COVID-19 subject 269

2021-01-08

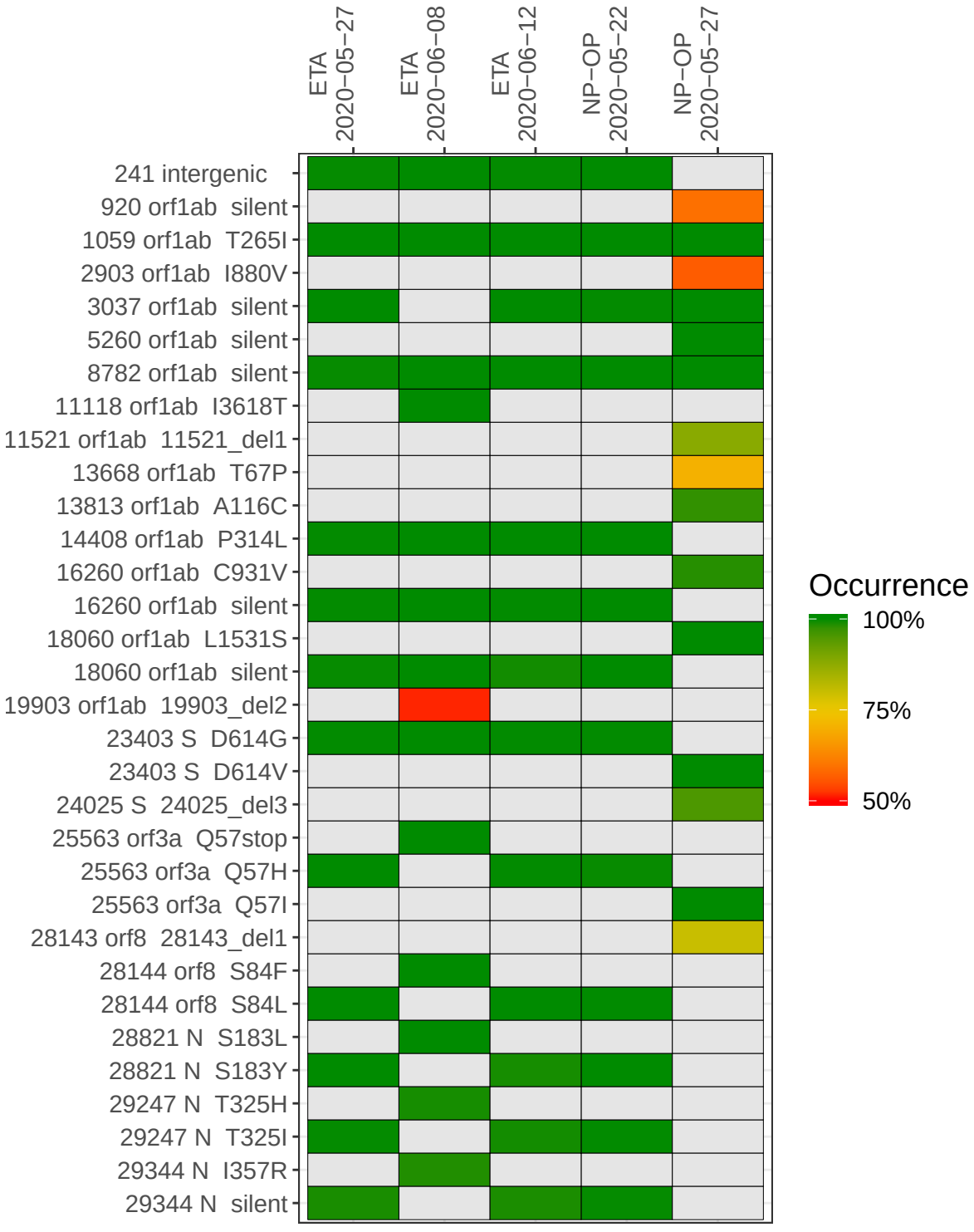
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

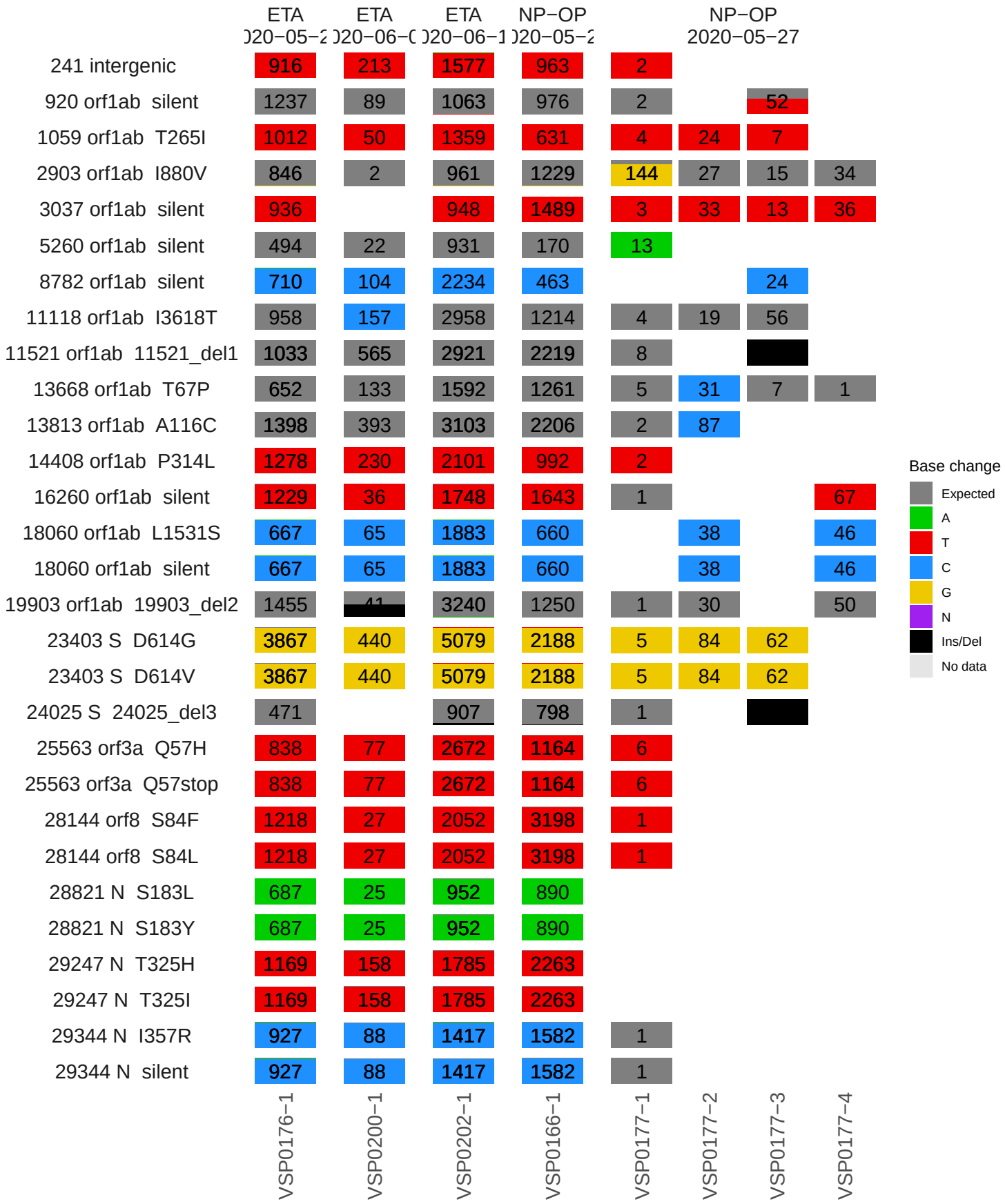
Table 1. Sample summary.

