

COVID-19 subject 256

2021-01-08

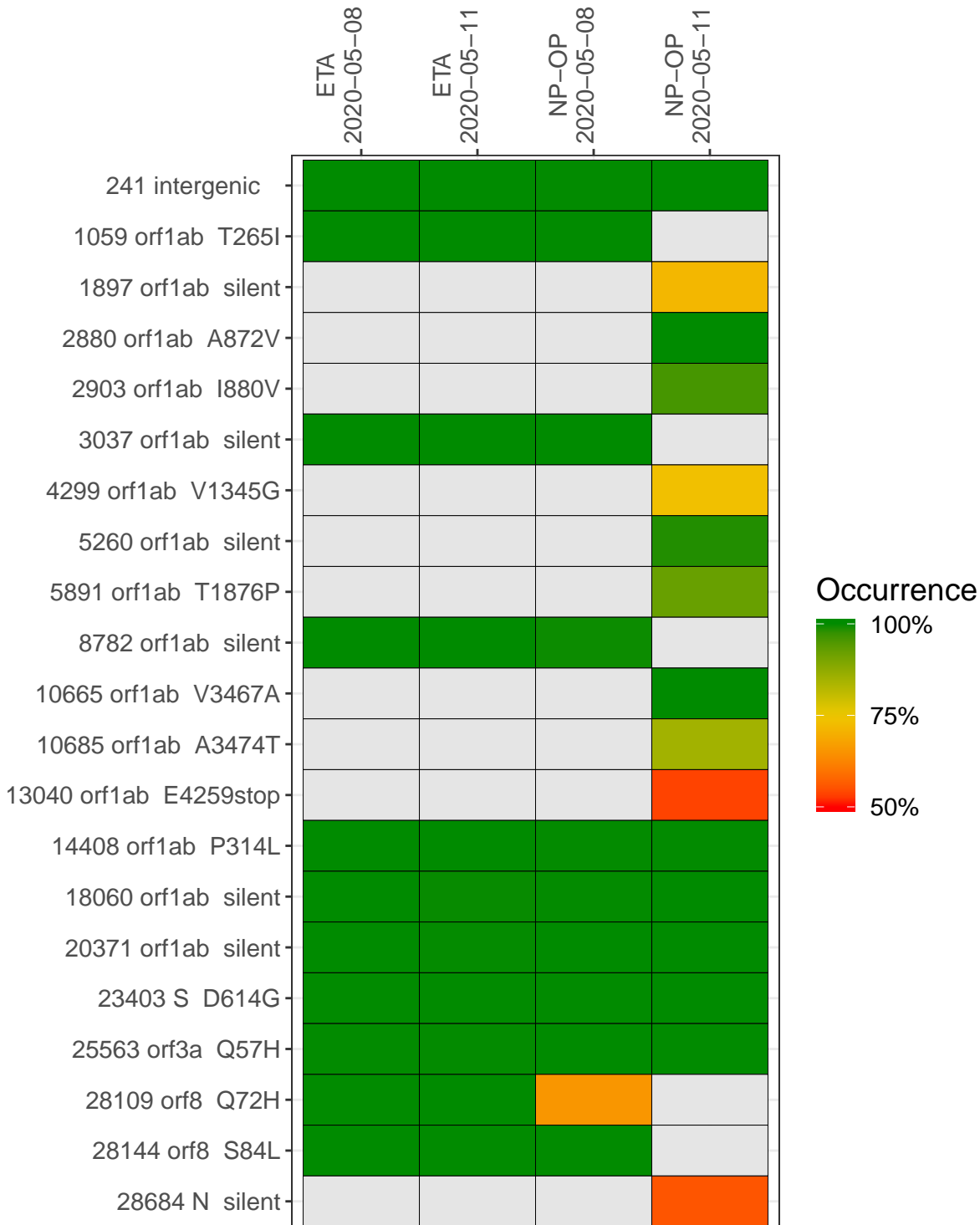
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found ([here](#)).

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	2020-05-08	29.68	100.0%	99.9%
VSP0118	composite	NA	NP-OP	2020-05-11	2.63	100.0%	58.2%
VSP0100-1	single experiment	2760000	ETA	2020-05-08	29.82	100.0%	99.7%
VSP0107-1	single experiment	595000	NP-OP	2020-05-08	29.89	100.0%	99.9%
VSP0107-2	single experiment	595000	NP-OP	2020-05-08	29.68	100.0%	99.8%
VSP0118-1	single experiment	269	NP-OP	2020-05-11	2.67	100.0%	53.5%
