

COVID-19 subject 251

2021-01-10

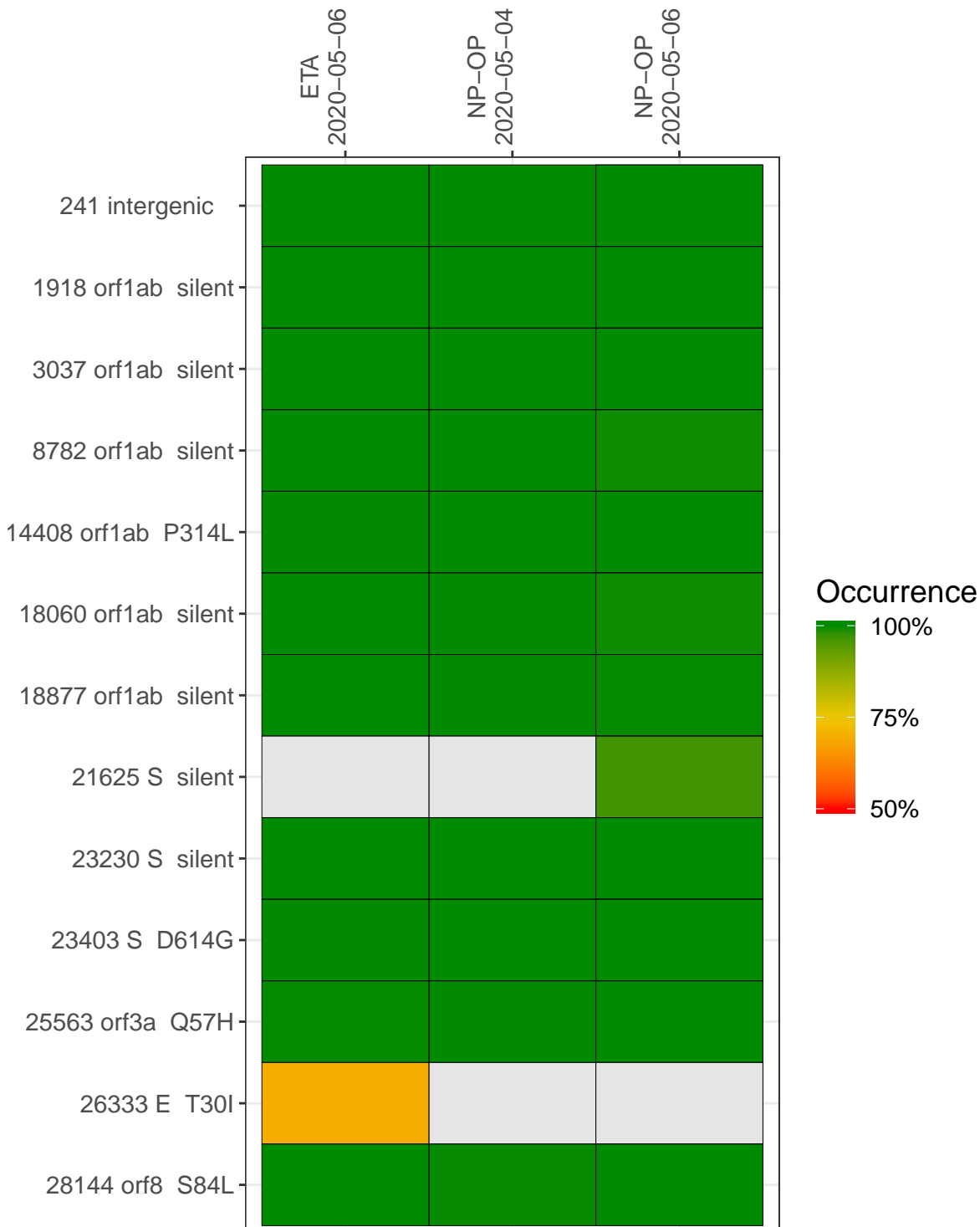
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found ([here](#)).

Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0065	composite	NA	NP-OP	2020-05-04	16.53	99.9%	99.8%
VSP0089	composite	NA	NP-OP	2020-05-06	30.00	99.9%	99.7%
VSP0065-1	single experiment	7550000	NP-OP	2020-05-04	16.47	99.9%	99.8%
VSP0065-2	single experiment	7550000	NP-OP	2020-05-04	29.85	99.8%	99.3%
VSP0088-1	single experiment	255500	ETA	2020-05-06	29.82	99.8%	99.8%
VSP0089-1	single experiment	570000	NP-OP	2020-05-06	29.91	99.9%	99.7%
VSP0089-2	single experiment	570000	NP-OP	2020-05-06	29.45	99.4%	98.6%
VSP0318-1	single experiment	890000	NP-OP	2020-05-06	24.51	99.8%	99.2%

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.