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	4.03	100.0%	73.8%
VSP0166-1	single experiment	NA	NP-OP	2020-05-22	29.84	100.0%	99.5%
VSP0176-1	single experiment	166000.0	ETA	2020-05-27	29.82	100.0%	99.8%
VSP0177-1	single experiment	59.7	NP-OP	2020-05-27	1.03	100.0%	18.6%
VSP0177-2	single experiment	NA	NP-OP	2020-05-27	1.01	100.0%	26.0%
VSP0177-3	single experiment	NA	NP-OP	2020-05-27	1.02	100.0%	35.5%
VSP0177-4	single experiment	NA	NP-OP	2020-05-27	0.93	100.0%	35.6%
VSP0200-1	single experiment	NA	ETA	2020-06-08	5.92	100.0%	82.1%
VSP0202-1	single experiment	16300.0	ETA	2020-06-12	29.83	100.0%	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.

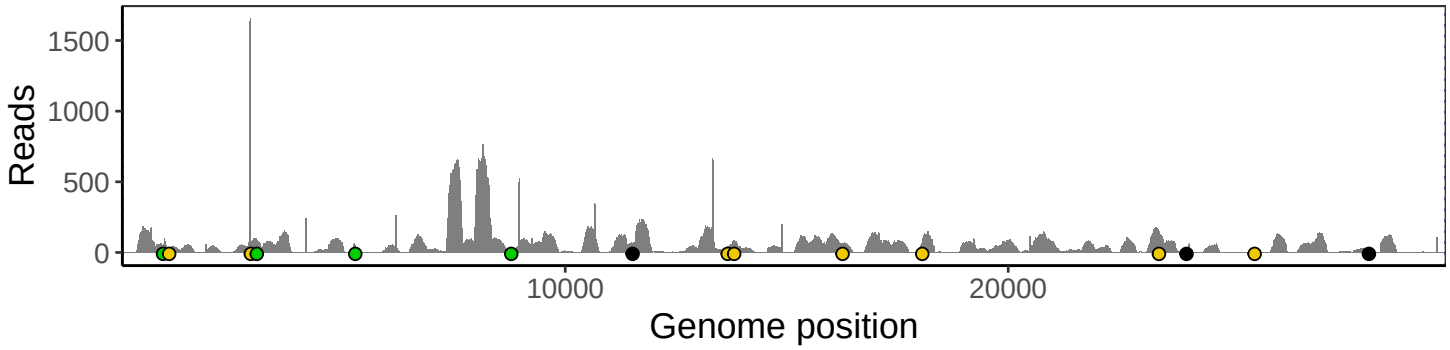



ETA 020−05−2
ETA 020−06−0
ETA 020−06−1
NP−OP 020−05−2
NP−OP 2020−05−27
241 intergenic
920 orf1ab silent
1059 orf1ab T265I
2903 orf1ab I880V
3037 orf1ab silent
5260 orf1ab silent
8782 orf1ab silent
11118 orf1ab I3618T
11521 orf1ab 11521_del1
13668 orf1ab T67P
13813 orf1ab A116C
14408 orf1ab P314L
16260 orf1ab silent
18060 orf1ab L1531S
18060 orf1ab silent
19903 orf1ab 19903_del2
23403 S D614G
23403 S D614V
24025 S 24025_del3
25563 orf3a Q57H
25563 orf3a Q57stop
28144 orf8 S84F
28144 orf8 S84L
28821 N S183L
28821 N S183Y
29247 N T325H
29247 N T325I
29344 N I357R
29344 N silent
916 213 1577 963 2
1237 89 1063 976 2 52
1012 50 1359 631 4 24 7
846 2 961 1229 144 27 15 34
936 948 1489 3 33 13 36
494 22 931 170 13
710 104 2234 463 24
958 157 2958 1214 4 19 56
1033 565 2921 2219 8
652 133 1592 1261 5 31 7 1
1398 393 3103 2206 2 87
1278 230 2101 992 2
1229 36 1748 1643 1 67
667 65 1883 660 38 46
667 65 1883 660 38 46
1455 41 3240 1250 1 30 50
3867 440 5079 2188 5 84 62
3867 440 5079 2188 5 84 62
471 907 798 1
838 77 2672 1164 6
838 77 2672 1164 6
1218 27 2052 3198 1
1218 27 2052 3198 1
687 25 952 890
687 25 952 890
1169 158 1785 2263
1169 158 1785 2263
927 88 1417 1582 1
927 88 1417 1582 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

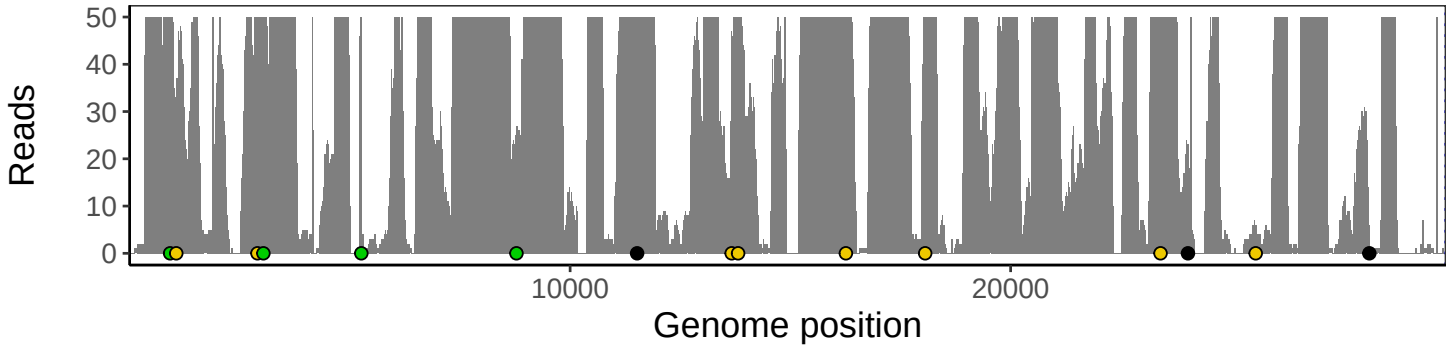
Analyses of individual experiments and composite results.

