

COVID-19 subject 242

2020-10-23

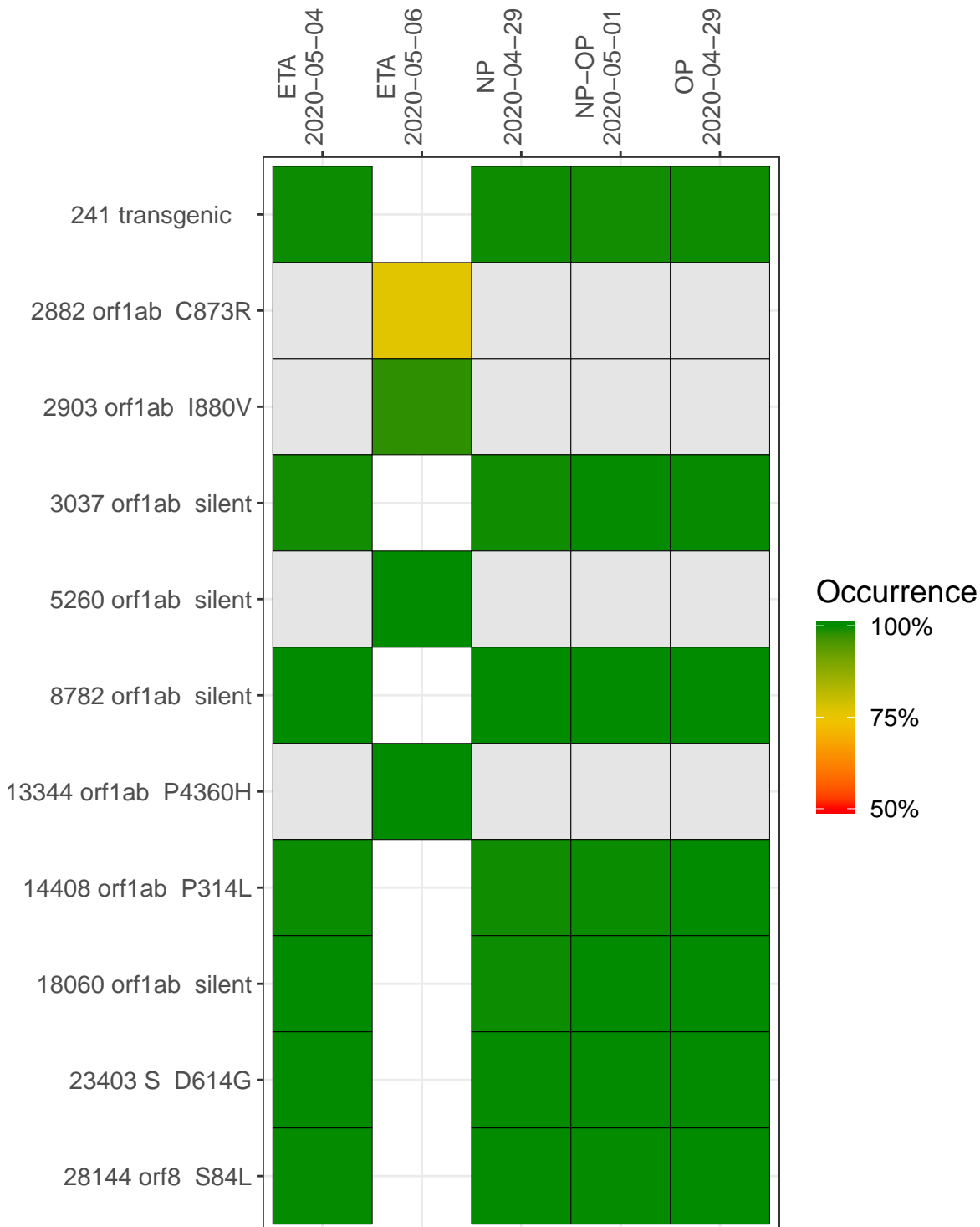
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found ([here](#)).

Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0044	composite	NA	NP	2020-04-29	29.88	99.9%	99.8%
VSP0085	composite	NA	ETA	2020-05-06	NA	6.4%	1.8%
VSP0044-1m	single experiment	NA	NP	2020-04-29	29.84	99.8%	99.7%
VSP0044-2	single experiment	1.975e+05	NP	2020-04-29	16.60	99.9%	99.7%
VSP0045-1	single experiment	6.670e+02	OP	2020-04-29	29.72	99.6%	99.2%
VSP0047-1	single experiment	2.220e+05	NP-OP	2020-05-01	29.89	99.9%	99.8%
VSP0052-1	single experiment	1.420e+06	ETA	2020-05-04	29.31	99.9%	99.7%
VSP0085-1	single experiment	8.540e+00	ETA	2020-05-06	NA	6.4%	1.8%
VSP0085-2	single experiment	4.270e+01	ETA	2020-05-06	NA	NA	NA
VSP0085-3	single experiment	4.270e+01	ETA	2020-05-06	NA	NA	NA
VSP0085-4	single experiment	4.270e+01	ETA	2020-05-06	NA	NA	NA

