COVID-19 subject 228

2020-09-04

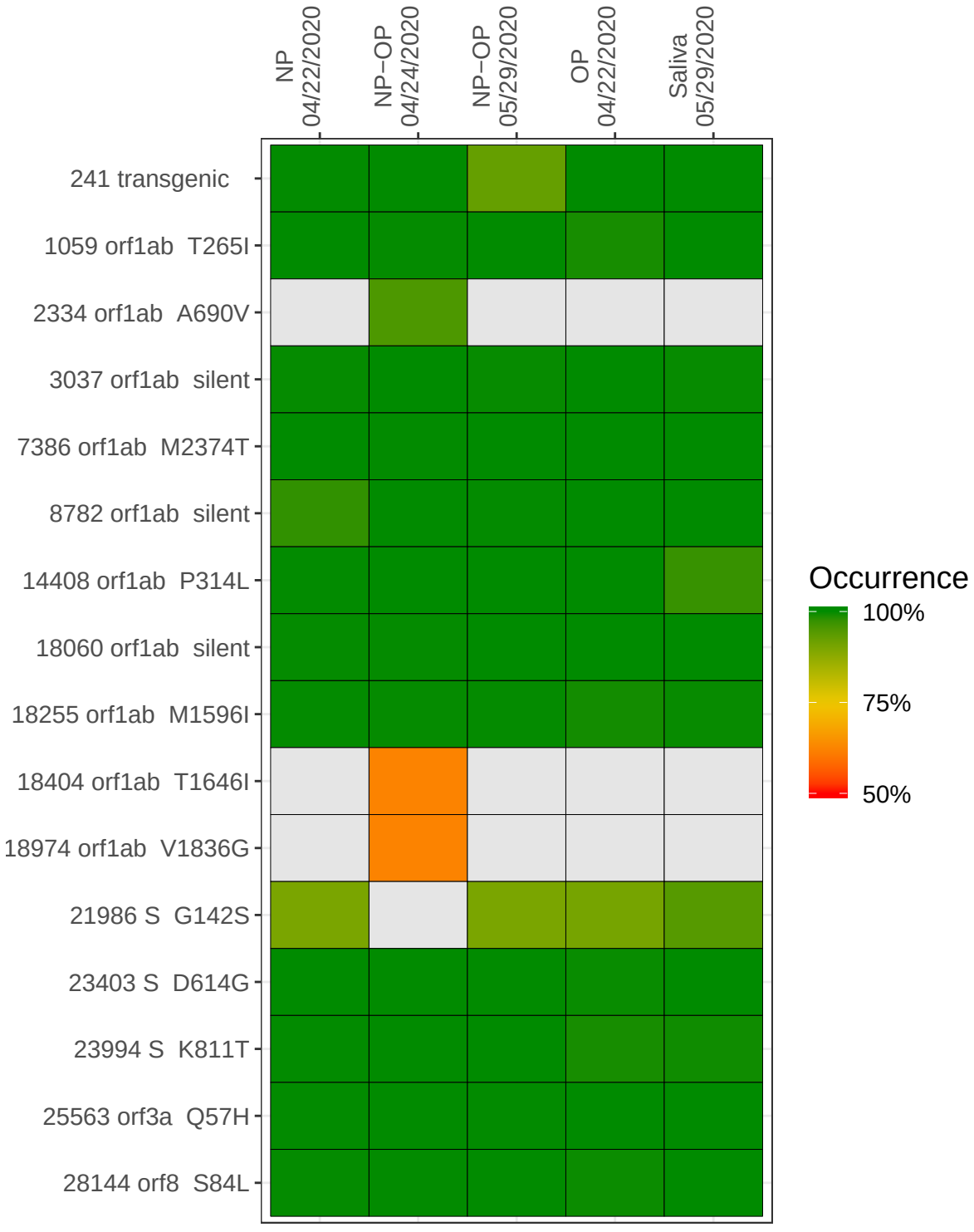
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

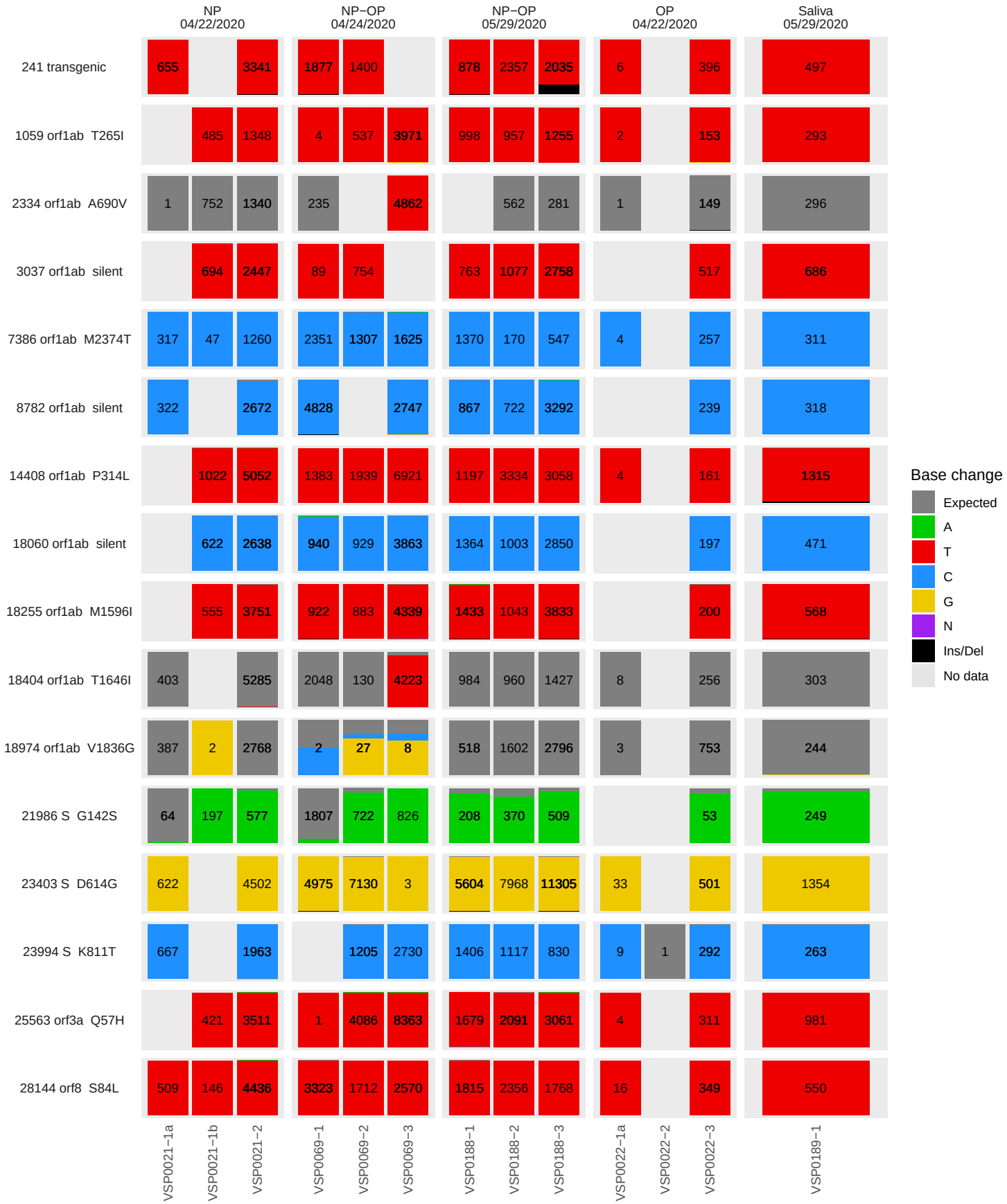
Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0021	composite	NA	NP	04/22/2020	29.82	99.8%	99.8%
VSP0022	composite	NA	OP	04/22/2020	29.68	99.8%	98.8%
VSP0069	composite	NA	NP-OP	04/24/2020	18.98	98.5%	98.5%
VSP0187	composite	NA	ETA	05/29/2020	NA	NA	NA
VSP0188	composite	NA	NP-OP	05/29/2020	29.90	99.8%	99.8%
VSP0021-1a	single experiment	2.20e+03	NP	04/22/2020	0.52	64.8%	61.9%
VSP0021-1b	single experiment	2.20e+03	NP	04/22/2020	0.57	63.0%	62.1%
VSP0021-2	single experiment	1.10e+04	NP	04/22/2020	29.82	99.8%	99.8%
VSP0022-1a	single experiment	2.68e+05	OP	04/22/2020	1.75	78.3%	37.7%
VSP0022-2	single experiment	1.34e+06	OP	04/22/2020	0.24	6.2%	0.0%
VSP0022-3	single experiment	1.34e+06	OP	04/22/2020	29.68	99.8%	98.8%
VSP0069-1	single experiment	9.75e+01	NP-OP	04/24/2020	6.54	92.2%	88.2%
VSP0069-2	single experiment	9.75e+01	NP-OP	04/24/2020	9.23	90.5%	90.0%
VSP0069-3	single experiment	9.75e+01	NP-OP	04/24/2020	6.37	87.1%	85.5%
VSP0187-1	single experiment	6.02e+01	ETA	05/29/2020	NA	NA	NA
VSP0187-2	single experiment	3.01e+02	ETA	05/29/2020	NA	NA	NA
VSP0188-1	single experiment	2.04e+03	NP-OP	05/29/2020	9.60	93.7%	93.5%
VSP0188-2	single experiment	1.02e+04	NP-OP	05/29/2020	22.61	99.1%	99.1%
VSP0188-3	single experiment	1.02e+04	NP-OP	05/29/2020	29.87	99.8%	99.8%
VSP0189-1	single experiment	8.51e+04	Saliva	05/29/2020	29.82	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.

