

COVID-19 subject 290

2021-01-10

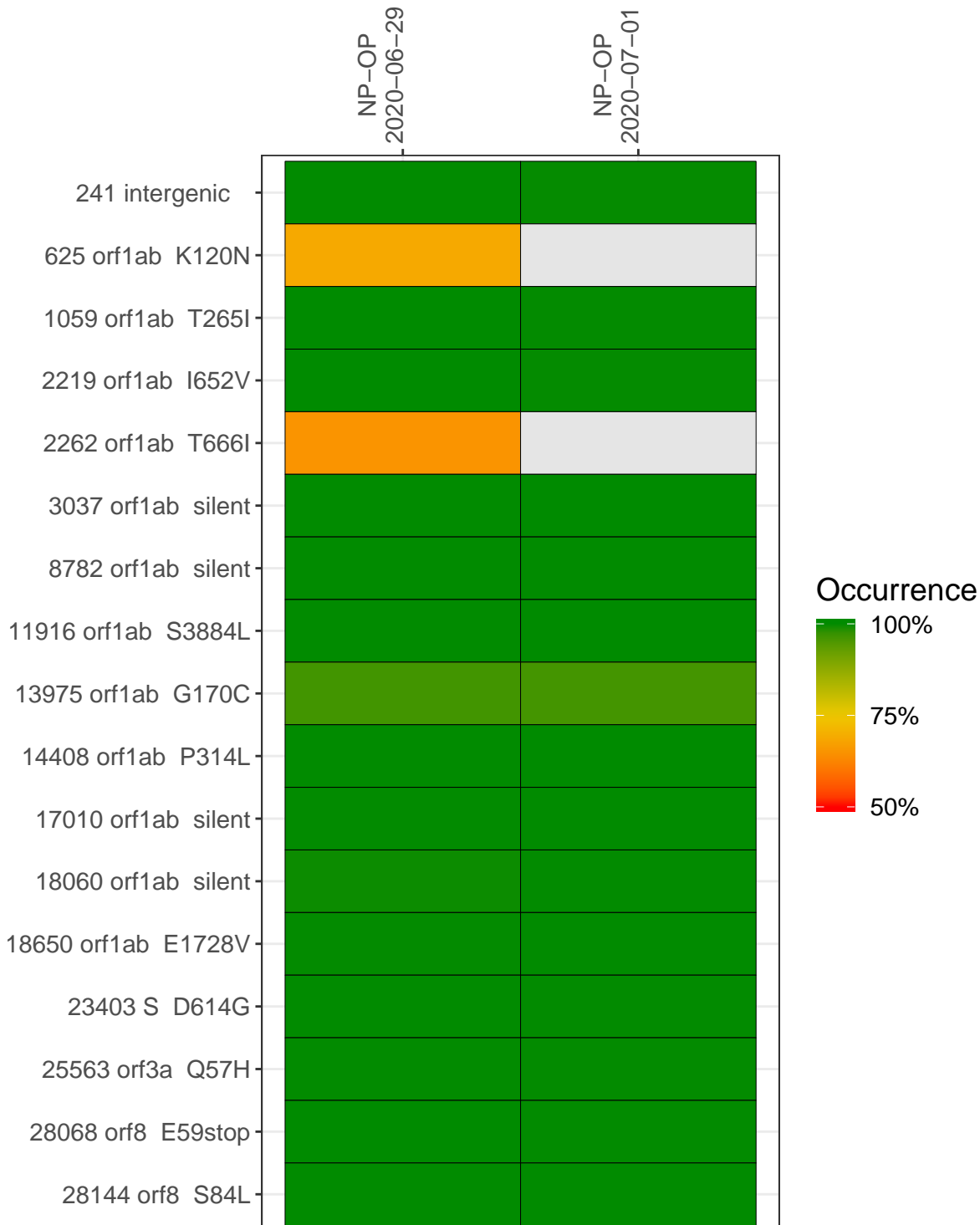
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found ([here](#)).

Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0230	composite	NA	NP-OP	2020-06-29	29.80	99.8%	99.8%
VSP0233	composite	NA	NP-OP	2020-07-01	24.18	99.8%	99.8%
VSP0230-1	single experiment	11750	NP-OP	2020-06-29	27.24	99.8%	99.8%
VSP0230-2	single experiment	11750	NP-OP	2020-06-29	29.80	99.8%	99.8%
VSP0233-1	single experiment	27900	NP-OP	2020-07-01	29.86	99.8%	99.8%
VSP0233-2	single experiment	27900	NP-OP	2020-07-01	28.54	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-OP 2020-06-29		NP-OP 2020-07-01	
241 intergenic	4012	4899	2987	3991
625 orf1ab K120N	1886	2667	1483	2459
1059 orf1ab T265I	1374	2005	1101	1830
2219 orf1ab I652V	1006	1081	836	1114
2262 orf1ab T666I	939	952	730	873
3037 orf1ab silent	2287	1770	2048	1325
8782 orf1ab silent	2653	1980	2173	1116
11916 orf1ab S3884L	2330	1956	2360	1799
13975 orf1ab G170C	1669	1493	2033	1297
14408 orf1ab P314L	3105	2749	2816	2043
17010 orf1ab silent	5467	5027	6012	5014
18060 orf1ab silent	1509	882	1437	794
18650 orf1ab E1728V	2754	2234	3062	2643
23403 S D614G	2744	3150	3603	4952
25563 orf3a Q57H	1613	2016	1722	2391
28068 orf8 E59stop	2046	1789	2610	2253
28144 orf8 S84L	1921	2105	2805	3007
	VSP0230-1	VSP0230-2	VSP0233-1	VSP0233-2

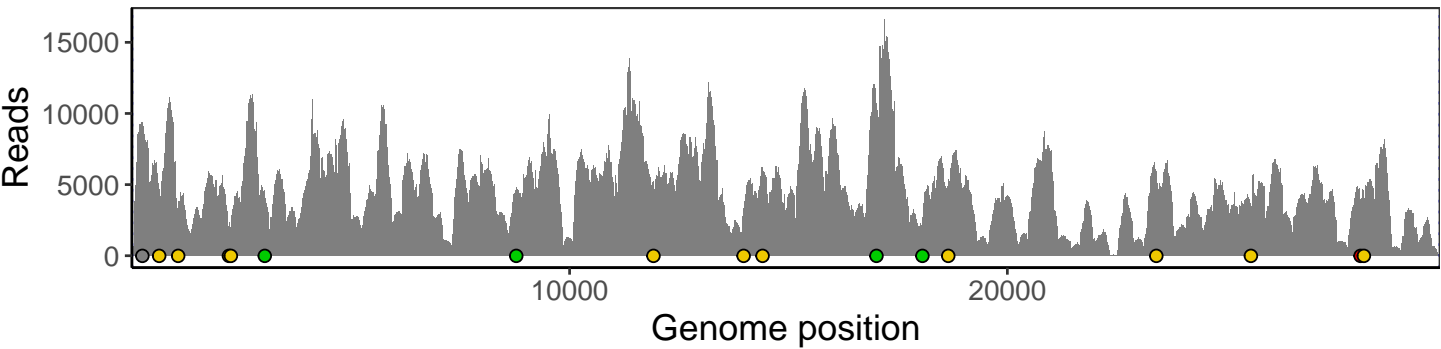
Base change

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

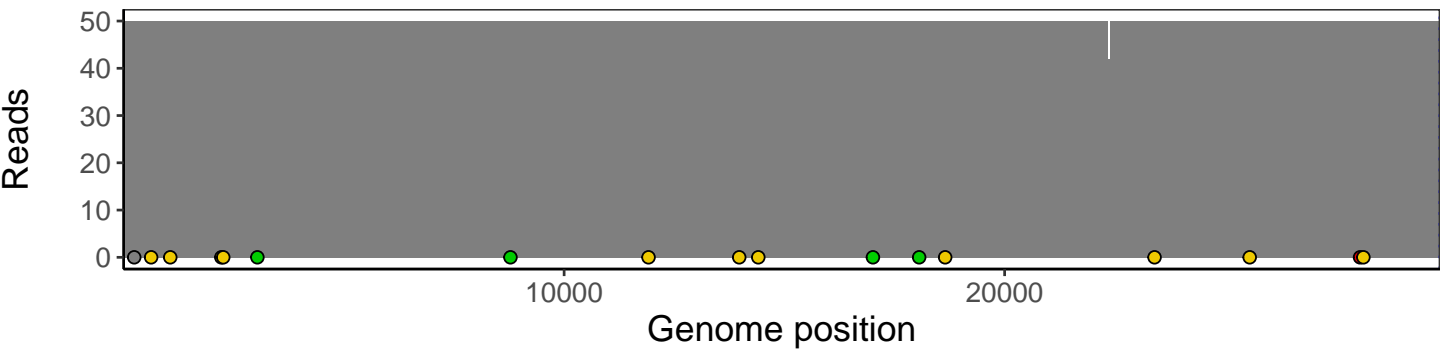
Analyses of individual experiments and composite results.