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 2020-05-04	ETA 2020-05-06	NP 2020-04-29	NP-OP 2020-05-01	OP 2020-04-29	
241 transgenic	2118		2572	1053	1530	1227
2882 orf1ab C873R	1600	52	605	1548	884	1667
2903 orf1ab I880V	339	150	107	1778	687	1258
3037 orf1ab silent	423		93	1958	784	1312
5260 orf1ab silent	45	5	41	566	45	565
8782 orf1ab silent	283		138	582	54	956
13344 orf1ab P4360H	2531	27	1204	1112	4436	3335
14408 orf1ab P314L	478		306	442	1726	4699
18060 orf1ab silent	166		68	613	300	1205
23403 S D614G	23788		16589	632	18016	2487
28144 orf8 S84L	3026		1639	891	3157	2881
	VSP0052-1	VSP0085-1	VSP0044-1m	VSP0044-2	VSP0047-1	VSP0045-1

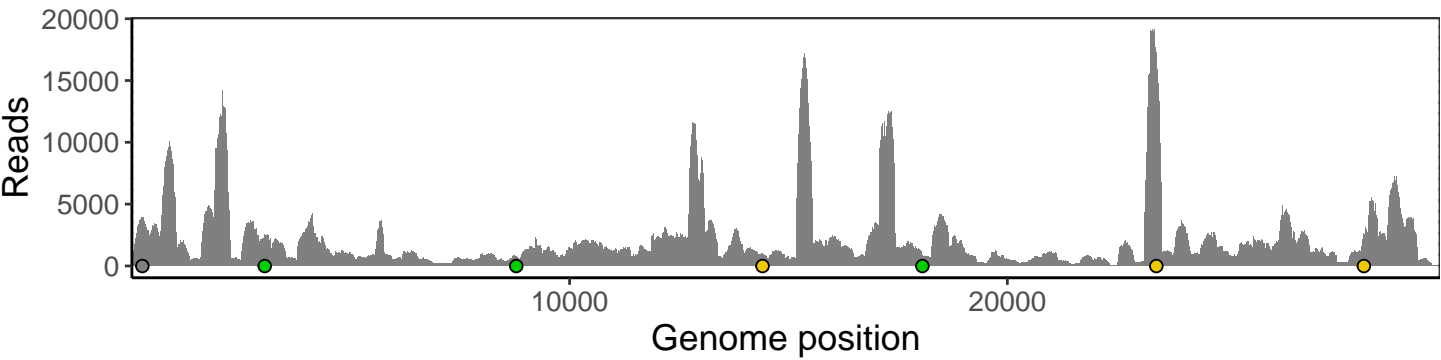
Base change

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

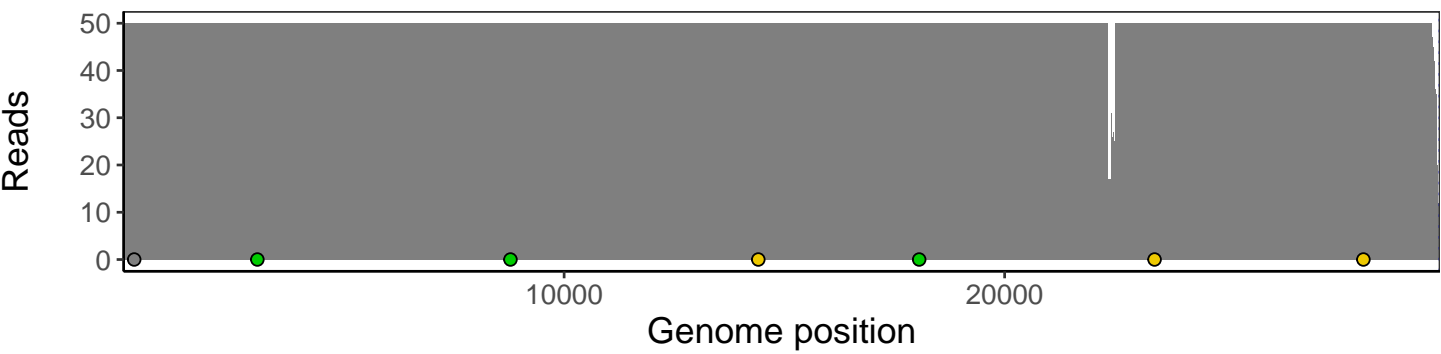
Analyses of individual experiments and composite results.

VSP0044 | 2020-04-29 | NP | 242n-tri | composite result

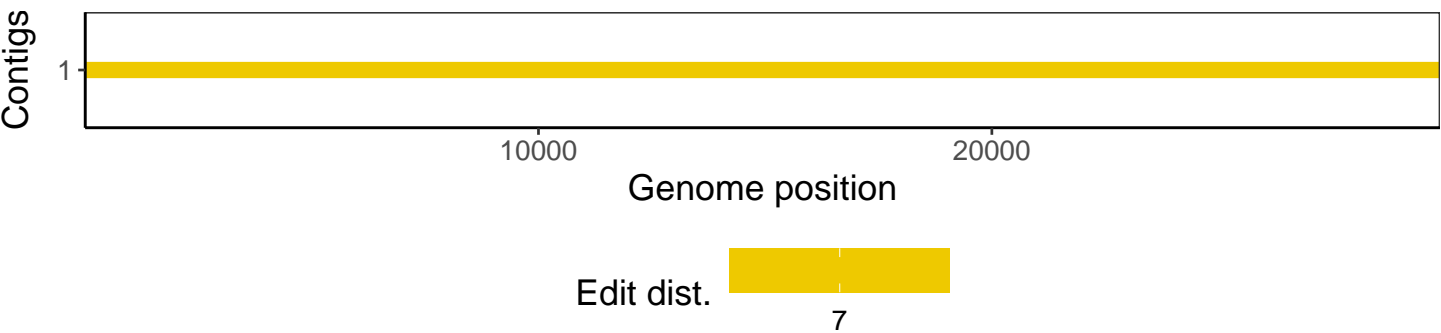
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

