

# COVID-19 subject 239

*2020-09-14*

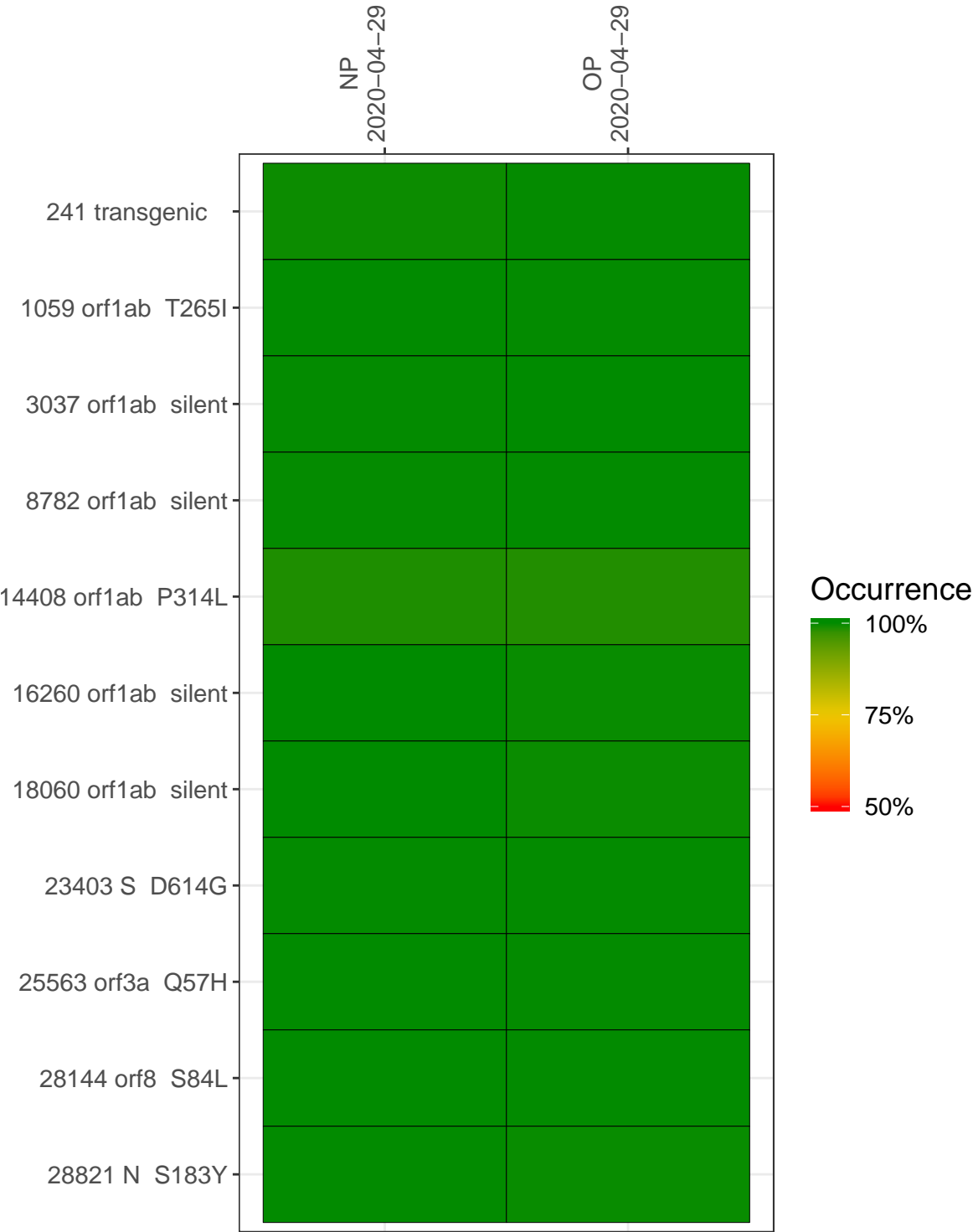
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found ([here](#)).

Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0041	composite	NA	NP	2020-04-29	30.06	99.9%	99.8%
VSP0042	composite	NA	OP	2020-04-29	27.48	99.8%	99.8%
VSP0041-1m	single experiment	NA	NP	2020-04-29	29.83	99.8%	99.8%
VSP0041-2	single experiment	NA	NP	2020-04-29	19.05	99.8%	99.5%
VSP0042-1m	single experiment	NA	OP	2020-04-29	1.12	70.2%	63.2%
VSP0042-2	single experiment	6490	OP	2020-04-29	1.09	81.0%	64.7%

**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 2020-04-29		OP 2020-04-29	
241 transgenic	2900	6732		3326
1059 orf1ab T265I	931	6745	1486	1
3037 orf1ab silent	750	510	1060	
8782 orf1ab silent	1968	292		2213
14408 orf1ab P314L	1591	523	1715	1
16260 orf1ab silent	639	498	1086	1
18060 orf1ab silent	918	296	1291	
23403 S D614G	4576	11495		4468
25563 orf3a Q57H	1598	13380	2385	8
28144 orf8 S84L	4368	1511	546	4780
28821 N S183Y	1381	2583	1	2065
	VSP00041-1m	VSP00041-2	VSP00042-1m	VSP00042-2

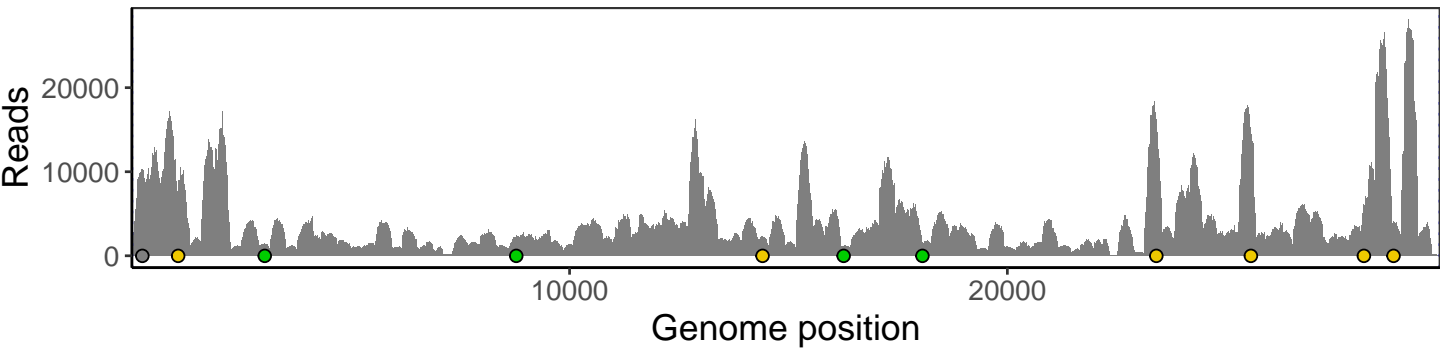
Base change

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

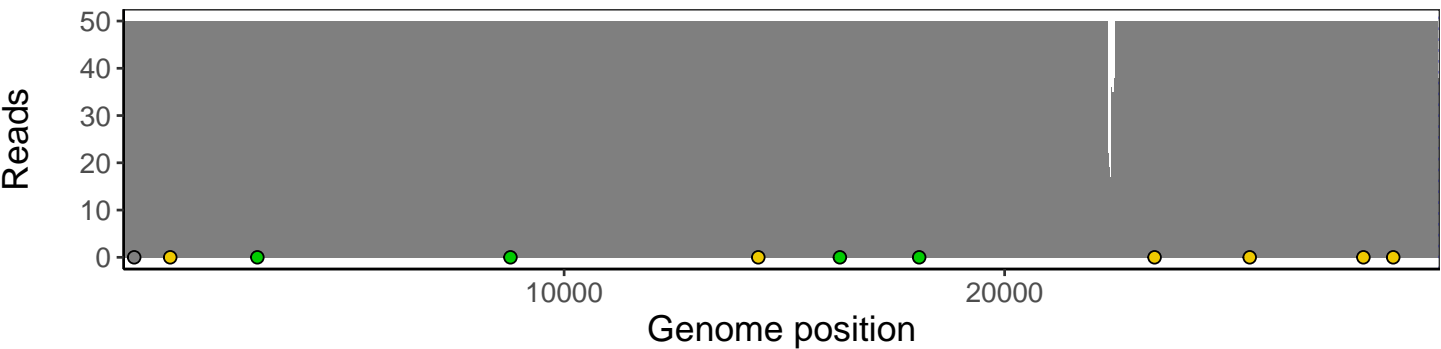
Analyses of individual experiments and composite results.

