

# COVID-19 subject 266

2021-01-08

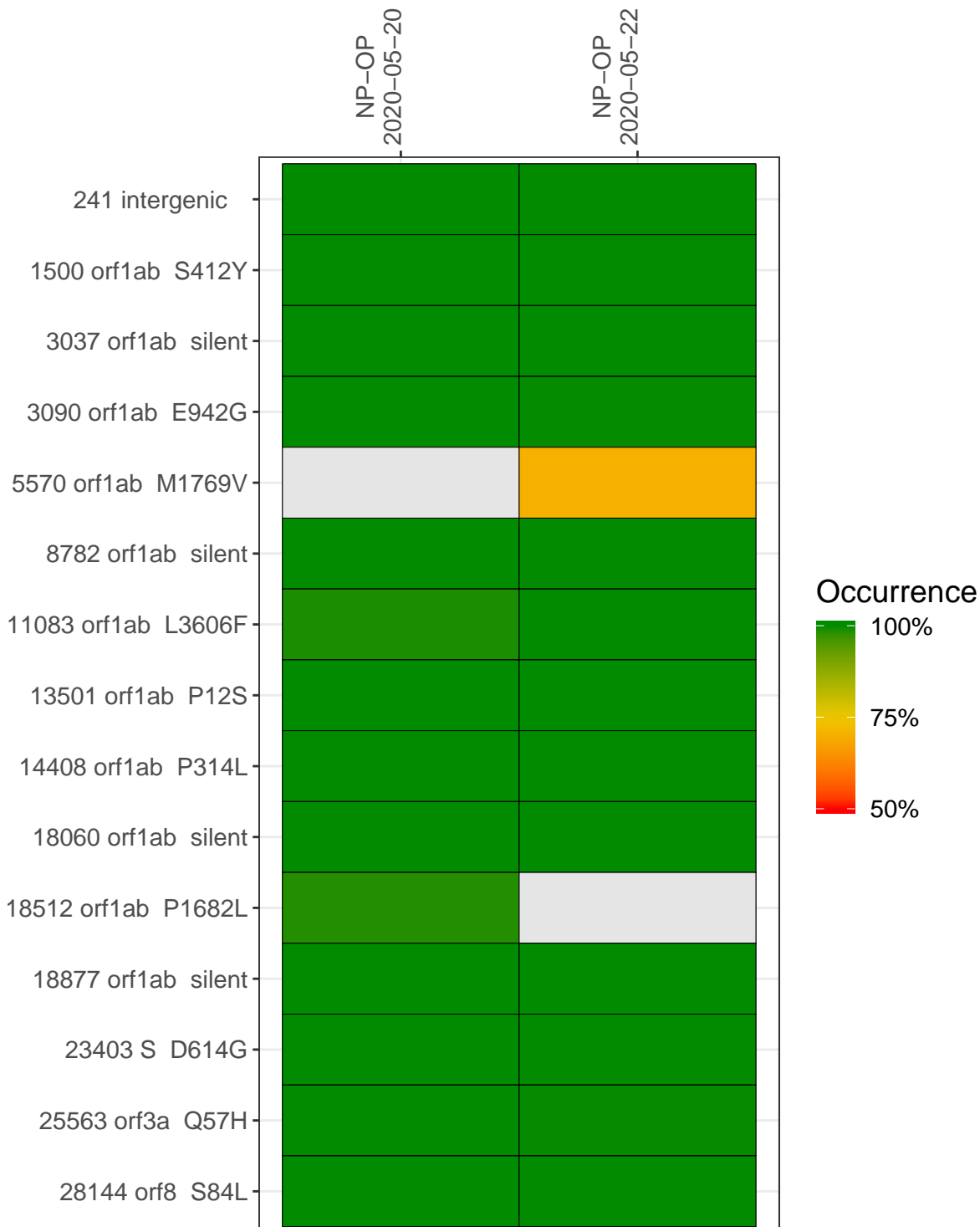
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found ([here](#)).

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	100.0%	99.0%
VSP0163	composite	NA	NP-OP	2020-05-22	29.75	100.0%	99.8%
VSP0155-1	single experiment	17000	NP-OP	2020-05-20	21.43	100.0%	98.5%
VSP0155-2	single experiment	85000	NP-OP	2020-05-20	22.33	100.0%	98.6%
VSP0163-1	single experiment	1530000	NP-OP	2020-05-22	29.75	100.0%	99.8%
VSP0163-2	single experiment	7650000	NP-OP	2020-05-22	29.84	100.0%	99.8%
VSP0319-1	single experiment	143500	NP-OP	2020-05-20	22.25	100.0%	98.5%
VSP0320-1	single experiment	5750000	NP-OP	2020-05-22	29.86	100.0%	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 intergenic	45	345	292	2677	1406	2626
1500 orf1ab S412Y	205	33	36	399	966	1619
3037 orf1ab silent	43	315	276	1910	1341	1869
3090 orf1ab E942G	48	440	346	2191	1181	1600
5570 orf1ab M1769V	34	60	77	716	1479	2187
8782 orf1ab silent	22	96	110	756	1486	2511
11083 orf1ab L3606F	112	153	151	636	979	845
13501 orf1ab P12S	36	89	82	658	1835	2973
14408 orf1ab P314L	61	81	98	1043	1917	2262
18060 orf1ab silent	32	83	62	749	1009	1258
18512 orf1ab P1682L	70	262	241	999	2723	3621
18877 orf1ab silent	59	392	379	1690	1794	2184
23403 S D614G	91	635	709	3001	2168	3063
25563 orf3a Q57H	48	283	270	2523	1274	1916
28144 orf8 S84L	80	245	288	1844	946	1292
	VSP0155-1	VSP0155-2	VSP0319-1	VSP0163-1	VSP0163-2	VSP0320-1

