

COVID-19 subject 266

2020-08-28

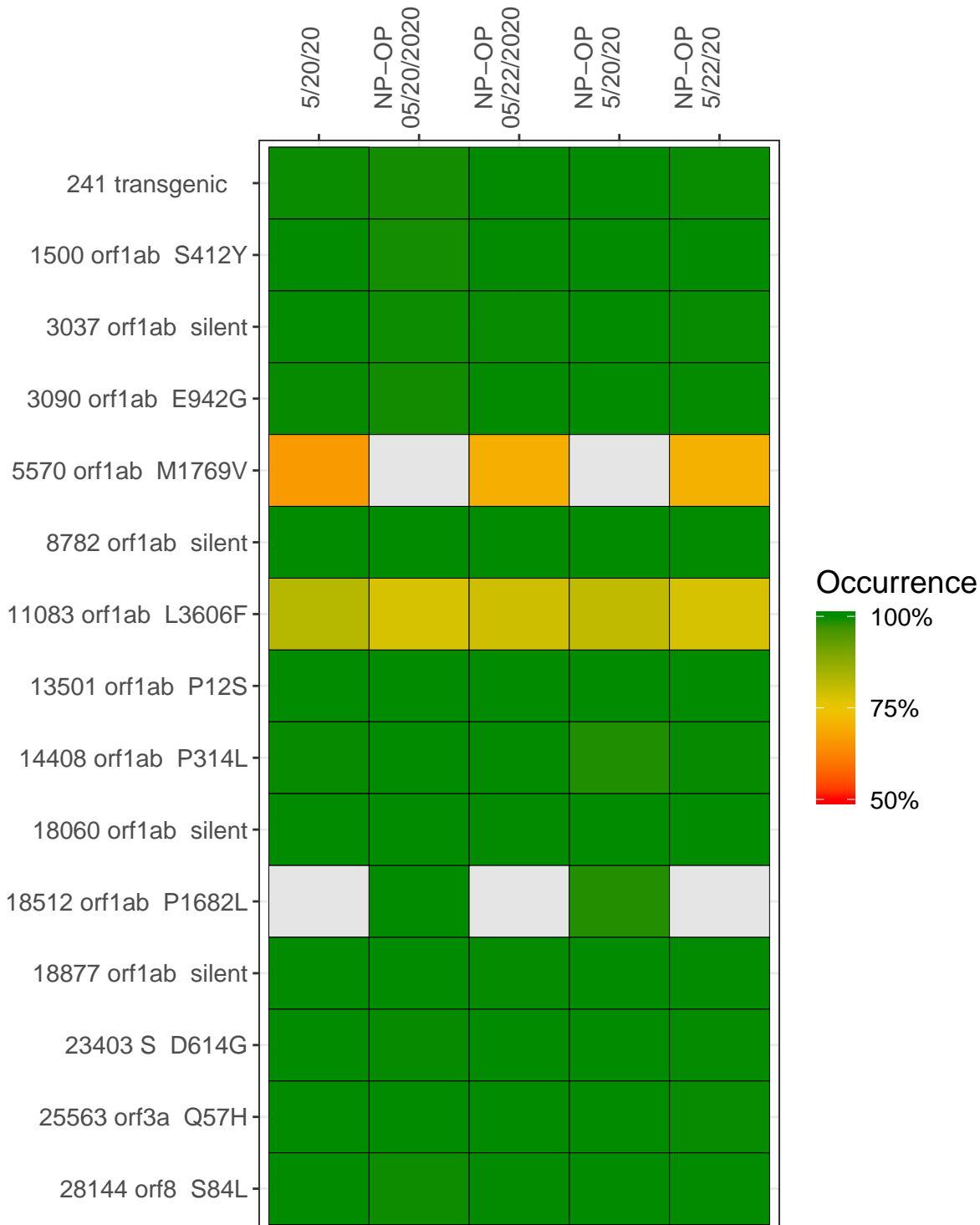
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found ([here](#)).

Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0155	composite	NA	NP-OP	05/20/2020	22.33	99.8%	99.0%
VSP0163	composite	NA	NP-OP	05/22/2020	29.75	99.9%	99.8%
VSP0155-1	single experiment	17000	NP-OP	05/20/2020	21.42	99.4%	98.2%
VSP0155-2	single experiment	85000	NP-OP	05/20/2020	22.33	99.7%	98.6%
VSP0163-1	single experiment	1530000	NP-OP	05/22/2020	29.75	99.9%	99.8%
VSP0163-2	single experiment	7650000	NP-OP	05/22/2020	29.84	99.9%	99.8%
VSP0262-1	single experiment	NA		5/20/20	29.98	99.9%	99.8%
VSP0263-1	single experiment	NA		5/20/20	29.86	99.9%	99.6%
VSP0319-1	single experiment	NA	NP-OP	5/20/20	22.25	99.3%	98.5%
VSP0320-1	single experiment	NA	NP-OP	5/22/20	29.86	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.



