

COVID-19 subject 269

2020-11-30

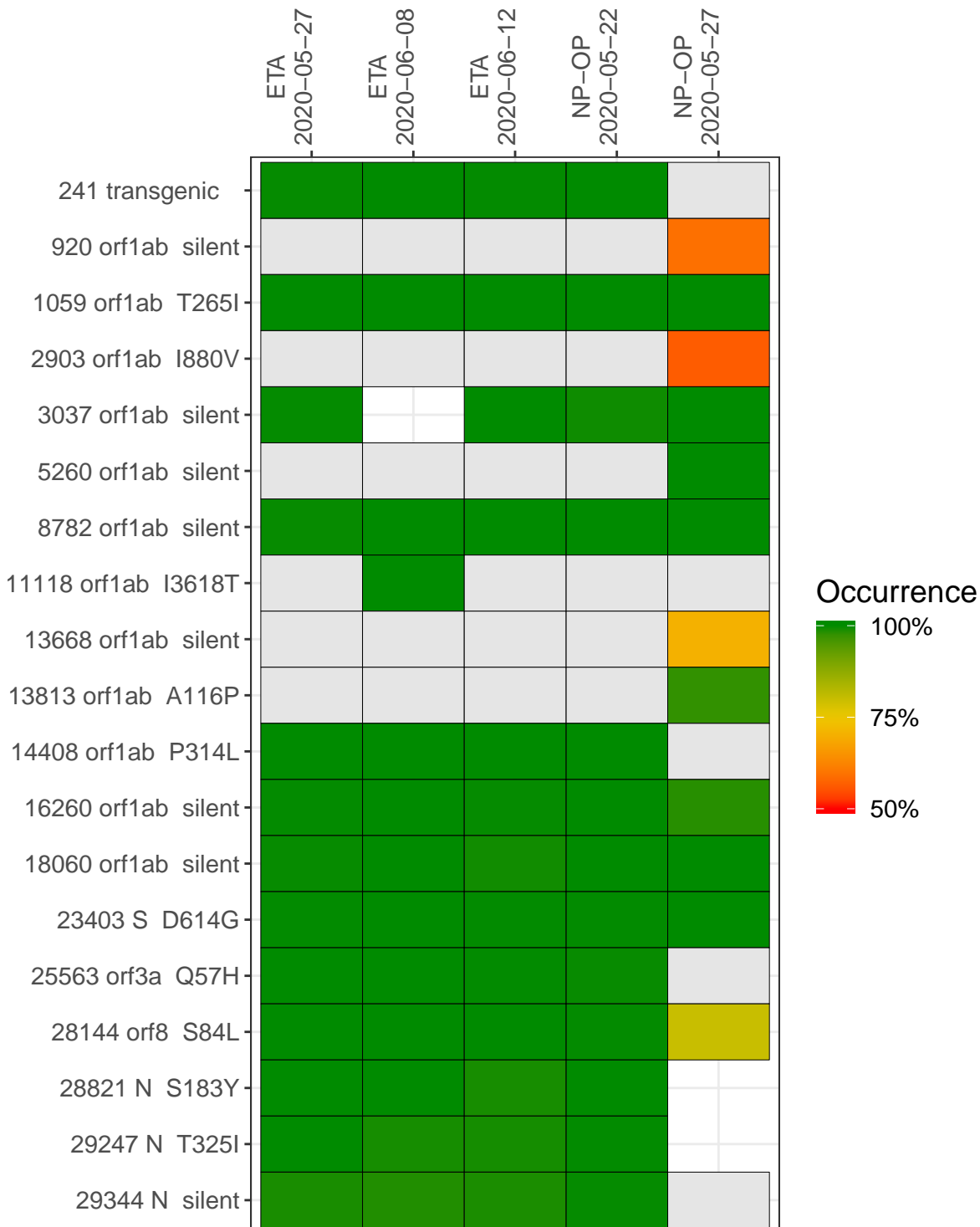
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found ([here](#)).

Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0177	composite	NA	NP-OP	2020-05-27	3.70	89.8%	72.9%
VSP0166-1	single experiment	NA	NP-OP	2020-05-22	29.84	99.8%	99.5%
VSP0176-1	single experiment	166000.0	ETA	2020-05-27	29.82	99.8%	99.8%
VSP0177-1	single experiment	59.7	NP-OP	2020-05-27	1.03	72.3%	17.5%
VSP0177-2	single experiment	NA	NP-OP	2020-05-27	1.00	31.5%	26.0%
VSP0177-3	single experiment	NA	NP-OP	2020-05-27	1.02	40.8%	35.0%
VSP0177-4	single experiment	NA	NP-OP	2020-05-27	0.93	38.4%	35.6%
VSP0200-1	single experiment	NA	ETA	2020-06-08	5.92	84.5%	82.0%
VSP0202-1	single experiment	16300.0	ETA	2020-06-12	29.83	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.