VSP0230 | 2020-06-29 | NP-OP | 290no-q | composite result

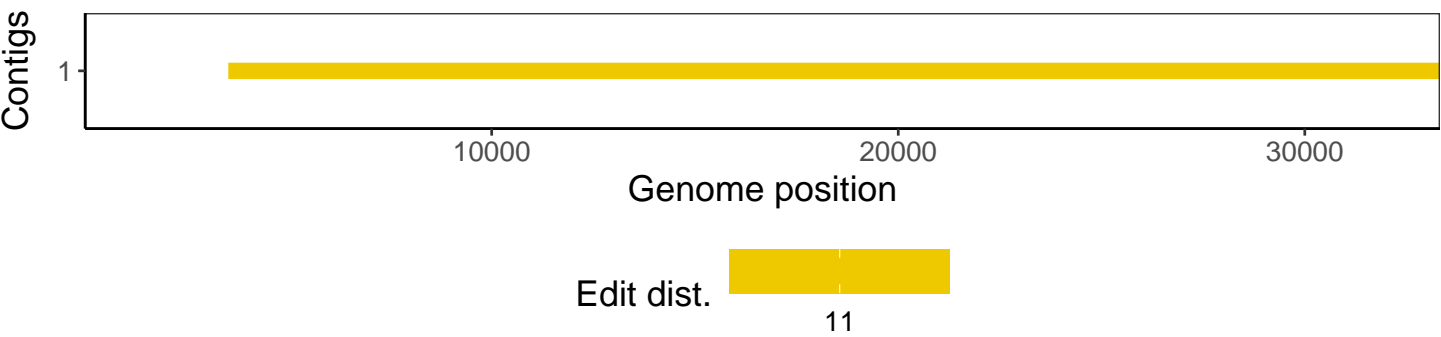
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



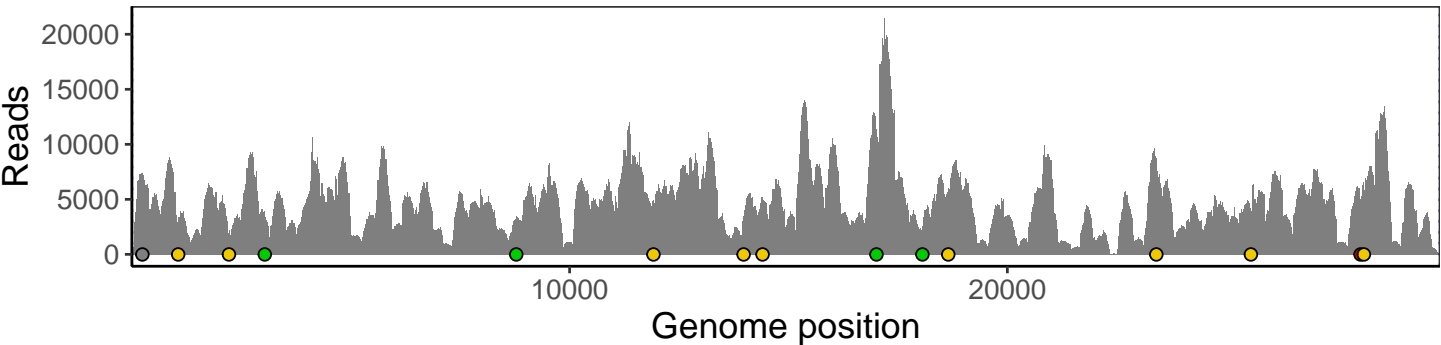
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