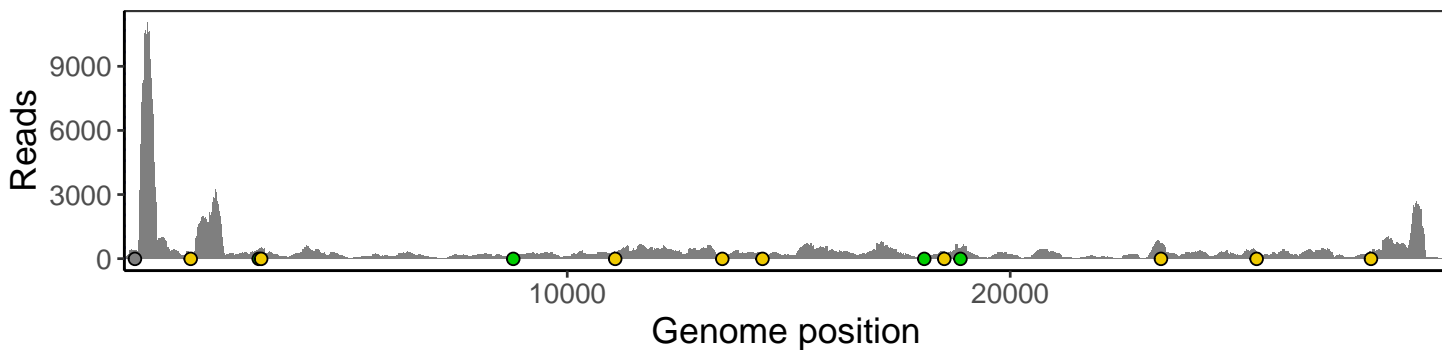
Base change

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

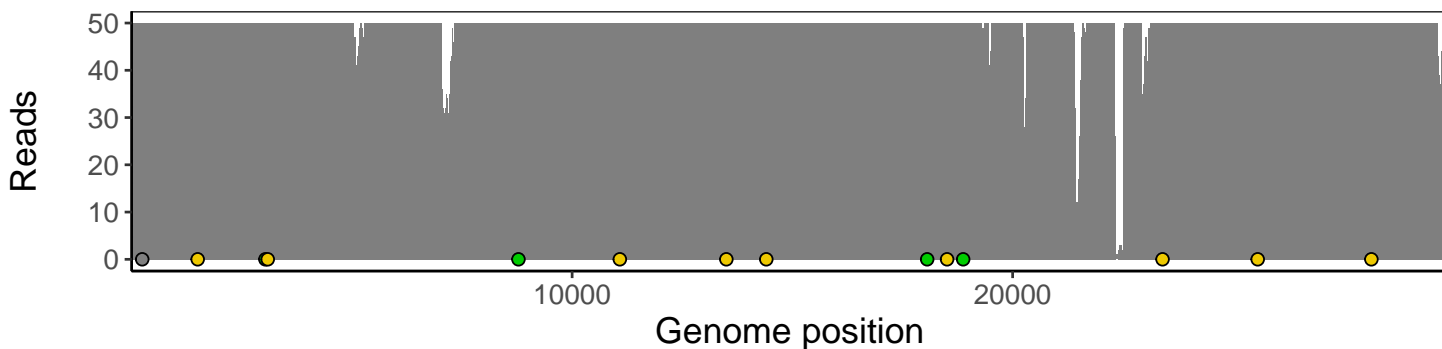
## Analyses of individual experiments and composite results.

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

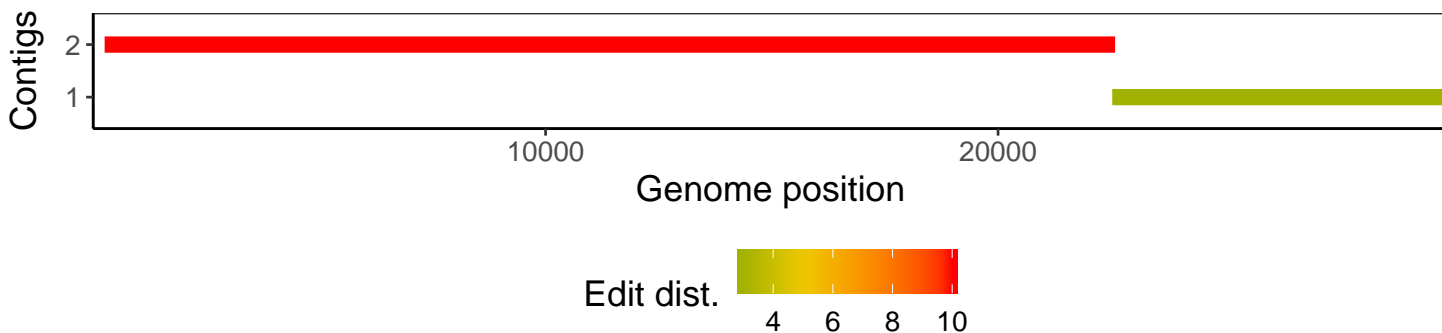
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



