

COVID-19 subject 266

2020-11-30

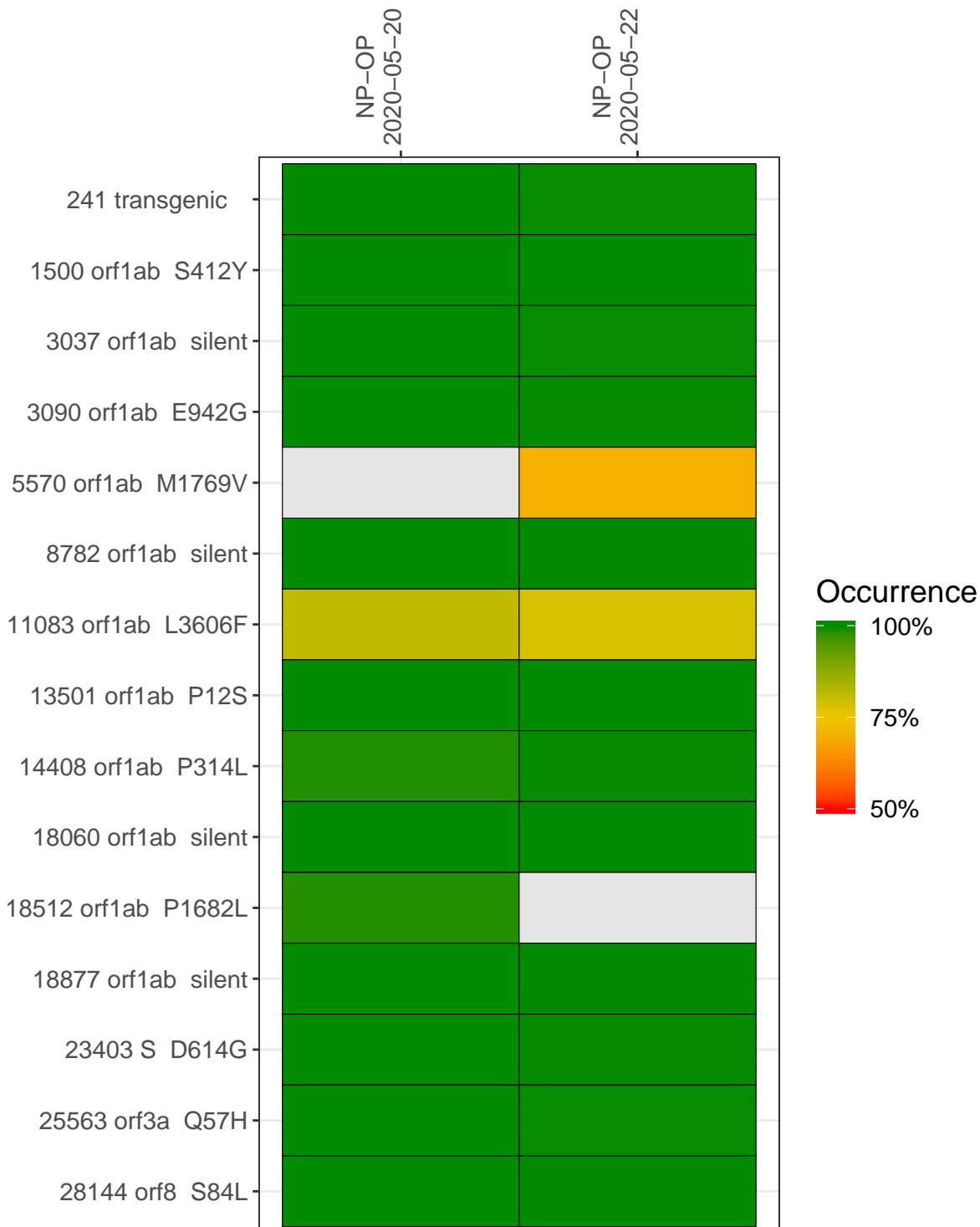
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found ([here](#)).

Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0155	composite	NA	NP-OP	2020-05-20	22.33	99.8%	99.0%
VSP0163	composite	NA	NP-OP	2020-05-22	29.75	99.9%	99.8%
VSP0155-1	single experiment	17000	NP-OP	2020-05-20	21.42	99.4%	98.2%
VSP0155-2	single experiment	85000	NP-OP	2020-05-20	22.33	99.7%	98.6%
VSP0163-1	single experiment	1530000	NP-OP	2020-05-22	29.75	99.9%	99.8%
VSP0163-2	single experiment	7650000	NP-OP	2020-05-22	29.84	99.9%	99.8%
VSP0319-1	single experiment	143500	NP-OP	2020-05-20	22.25	99.3%	98.5%
VSP0320-1	single experiment	5750000	NP-OP	2020-05-22	29.86	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 2020-05-20			NP-OP 2020-05-22		
241 transgenic	37	335	283	2589	1388	2515
1500 orf1ab S412Y	133	33	34	379	957	1521
3037 orf1ab silent	33	313	272	1859	1321	1757
3090 orf1ab E942G	38	436	343	2123	1167	1512
5570 orf1ab M1769V	29	60	74	699	1463	2078
8782 orf1ab silent	17	91	107	728	1469	2376
11083 orf1ab L3606F	78	151	148	585	968	802
13501 orf1ab P12S	31	86	77	608	1806	2796
14408 orf1ab P314L	46	79	94	995	1890	2157