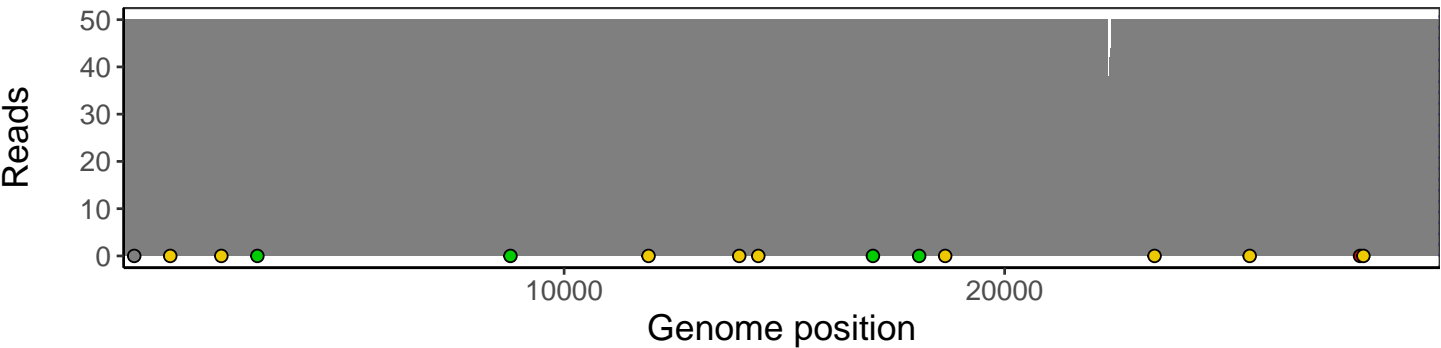
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



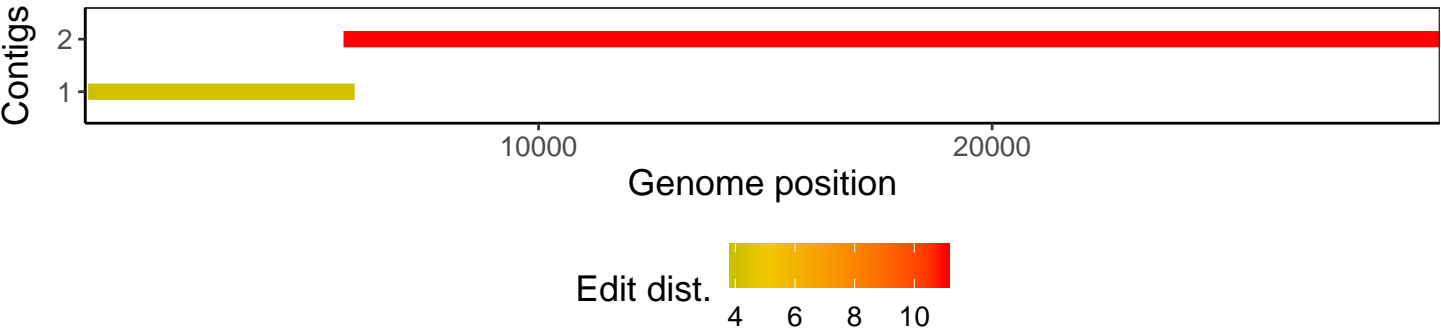
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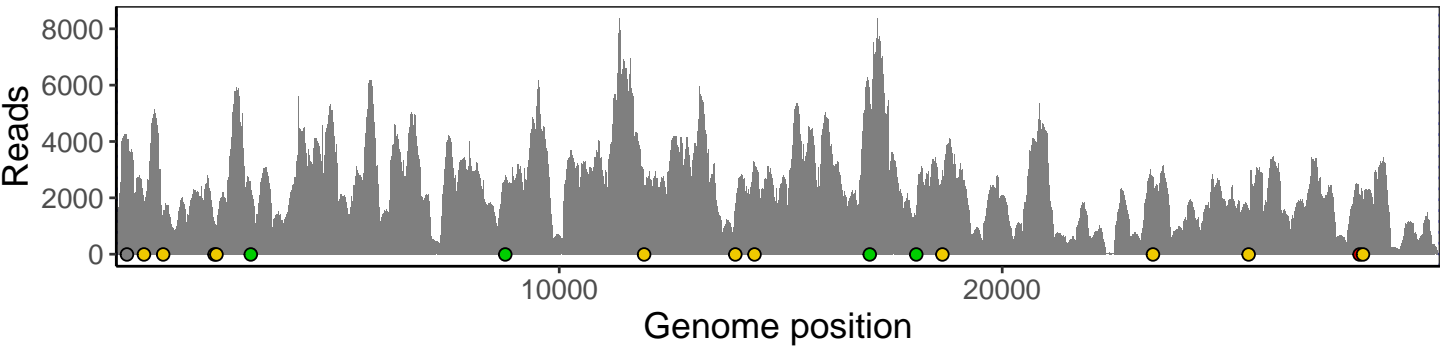