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

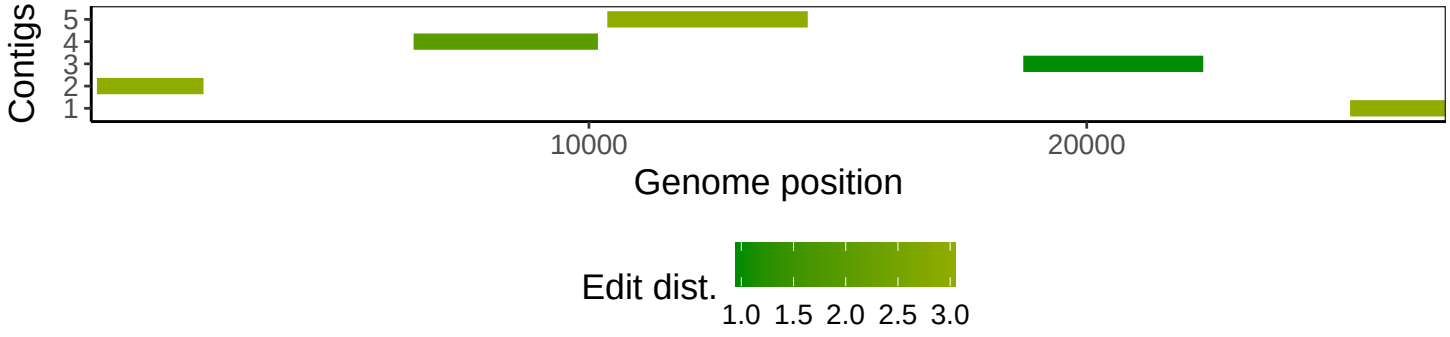
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

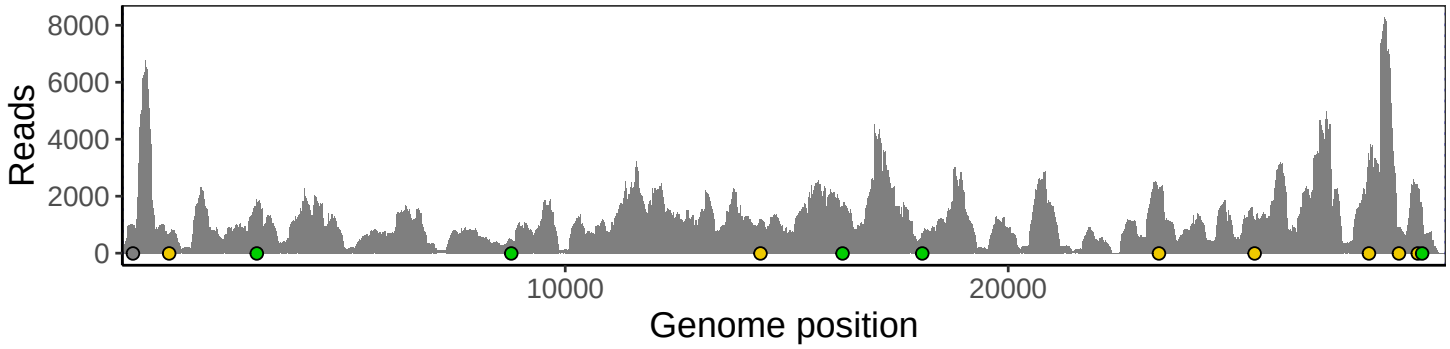


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

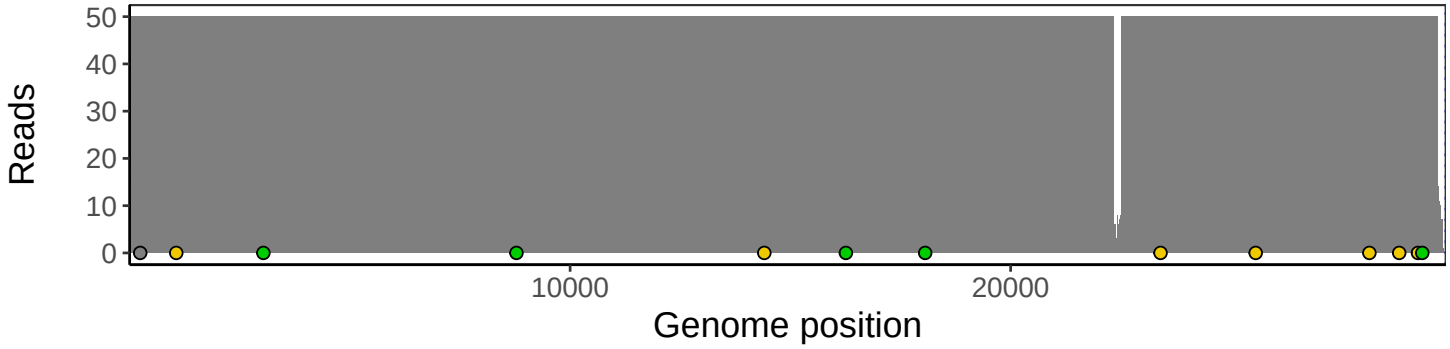


VSP0166-1 | 2020-05-22 | NP-OP | 269no-q | genomes | single experiment

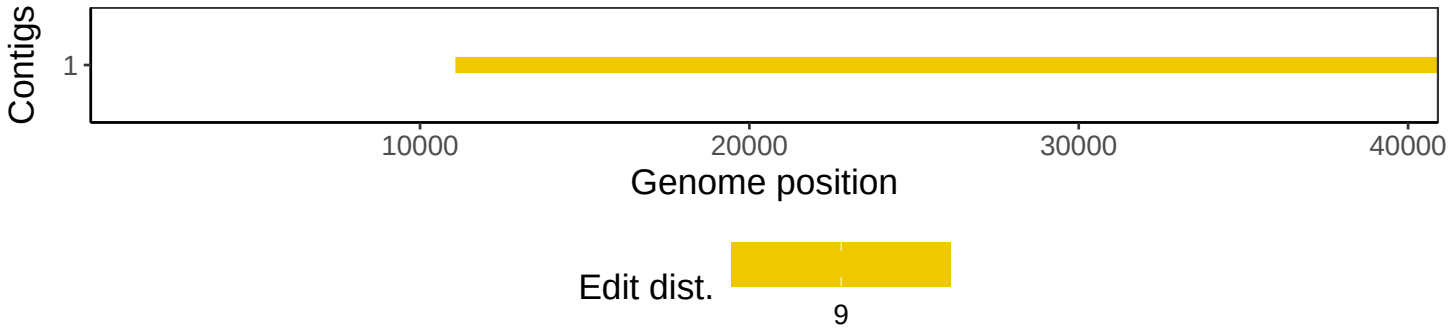
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