	ETA 2020-05-06	NP-OP 2020-05-04		NP-OP 2020-05-06		
241 intergenic	1436	1338	5028	2312	589	628
1918 orf1ab silent	1624	1479	4395	1752	1363	521
3037 orf1ab silent	1249	2670	1565	1873	286	902
8782 orf1ab silent	1148	2360	234	1929	108	322
14408 orf1ab P314L	2616	2107	65	3835	193	214
18060 orf1ab silent	1268	2580	483	1856	188	307
18877 orf1ab silent	3411	4348	178	4456	759	754
21625 S silent	271	1562	17	543	39	83
23230 S silent	2771	2136	3374	3564	1075	503
23403 S D614G	3869	2639	4201	4873	1296	590
25563 orf3a Q57H	1129	1416	4152	1506	496	377
26333 E T30I	1351	1575	573	2002	288	278
28144 orf8 S84L	2405	1067	116	3851	512	474
	VSP0088-1	VSP0065-1	VSP0065-2	VSP0089-1	VSP0089-2	VSP0318-1

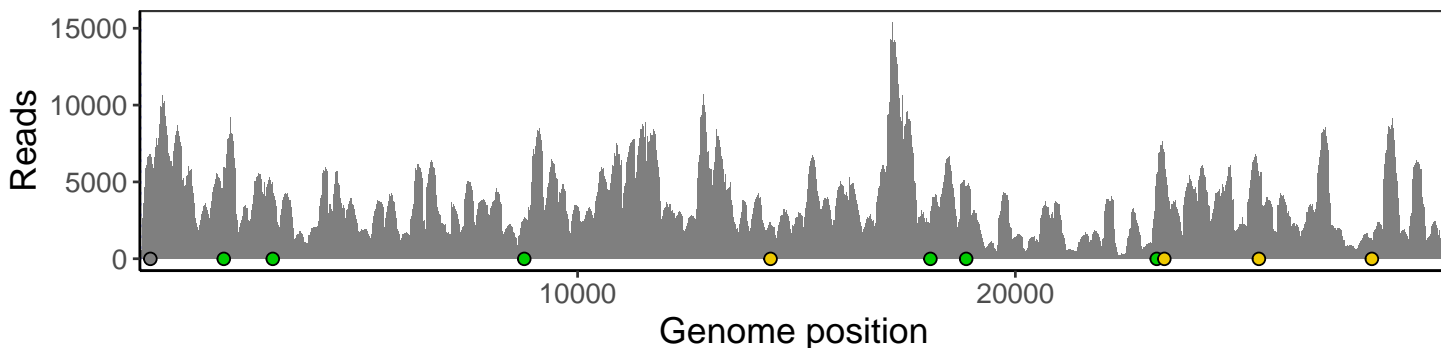
Base change

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

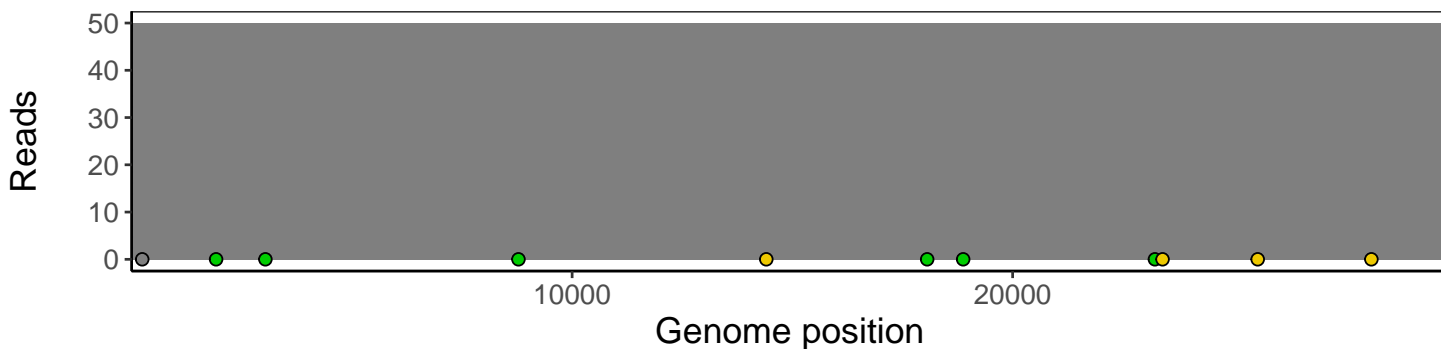