VSP0041 | 2020-04-29 | NP | 239n-tri | composite result

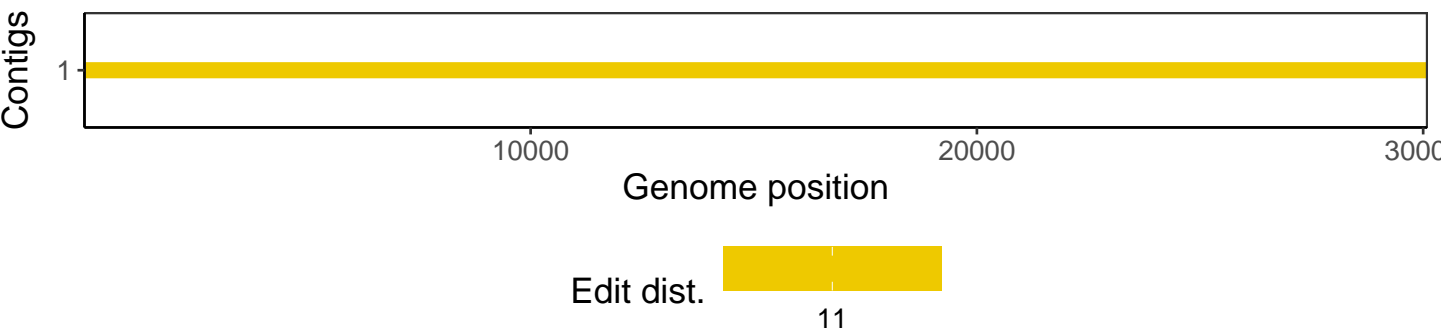
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



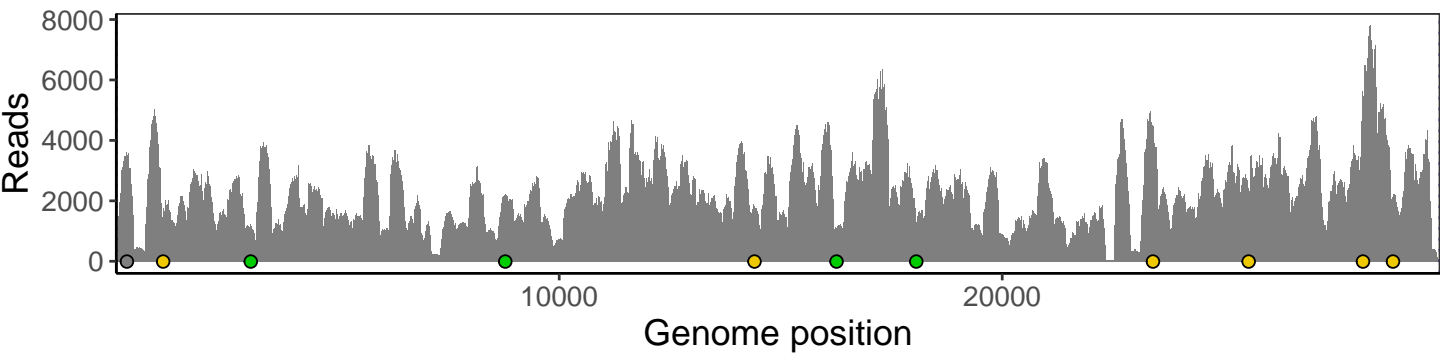
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



