

COVID-19 subject 272

2021-01-10

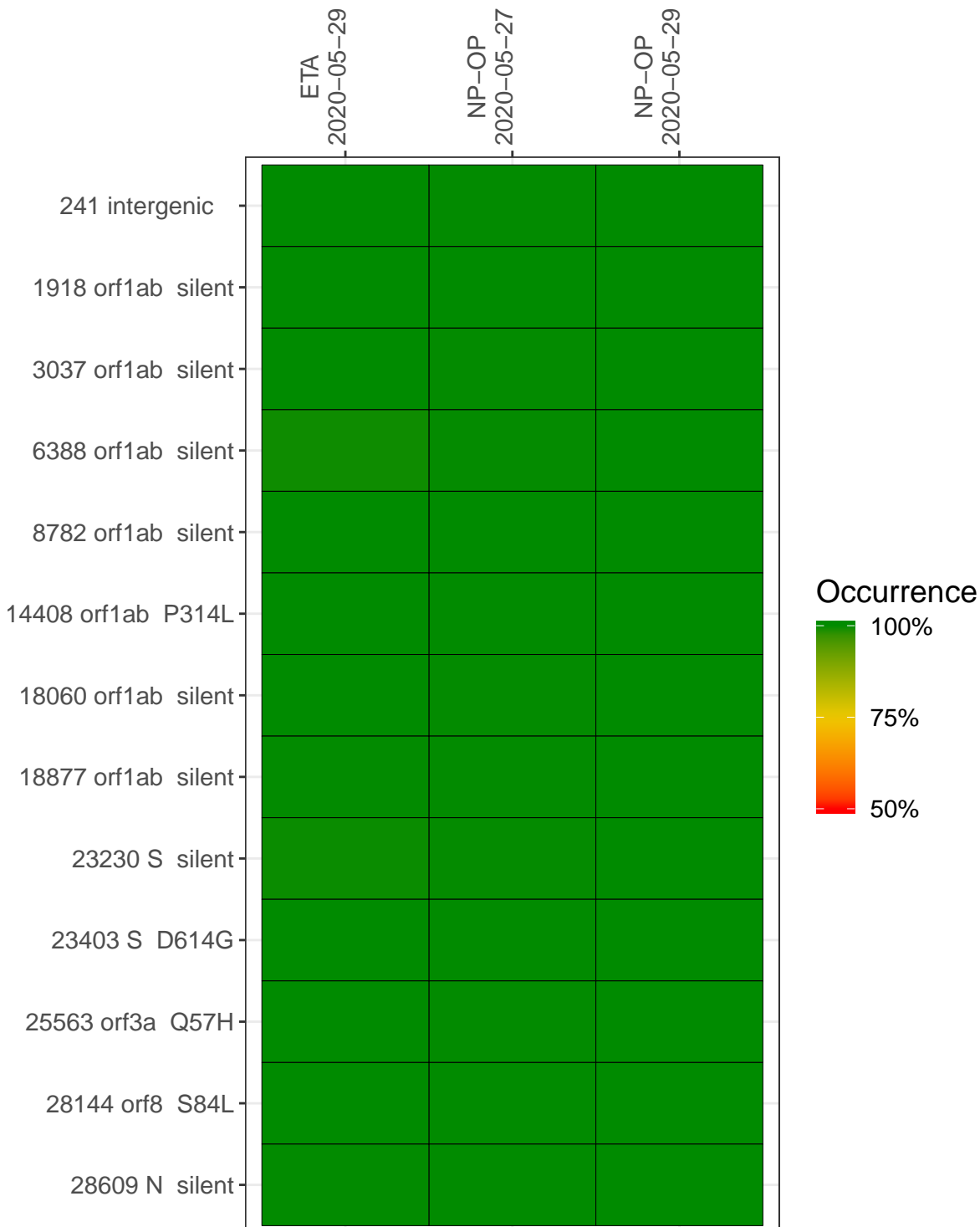
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found ([here](#)).

Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0179-1	single experiment	14500	NP-OP	2020-05-27	29.41	99.8%	99.8%
VSP0195-1	single experiment	1530000	ETA	2020-05-29	25.63	99.8%	98.7%
VSP0196-1	single experiment	14300	NP-OP	2020-05-29	22.29	99.5%	99.0%
VSP0260-1	single experiment	NA	Stool	2020-06-17	NA	3.5%	0.0%

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 2020-05-29	NP-OP 2020-05-27	NP-OP 2020-05-29
241 intergenic	259	1896	51
1918 orf1ab silent	2992	1830	39
3037 orf1ab silent	1163	1569	66
6388 orf1ab silent	590	2892	168
8782 orf1ab silent	880	1497	49
14408 orf1ab P314L	979	2962	77
18060 orf1ab silent	475	1343	32
18877 orf1ab silent	1954	2561	65
23230 S silent	855	2913	191
23403 S D614G	1155	3898	204
25563 orf3a Q57H	2733	2086	29
28144 orf8 S84L	1178	4930	159
28609 N silent	1889	6474	339
	VSP0195-1	VSP0179-1	VSP0196-1

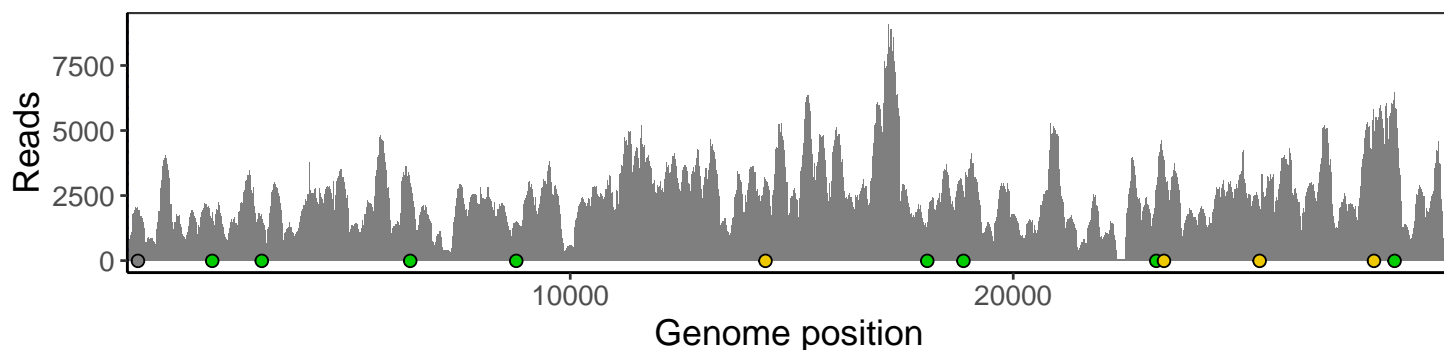
Base change

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

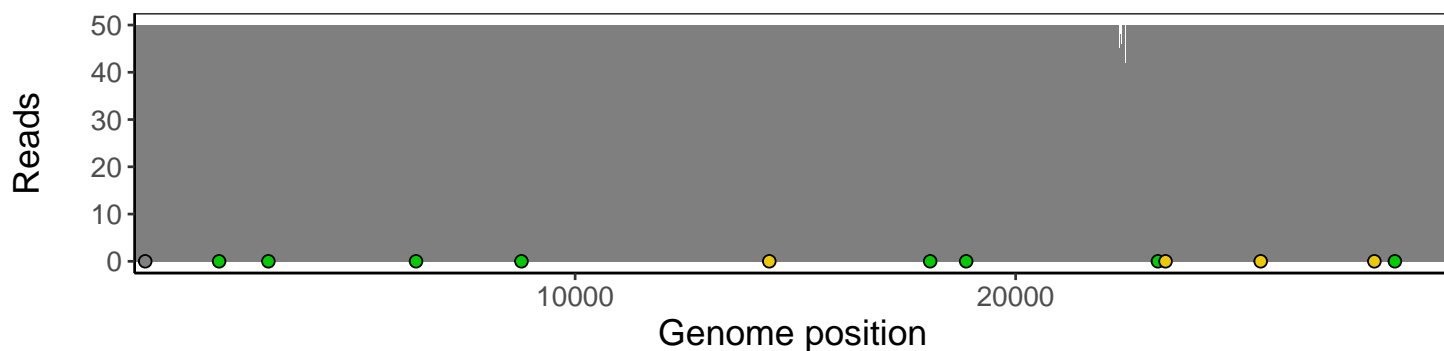
Analyses of individual experiments and composite results.