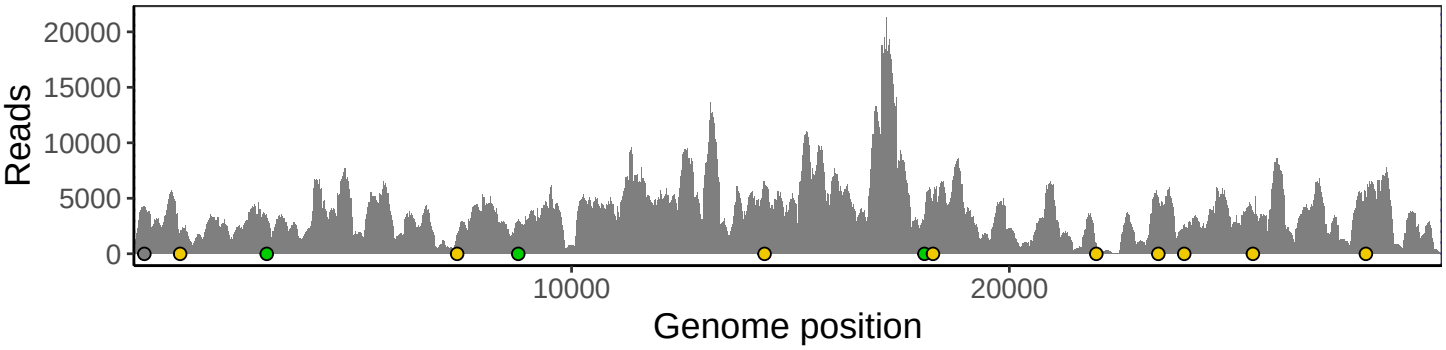



NP
04/22/2020
NP−OP
04/24/2020
NP−OP
05/29/2020
OP
04/22/2020
Saliva
05/29/2020
241 transgenic
655
3341
1877
1400
878
2357
2035
6
396
497
1059 orf1ab T265I
485
1348
4
537
3971
998
957
1255
2
153
293
2334 orf1ab A690V
1
752
1340
235
4862
562
281
1
149
296
3037 orf1ab silent
694
2447
89
754
763
1077
2758
517
686
7386 orf1ab M2374T
317
47
1260
2351
1307
1625
1370
170
547
4
257
311
8782 orf1ab silent
322
2672
4828
2747
867
722
3292
239
318
14408 orf1ab P314L
1022
5052
1383
1939
6921
1197
3334
3058
4
161
1315
18060 orf1ab silent
622
2638
940
929
3863
1364
1003
2850
197
471
18255 orf1ab M1596I
555
3751
922
883
4339
1433
1043
3833
200
568
18404 orf1ab T1646I
403
5285
2048
130
4223
984
960
1427
8
256
303
18974 orf1ab V1836G
387
2
2768
2
27
8
518
1602
2796
3
753
244
21986 S G142S
64
197
577
1807
722
826
208
370
509
53
249
23403 S D614G
622
4502
4975
7130
3
5604
7968
11305
33
501
1354
23994 S K811T
667
1963
1205
2730
1406
1117
830
9
1
292
263
25563 orf3a Q57H
421
3511
1
4086
8363
1679
2091
3061
4
311
981
28144 orf8 S84L
509
146
4436
3323
1712
2570
1815
2356
1768
16
349
550
VSP0021−1a
VSP0021−1b
VSP0021−2
VSP0069−1
VSP0069−2
VSP0069−3
VSP0188−1
VSP0188−2
VSP0188−3
VSP0022−1a
VSP0022−2
VSP0022−3
VSP0189−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

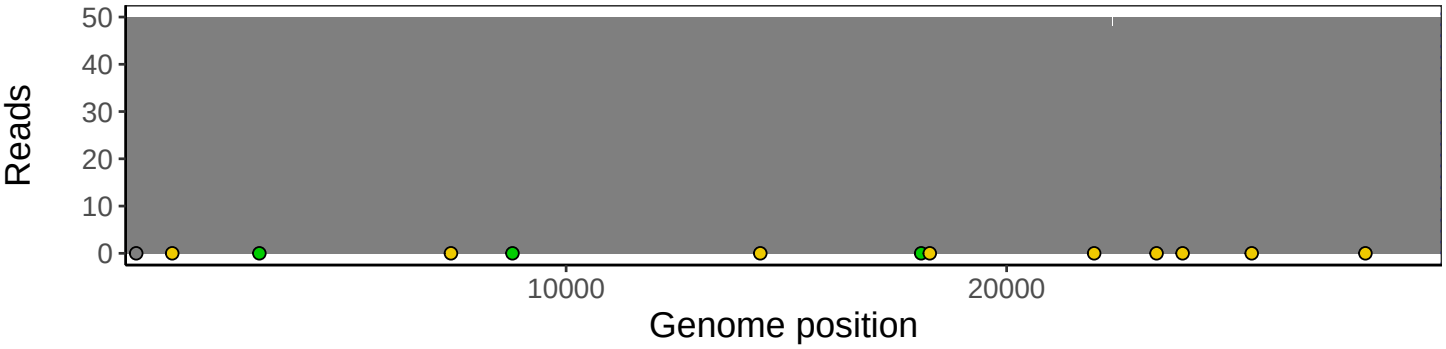
Analyses of individual experiments and composite results.

VSP0021 | 04/22/2020 | NP | 228n | composite result

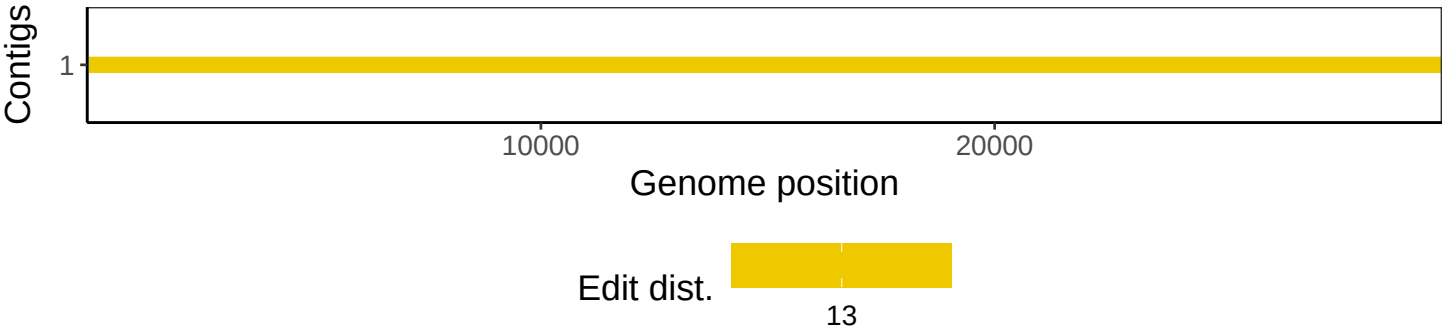
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