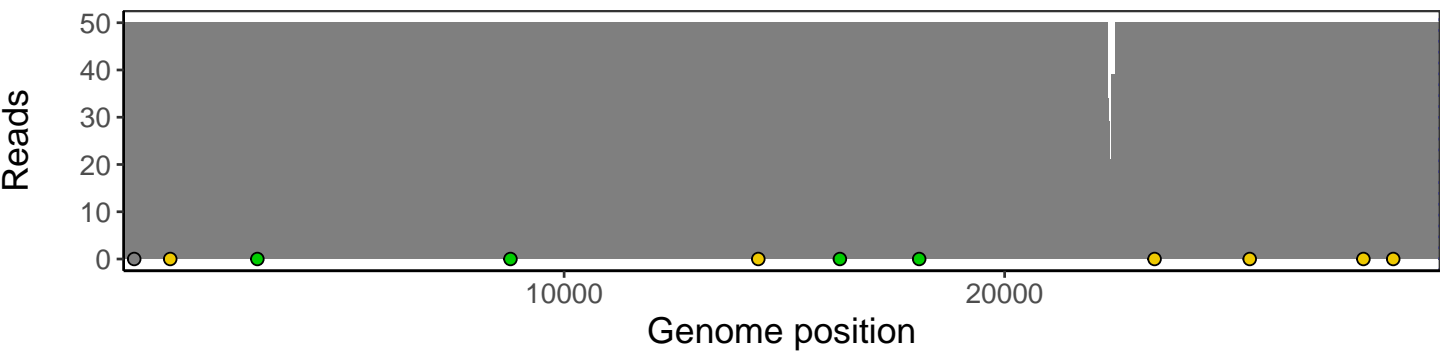
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



