COVID-19 subject 237

2020-09-14

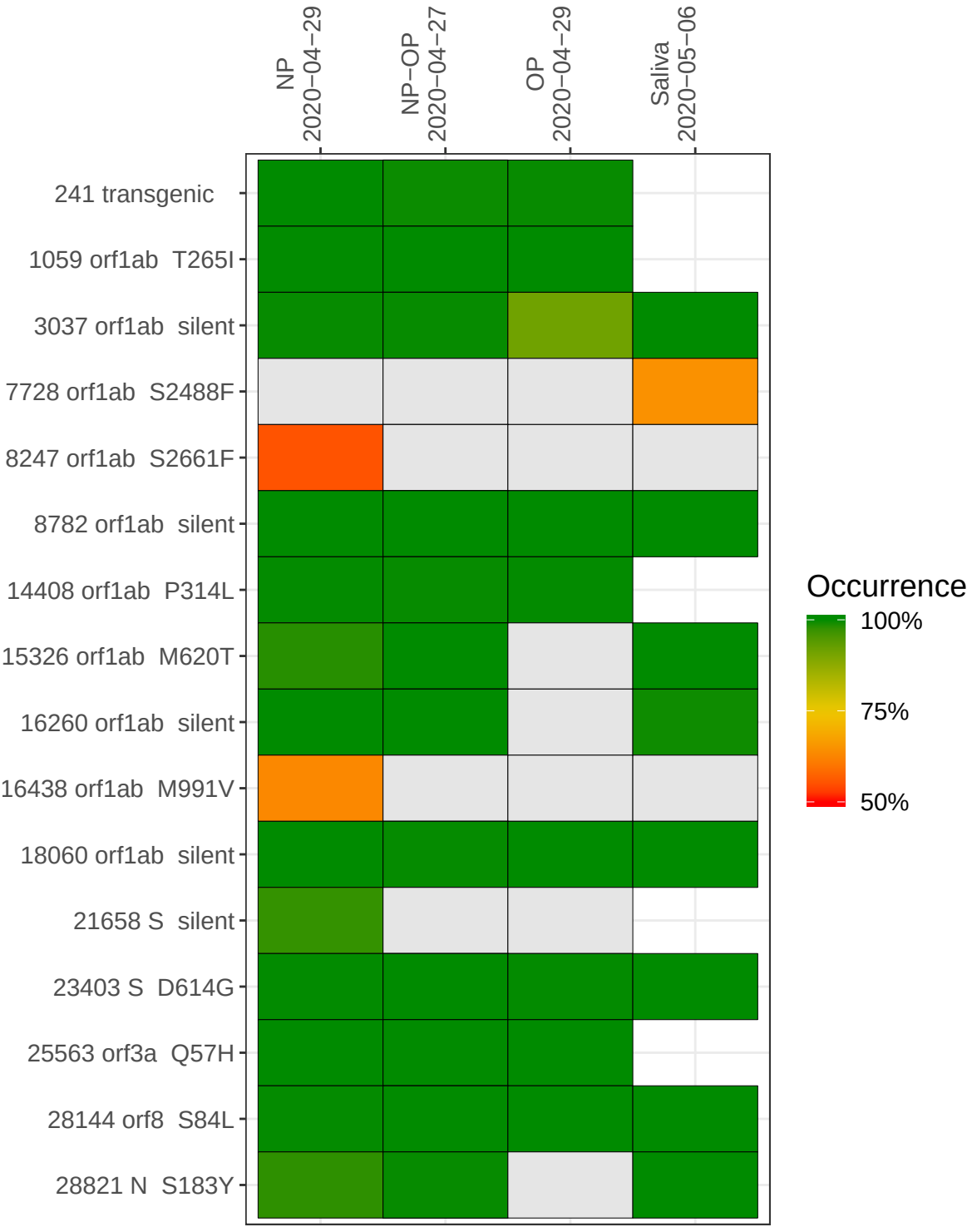
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

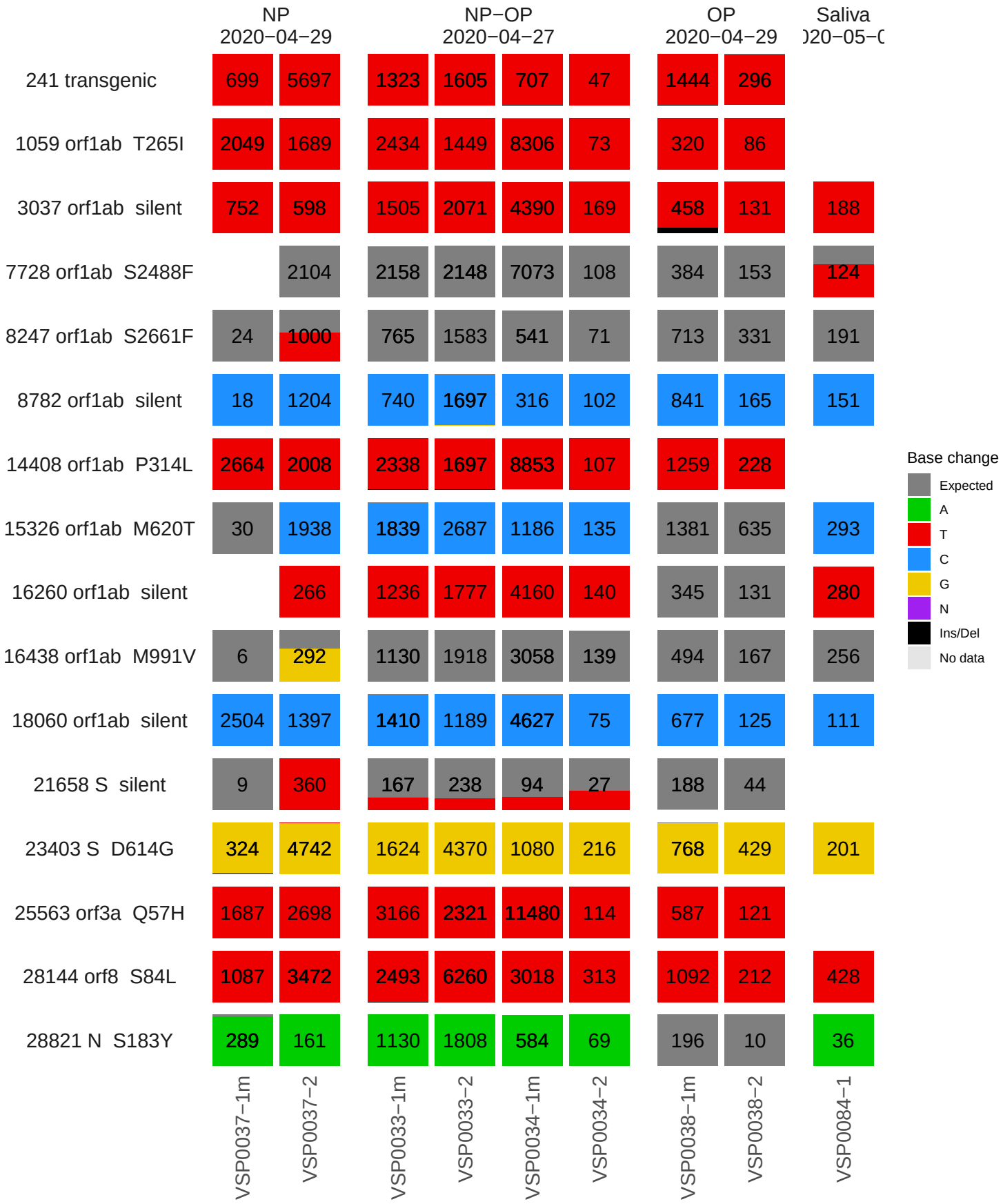
Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0033	composite	NA	NP-OP	2020-04-27	29.97	99.9%	99.8%
VSP0034	composite	NA	NP-OP	2020-04-27	29.84	99.8%	99.8%
VSP0037	composite	NA	NP	2020-04-29	24.92	99.3%	98.9%
VSP0038	composite	NA	OP	2020-04-29	29.92	99.9%	99.5%
VSP0033-1m	single experiment	NA	NP-OP	2020-04-27	28.58	99.9%	99.8%
VSP0033-2	single experiment	2985	NP-OP	2020-04-27	29.89	99.9%	99.5%
VSP0034-1m	single experiment	NA	NP-OP	2020-04-27	29.81	99.8%	99.8%
VSP0034-2	single experiment	1895000	NP-OP	2020-04-27	22.45	98.8%	98.5%
VSP0037-1m	single experiment	NA	NP	2020-04-29	6.66	89.3%	86.2%
VSP0037-2	single experiment	770	NP	2020-04-29	11.42	95.2%	94.4%
VSP0038-1m	single experiment	NA	OP	2020-04-29	22.46	99.9%	99.3%
VSP0038-2	single experiment	2060	OP	2020-04-29	22.32	99.7%	98.9%
VSP0084-1	single experiment	NA	Saliva	2020-05-06	4.70	78.5%	77.0%

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.

