

COVID-19 subject 290

2020-11-30

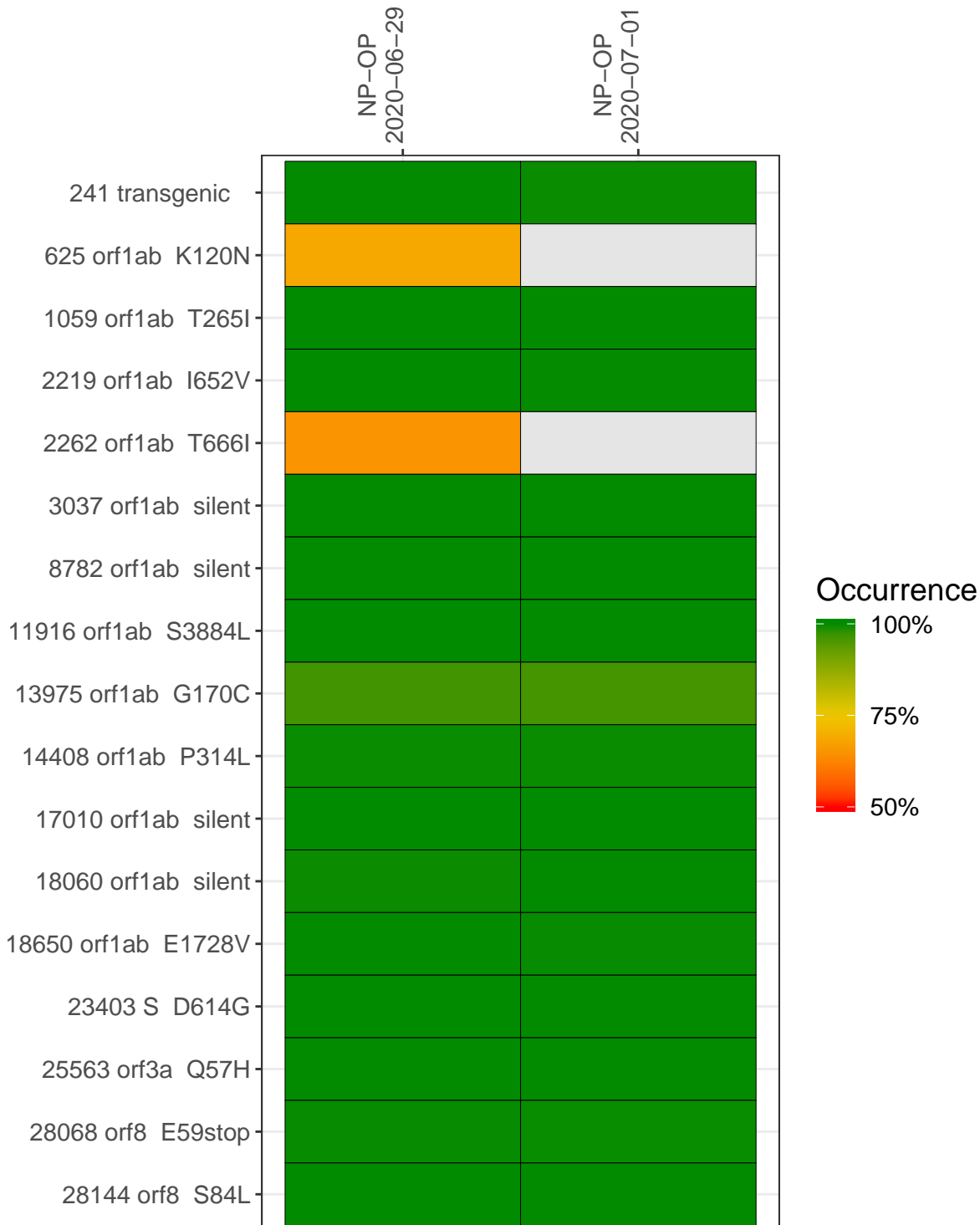
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found ([here](#)).