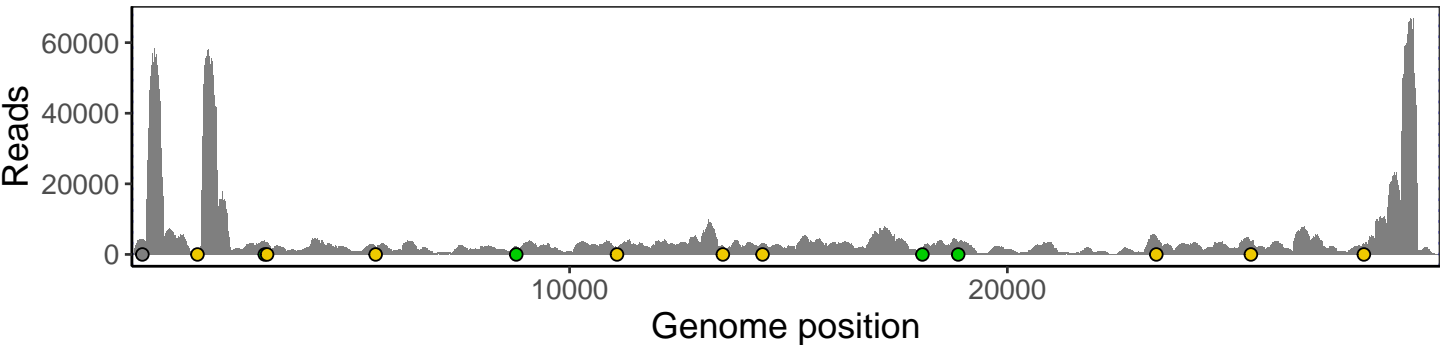
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



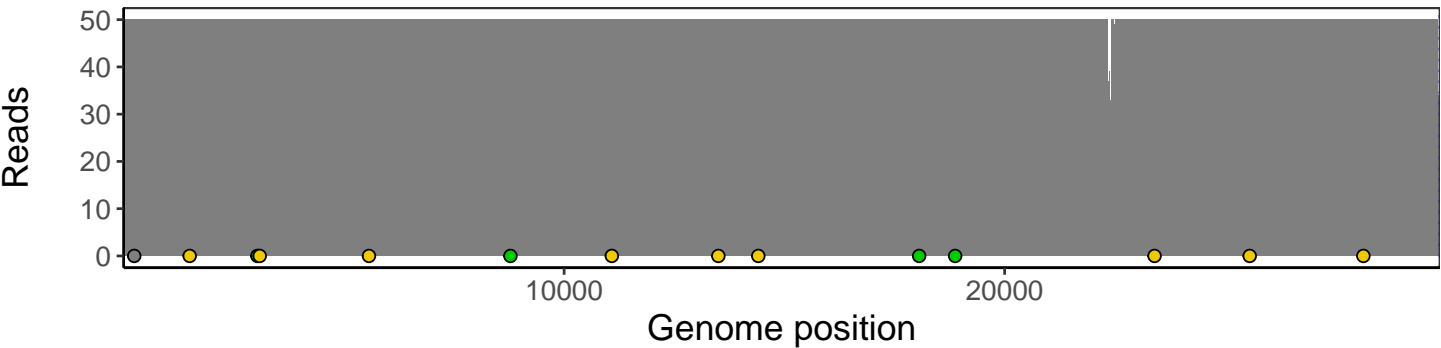
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



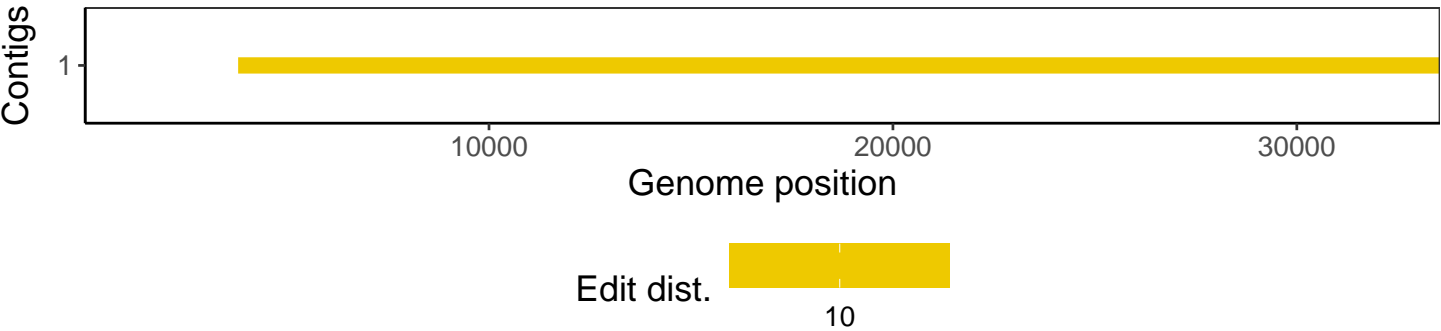
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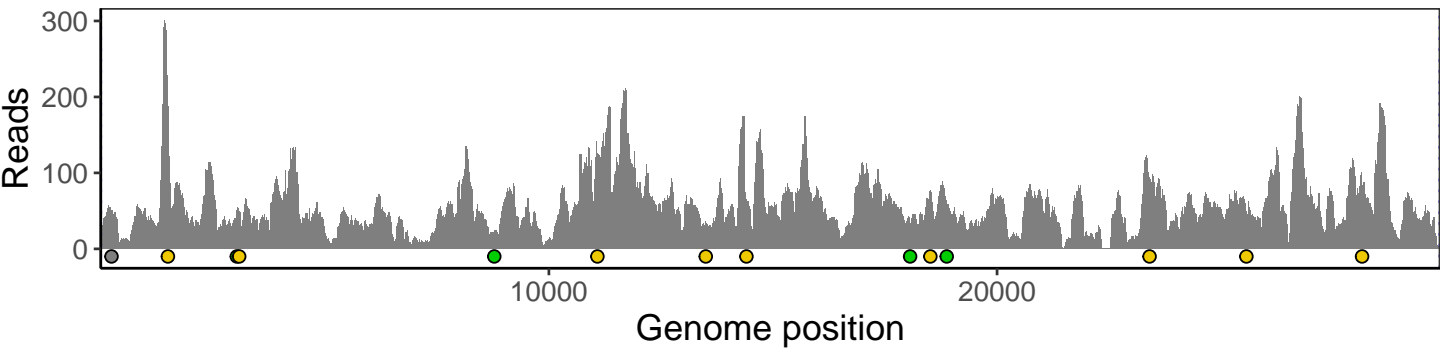
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



