

COVID-19 subject 256

2020-08-28

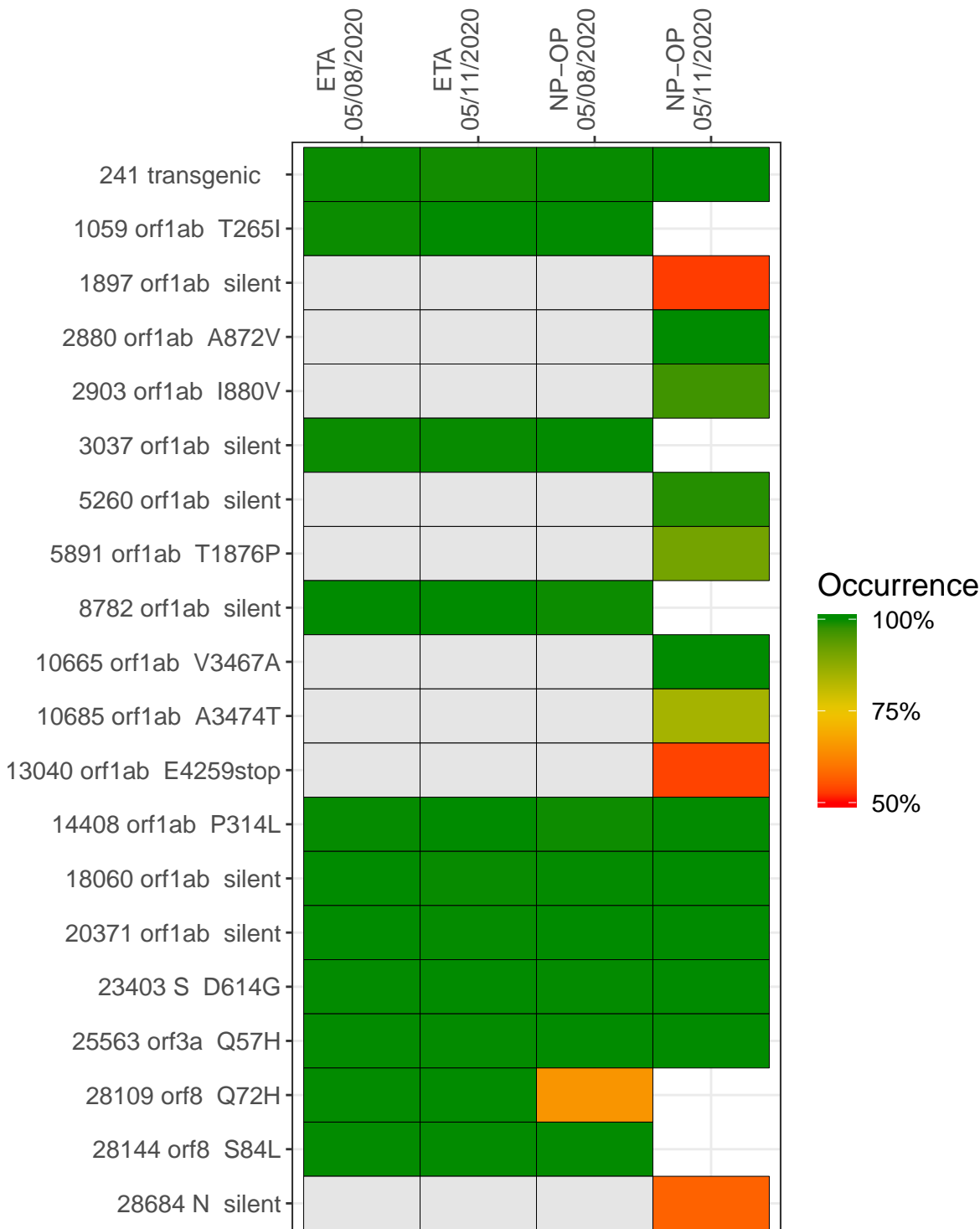
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found ([here](#)).

Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0107	composite	NA	NP-OP	05/08/2020	30.07	99.9%	99.9%
VSP0118	composite	NA	NP-OP	05/11/2020	2.63	62.0%	58.1%
VSP0100-1	single experiment	2760000	ETA	05/08/2020	29.82	99.7%	99.7%
VSP0107-1	single experiment	595000	NP-OP	05/08/2020	29.88	99.9%	99.8%
VSP0107-2	single experiment	595000	NP-OP	05/08/2020	30.07	99.9%	99.8%
VSP0118-1	single experiment	269	NP-OP	05/11/2020	2.67	56.6%	53.6%
VSP0118-2	single experiment	1345	NP-OP	05/11/2020	0.46	8.9%	5.5%
VSP0118-3	single experiment	1345	NP-OP	05/11/2020	0.54	10.5%	7.6%
VSP0118-4	single experiment	1345	NP-OP	05/11/2020	0.53	10.3%	6.7%
VSP0123-1	single experiment	123000	ETA	05/11/2020	29.89	99.9%	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.



