

COVID-19 subject 247

2021-01-10

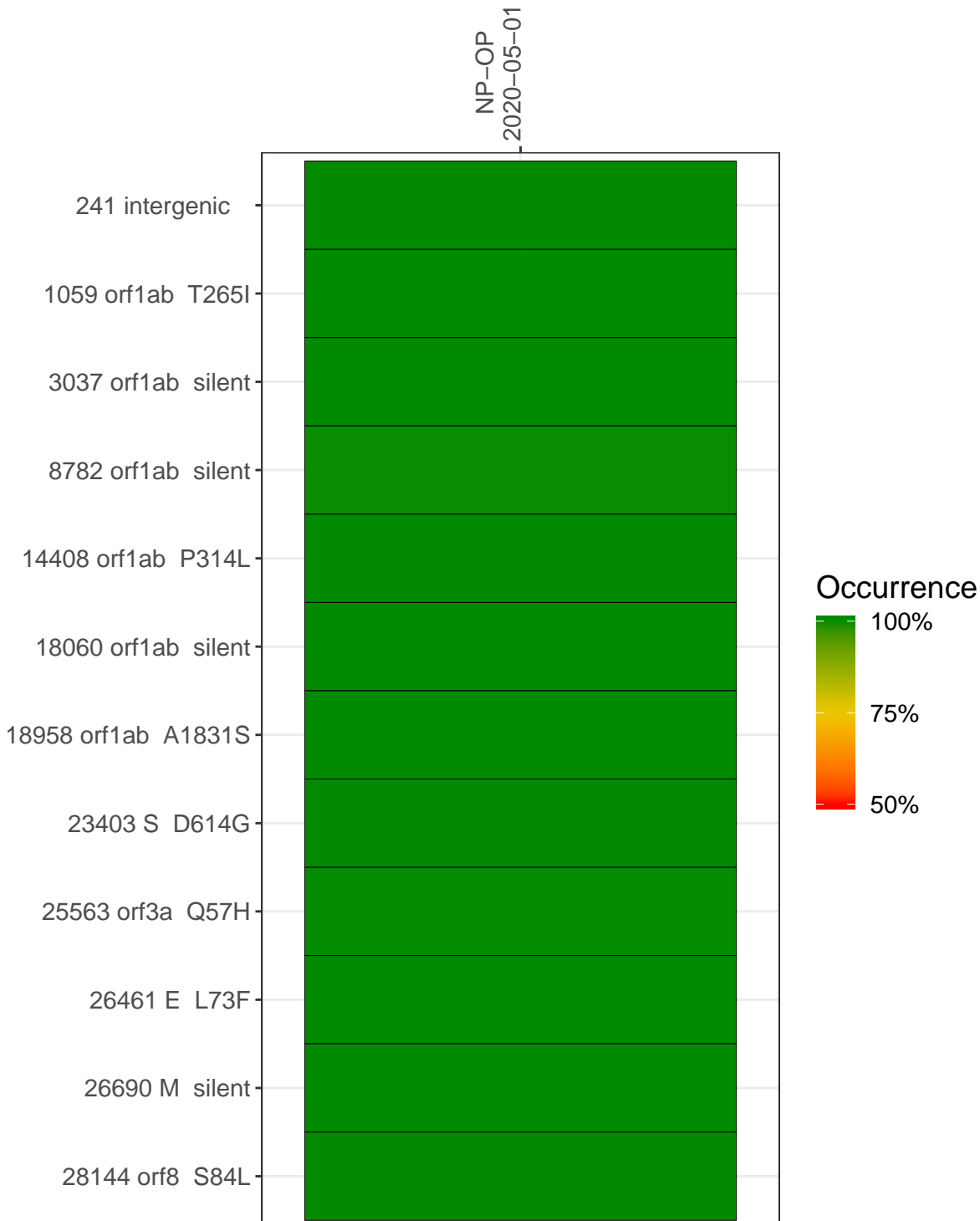
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found ([here](#)).

Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0050	composite	NA	NP-OP	2020-05-01	21.42	99.2%	99.0%
VSP0050-1	single experiment	2190	NP-OP	2020-05-01	4.73	83.3%	81.3%
VSP0050-2	single experiment	2190	NP-OP	2020-05-01	7.49	91.5%	89.8%
VSP0050-3	single experiment	2190	NP-OP	2020-05-01	10.14	97.7%	96.5%
VSP0050-4	single experiment	2190	NP-OP	2020-05-01	10.21	90.7%	90.1%

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
2020-05-01

	VSP0050-1	VSP0050-2	VSP0050-3	VSP0050-4
241 intergenic	151	319	675	502
1059 orf1ab T265I	63	445	115	249
3037 orf1ab silent	33	301	600	102
8782 orf1ab silent		1	1012	
14408 orf1ab P314L	208	673	598	1084
18060 orf1ab silent	53	337	202	354
18958 orf1ab A1831S	7	403	150	546
23403 S D614G	730	1746	2720	1638
25563 orf3a Q57H	81	339	265	371
26461 E L73F	425	240	514	169
26690 M silent	504	526	1144	984
28144 orf8 S84L	534	1174	508	410

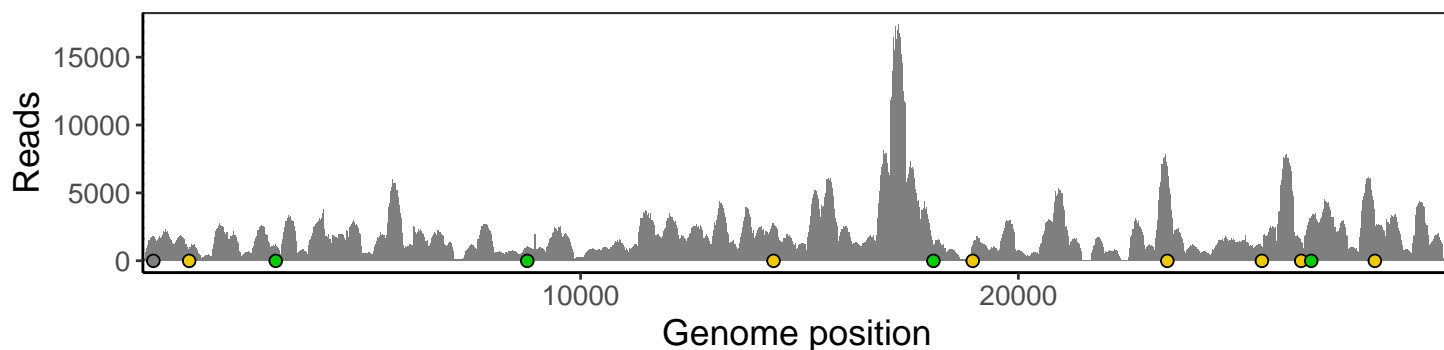
Base change

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

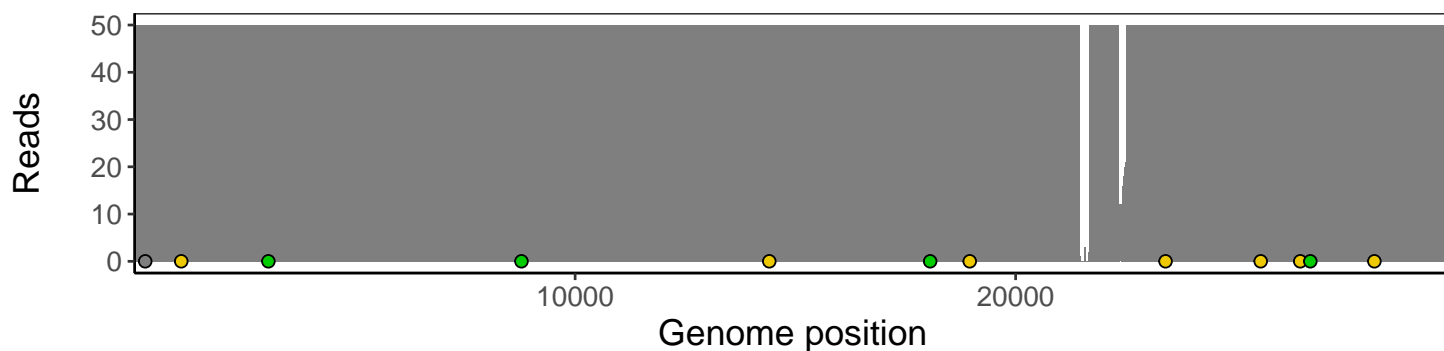
Analyses of individual experiments and composite results.