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	29.91	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 transgenic	3967	4857	2955	3946
625 orf1ab K120N	1845	2627	1456	2418
1059 orf1ab T265I	1358	1983	1090	1802
2219 orf1ab I652V	986	1071	823	1093
2262 orf1ab T666I	922	939	718	861
3037 orf1ab silent	2249	1747	2020	1310
8782 orf1ab silent	2614	1954	2131	1102
11916 orf1ab S3884L	2290	1937	2332	1774
13975 orf1ab G170C	1648	1479	2005	1274
14408 orf1ab P314L	3062	2713	2777	2014
17010 orf1ab silent	5401	4979	5921	4958
18060 orf1ab silent	1483	875	1414	782
18650 orf1ab E1728V	2721	2211	3021	2614
23403 S D614G	2708	3119	3543	4886
25563 orf3a Q57H	1593	1990	1710	2365
28068 orf8 E59stop	2020	1773	2570	2228
28144 orf8 S84L	1897	2080	2768	2966
	VSP0230-1	VSP0230-2	VSP0233-1	VSP0233-2

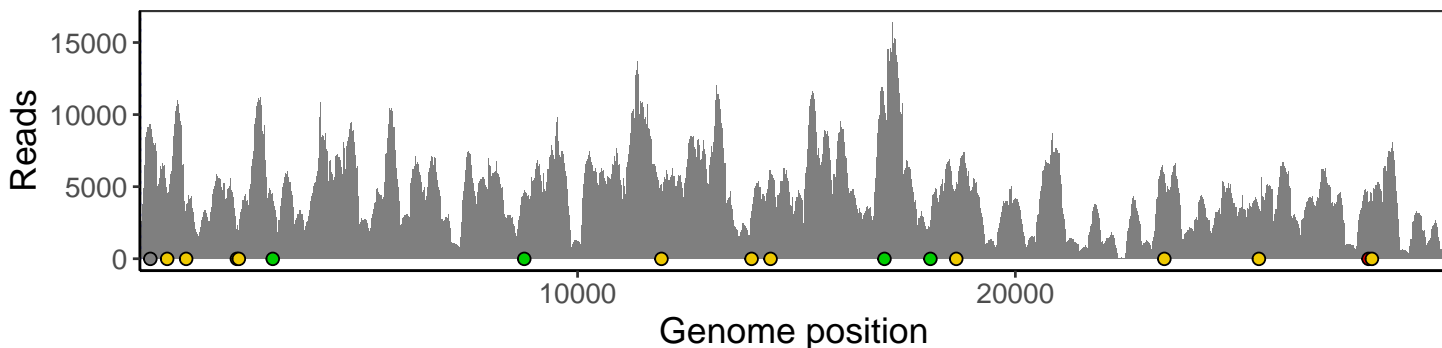
Base change

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

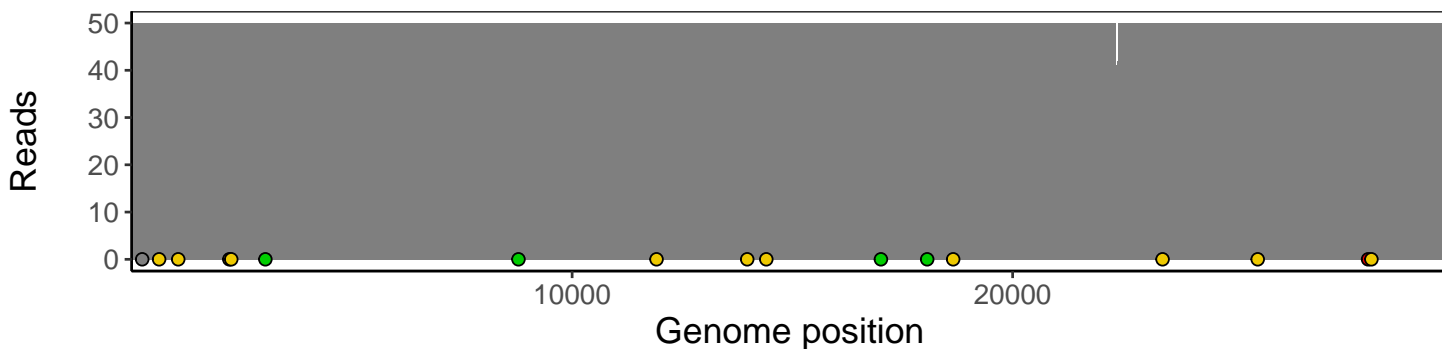
Analyses of individual experiments and composite results.