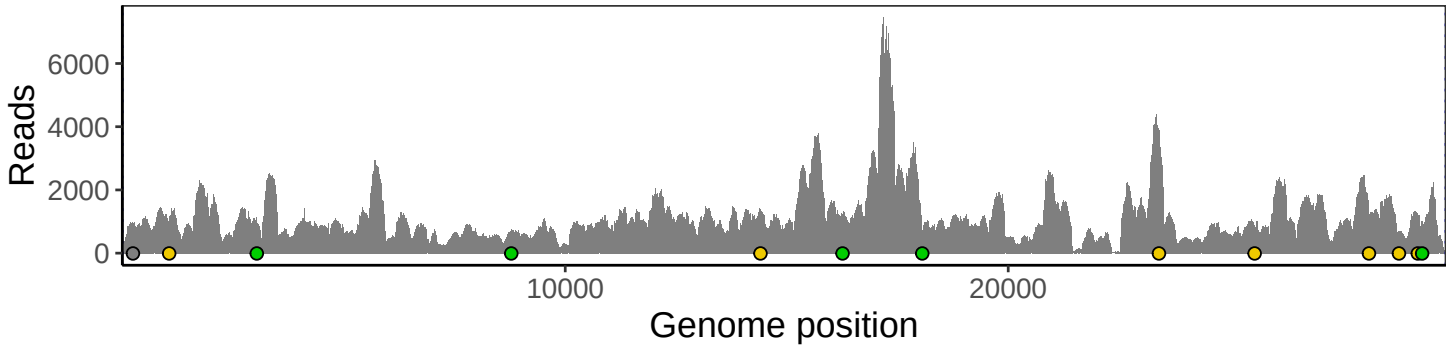


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

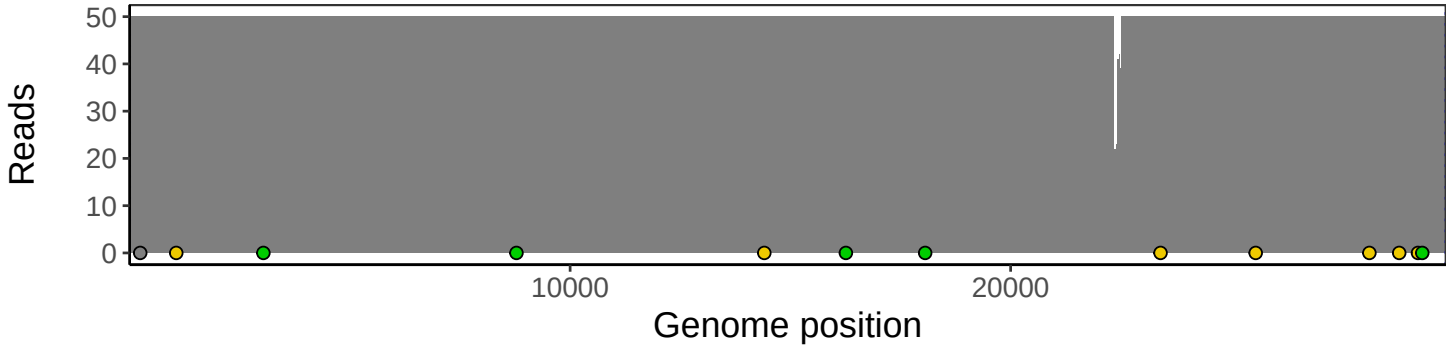


VSP0176-1 | 2020-05-27 | ETA | 269e-q | 166000 genomes | single experiment

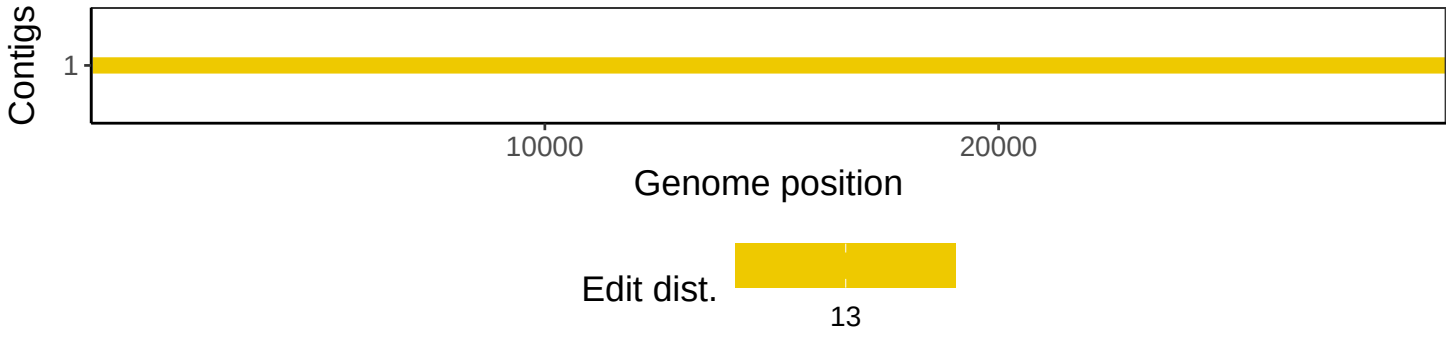
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