VSP0118-2	single experiment	1345	NP-OP	2020-05-11	0.60	100.0%	5.7%
VSP0118-3	single experiment	1345	NP-OP	2020-05-11	0.56	100.0%	7.8%
VSP0118-4	single experiment	1345	NP-OP	2020-05-11	0.60	100.0%	6.8%
VSP0123-1	single experiment	123000	ETA	2020-05-11	29.26	100.0%	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 020-05-0	ETA 020-05-1	NP-OP 2020-05-08		NP-OP 2020-05-11			
241 intergenic	1031	2202	5510	2102	997			
1059 orf1ab T265I	2382	1841	6298	1771				
1897 orf1ab silent	7054	3413	11605	3034	8	13	2	5
2880 orf1ab A872V	814	1563	1835	2680	31			
2903 orf1ab I880V	409	1025	1922	2686	222	62	28	10
3037 orf1ab silent	412	1215	2019	2731				
4299 orf1ab V1345G	3991	2882	5723	1824		1	8	6
5260 orf1ab silent	27	621	20	512	10	52	44	58
5891 orf1ab T1876P	1882	3879	457	2394		8		5
8782 orf1ab silent	66	1432	39	1035				
10665 orf1ab V3467A	632	2369	828	1246		28	12	21
10685 orf1ab A3474T	813	2638	1785	1587	1	9	3	7
13040 orf1ab E4259stop	9636	4233	8136	3514	2906			
14408 orf1ab P314L	805	2329	3311	1314	2400			
18060 orf1ab silent	179	617	1407	1381	2631			
20371 orf1ab silent	31	1051	18	260	1091			
23403 S D614G	19208	5794	8981	6619	1286			1
25563 orf3a Q57H	2559	3203	5472	2913	1	42531		
28109 orf8 Q72H	2791	4868	4173	7073				