VSP0050 | 2020-05-01 | NP-OP | 247-qia | composite result

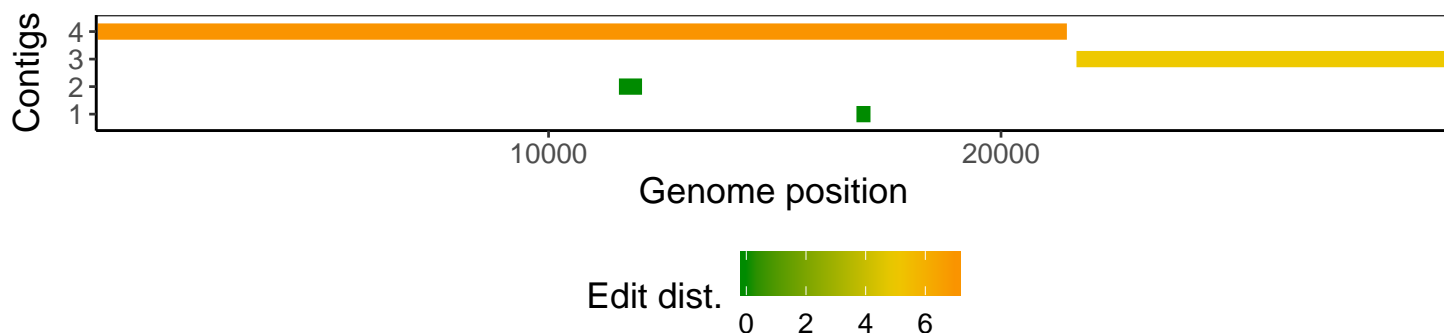
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



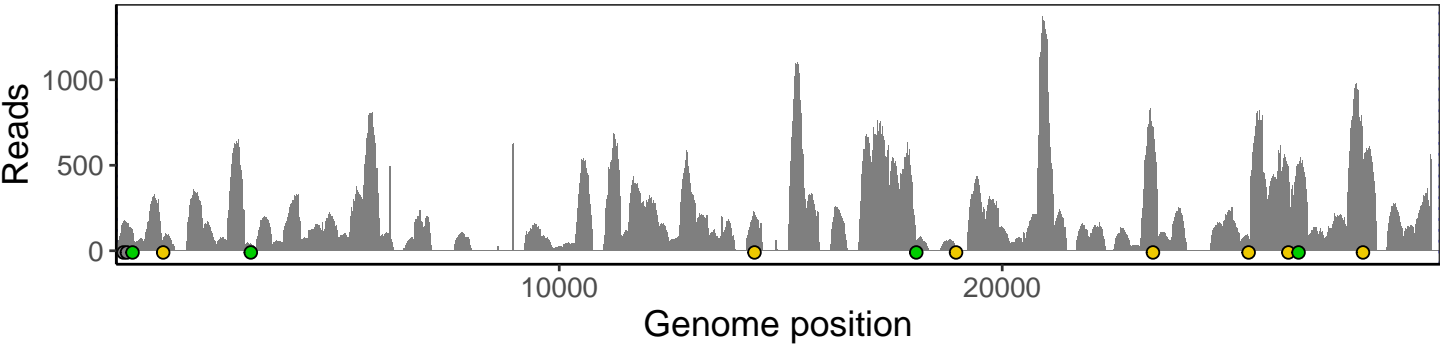
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