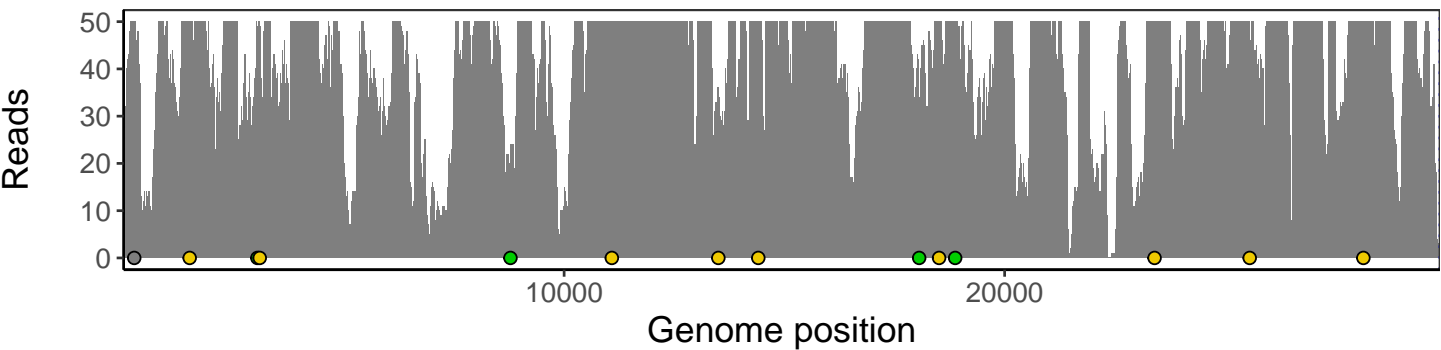
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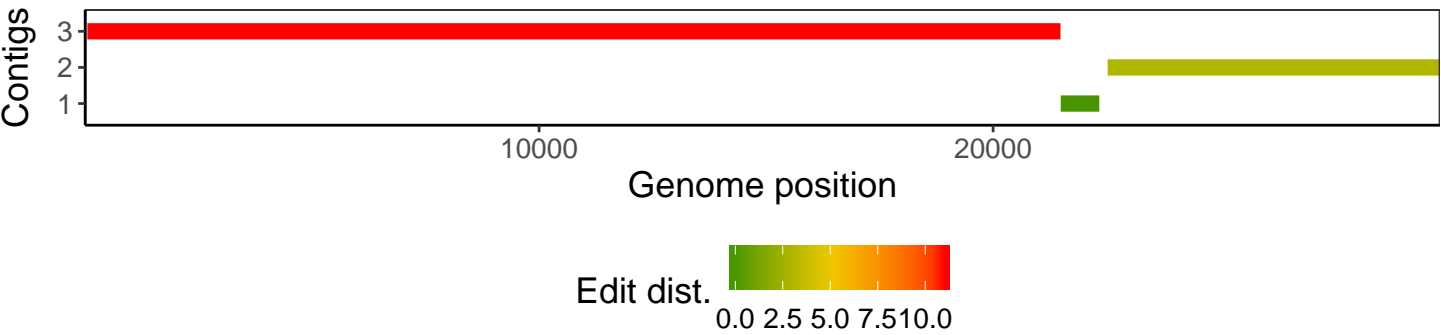
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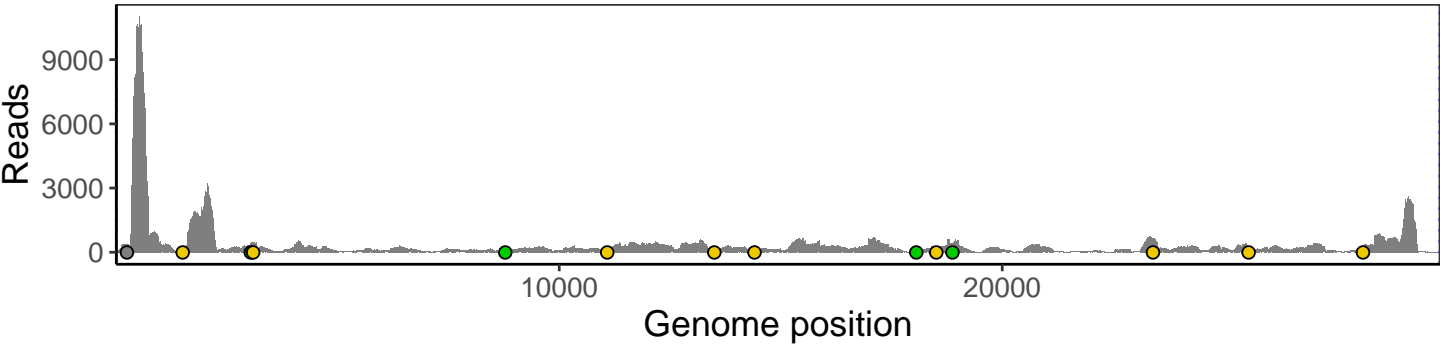
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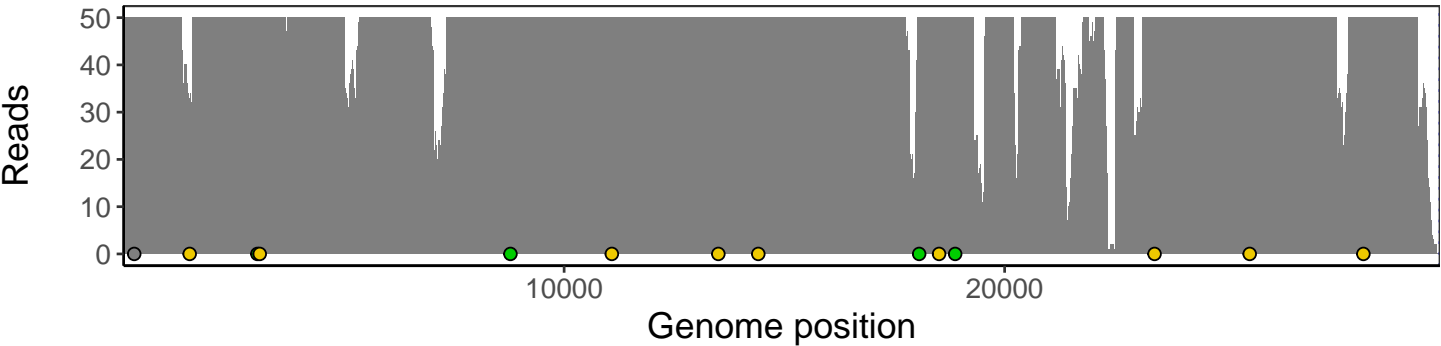
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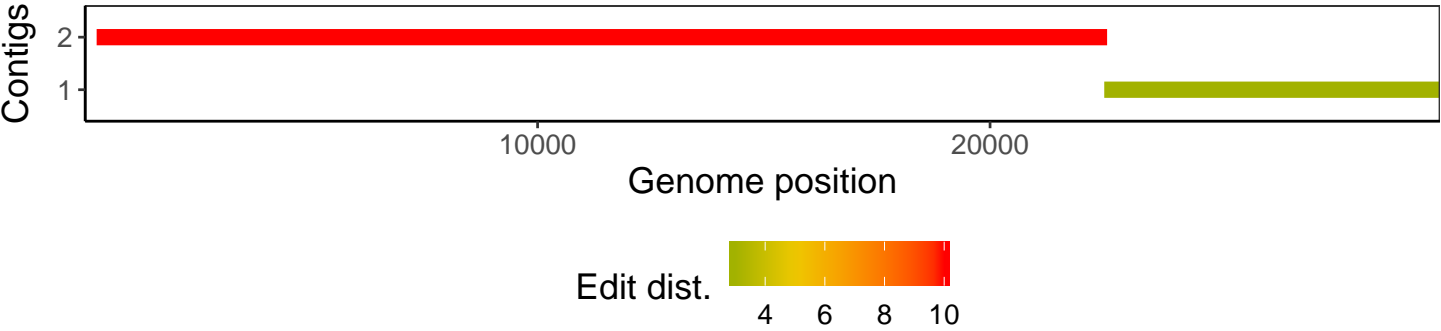
