

# COVID-19 subject 228

2020-11-30

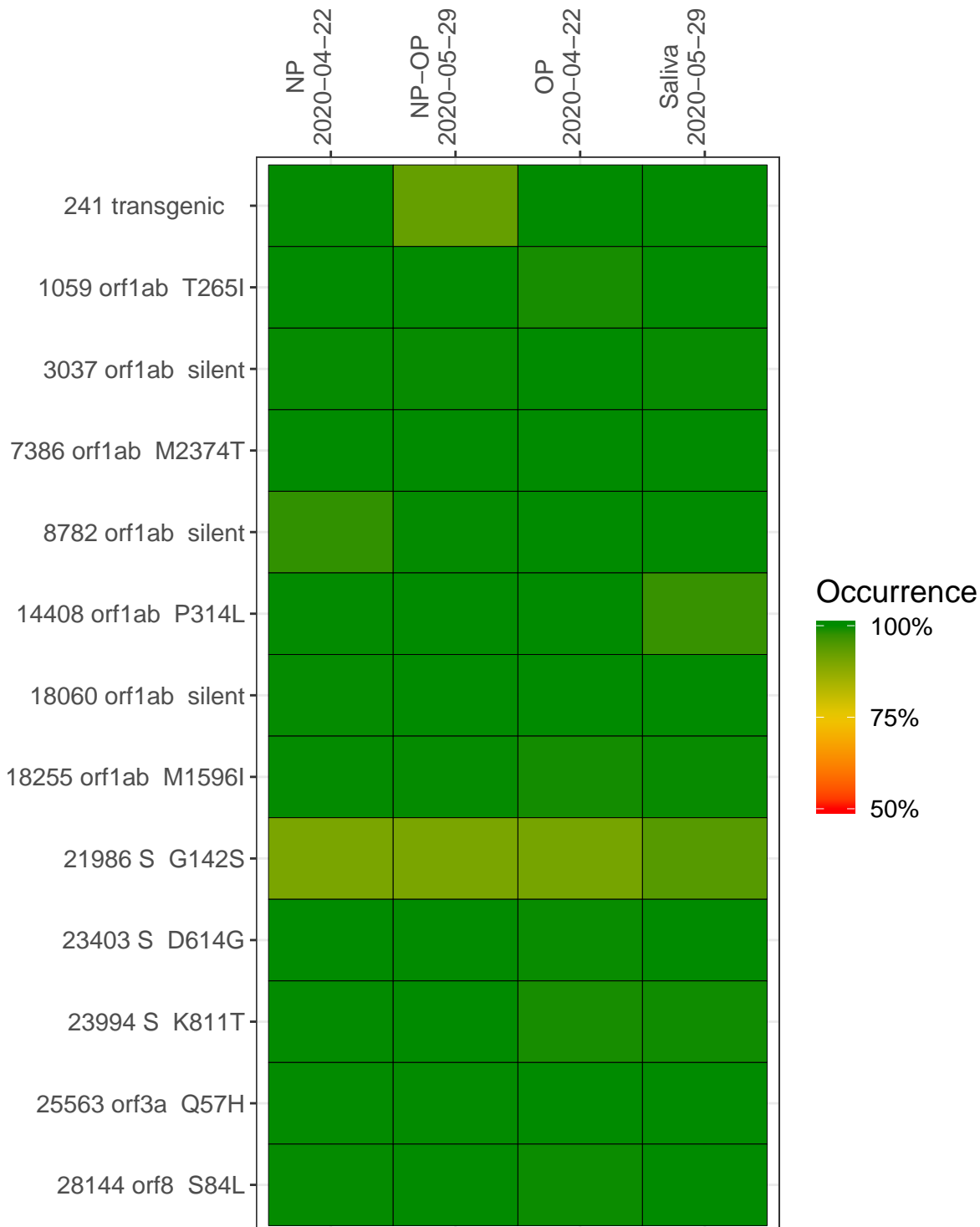
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found ([here](#)).

Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0021	composite	NA	NP	2020-04-22	29.82	99.8%	99.8%
VSP0022	composite	NA	OP	2020-04-22	29.68	99.8%	98.8%
VSP0187	composite	NA	ETA	2020-05-29	NA	NA	NA
VSP0188	composite	NA	NP-OP	2020-05-29	29.90	99.8%	99.8%
VSP0021-1m	single experiment	NA	NP	2020-04-22	29.82	99.8%	99.7%
VSP0021-2	single experiment	1.10e+04	NP	2020-04-22	29.82	99.8%	99.8%
VSP0022-1a	single experiment	2.68e+05	OP	2020-04-22	1.75	78.3%	37.7%
VSP0022-2	single experiment	1.34e+06	OP	2020-04-22	0.24	6.2%	0.0%
VSP0022-3	single experiment	1.34e+06	OP	2020-04-22	29.68	99.8%	98.8%
VSP0187-1	single experiment	6.02e+01	ETA	2020-05-29	NA	NA	NA
VSP0187-2	single experiment	3.01e+02	ETA	2020-05-29	NA	NA	NA
VSP0188-1	single experiment	2.04e+03	NP-OP	2020-05-29	9.60	93.7%	93.5%
VSP0188-2	single experiment	1.02e+04	NP-OP	2020-05-29	22.61	99.1%	99.1%
VSP0188-3	single experiment	1.02e+04	NP-OP	2020-05-29	29.87	99.8%	99.8%
VSP0189-1	single experiment	8.51e+04	Saliva	2020-05-29	29.82	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 2020-04-22		NP-OP 2020-05-29			OP 2020-04-22		Saliva 2020-05-2	
241 transgenic	655	3341	878	2357	2035	6		396	497
1059 orf1ab T265I	486	1348	998	957	1255	2		153	293
3037 orf1ab silent	695	2447	763	1077	2758			517	686
7386 orf1ab M2374T	364	1260	1370	170	547	4		257	311
8782 orf1ab silent	322	2672	867	722	3292			239	318
14408 orf1ab P314L	1024	5052	1197	3334	3058	4		161	1315
18060 orf1ab silent	622	2638	1364	1003	2850			197	471
18255 orf1ab M1596I	555	3751	1433	1043	3833			200	568
21986 S G142S	261	577	208	370	509			53	249
23403 S D614G	622	4502	5604	7968	11305	33		501	1354
23994 S K811T	667	1963	1406	1117	830	9	1	292	263
25563 orf3a Q57H	421	3511	1679	2091	3061	4		311	981
28144 orf8 S84L	655	4436	1815	2356	1768	16		349	550
	VSP0021-1m	VSP0021-2	VSP0188-1	VSP0188-2	VSP0188-3	VSP0022-1a	VSP0022-2	VSP0022-3	VSP0189-1