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

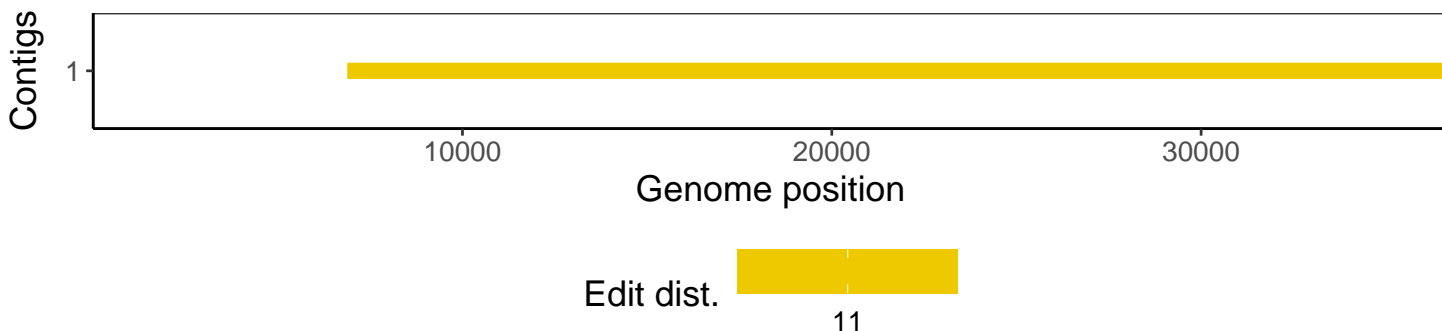
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



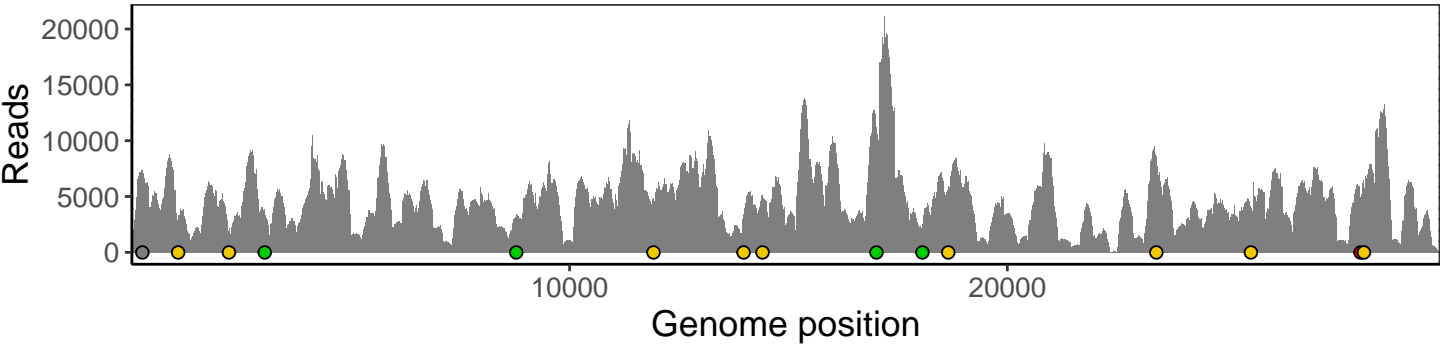
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