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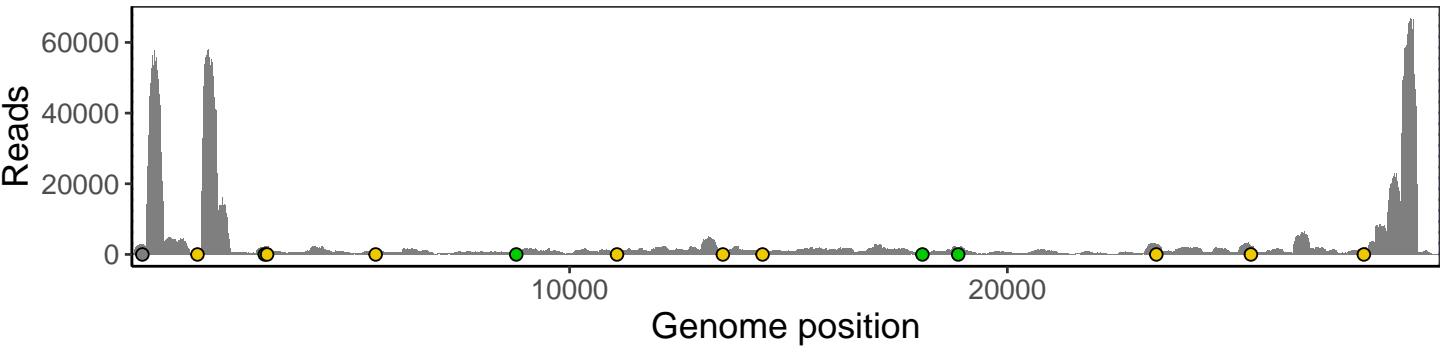
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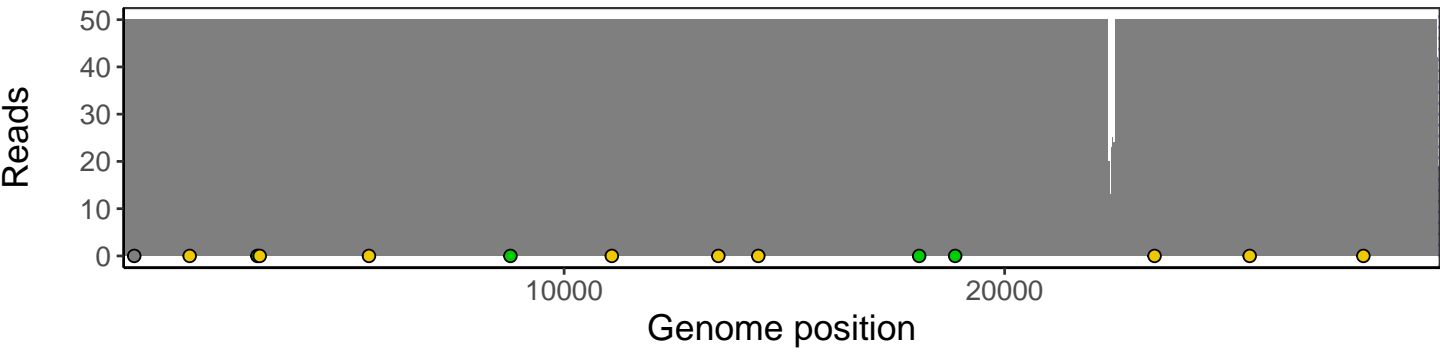
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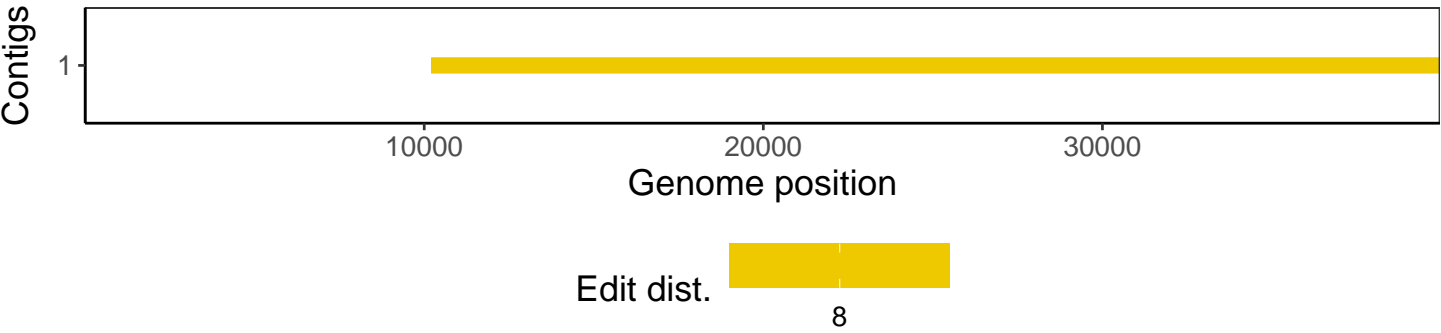
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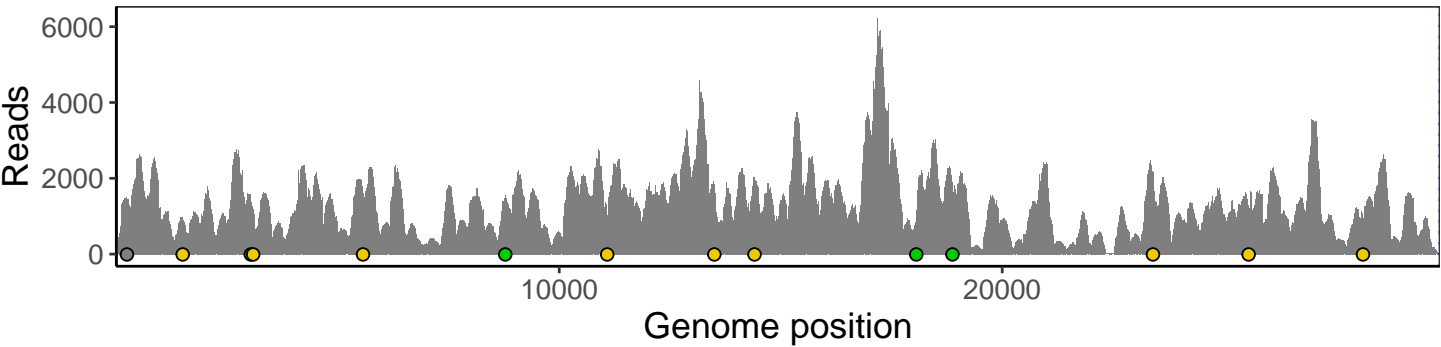