	ETA 05/08/2020	ETA 05/11/2020	NP-OP 05/08/2020		NP-OP 05/11/2020			
241 transgenic	955	2086	5416	1962	921			
1059 orf1ab T265I	2253	1752	6183	1696				
1897 orf1ab silent	6774	3246	11385	2913	10	6		1
2880 orf1ab A872V	775	1517	1801	2604	32			
2903 orf1ab I880V	395	984	1886	2602	214	30	16	2
3037 orf1ab silent	400	1167	1979	2649				
5260 orf1ab silent	25	600	20	487	10	51	36	48
5891 orf1ab T1876P	1796	3683	443	2334		6		5
8782 orf1ab silent	63	1367	39	996				
10665 orf1ab V3467A	619	2291	812	1128		20	9	14
10685 orf1ab A3474T	789	2560	1747	1457	1	5	2	5
13040 orf1ab E4259stop	9305	4098	7995	3241	2800			
14408 orf1ab P314L	779	2264	3269	1256	2256			
18060 orf1ab silent	174	596	1395	1315	2494			
20371 orf1ab silent	29	1003	16	237	1036			
23403 S D614G	18281	5494	8814	6352	1208			1
25563 orf3a Q57H	2425	3050	5380	2757	1	40764		
28109 orf8 Q72H	2707	4710	4078	6873				
28144 orf8 S84L	4380	4192	1486	7624				
28684 N silent	4593	3961	11661	5321	1		6	
	VSP0100-1	VSP0123-1	VSP0107-1	VSP0107-2	VSP0118-1	VSP0118-2	VSP0118-3	VSP0118-4

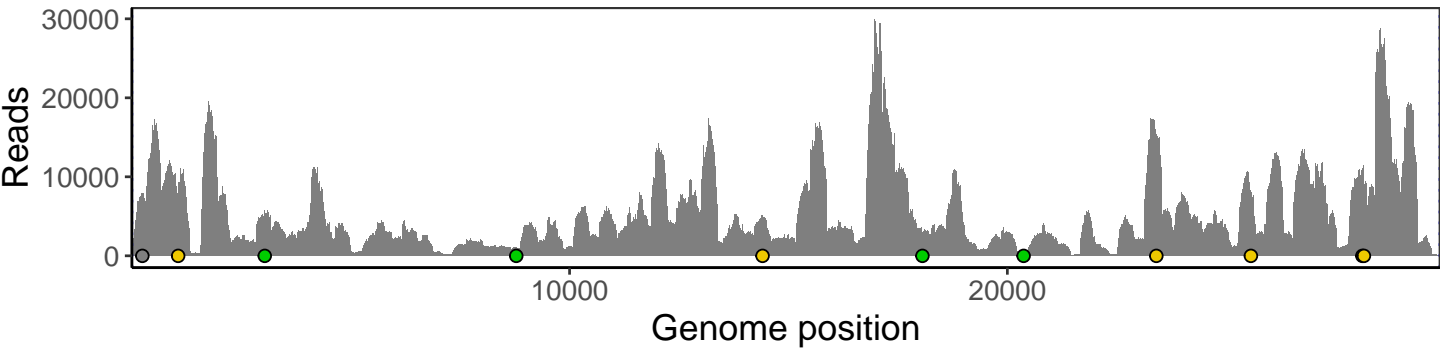
Base change

Expected	