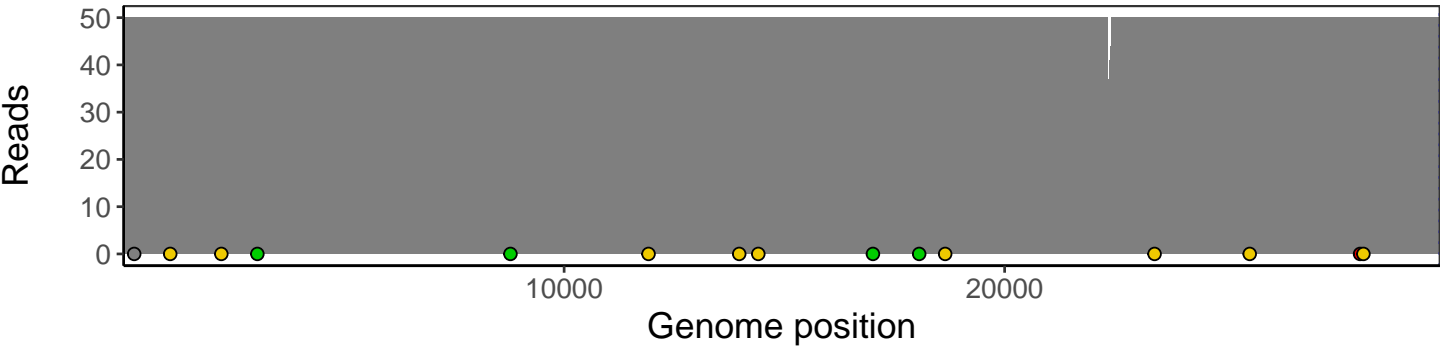
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



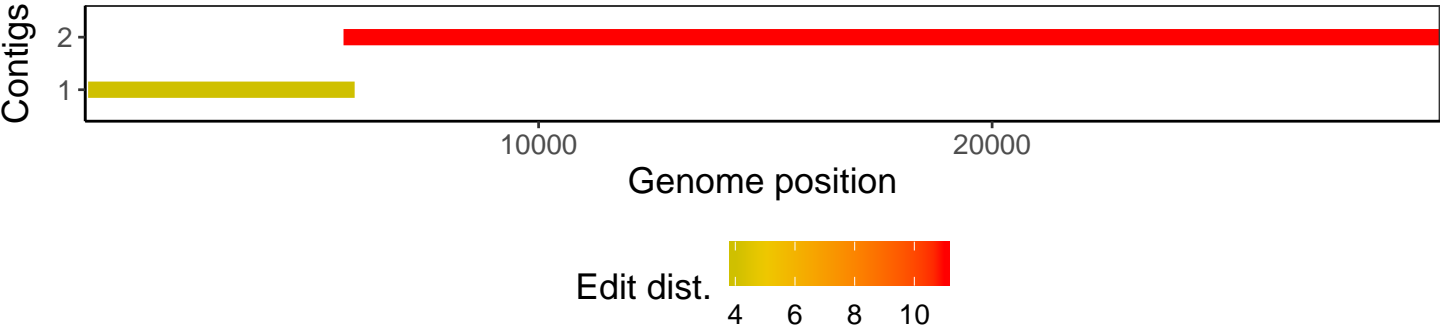
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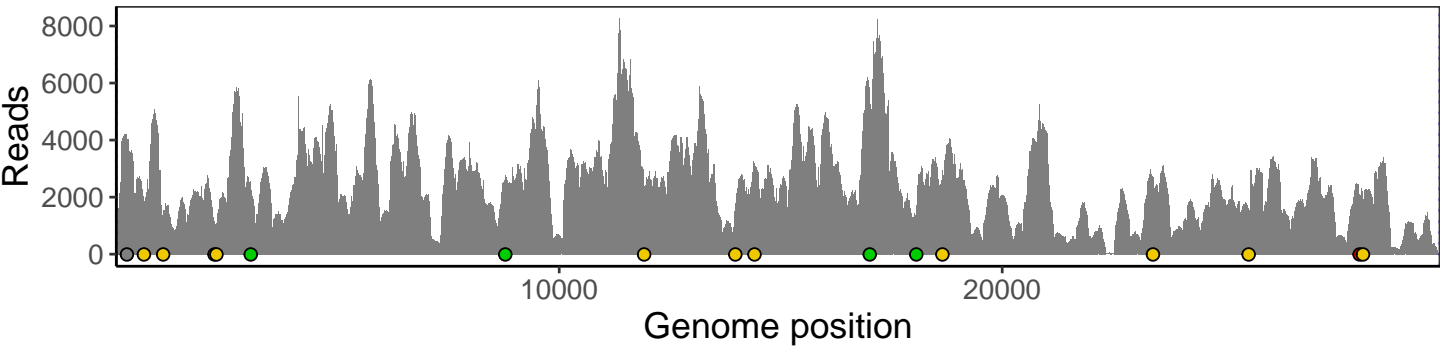