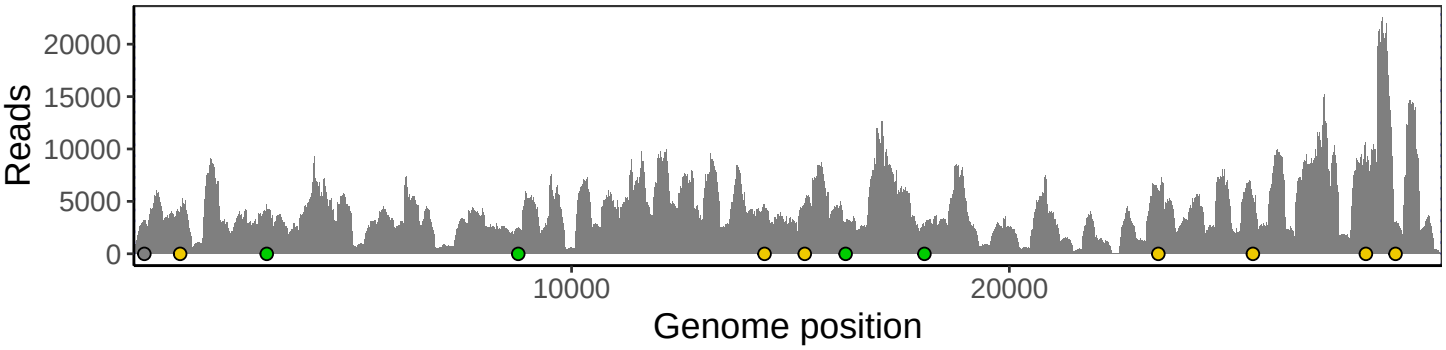



NP
2020−04−29
NP−OP
2020−04−27
OP
2020−04−29
Saliva
)20−05−(
241 transgenic
1059 orf1ab T265I
3037 orf1ab silent
7728 orf1ab S2488F
8247 orf1ab S2661F
8782 orf1ab silent
14408 orf1ab P314L
15326 orf1ab M620T
16260 orf1ab silent
16438 orf1ab M991V
18060 orf1ab silent
21658 S silent
23403 S D614G
25563 orf3a Q57H
28144 orf8 S84L
28821 N S183Y
699 5697 1323 1605 707 47 1444 296
2049 1689 2434 1449 8306 73 320 86
752 598 1505 2071 4390 169 458 131 188
2104 2158 2148 7073 108 384 153 124
24 1000 765 1583 541 71 713 331 191
18 1204 740 1697 316 102 841 165 151
2664 2008 2338 1697 8853 107 1259 228
30 1938 1839 2687 1186 135 1381 635 293
266 1236 1777 4160 140 345 131 280
6 292 1130 1918 3058 139 494 167 256
2504 1397 1410 1189 4627 75 677 125 111
9 360 167 238 94 27 188 44
324 4742 1624 4370 1080 216 768 429 201
1687 2698 3166 2321 11480 114 587 121
1087 3472 2493 6260 3018 313 1092 212 428
289 161 1130 1808 584 69 196 10 36
Base change
Expected
A
T
C
G
N
Ins/Del
No data
VSP0037−1m
VSP0037−2
VSP0033−1m
VSP0033−2
VSP0034−1m
VSP0034−2
VSP0038−1m
VSP0038−2
VSP0084−1

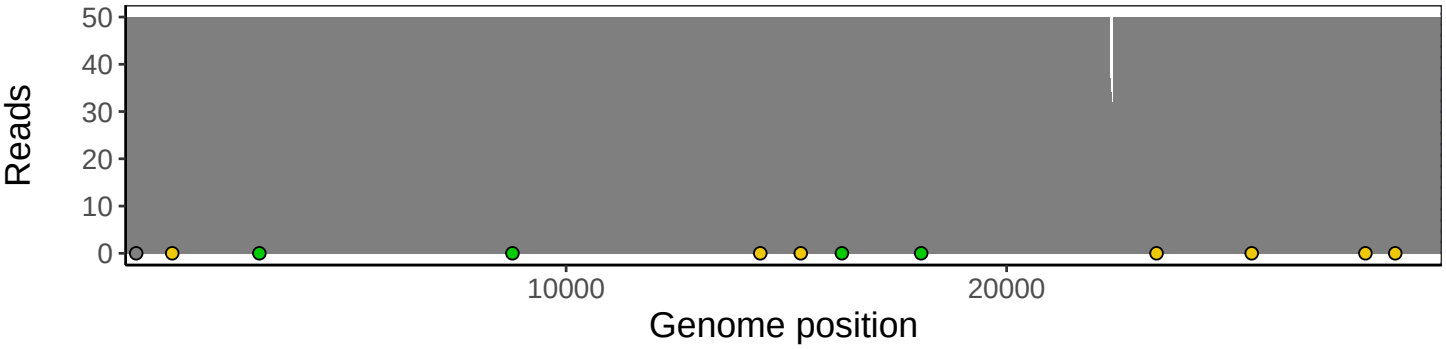
Analyses of individual experiments and composite results.

VSP0033 | 2020-04-27 | NP-OP | 237-tri | composite result

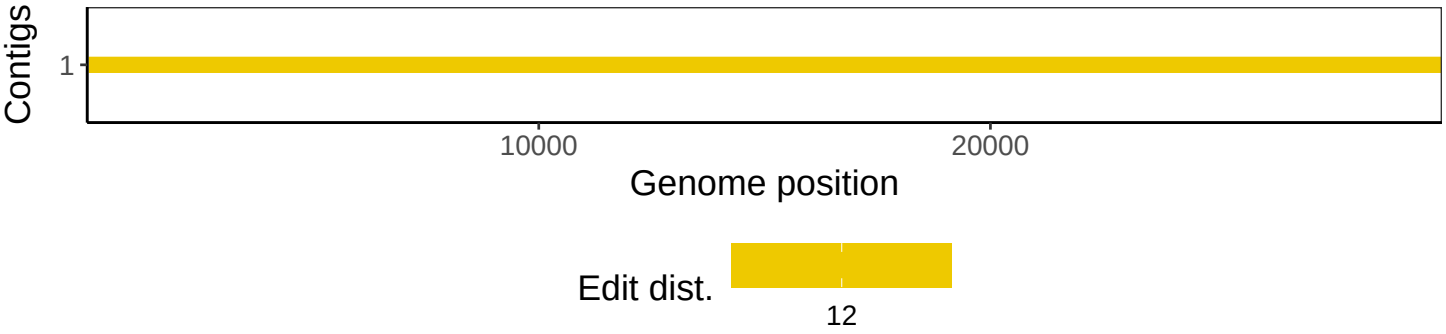
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