A	
T	
C	
G	
N	
Ins/Del	
No data	

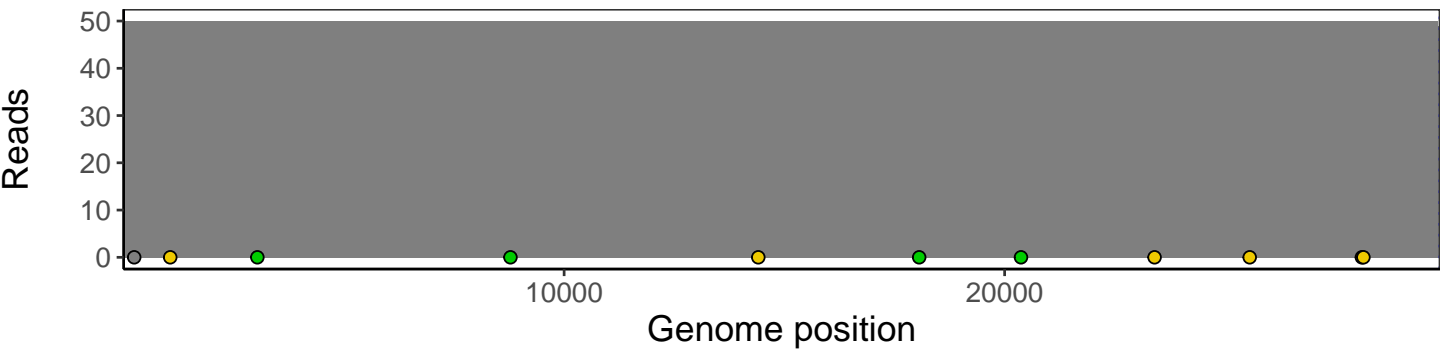
Analyses of individual experiments and composite results.

VSP0107 | 05/08/2020 | NP-OP | 256no-t | composite result

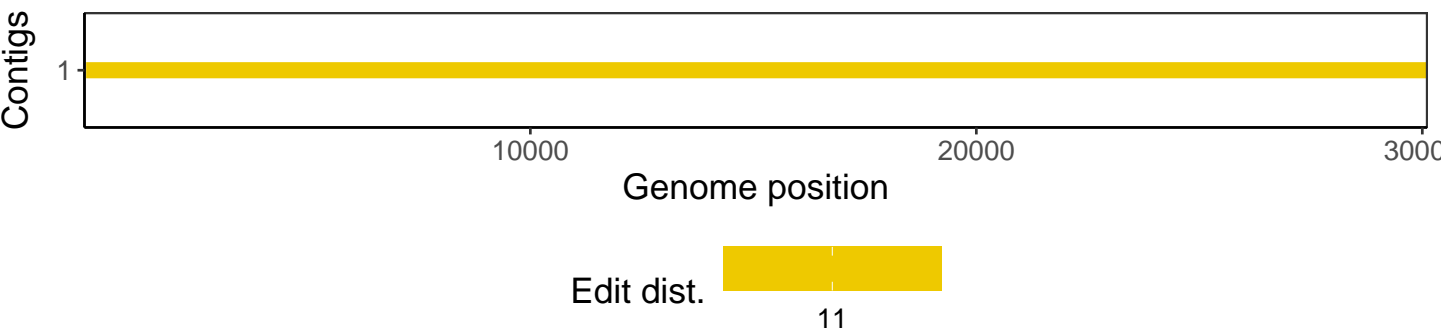
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



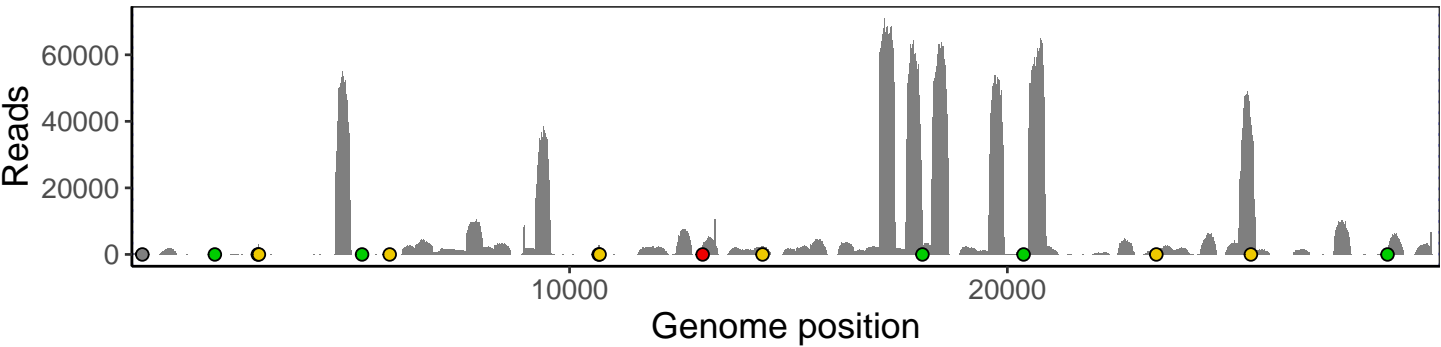
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



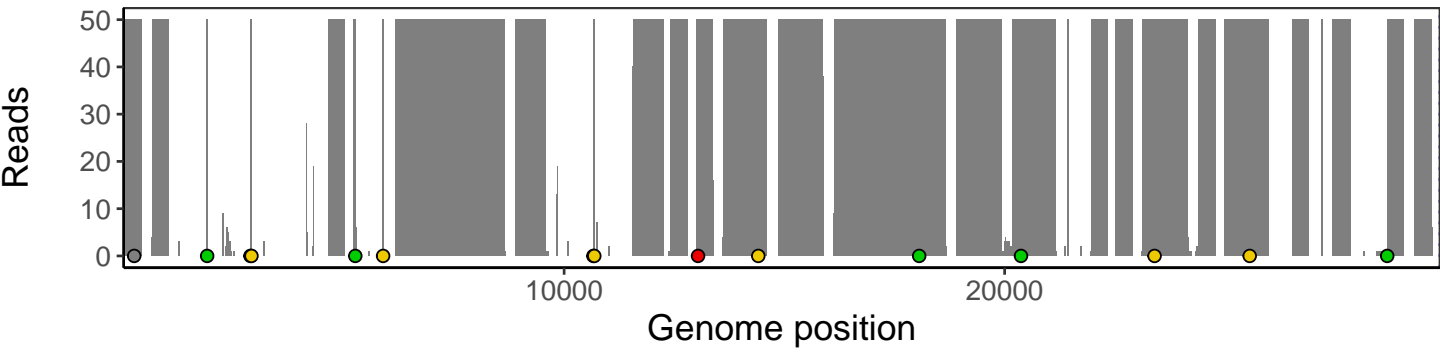
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



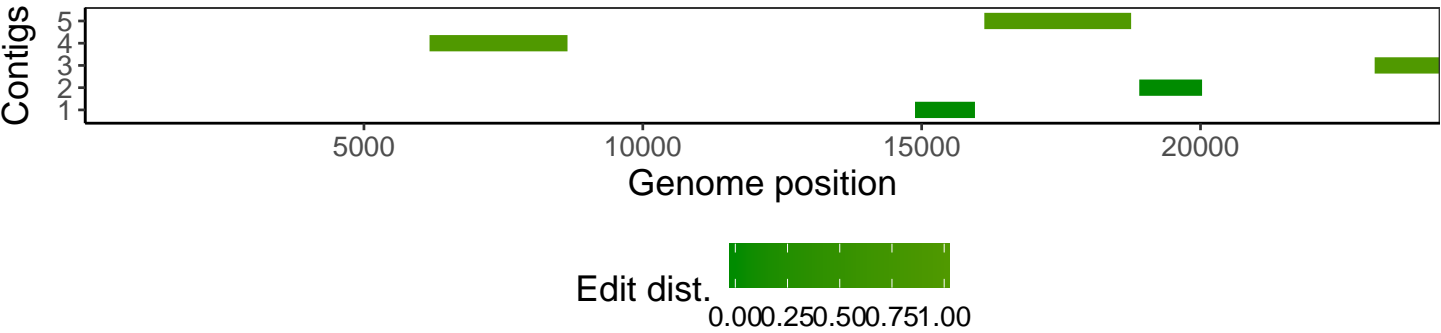
