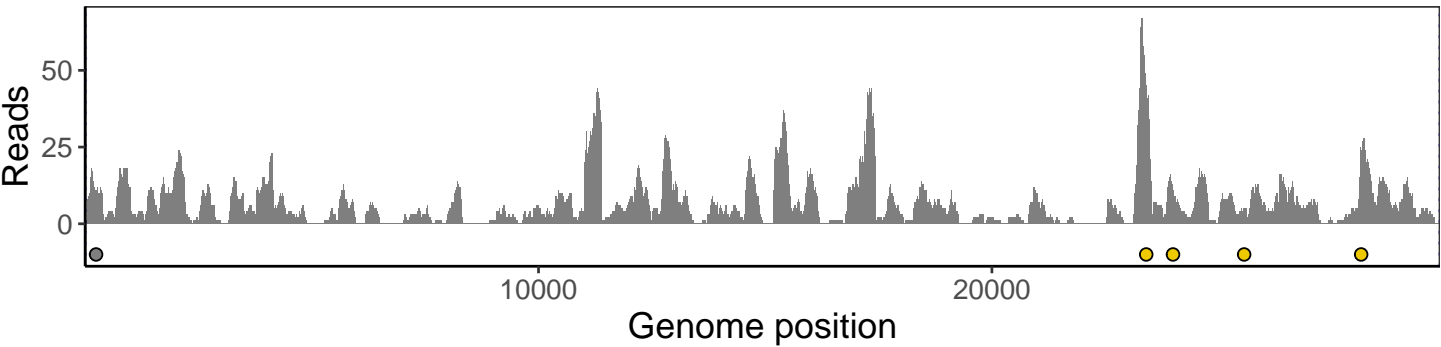
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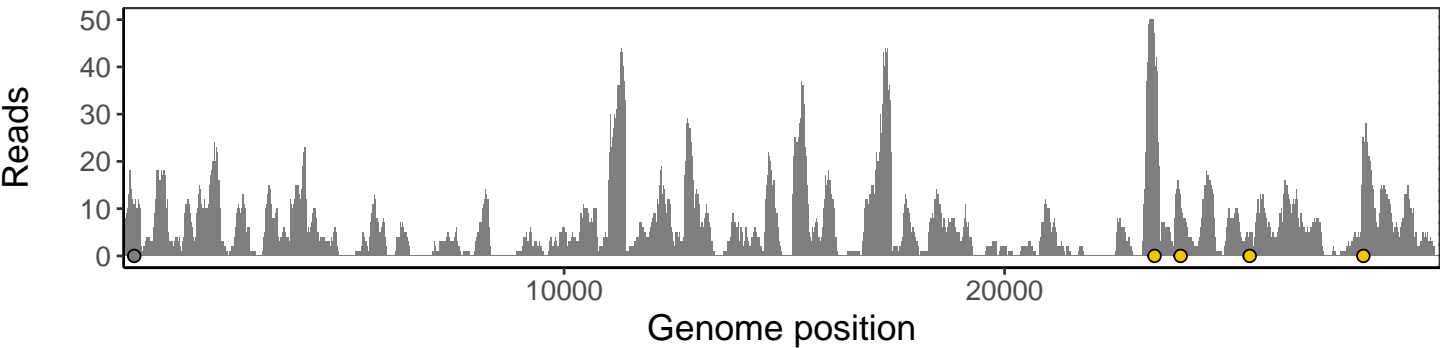
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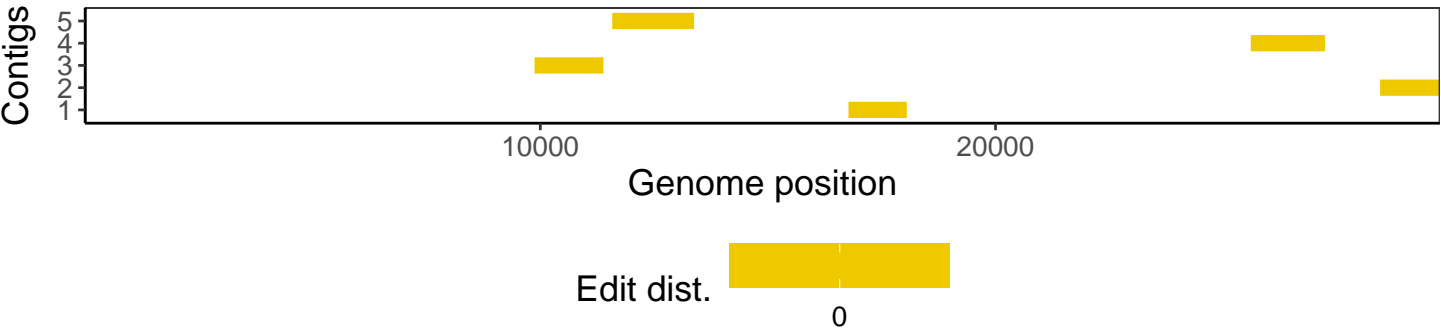
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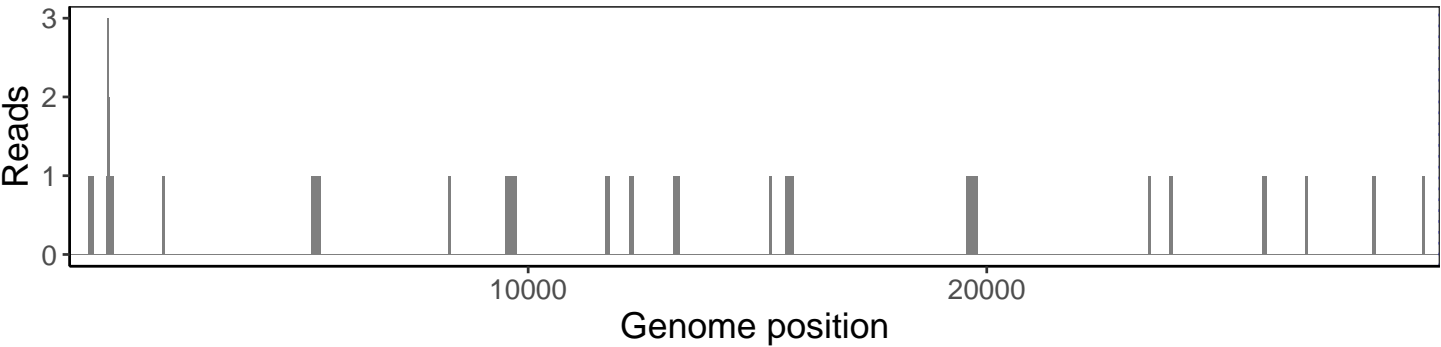