Analyses of individual experiments and composite results.

VSP0065 | 2020-05-04 | NP-OP | 251-q | composite result

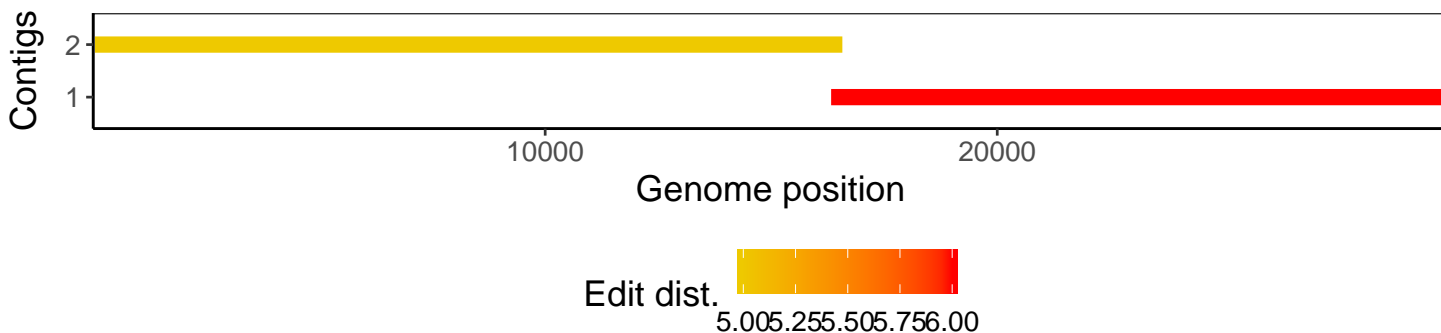
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



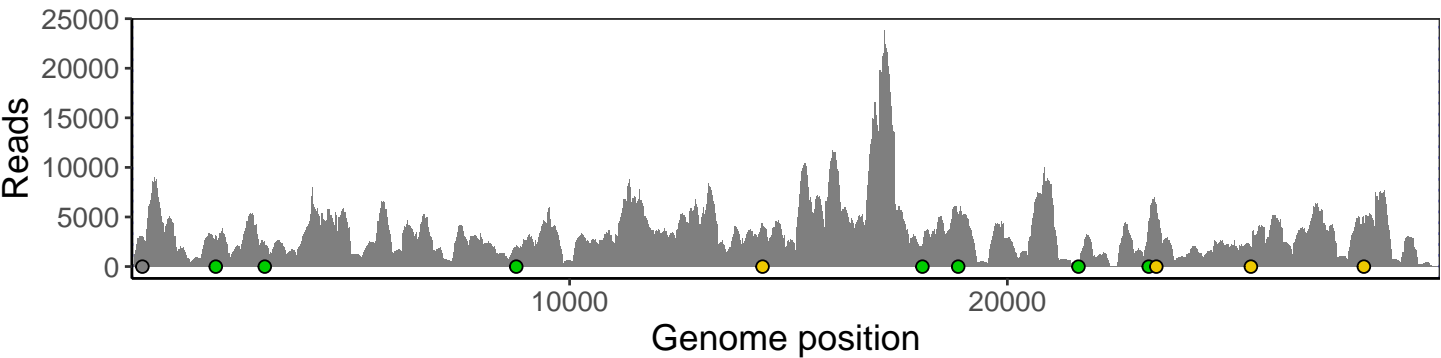
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



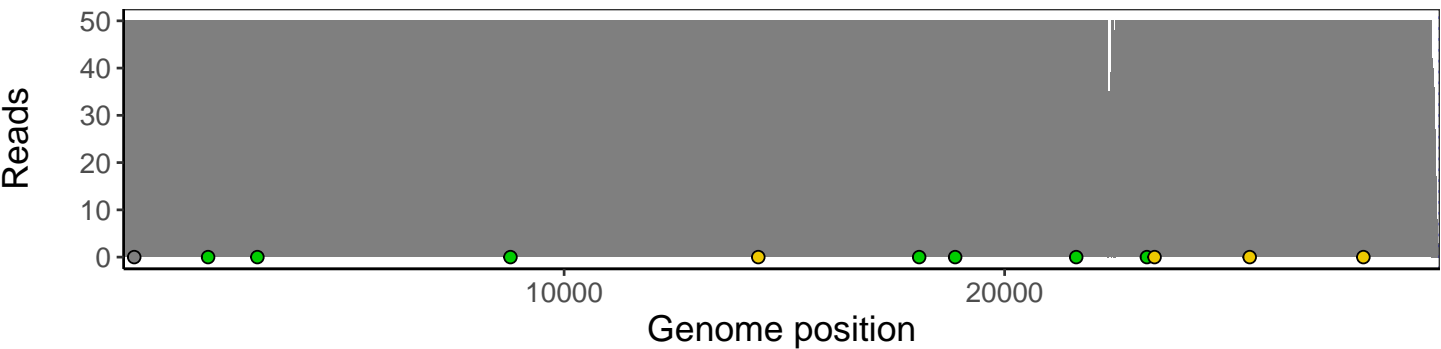
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