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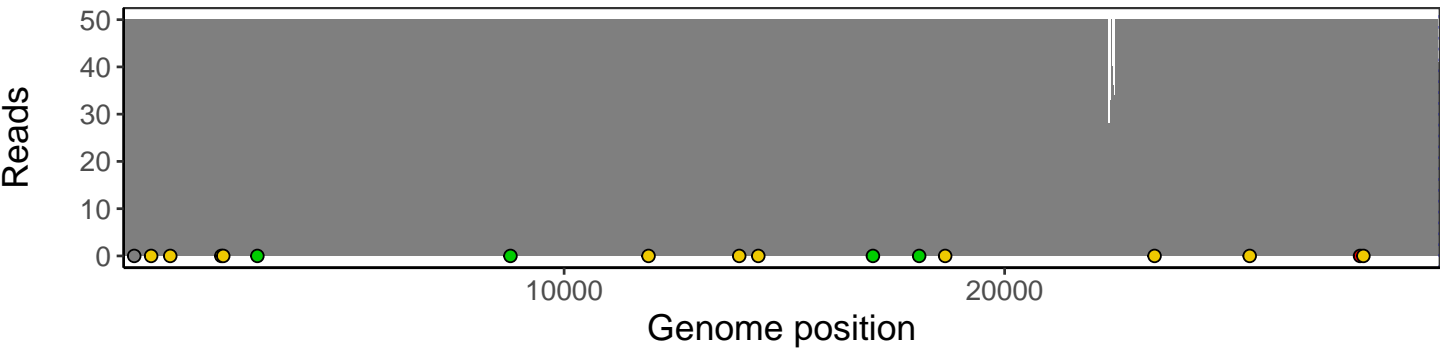
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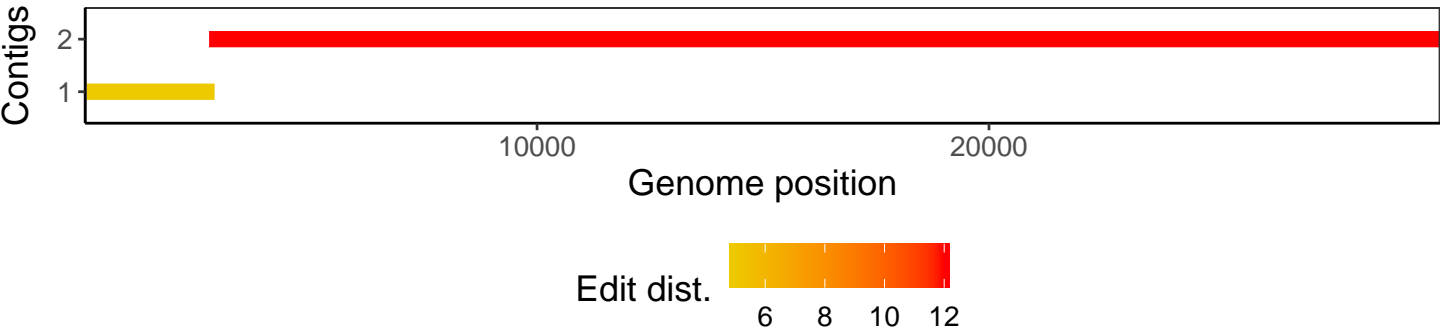
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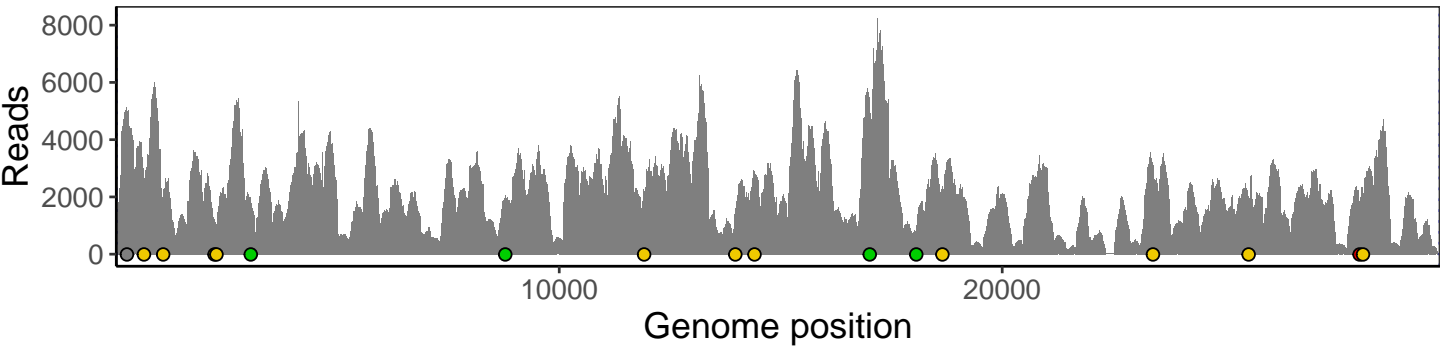