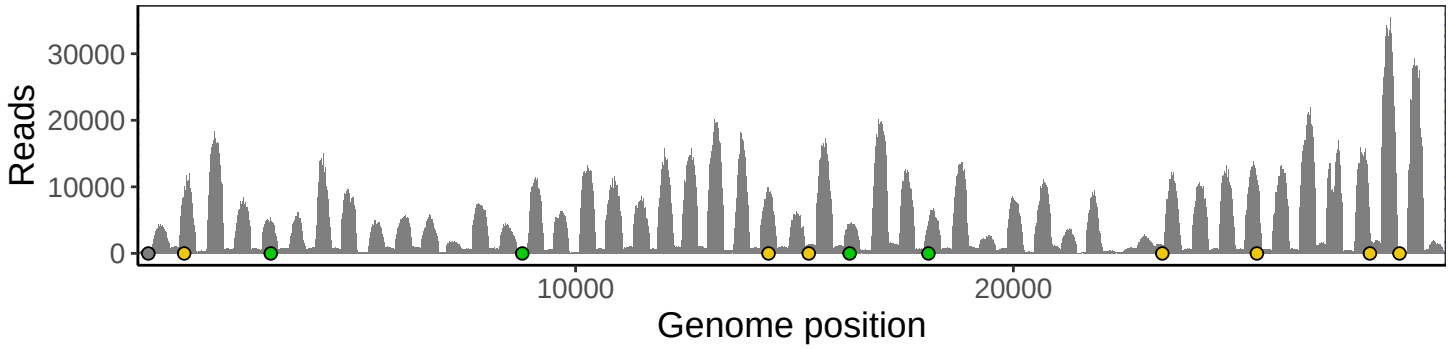


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

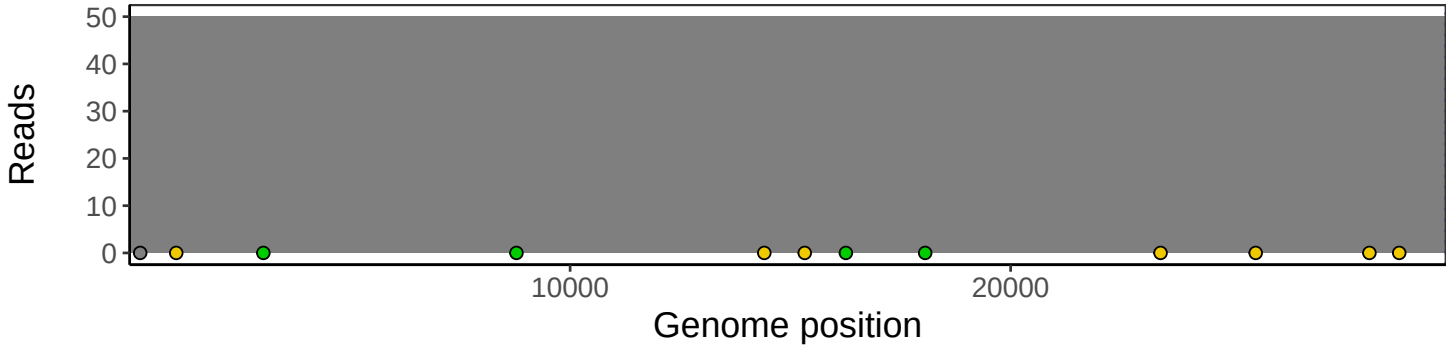


VSP0034 | 2020-04-27 | NP-OP | 237-qia | composite result

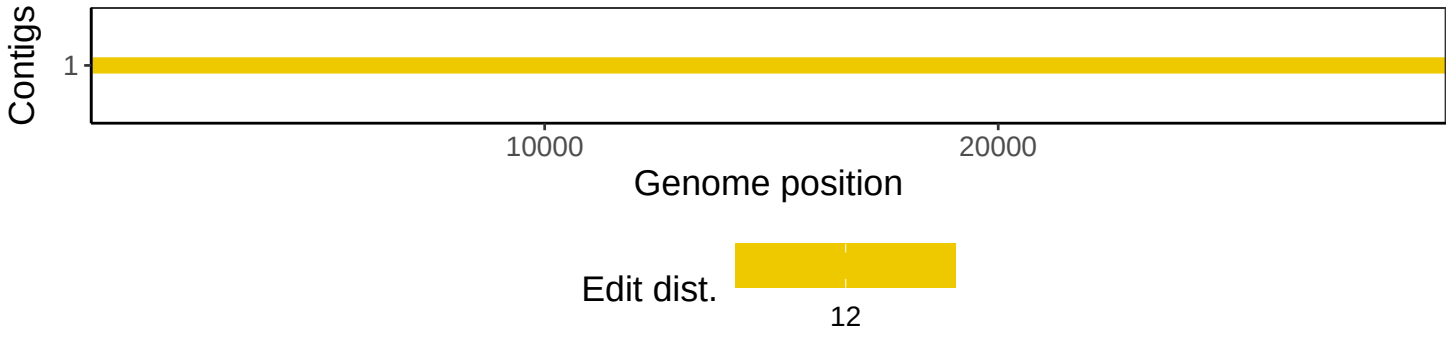
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

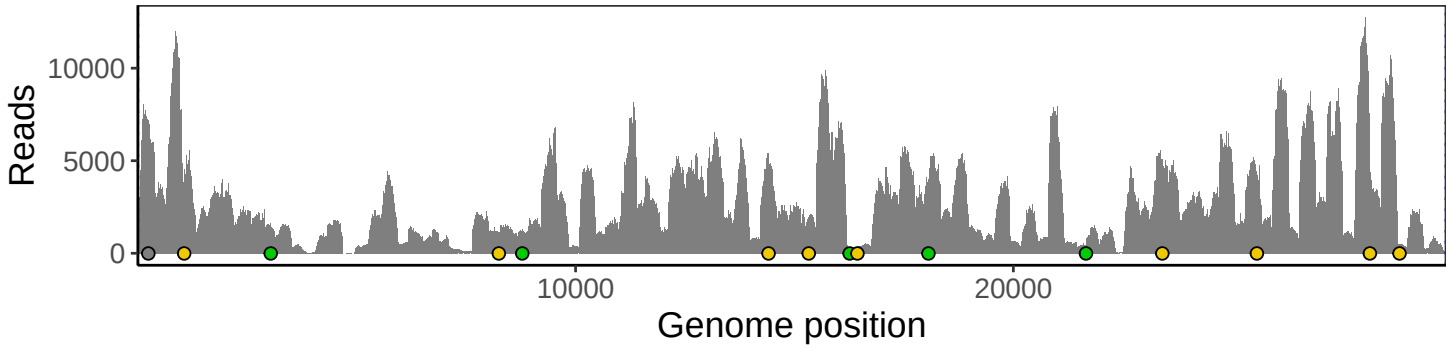


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

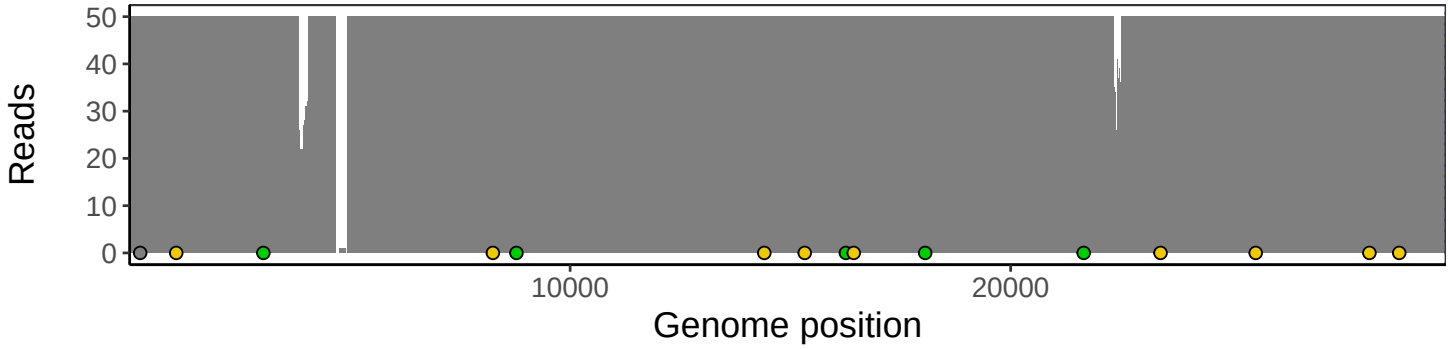


VSP0037 | 2020-04-29 | NP | 237n-tri | composite result

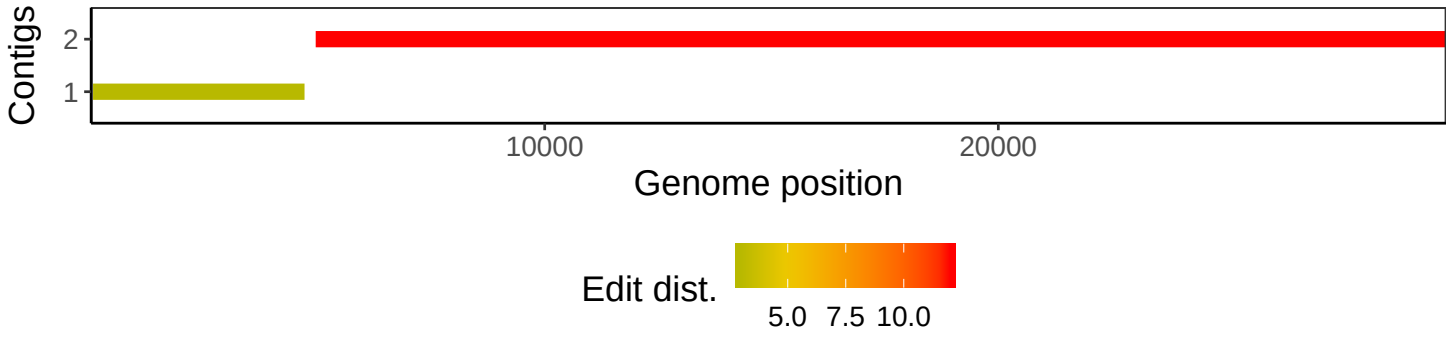
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