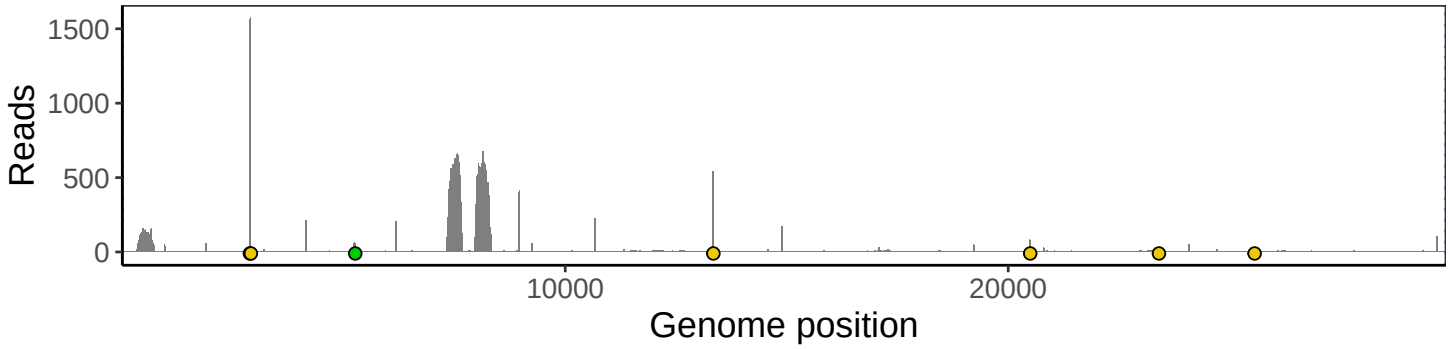


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

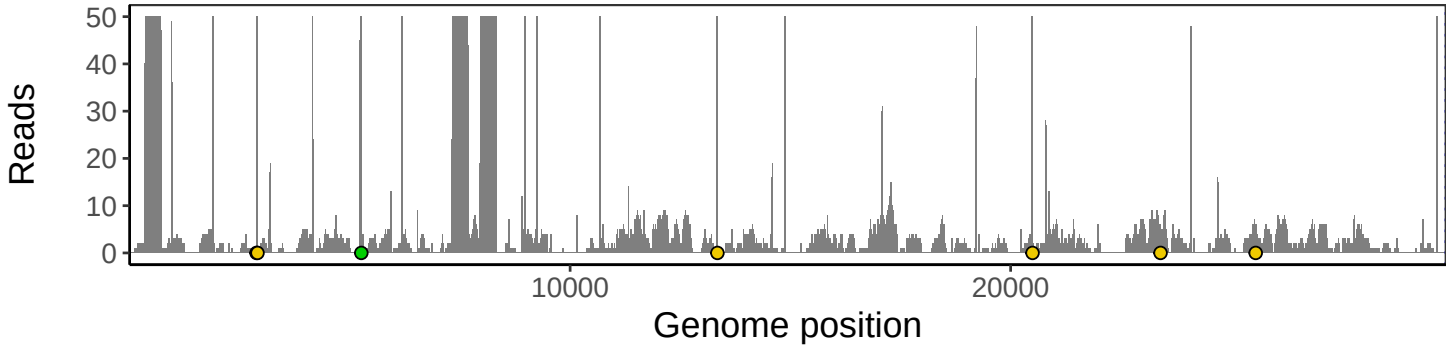


VSP0177-1 | 2020-05-27 | NP-OP | 269no-q | 59.7 genomes | single experiment

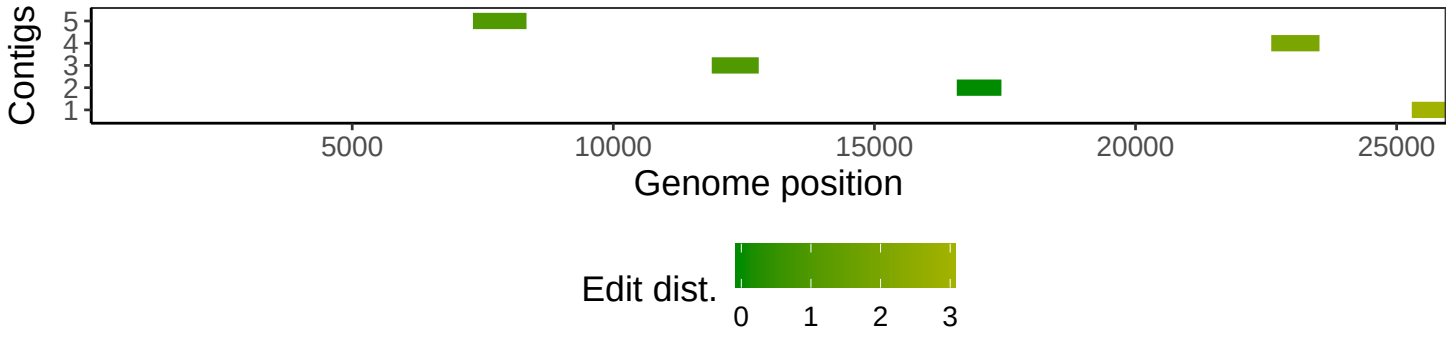
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