VSP0179-1 | 2020-05-27 | NP-OP | 272no-q | 14500 genomes | single experiment

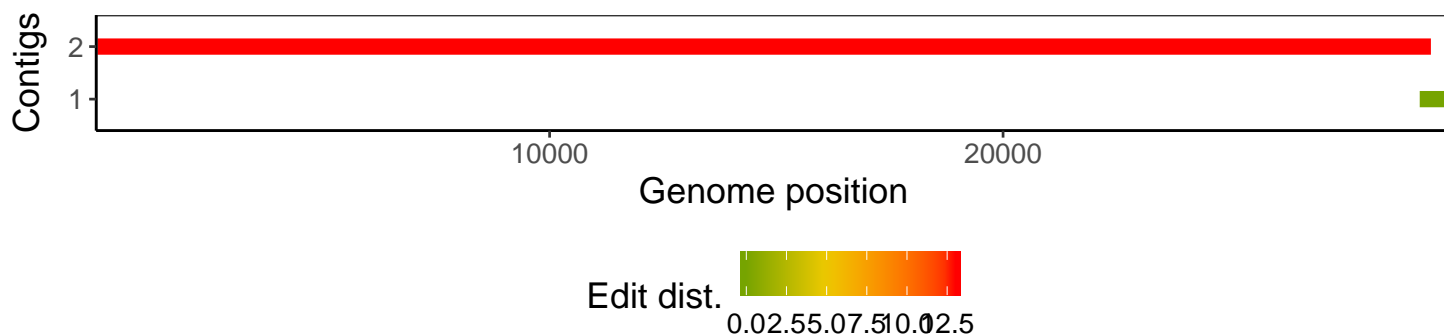
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



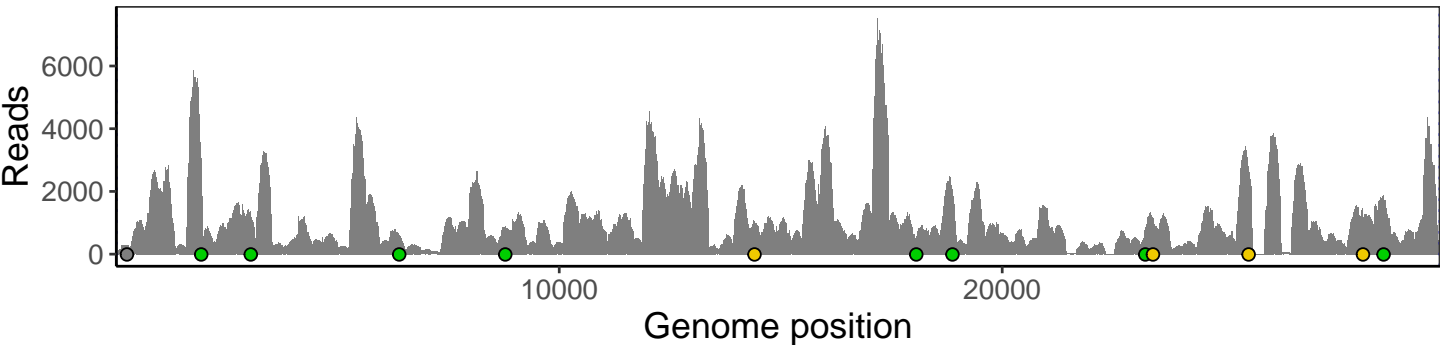
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