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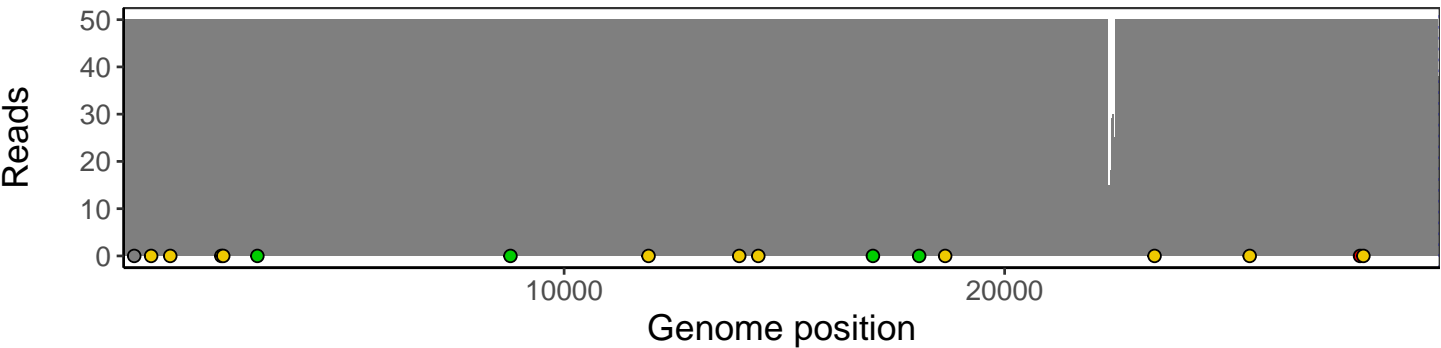
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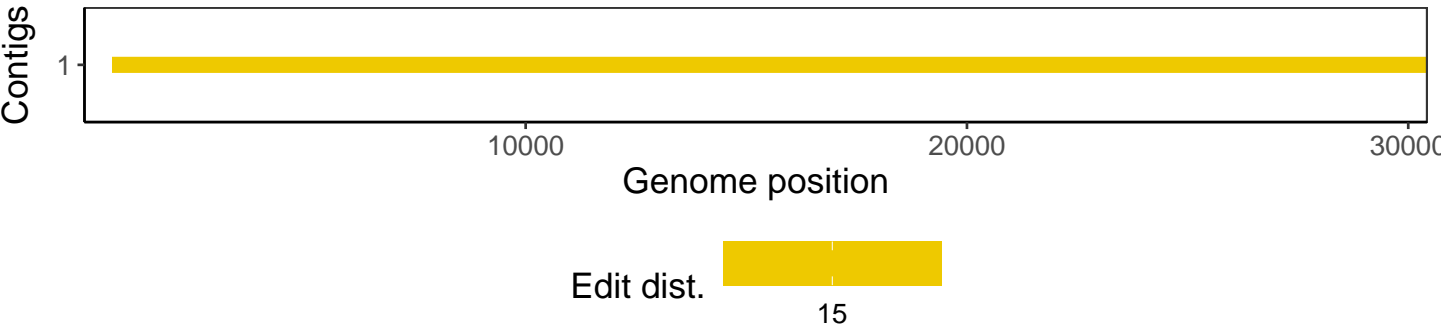