	5/20/20		NP-OP 05/20/2020		NP-OP 05/22/2020		NP-OP 5/20/20	NP-OP 5/22/20
241 transgenic	1137	436	37	335	2589	1388	283	2515
1500 orf1ab S412Y	2310	136	133	33	379	957	34	1521
3037 orf1ab silent	3005	814	33	313	1859	1321	272	1757
3090 orf1ab E942G	2652	707	38	436	2123	1167	343	1512
5570 orf1ab M1769V	2732	252	29	60	699	1463	74	2078
8782 orf1ab silent	3355	290	17	91	728	1469	107	2376
11083 orf1ab L3606F	2296	725	78	151	585	968	148	802
13501 orf1ab P12S	4569	311	31	86	608	1806	77	2796
14408 orf1ab P314L	3294	737	46	79	995	1890	94	2157
18060 orf1ab silent	1809	278	25	82	703	997	60	1184
18512 orf1ab P1682L	4515	1495	63	257	901	2685	240	3440
18877 orf1ab silent	3078	1036	47	388	1644	1762	375	2064
23403 S D614G	3628	1281	72	620	2914	2132	703	2907
25563 orf3a Q57H	2402	773	35	277	2440	1256	264	1819
28144 orf8 S84L	1677	601	68	242	1792	937	286	1221
	VSP0262-1	VSP0263-1	VSP0155-1	VSP0155-2	VSP0163-1	VSP0163-2	VSP0319-1	VSP0320-1

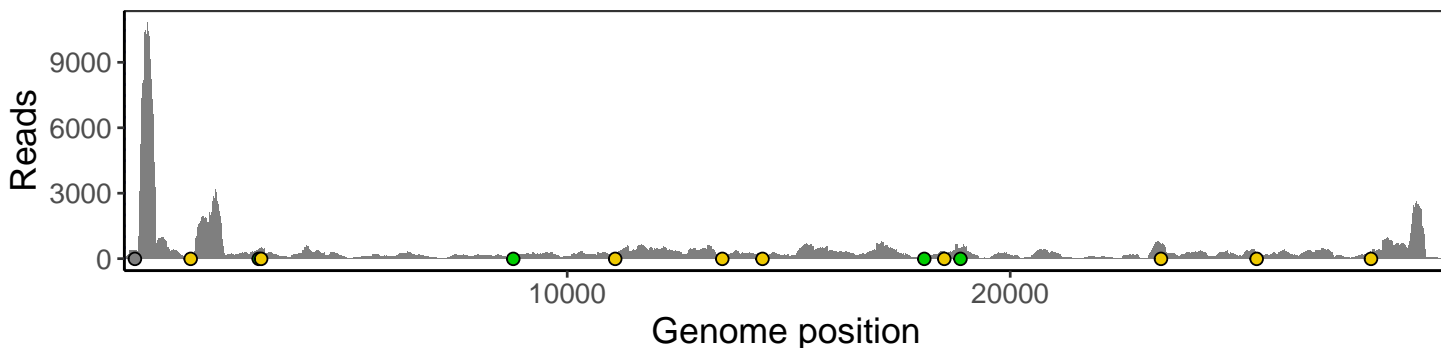
Base change



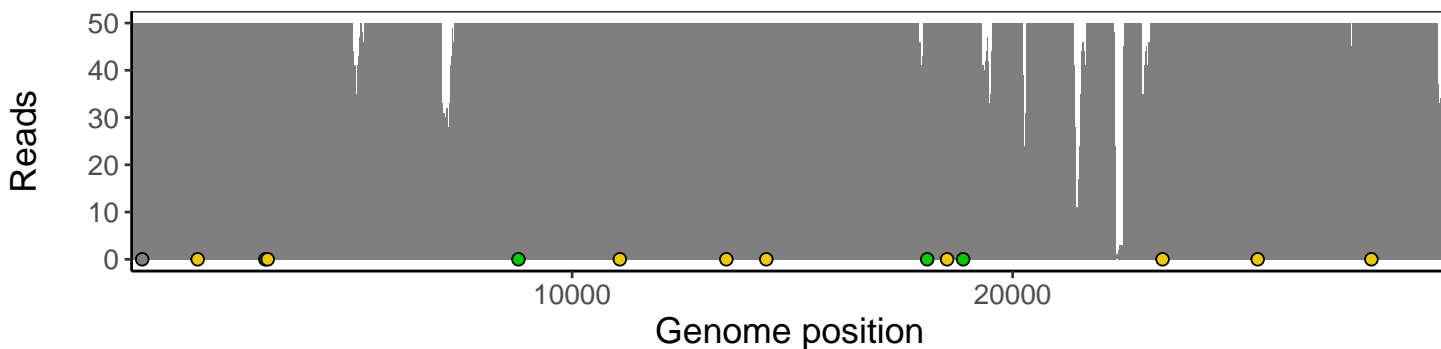