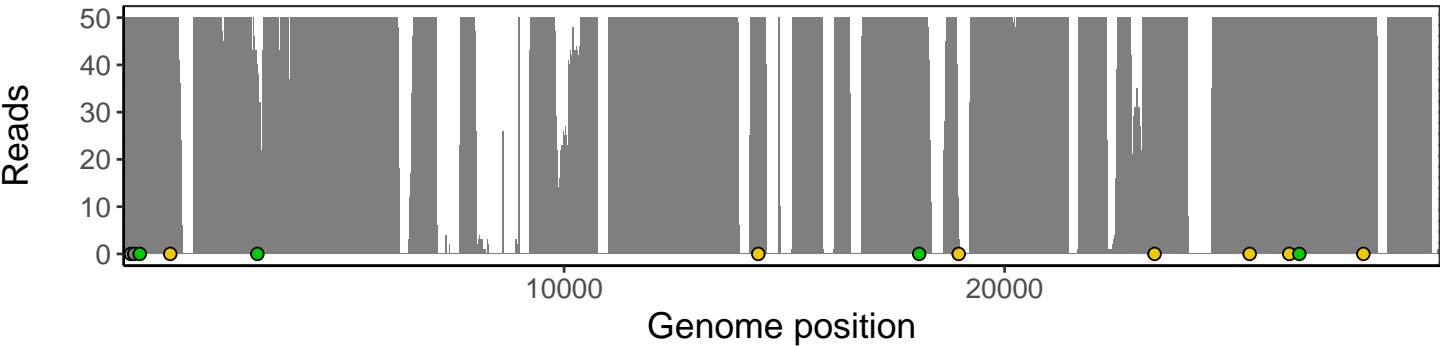
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