18060 orf1ab silent	25	82	60	703	997	1184
18512 orf1ab P1682L	63	257	240	901	2685	3440
18877 orf1ab silent	47	388	375	1644	1762	2064
23403 S D614G	72	620	703	2914	2132	2907
25563 orf3a Q57H	35	277	264	2440	1256	1819
28144 orf8 S84L	68	242	286	1792	937	1221
	VSP0155-1	VSP0155-2	VSP0319-1	VSP0163-1	VSP0163-2	VSP0320-1

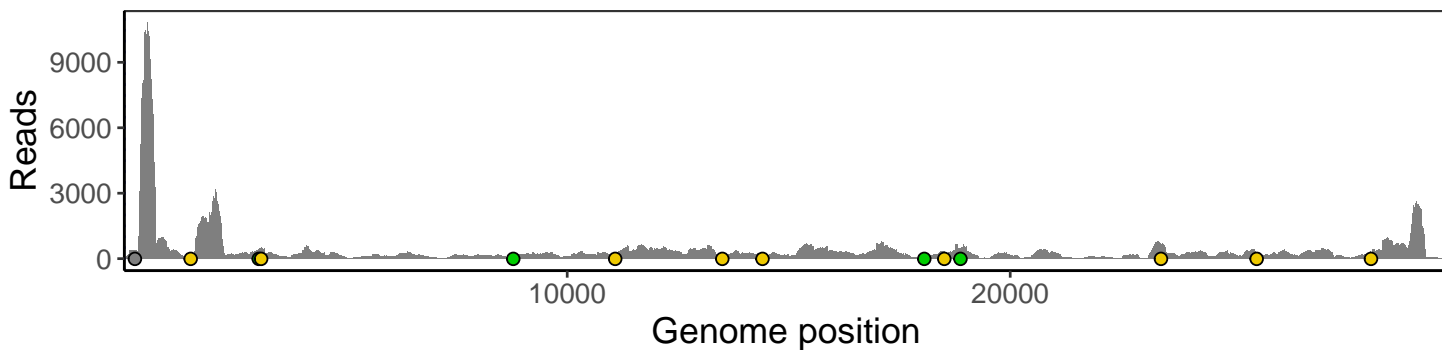
Base change

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

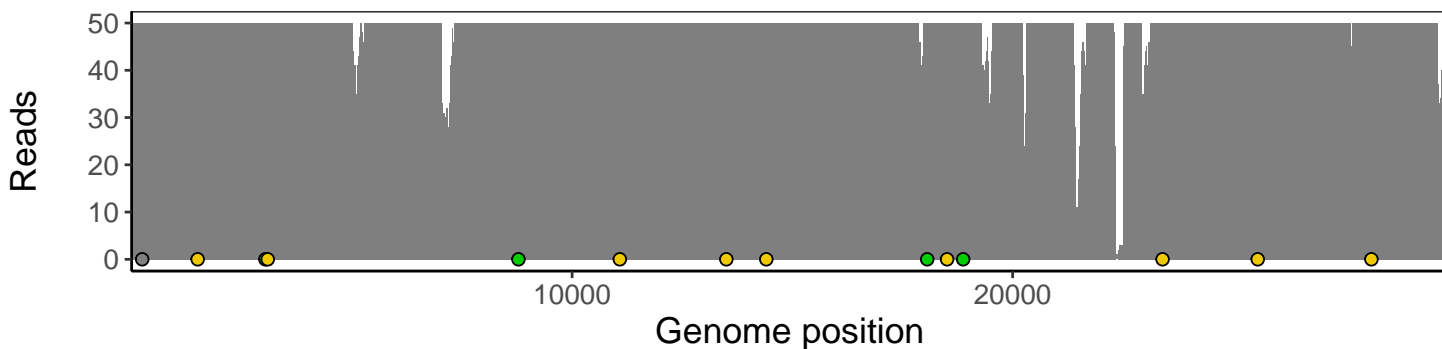
Analyses of individual experiments and composite results.