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



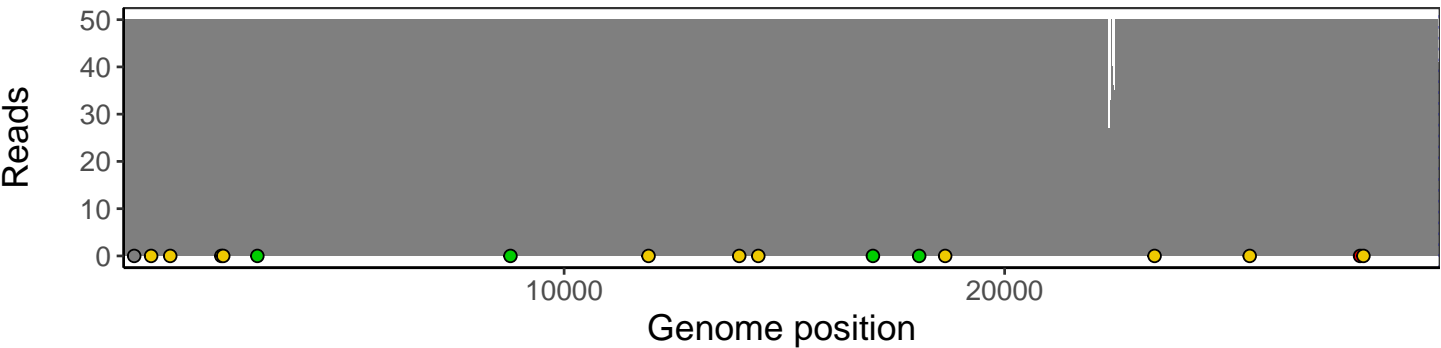
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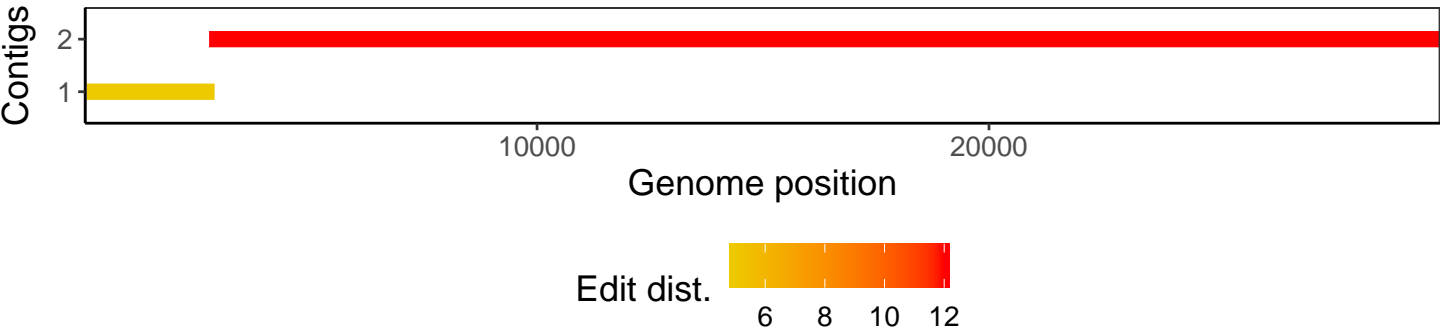
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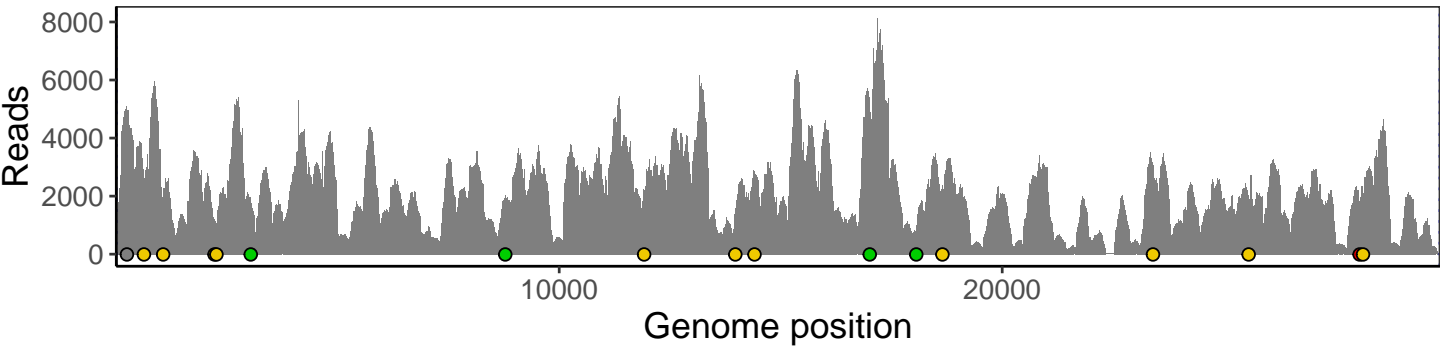