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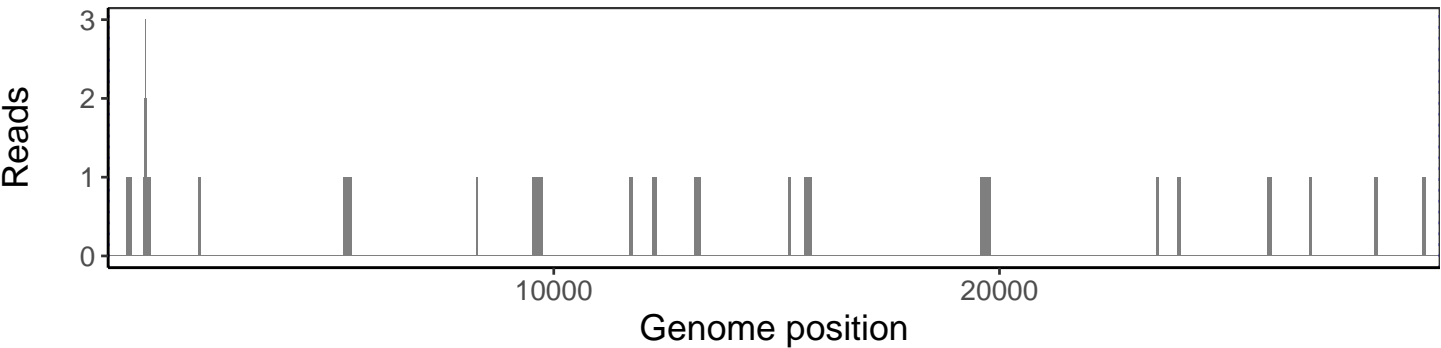
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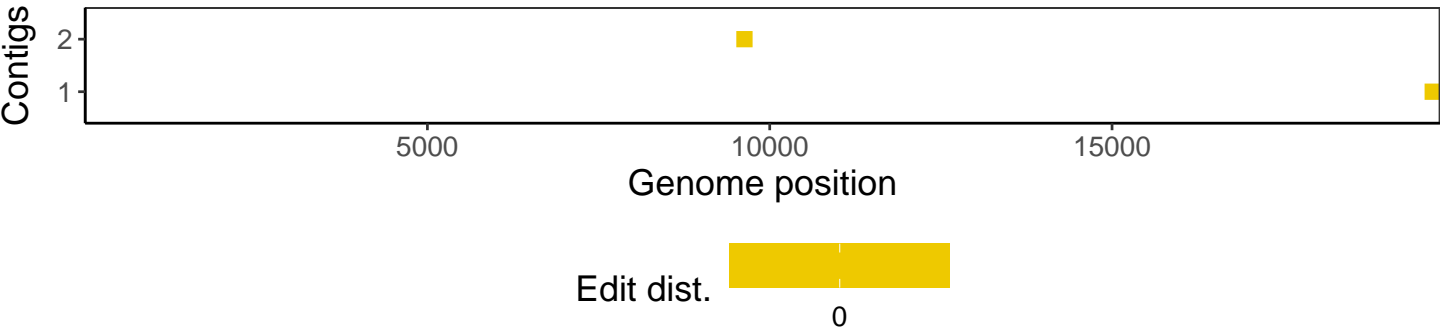
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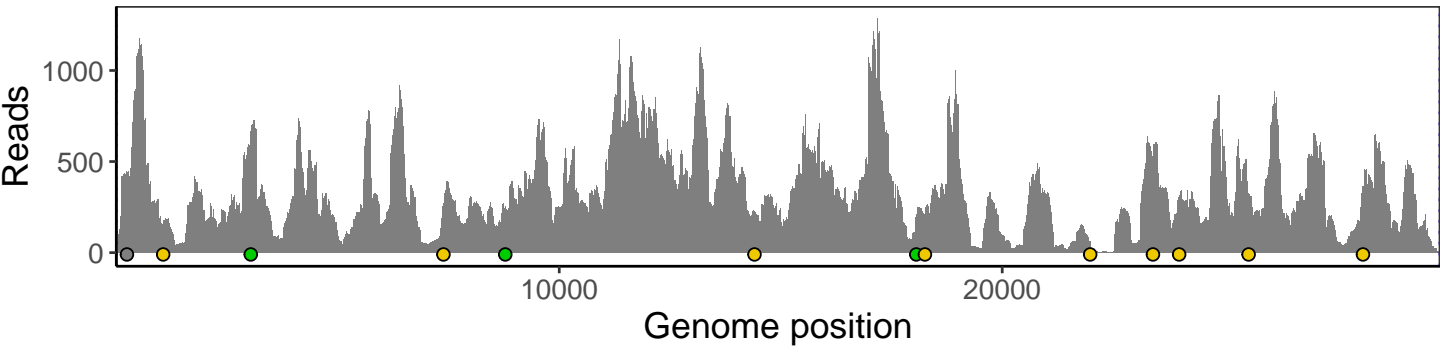