28144 orf8 S84L	4549	4351	1518	7772				
28684 N silent	4798	4112	11910	5479	1		8	
	VSP0100-1	VSP0123-1	VSP0107-1	VSP0107-2	VSP0118-1	VSP0118-2	VSP0118-3	VSP0118-4

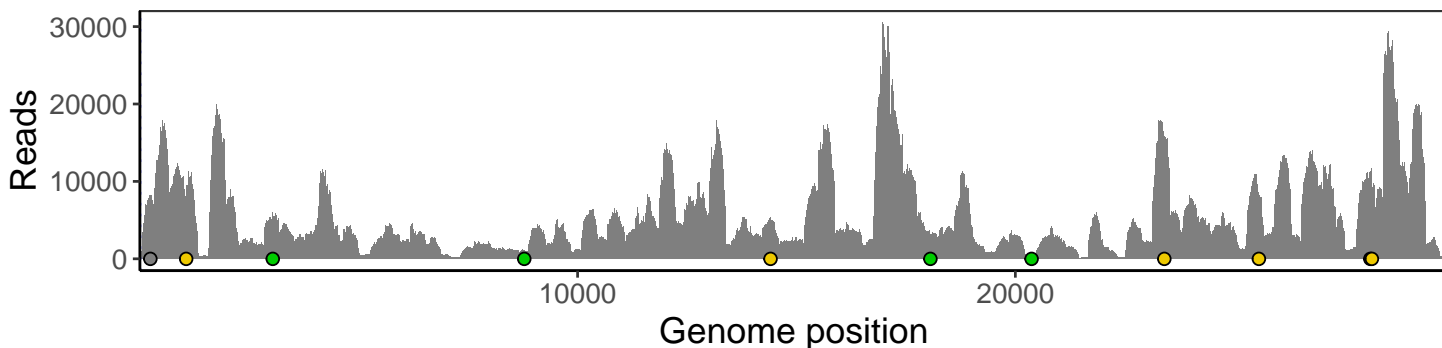
Base change

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

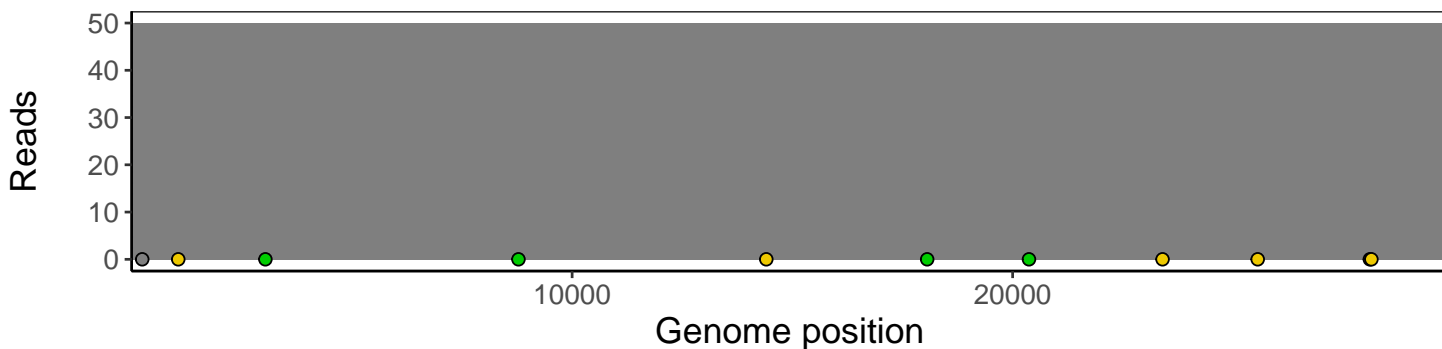
Analyses of individual experiments and composite results.

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

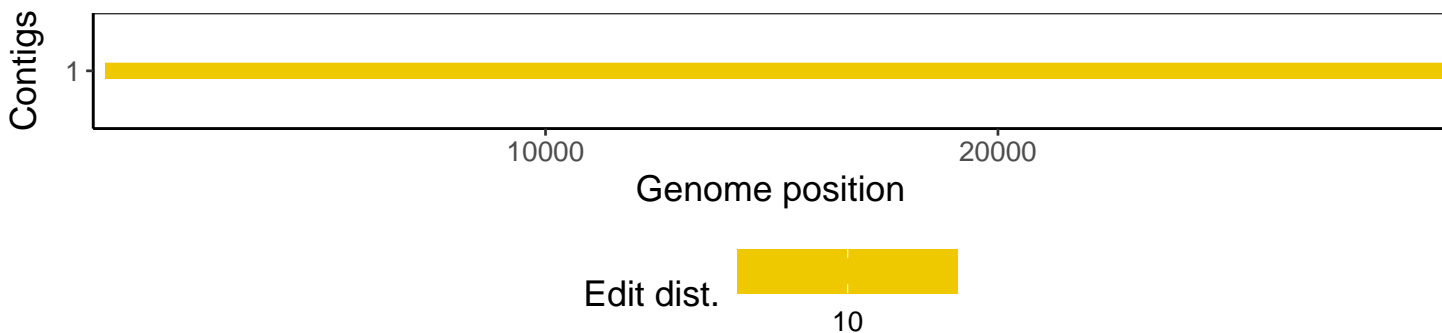
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



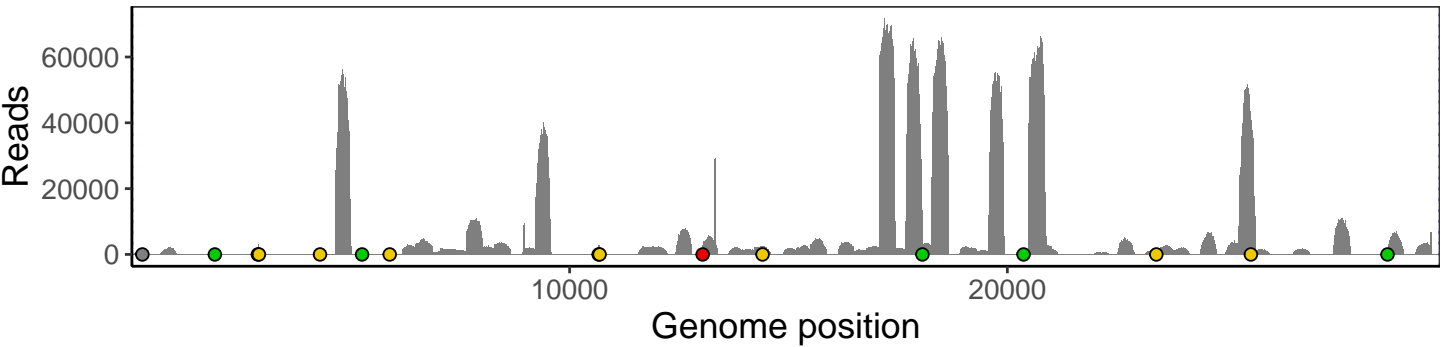