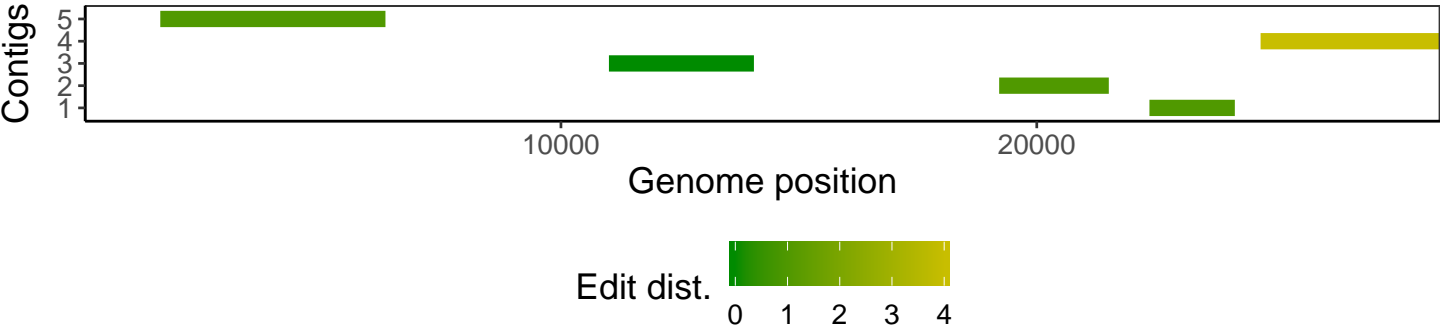
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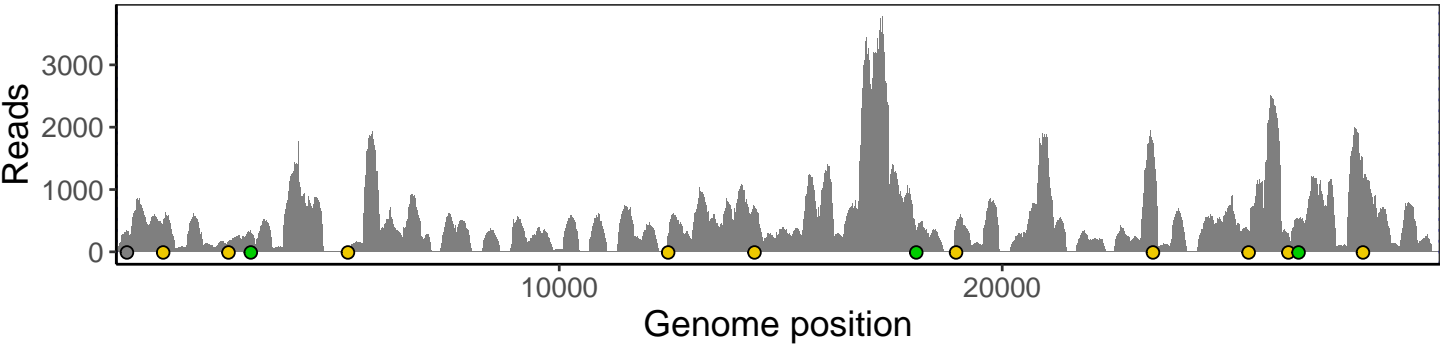
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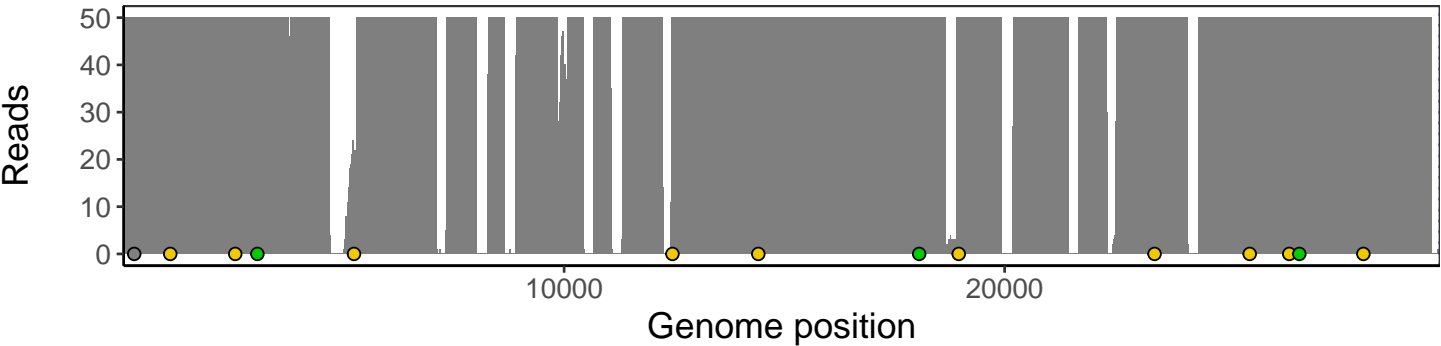
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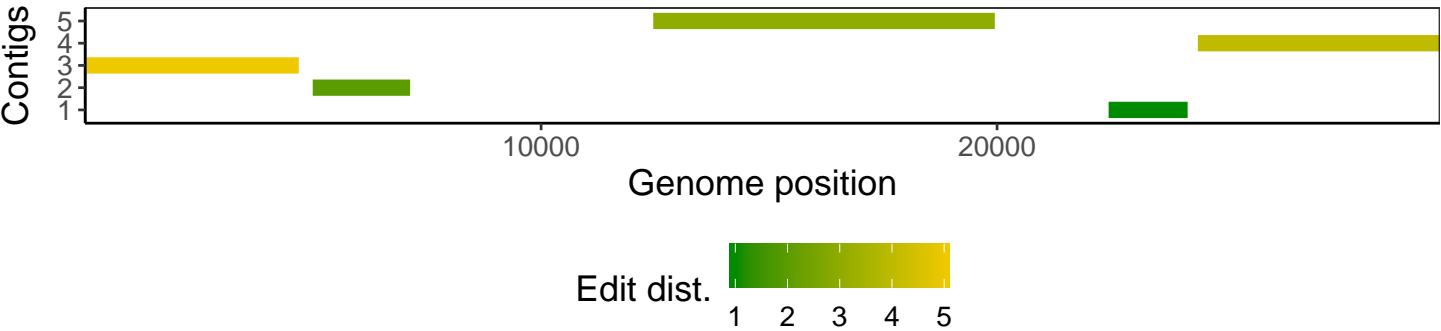