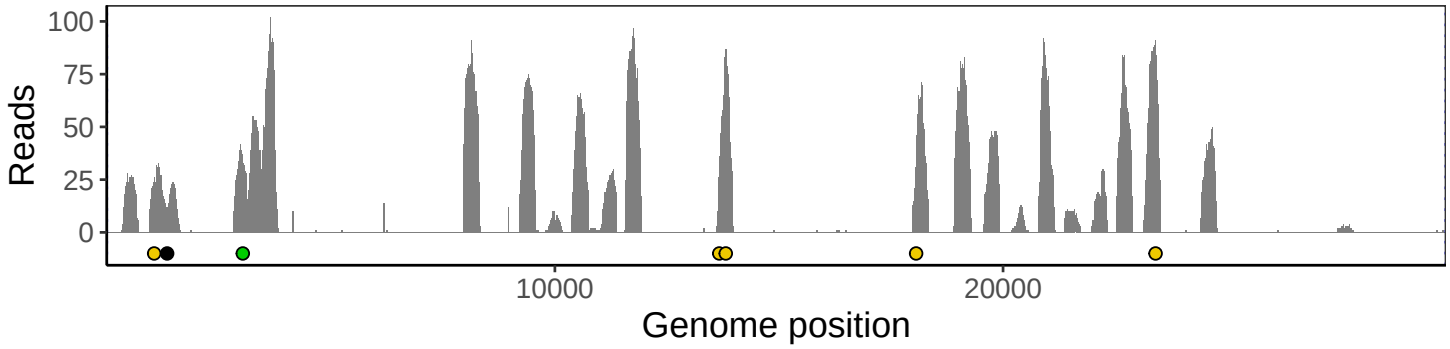


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

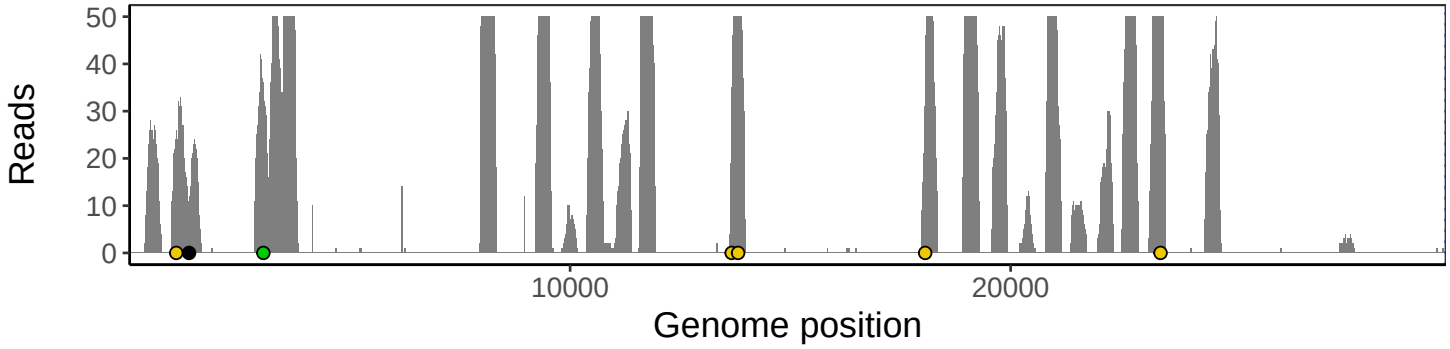


VSP0177-2 | 2020-05-27 | NP-OP | 269no-q | genomes | single experiment

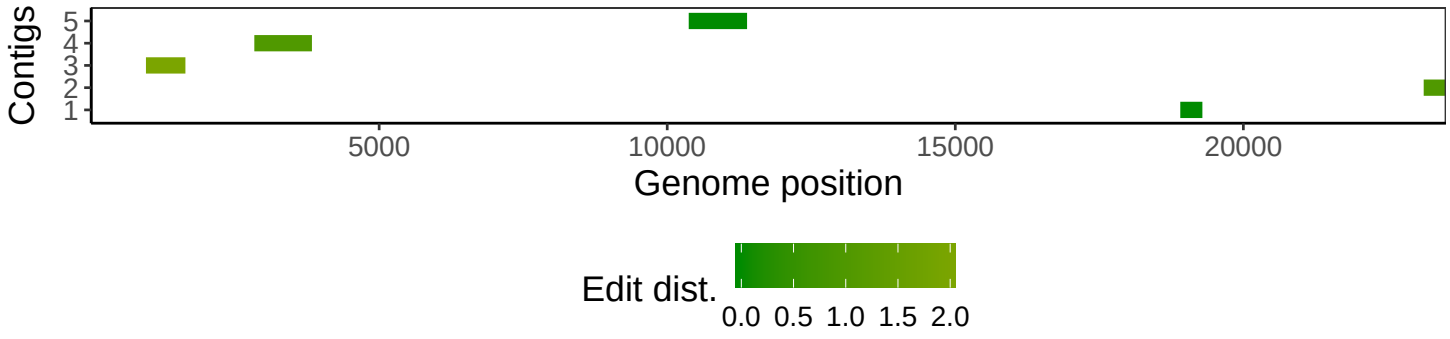
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

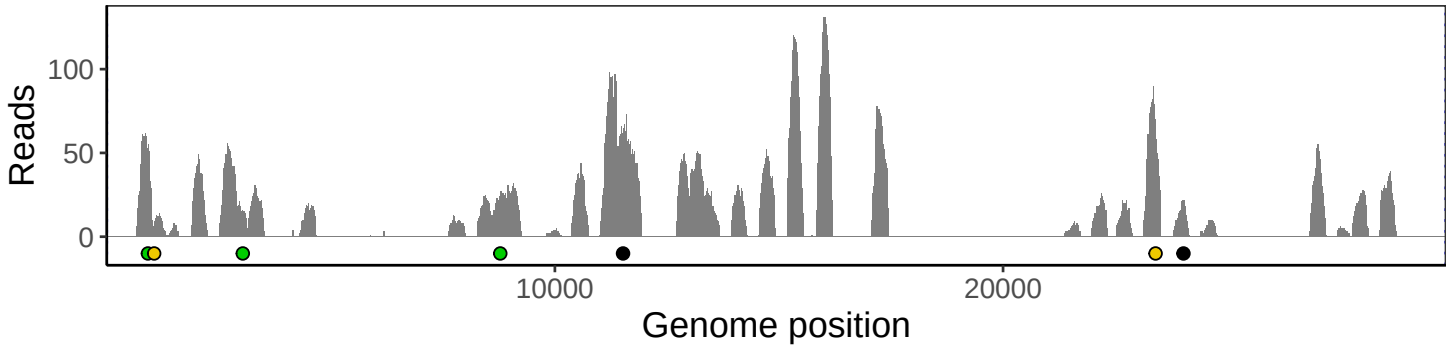


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

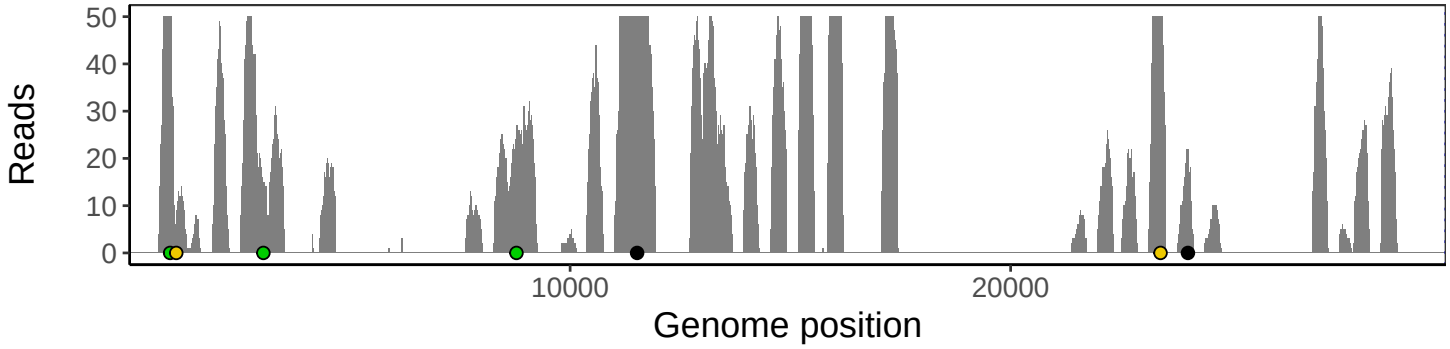


VSP0177-3 | 2020-05-27 | NP-OP | 269no-q | genomes | single experiment

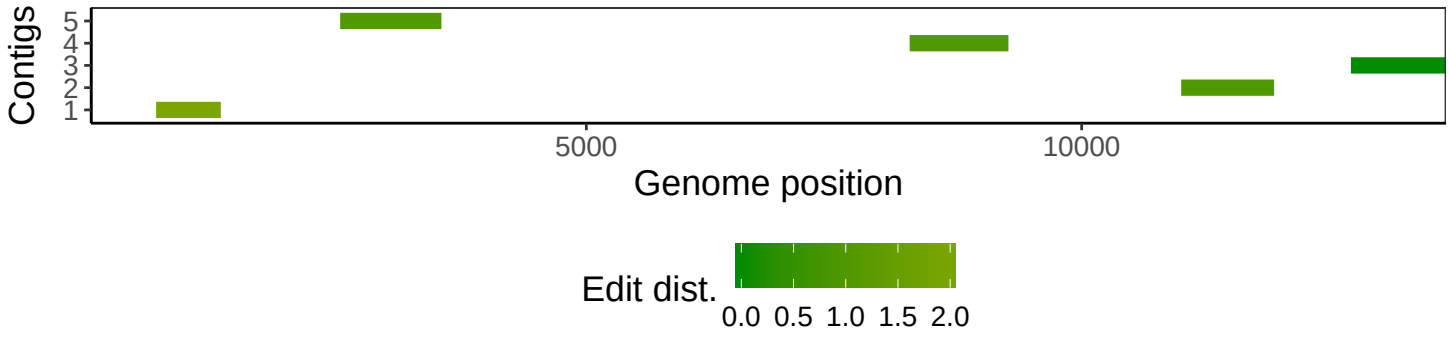
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