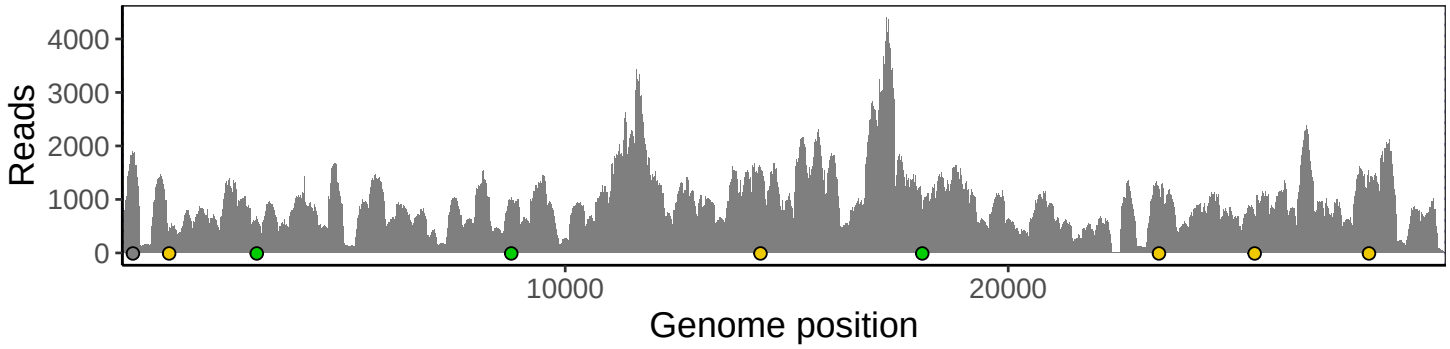


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

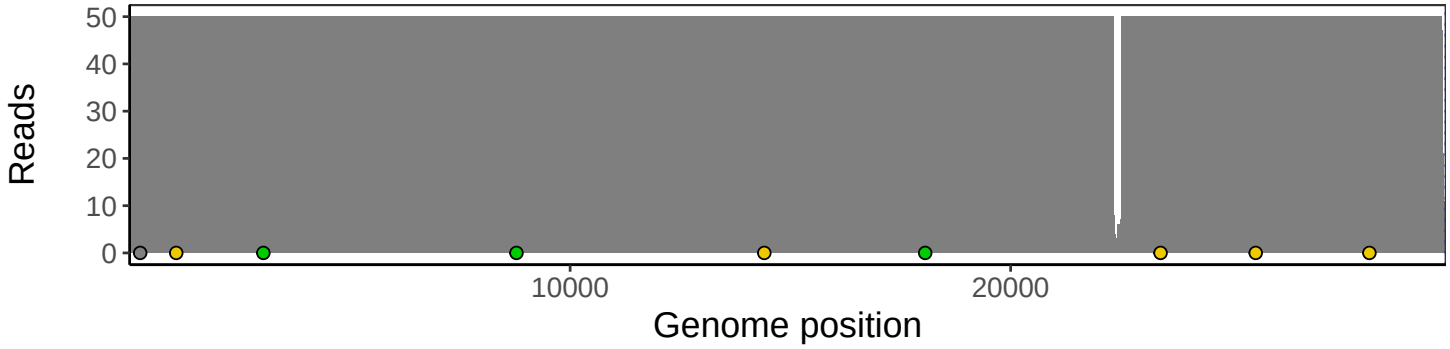


VSP0038 | 2020-04-29 | OP | 237o-tri | composite result

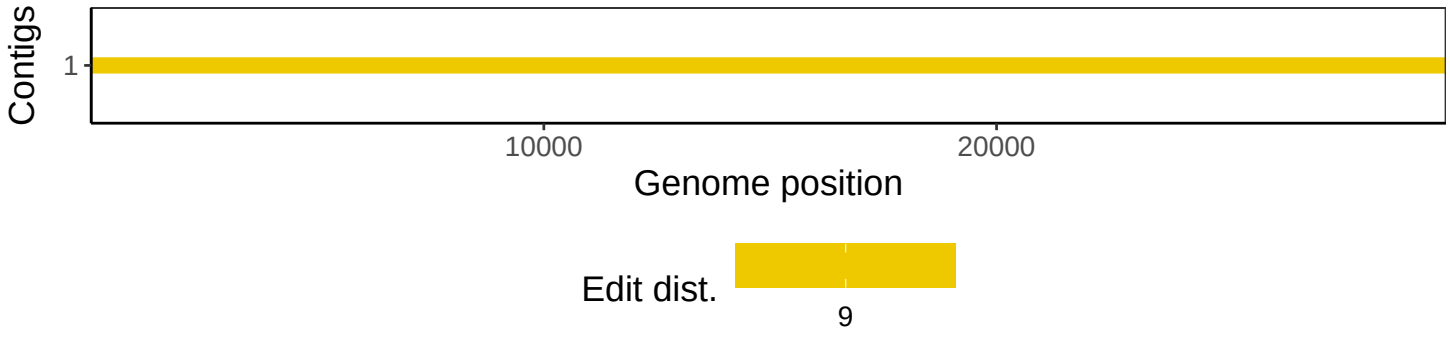
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

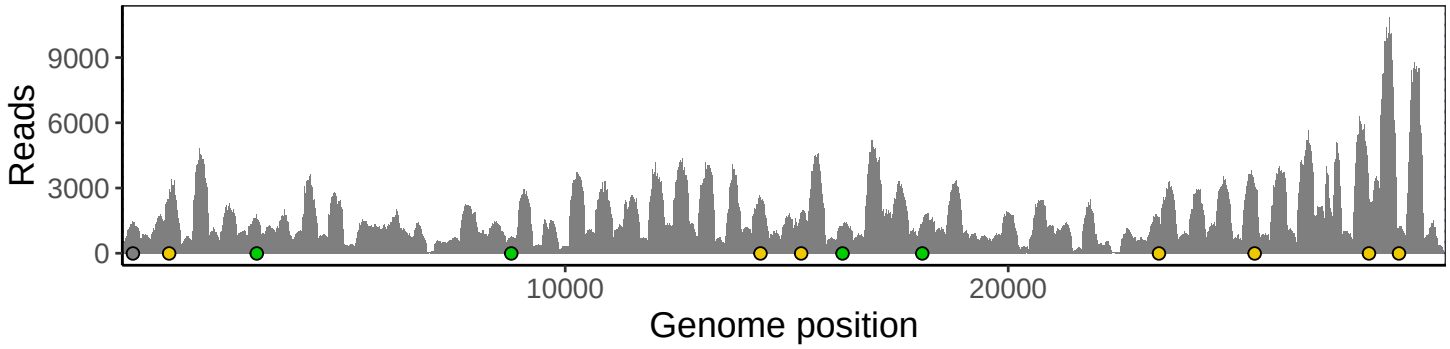


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

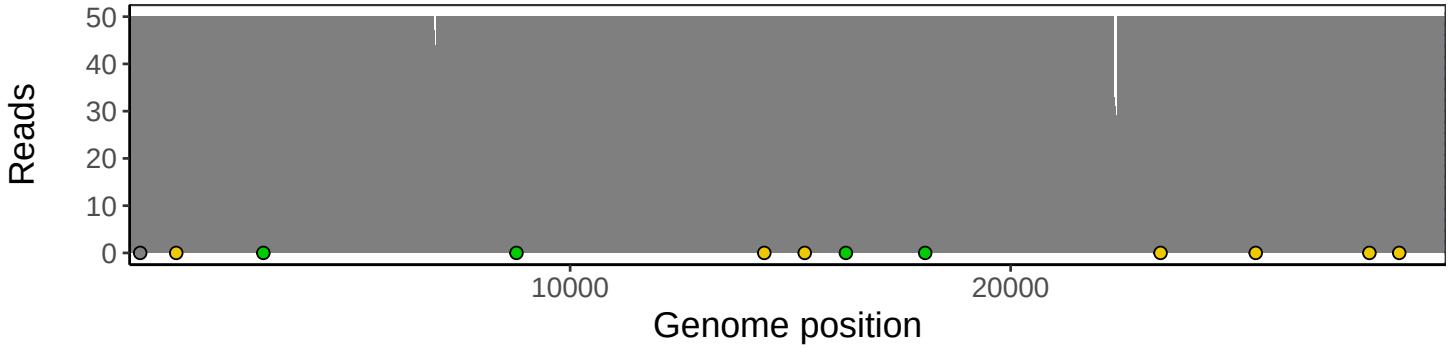


VSP0033-1m | 2020-04-27 | NP-OP | 237-tri | genomes | single experiment

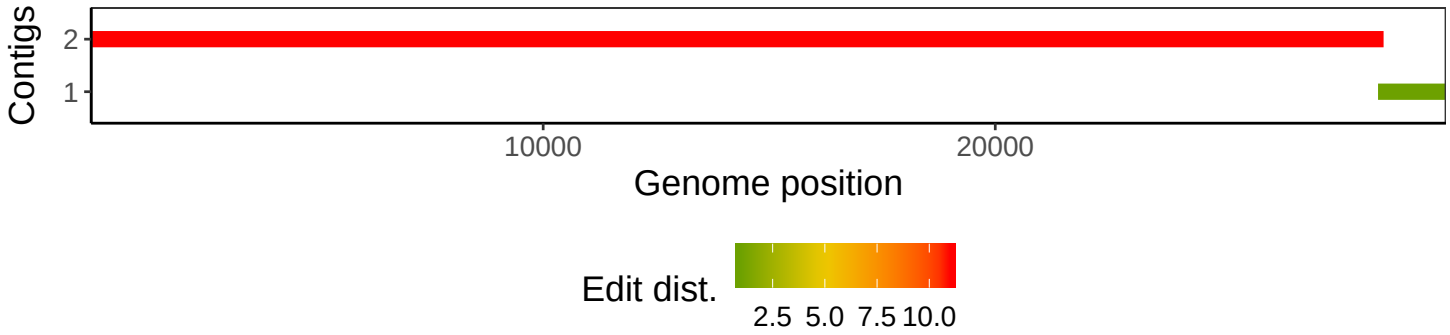
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