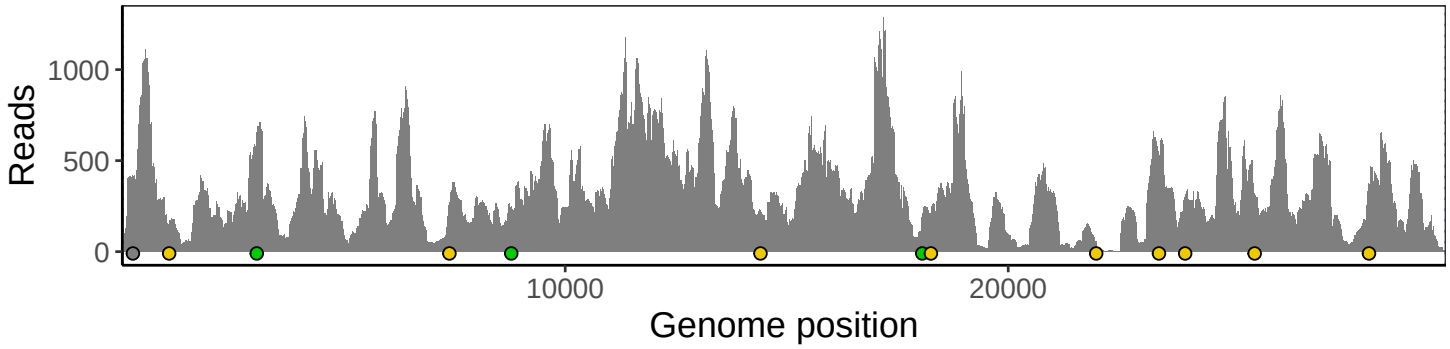


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

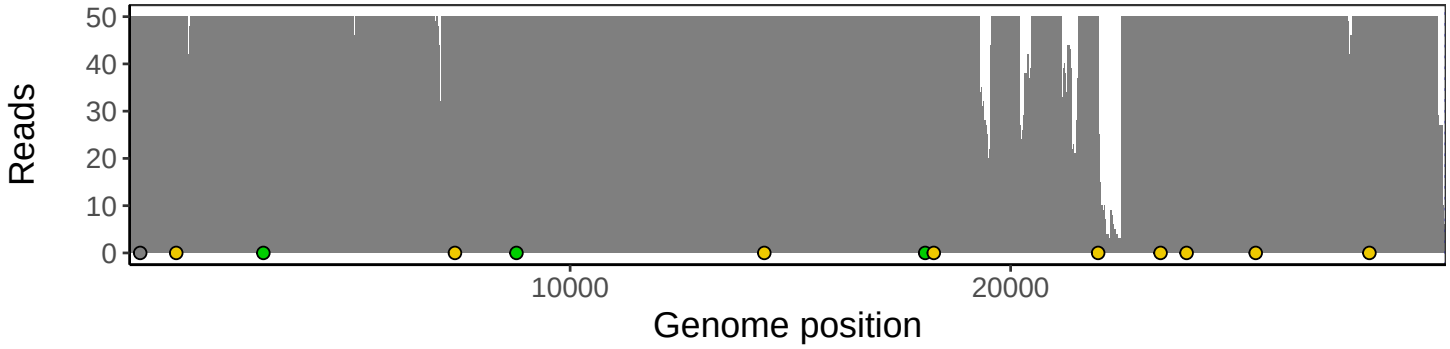


VSP0022 | 04/22/2020 | OP | 228o | composite result

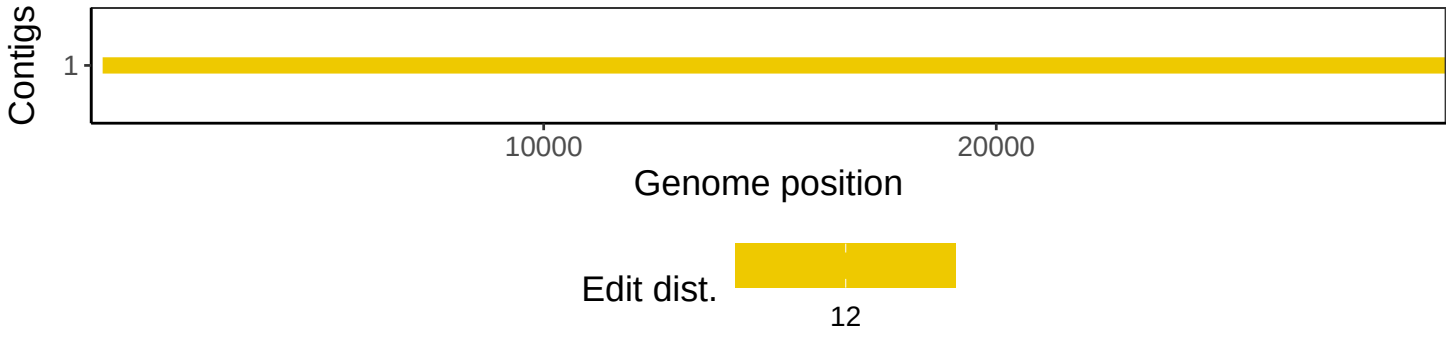
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

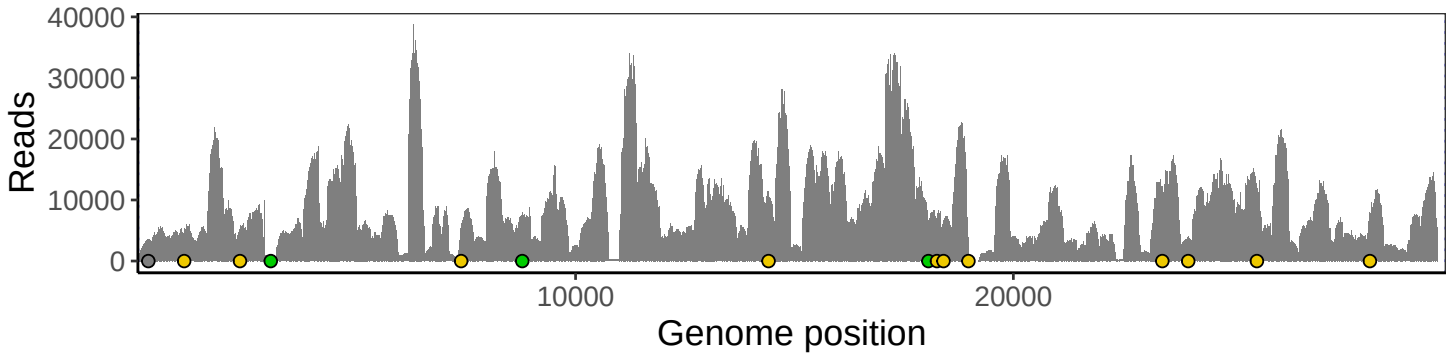


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

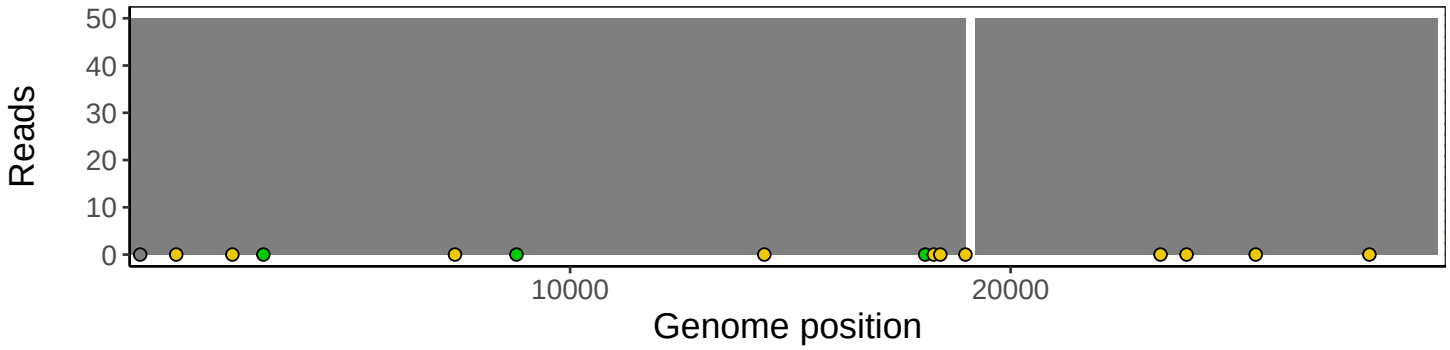


VSP0069 | 04/24/2020 | NP-OP | 228no-t | composite result

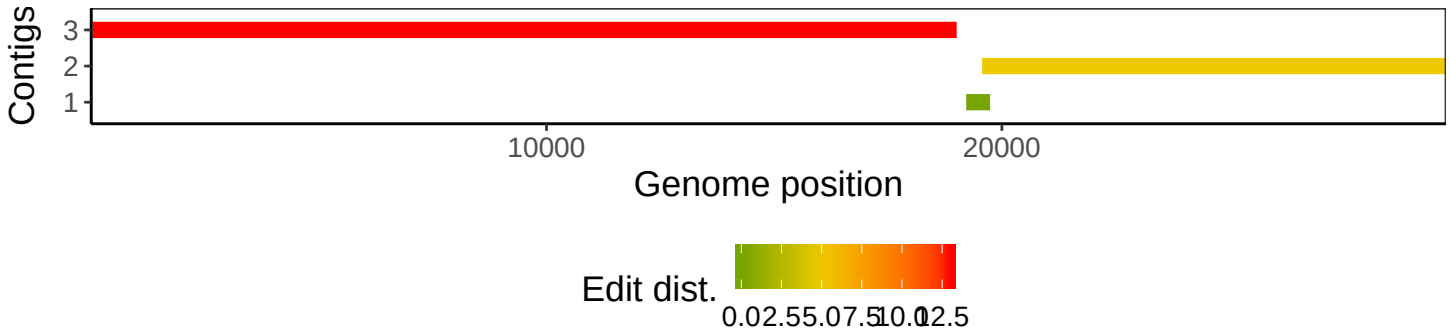
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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.