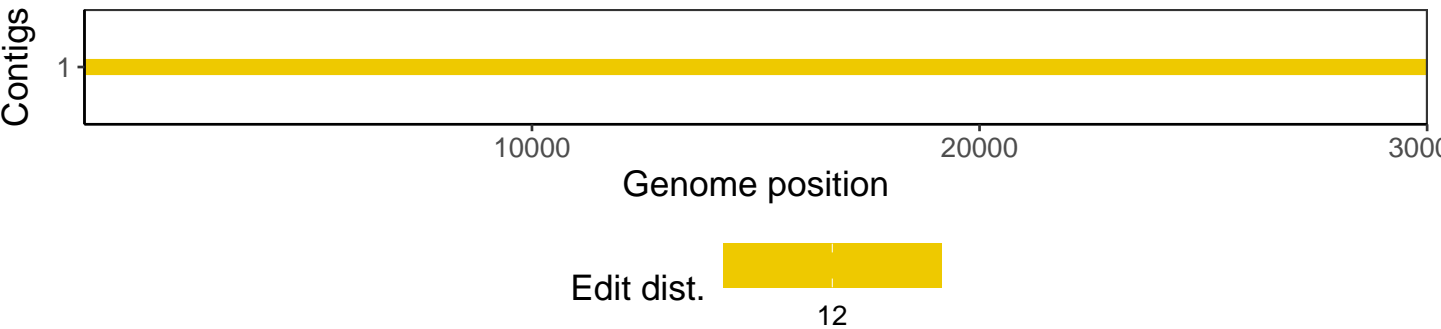
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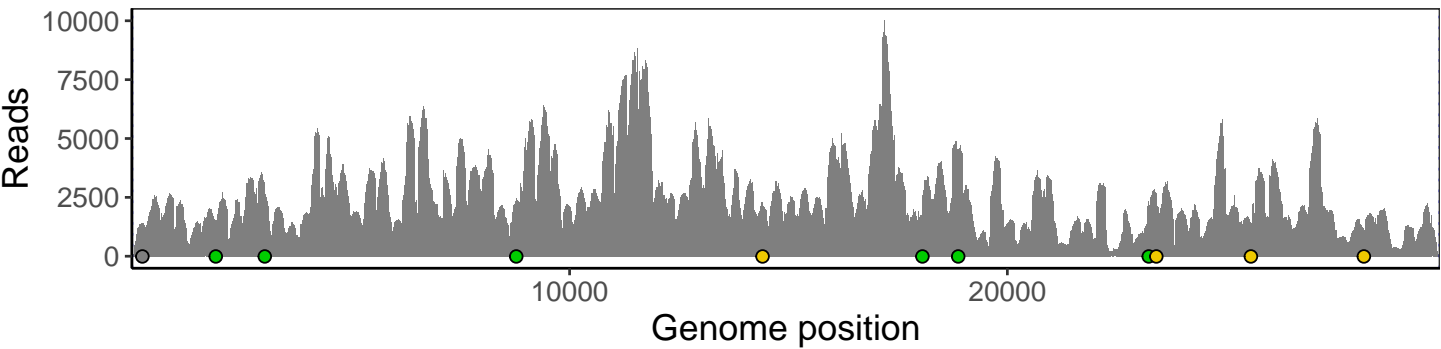
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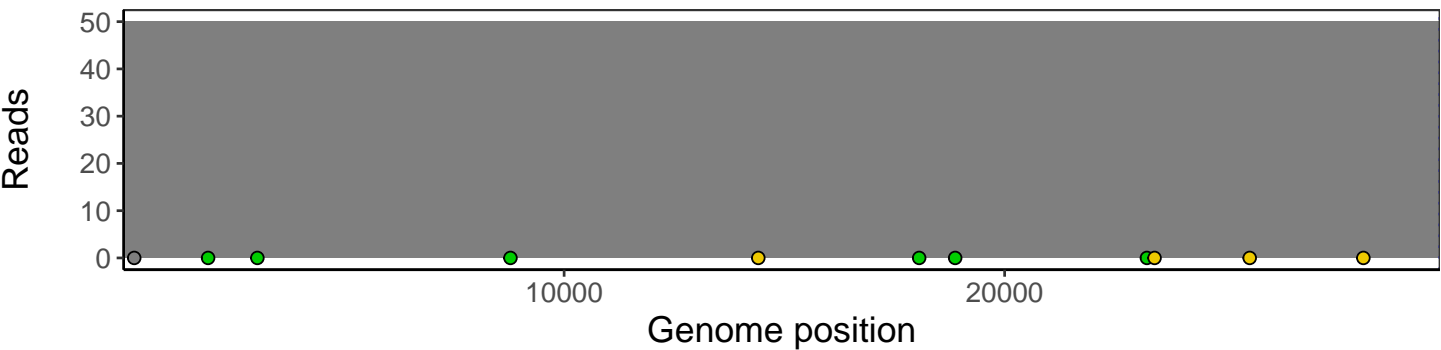
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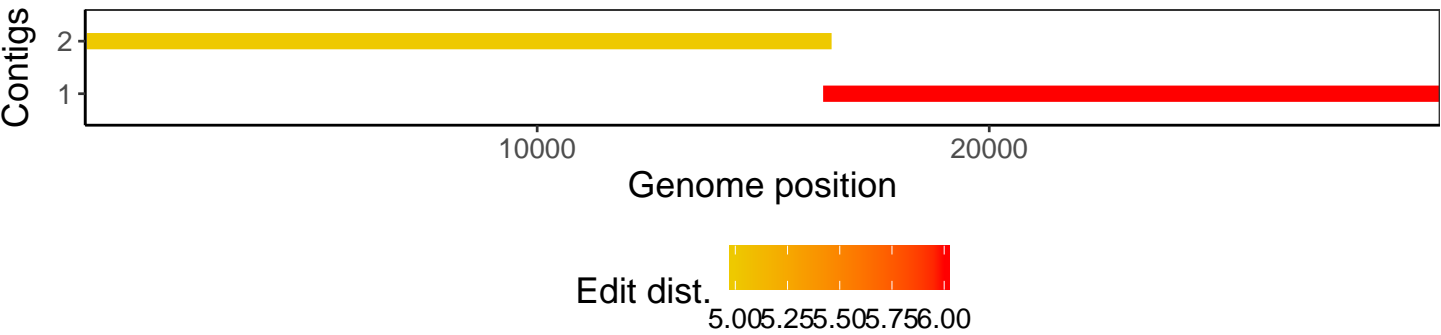
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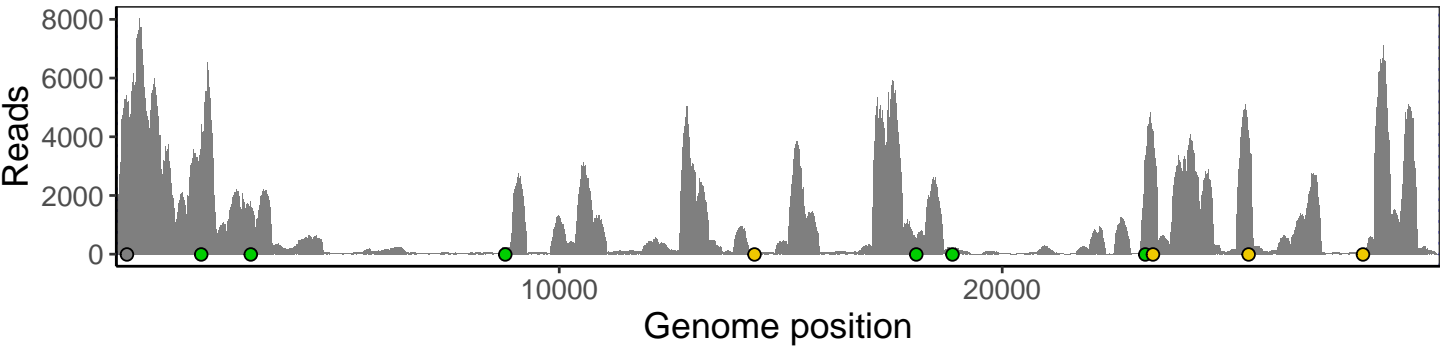