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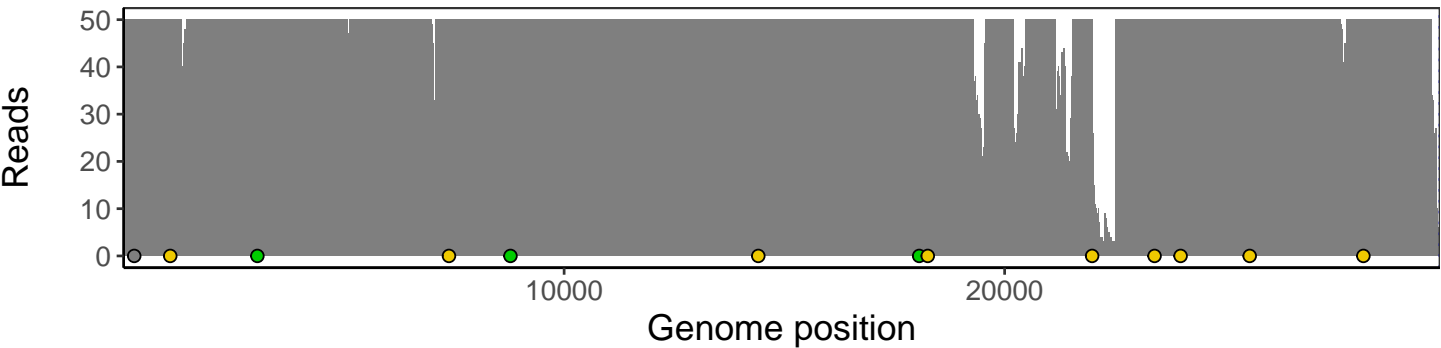
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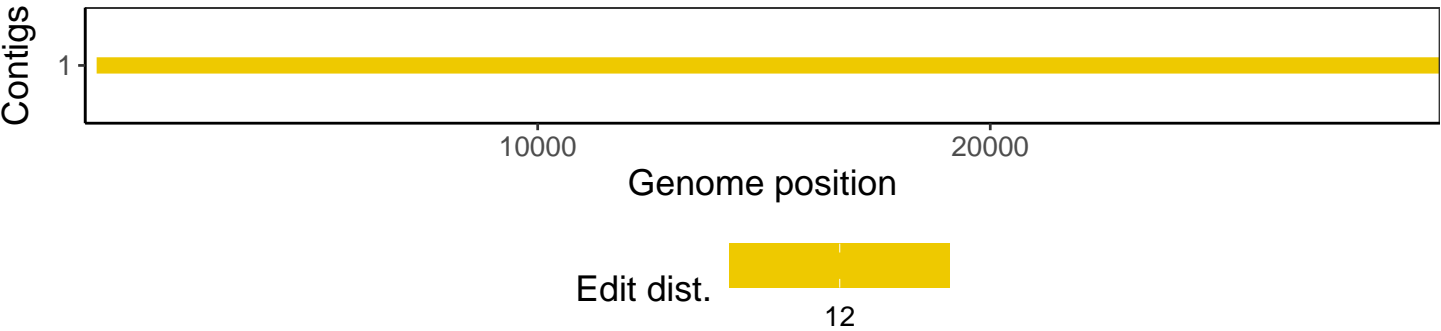
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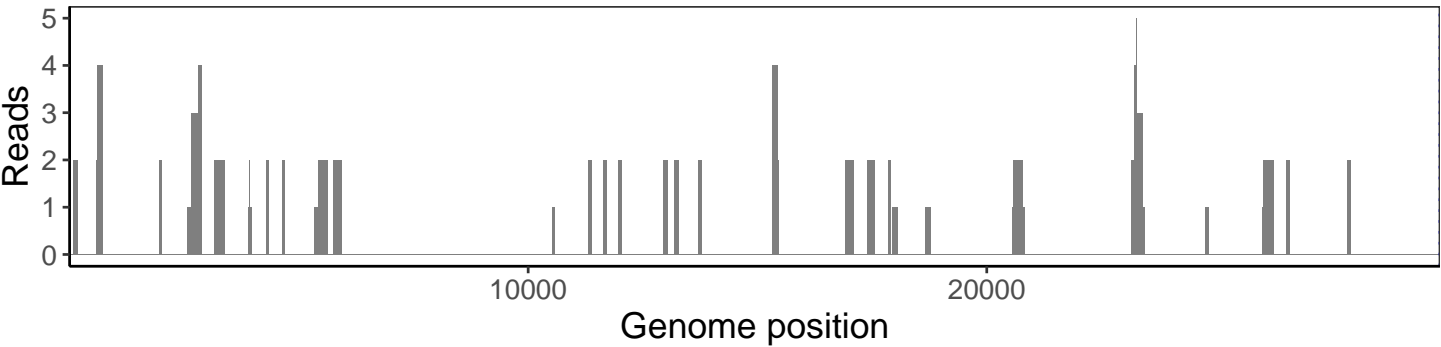