VSP0155 | 2020-05-20 | NP-OP | 266no-q | composite result

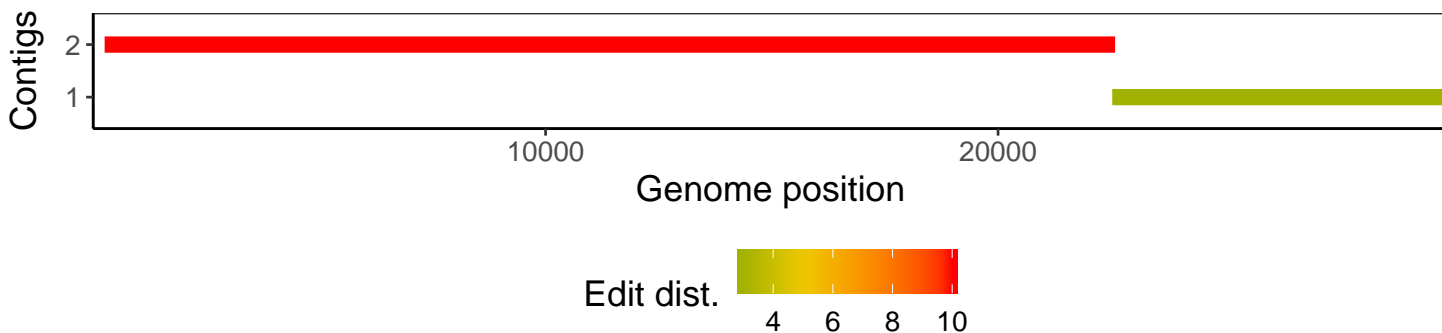
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



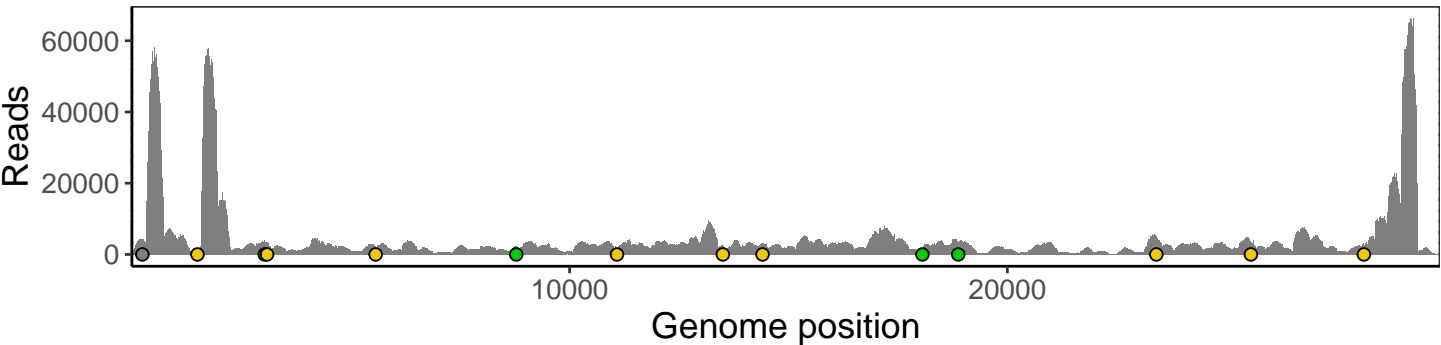
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



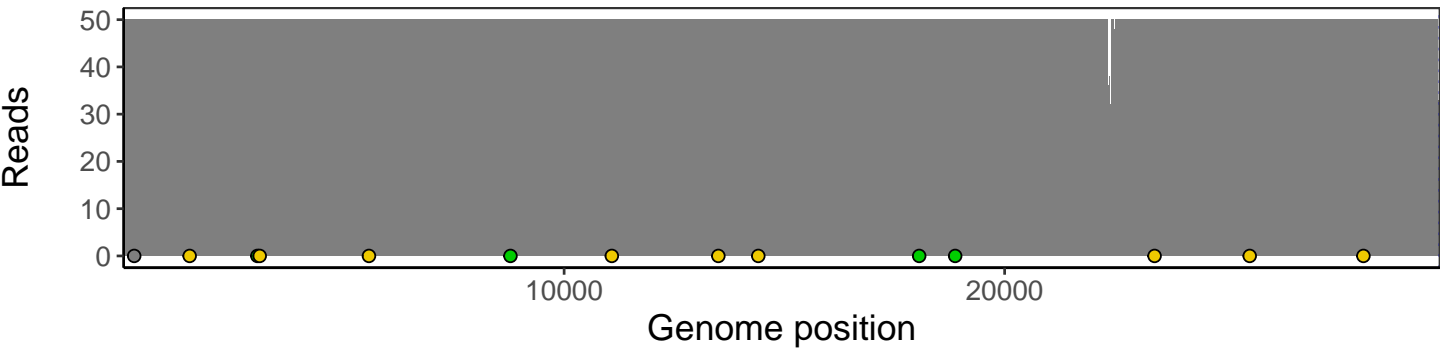
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



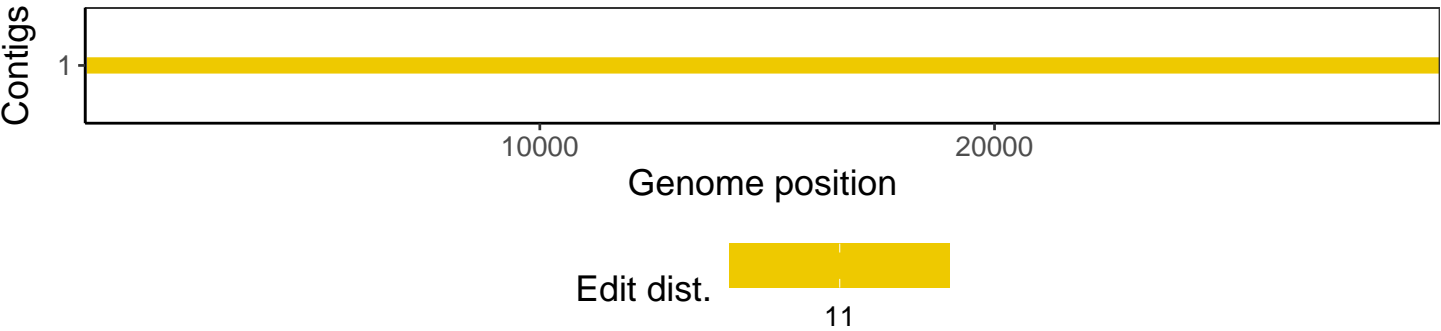
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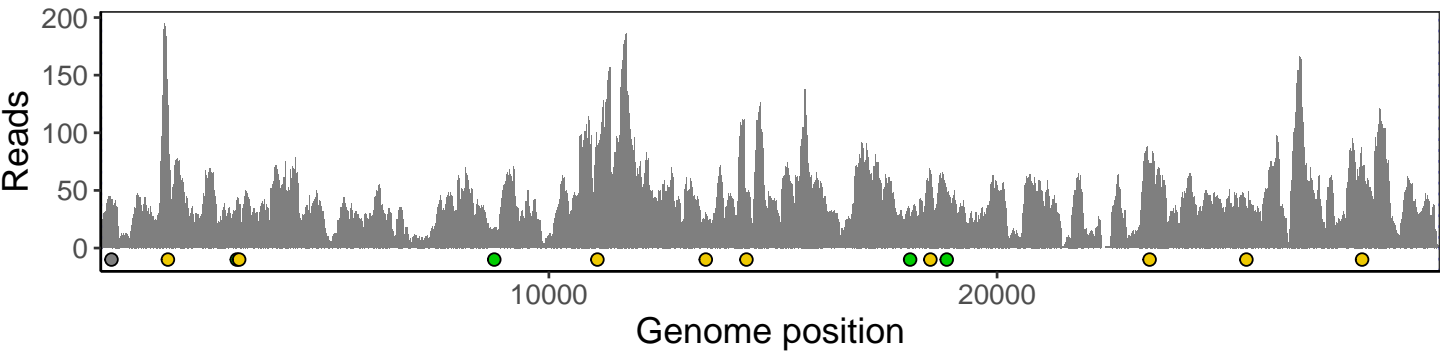
