

COVID-19 subject 247

2020-10-23

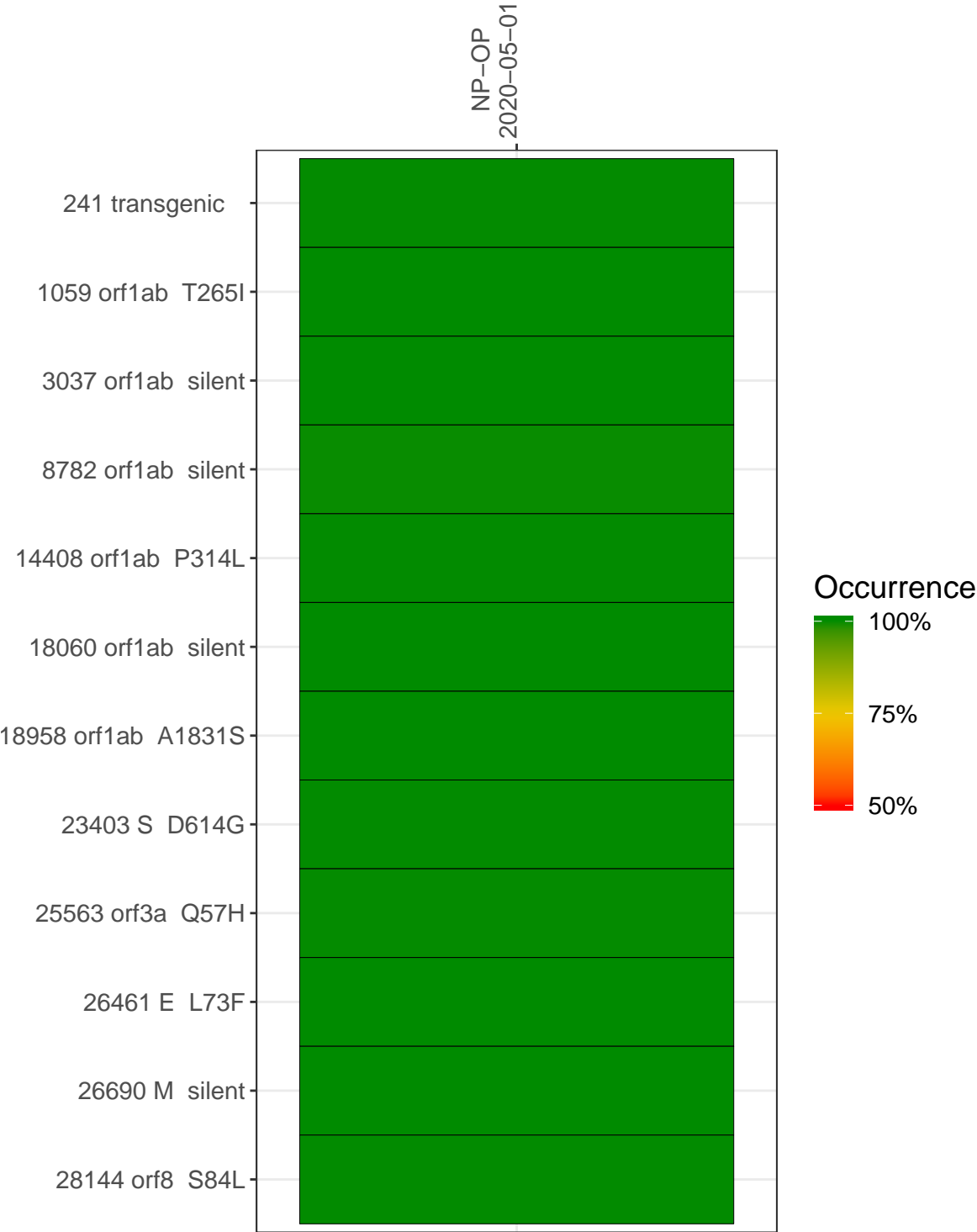
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found ([here](#)).