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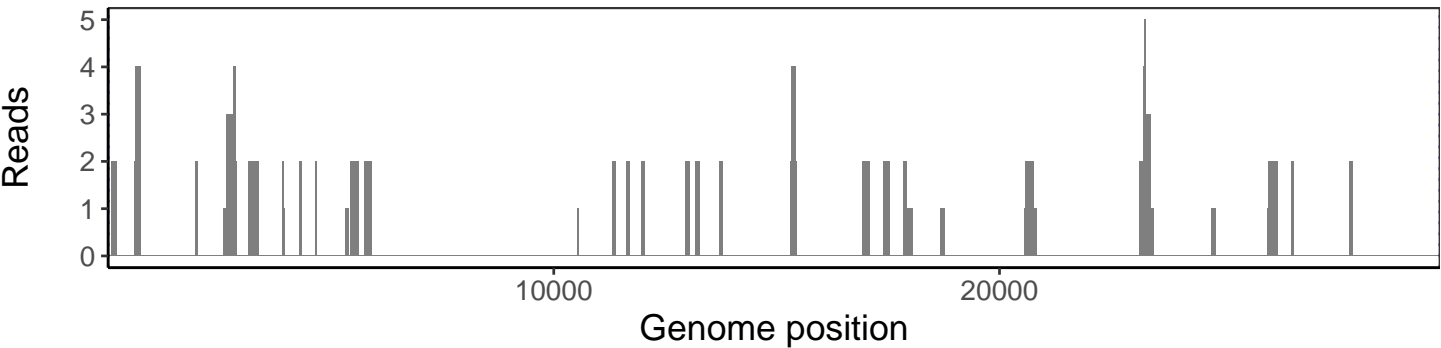
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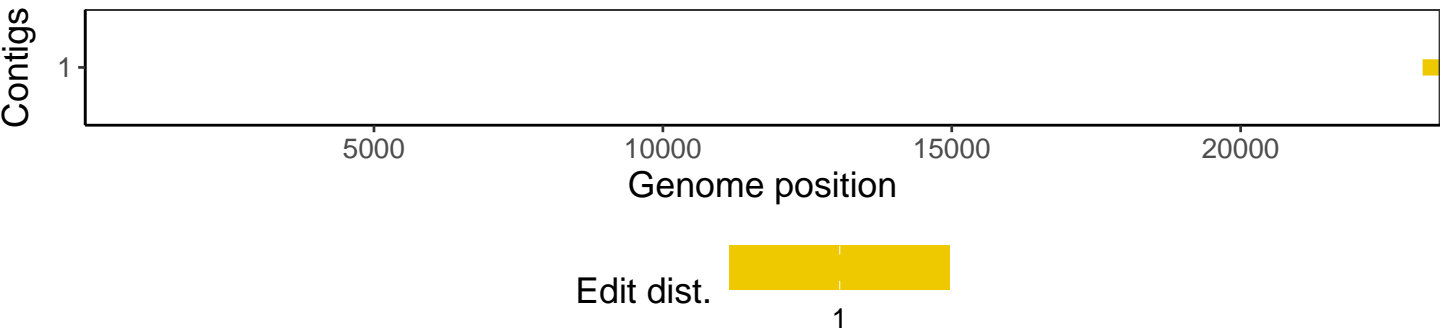
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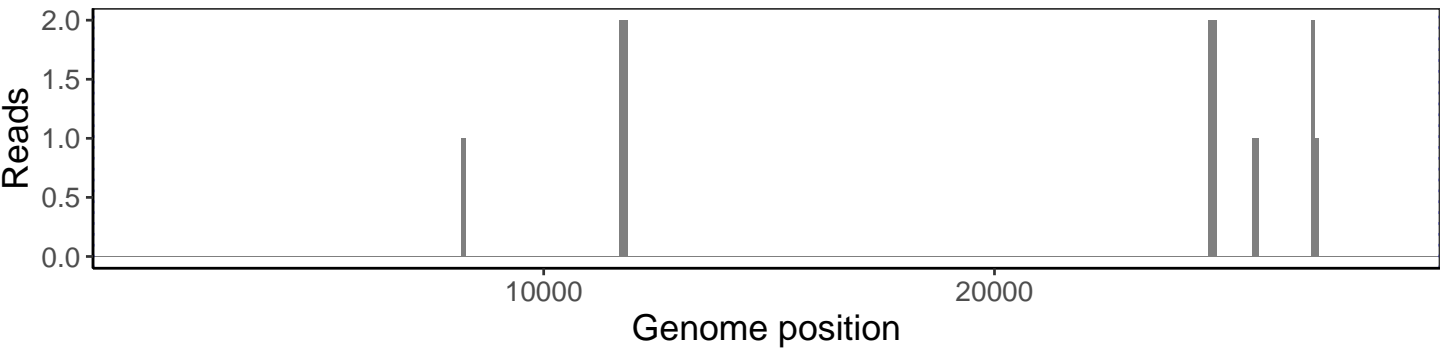