Base change

Expected

A

T

C

G

N

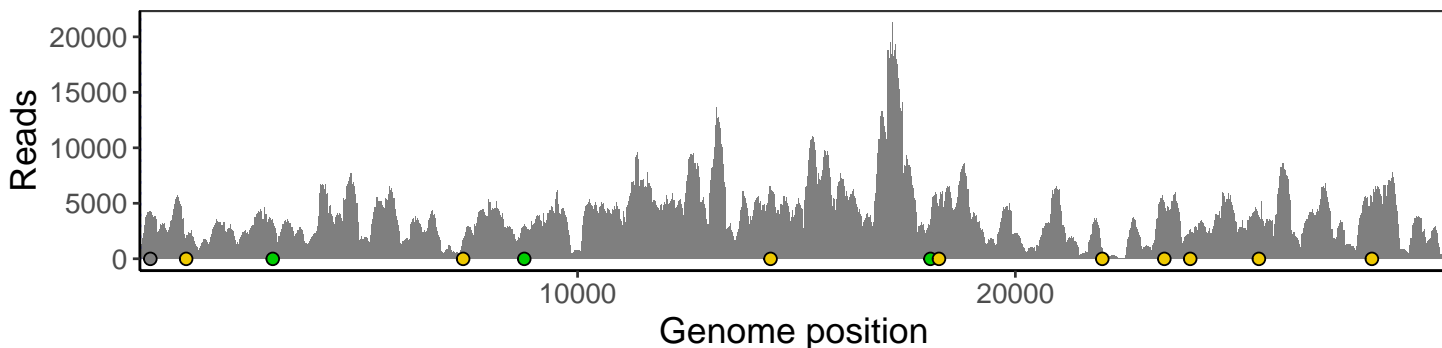
Ins/Del

No data

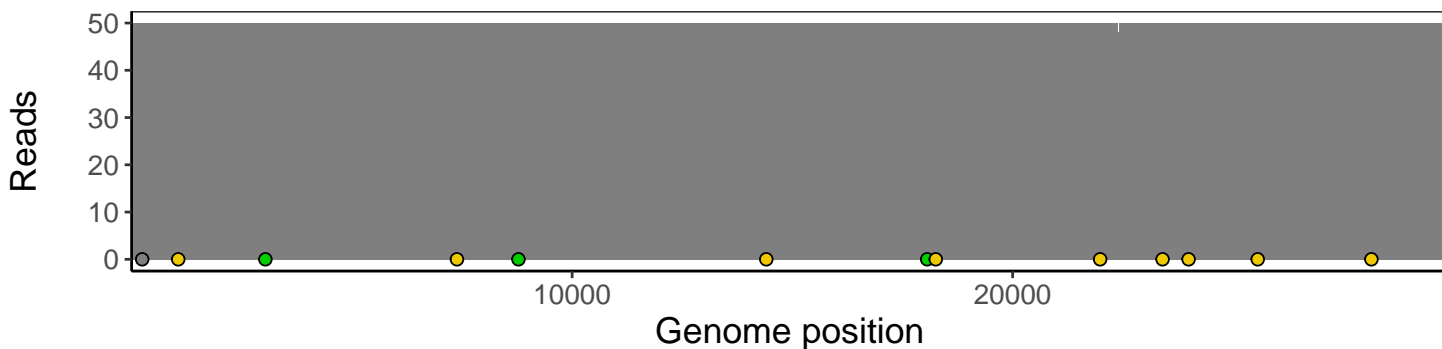
## Analyses of individual experiments and composite results.

VSP0021 | 2020-04-22 | NP | 228n | composite result

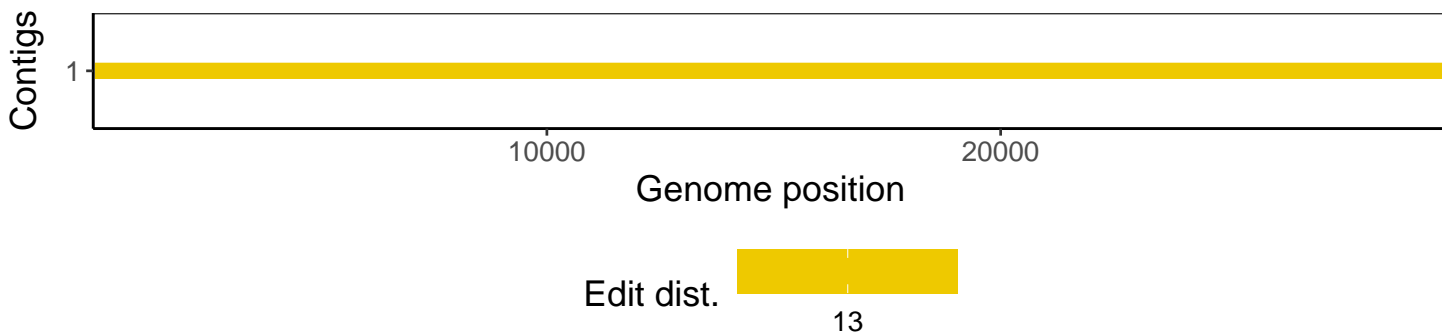
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



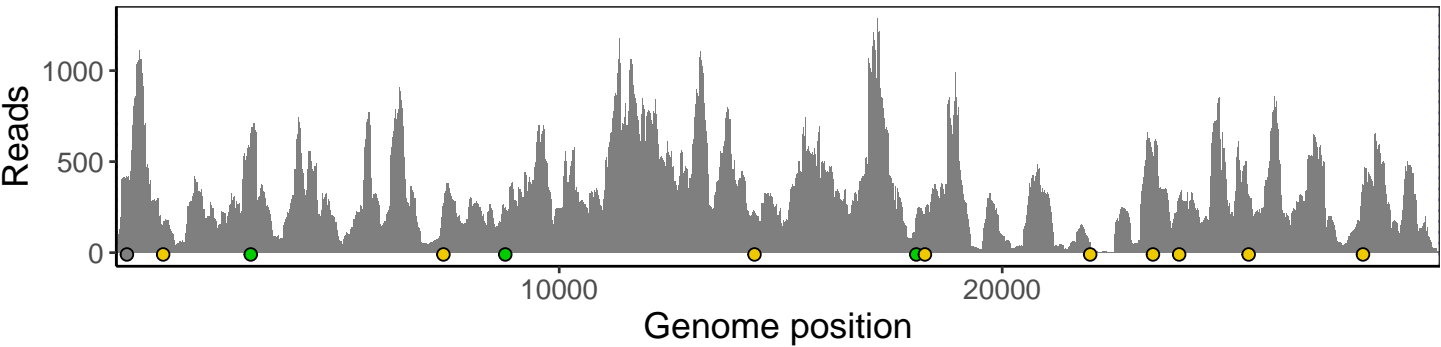
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



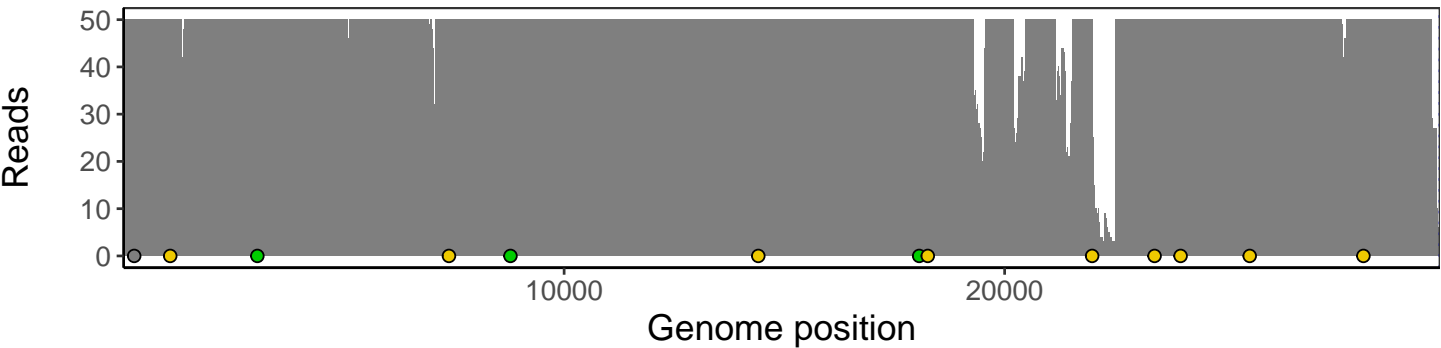
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