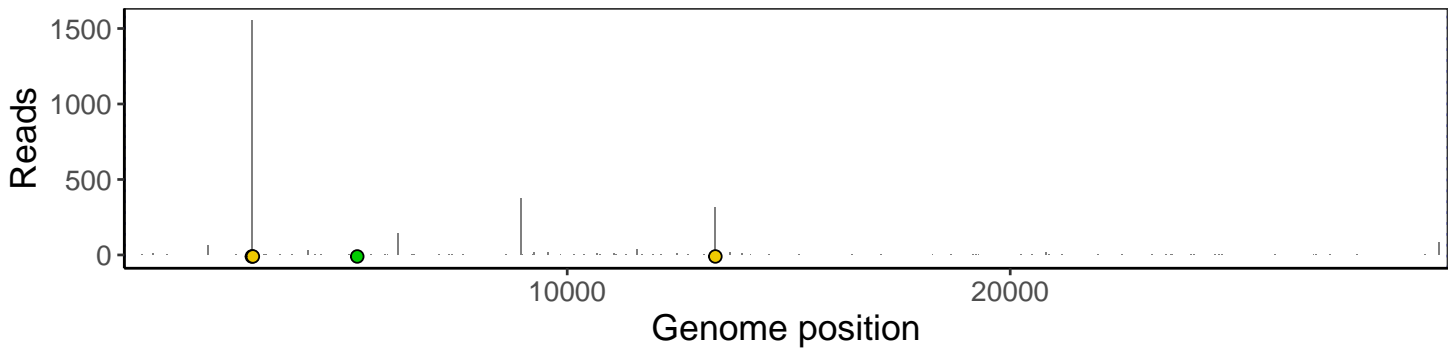


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

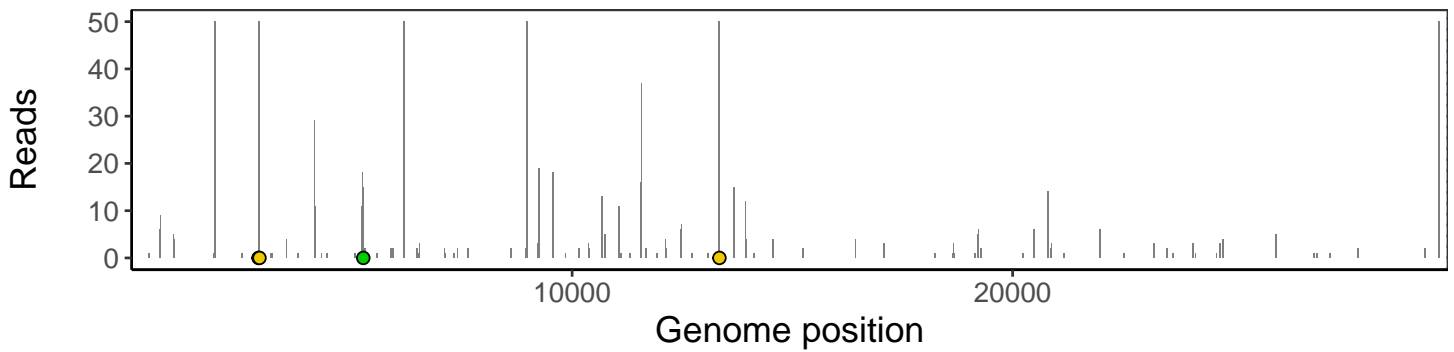


VSP0085 | 2020-05-06 | ETA | 242e-q | composite result

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.

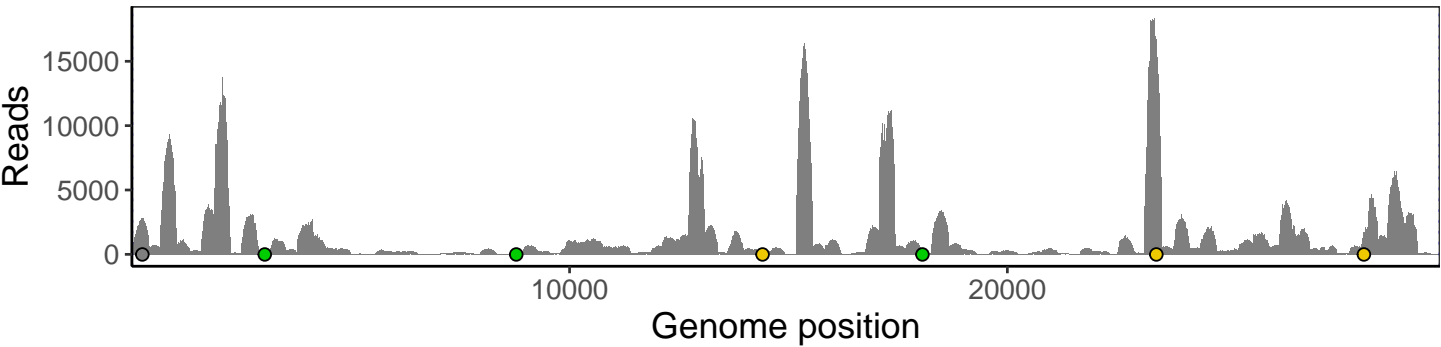


Excerpt from plot above focusing on reads coverage from 0 to 50 NT.