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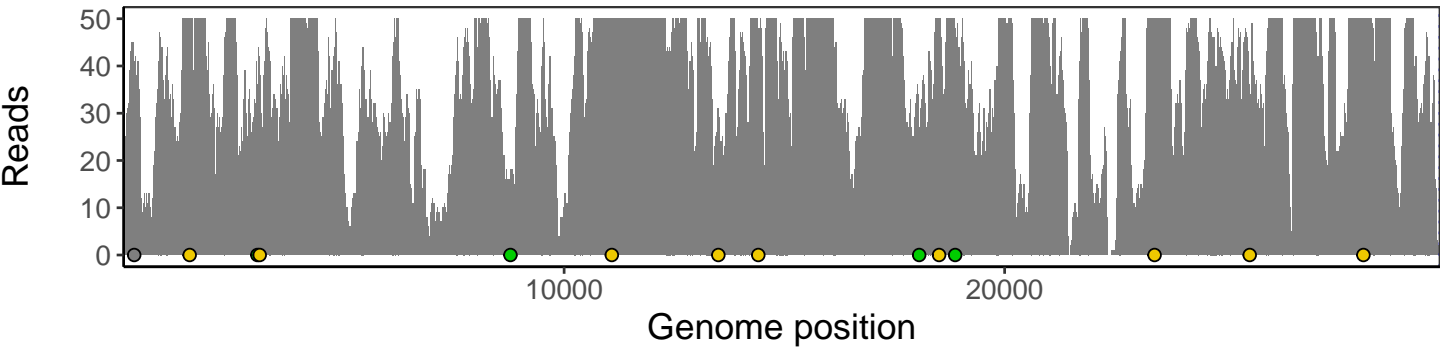
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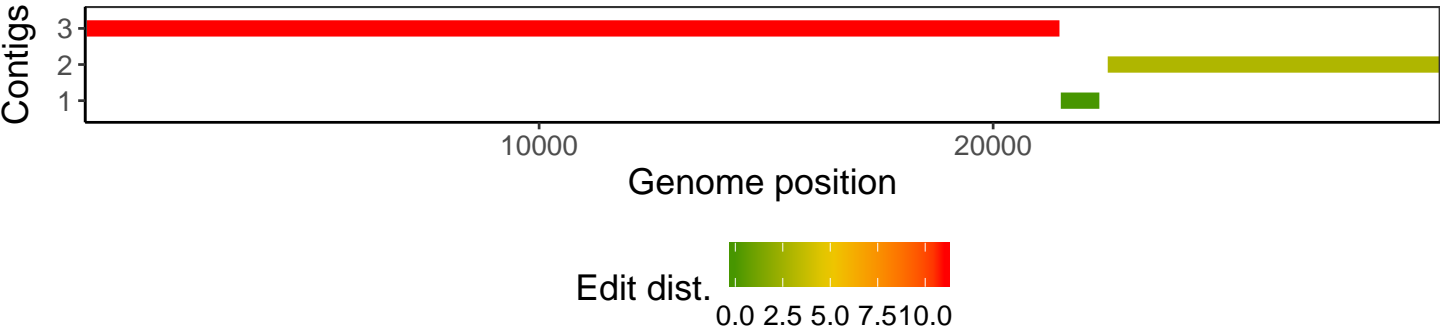
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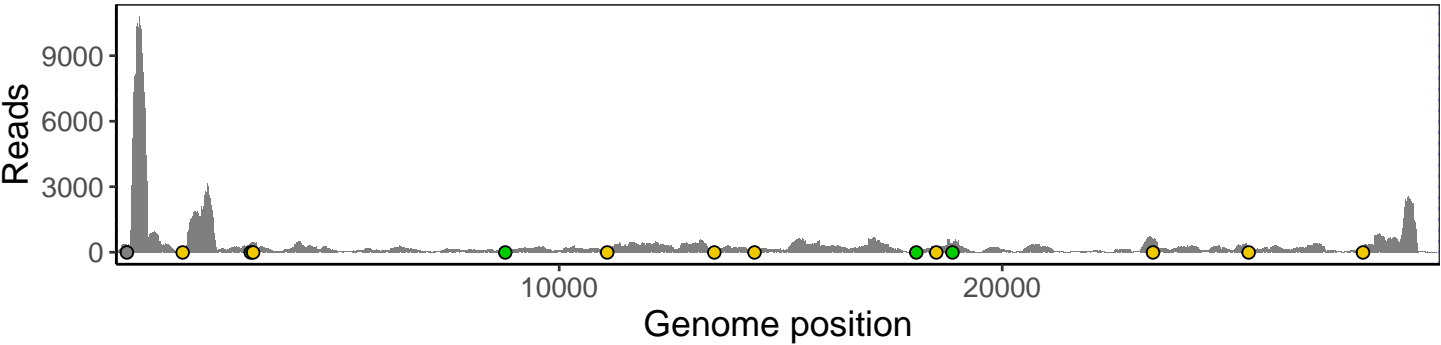
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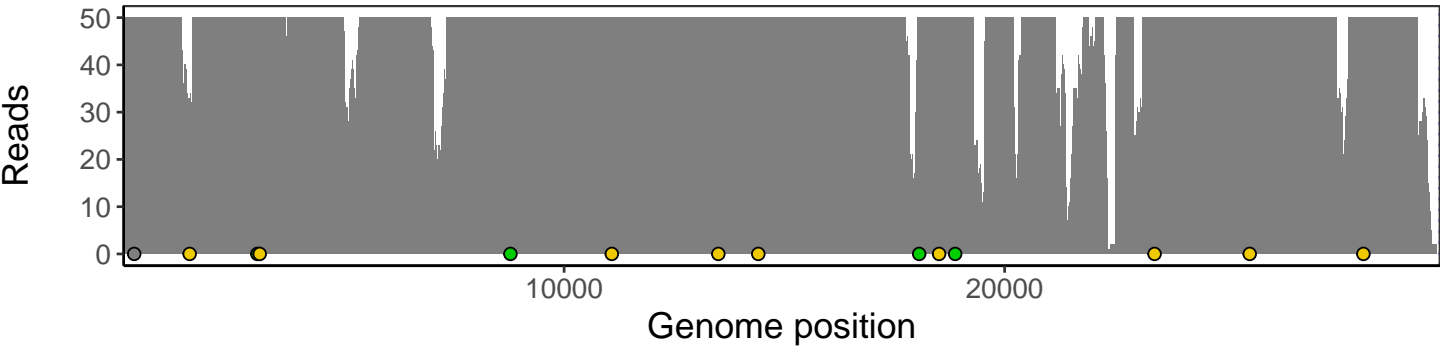
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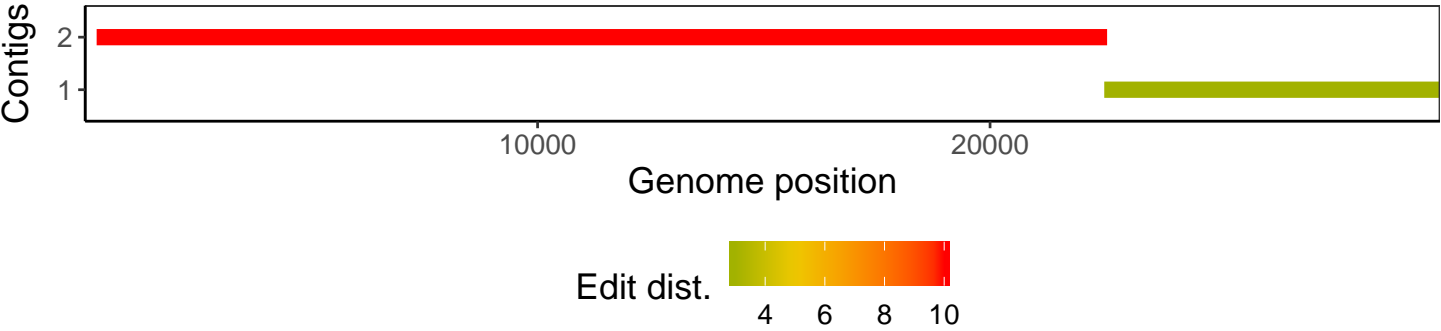
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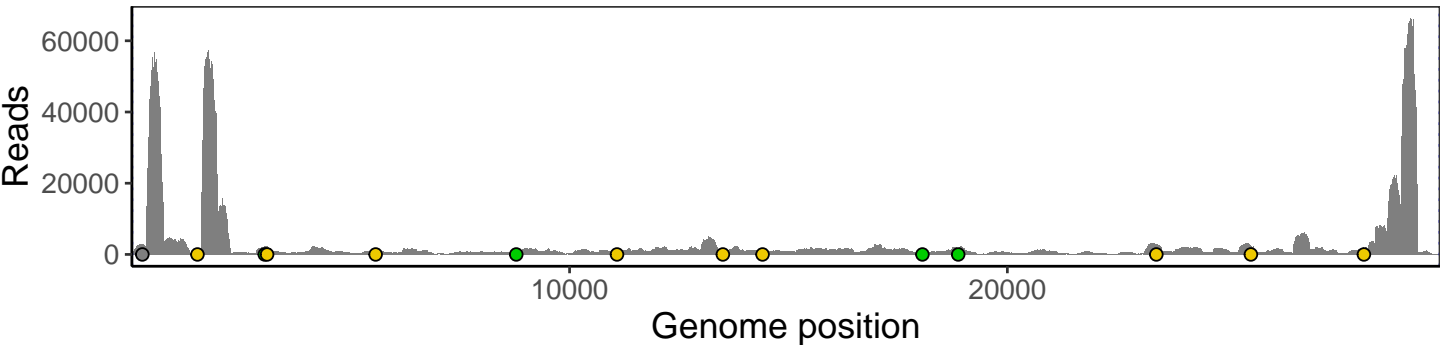