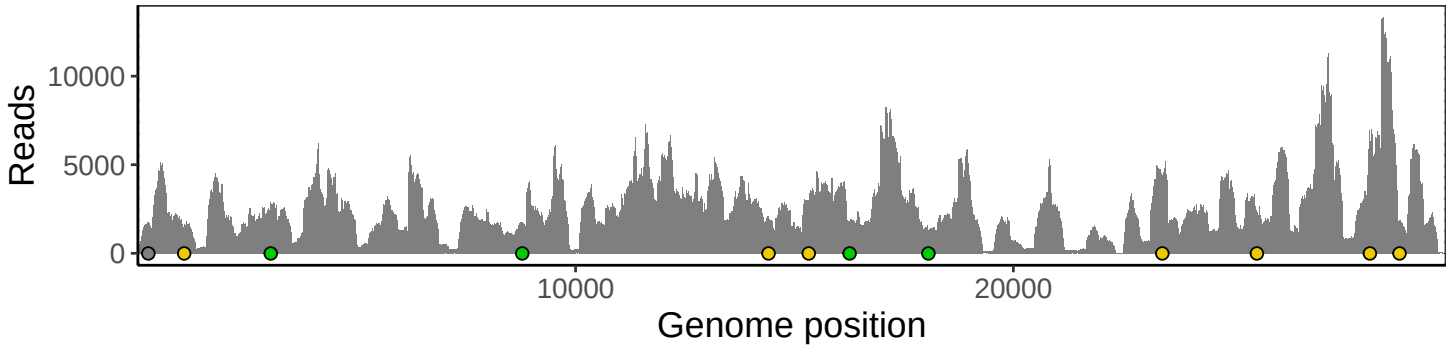


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

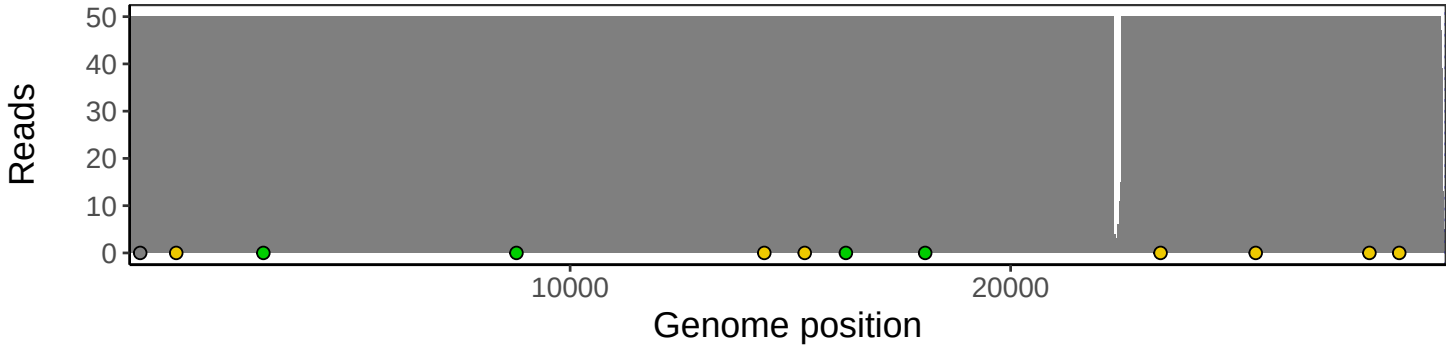


VSP0033-2 | 2020-04-27 | NP-OP | 237-tri | 2985 genomes | single experiment

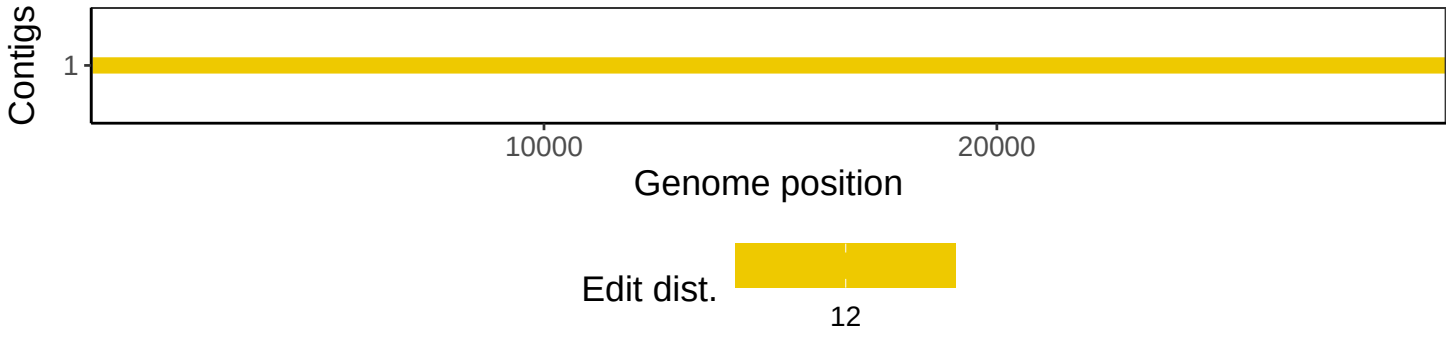
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

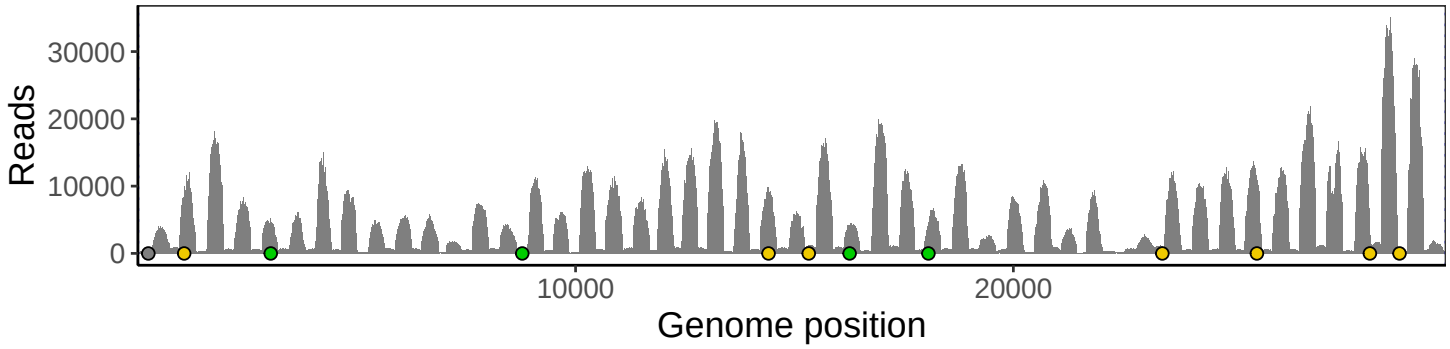


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

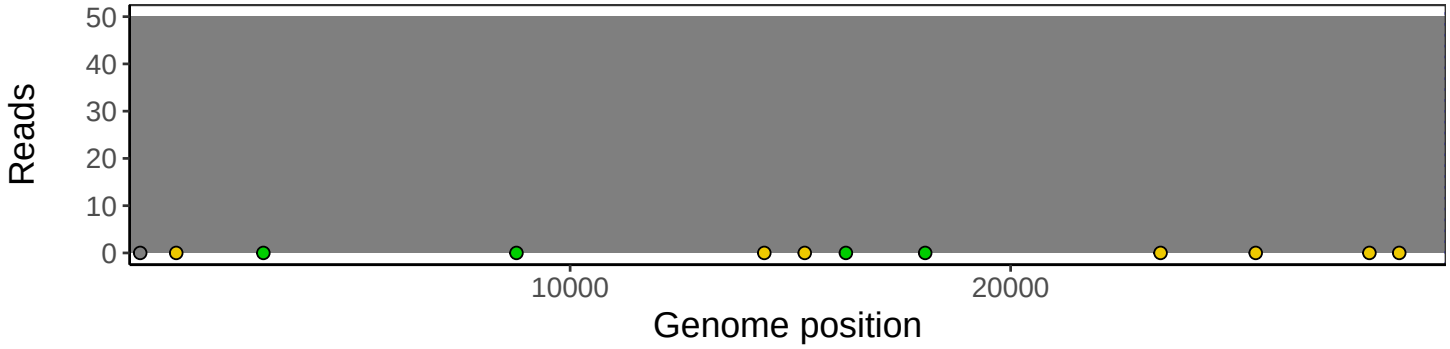


VSP0034-1m | 2020-04-27 | NP-OP | 237-qia | genomes | single experiment

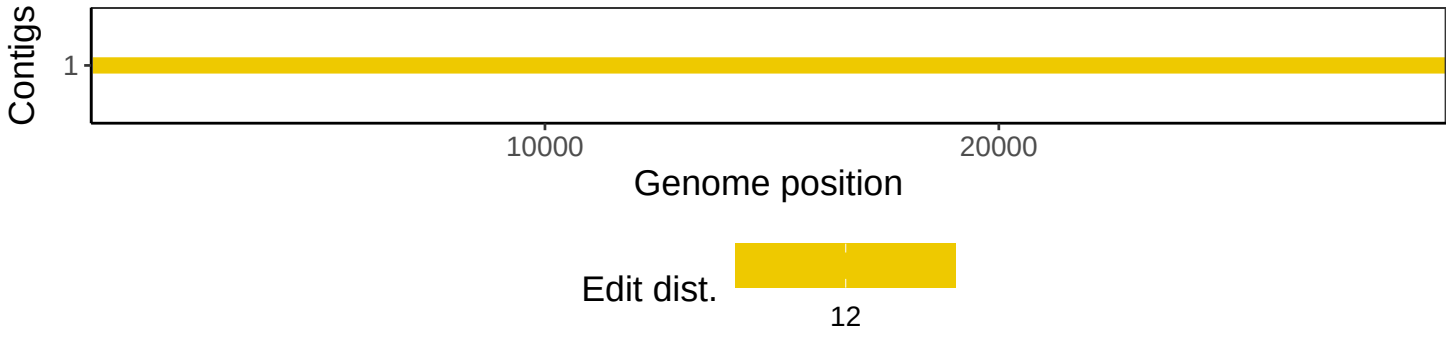
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