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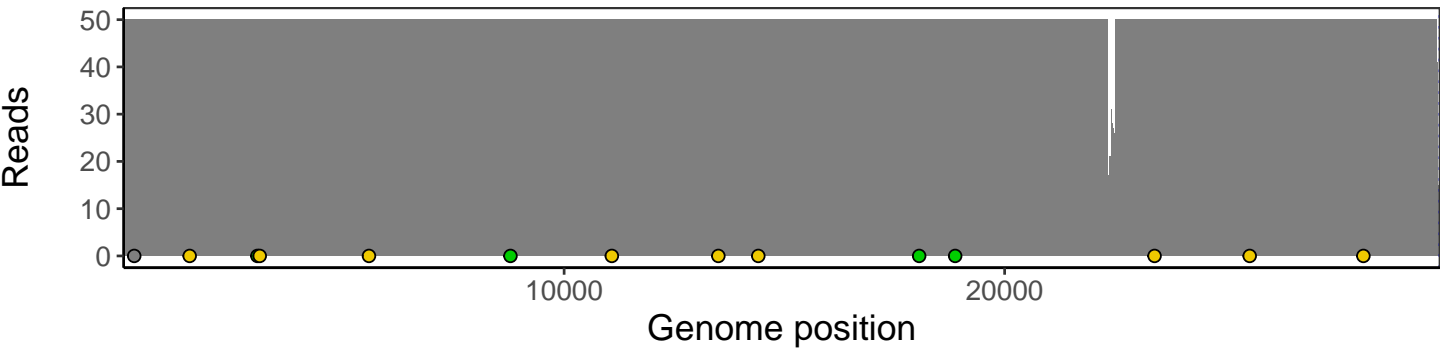