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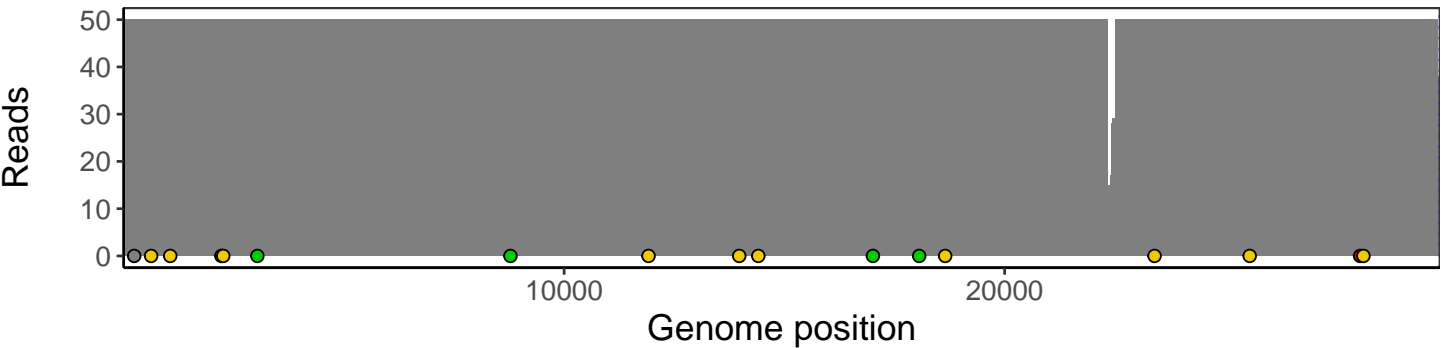
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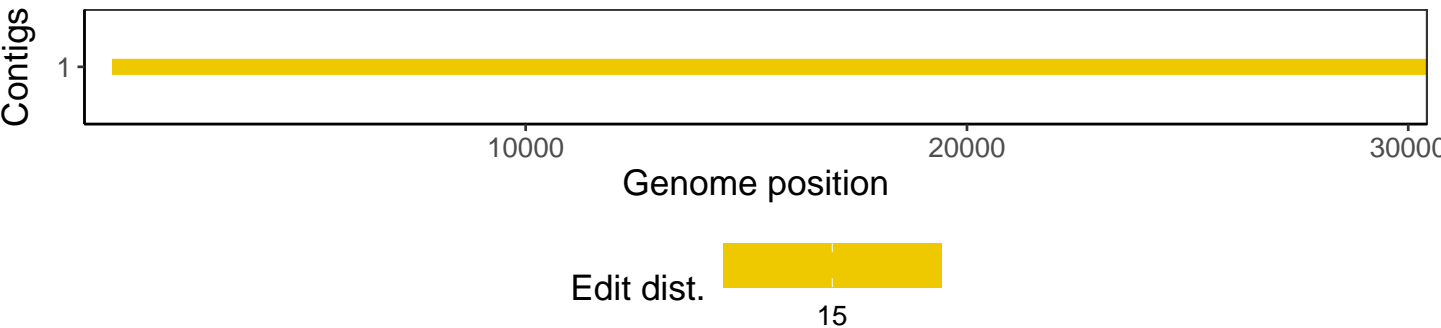