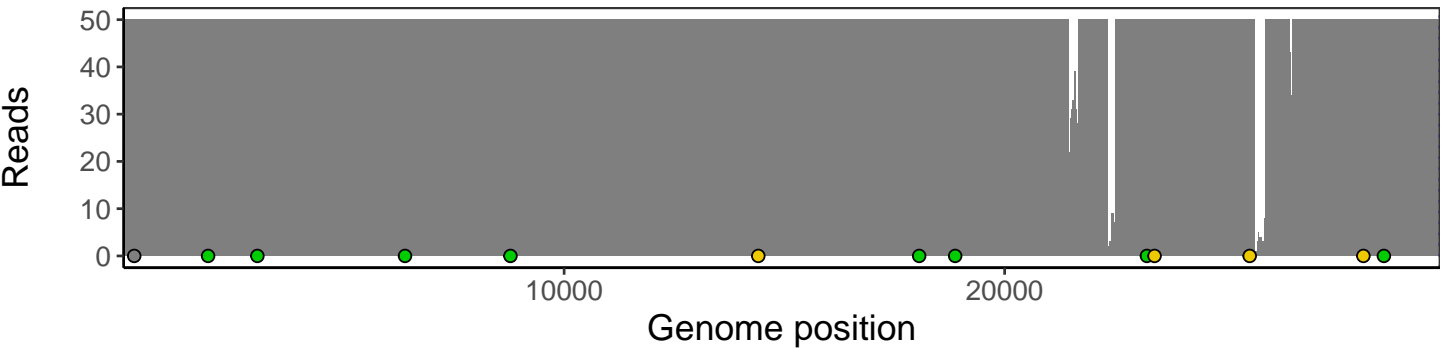
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



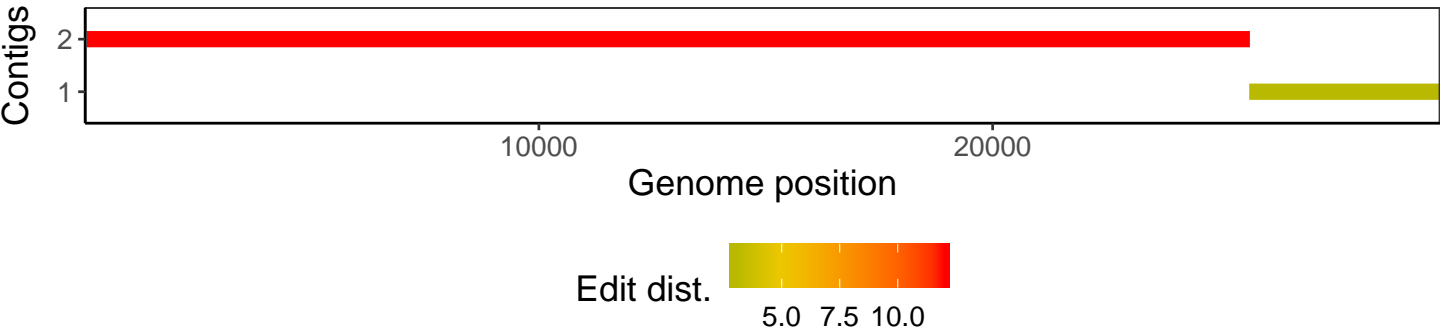
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