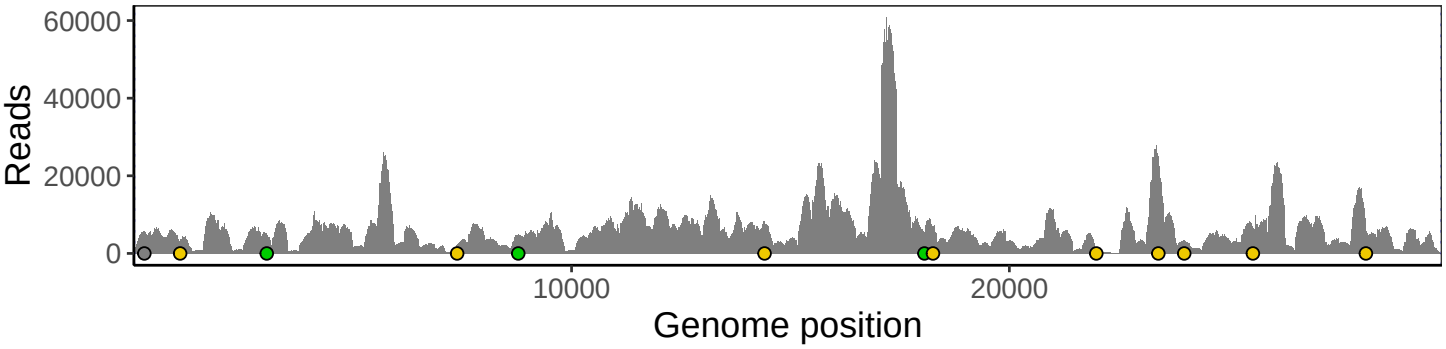


No pileup data available.

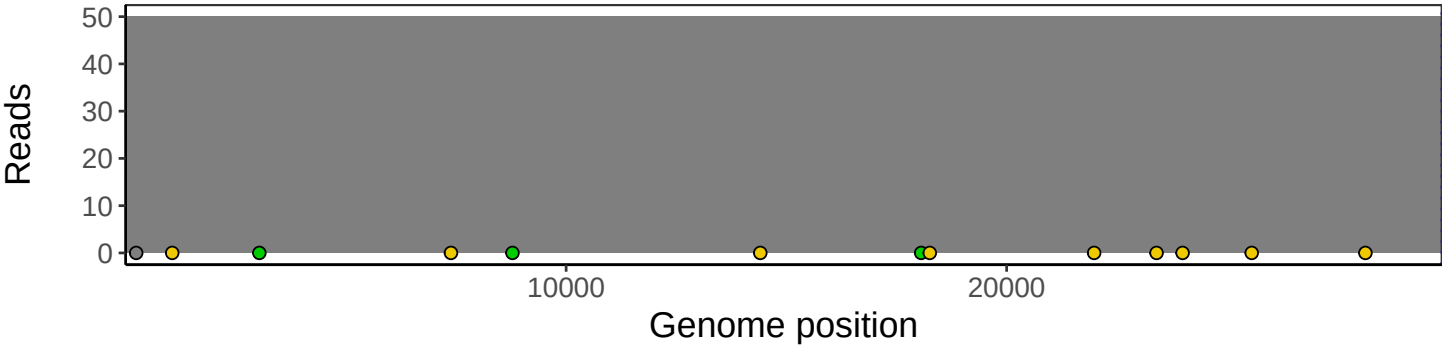
No contig data available.

VSP0188 | 05/29/2020 | NP-OP | 228no-q | composite result

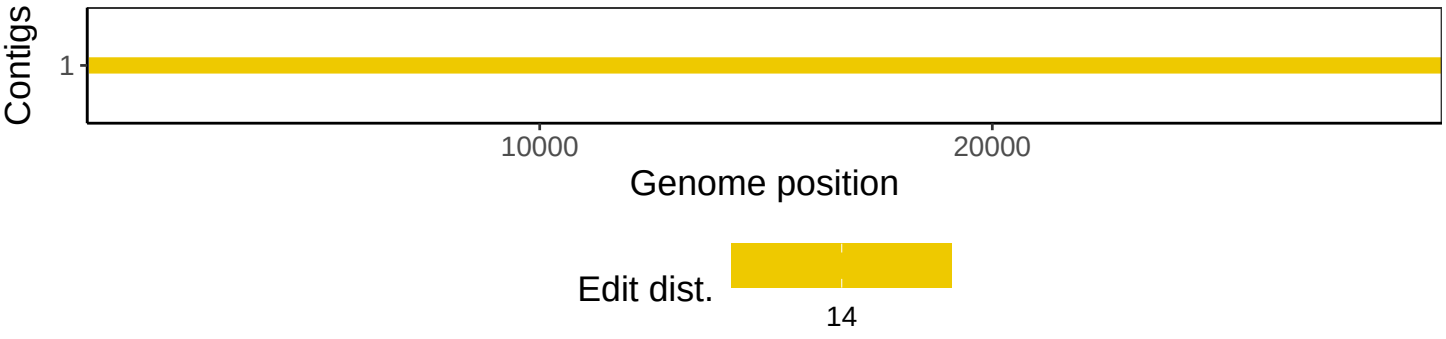
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

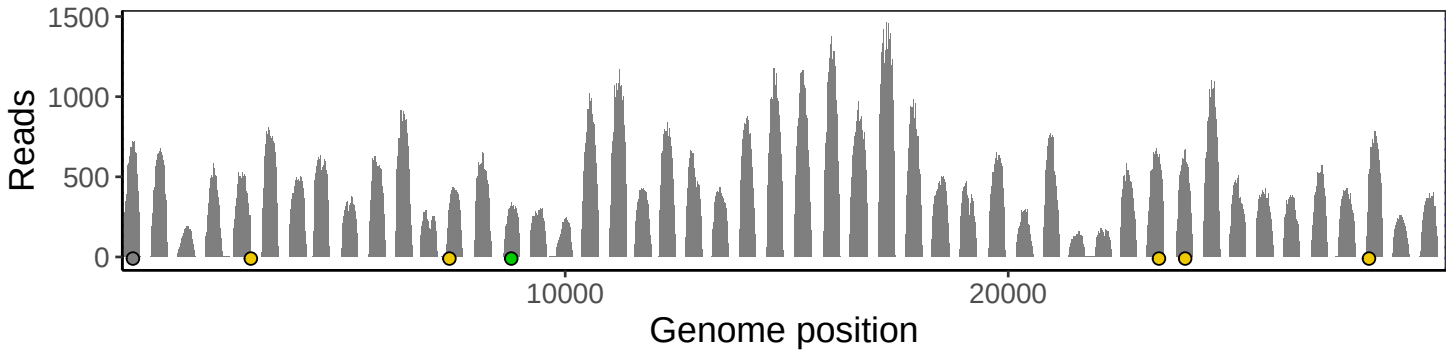


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

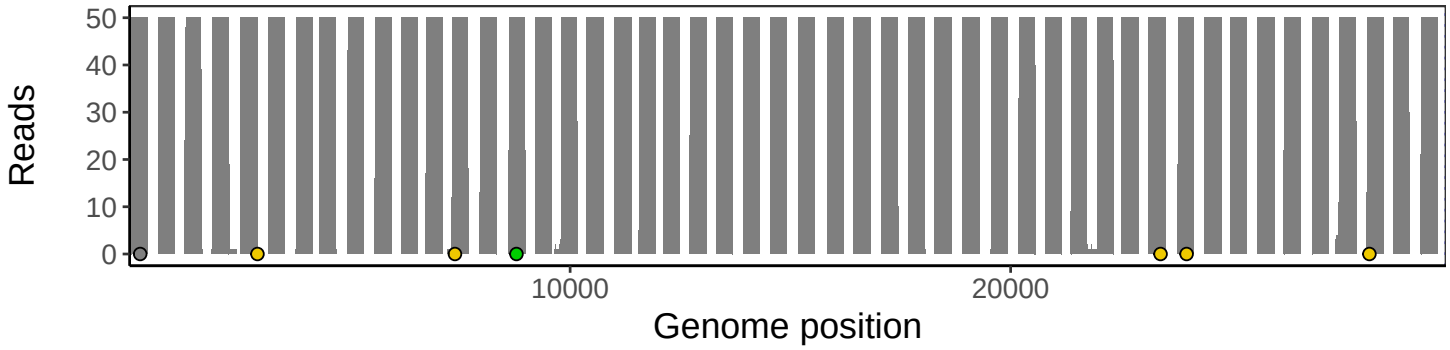


VSP0021-1a | 04/22/2020 | NP | 228n | 2200 genomes | single experiment

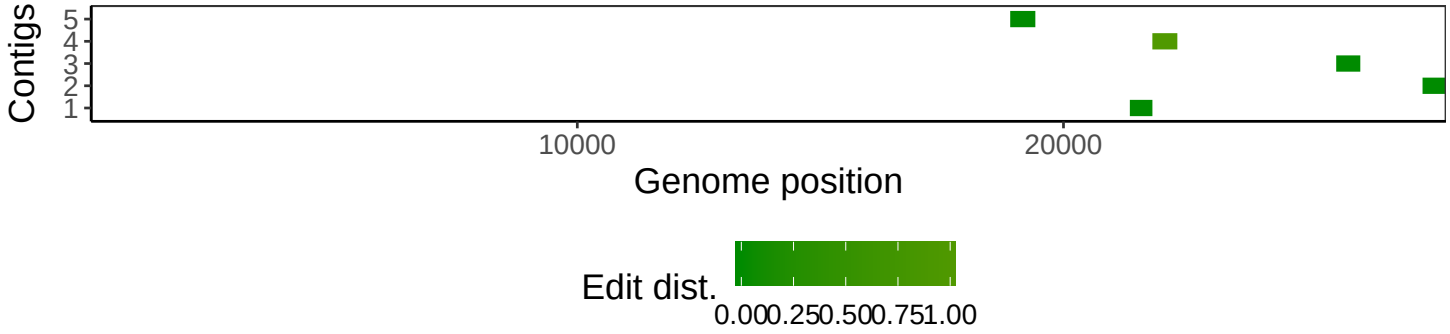
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