Analyses of individual experiments and composite results.

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

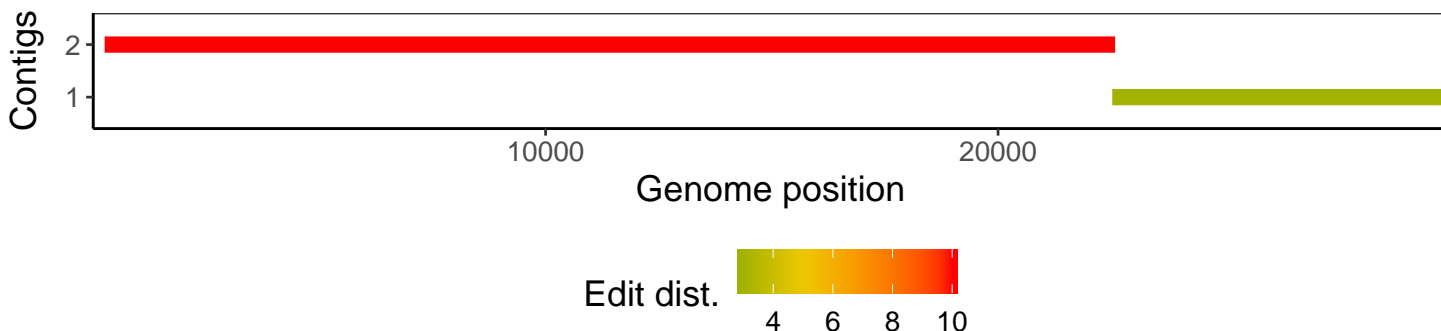
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



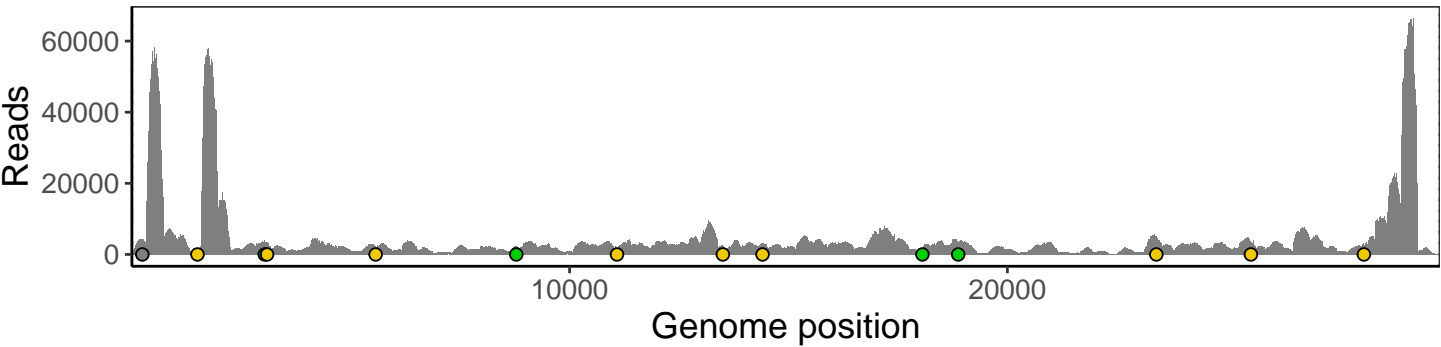
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



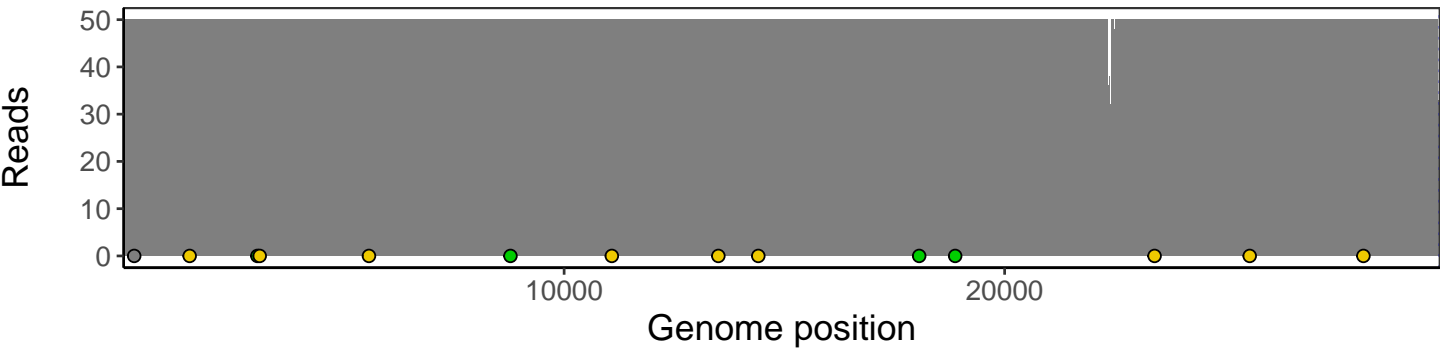
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



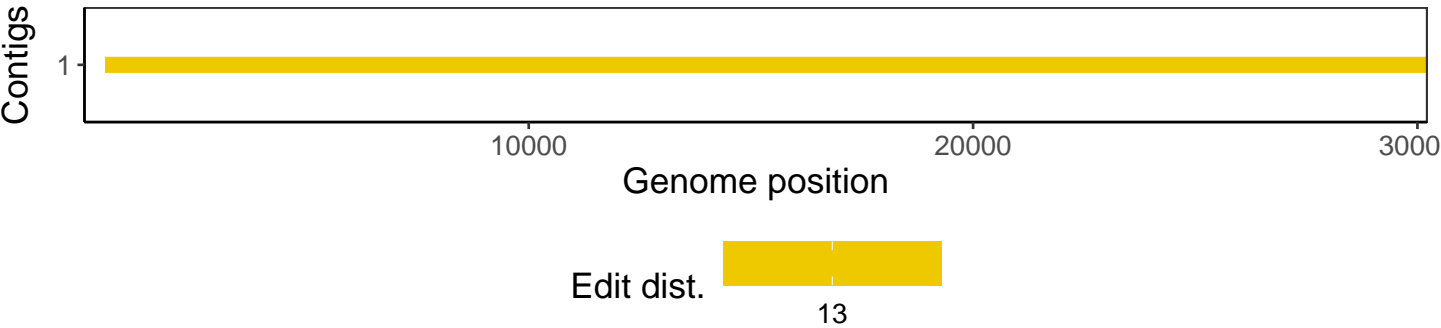
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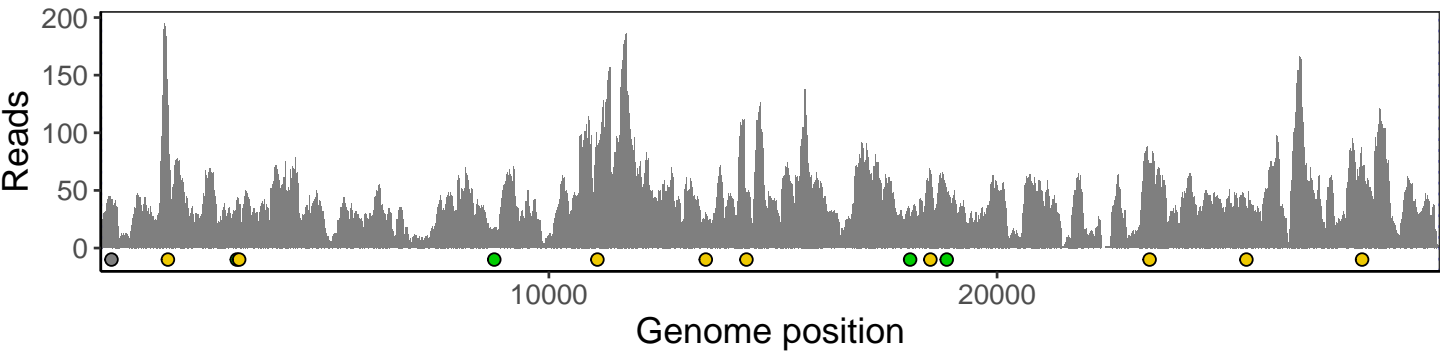