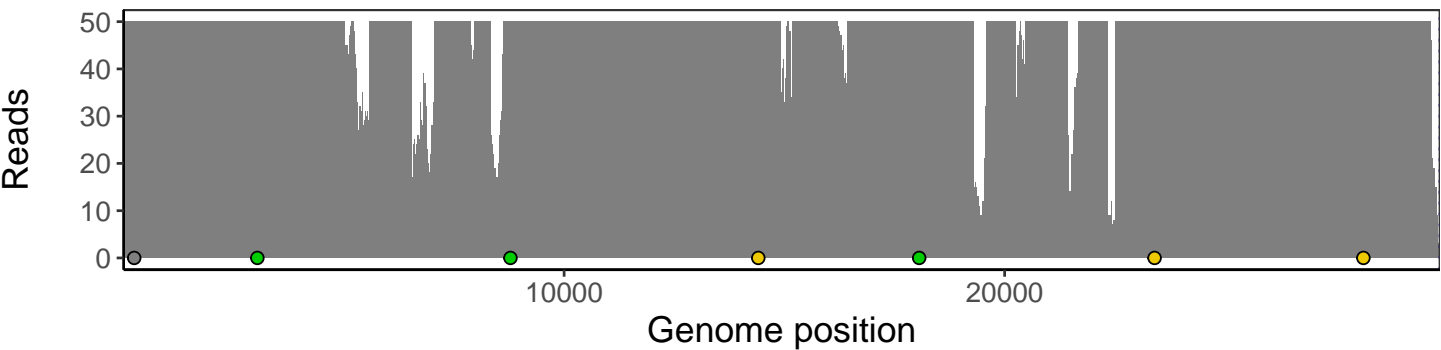


No contig data available.

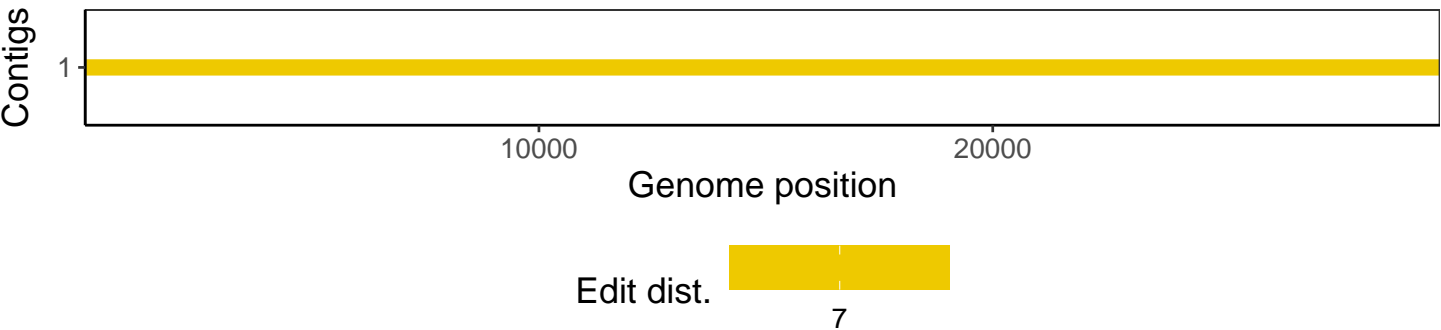
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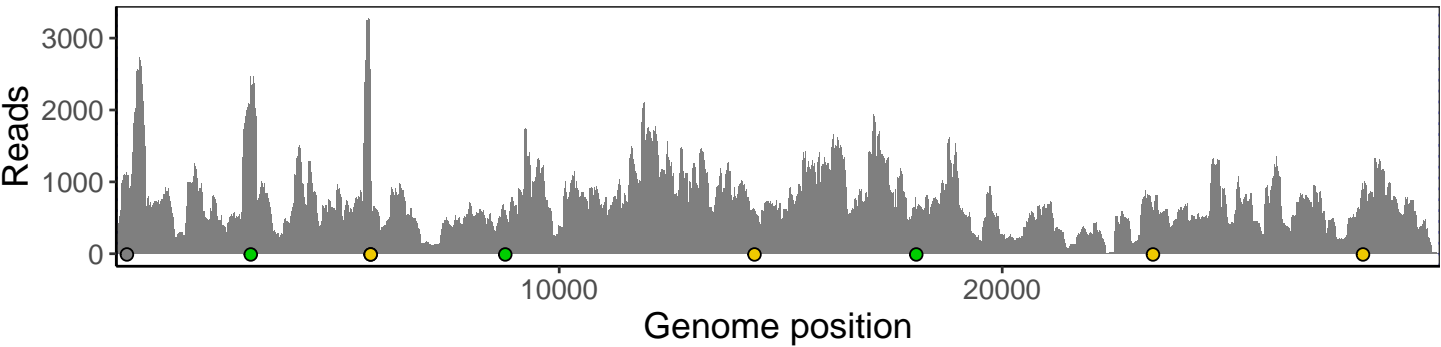
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