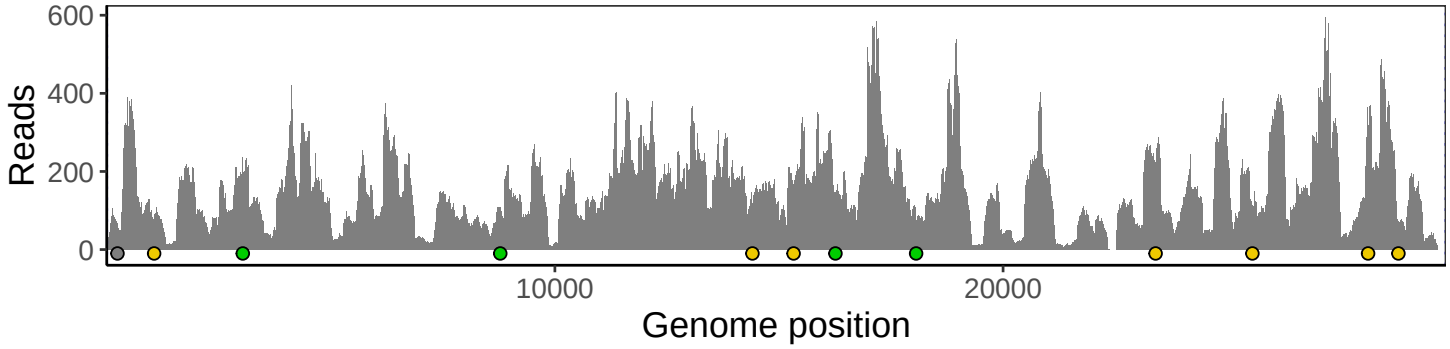


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

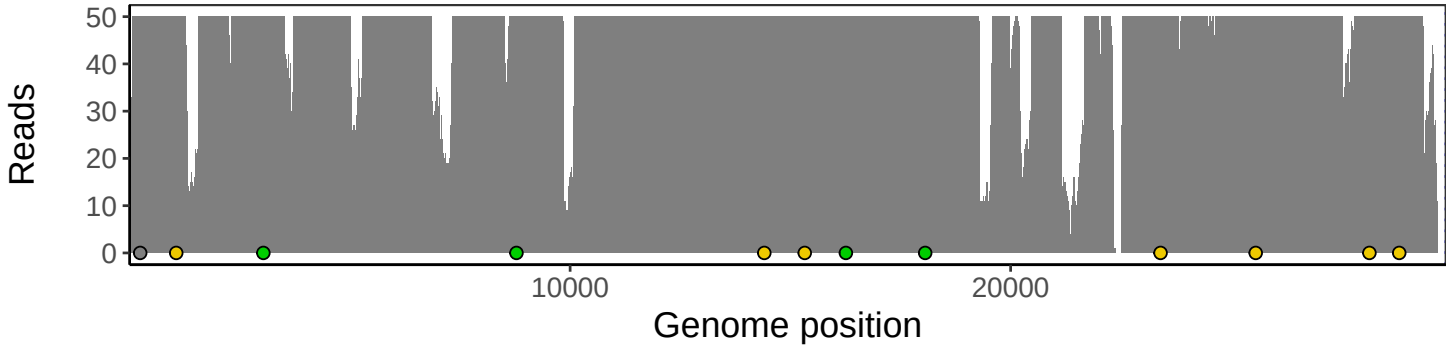


VSP0034-2 | 2020-04-27 | NP-OP | 237-qia | 1895000 genomes | single experiment

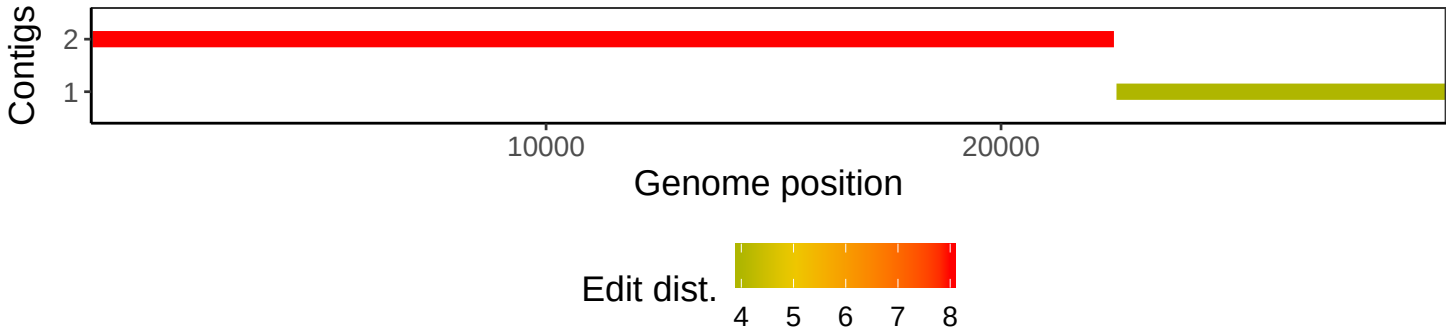
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

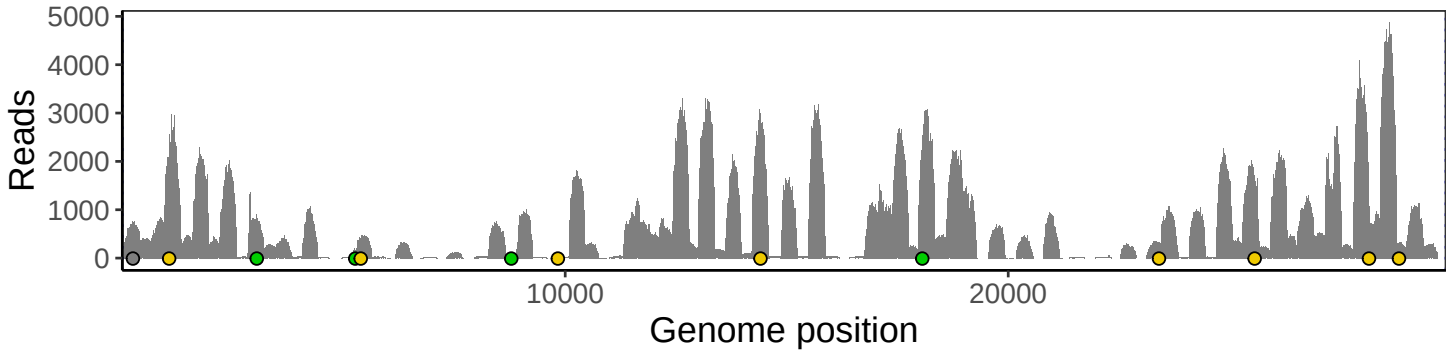


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

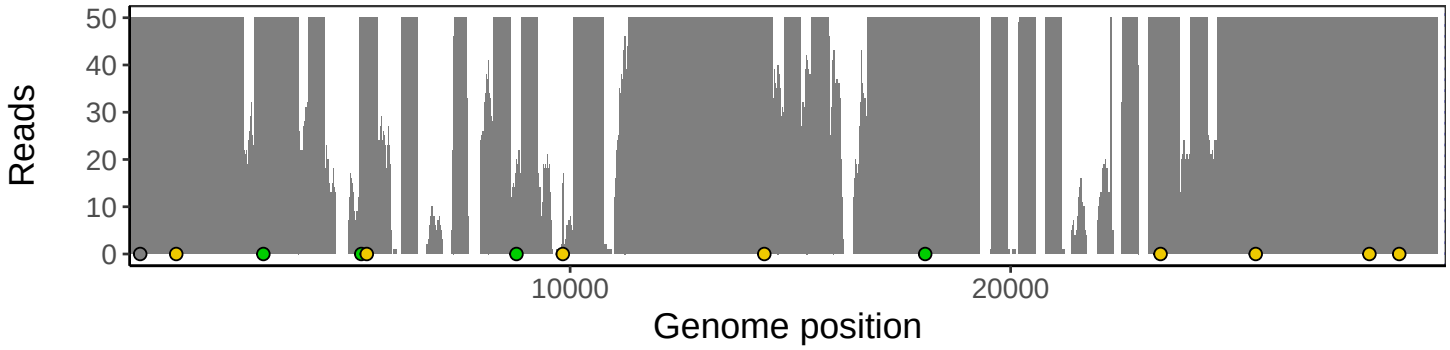


VSP0037-1m | 2020-04-29 | NP | 237n-tri | genomes | single experiment

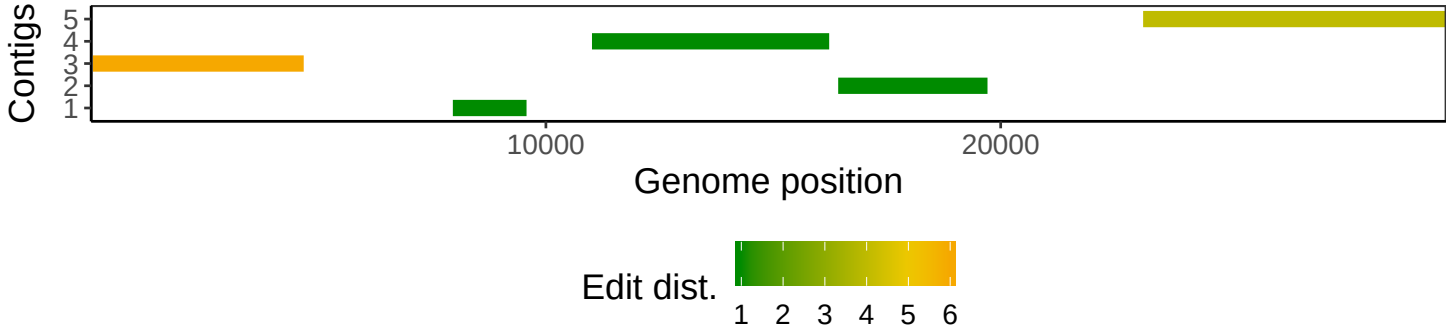
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