	ETA 020-05-2	ETA 020-06-0	ETA 020-06-1	NP-OP 020-05-2	NP-OP 2020-05-27			
241 transgenic	906	211	1544	891	2			
920 orf1ab silent	1214	88	1045	948	2		52	
1059 orf1ab T265I	987	47	1333	608	4	23	6	
2903 orf1ab I880V	829	2	948	1177	144	27	15	34
3037 orf1ab silent	918		932	1416	3	32	13	36
5260 orf1ab silent	485	22	909	165	12			
8782 orf1ab silent	704	104	2189	441			24	
11118 orf1ab I3618T	951	153	2907	1179	4	16	55	
13668 orf1ab silent	638	131	1570	1225	5	31	7	1
13813 orf1ab A116P	1374	386	3051	2137	2	86		
14408 orf1ab P314L	1257	227	2057	942	2			
16260 orf1ab silent	1211	34	1722	1563	1			66
18060 orf1ab silent	655	62	1852	631		38		46
23403 S D614G	3805	432	4971	2122	5	83	62	
25563 orf3a Q57H	828	76	2614	1110	4			
28144 orf8 S84L	1197	27	2018	3122	1			
28821 N S183Y	667	24	925	846				
29247 N T325I	1148	157	1741	2161				
29344 N silent	914	87	1386	1508	1			
	VSP0176-1	VSP0200-1	VSP0202-1	VSP0166-1	VSP0177-1	VSP0177-2	VSP0177-3	VSP0177-4

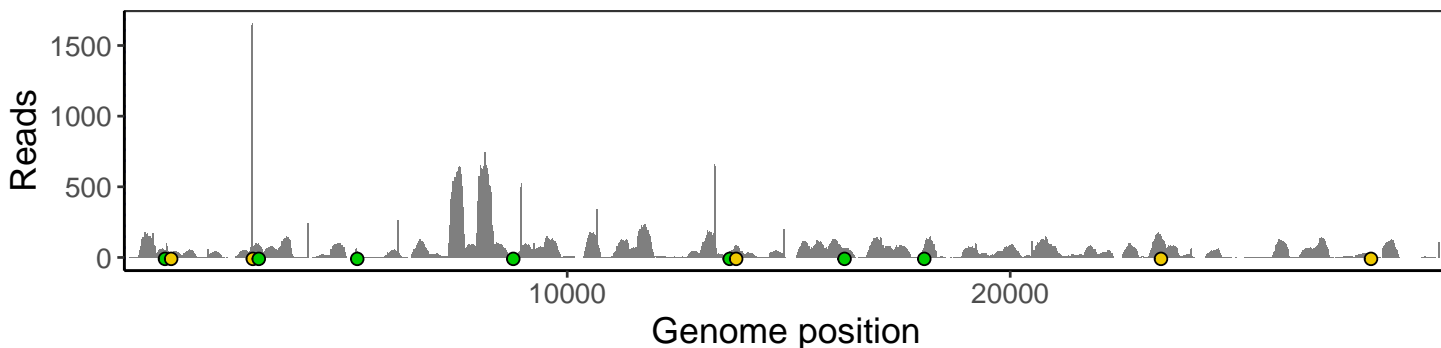
Base change

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

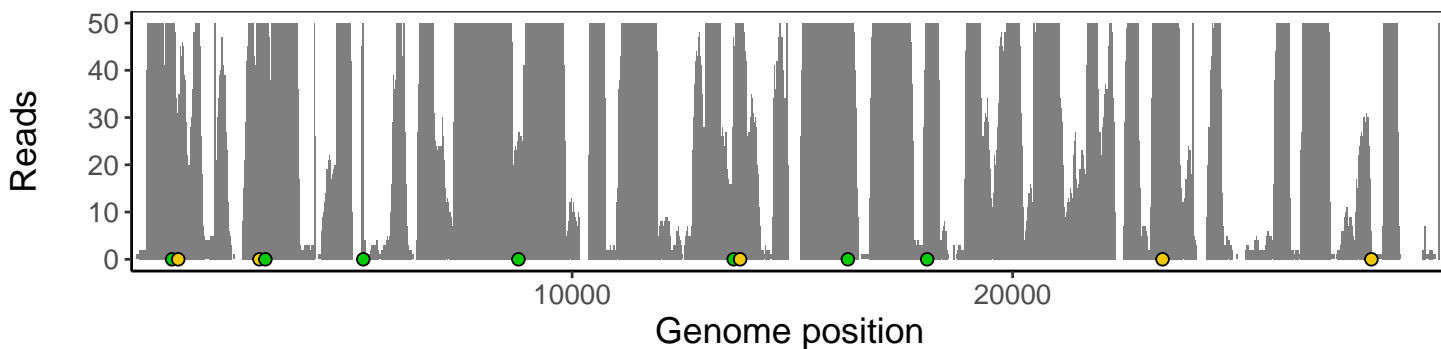
Analyses of individual experiments and composite results.

VSP0177 | 2020-05-27 | NP-OP | 269no-q | composite result

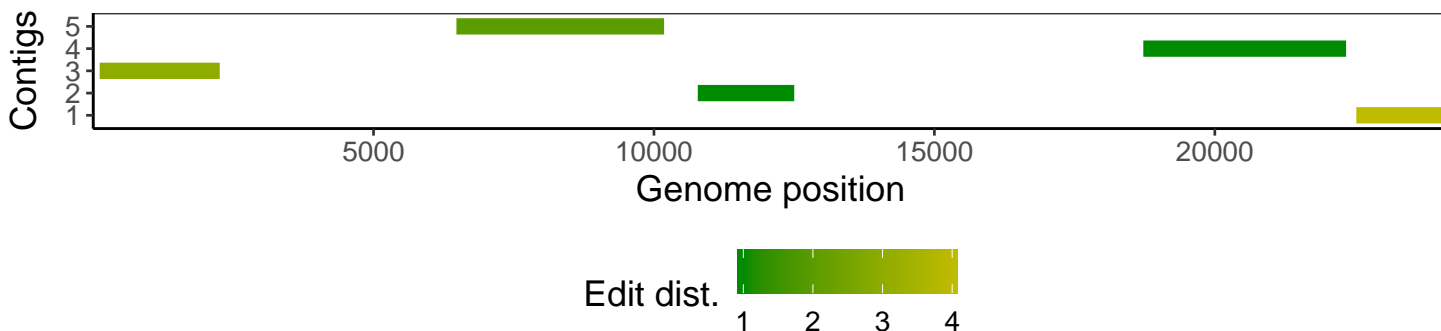
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