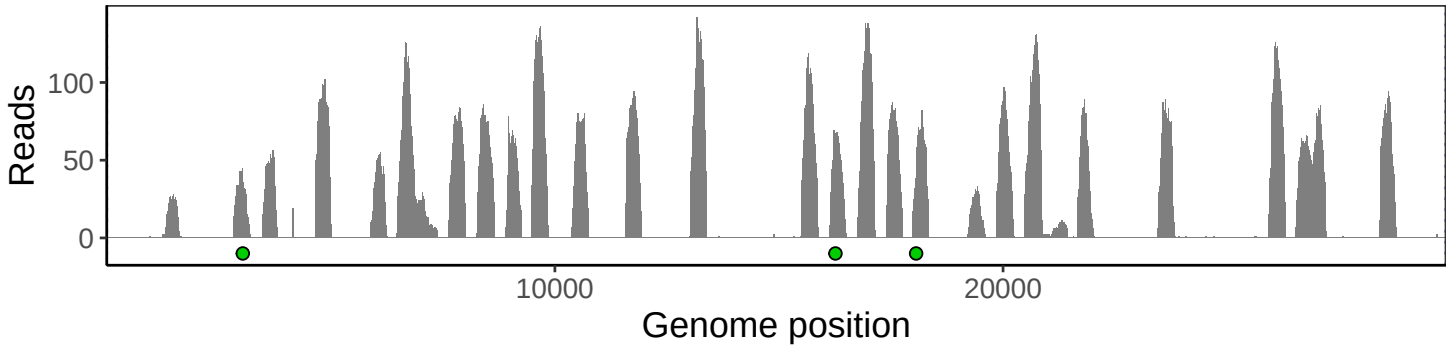


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

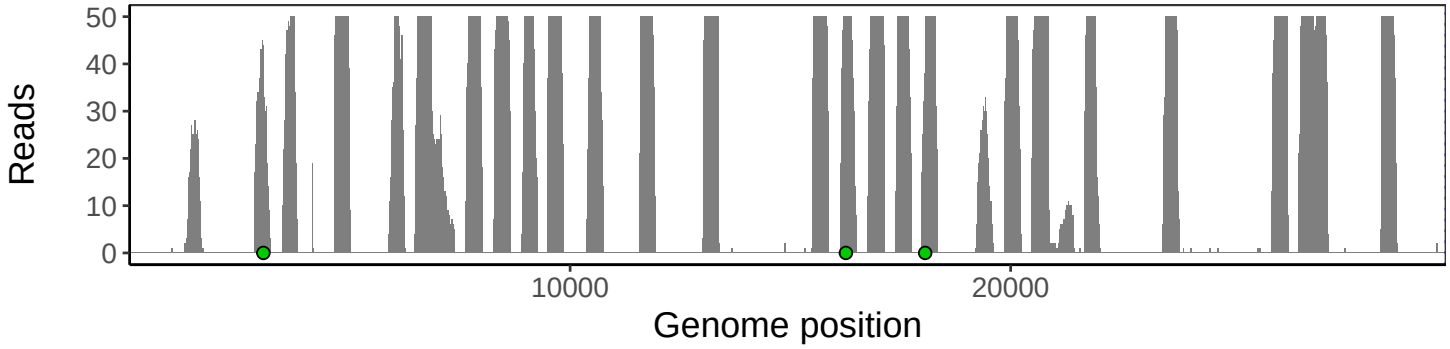


VSP0177-4 | 2020-05-27 | NP-OP | 269no-q | genomes | single experiment

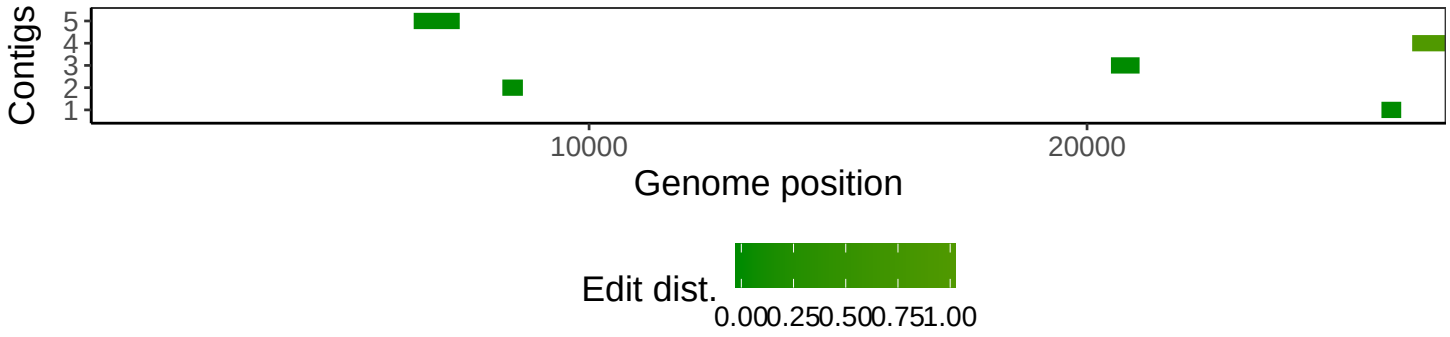
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