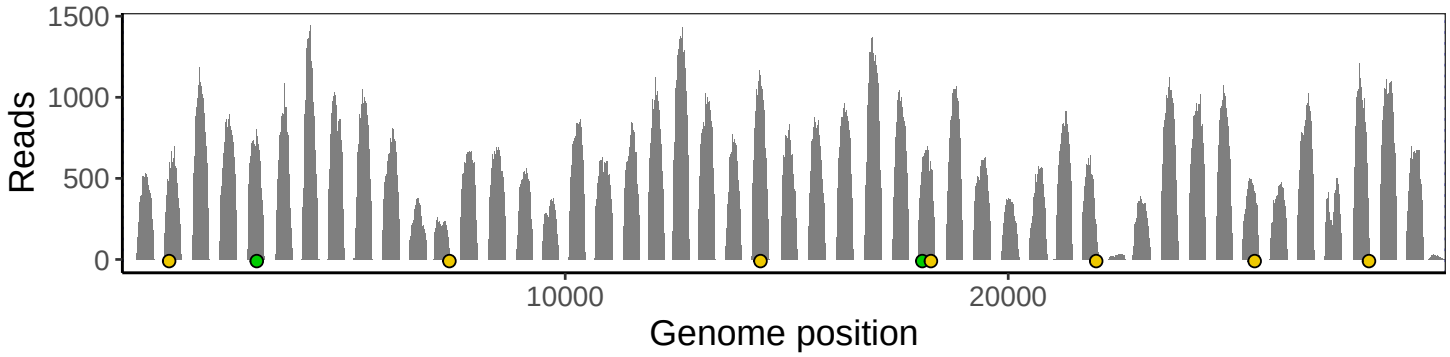


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

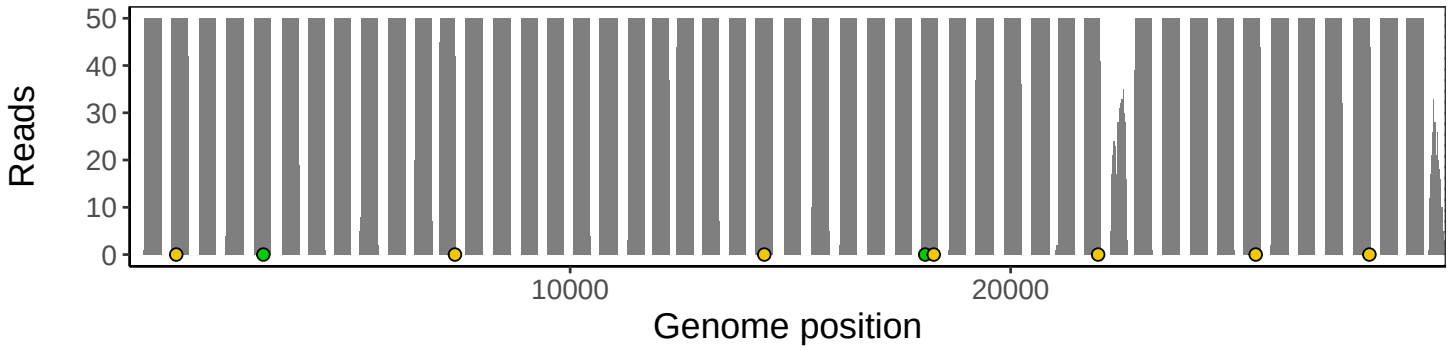


VSP0021-1b | 04/22/2020 | NP | 228n | 2200 genomes | single experiment

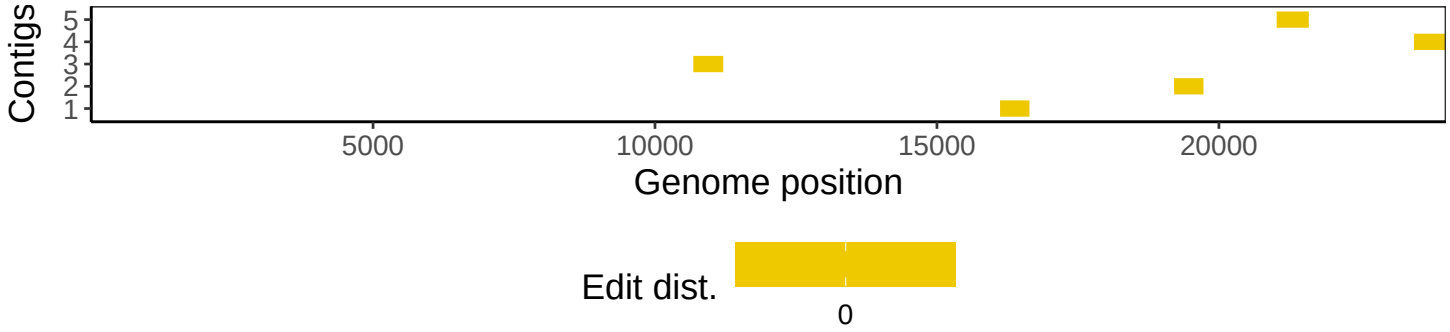
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