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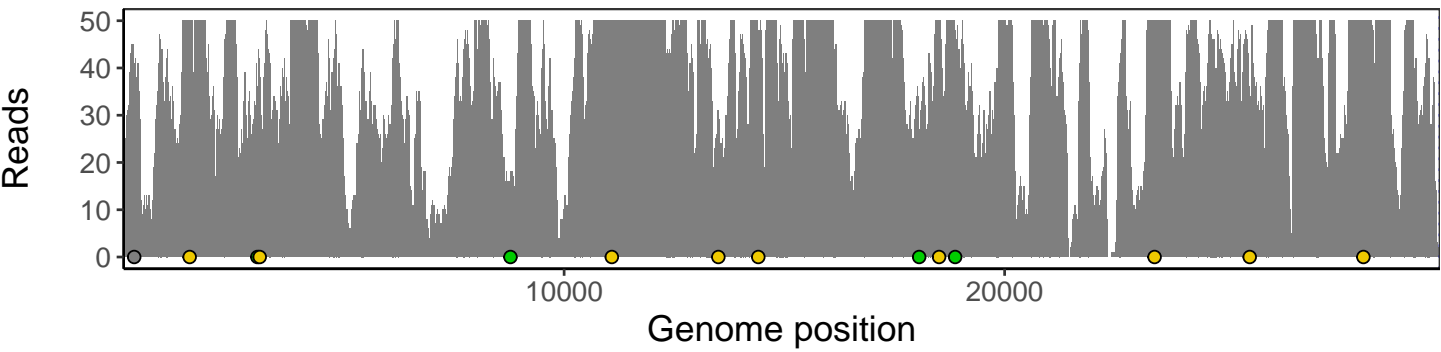
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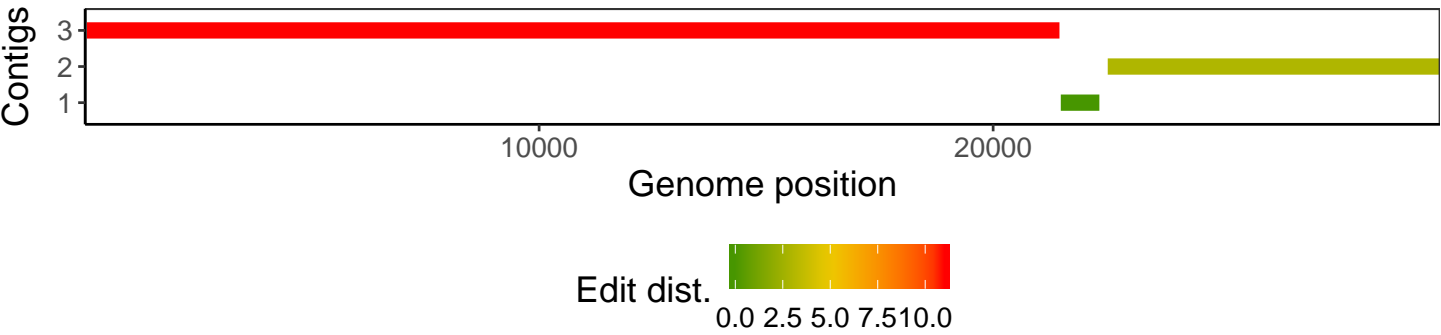
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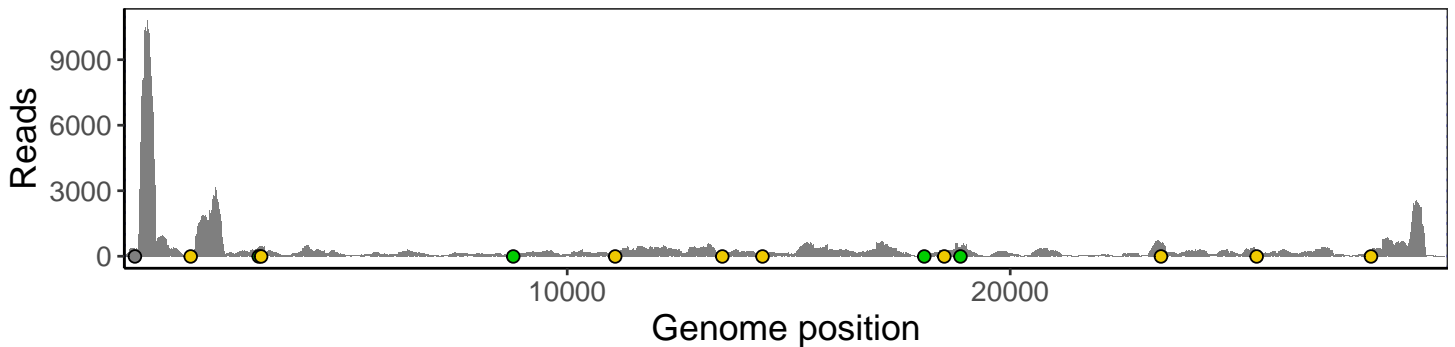
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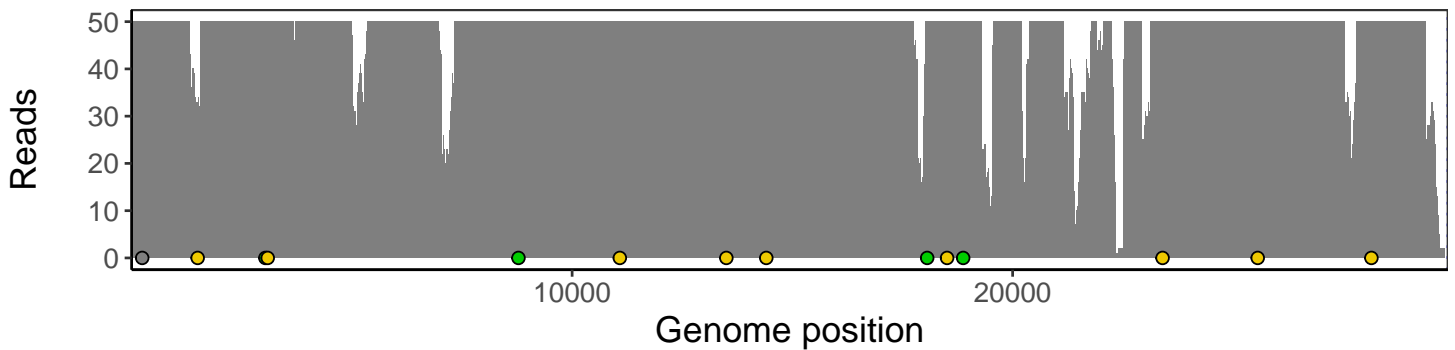
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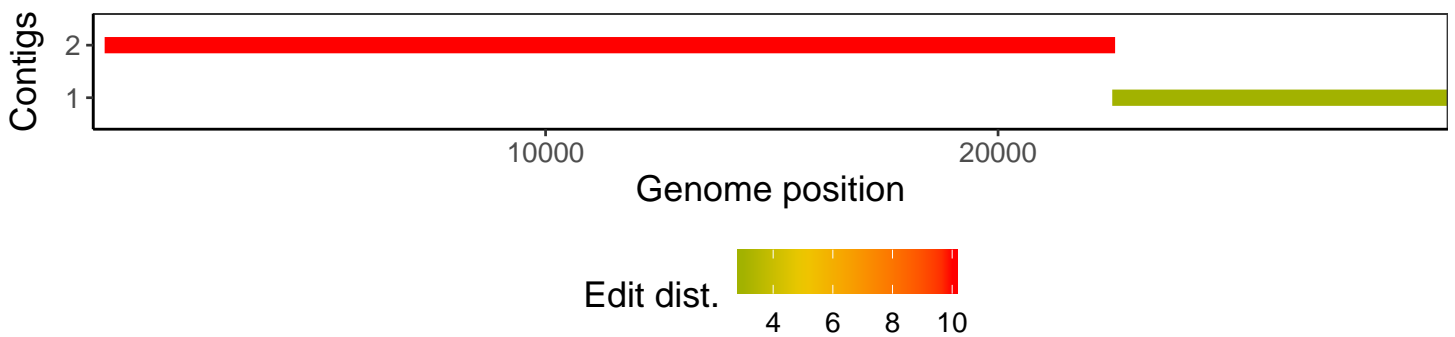
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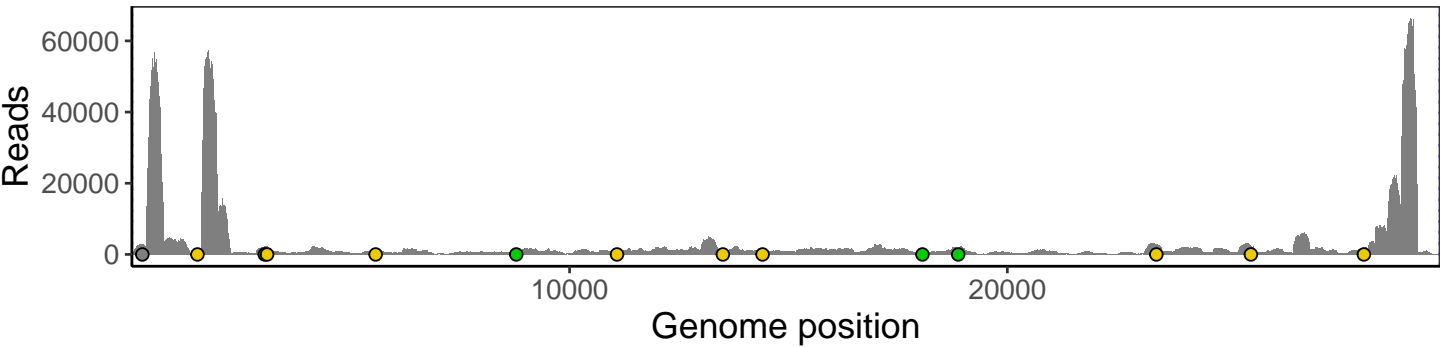