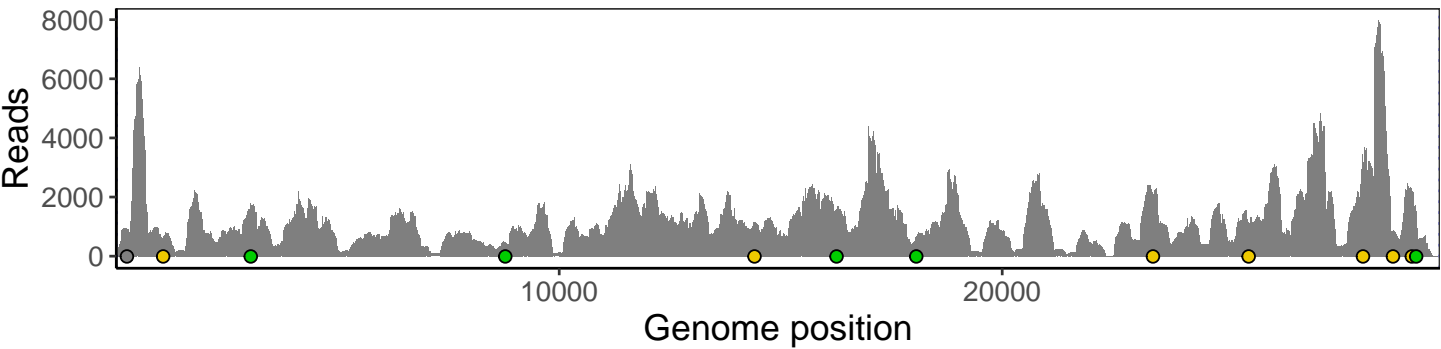
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



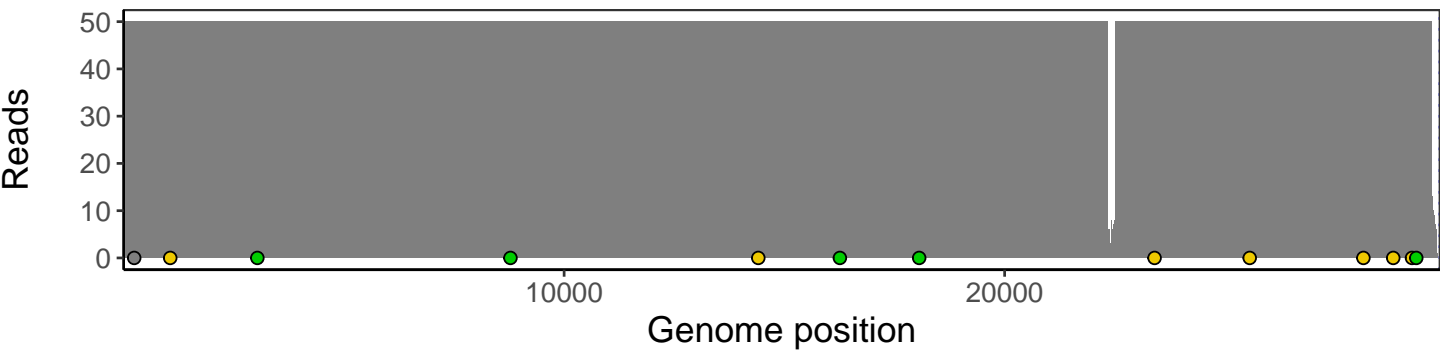
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



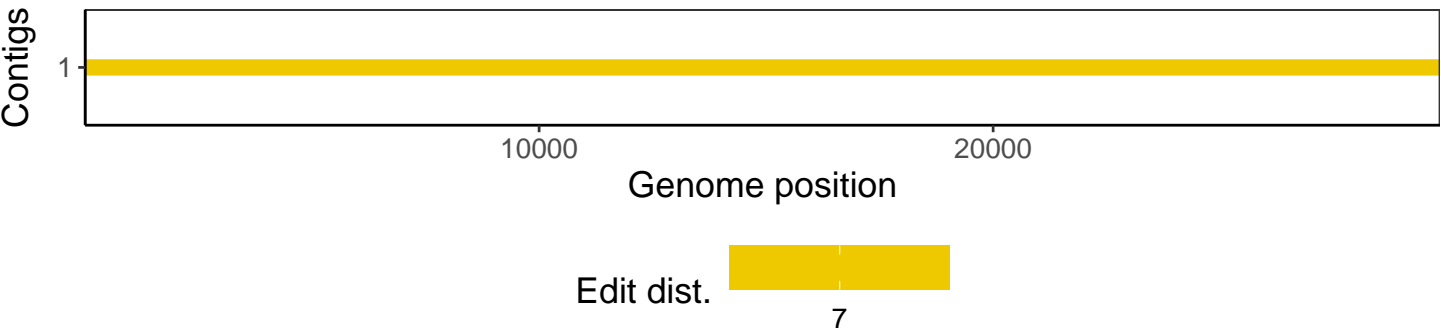
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