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 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
2020-05-01

	VSP0050-1	VSP0050-2	VSP0050-3	VSP0050-4
241 transgenic	151	314	646	495
1059 orf1ab T265I	63	437	112	246
3037 orf1ab silent	33	296	587	100
8782 orf1ab silent		1	991	
14408 orf1ab P314L	202	656	587	1064
18060 orf1ab silent	52	328	197	340
18958 orf1ab A1831S	7	397	145	537
23403 S D614G	717	1716	2647	1611
25563 orf3a Q57H	80	332	254	366
26461 E L73F	415	236	499	168
26690 M silent	498	516	1119	974
28144 orf8 S84L	520	1160	493	400

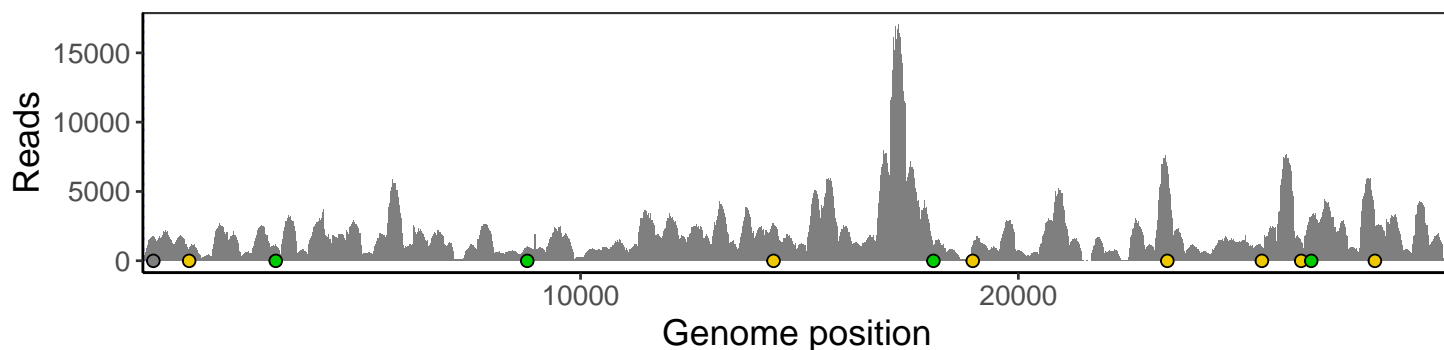
Base change

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

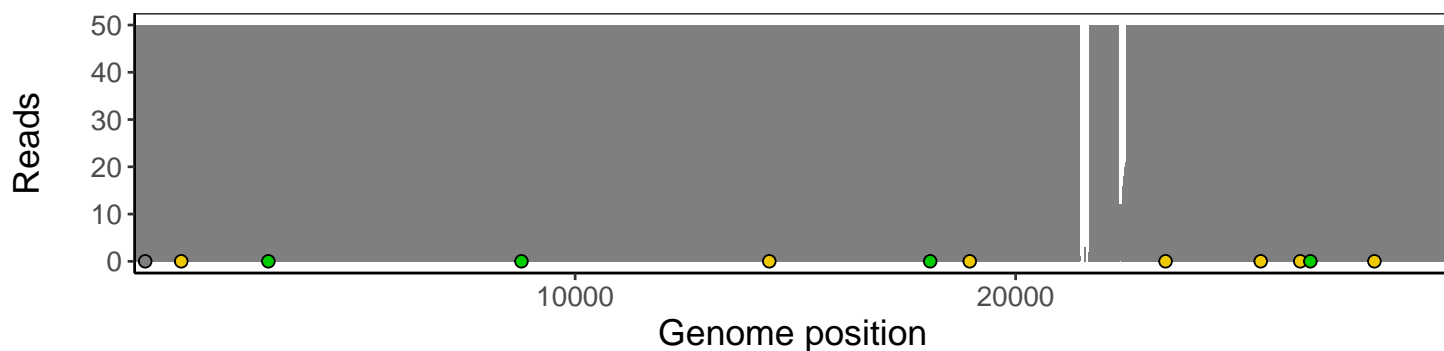
Analyses of individual experiments and composite results.