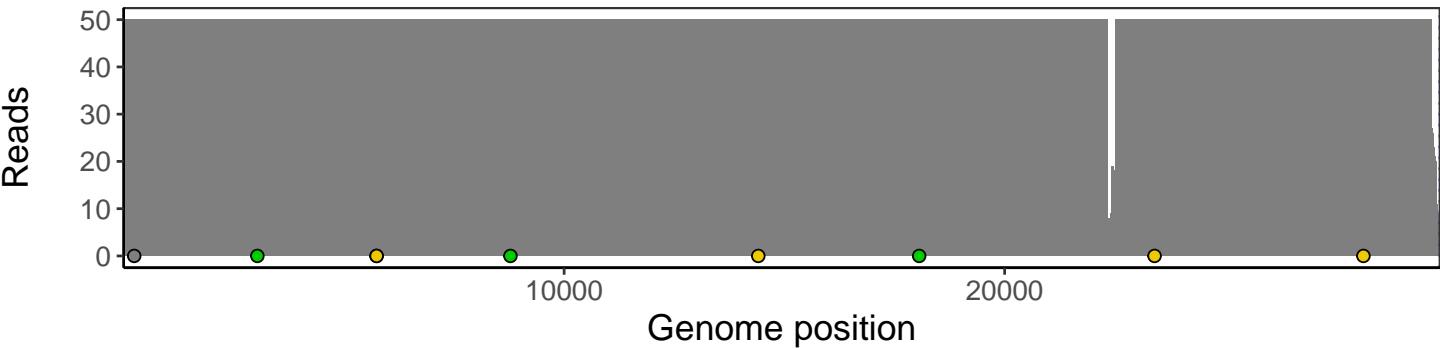
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



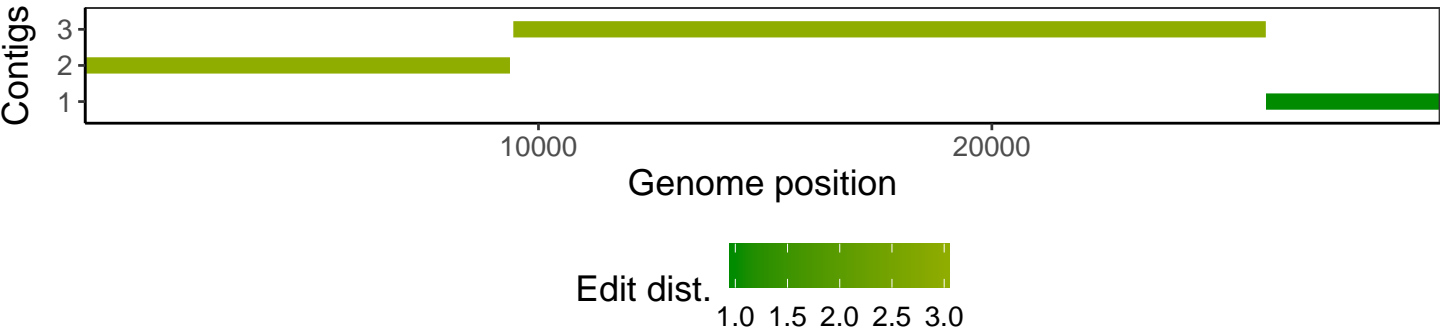
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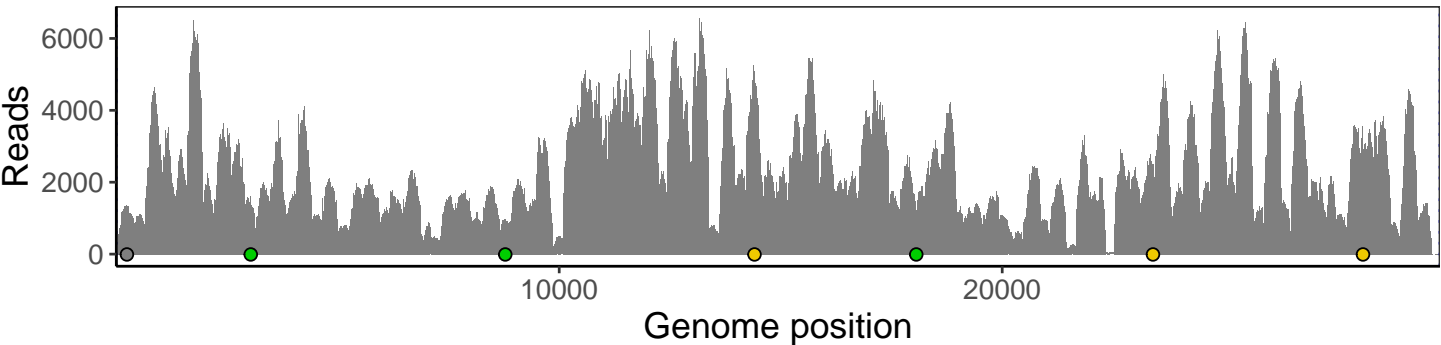
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



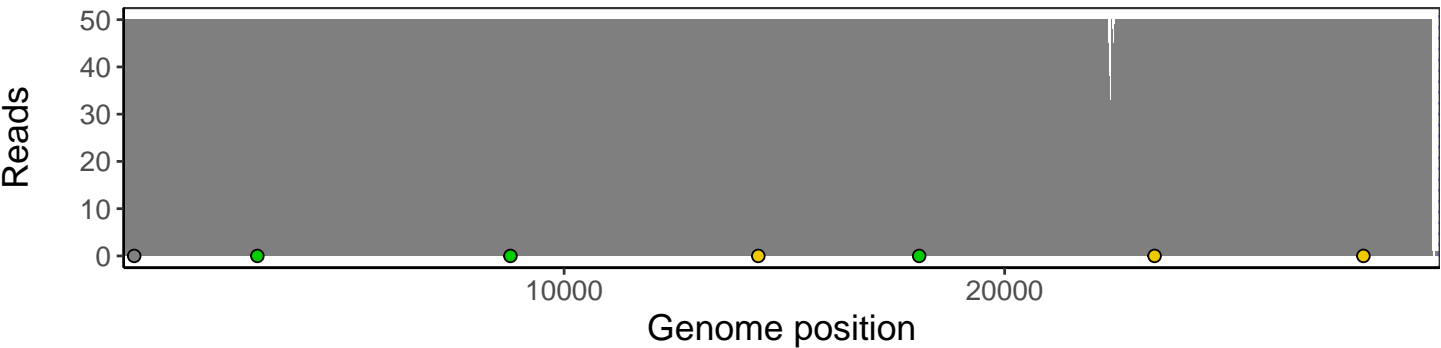
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