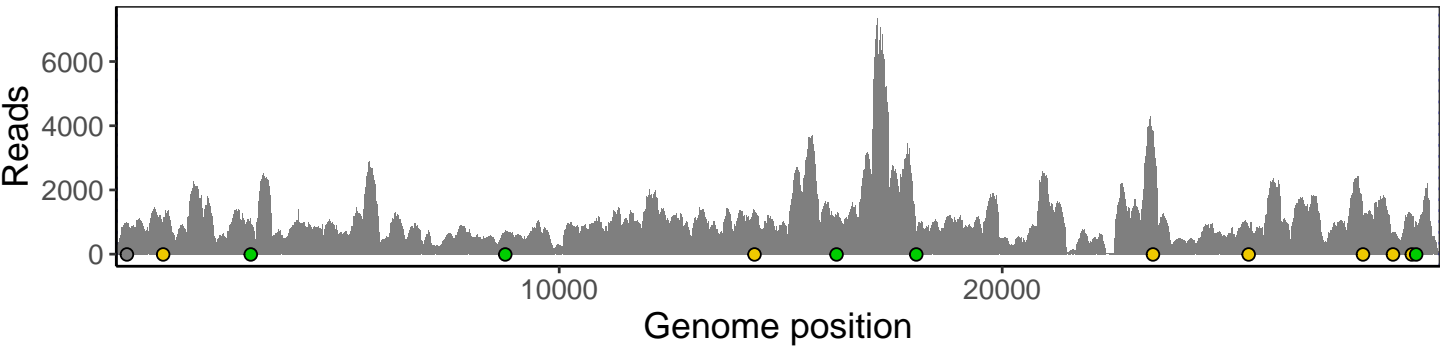
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



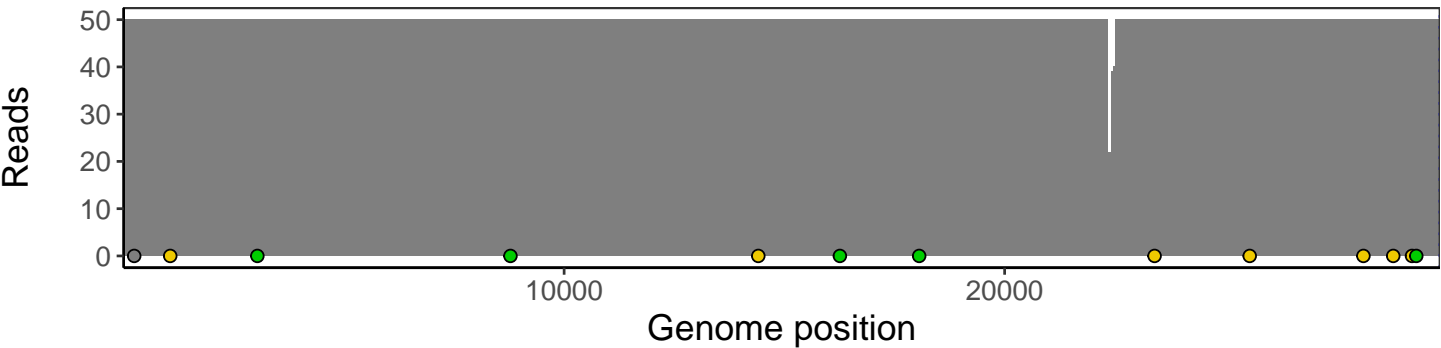
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



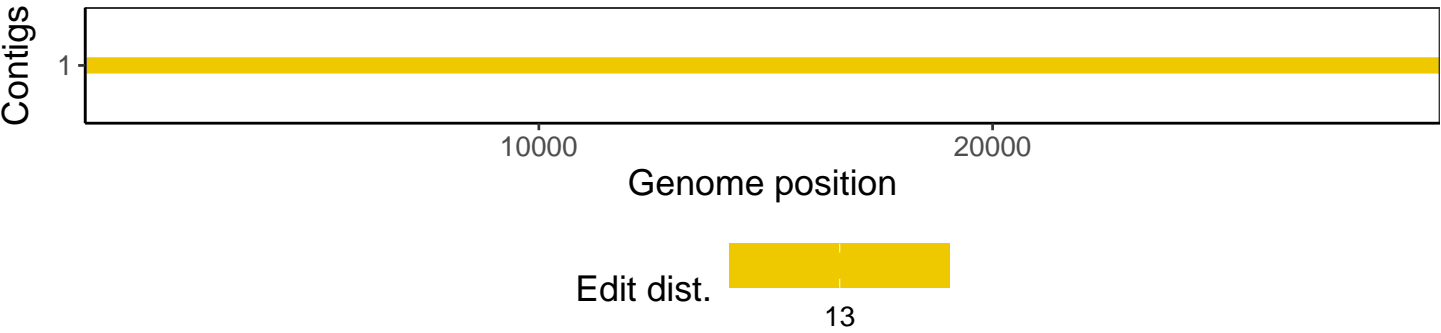
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



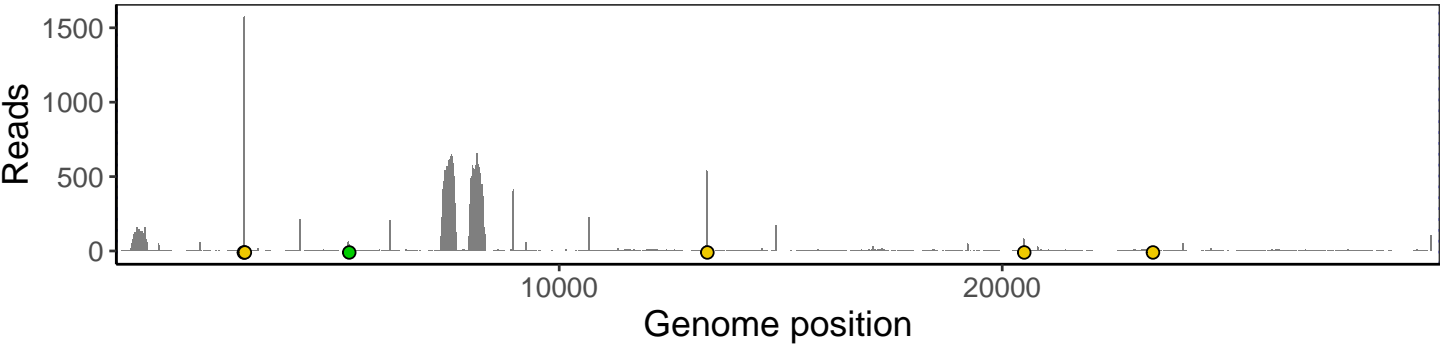
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