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

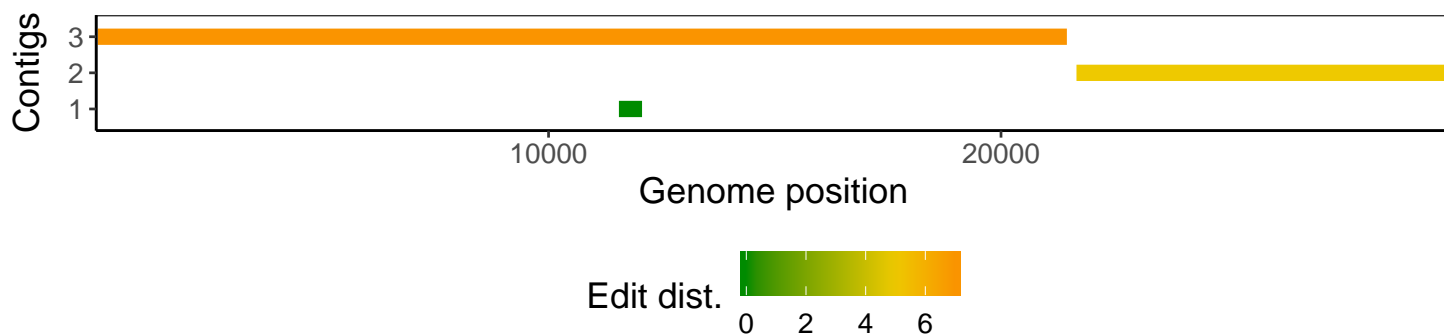
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



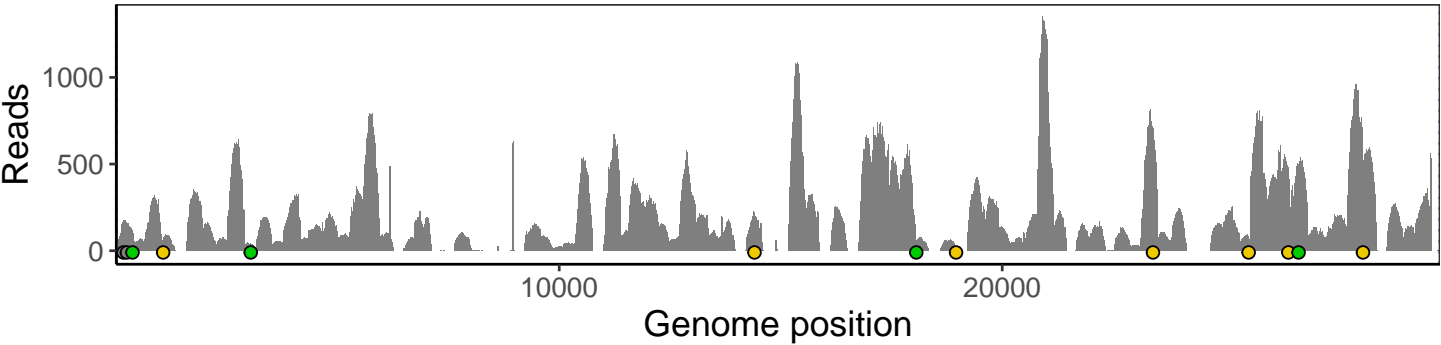
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