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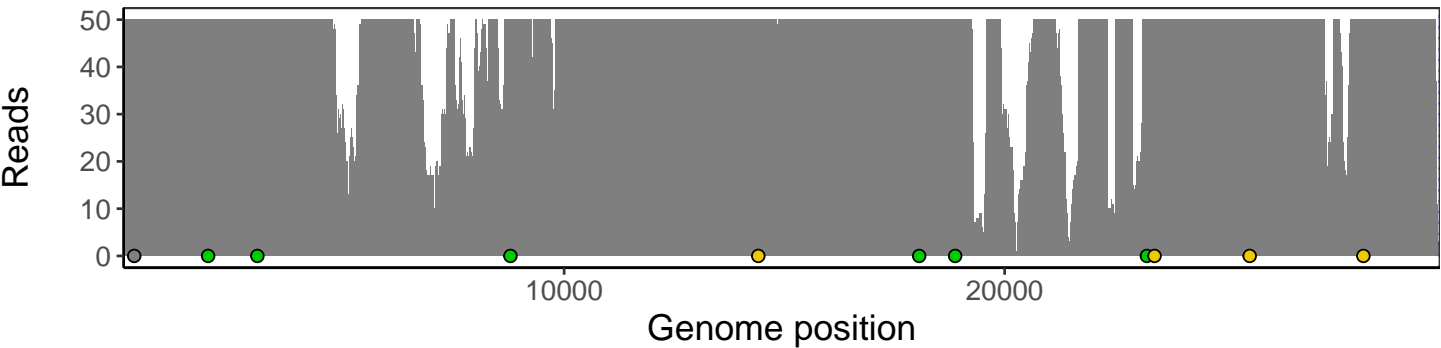
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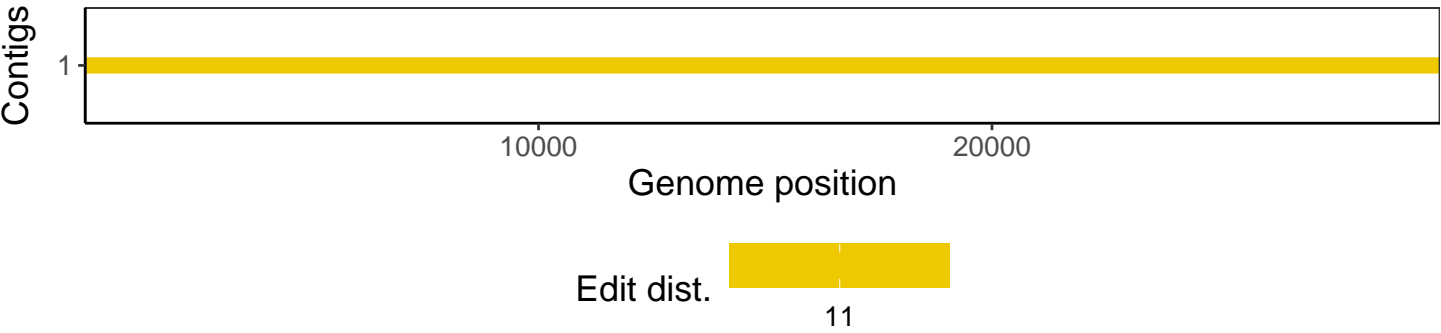
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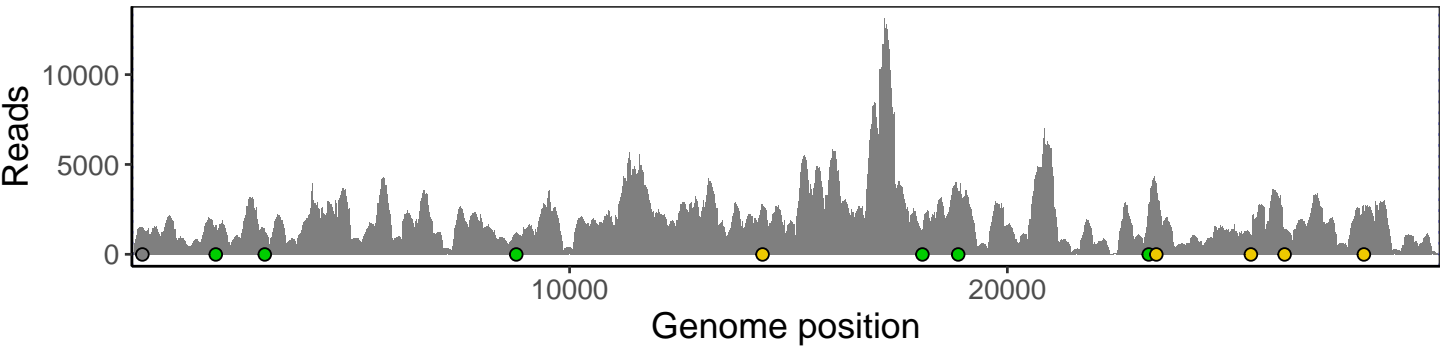
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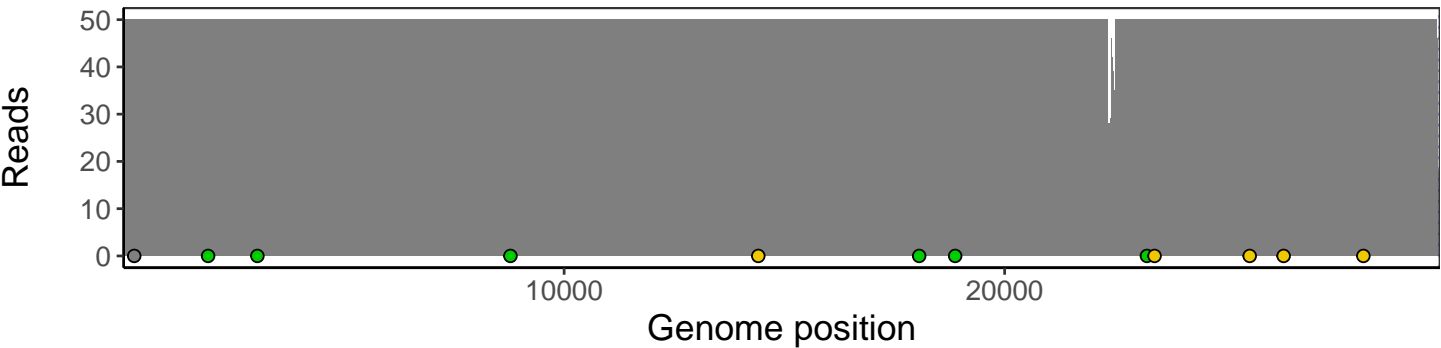
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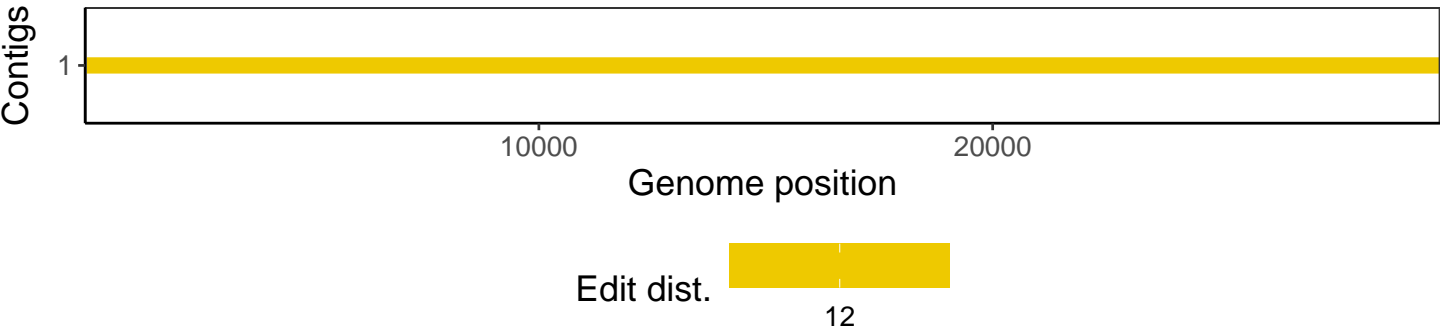