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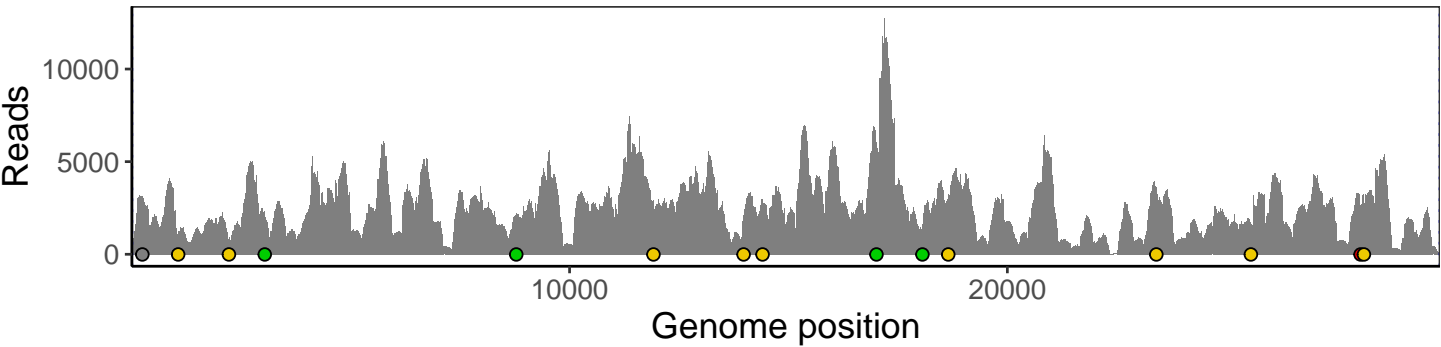
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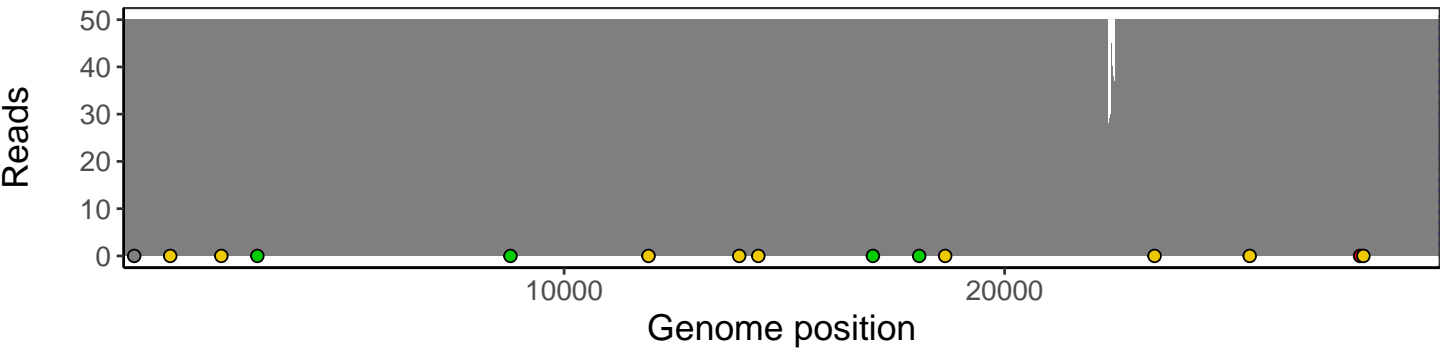
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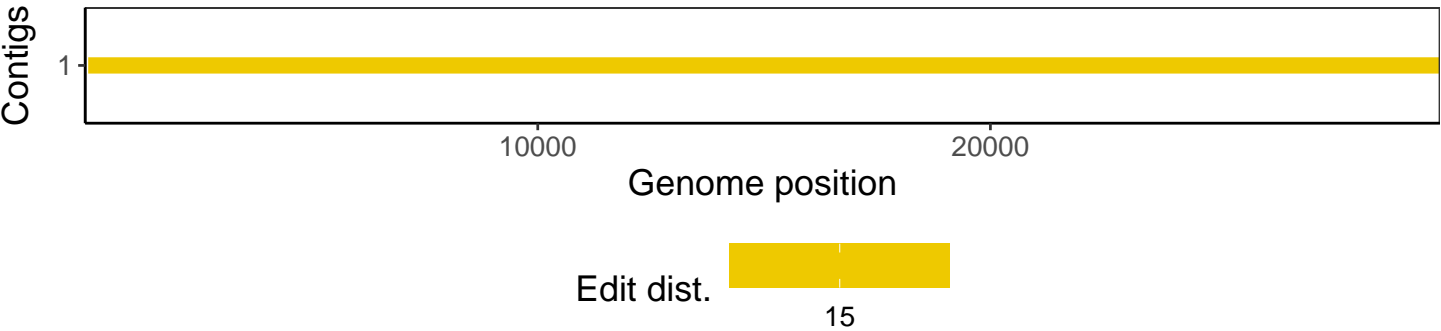