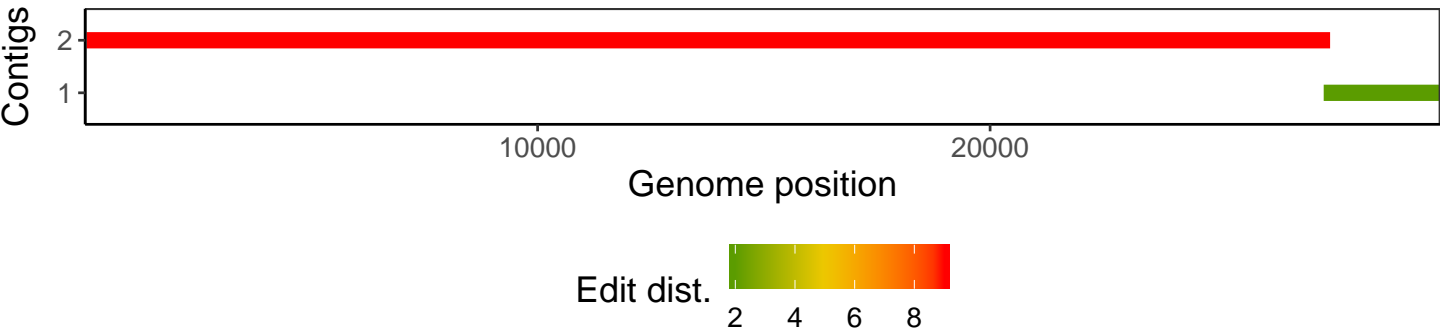
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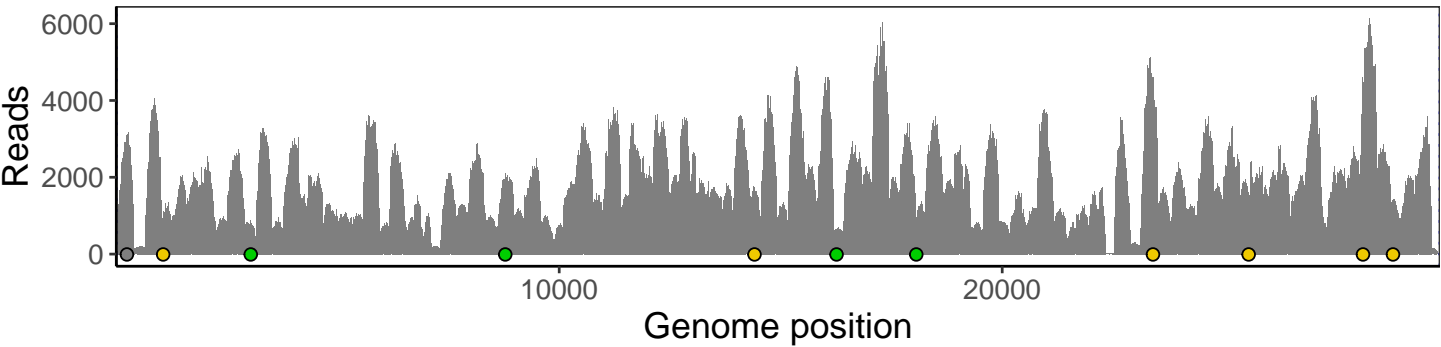
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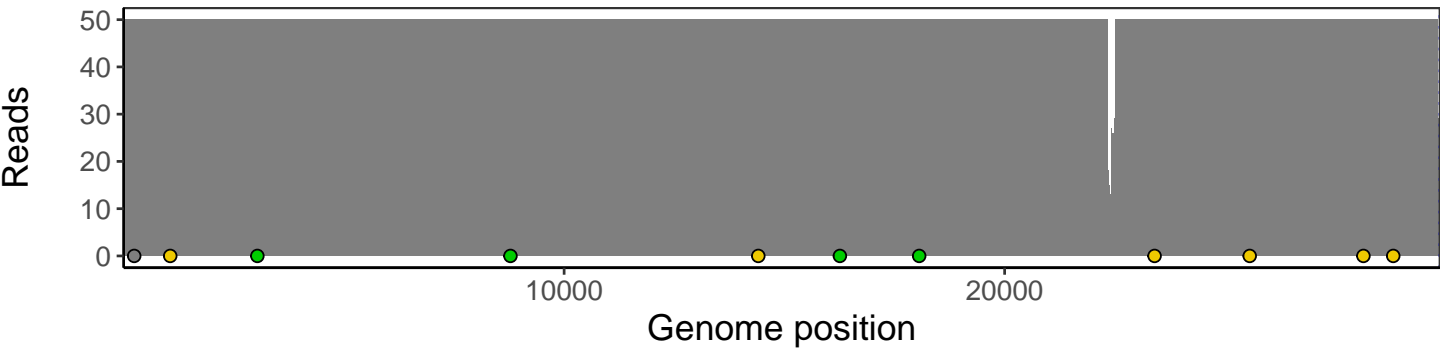
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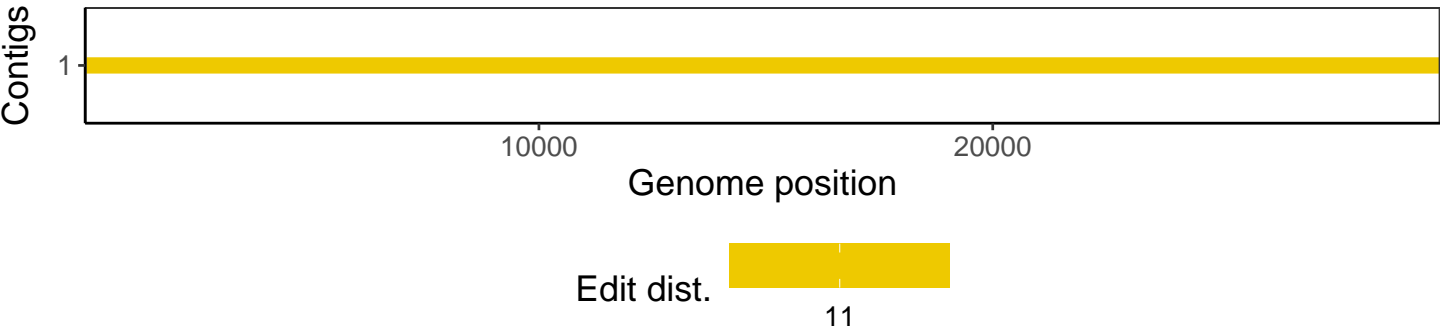