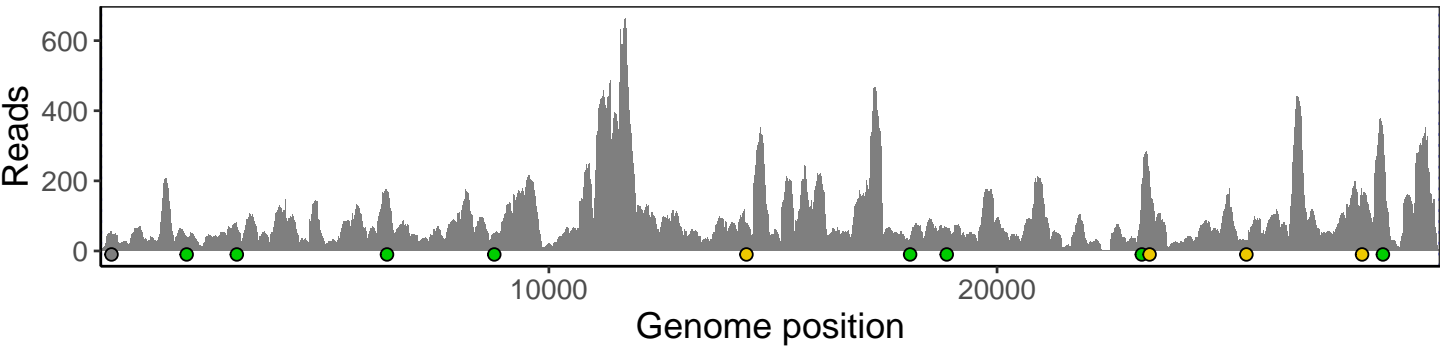
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



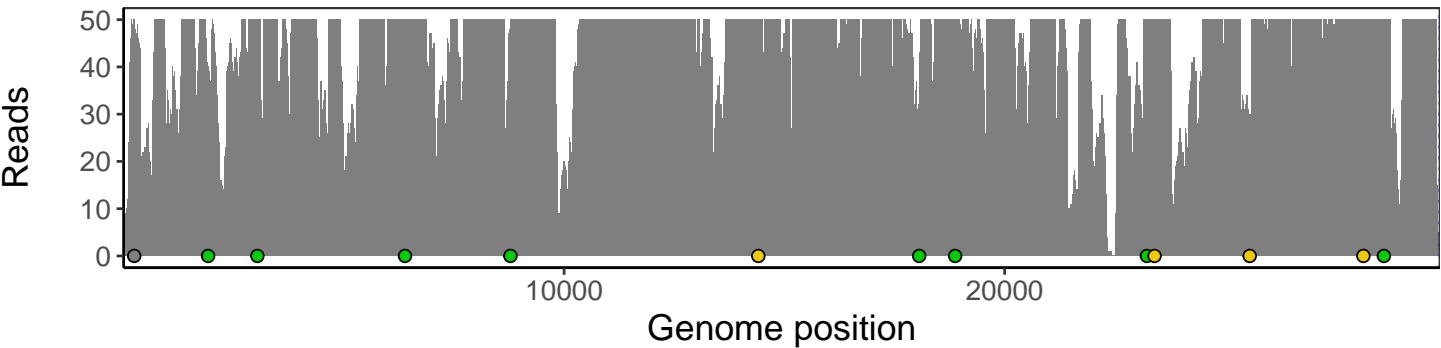
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



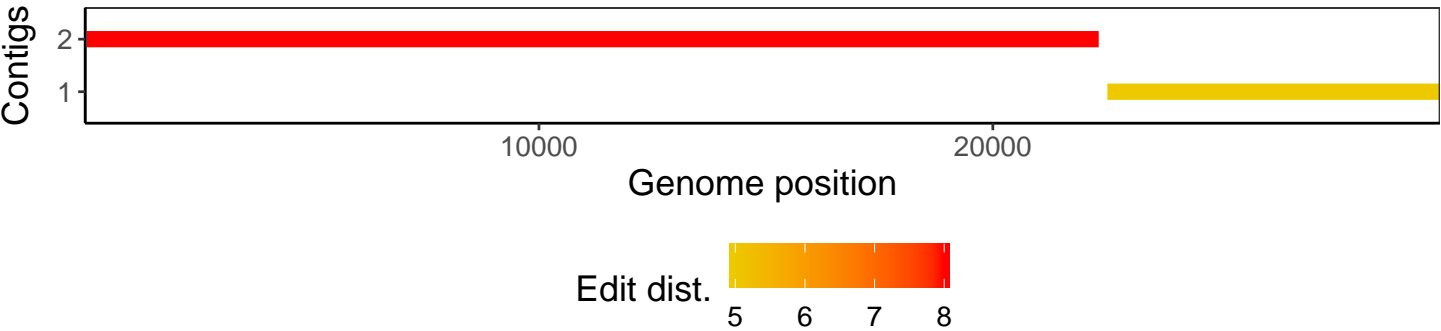
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