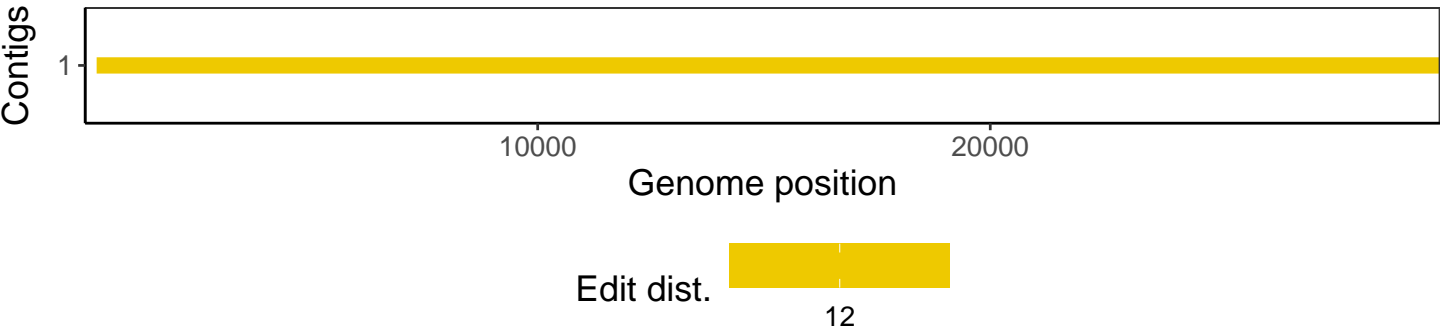
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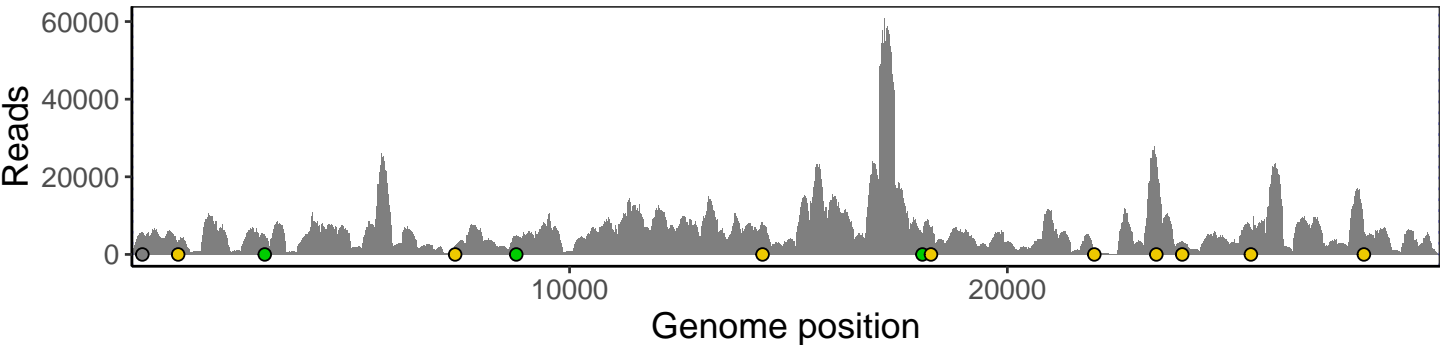


VSP0187 | 2020-05-29 | ETA | 228e-q | composite result

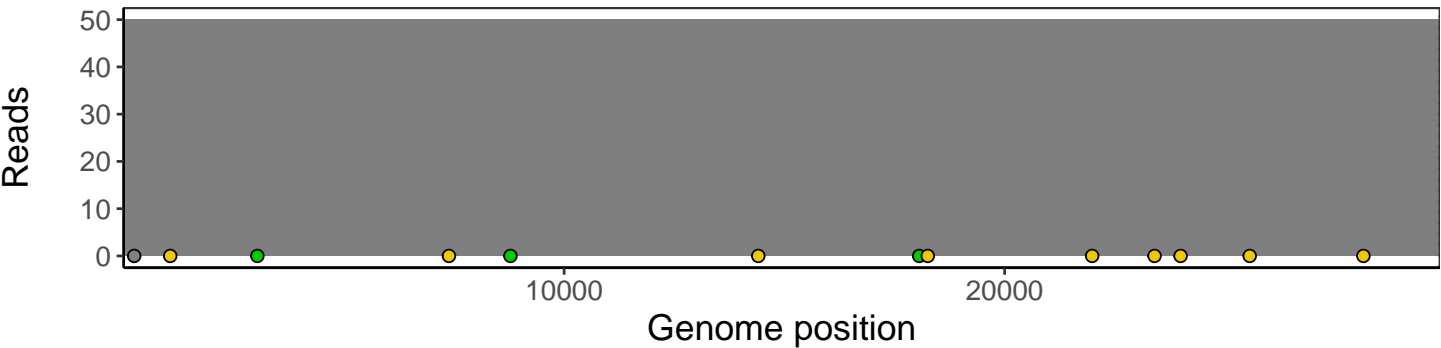
No pileup data available.

No contig data available.

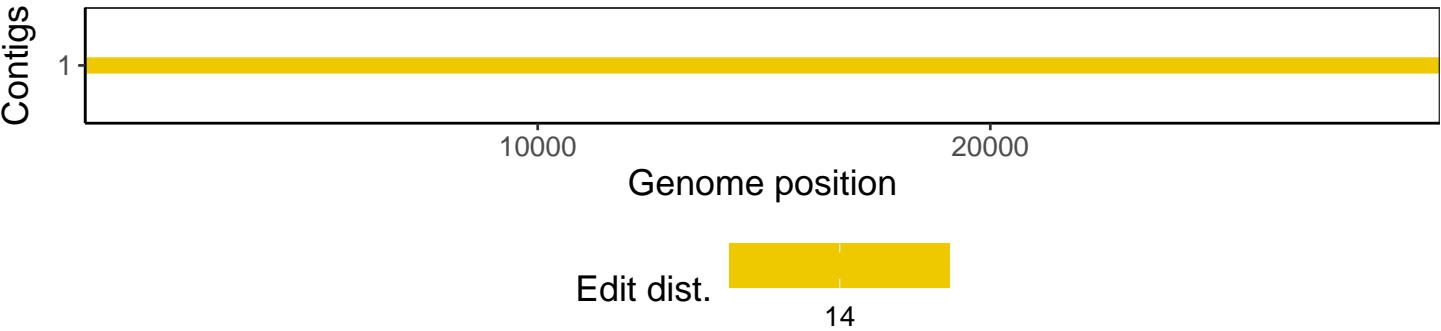
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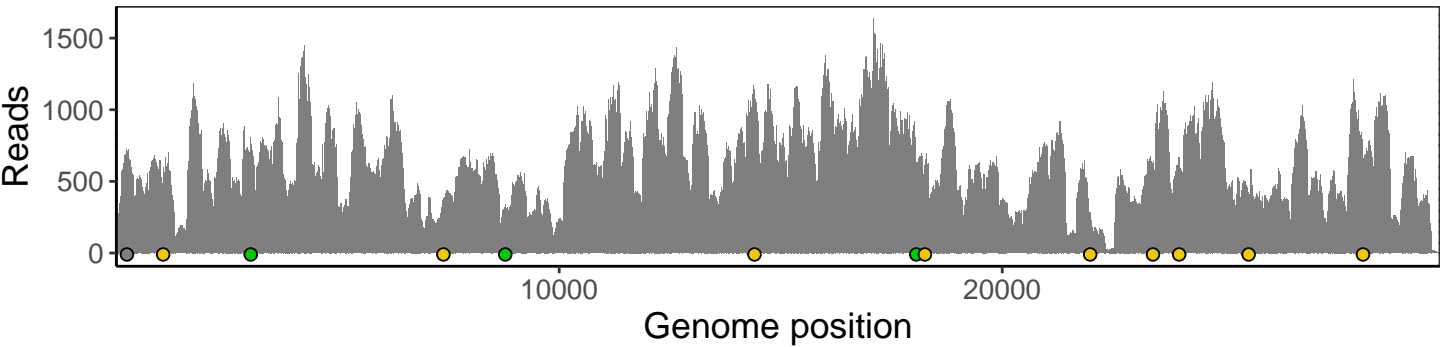
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