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



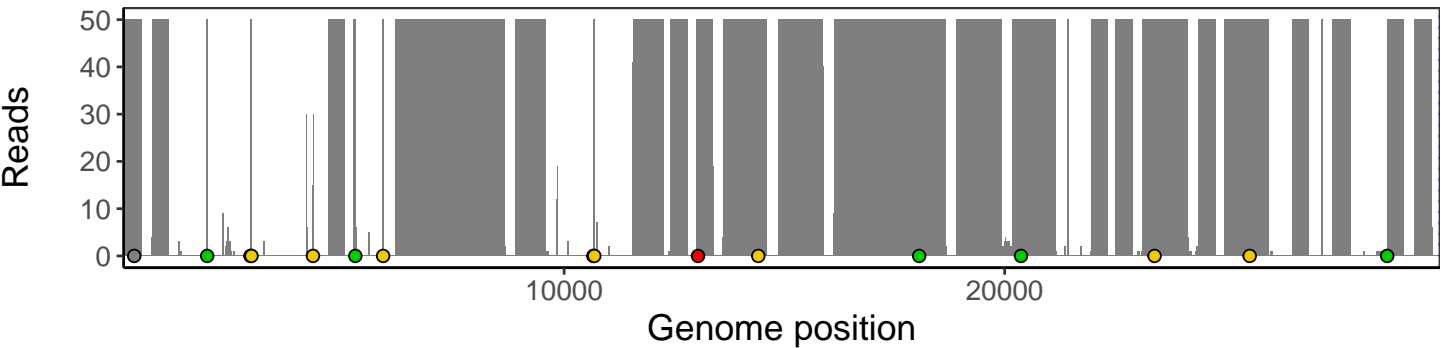
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



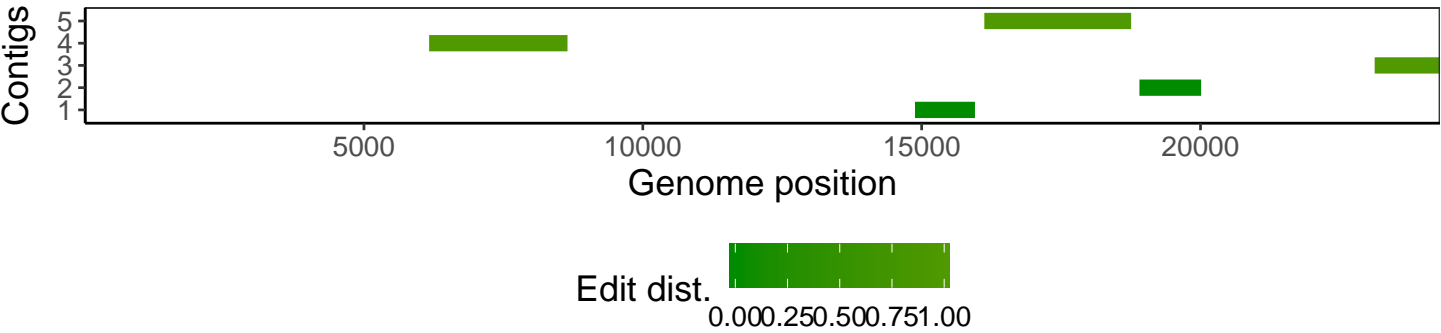
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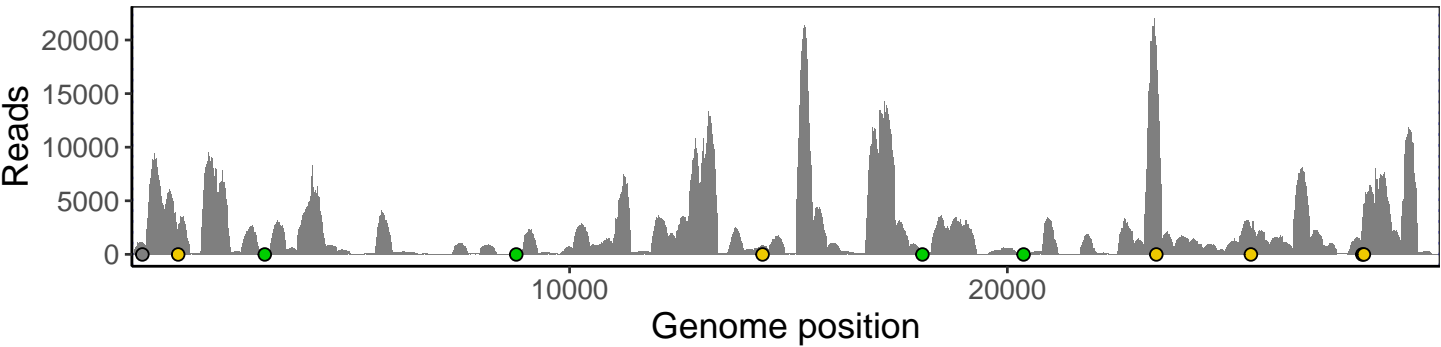
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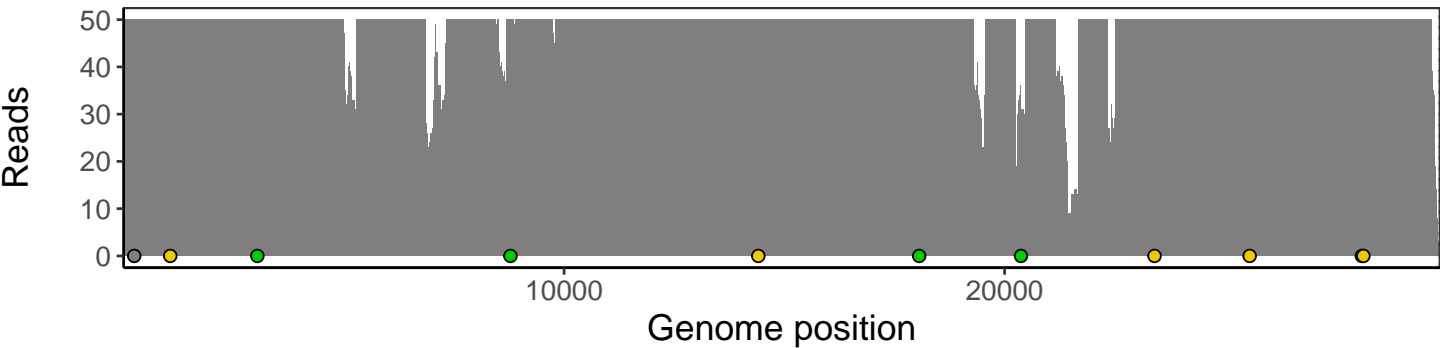
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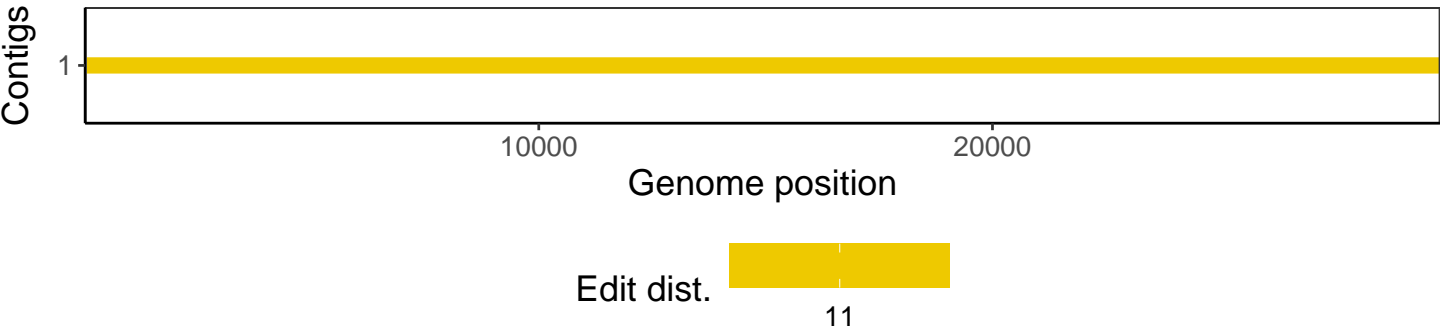
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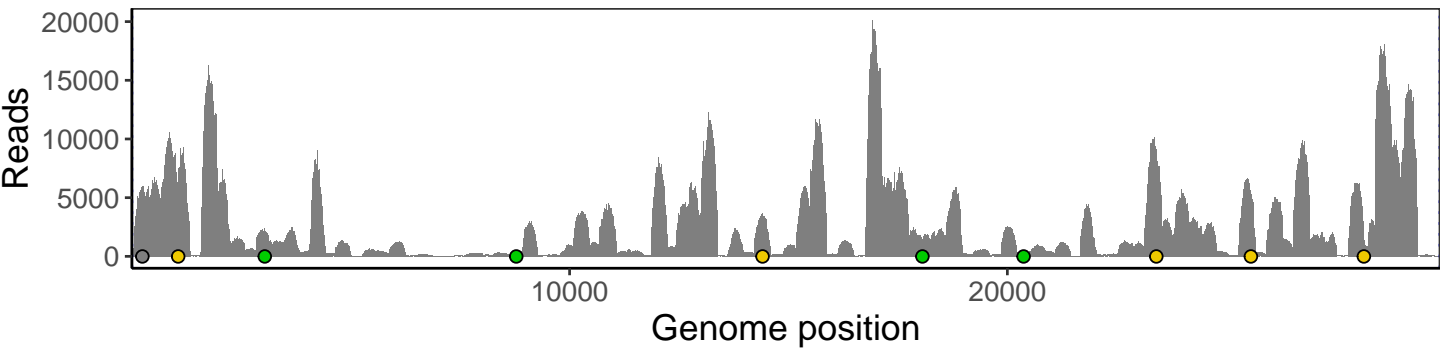