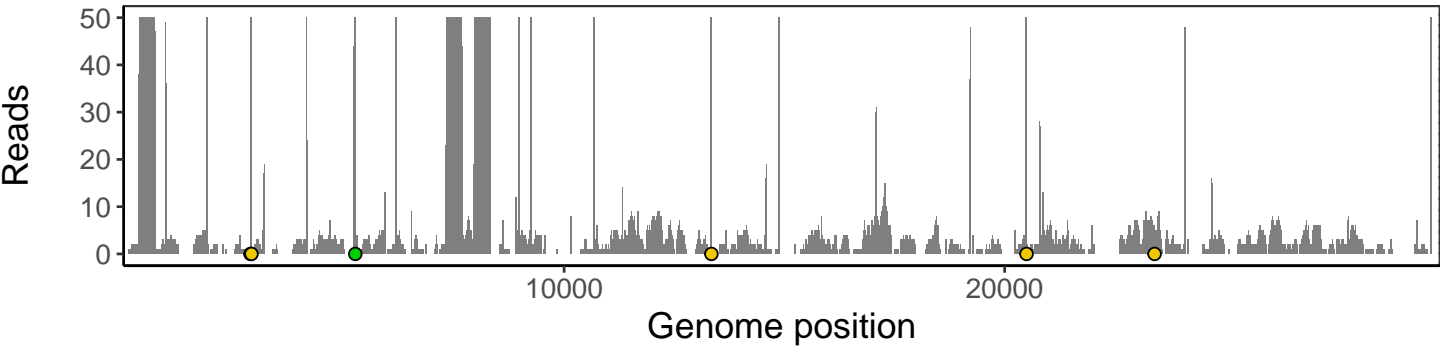
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



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.



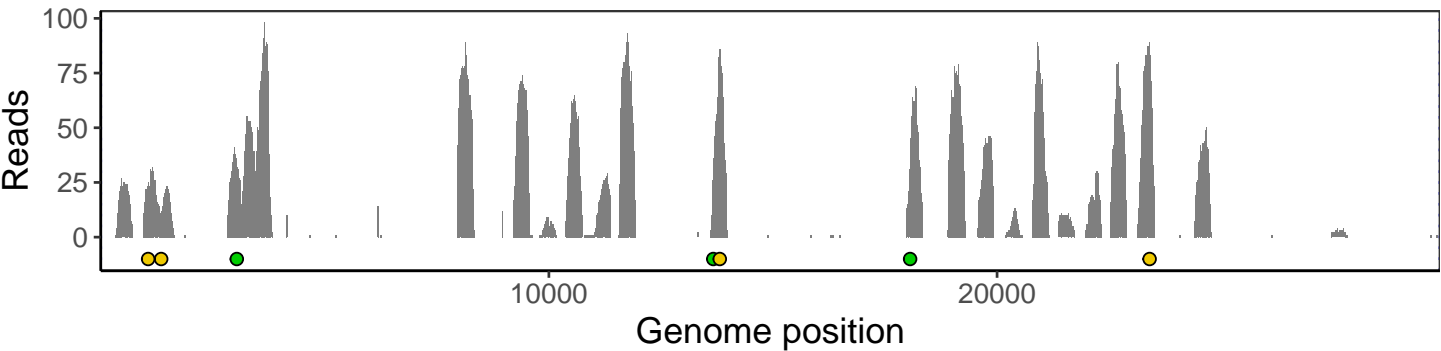
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



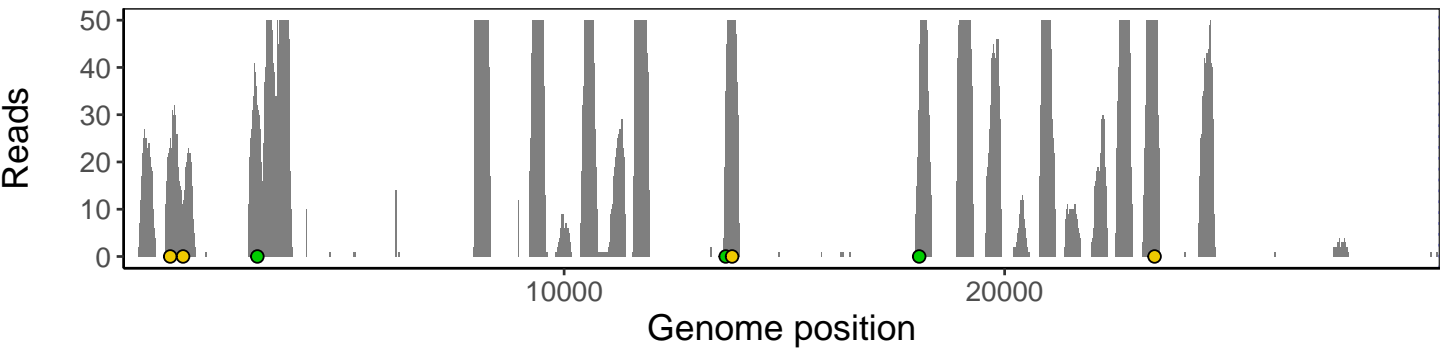
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