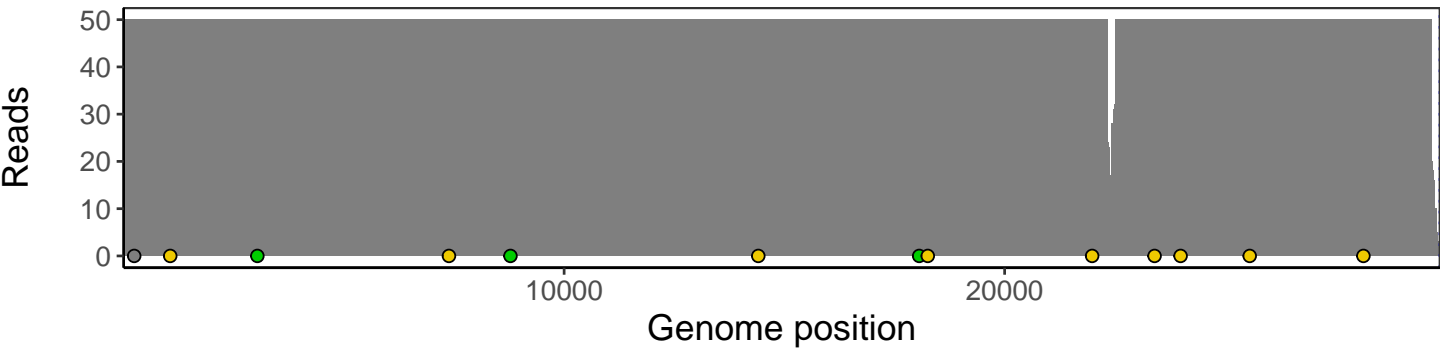
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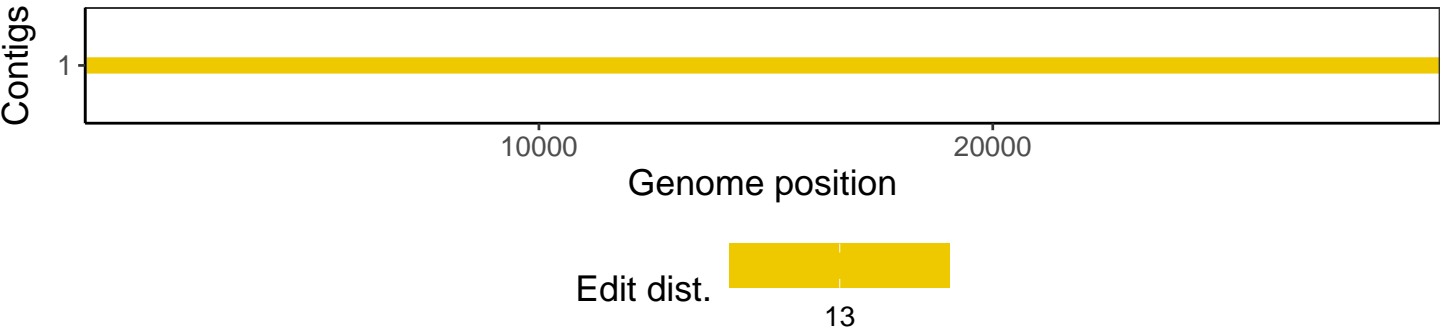
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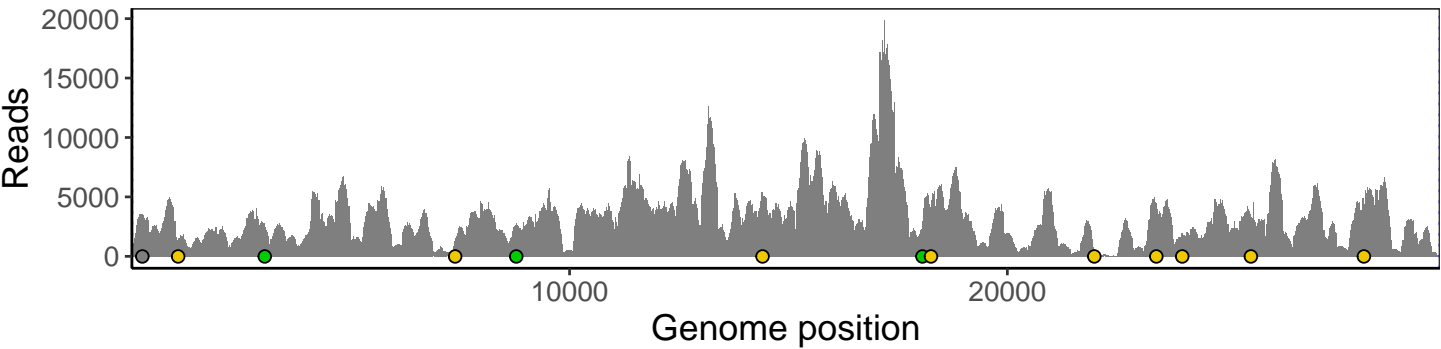


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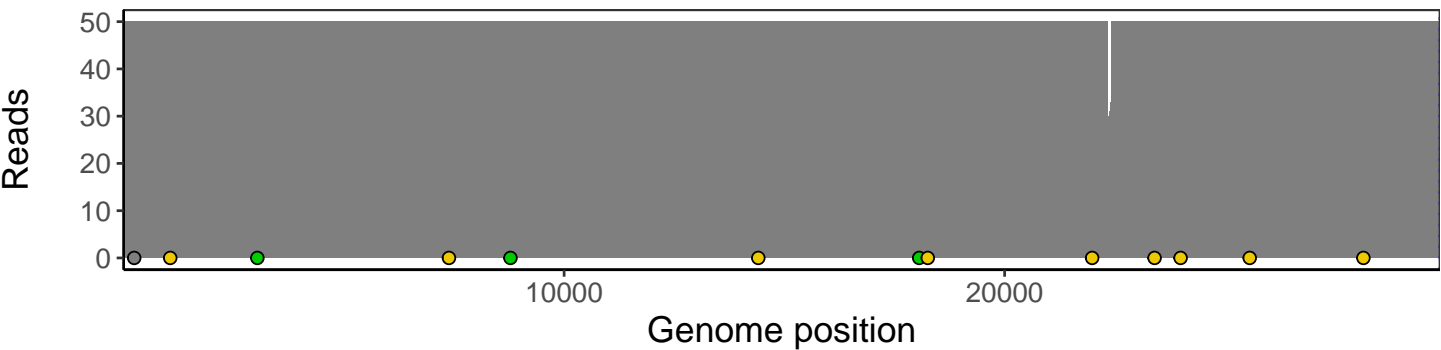




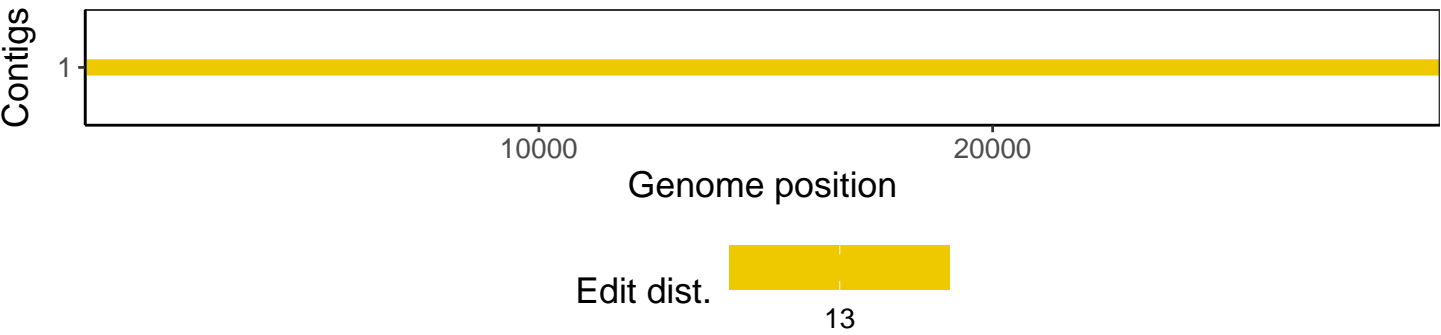
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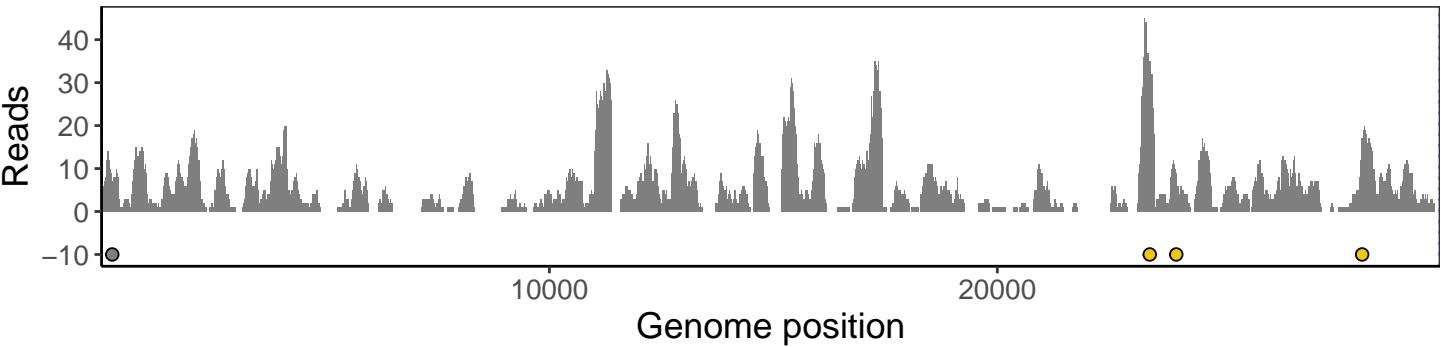
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