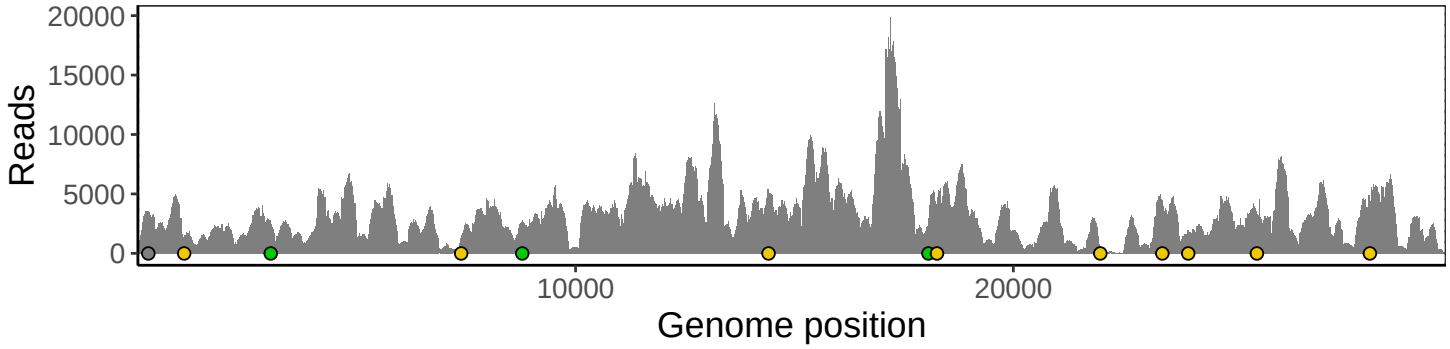


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

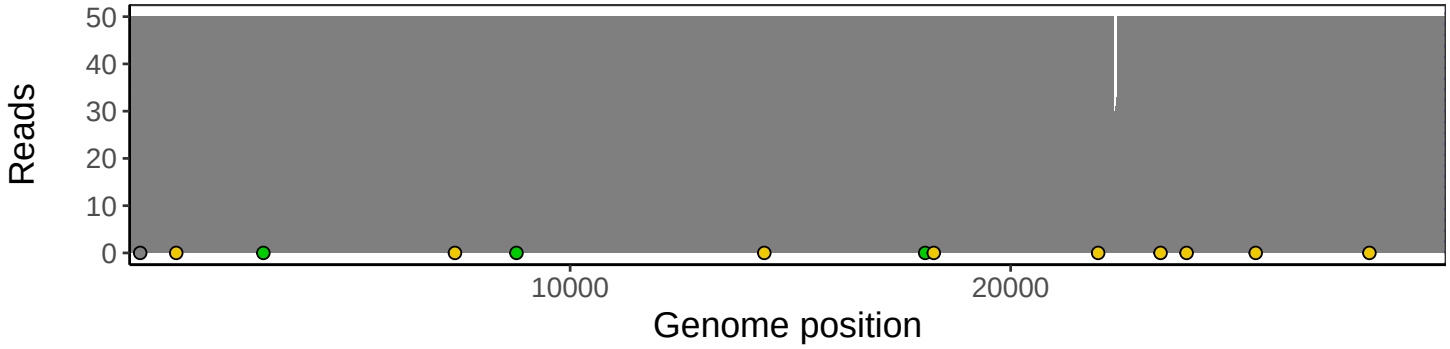


VSP0021-2 | 04/22/2020 | NP | 228n | 11000 genomes | single experiment

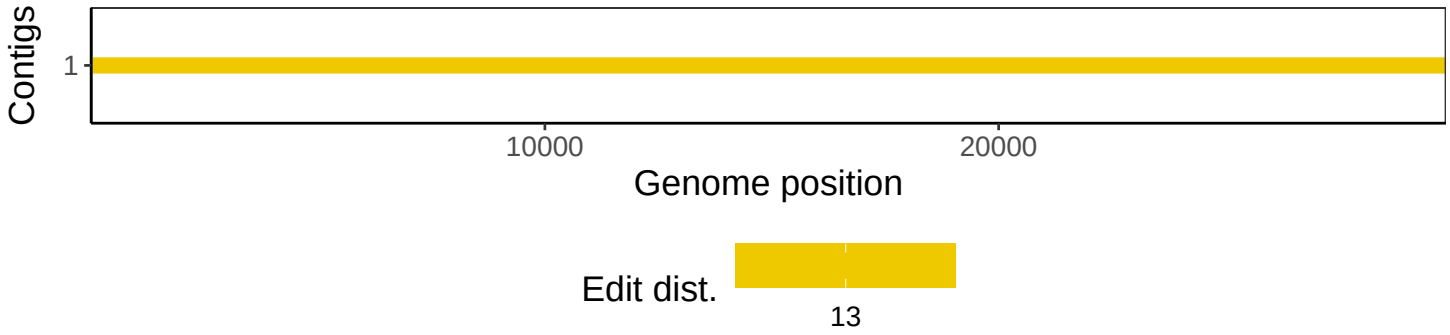
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

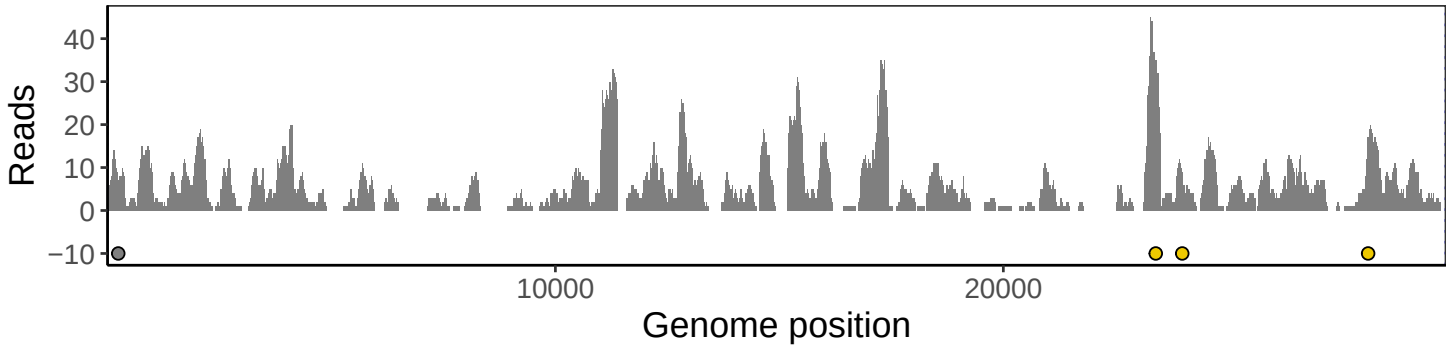


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

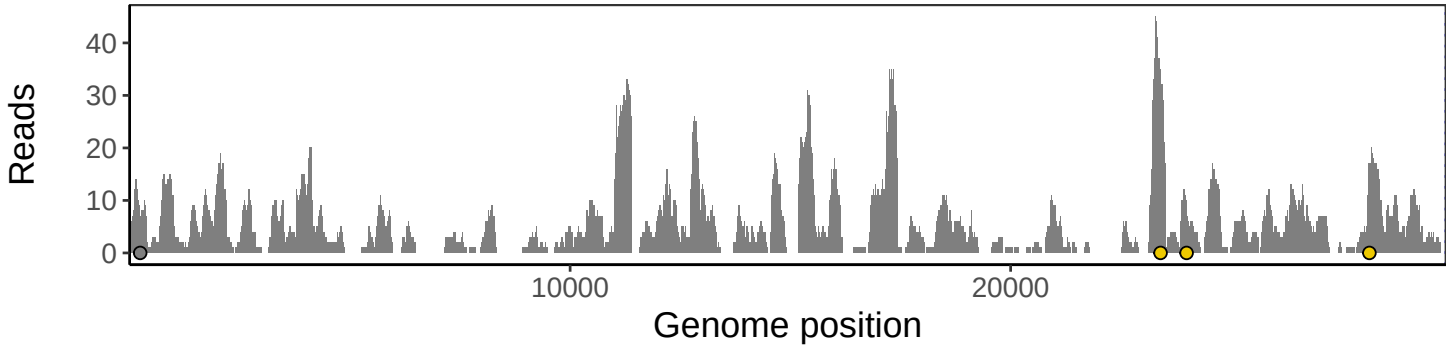


VSP0022-1a | 04/22/2020 | OP | 228o | 268000 genomes | single experiment

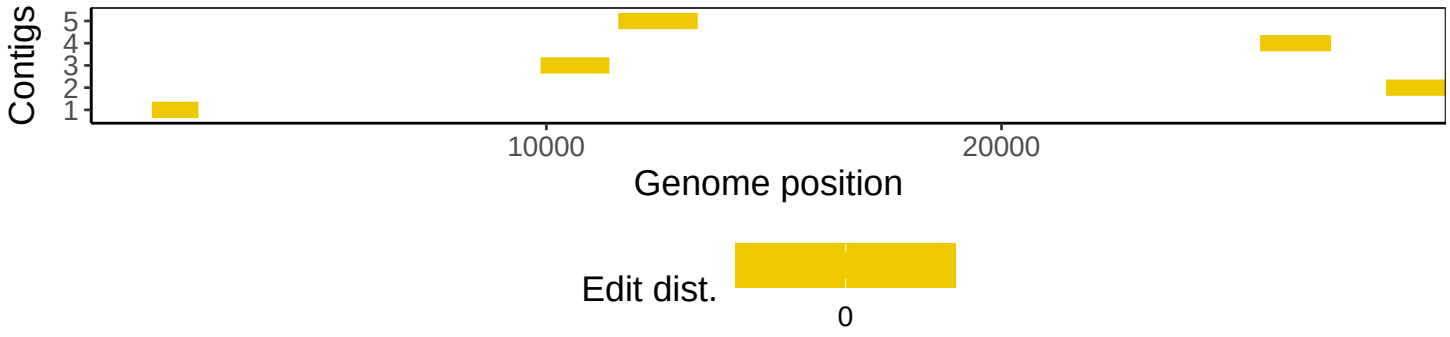
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