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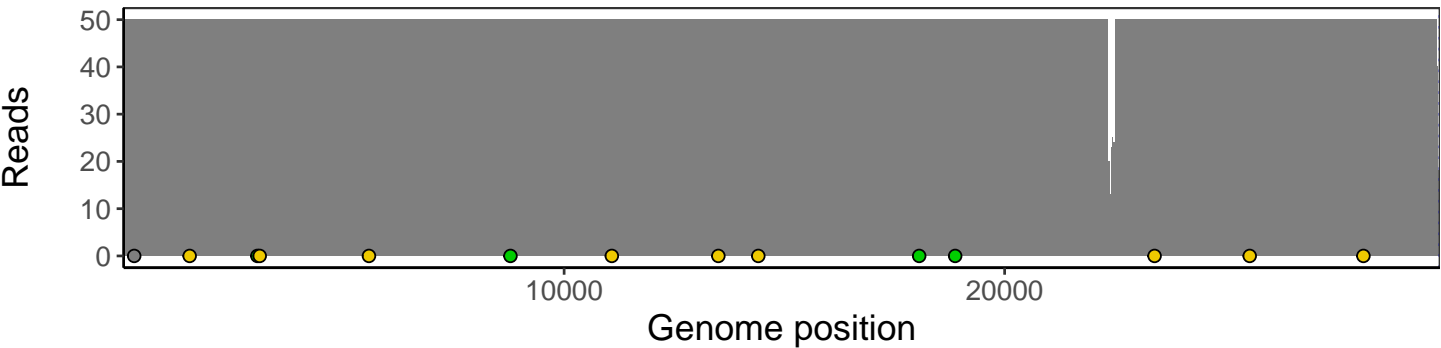
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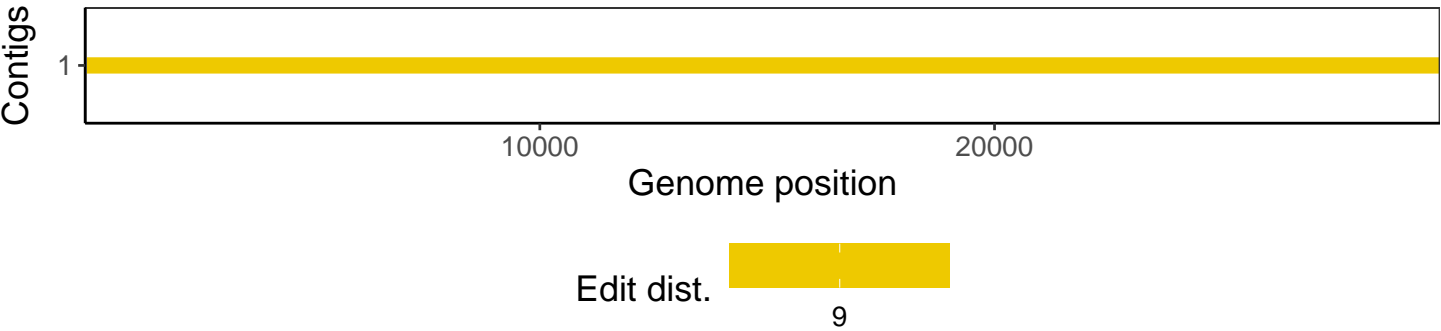
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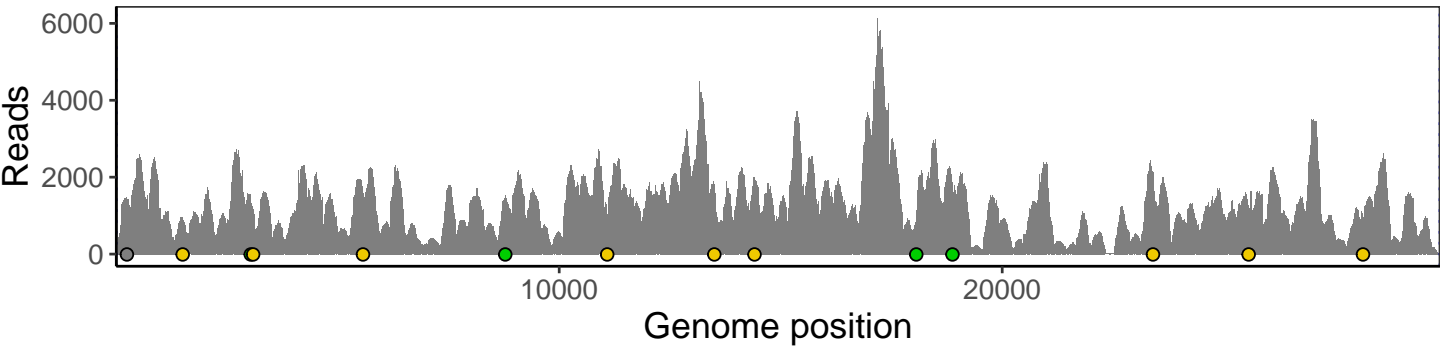
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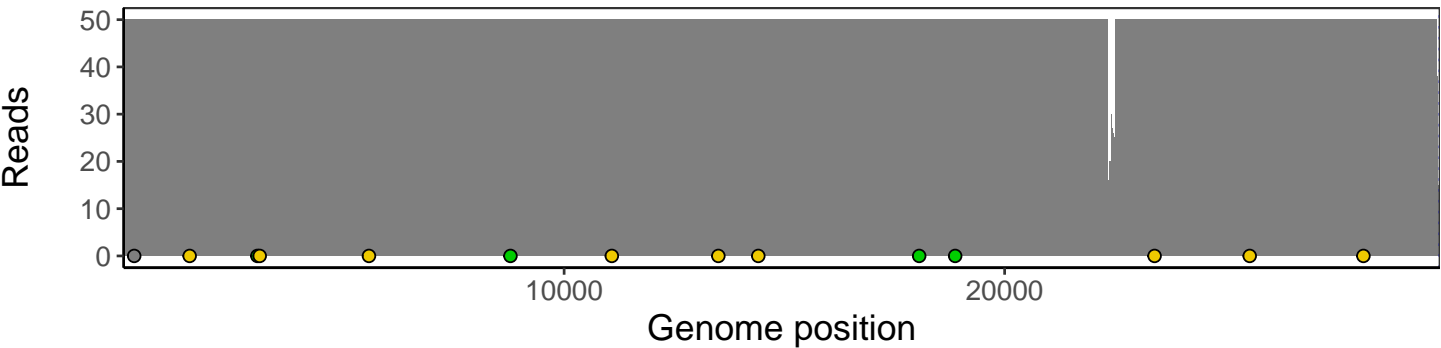
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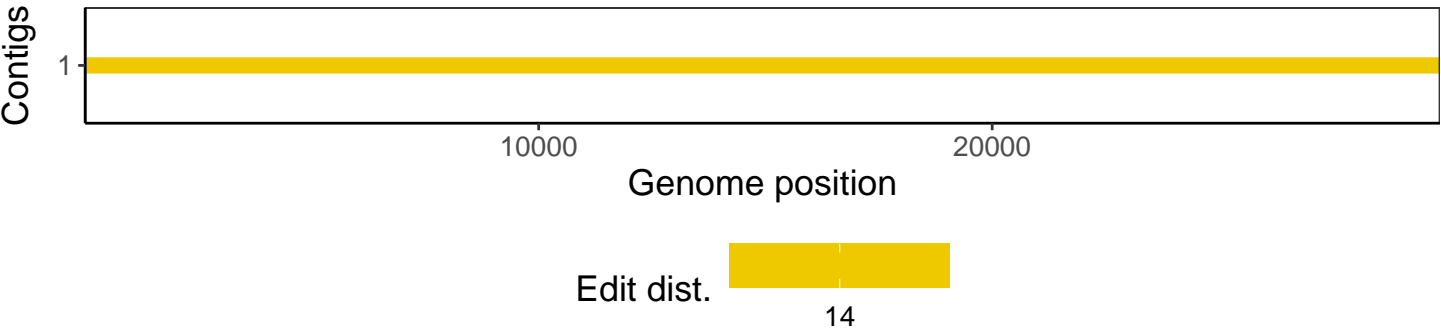