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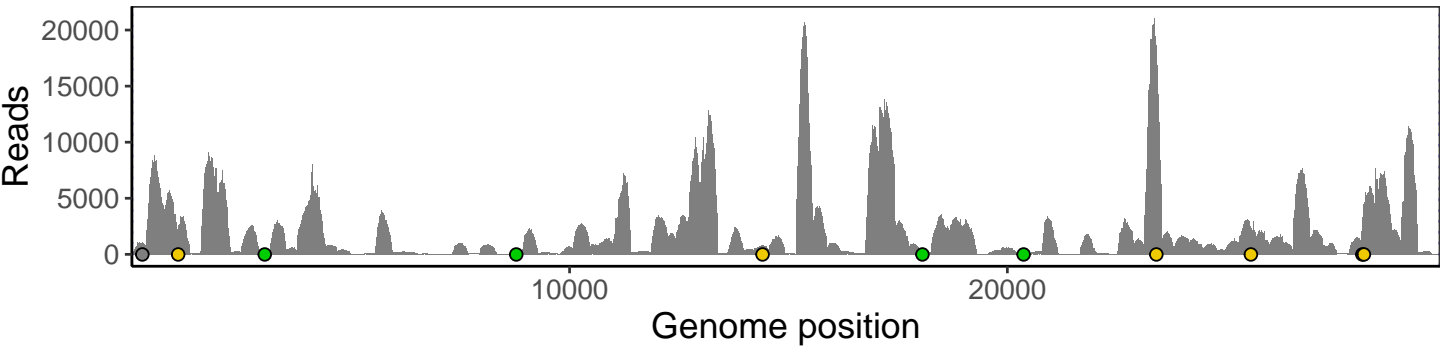
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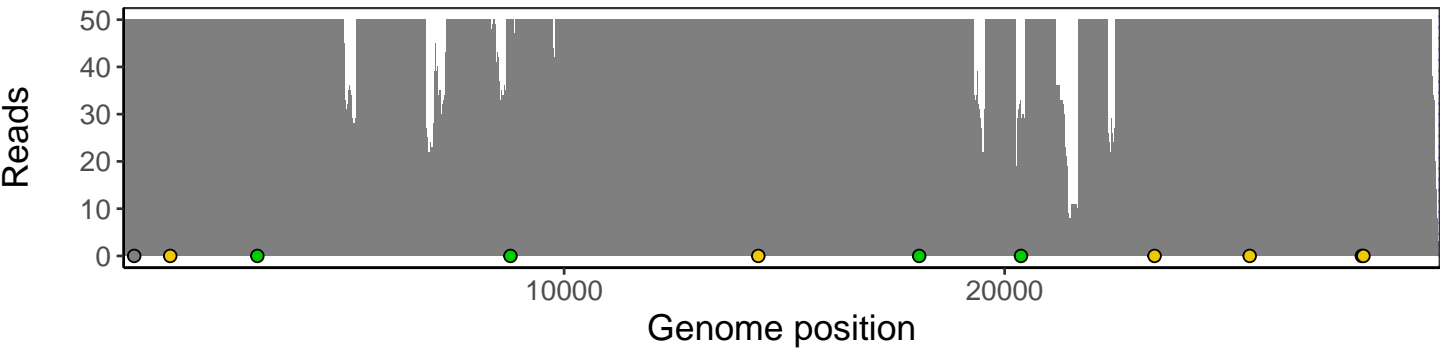
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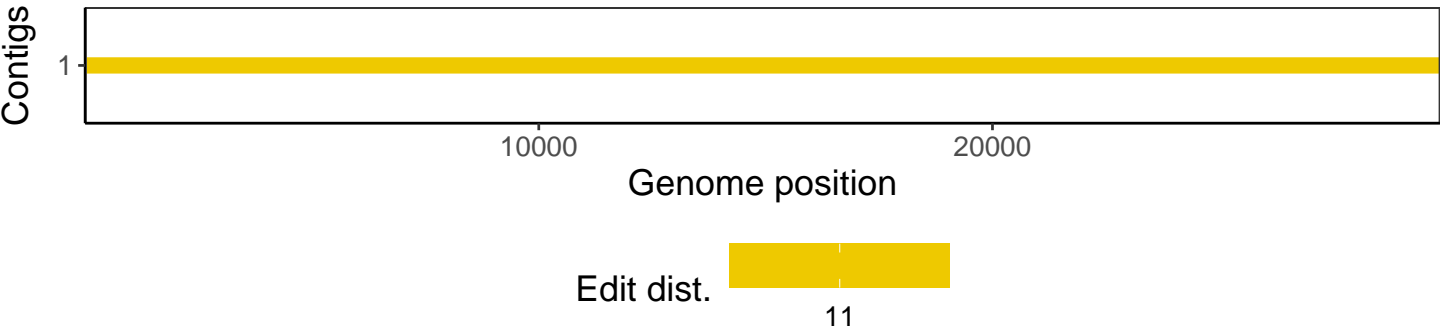
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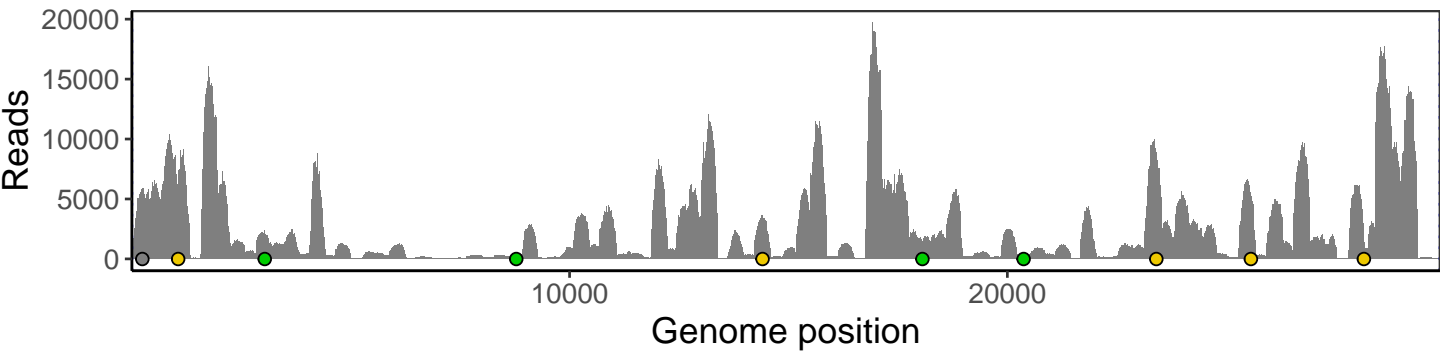
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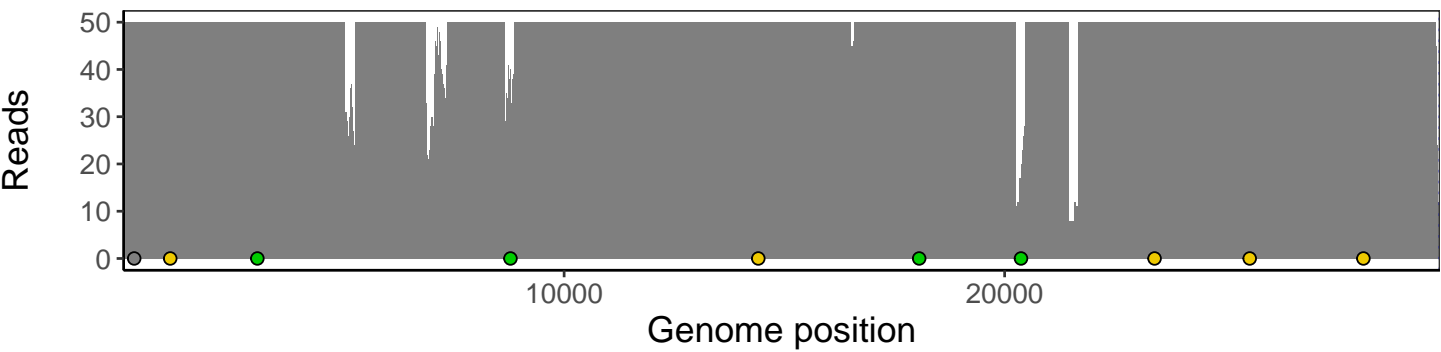
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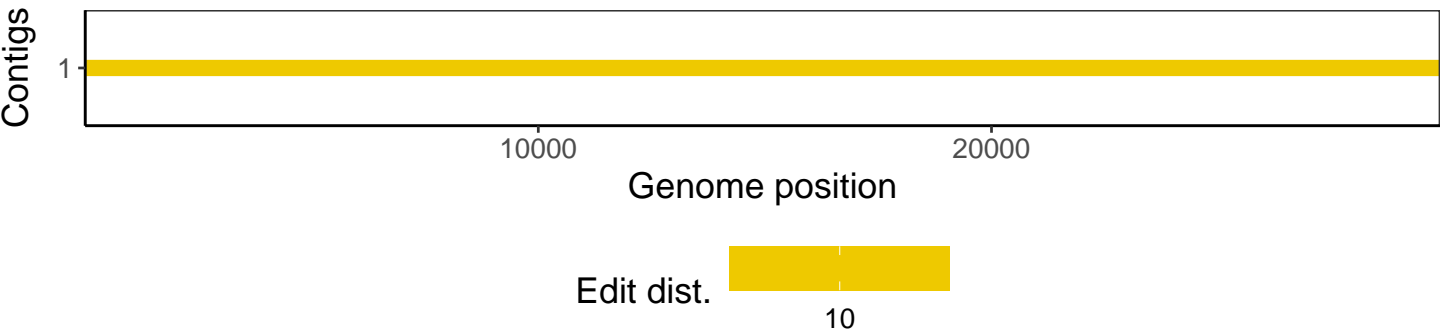