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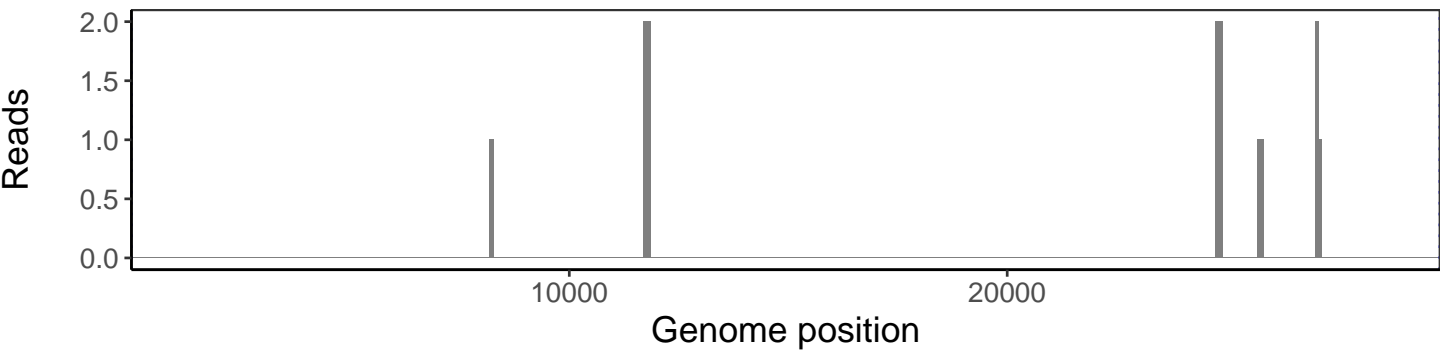
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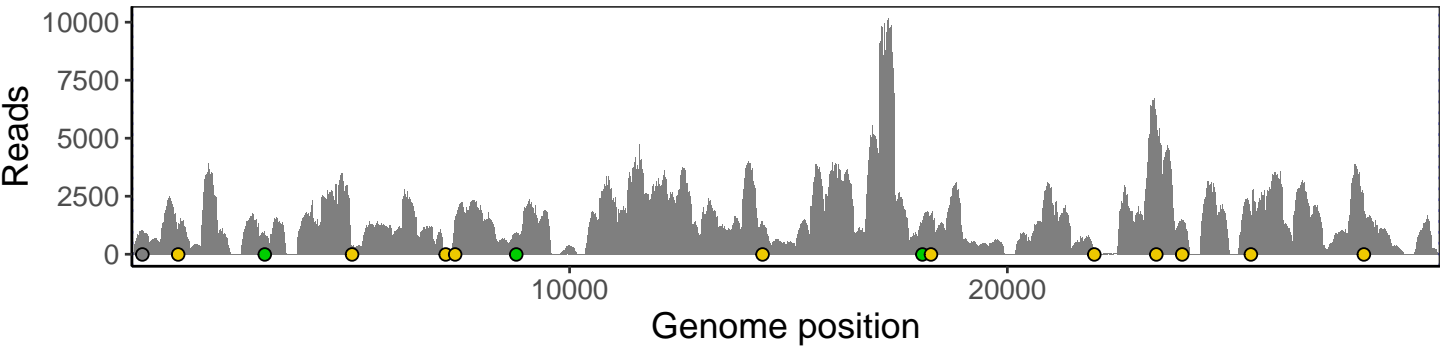


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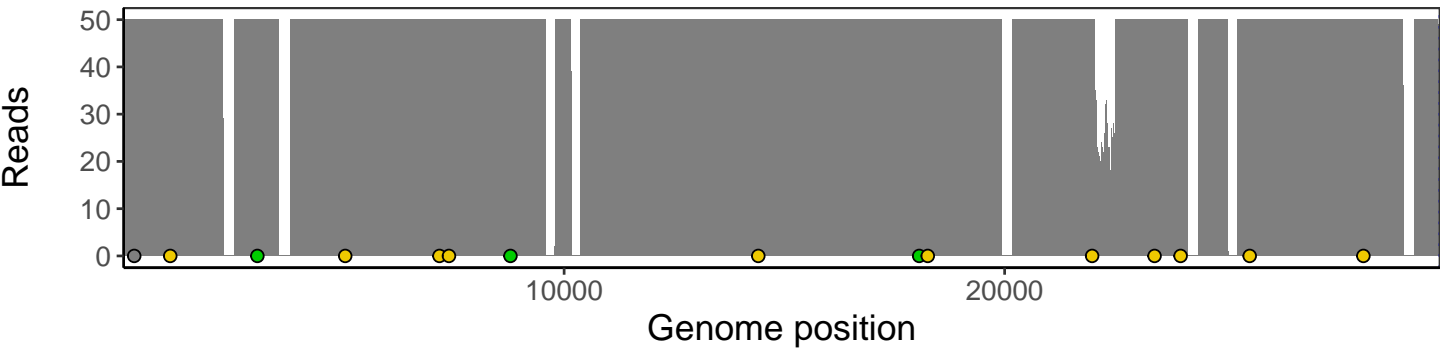


No contig data available.