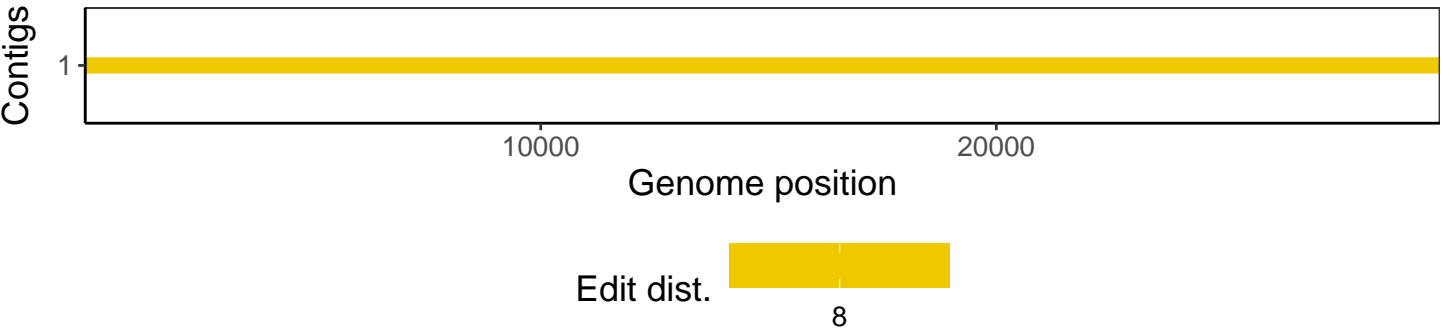
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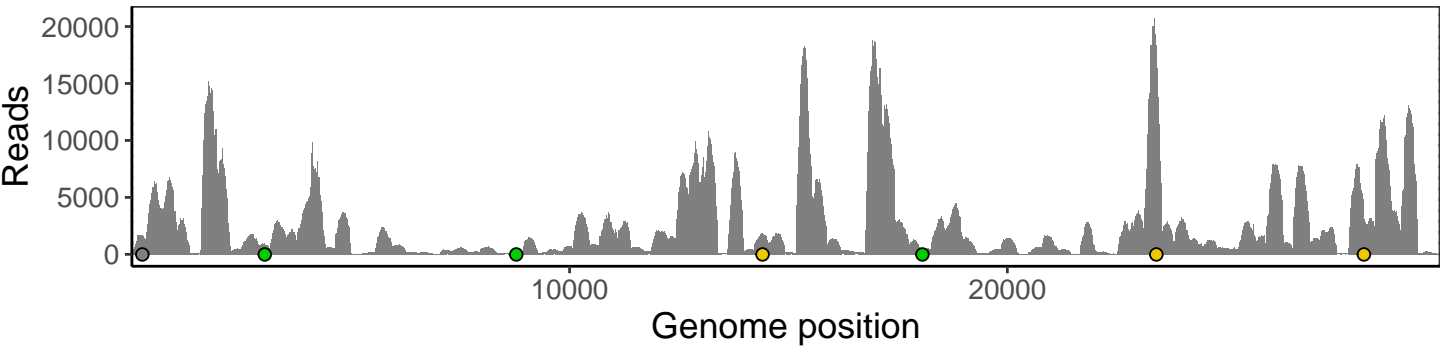
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



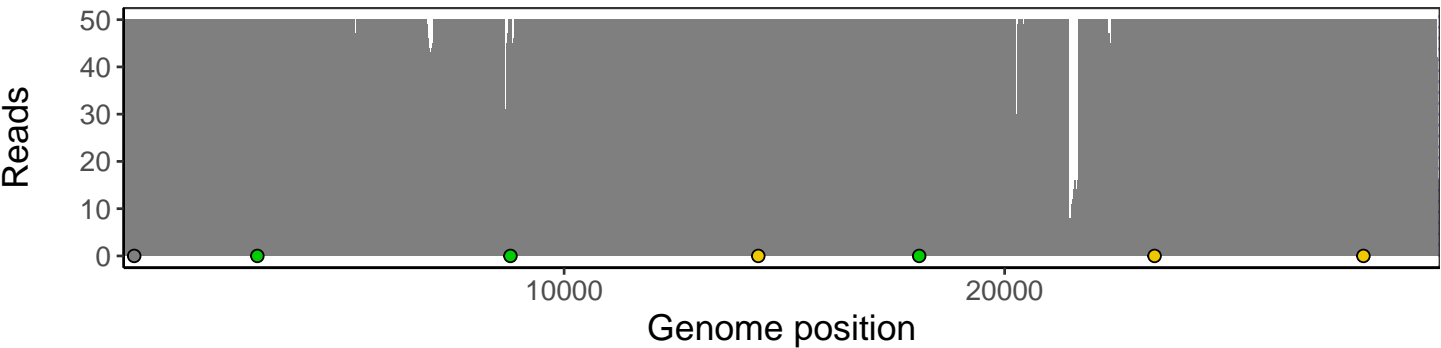
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