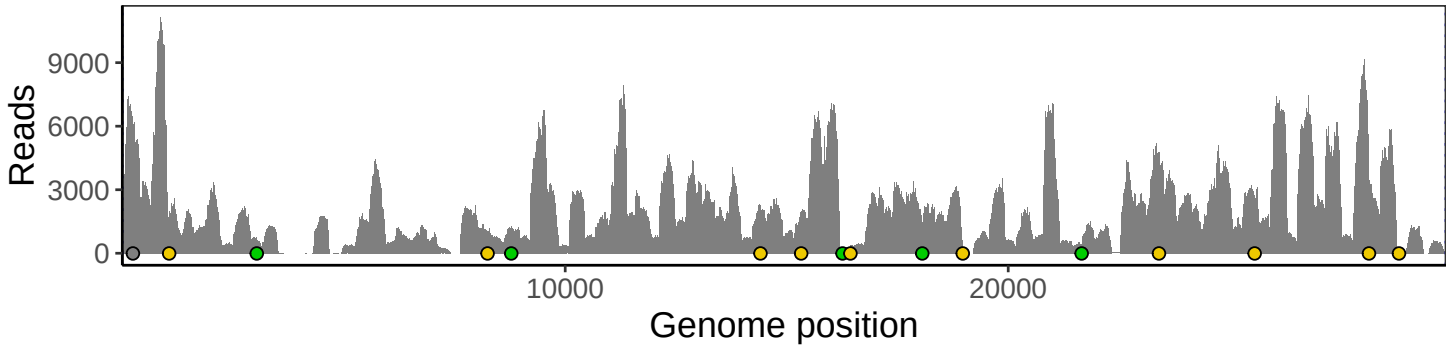


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

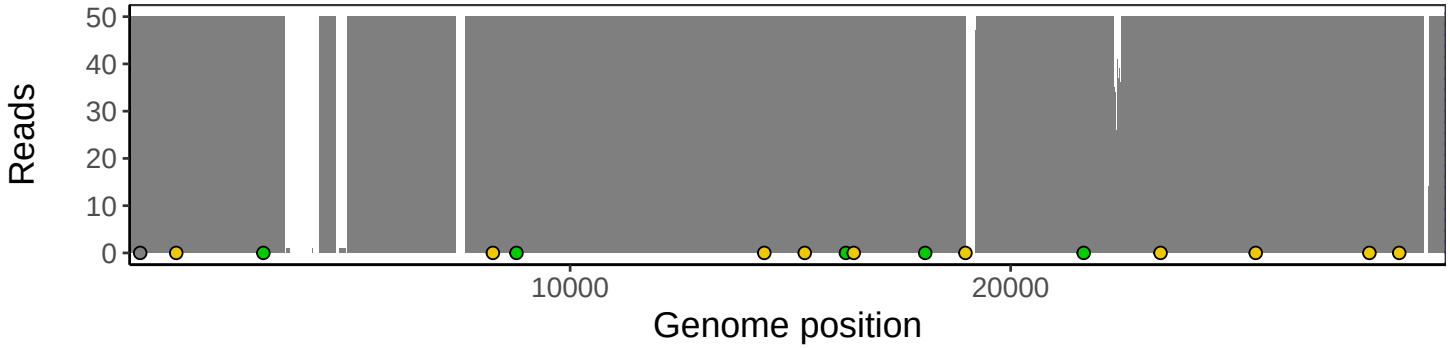


VSP0037-2 | 2020-04-29 | NP | 237n-tri | 770 genomes | single experiment

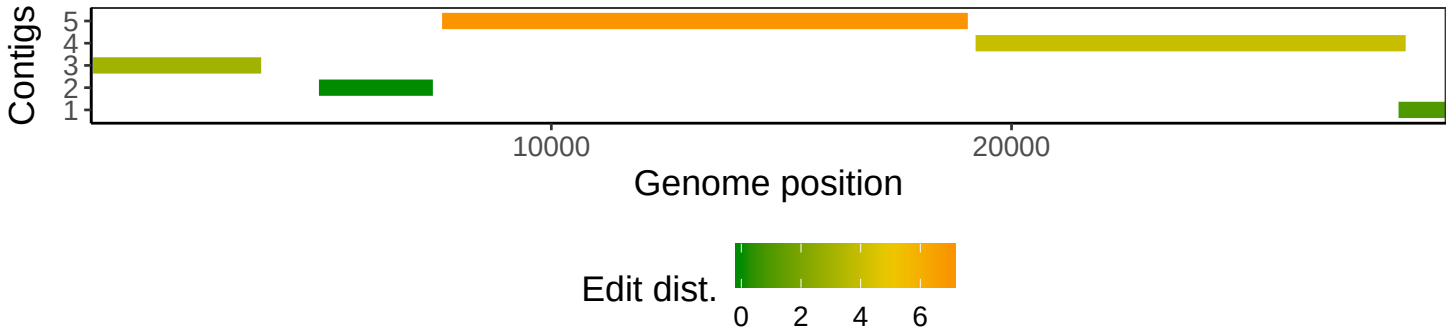
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

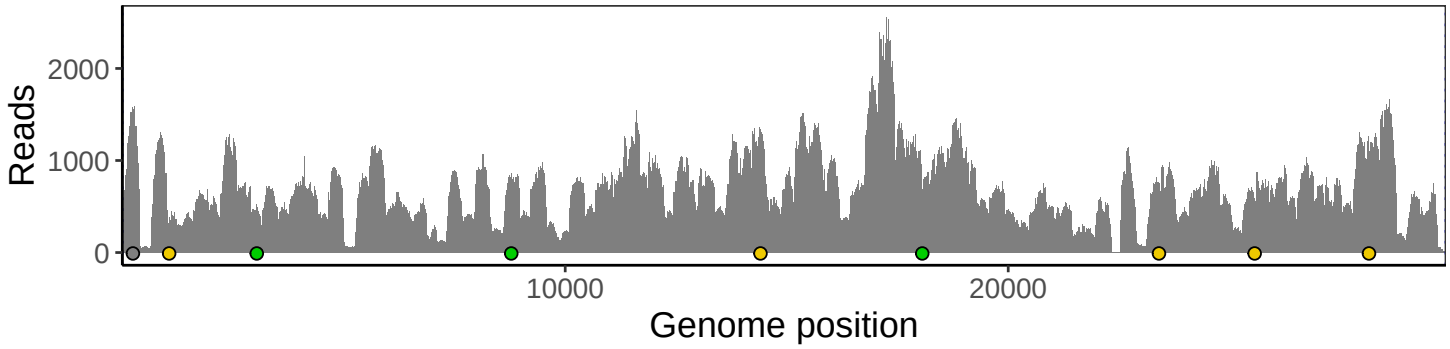


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

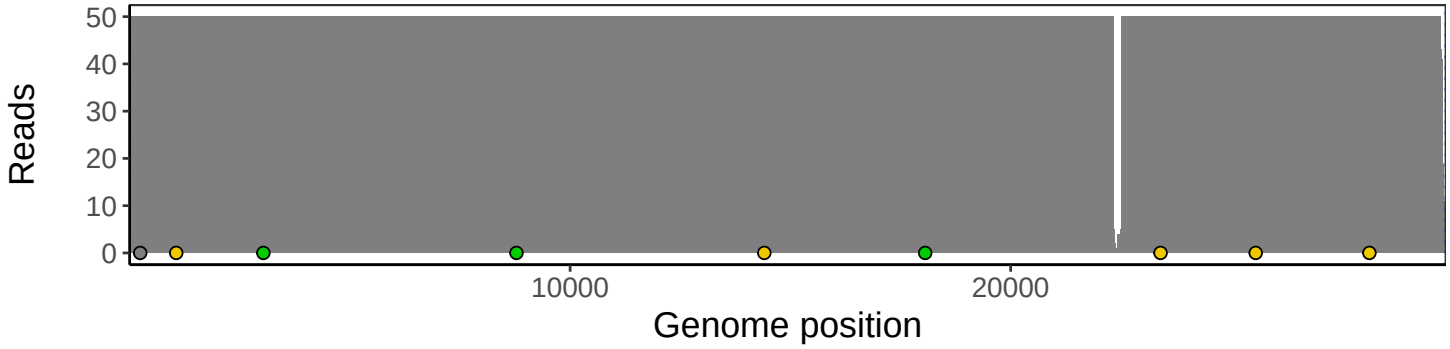


VSP0038-1m | 2020-04-29 | OP | 237o-tri | genomes | single experiment

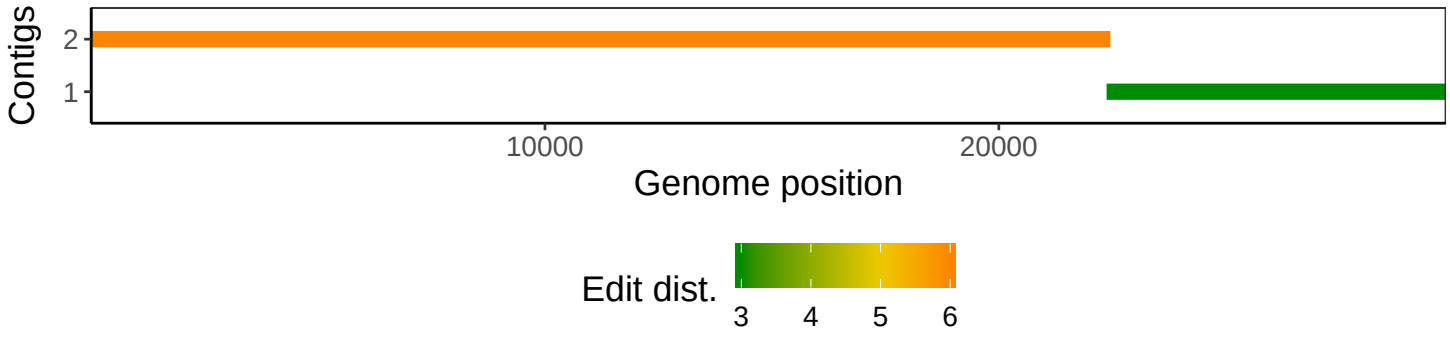
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