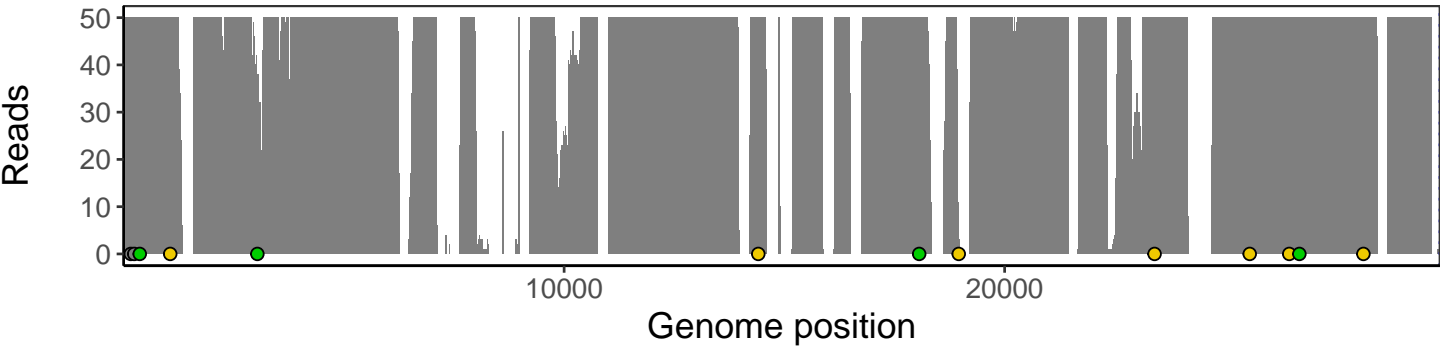
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



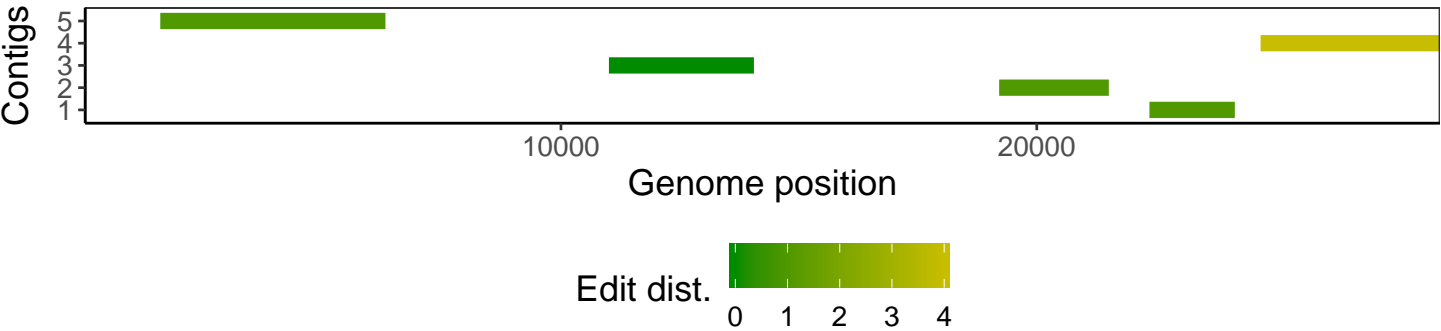
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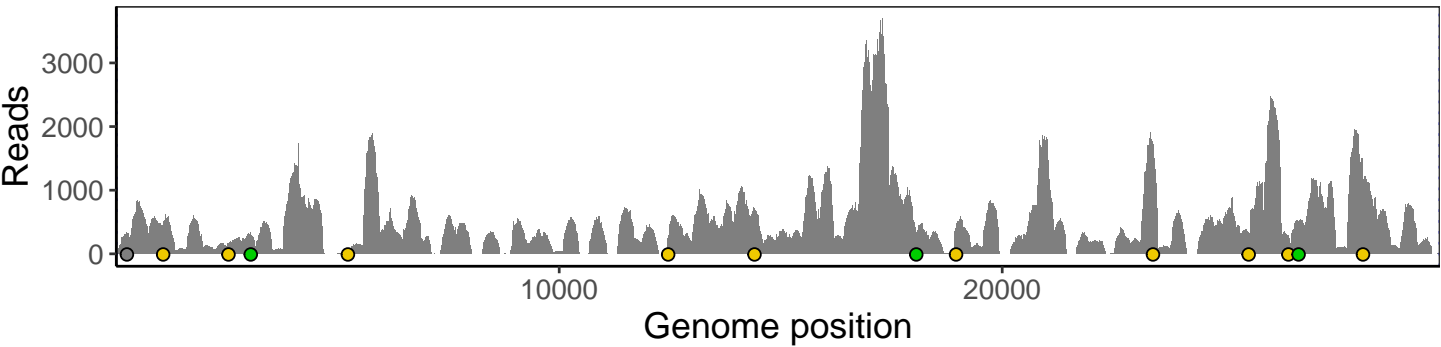
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