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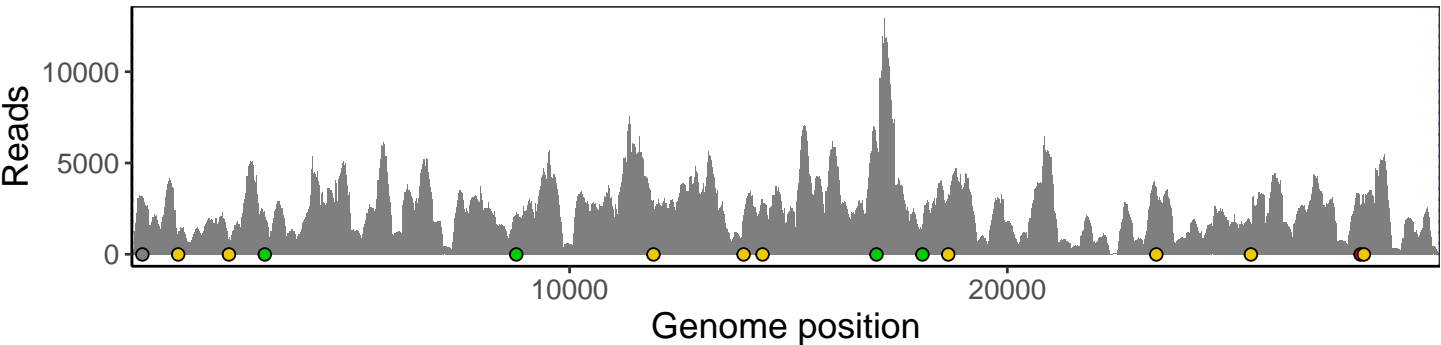
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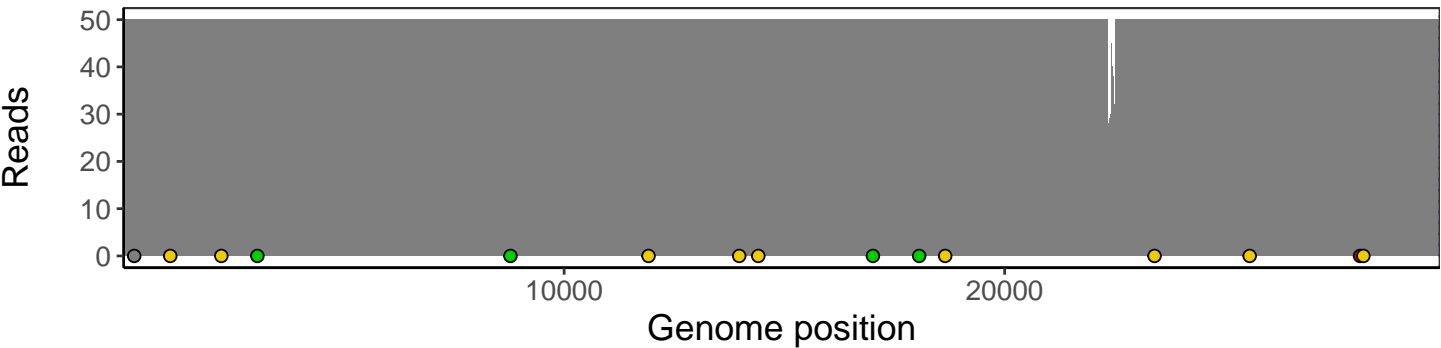
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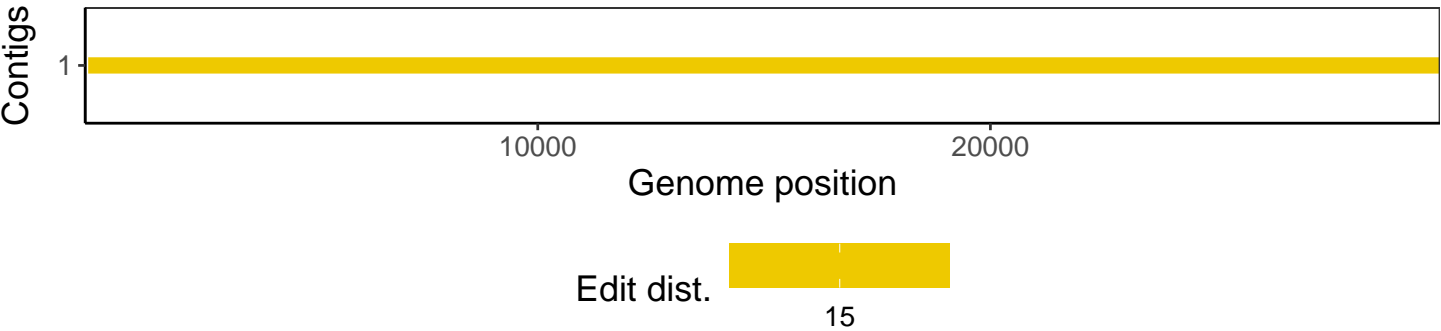