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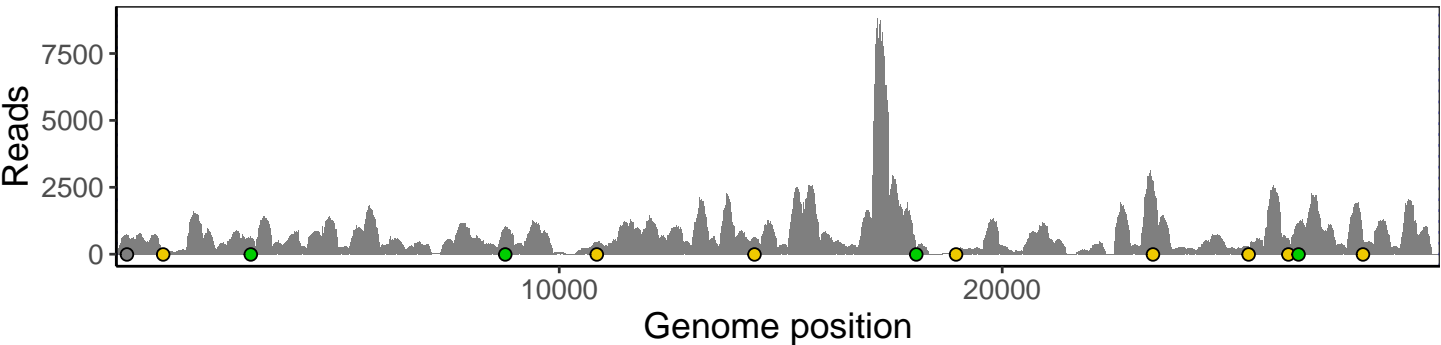
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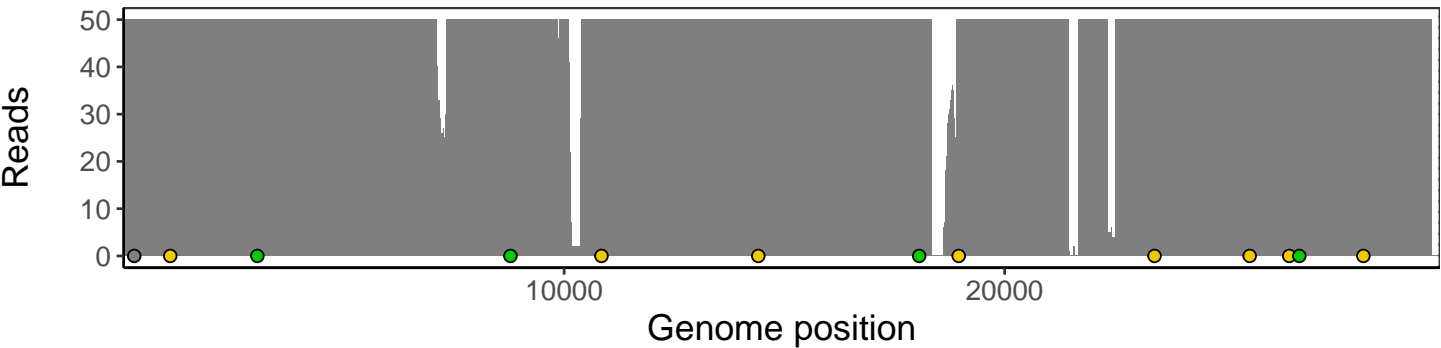
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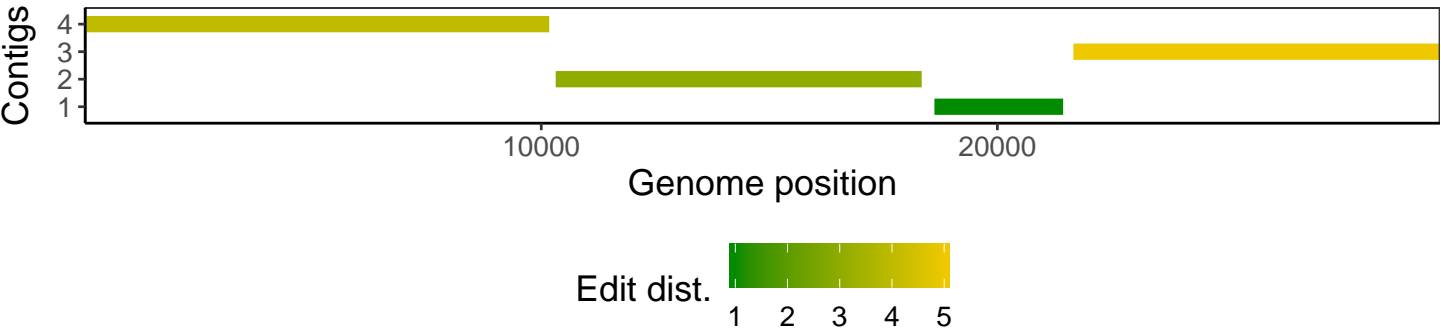