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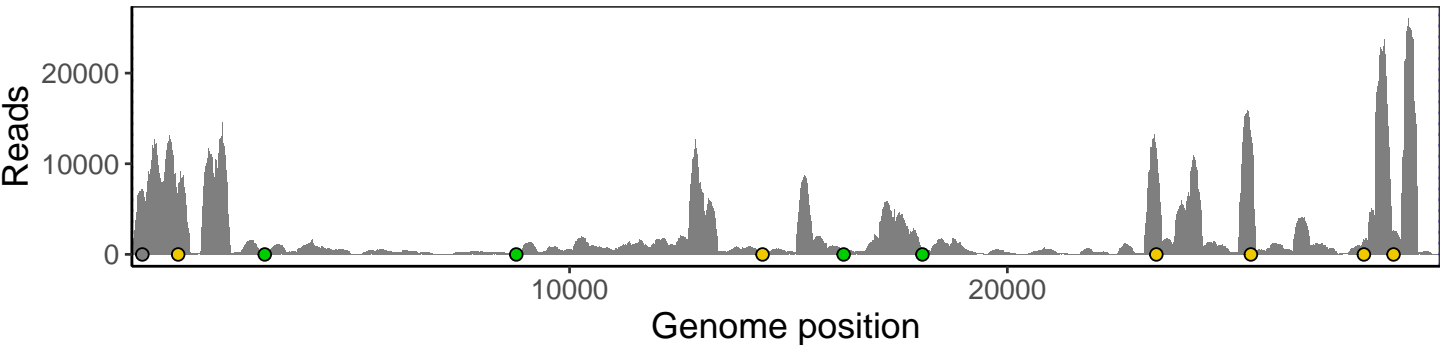
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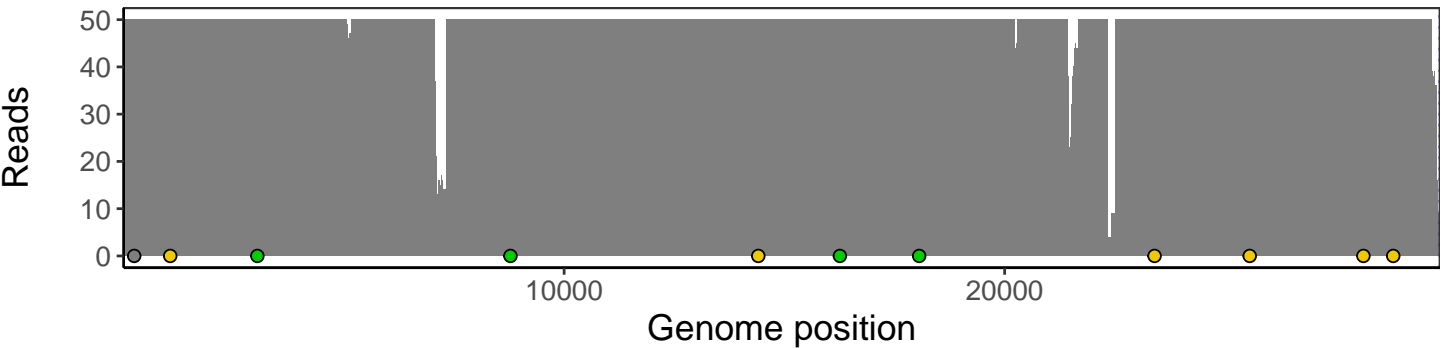
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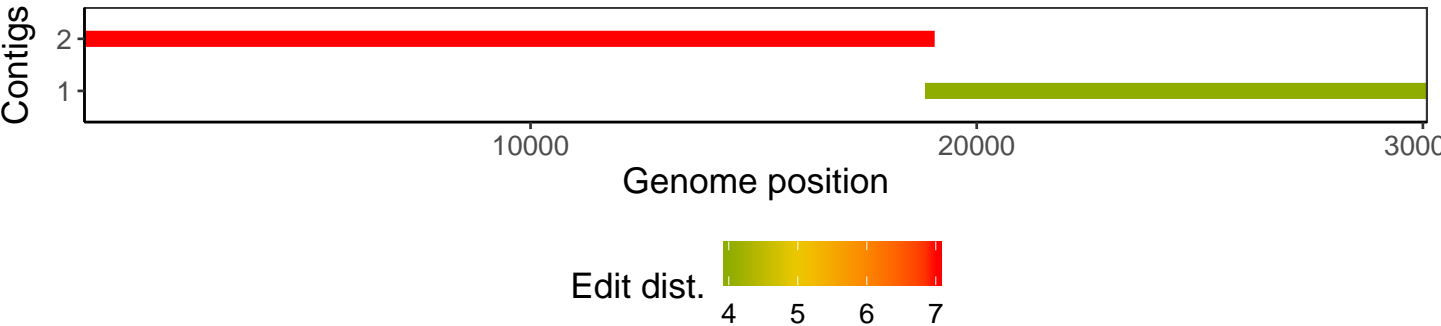
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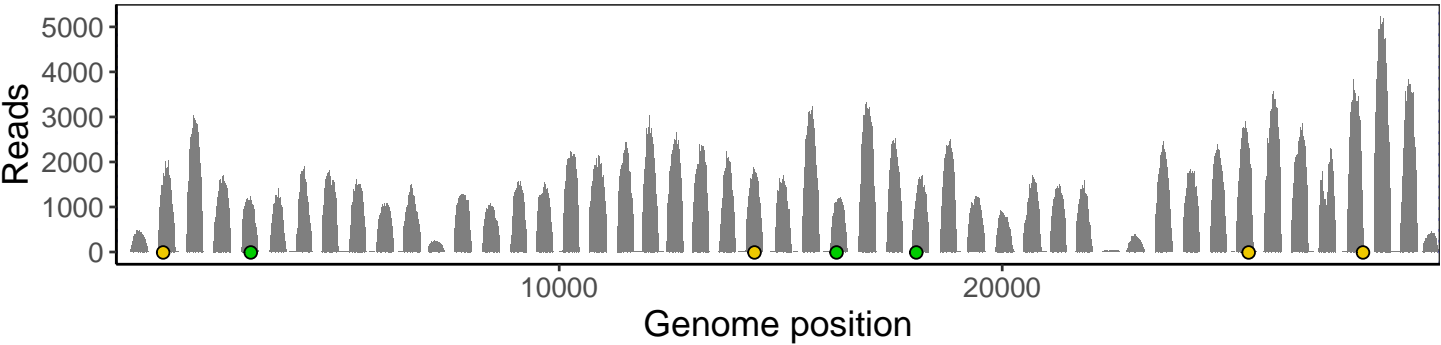