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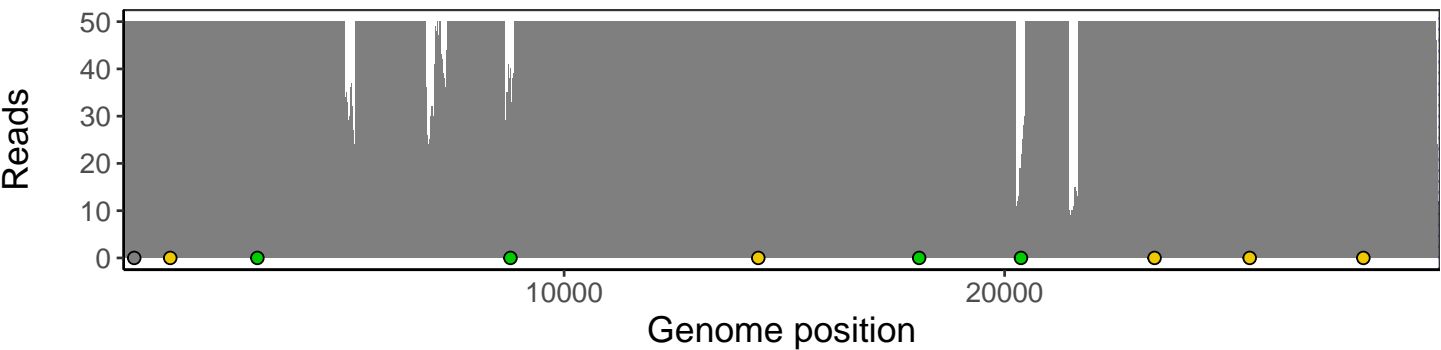
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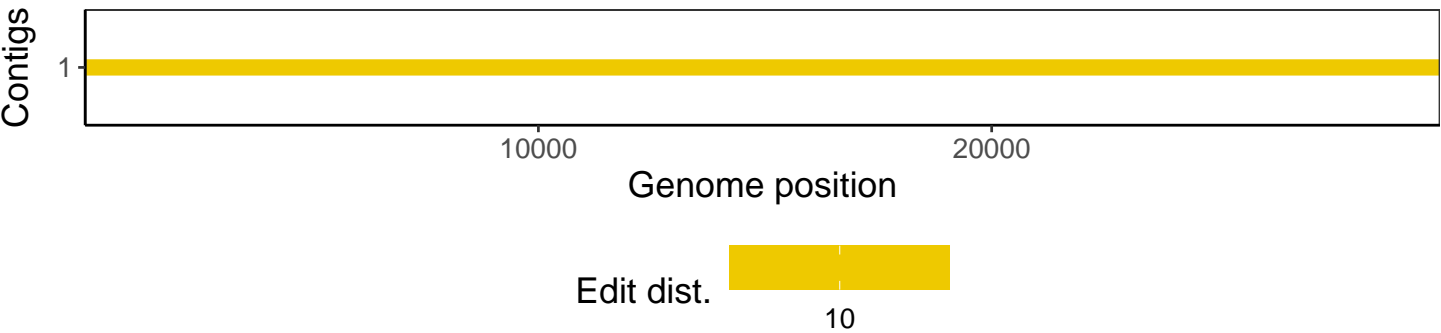
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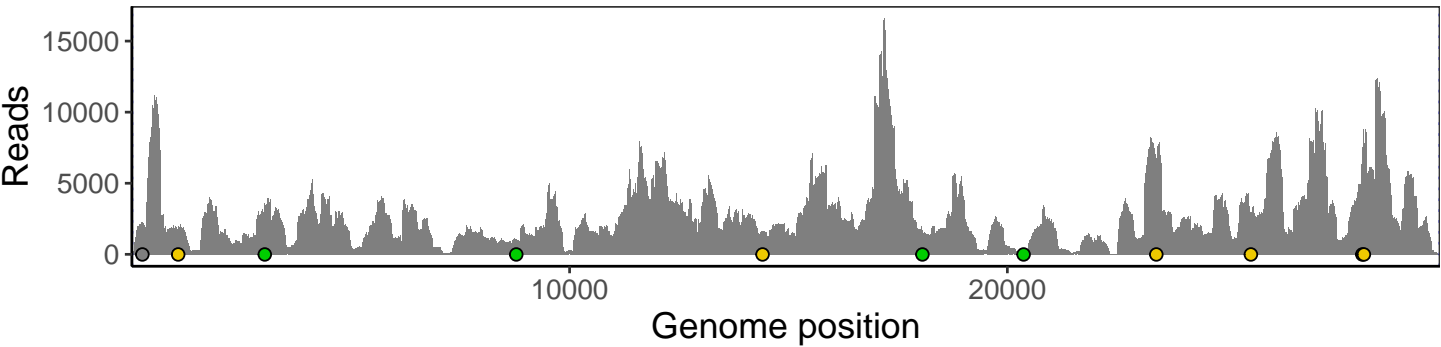
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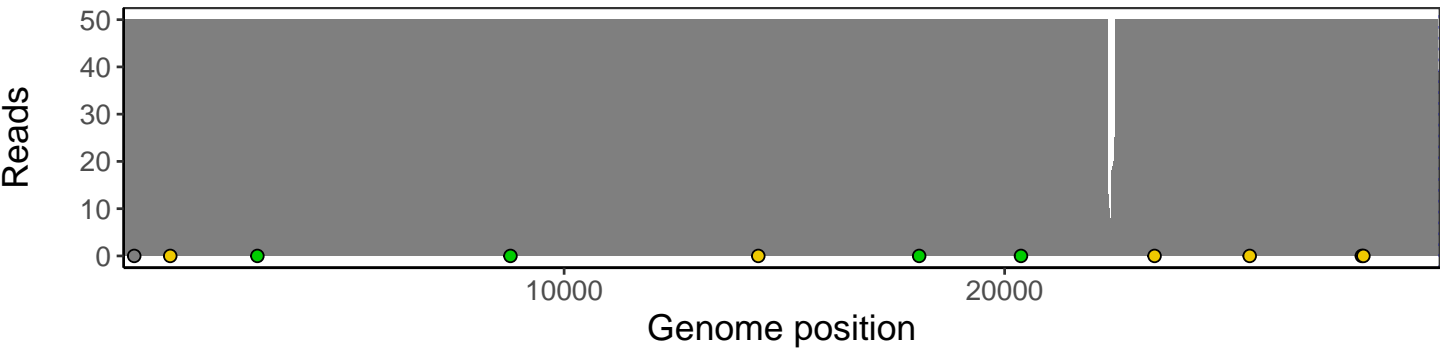
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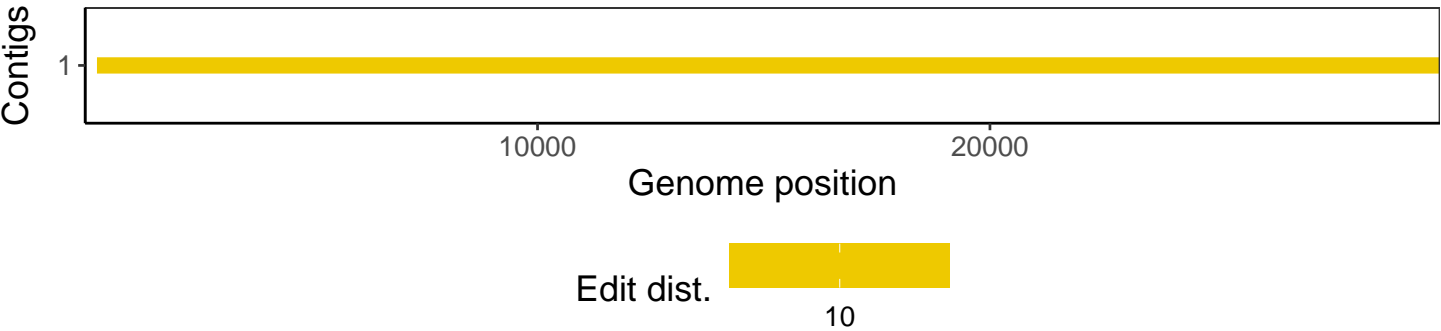
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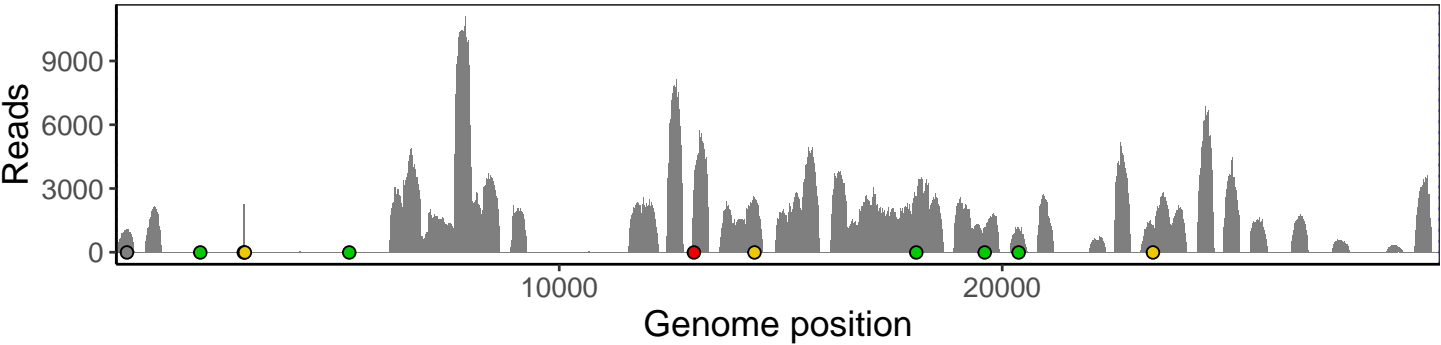
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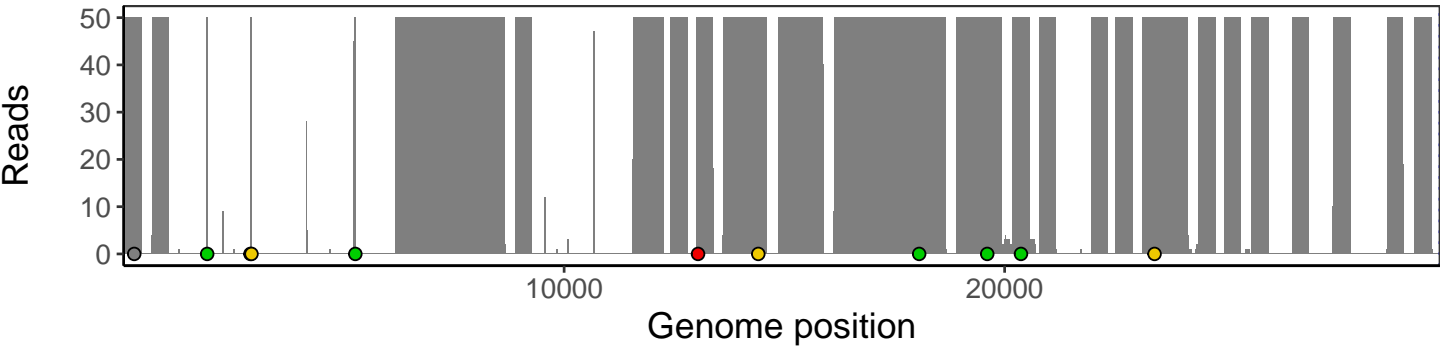