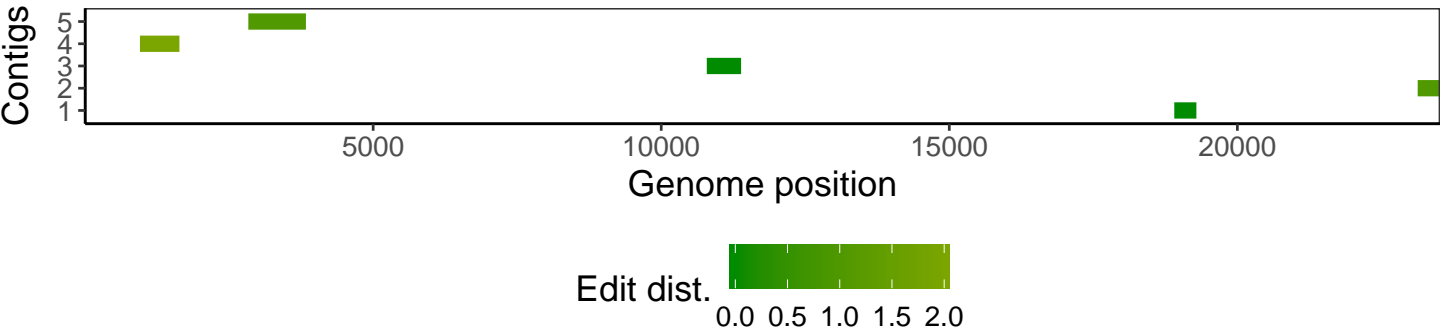
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



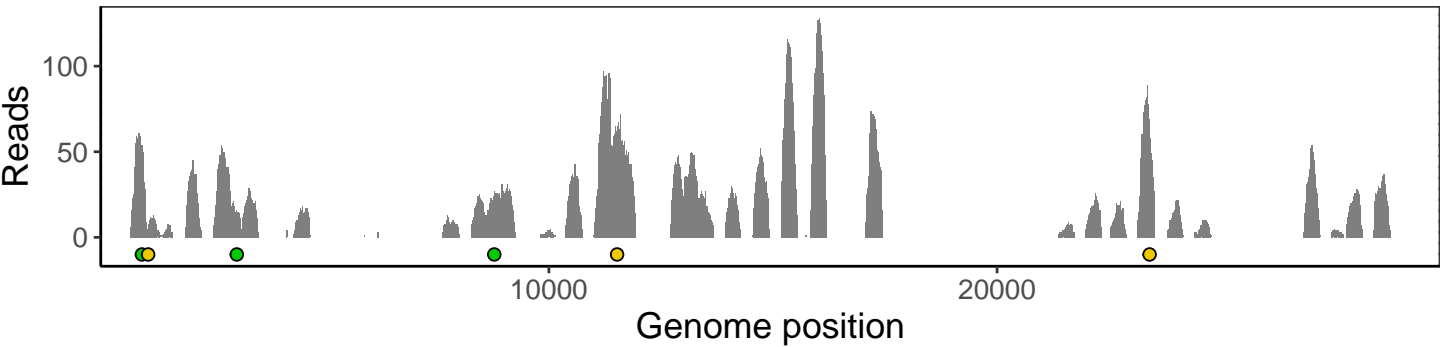
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



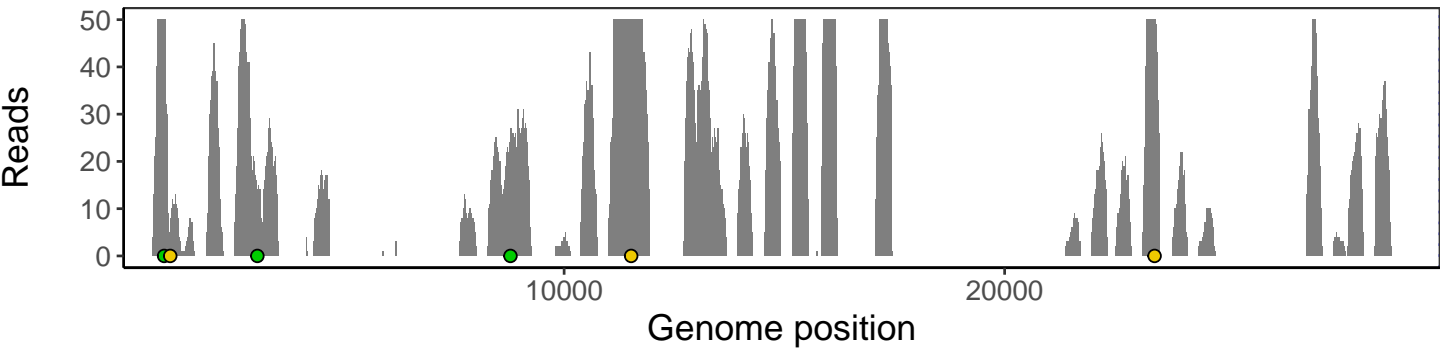
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



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.