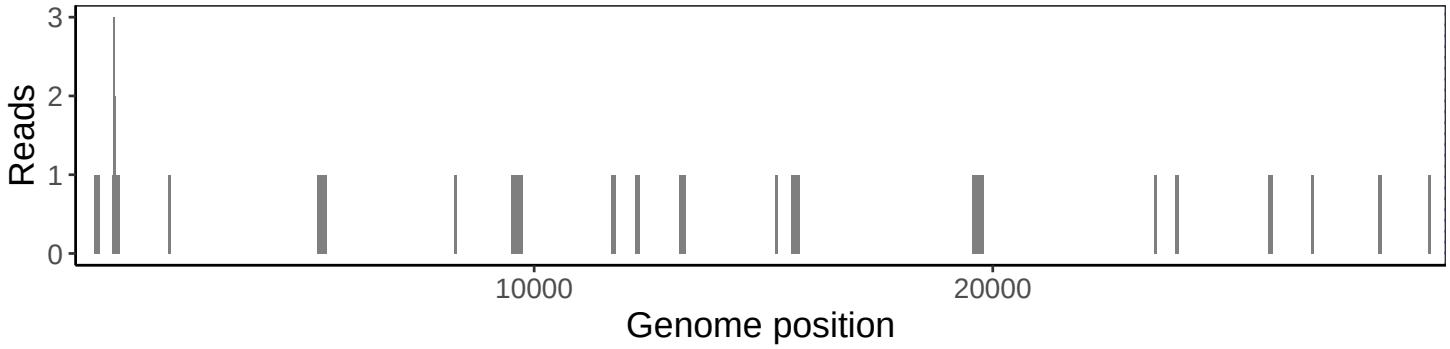


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

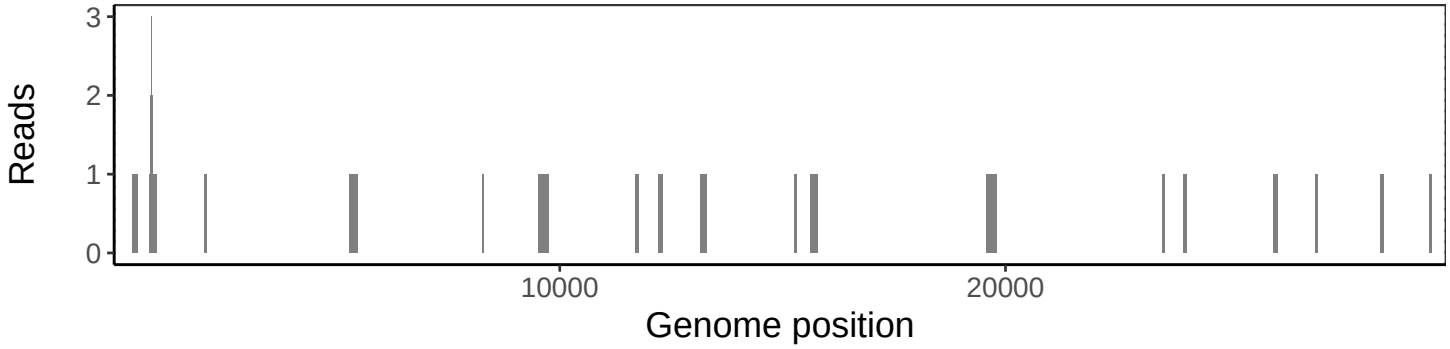


VSP0022-2 | 04/22/2020 | OP | 228o | 1340000 genomes | single experiment

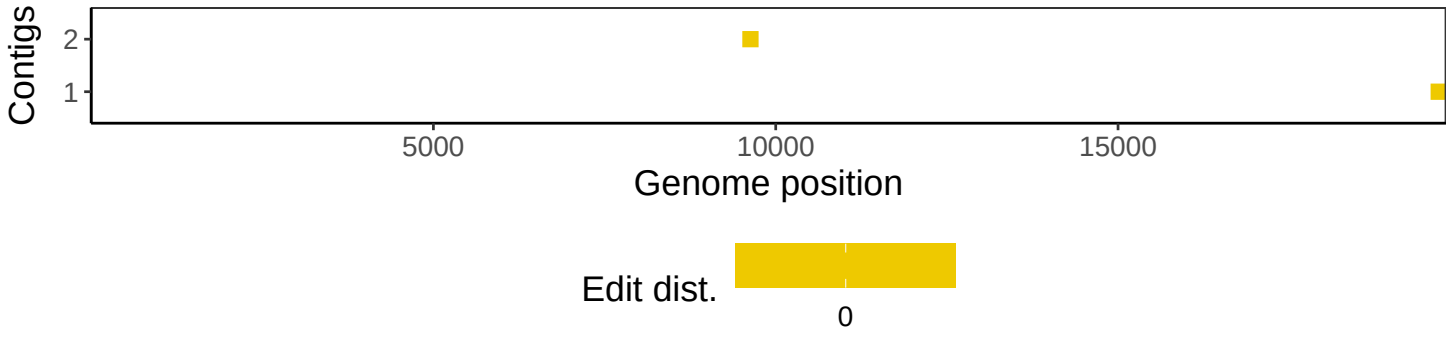
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

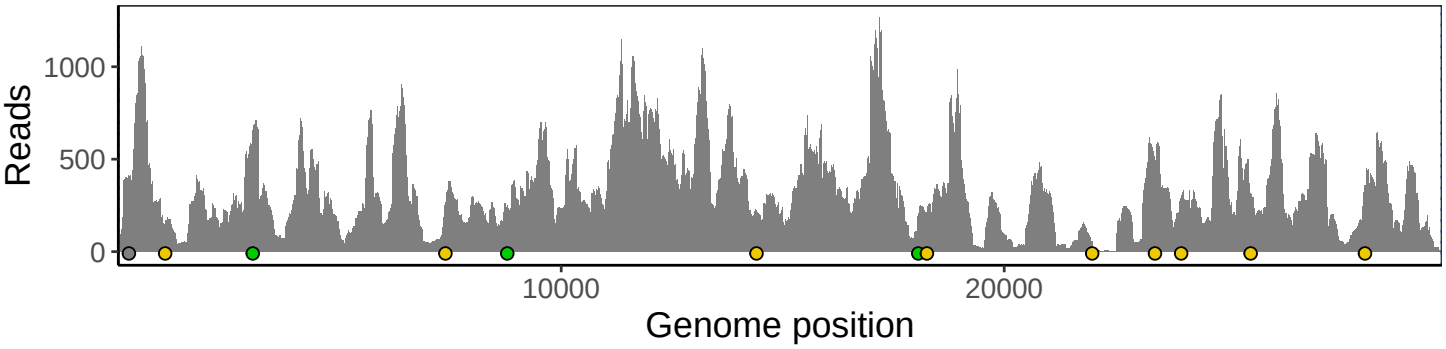


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

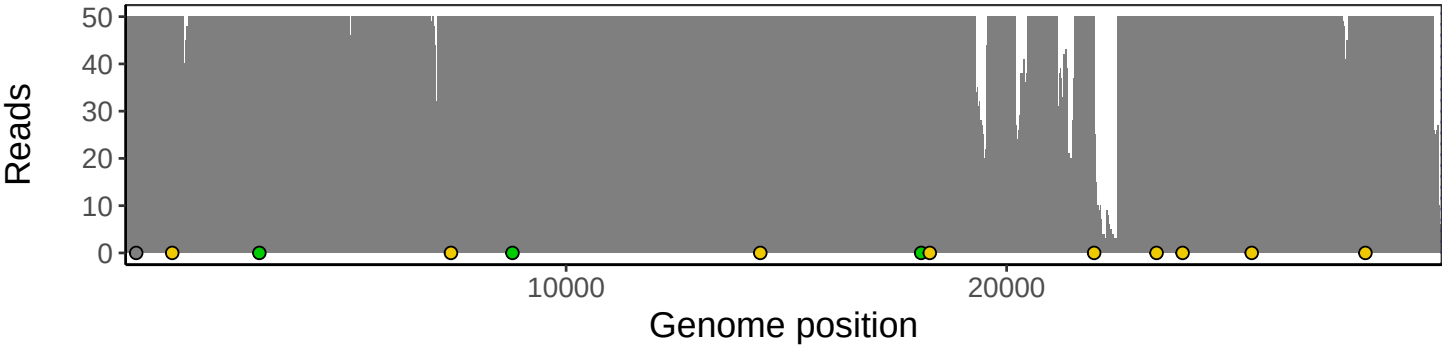


VSP0022-3 | 04/22/2020 | OP | 228o | 1340000 genomes | single experiment

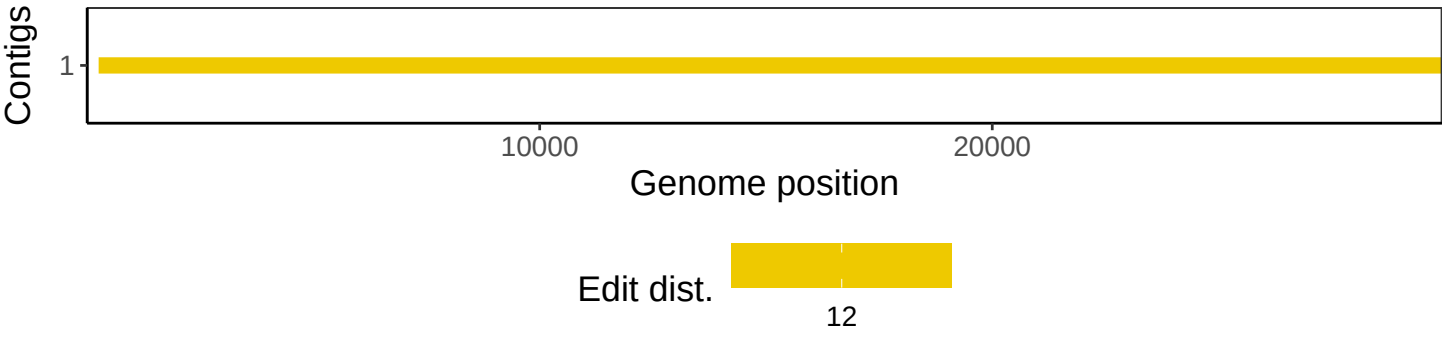
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