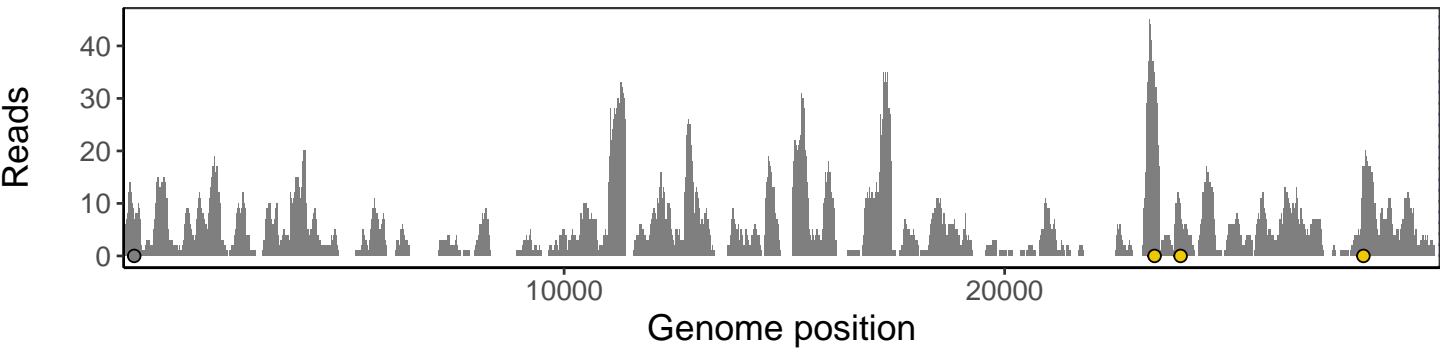
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



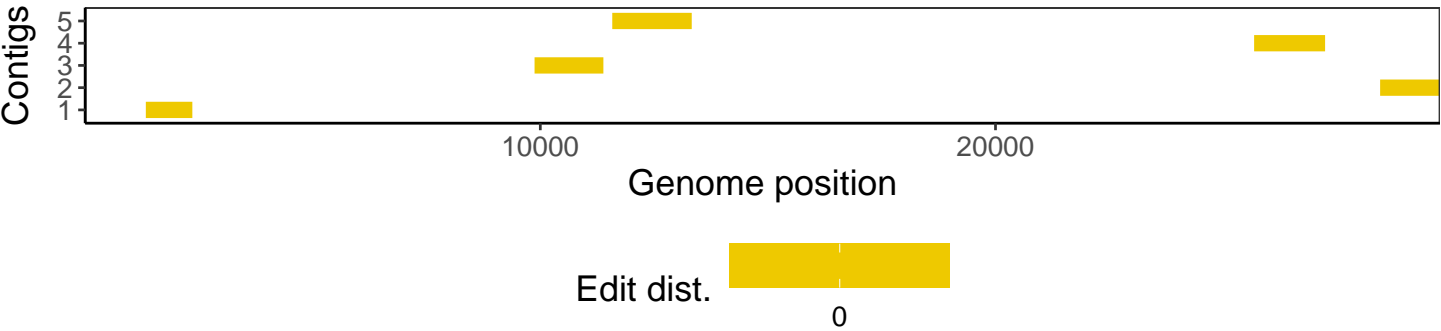
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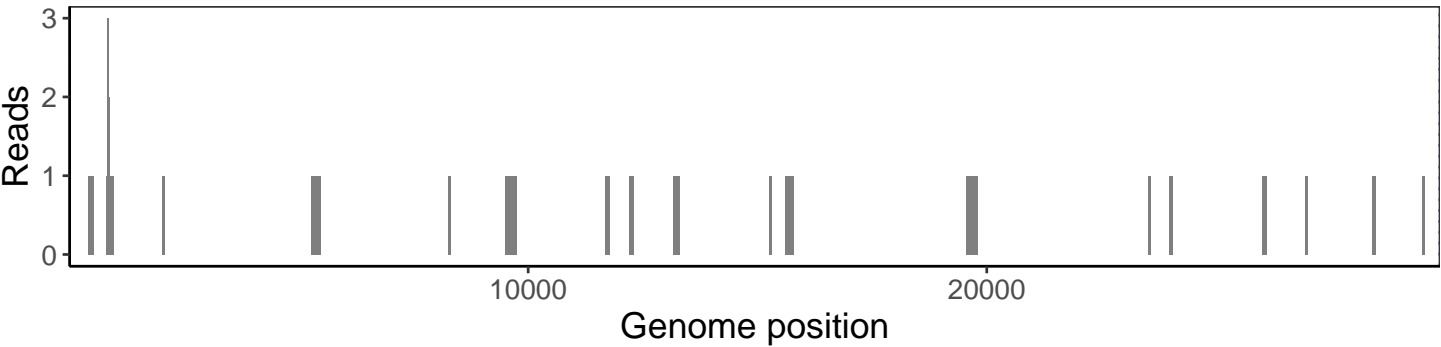
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