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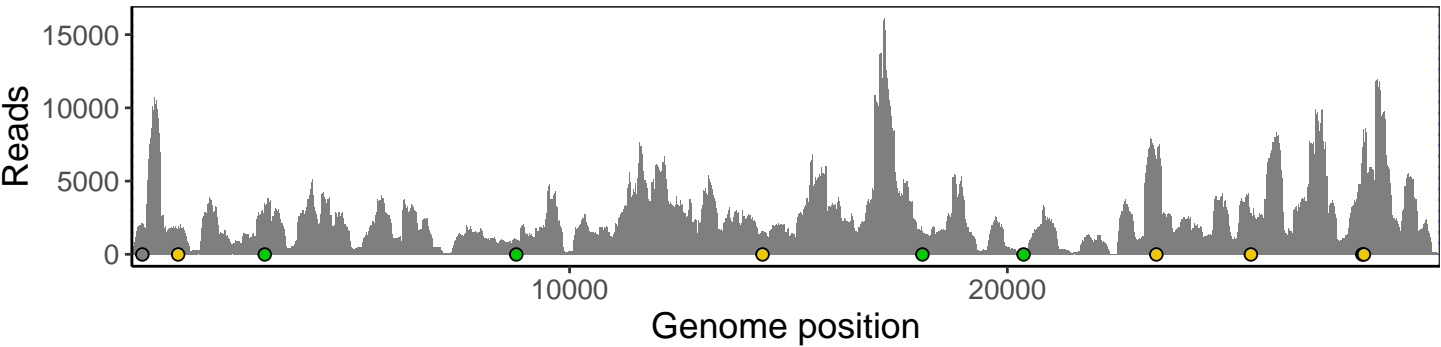
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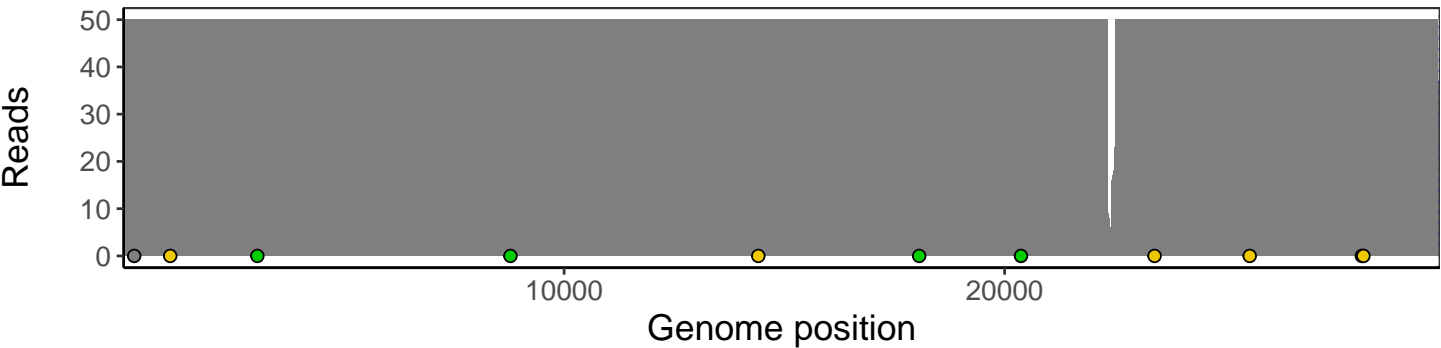
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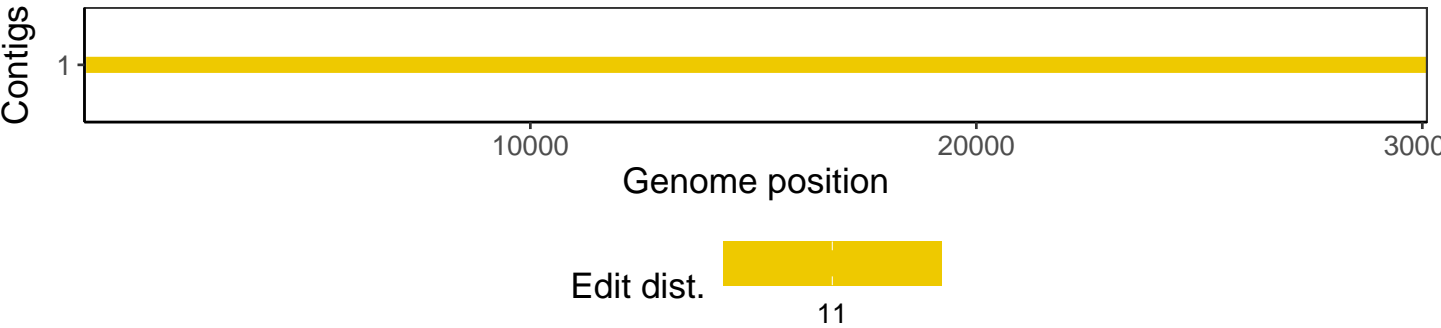
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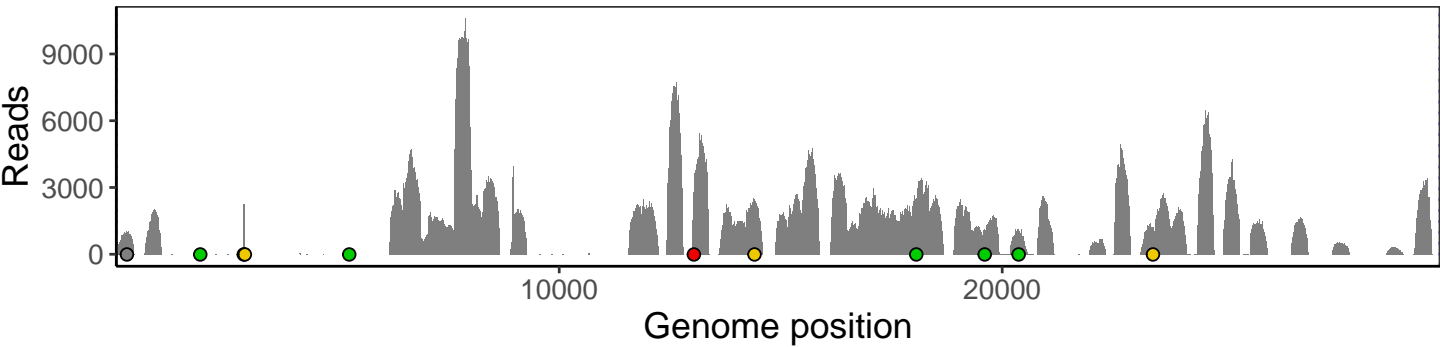
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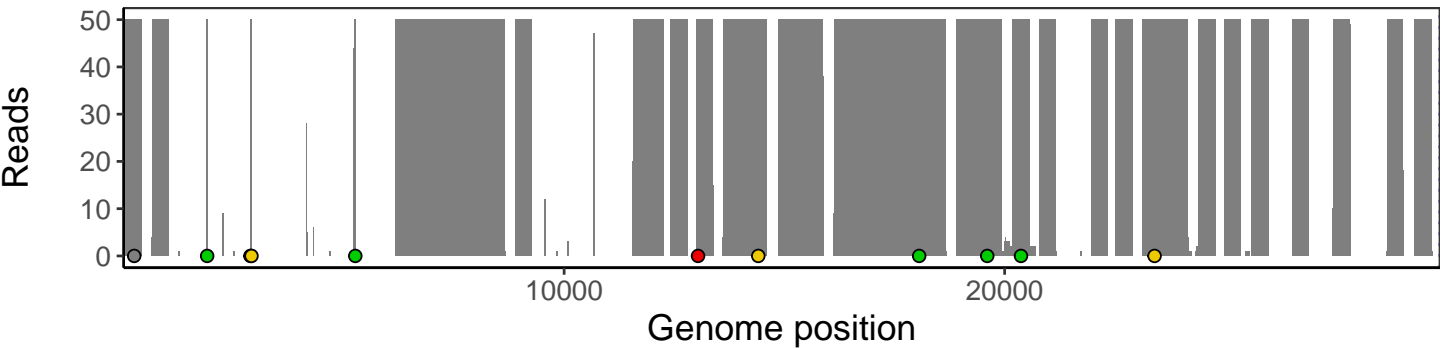
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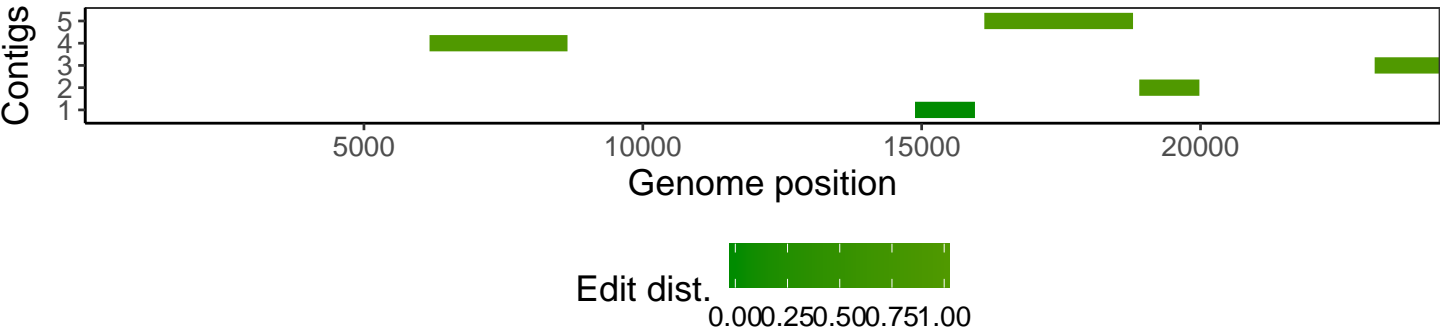