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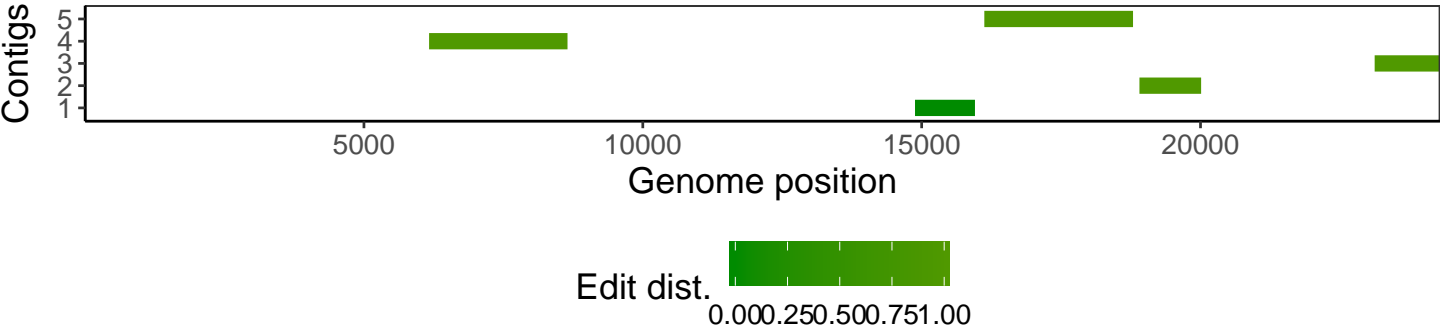
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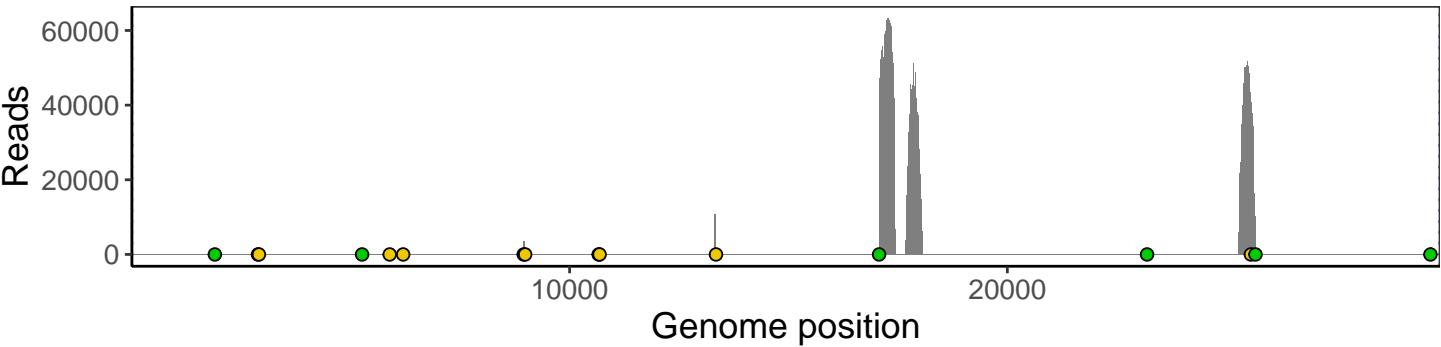
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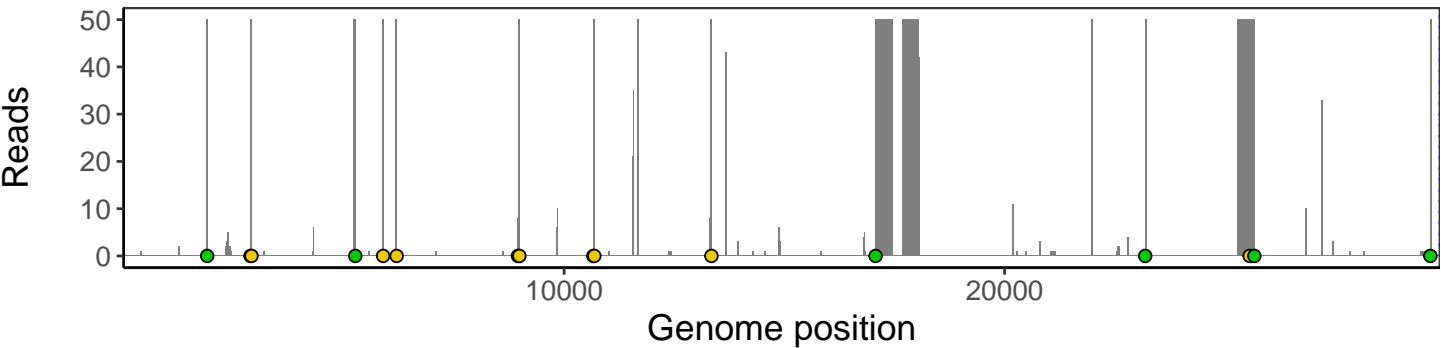
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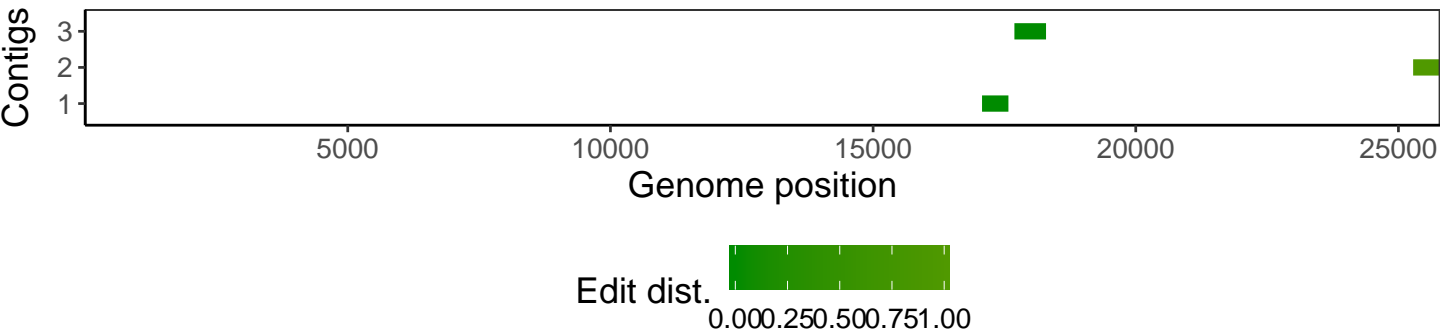
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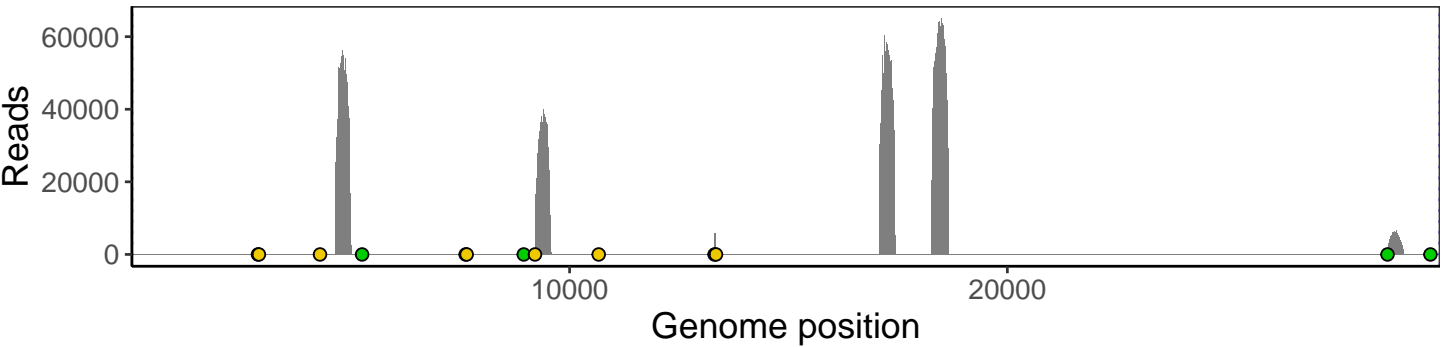
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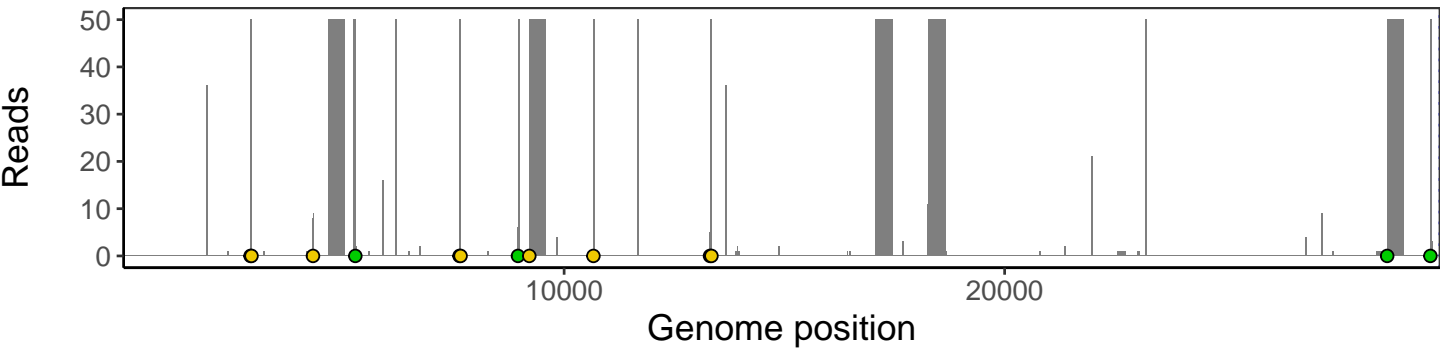