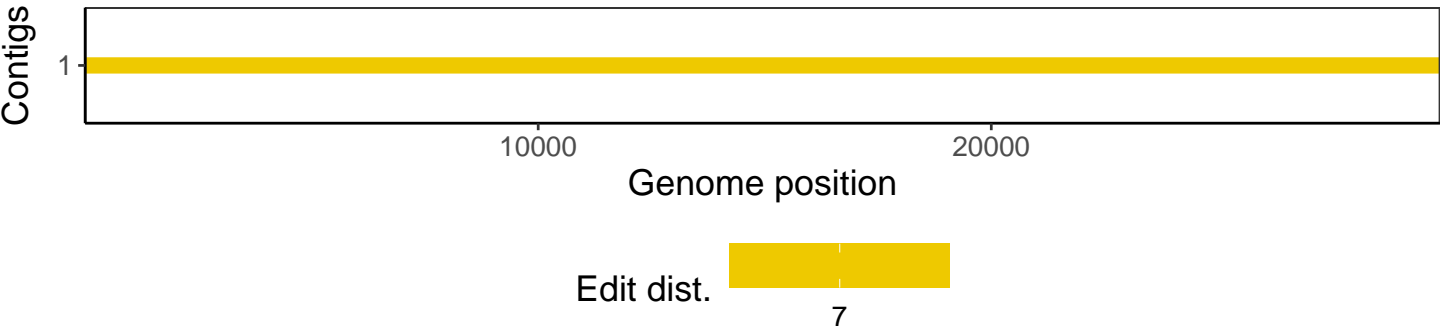
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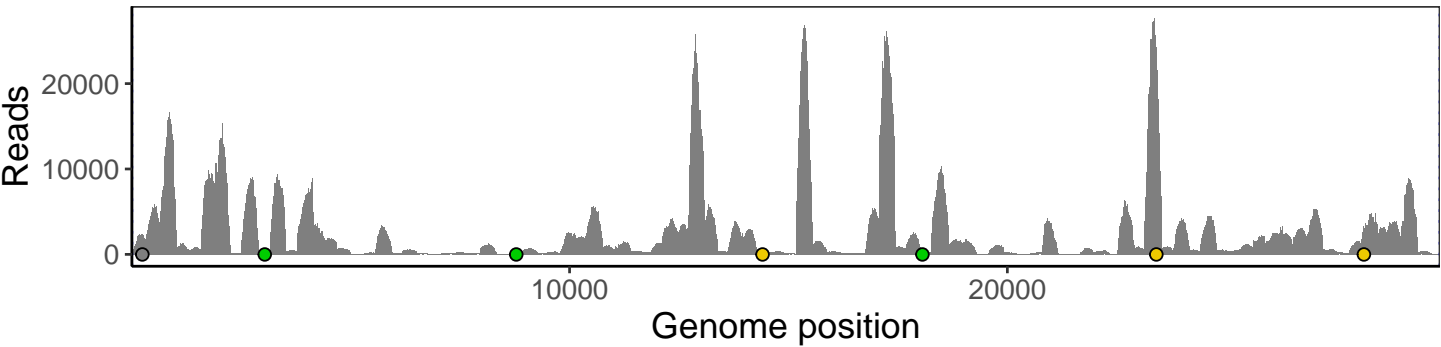
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



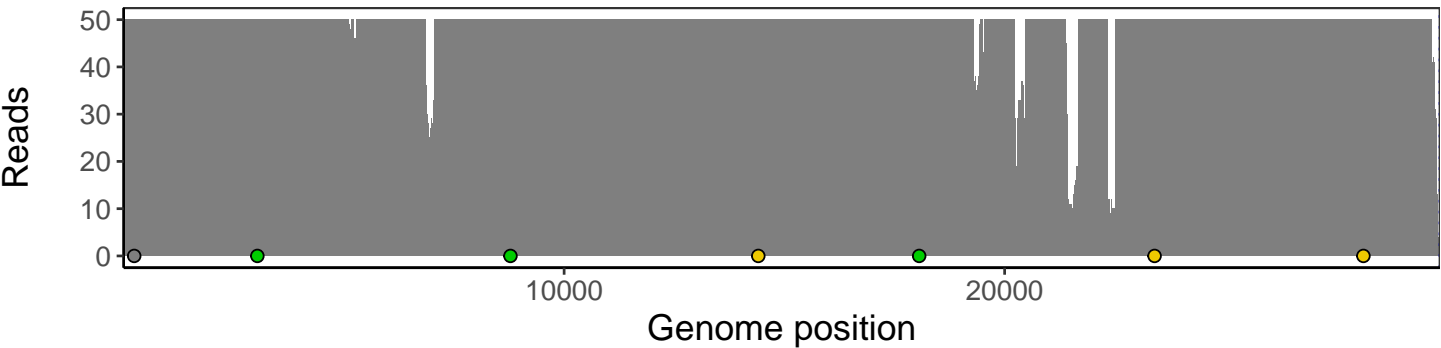
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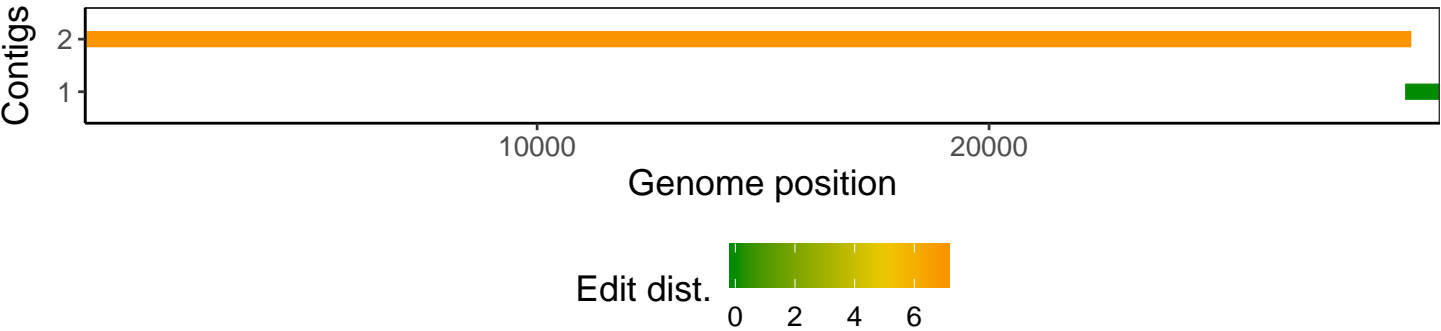
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Excerpt from plot above focusing on reads coverage from 0 to 50 NT.