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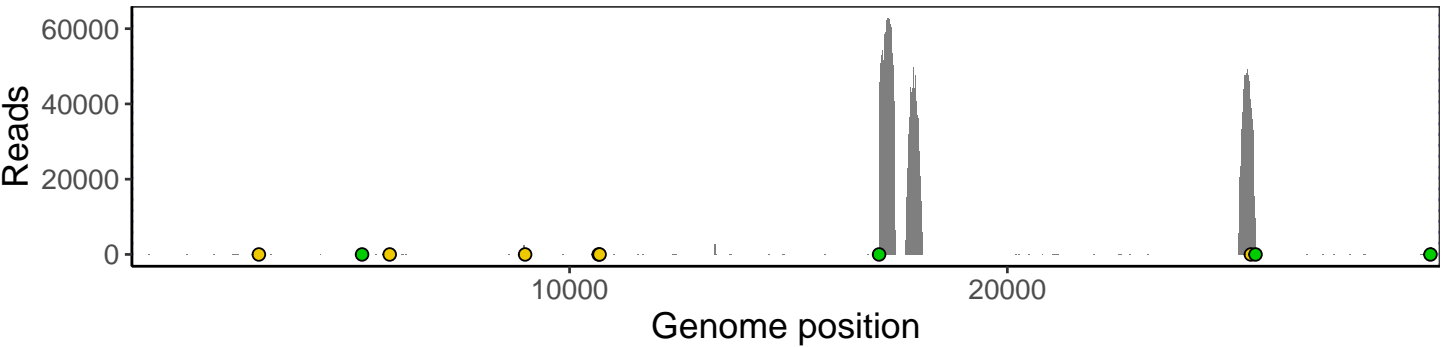
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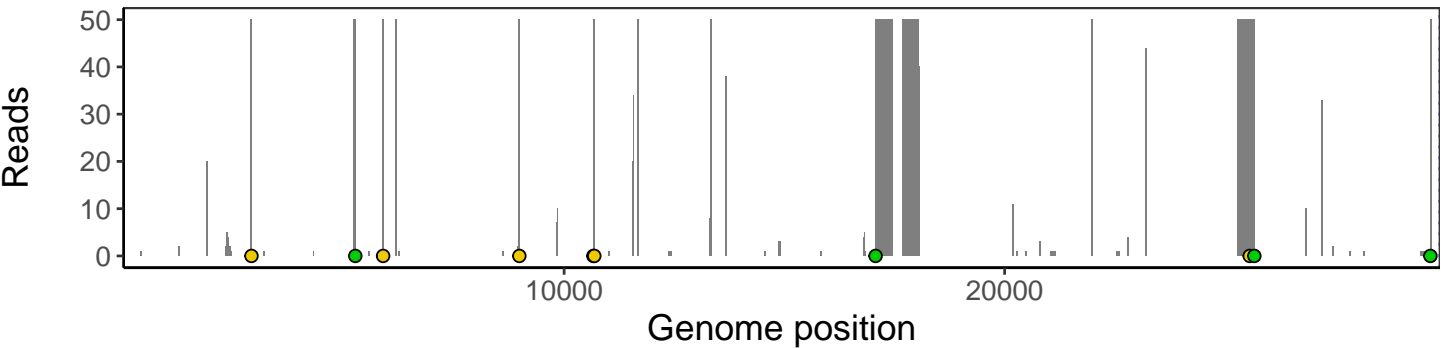
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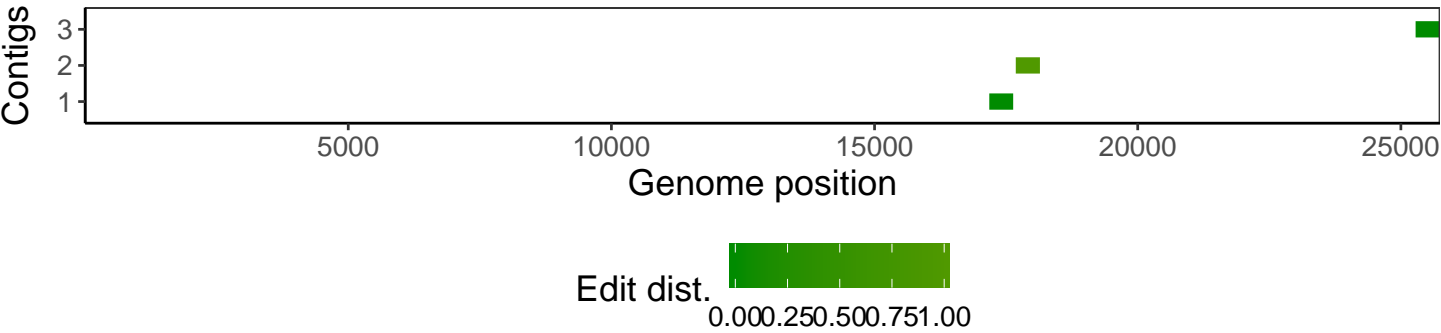
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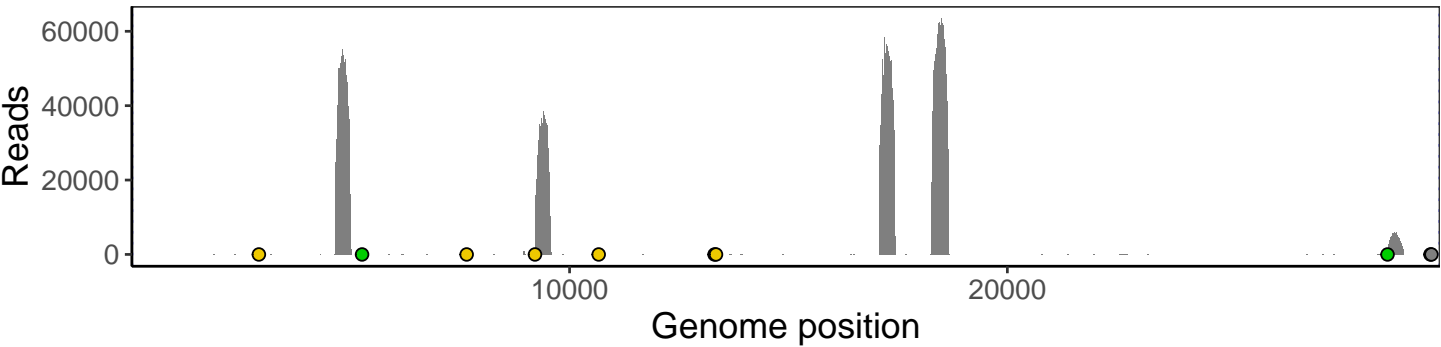
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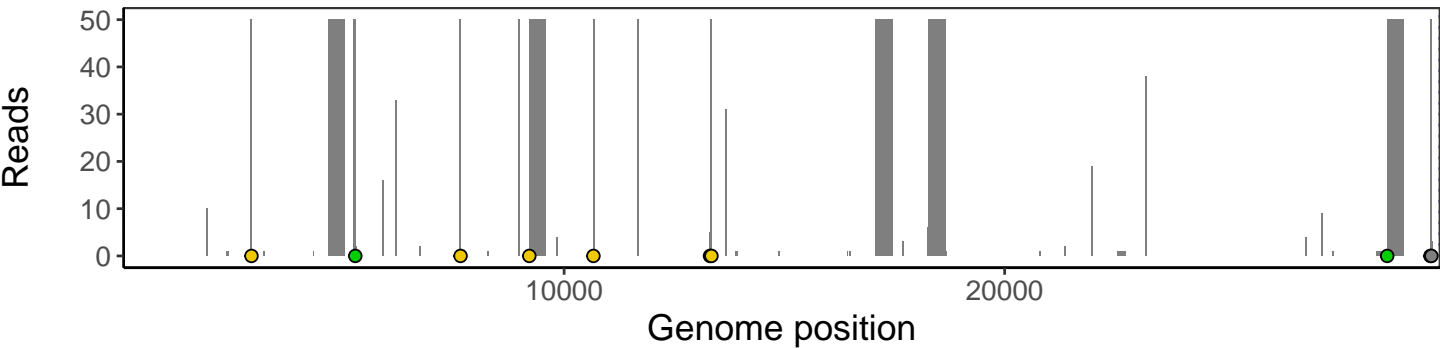
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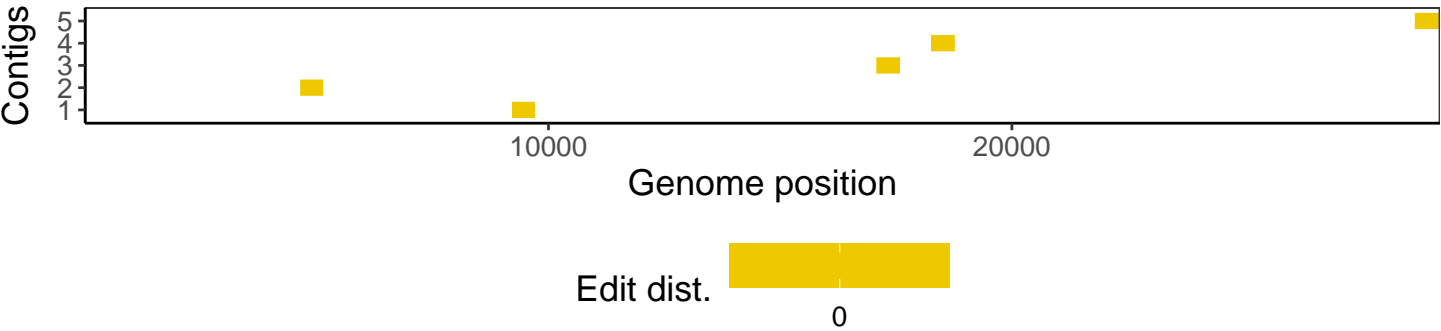