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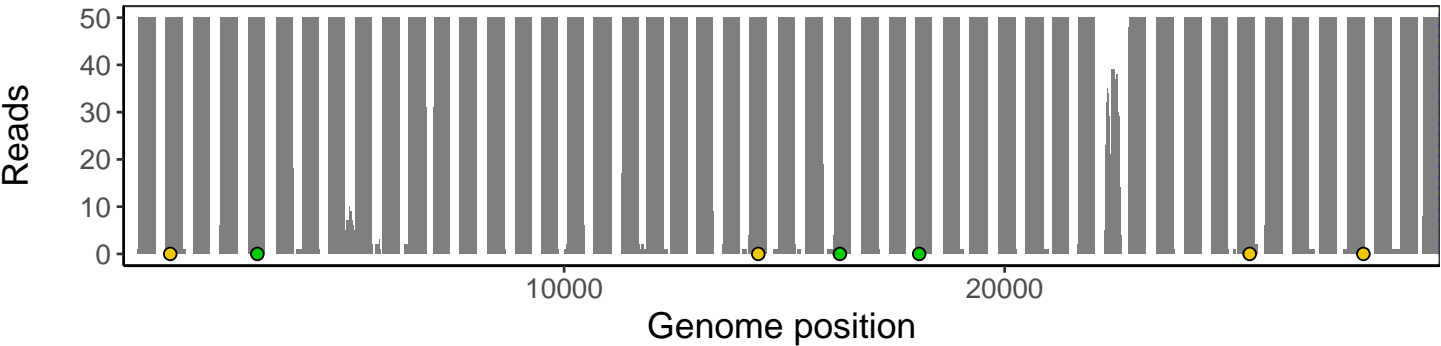
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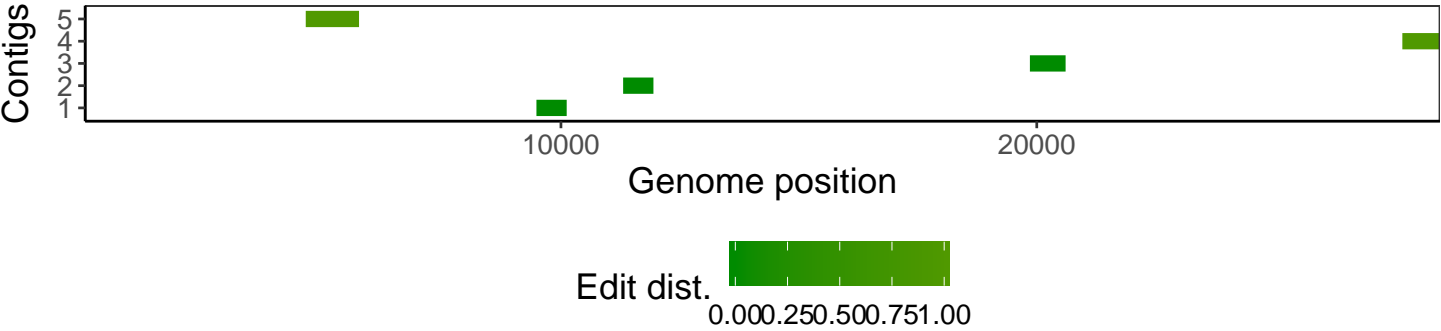
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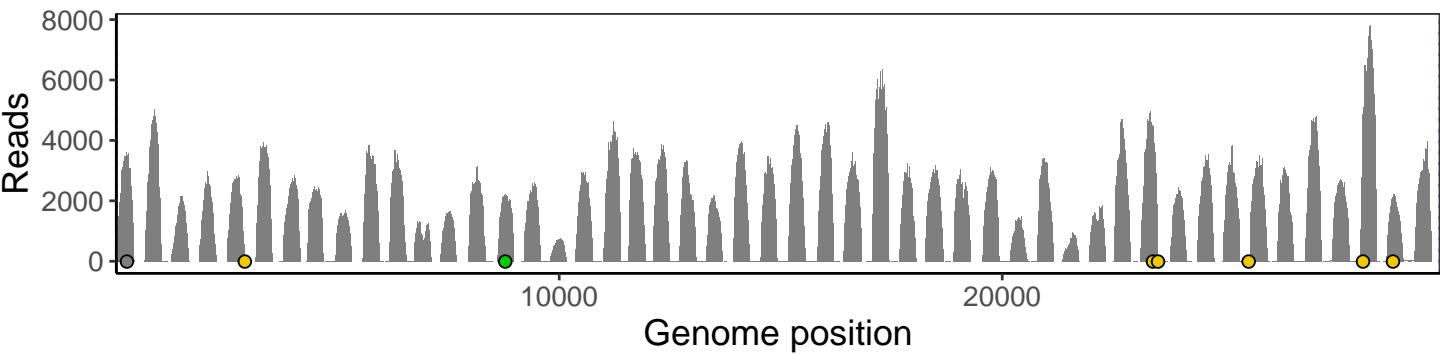