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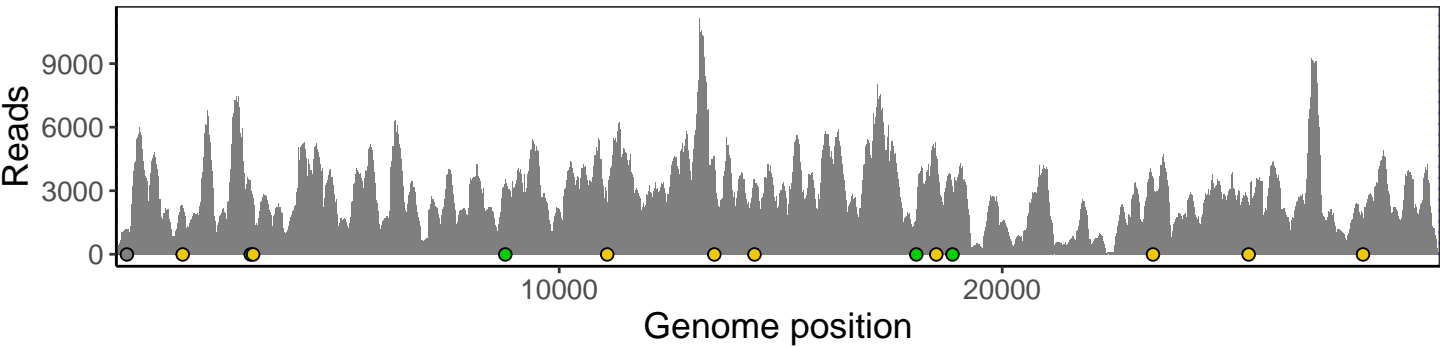
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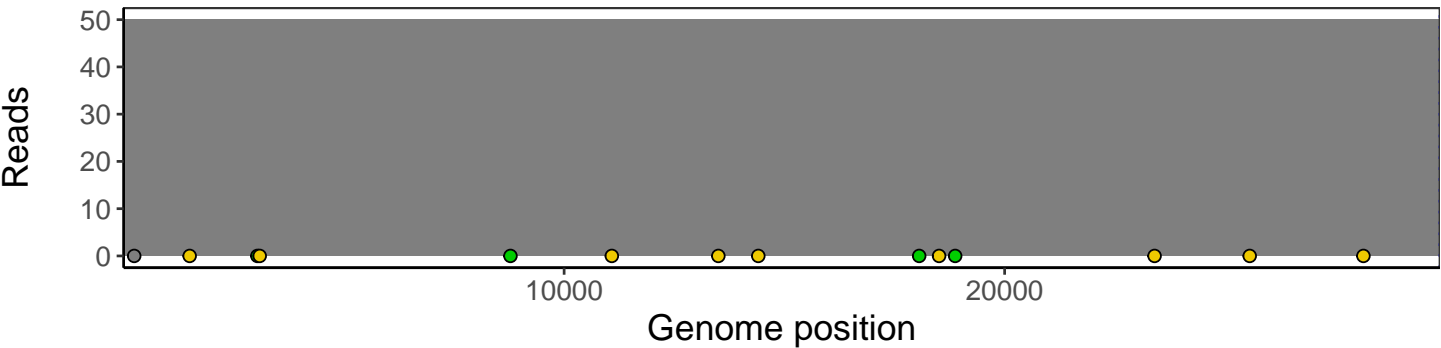
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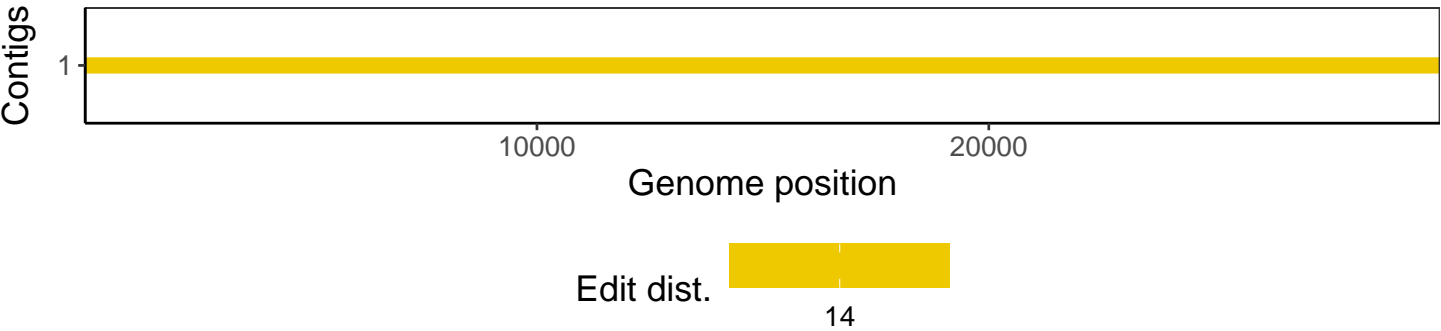
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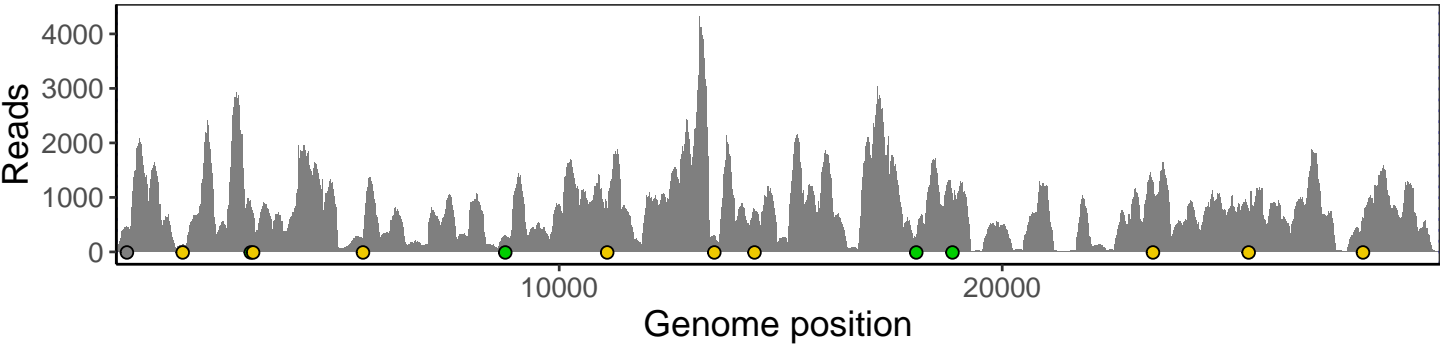
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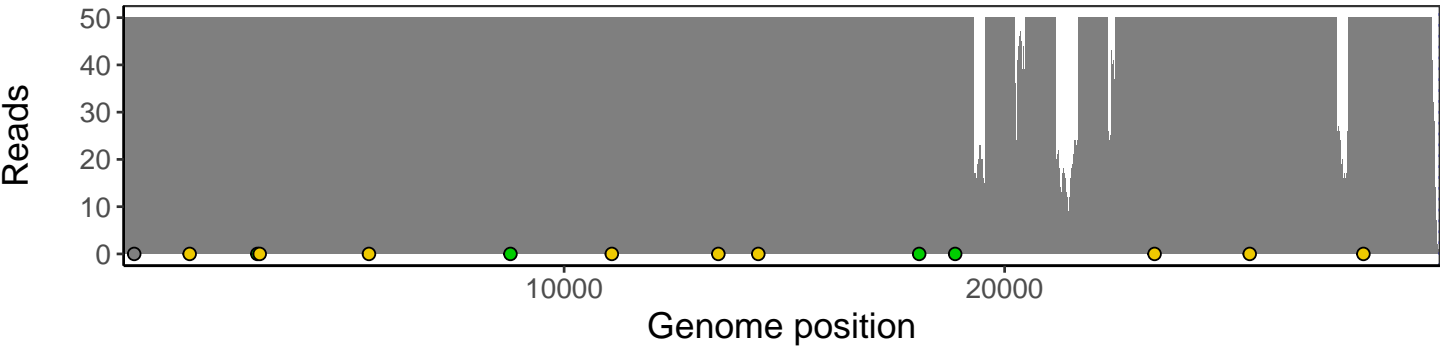
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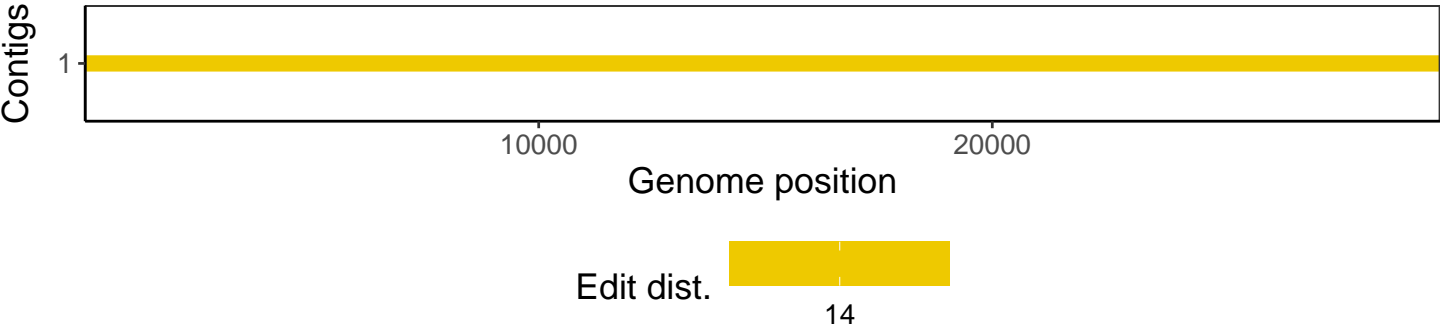