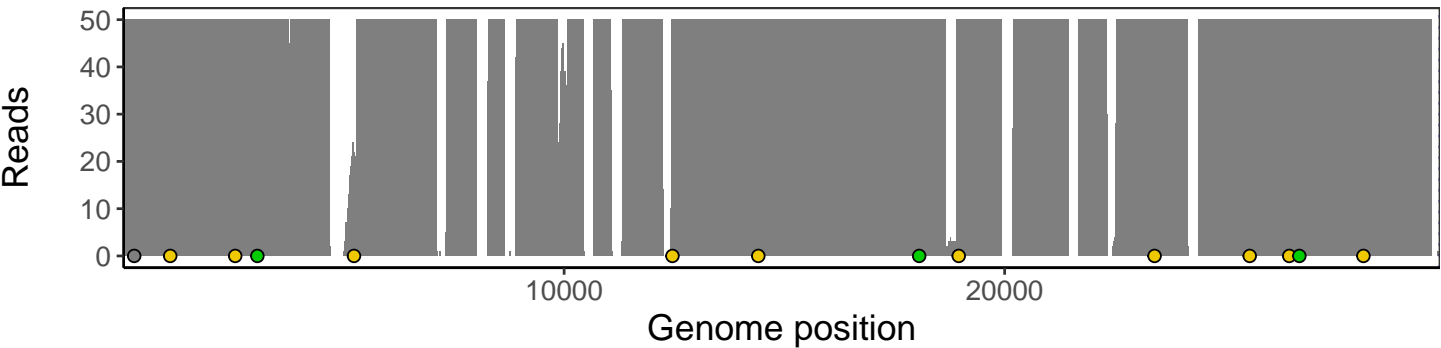
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