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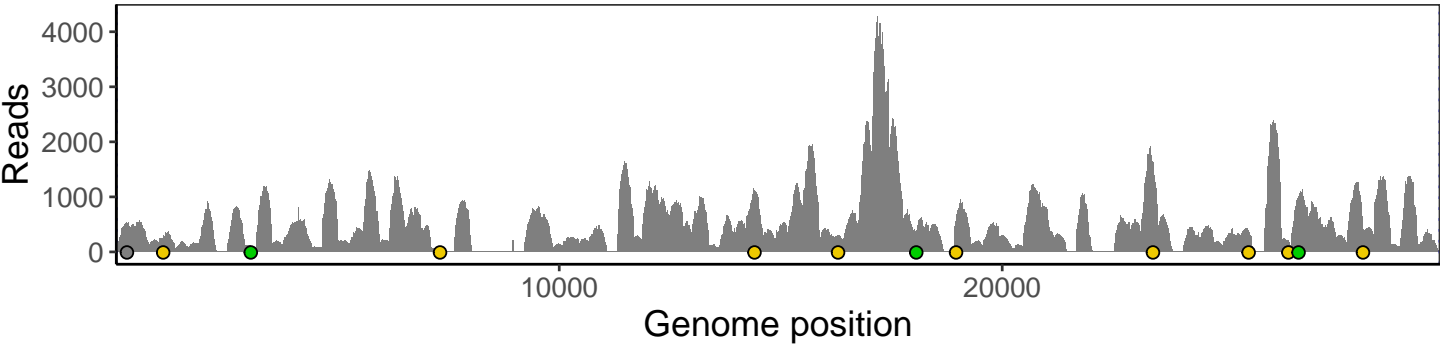
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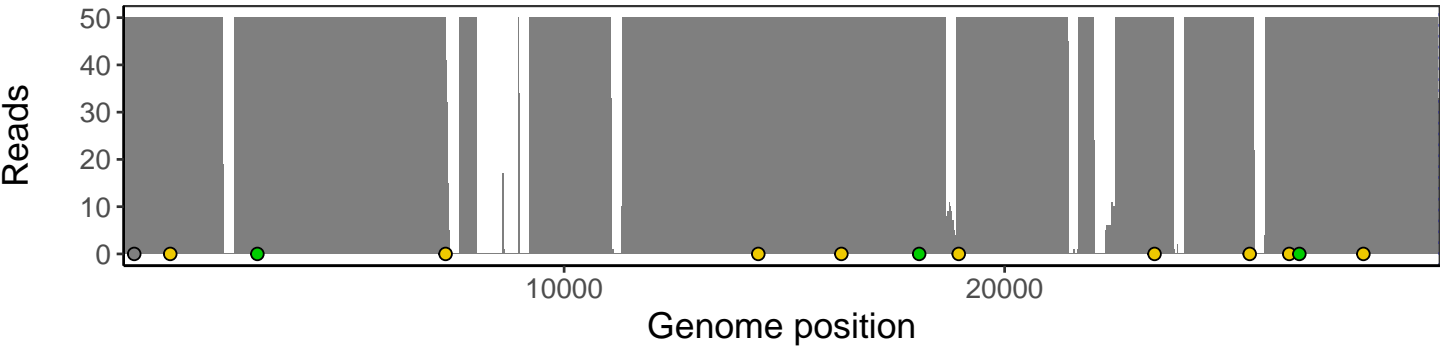
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