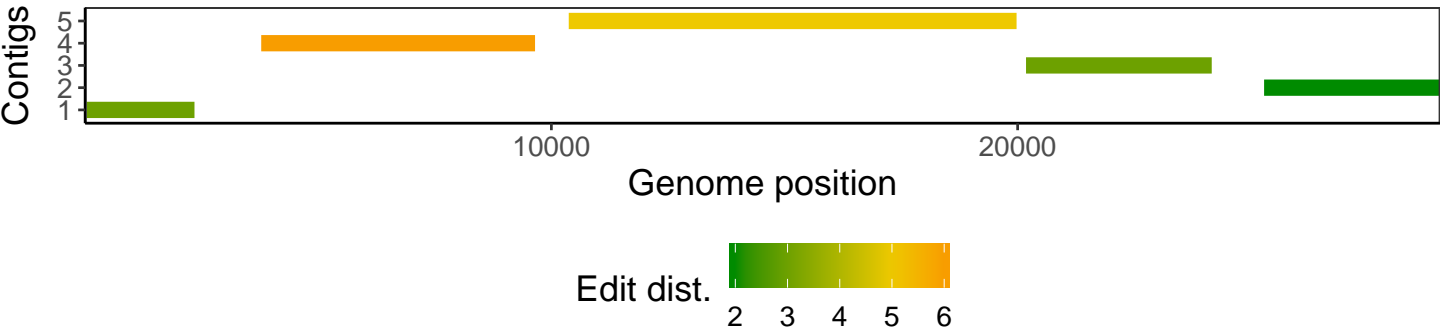
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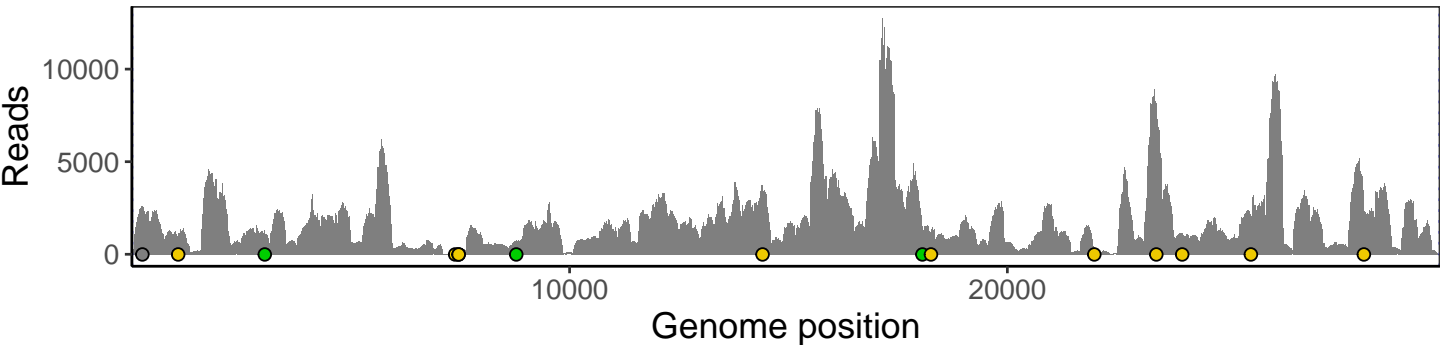
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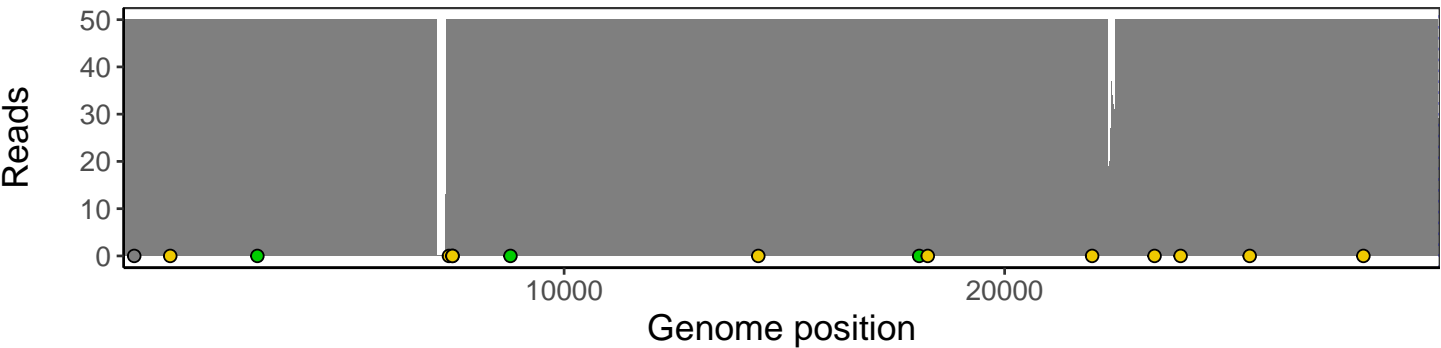
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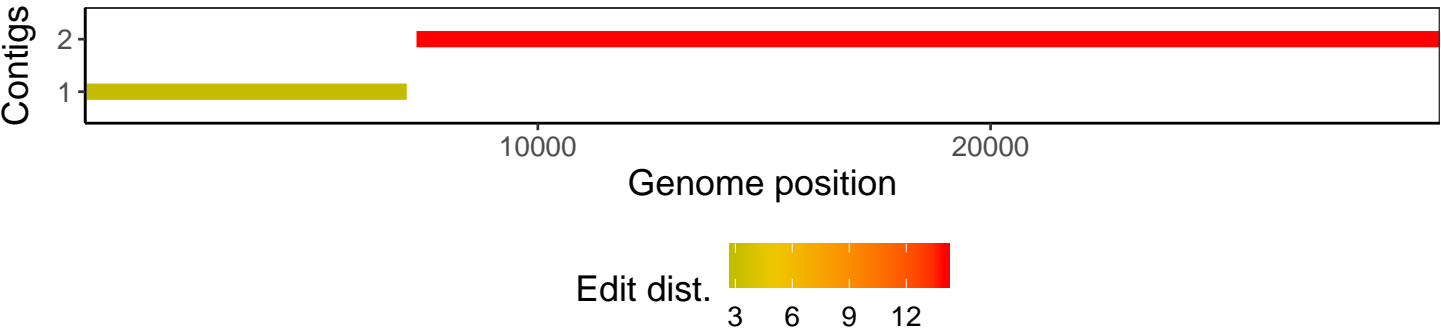