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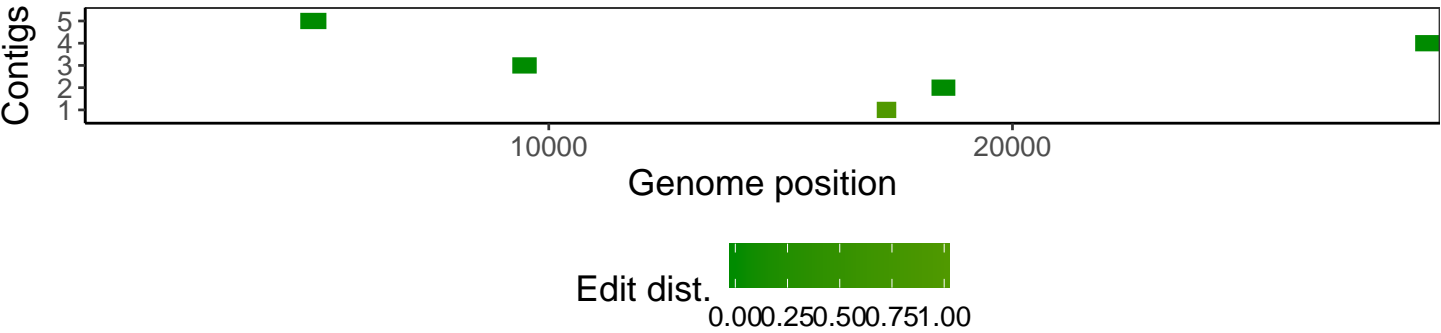
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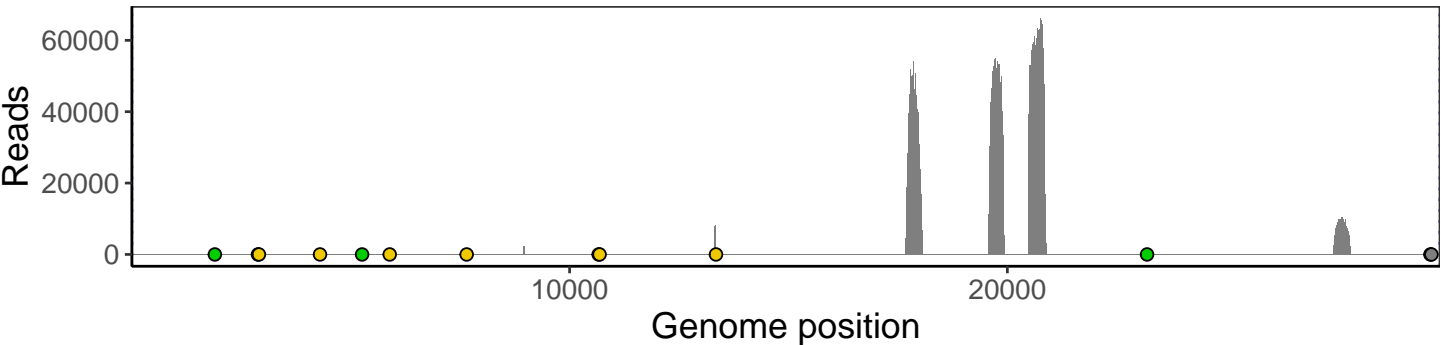
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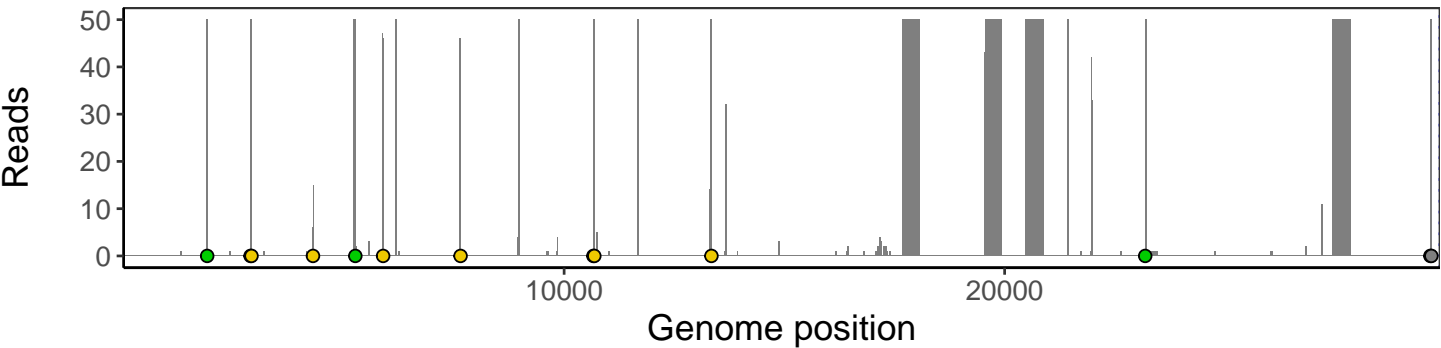
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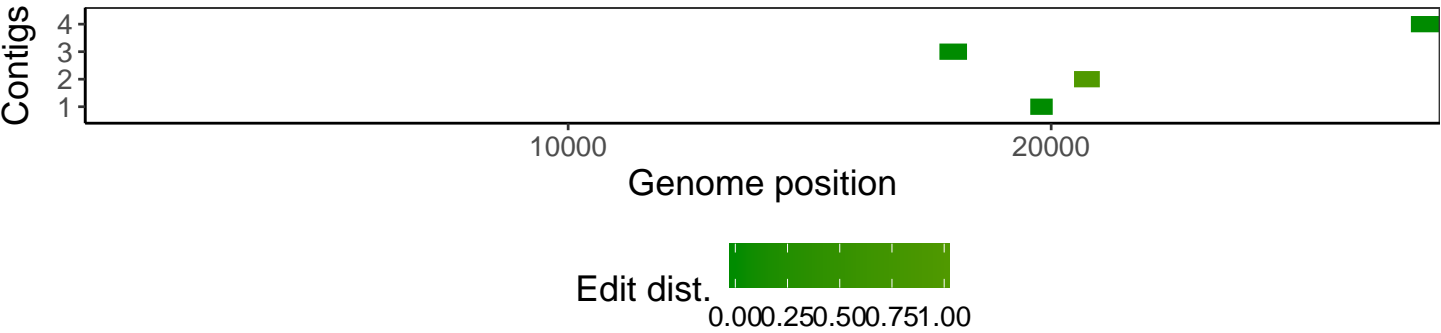
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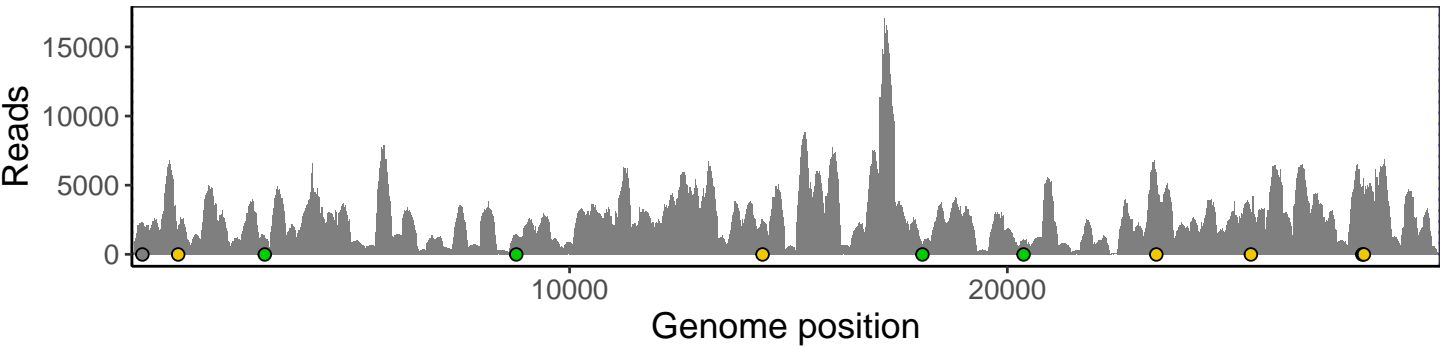
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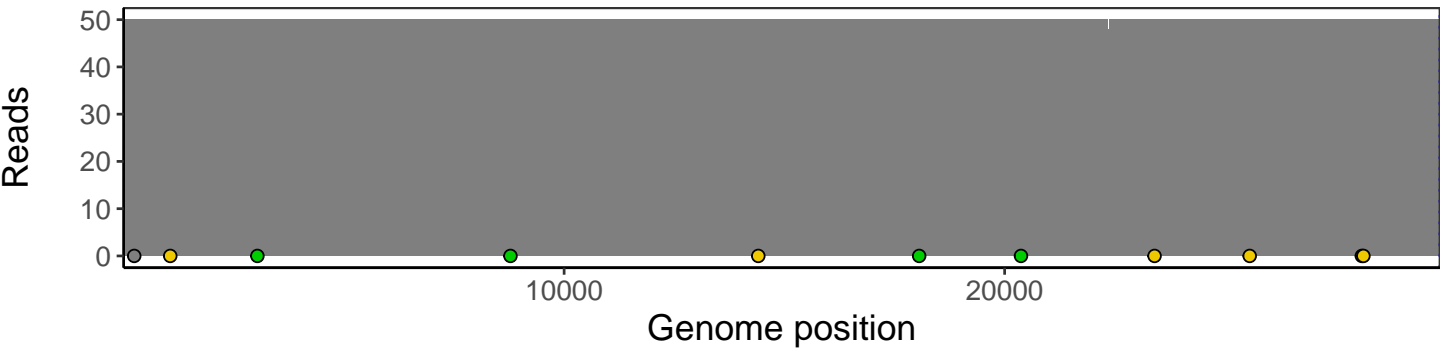
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