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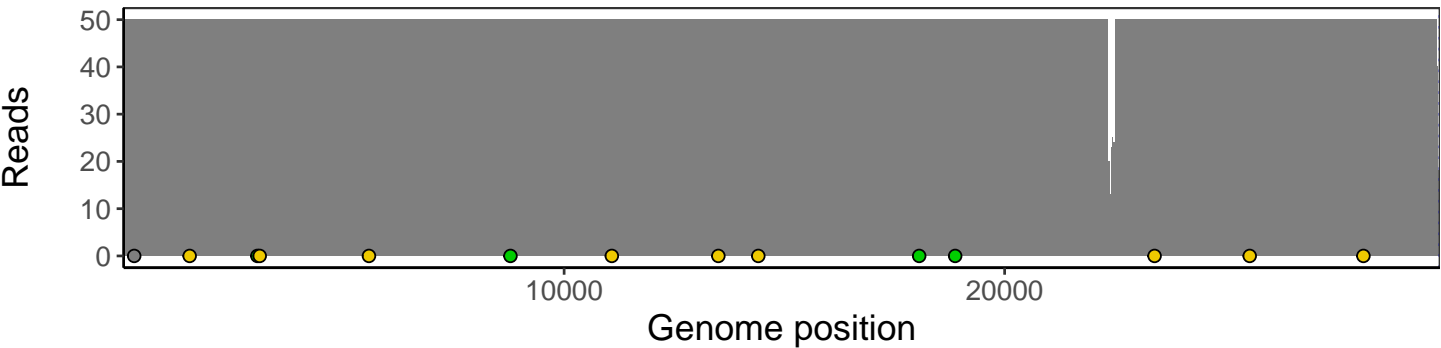
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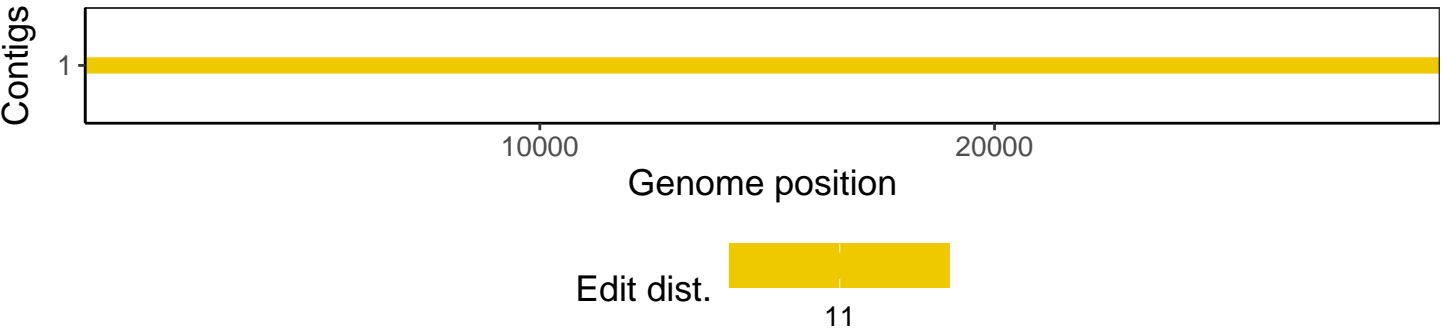
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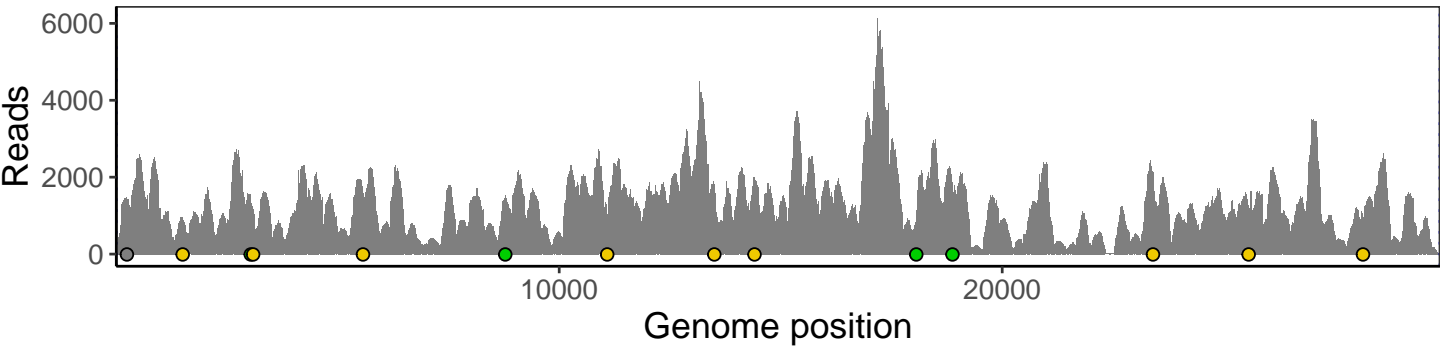
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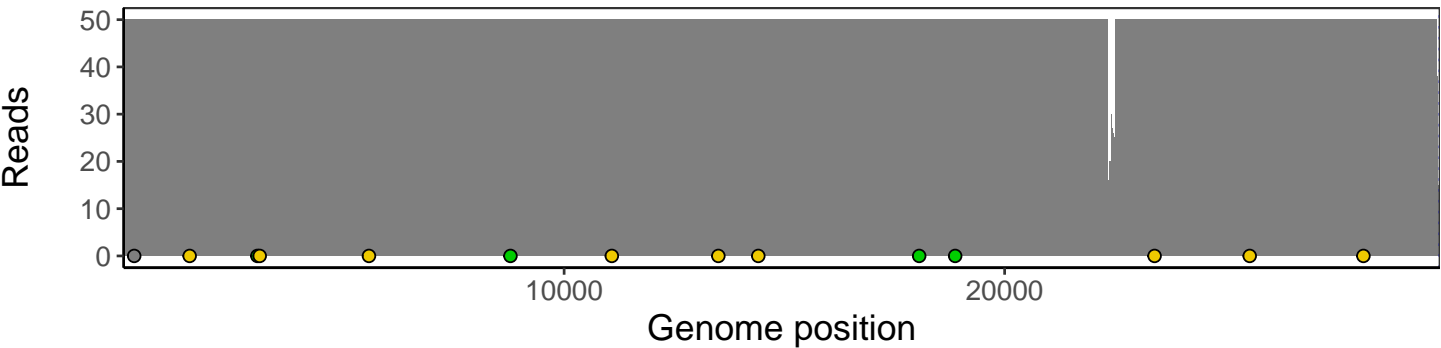
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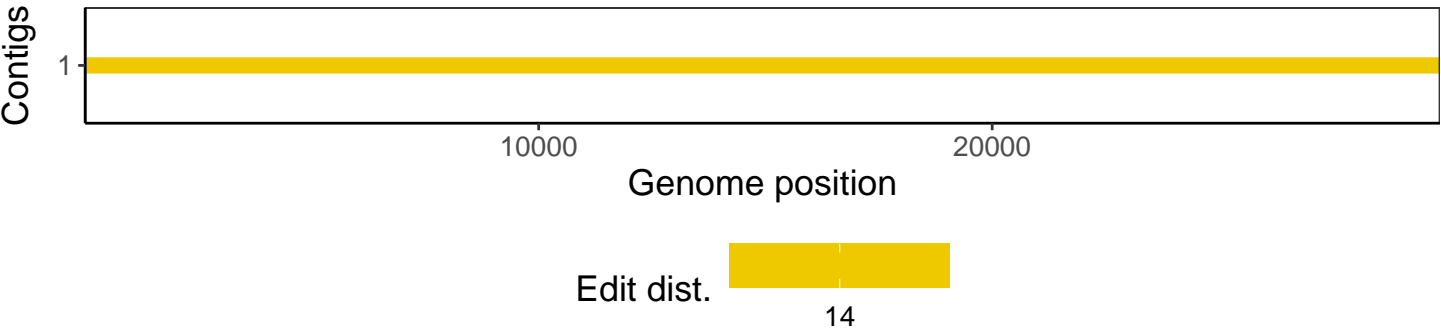