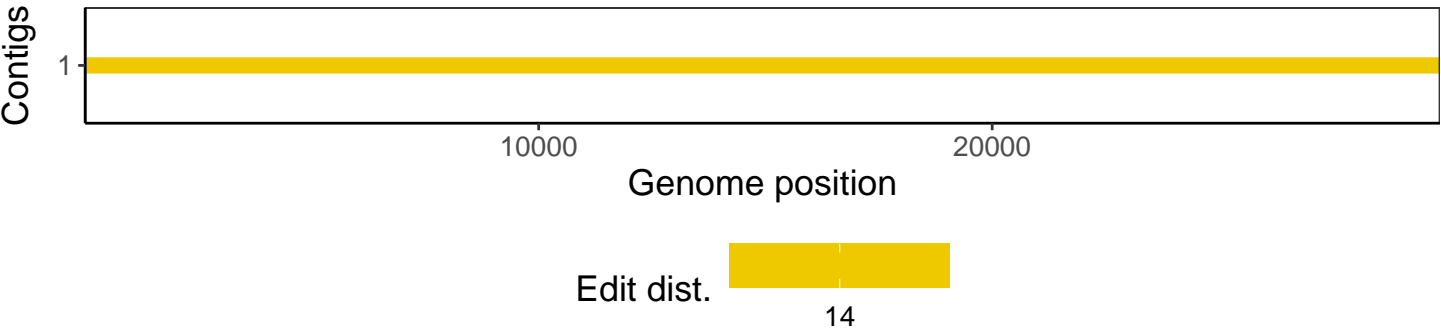
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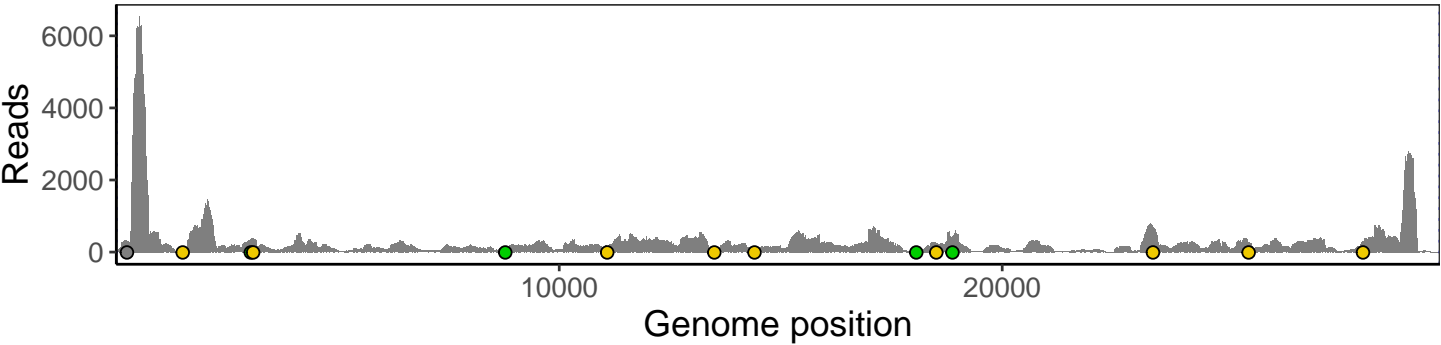
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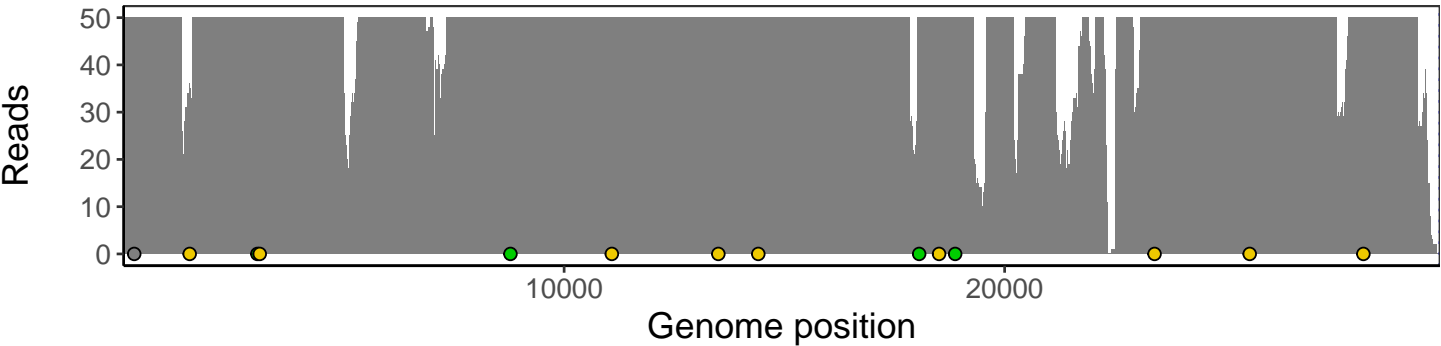
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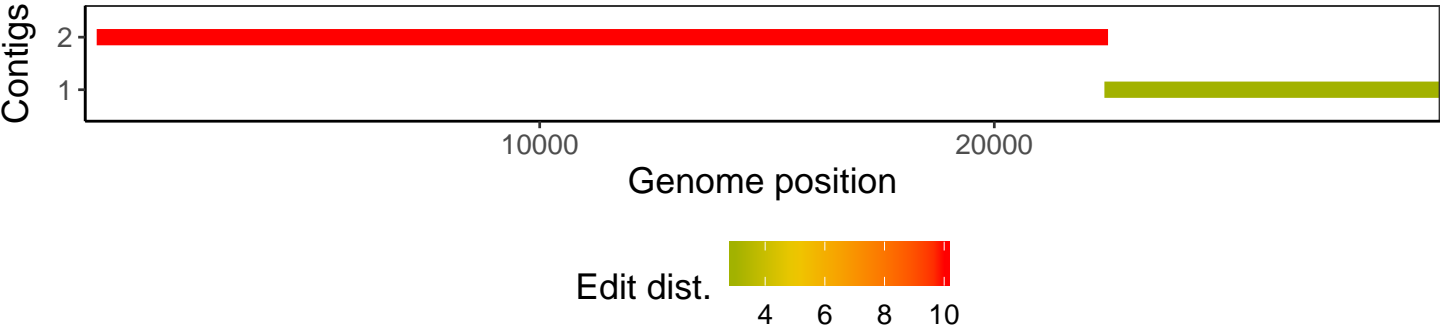