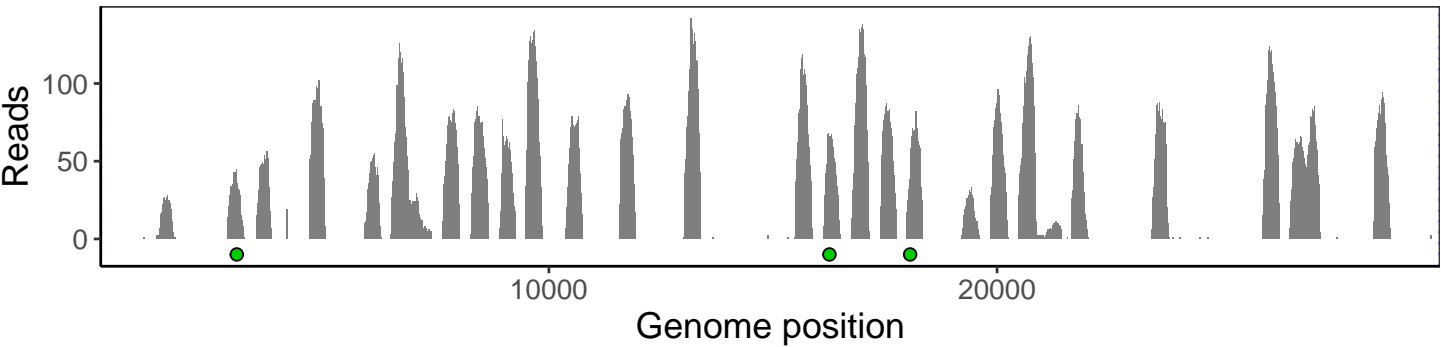
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



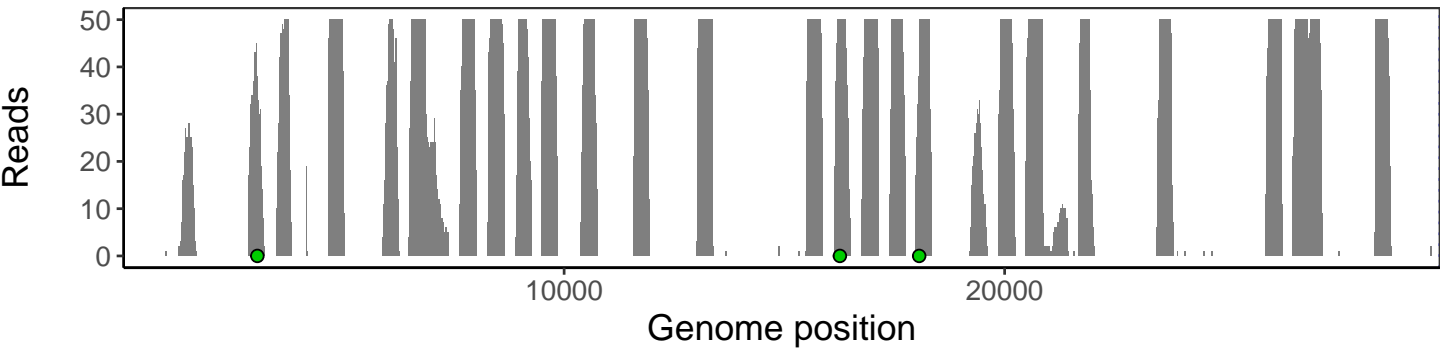
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



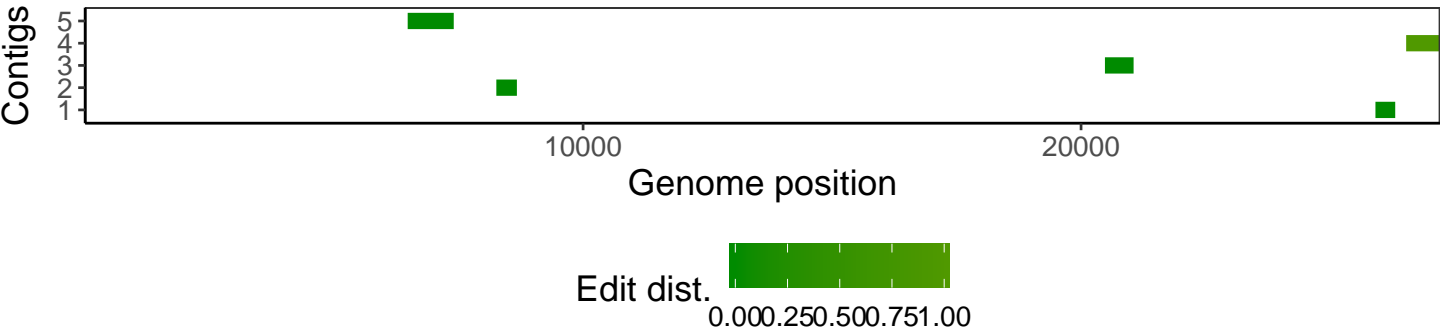
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



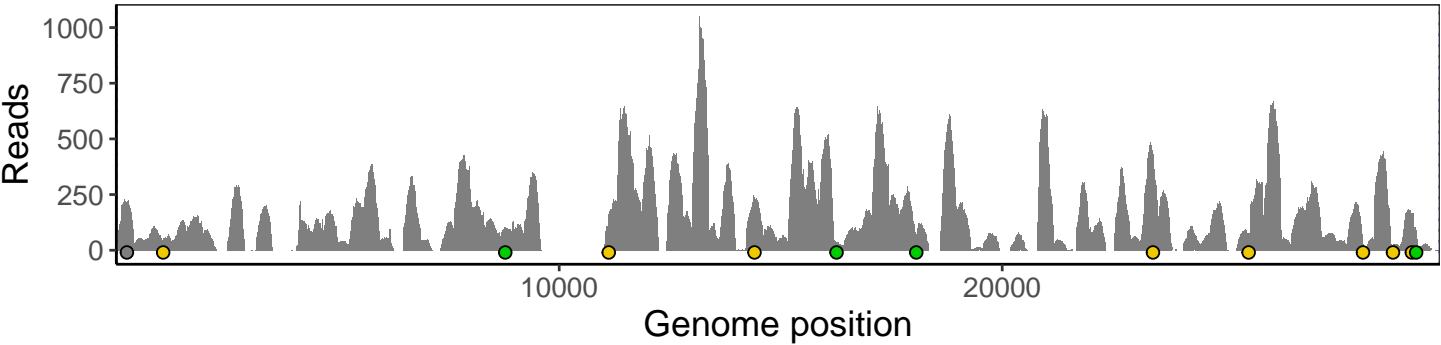
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