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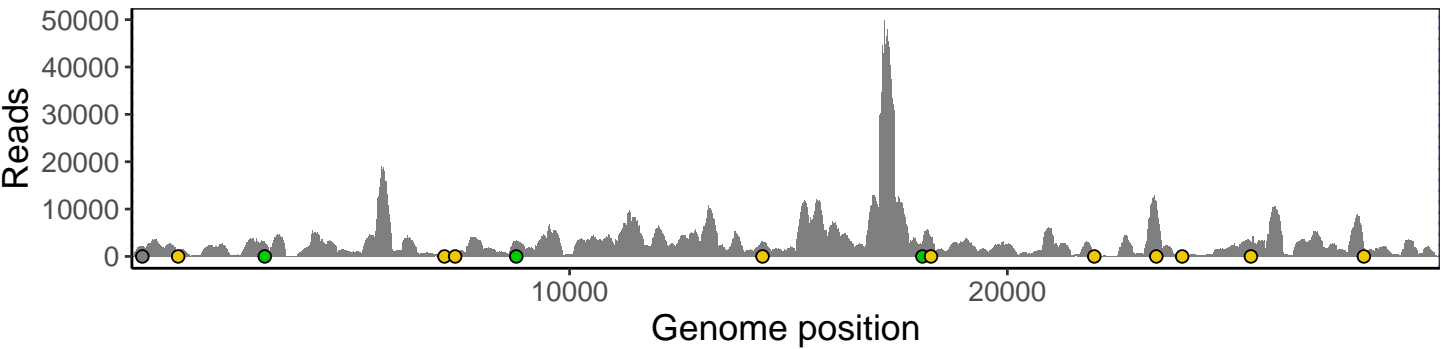
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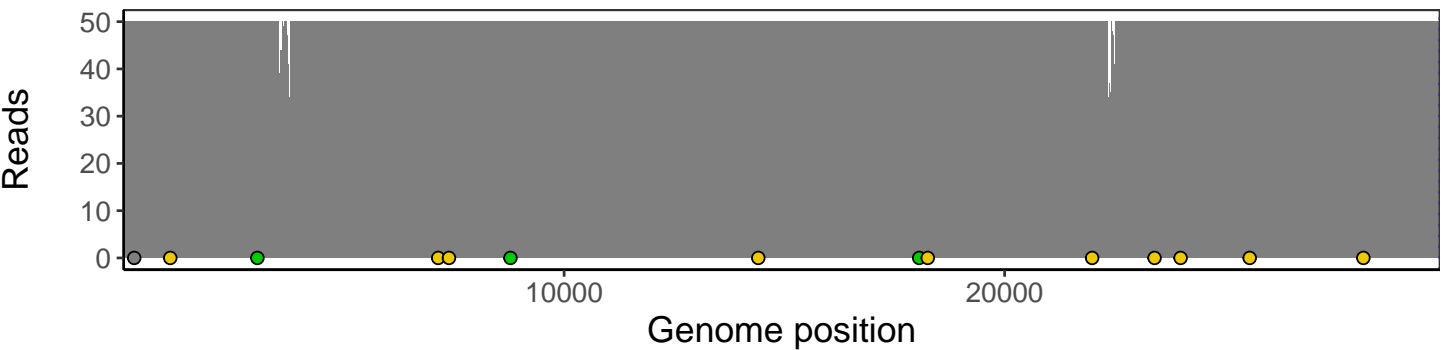
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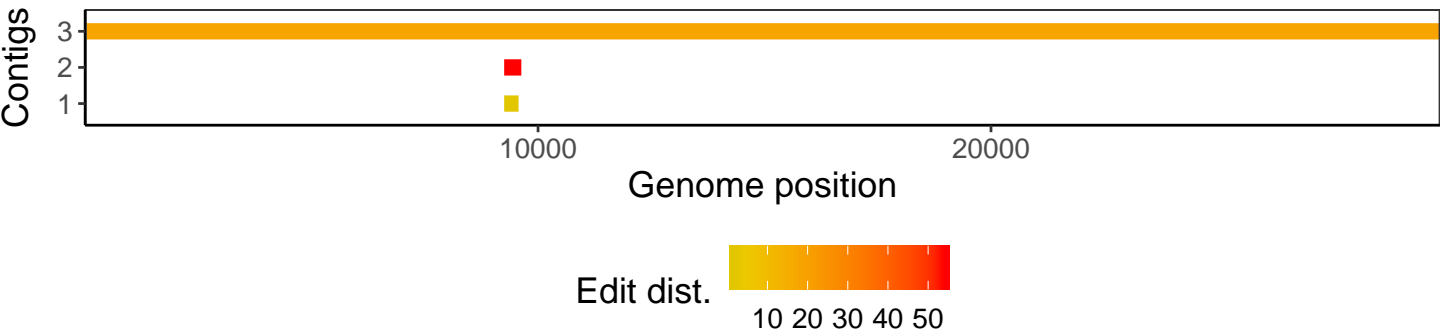