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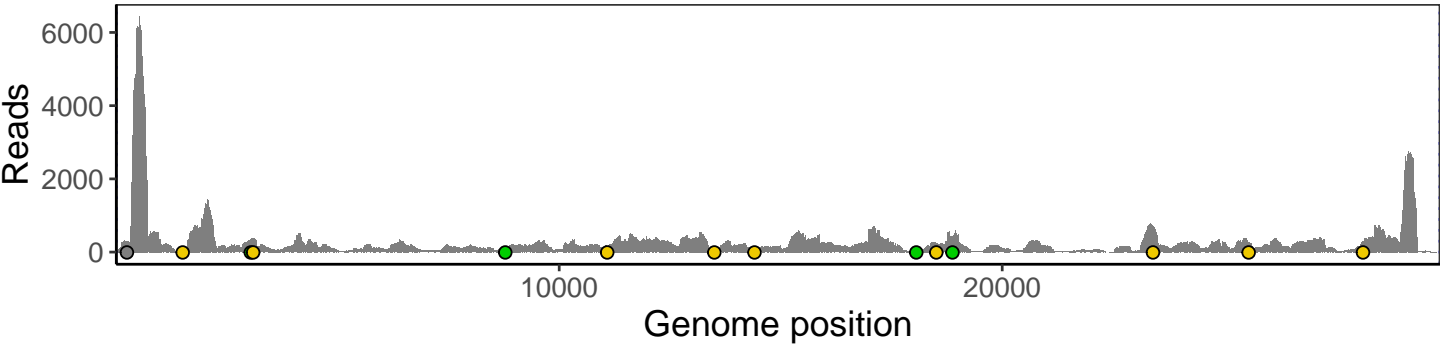
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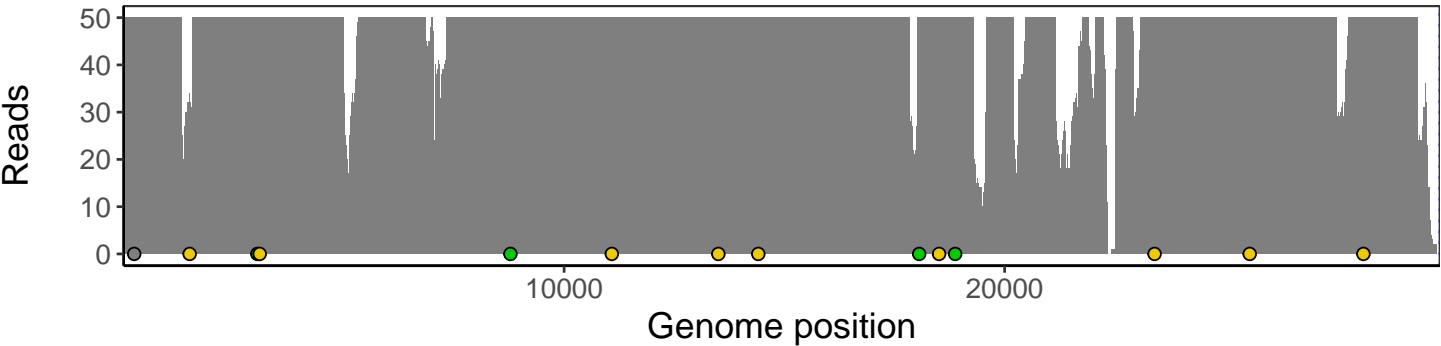
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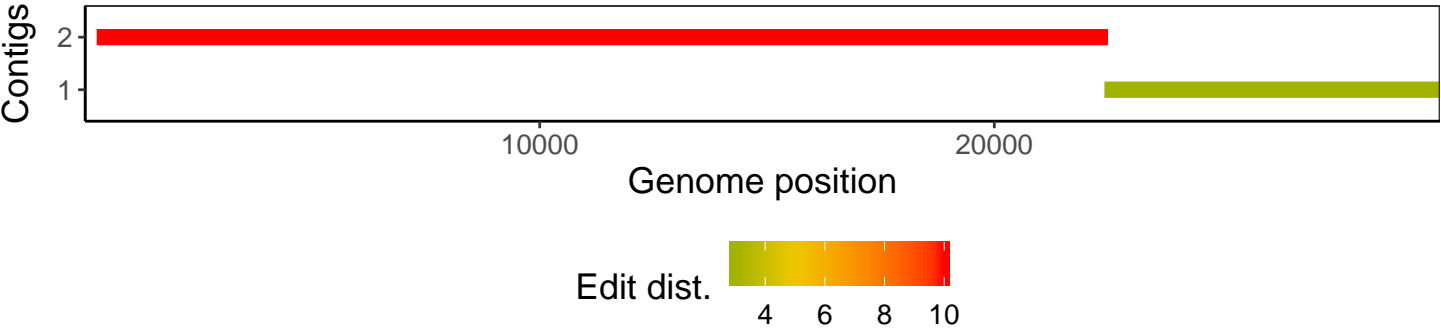
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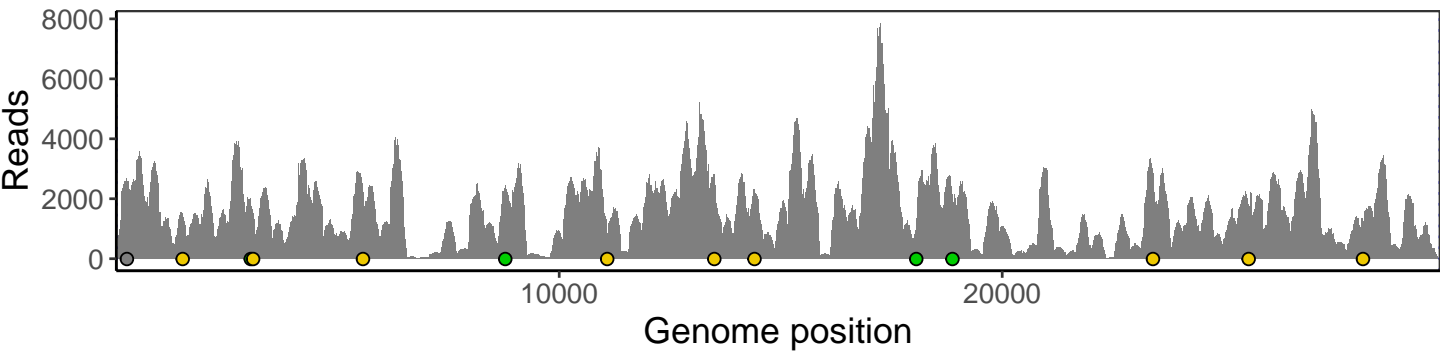
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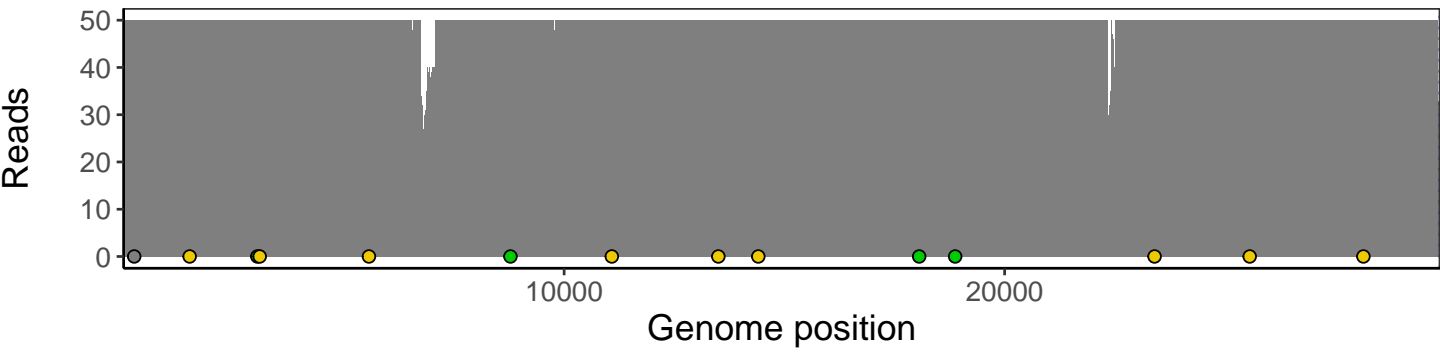
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