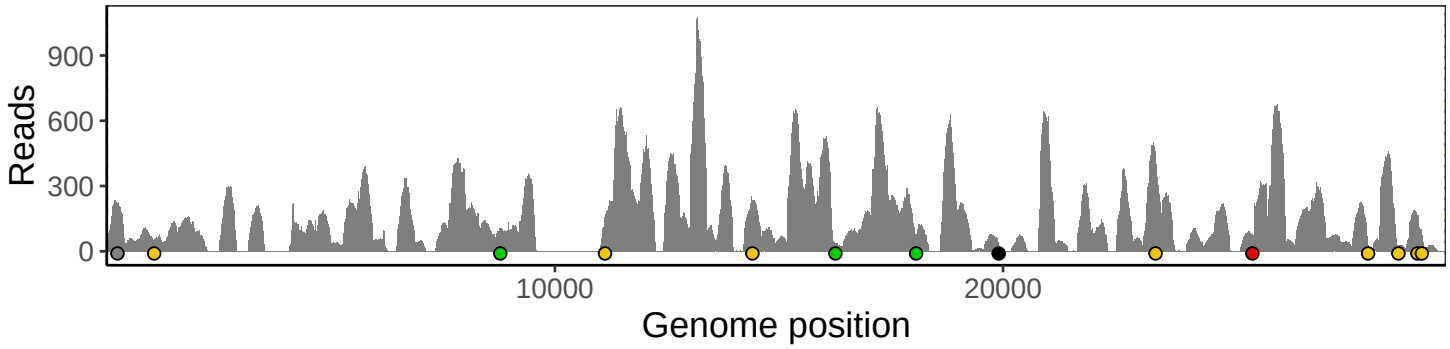


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

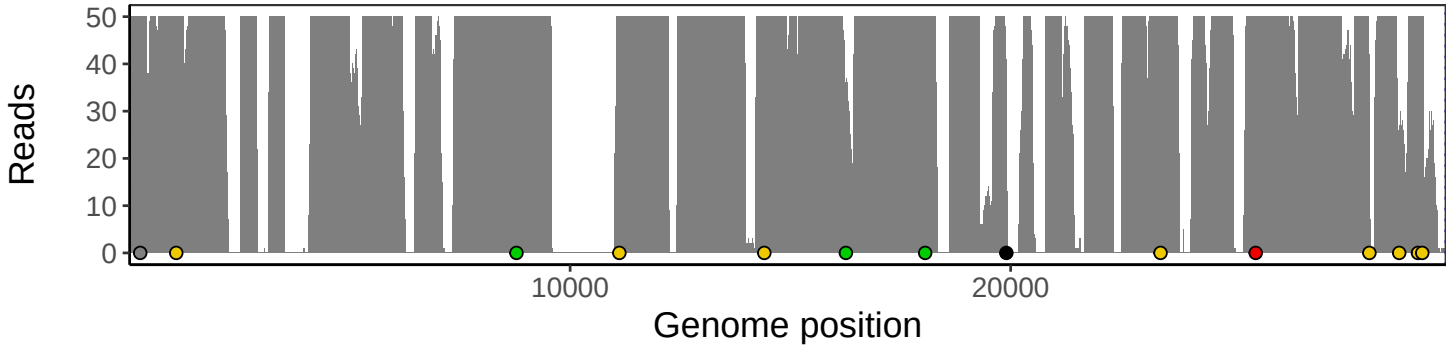


VSP0200-1 | 2020-06-08 | ETA | 269e-q | genomes | single experiment

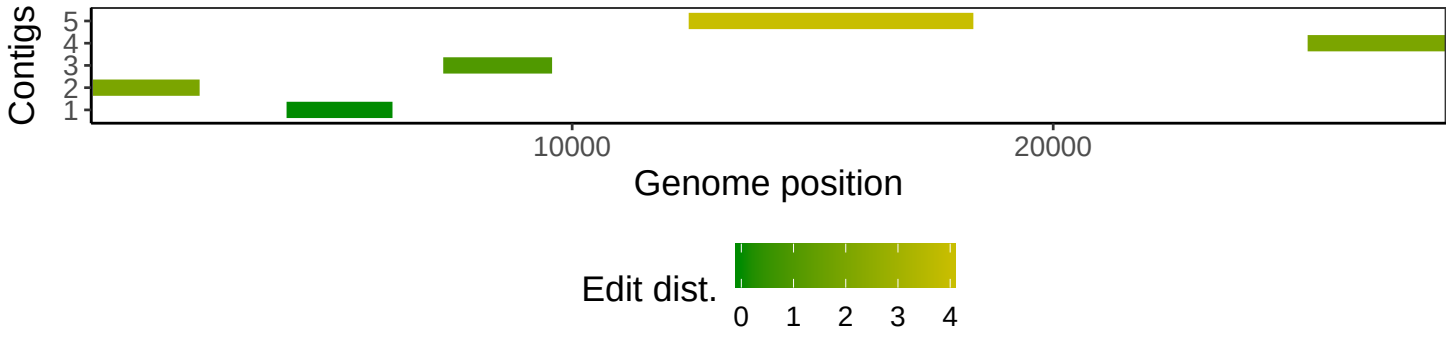
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

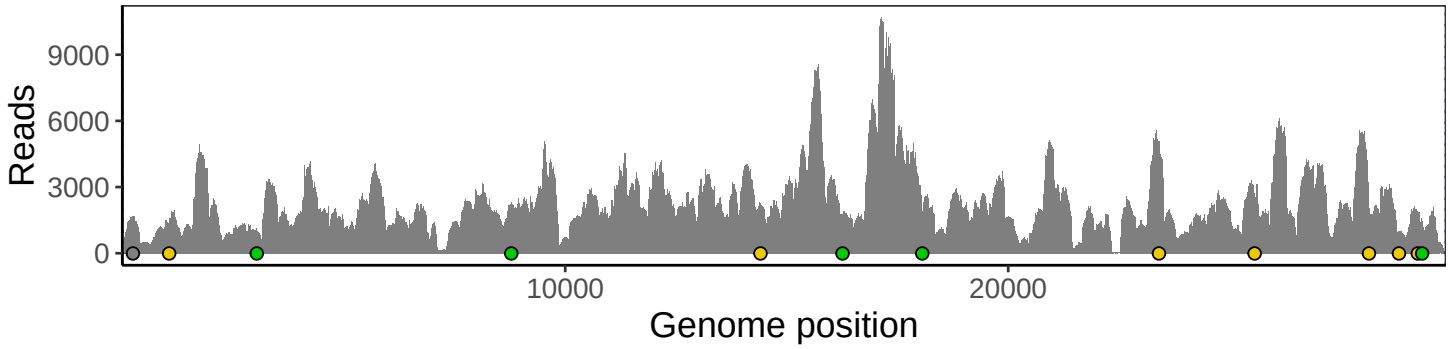


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

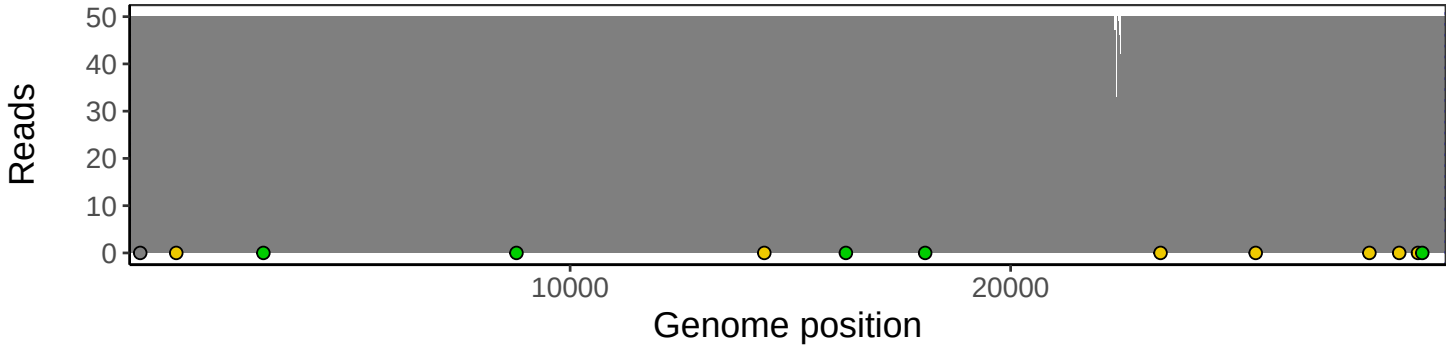


VSP0202-1 | 2020-06-12 | ETA | 269e-q | 16300 genomes | single experiment

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.



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