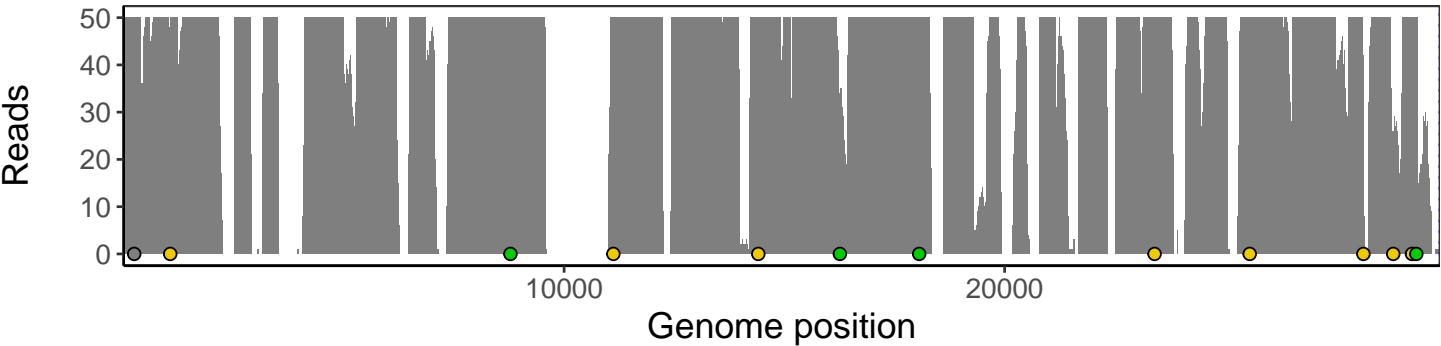
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



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.



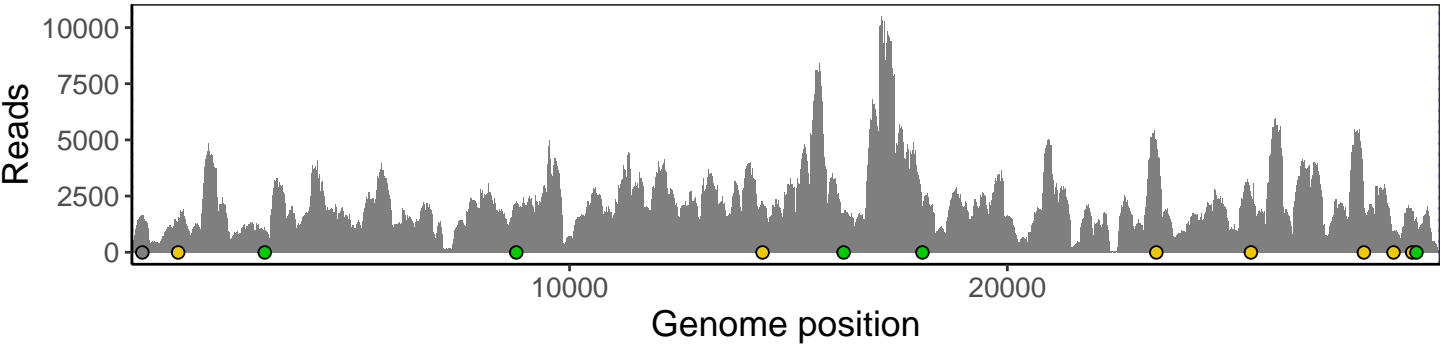
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



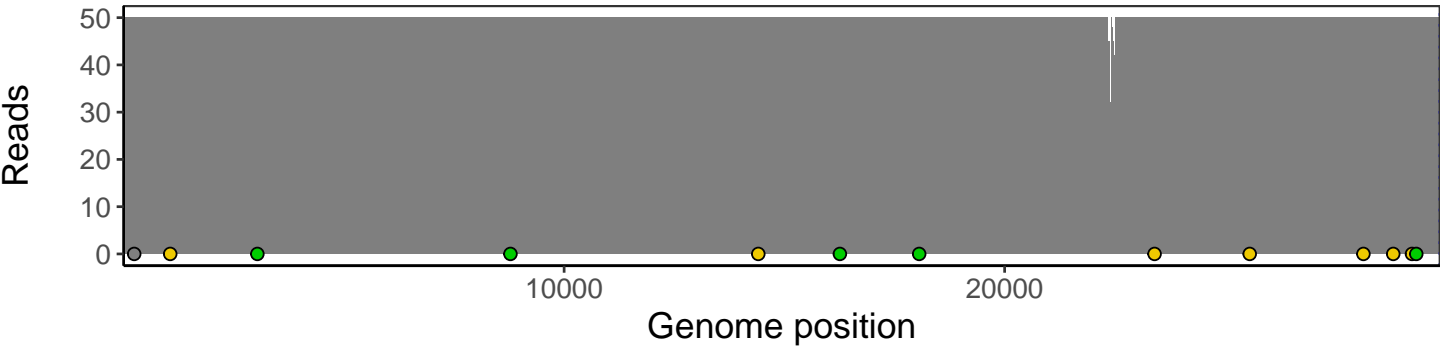
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



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.