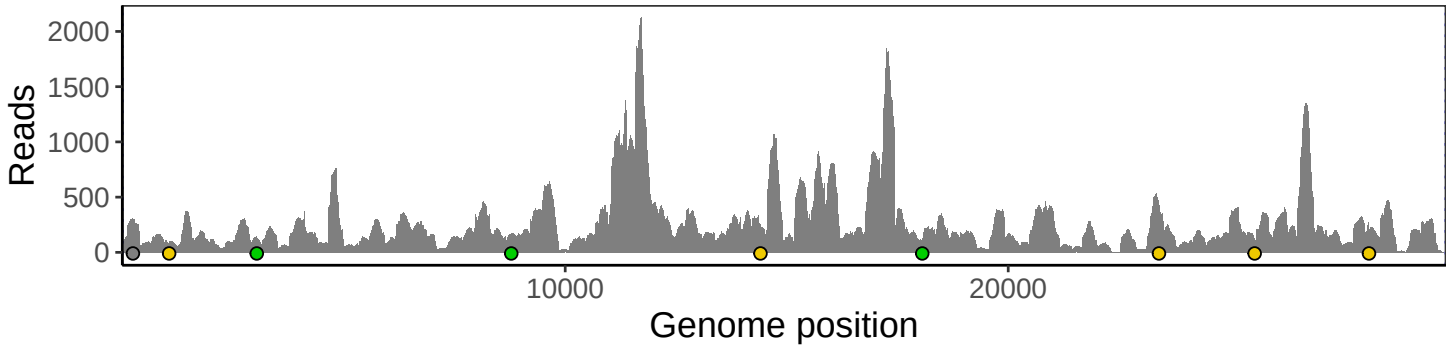


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

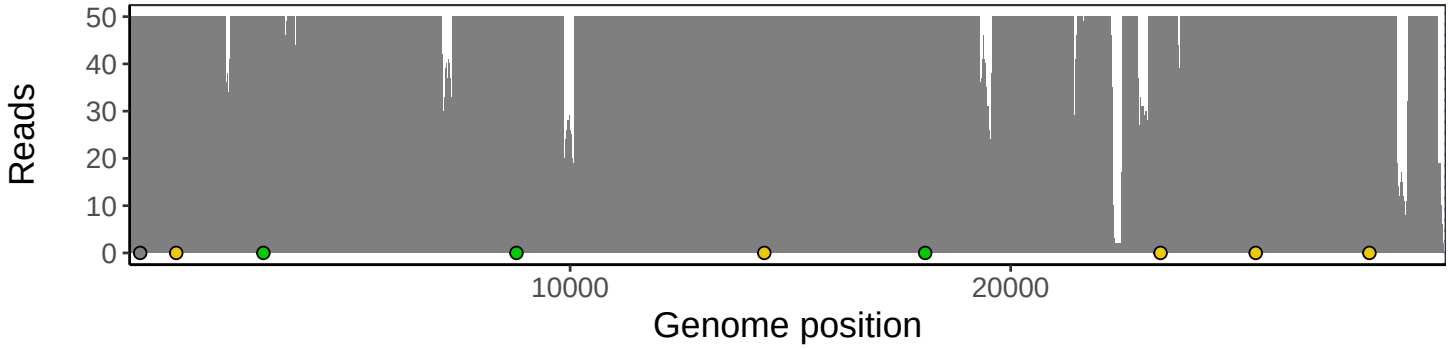


VSP0038-2 | 2020-04-29 | OP | 237o-tri | 2060 genomes | single experiment

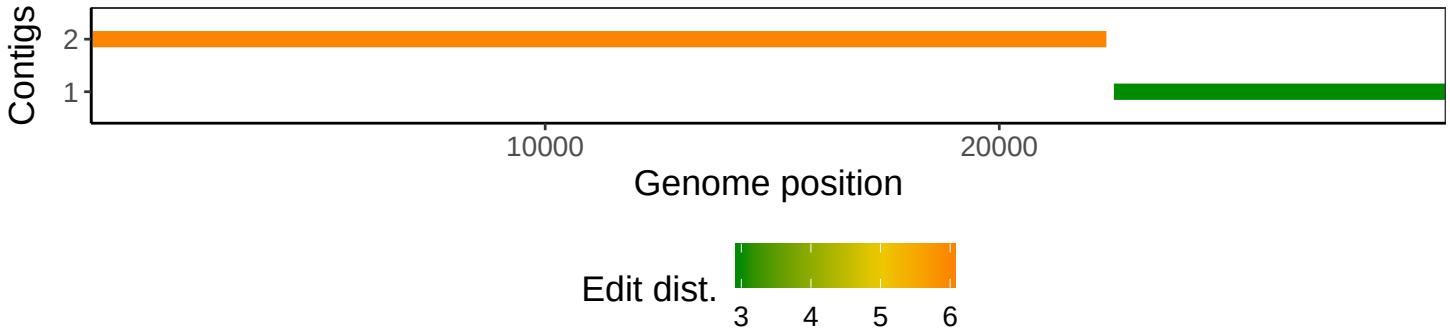
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

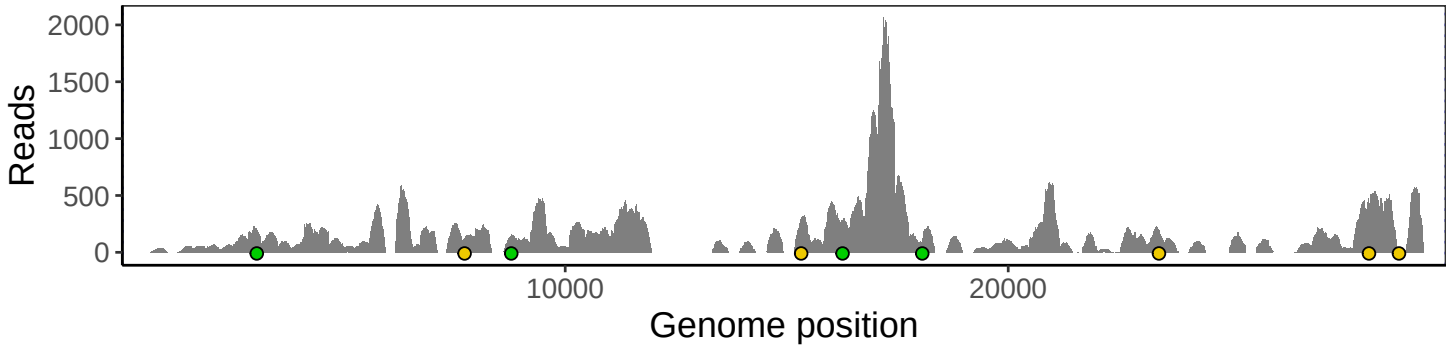


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

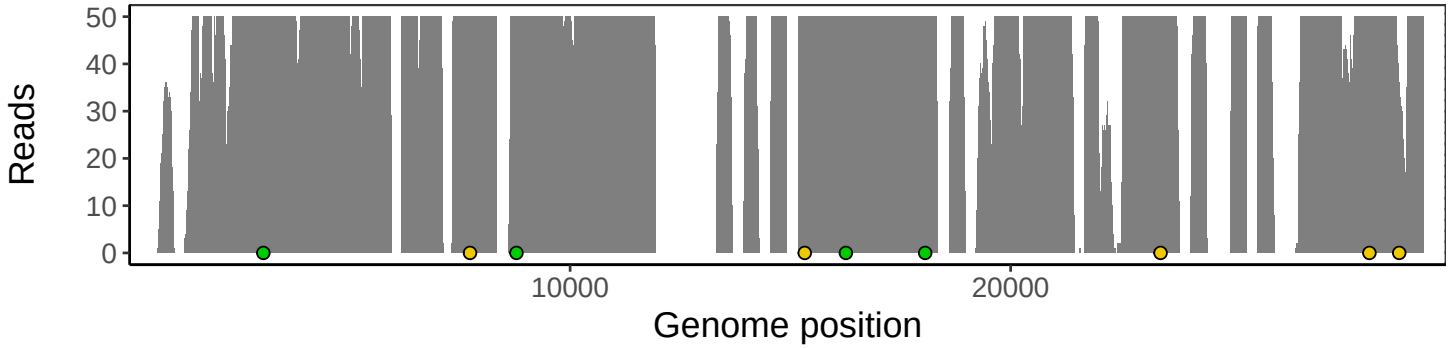


VSP0084-1 | 2020-05-06 | Saliva | 237s-q | genomes | single experiment

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.