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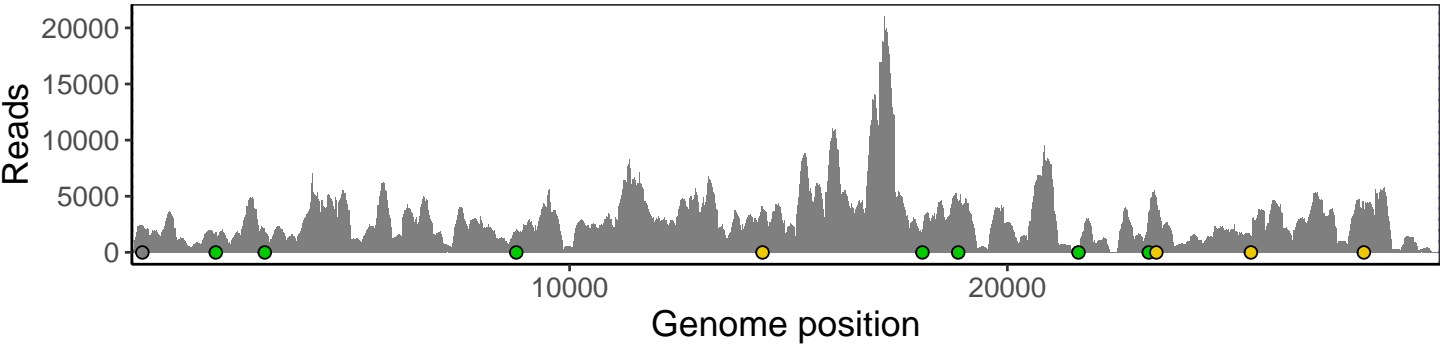
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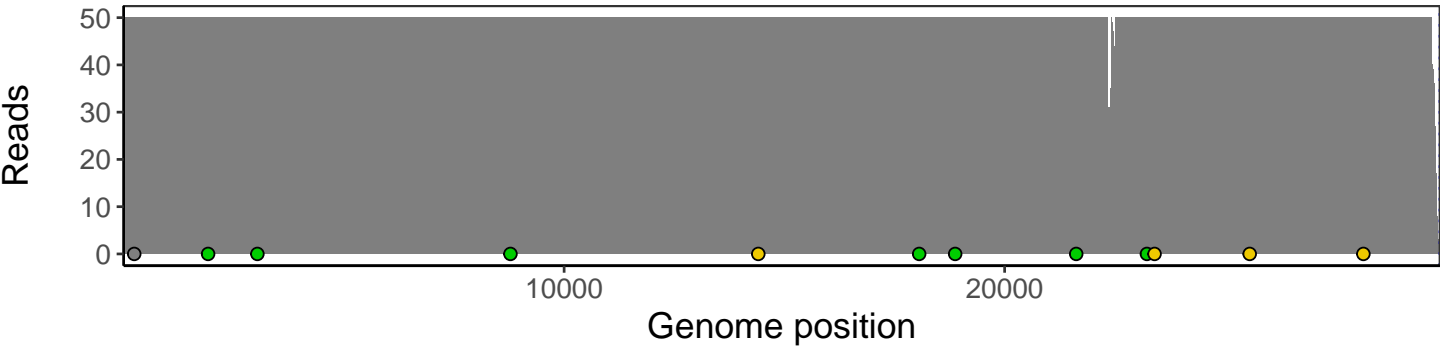
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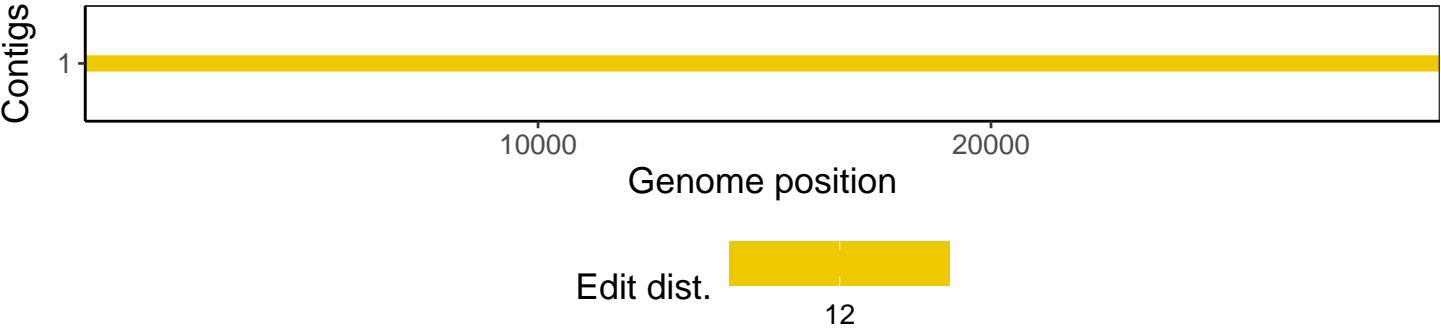
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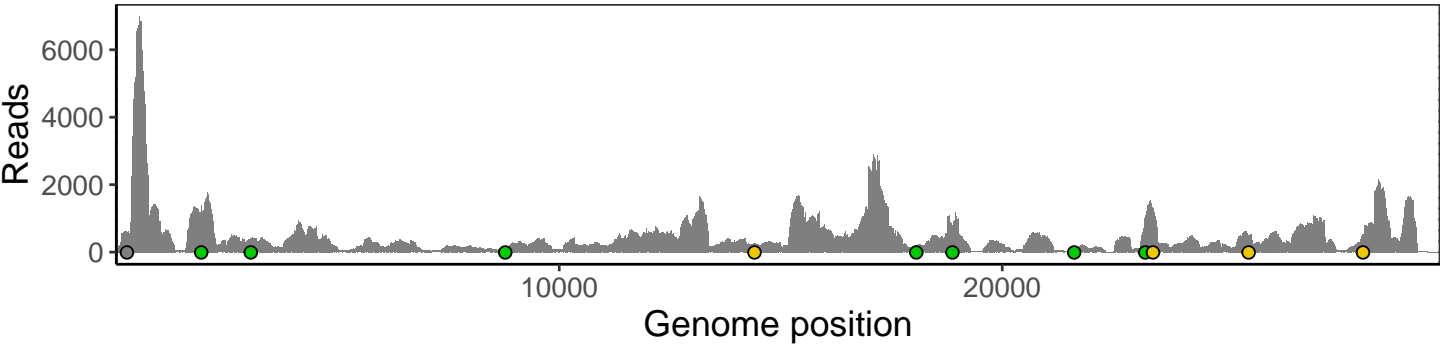