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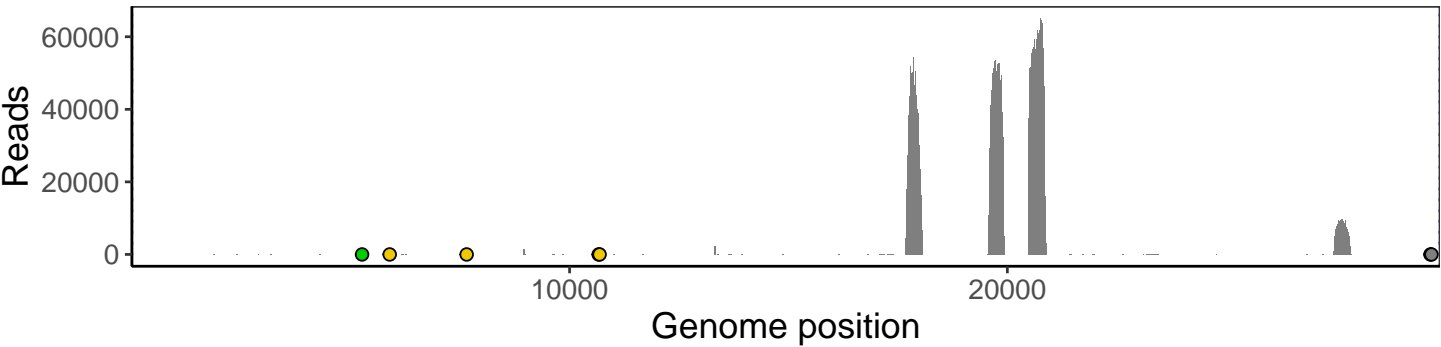
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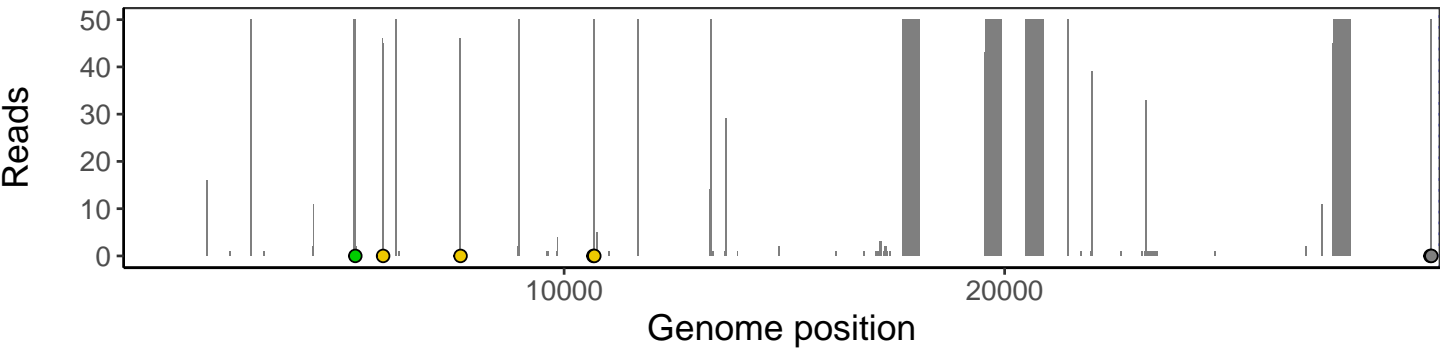
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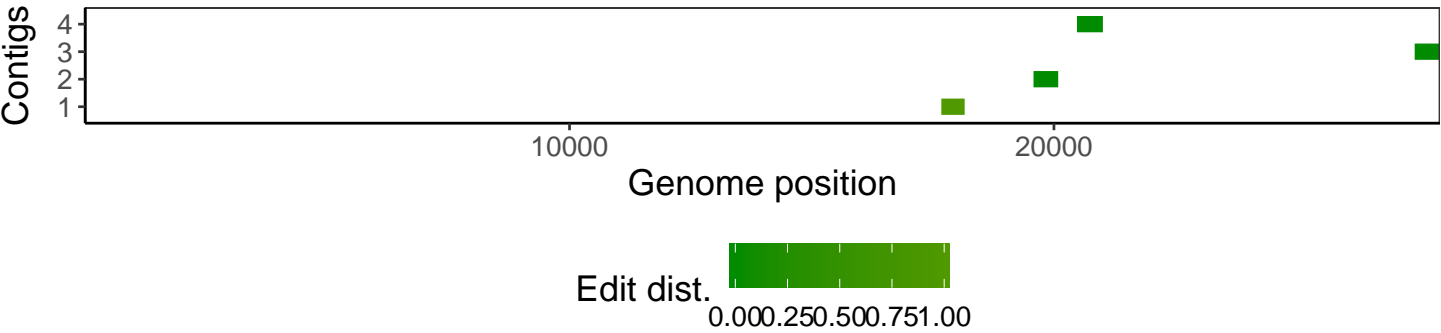
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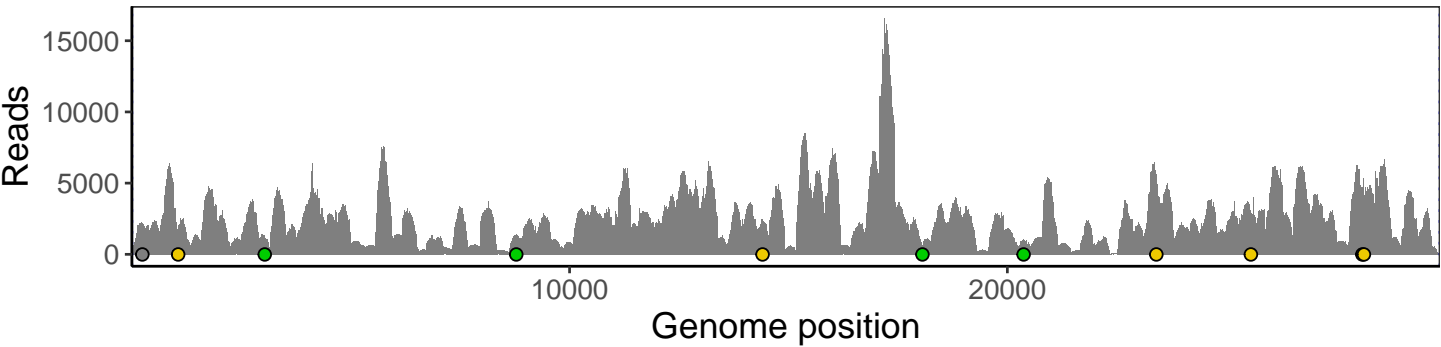
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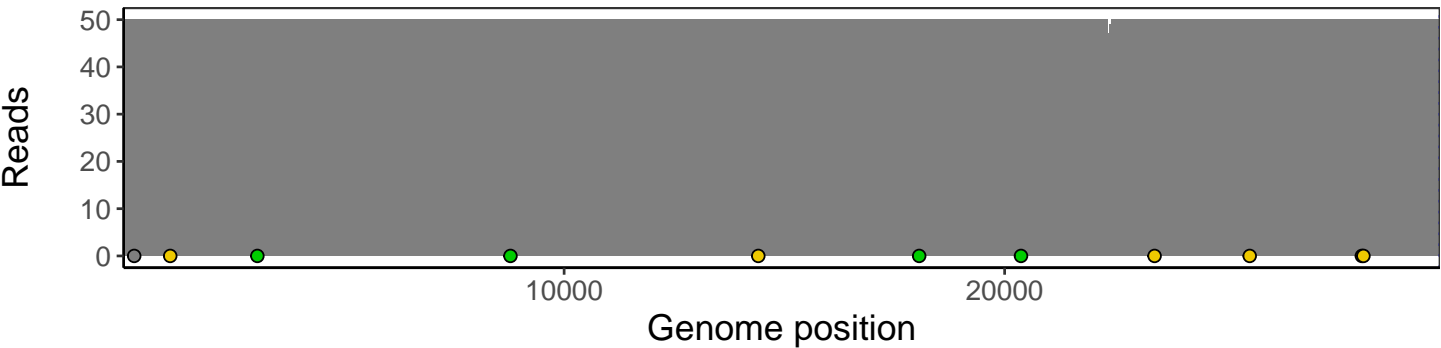
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