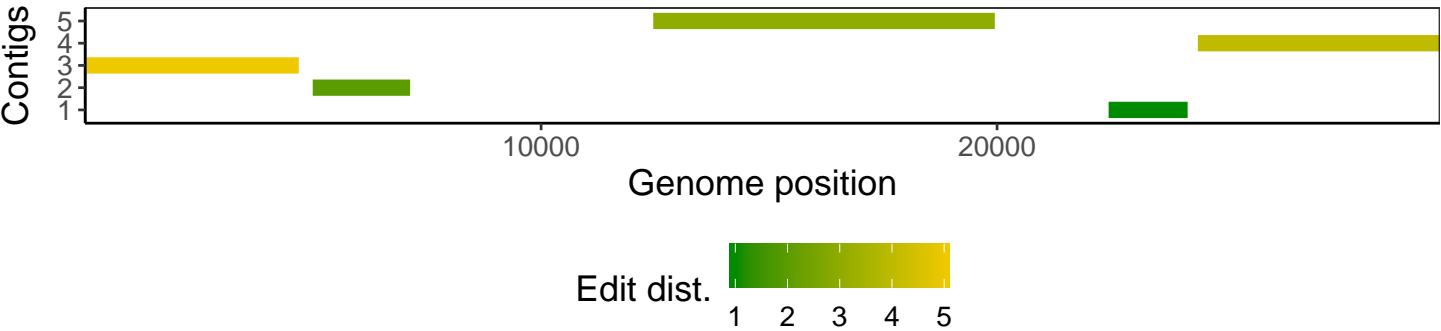
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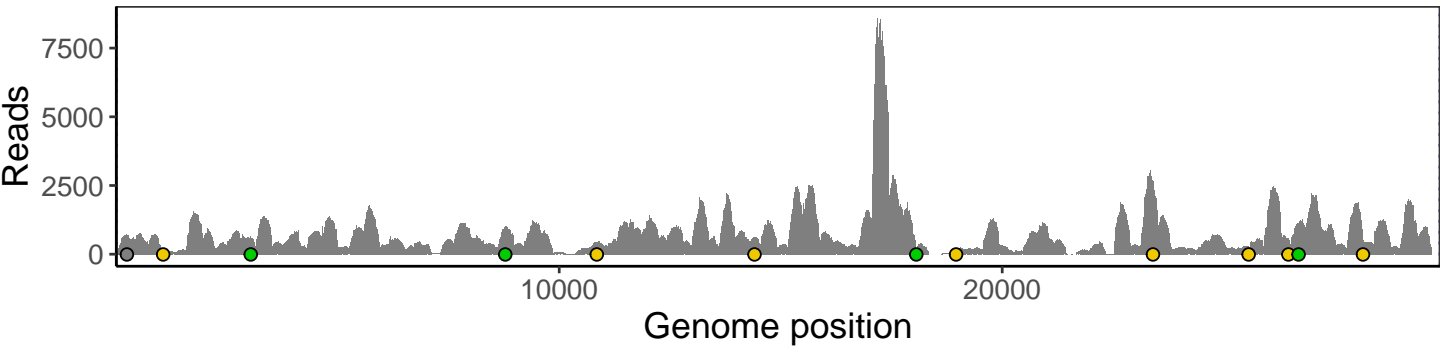
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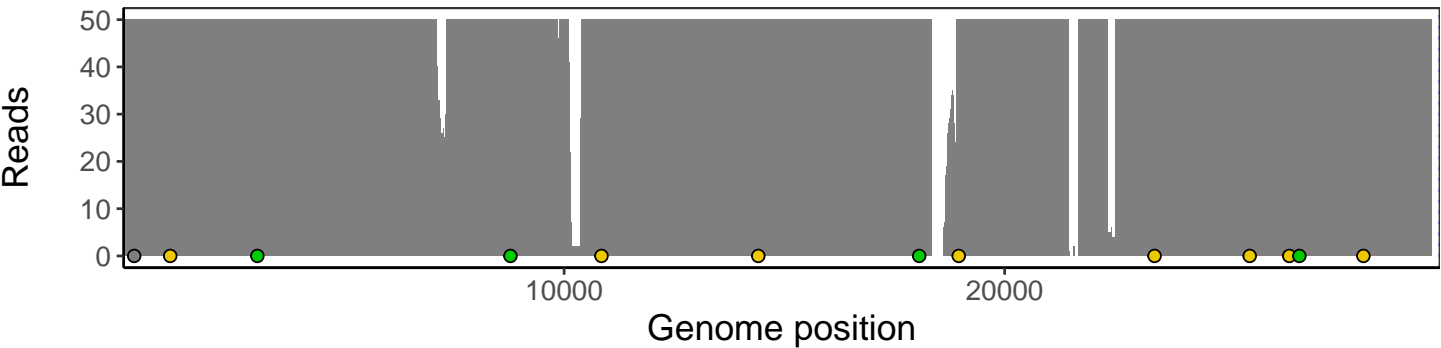
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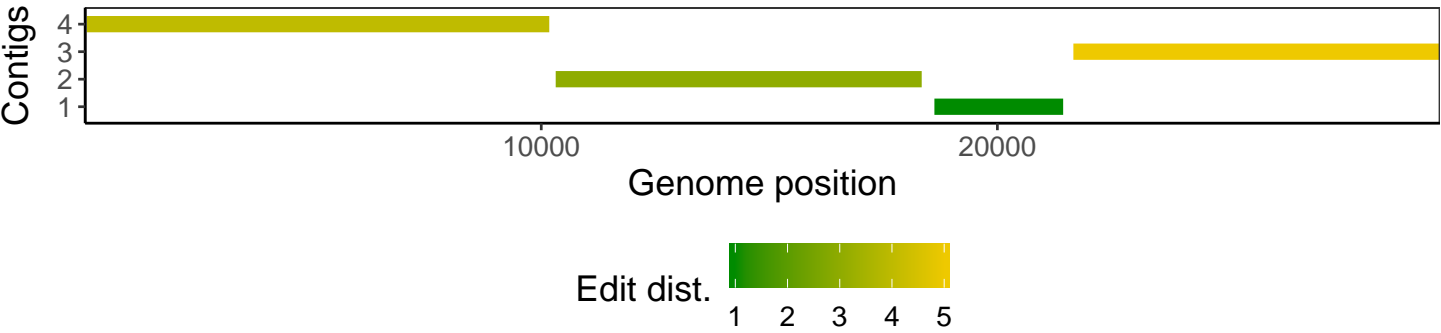
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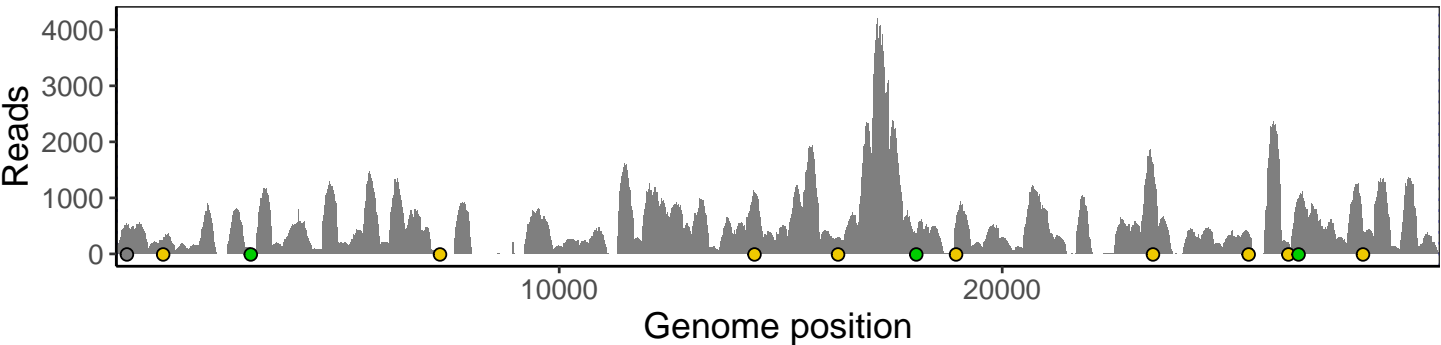
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