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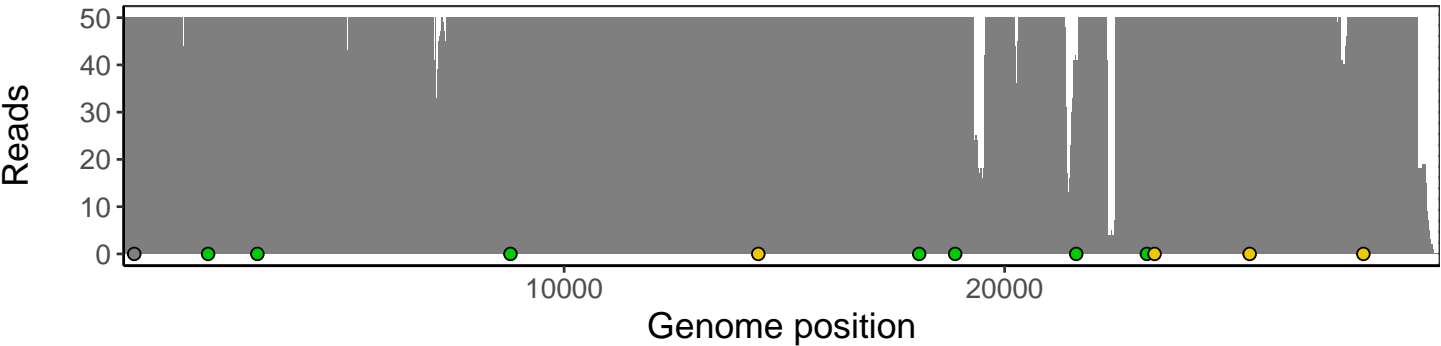
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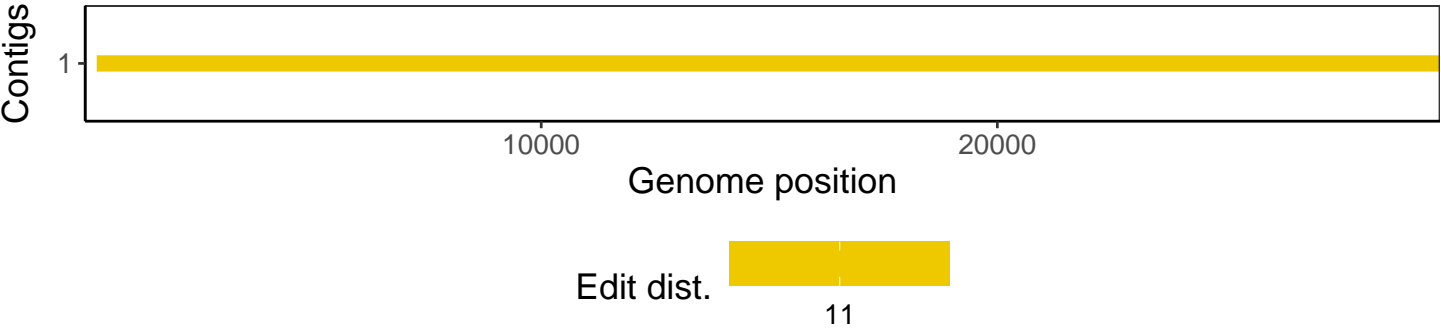
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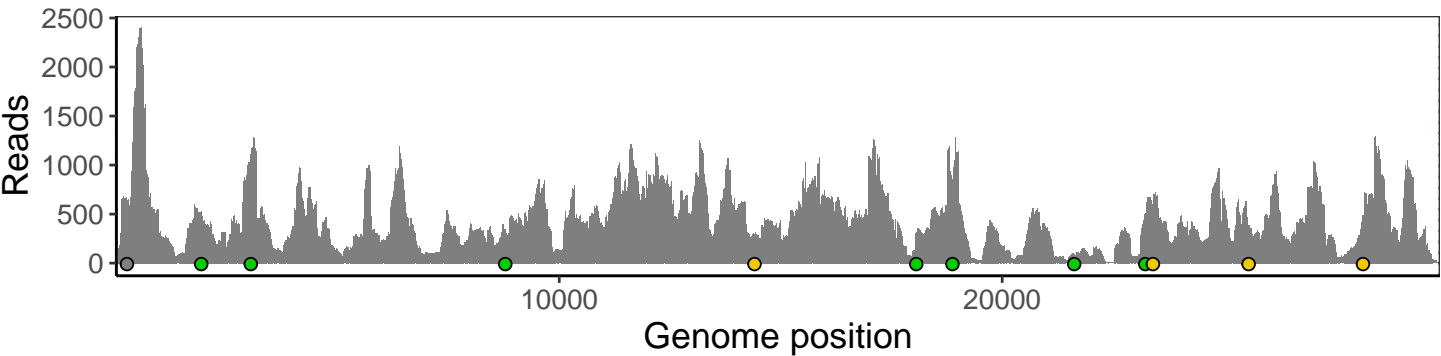
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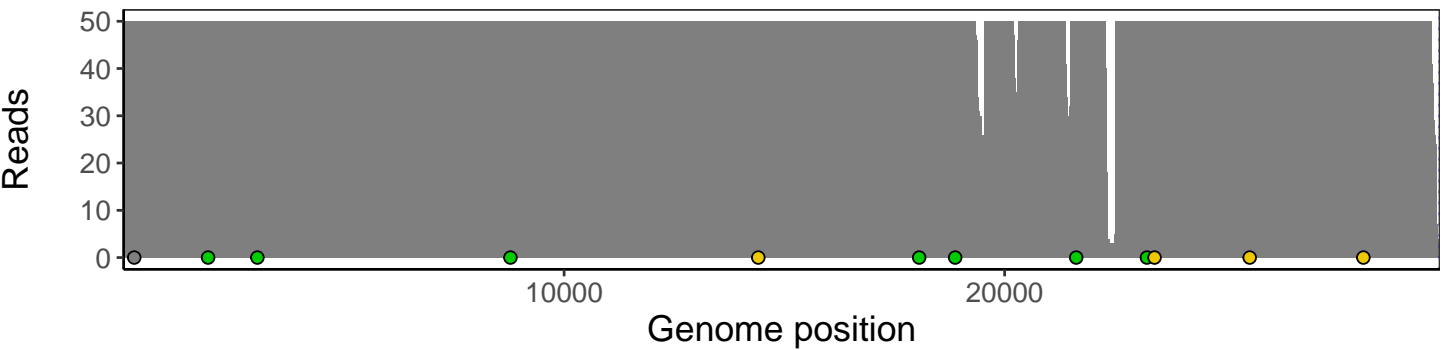
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