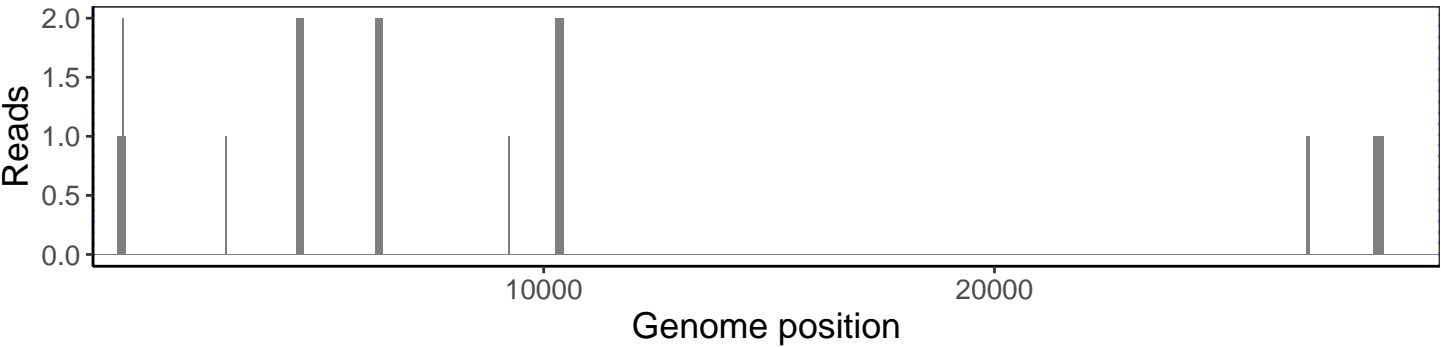
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



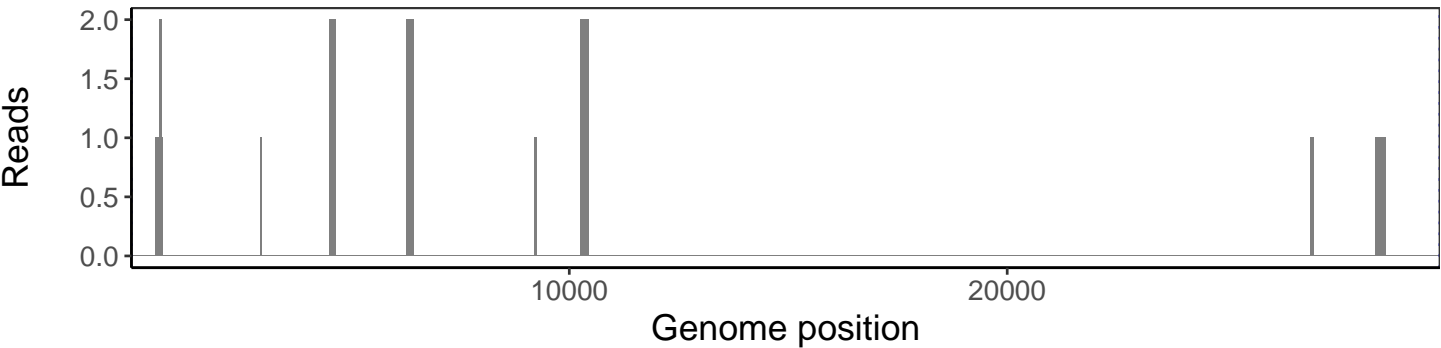
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



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.