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

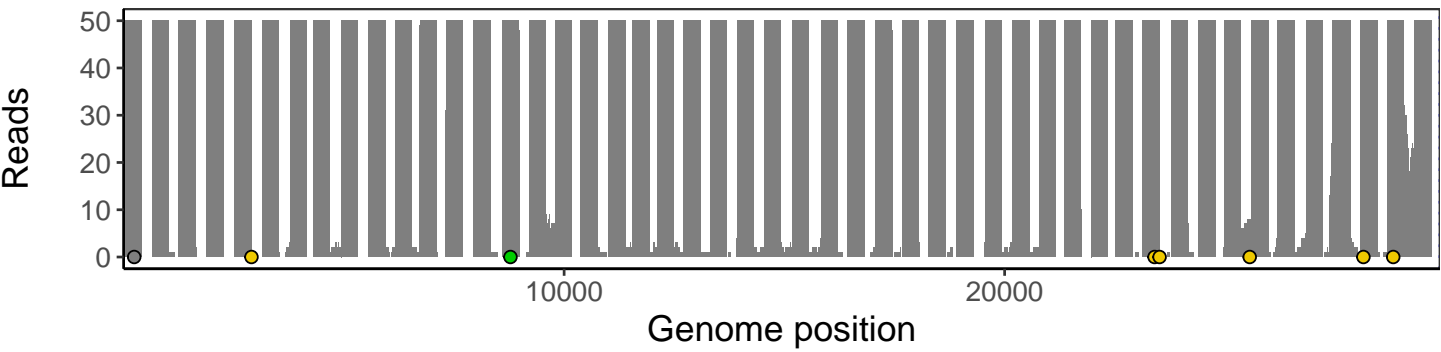




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