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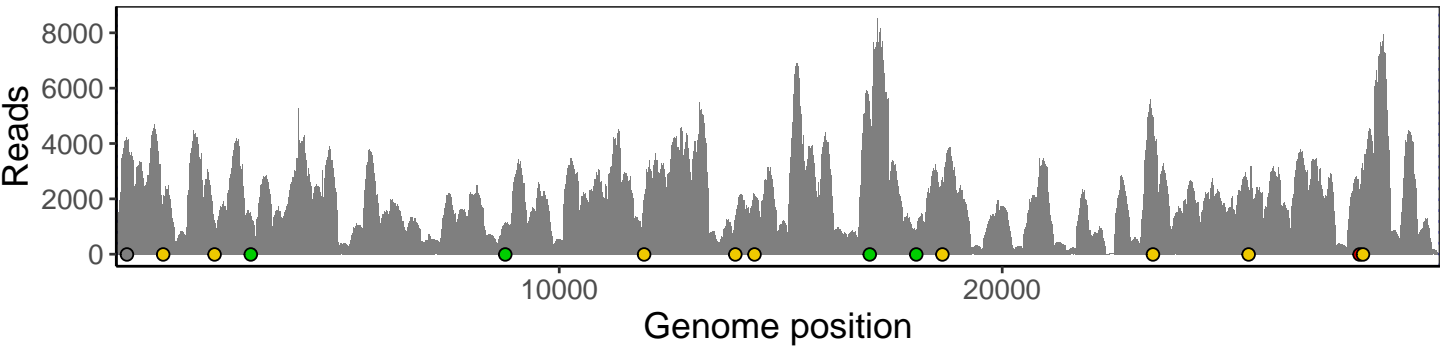
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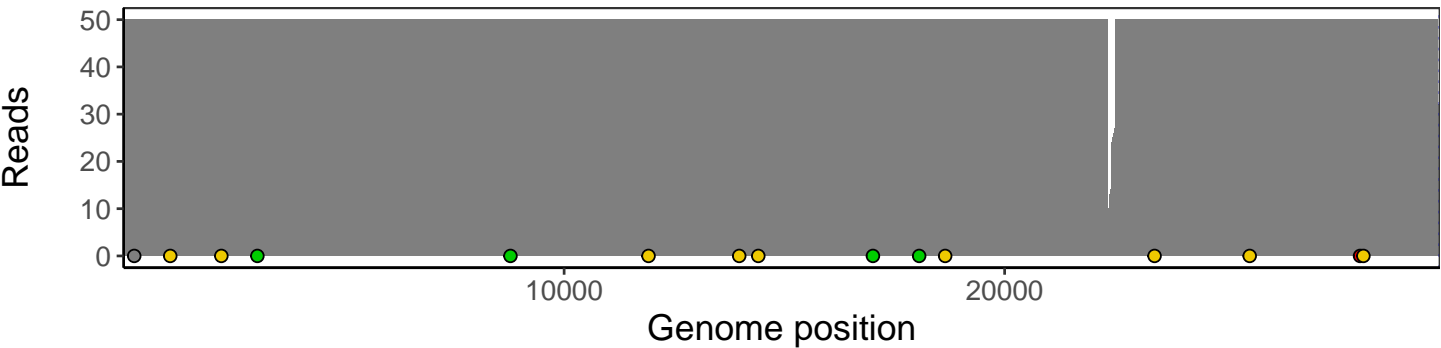
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