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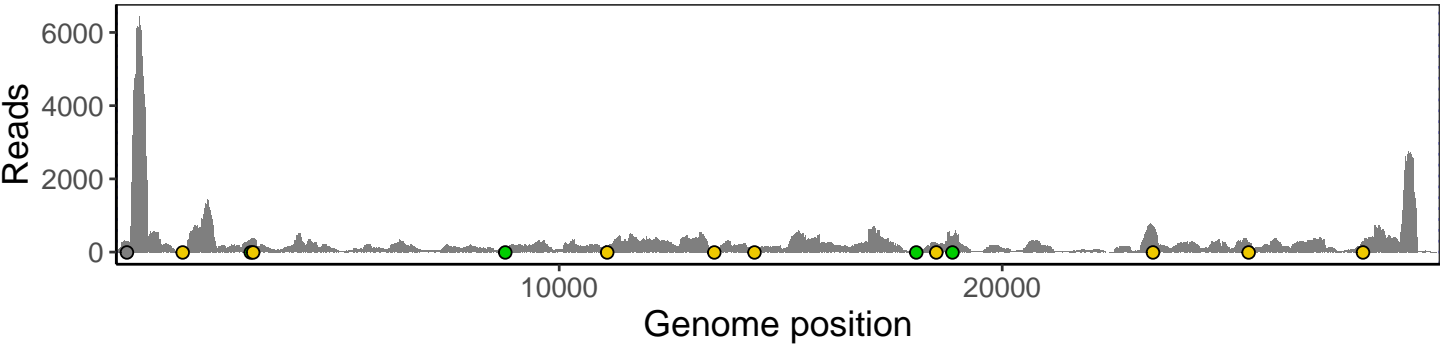
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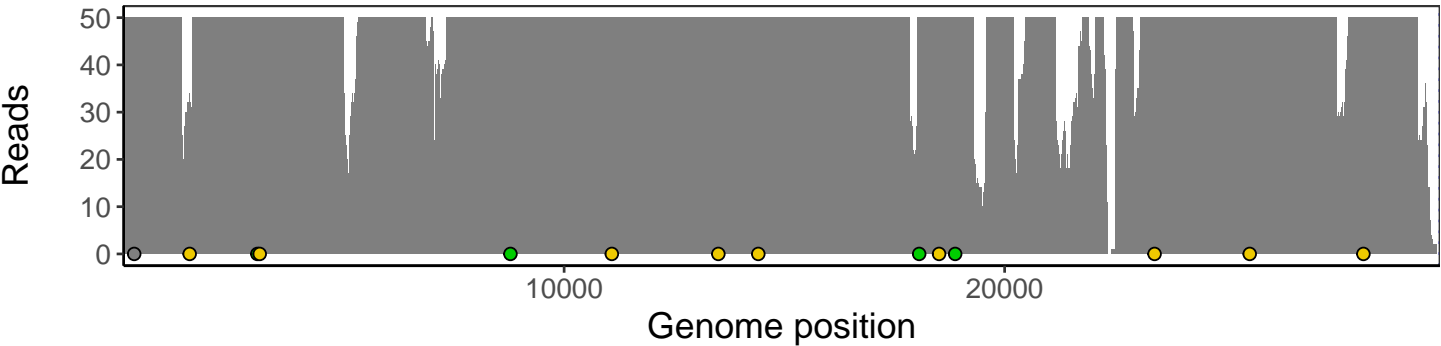
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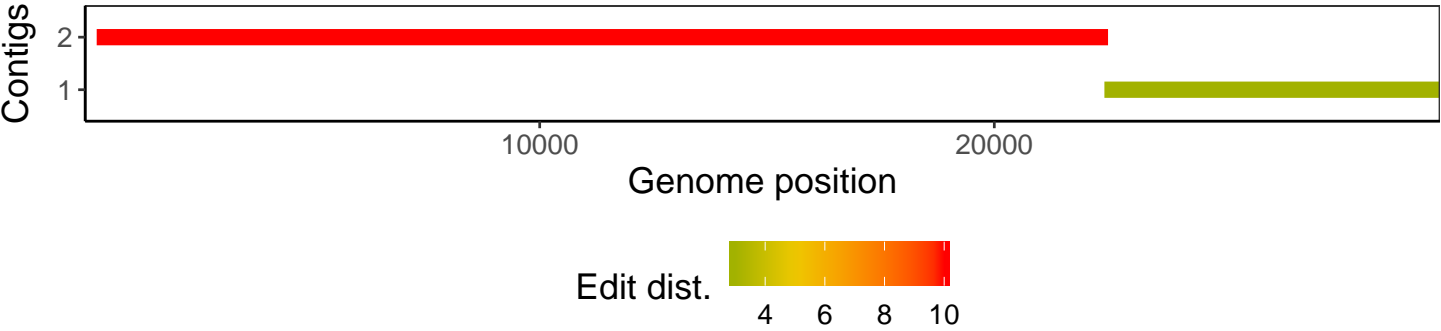
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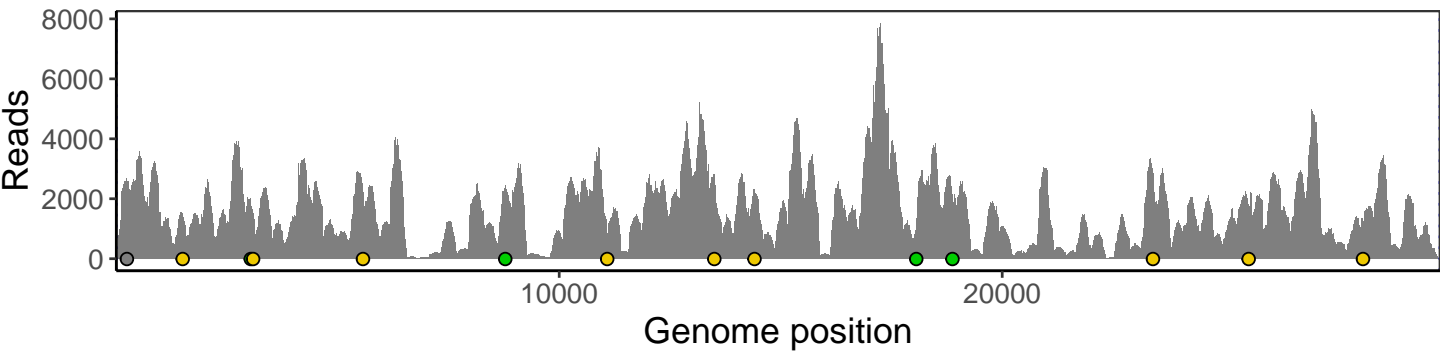
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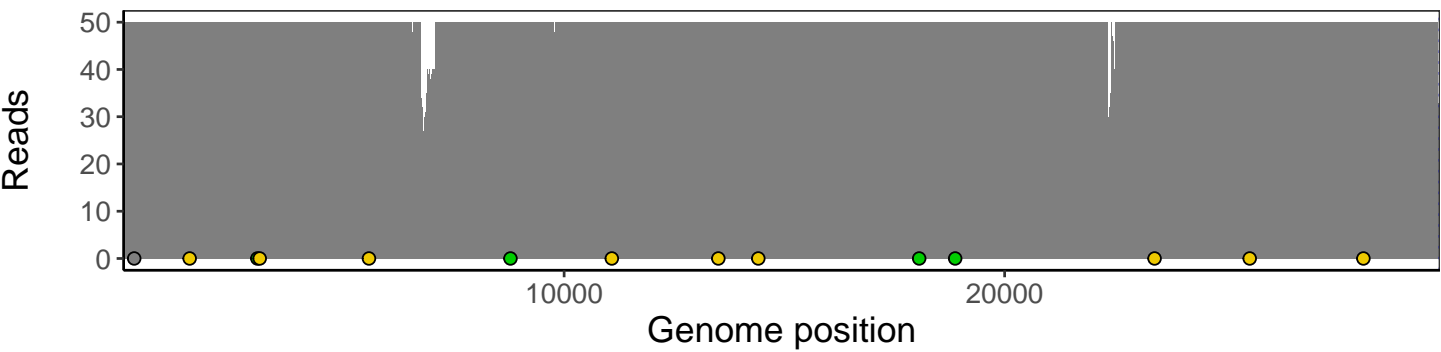
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