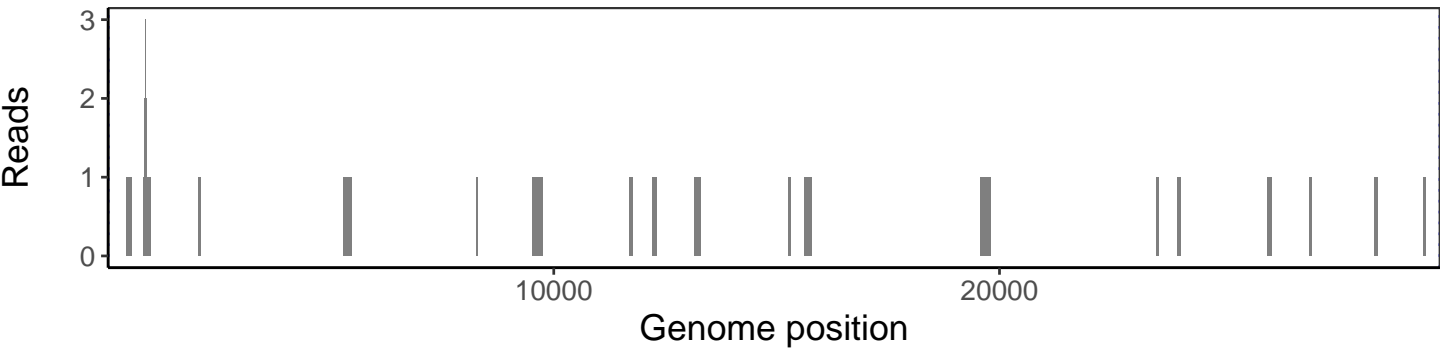
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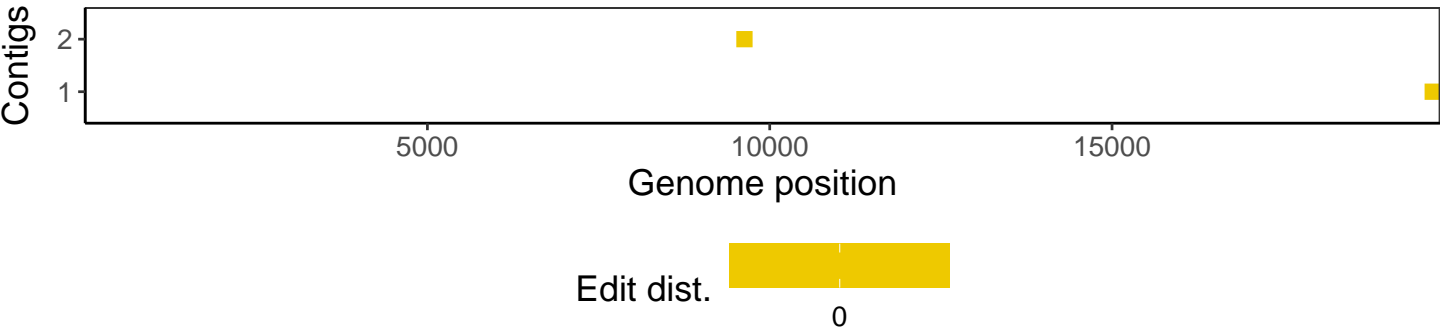
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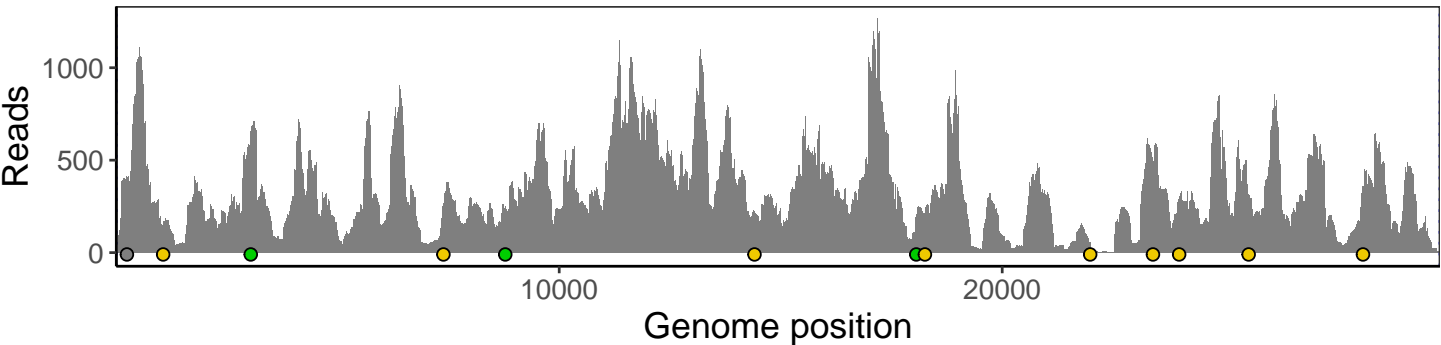
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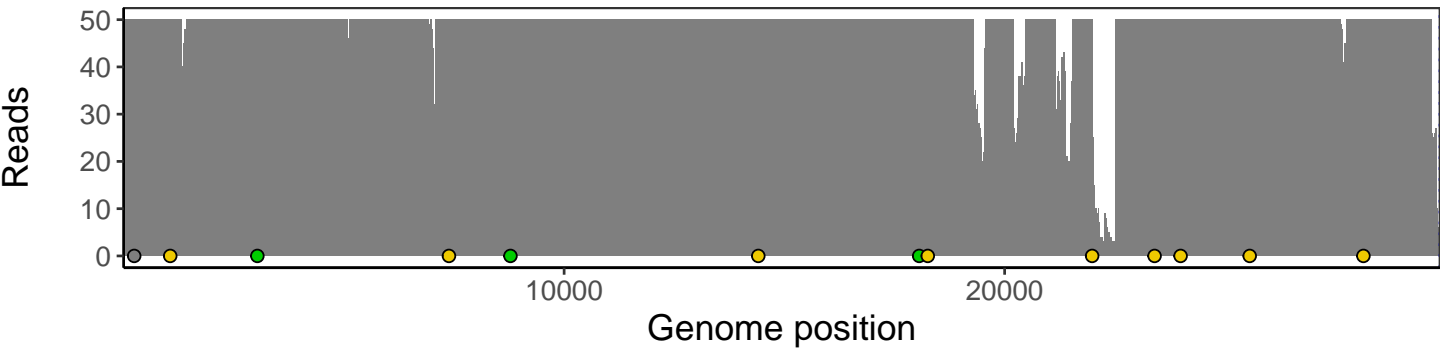
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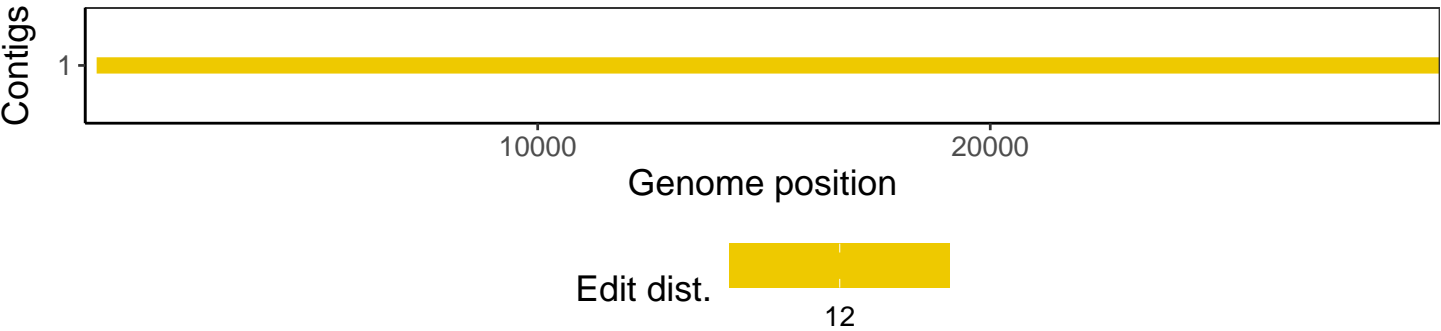
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Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



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



VSP0187-1 | 2020-05-29 | ETA | 228e-q | 60.2 genomes | single experiment

No pileup data available.

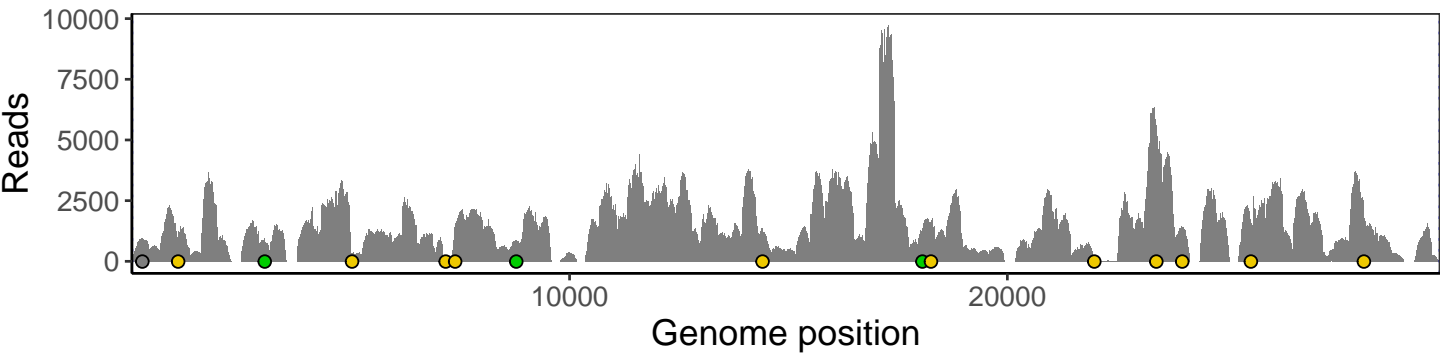
No contig data available.