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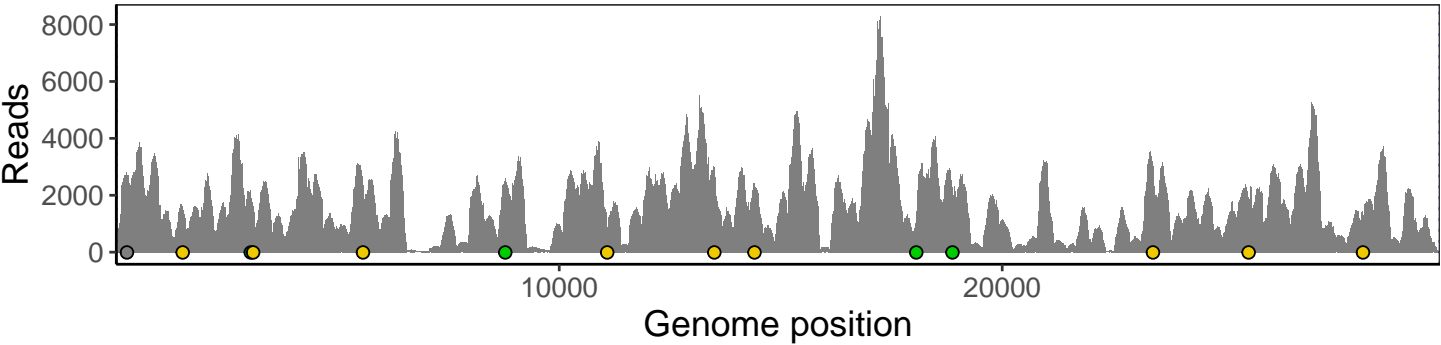
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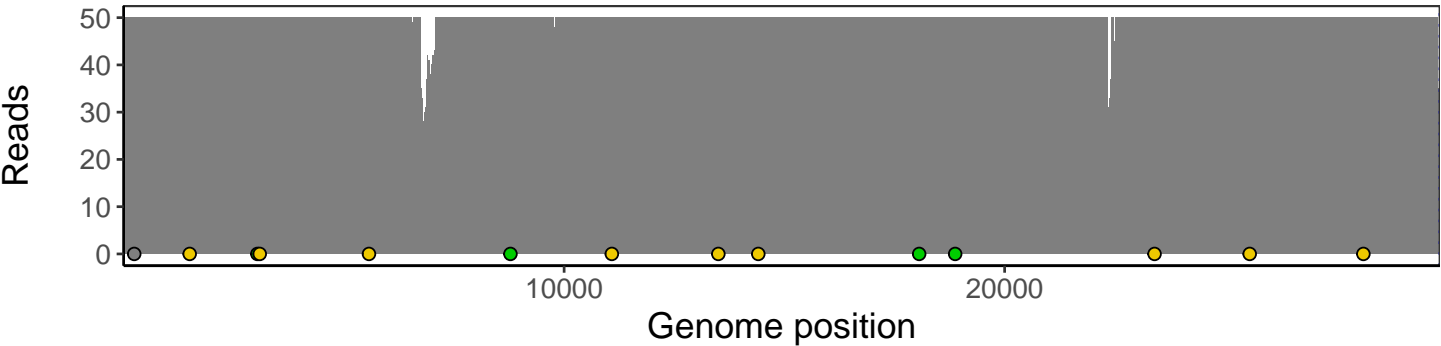
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