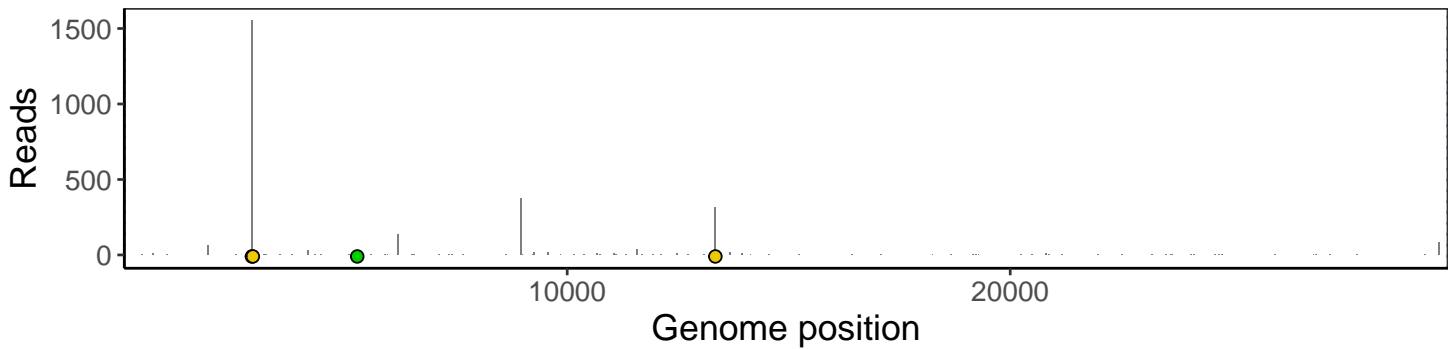


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

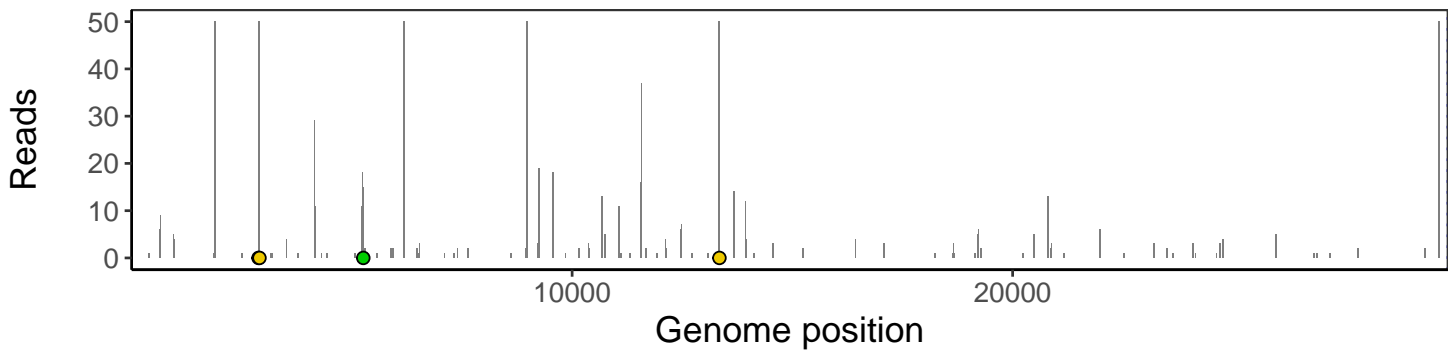


VSP0085-1 | 2020-05-06 | ETA | 242e-q | 8.54 genomes | single experiment

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.



No contig data available.

VSP0085-2 | 2020-05-06 | ETA | 242e-q | 42.7 genomes | single experiment

No pileup data available.

No contig data available.

VSP0085-3 | 2020-05-06 | ETA | 242e-q | 42.7 genomes | single experiment

No pileup data available.

No contig data available.

VSP0085-4 | 2020-05-06 | ETA | 242e-q | 42.7 genomes | single experiment

No pileup data available.

No contig data available.