VSP0187-2 | 2020-05-29 | ETA | 228e-q | 301 genomes | single experiment

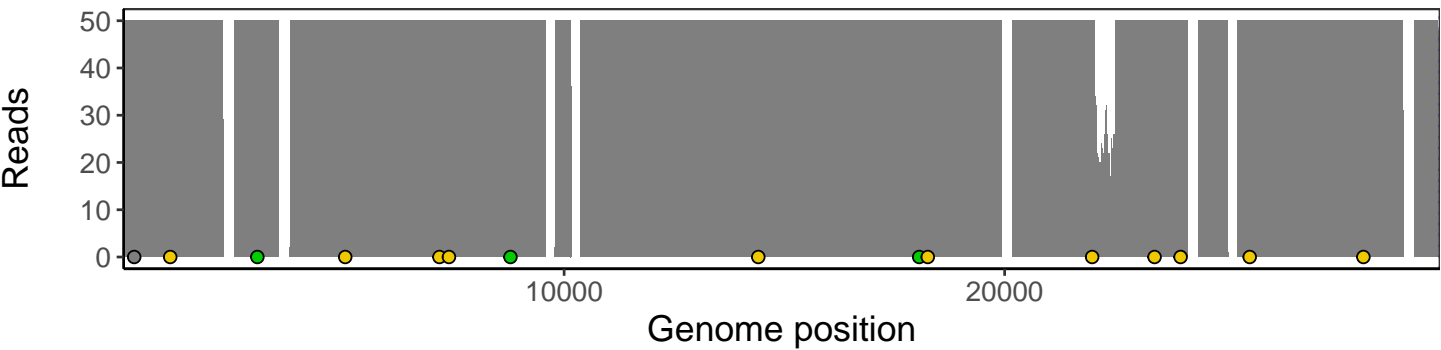
No pileup data available.

No contig data available.

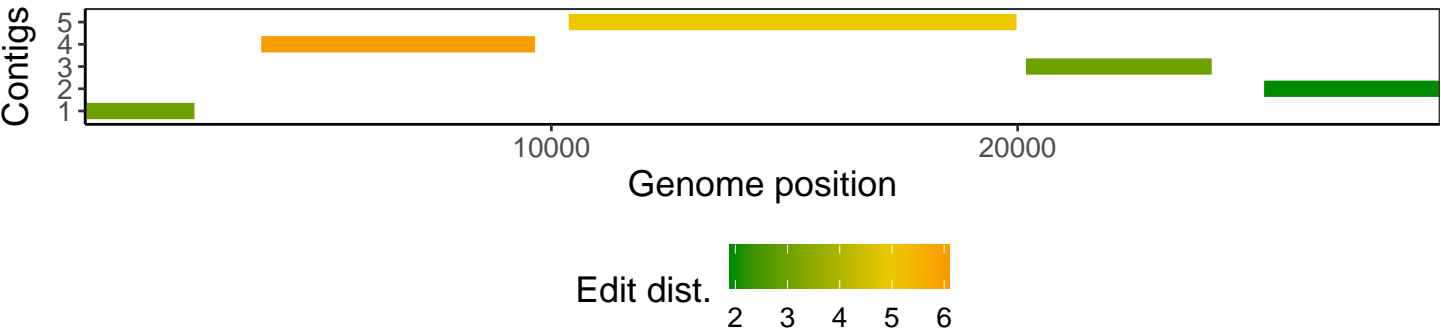
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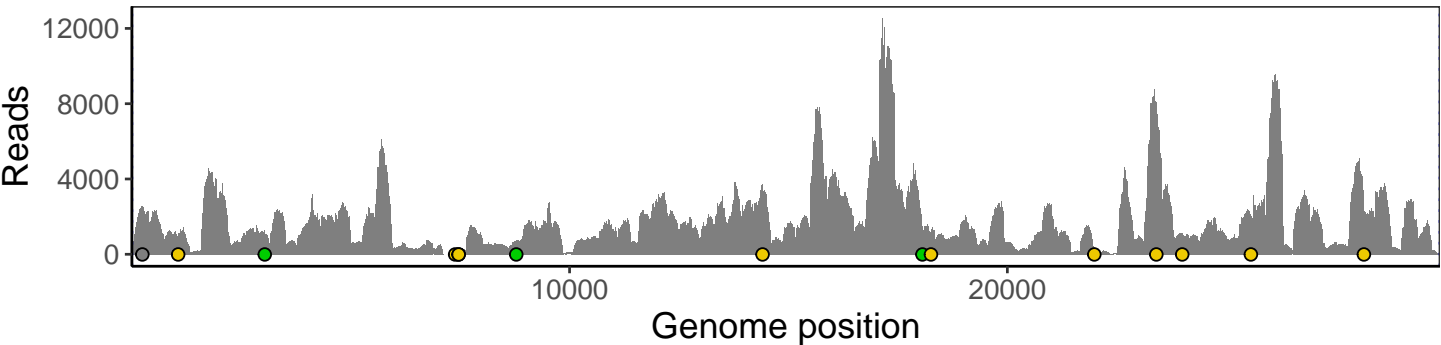
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



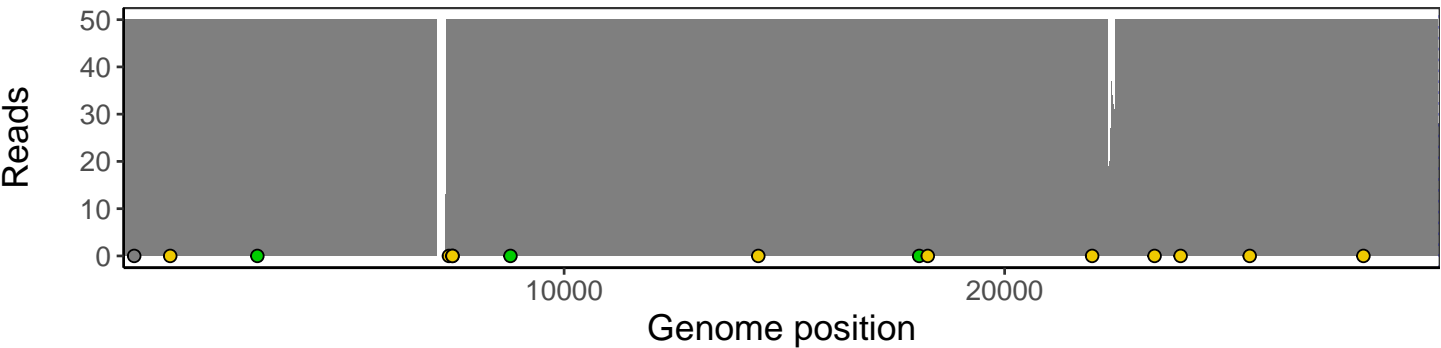
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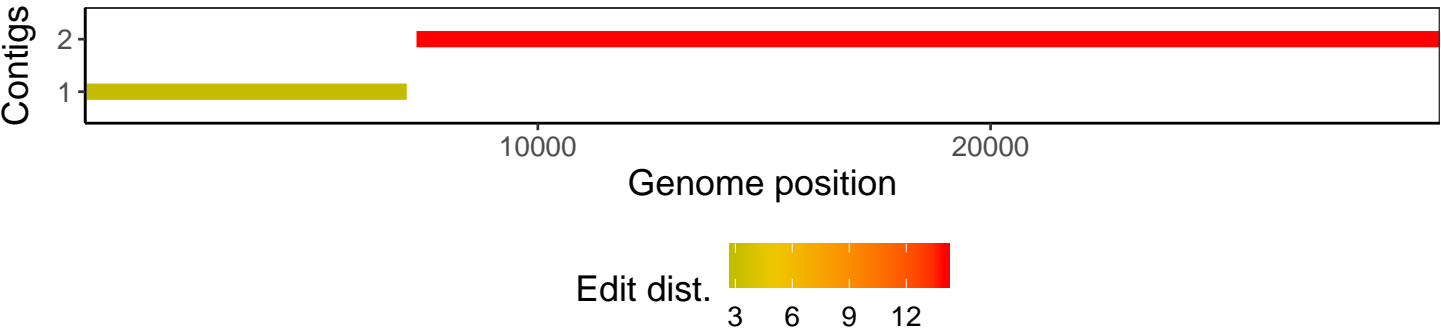
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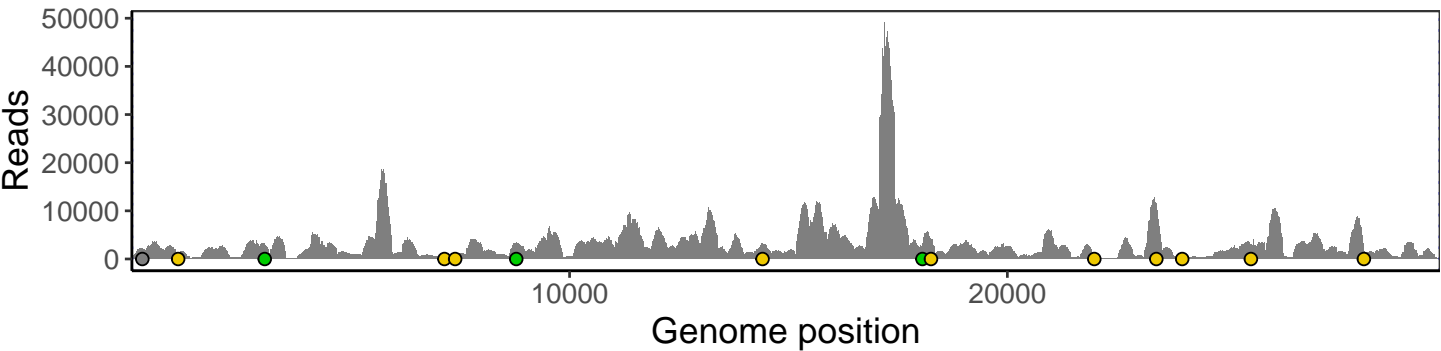