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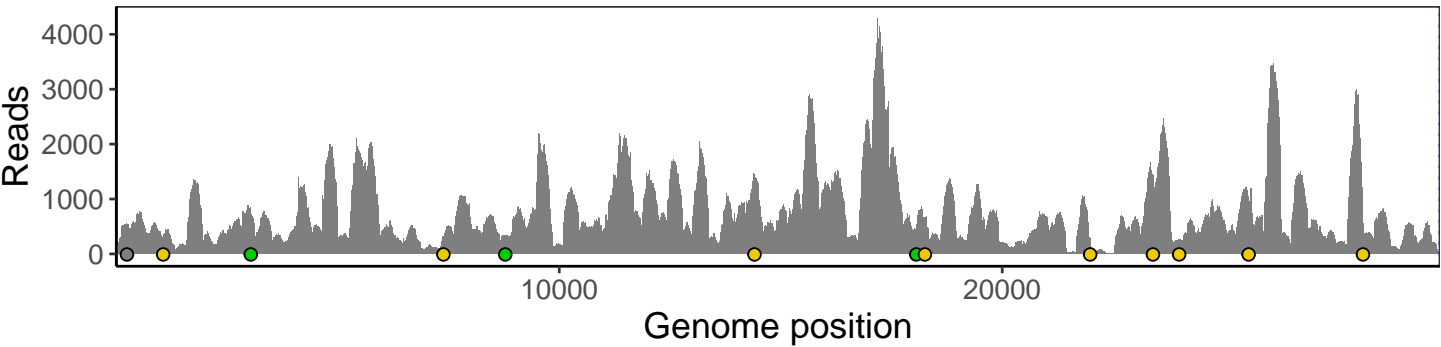
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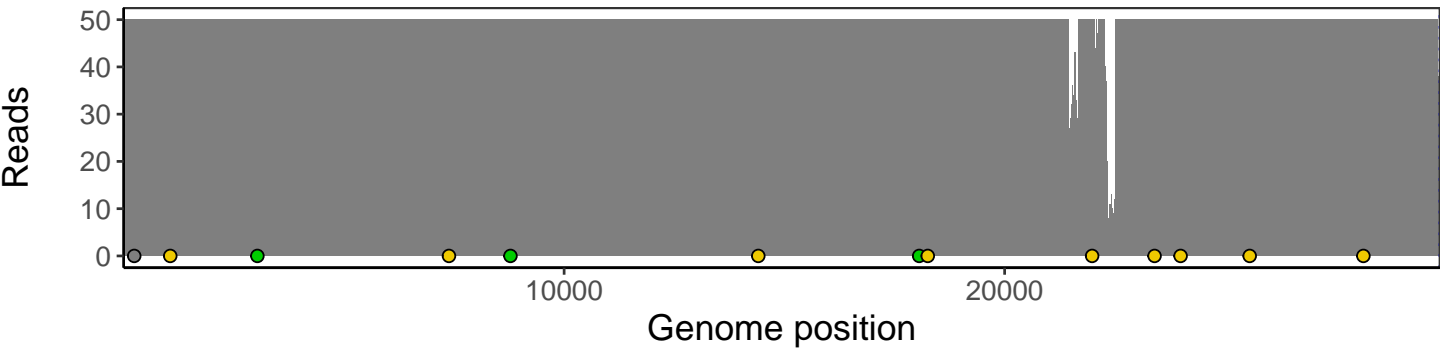
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