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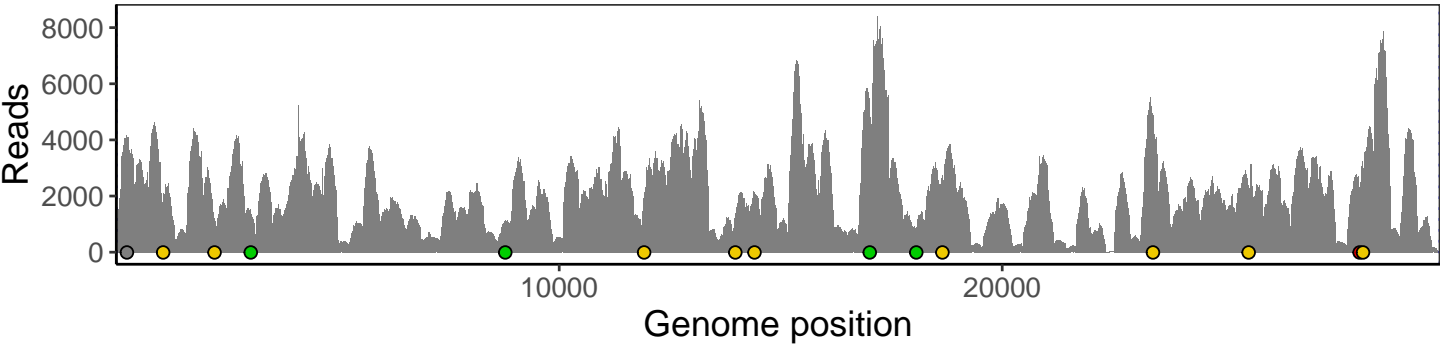
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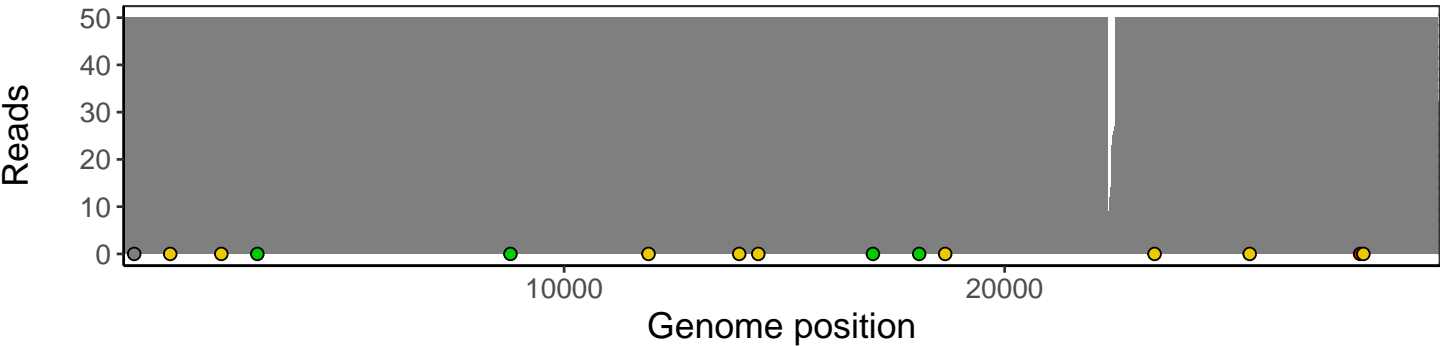
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