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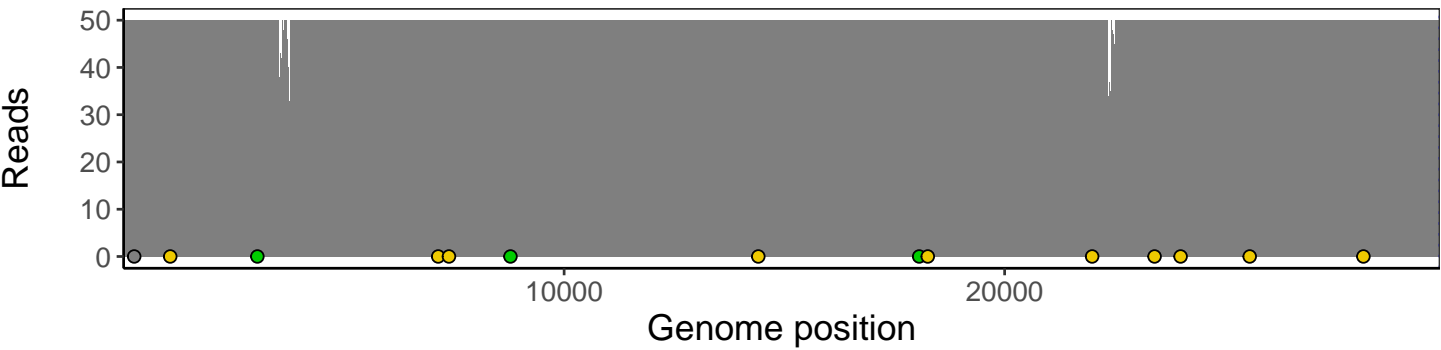




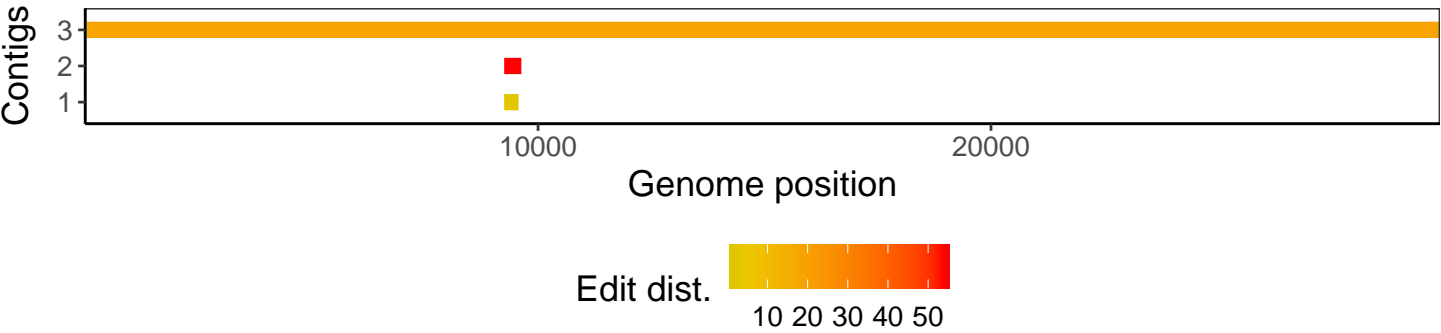
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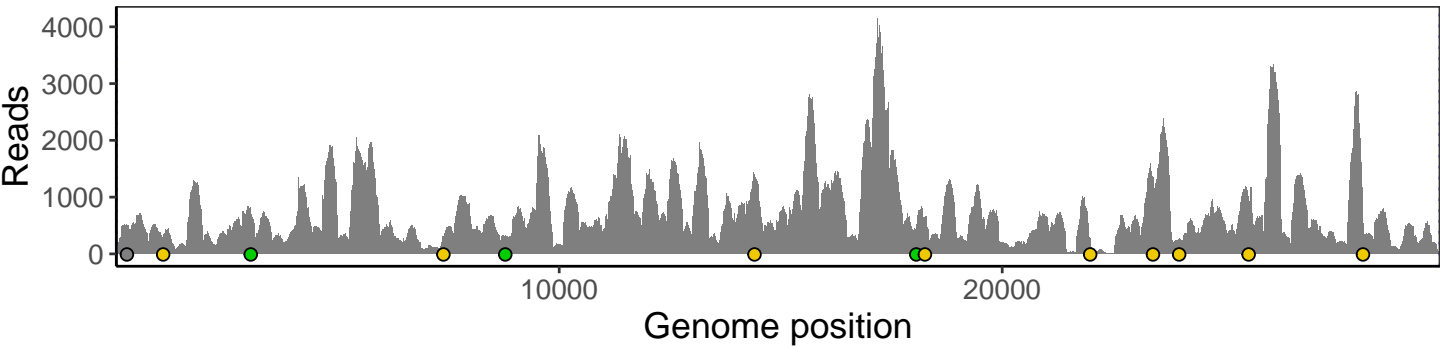
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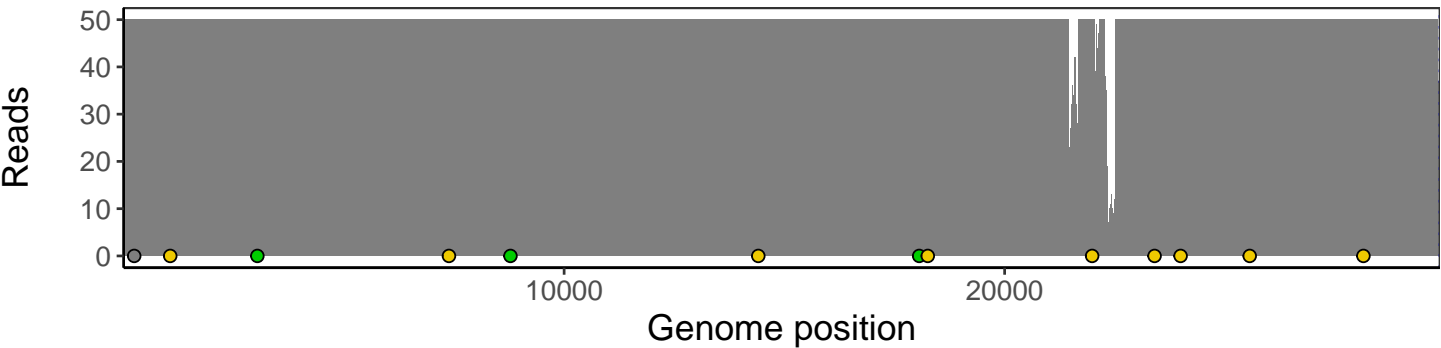
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