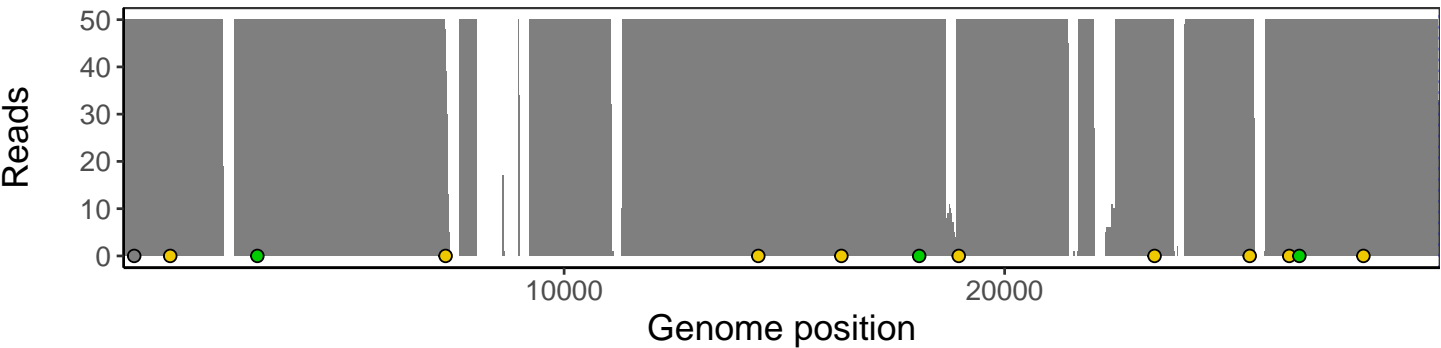
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