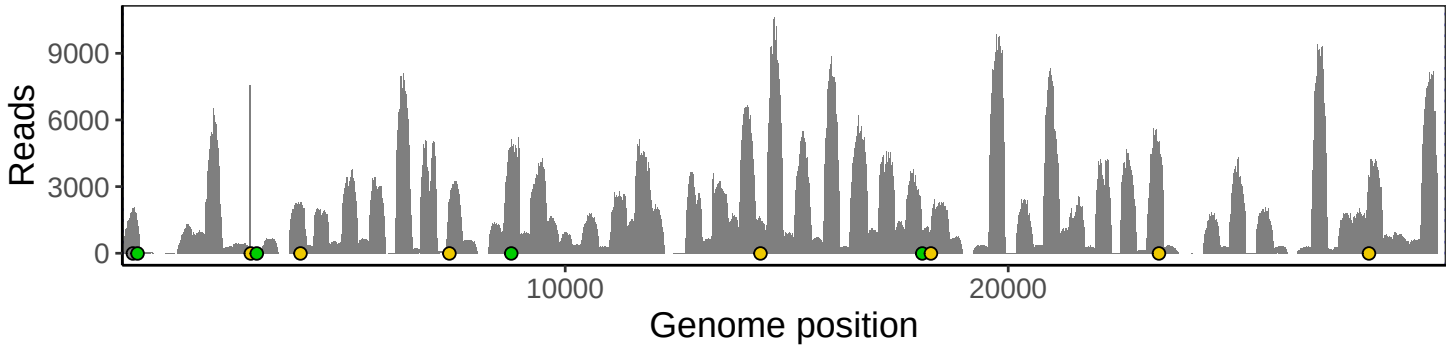


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

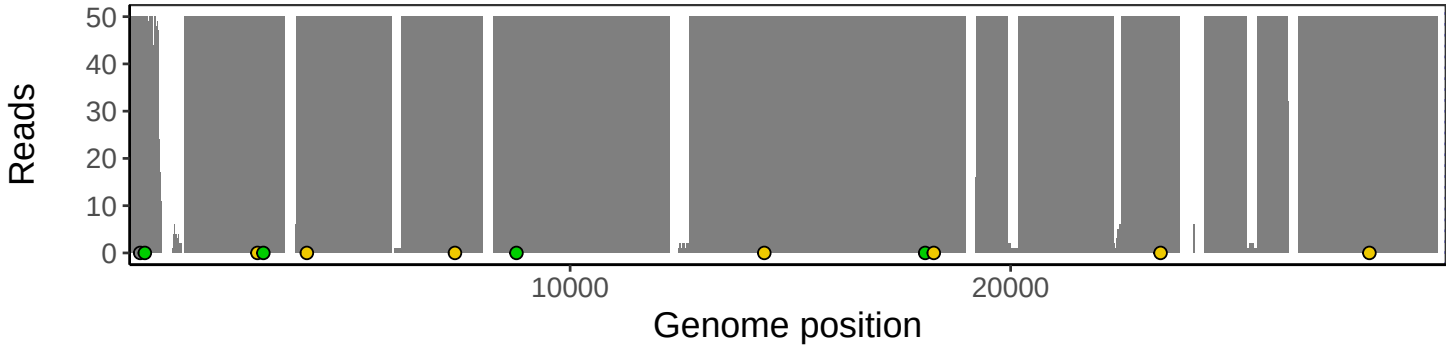


VSP0069-1 | 04/24/2020 | NP-OP | 228no-t | 97.5 genomes | single experiment

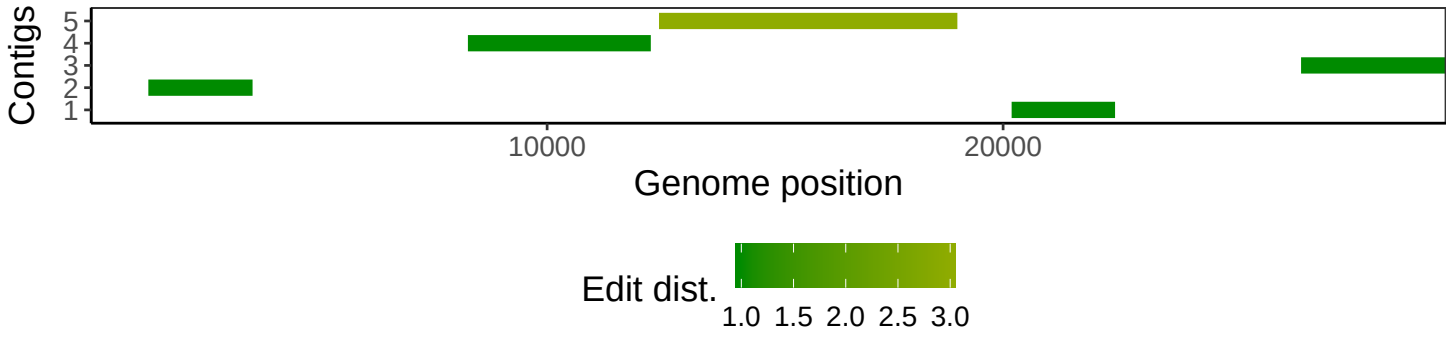
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

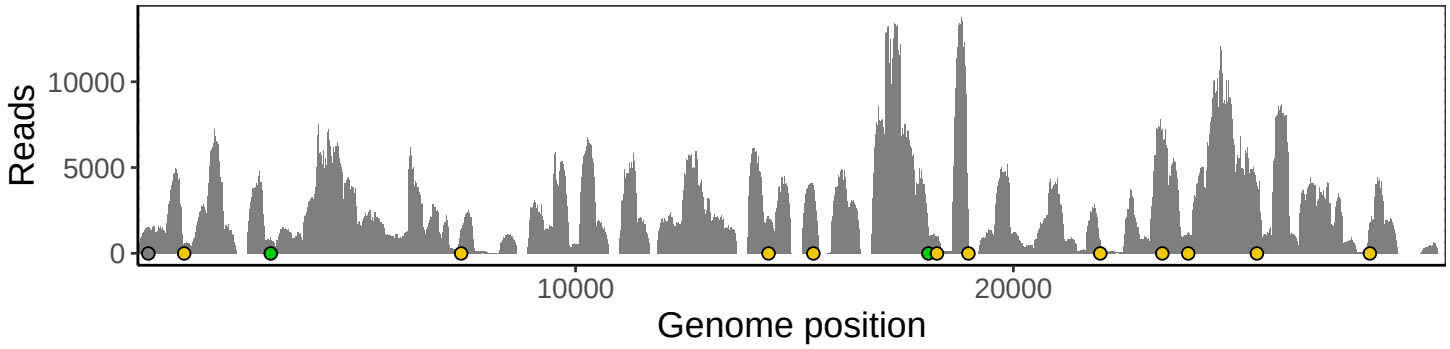


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

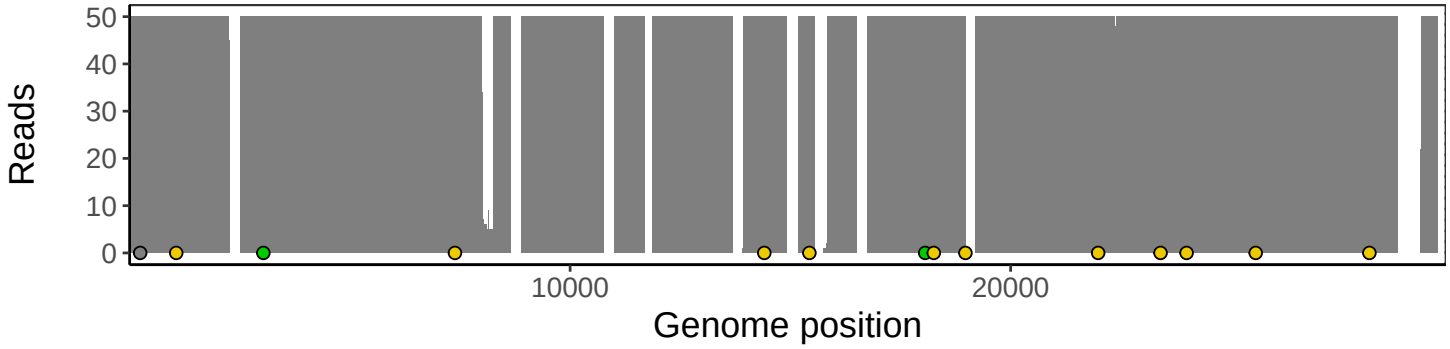


VSP0069-2 | 04/24/2020 | NP-OP | 228no-t | 97.5 genomes | single experiment

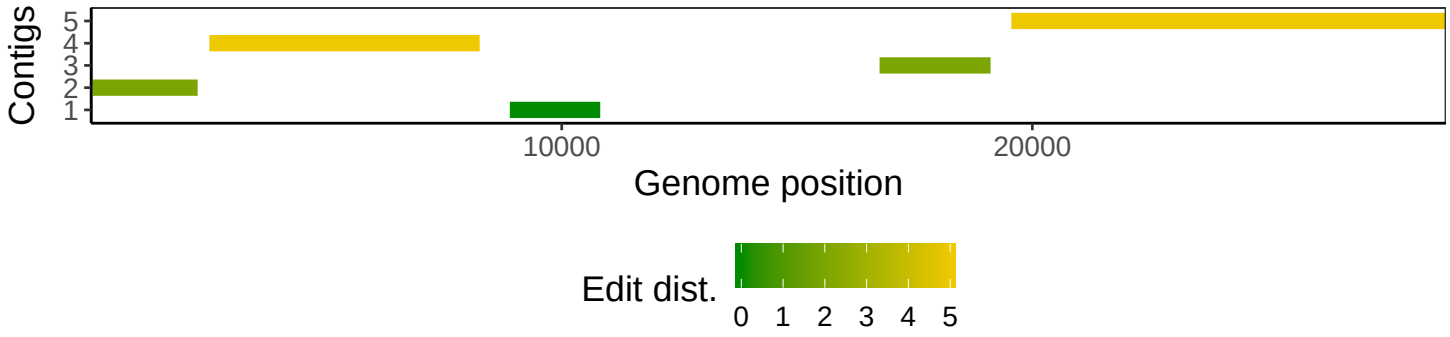
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

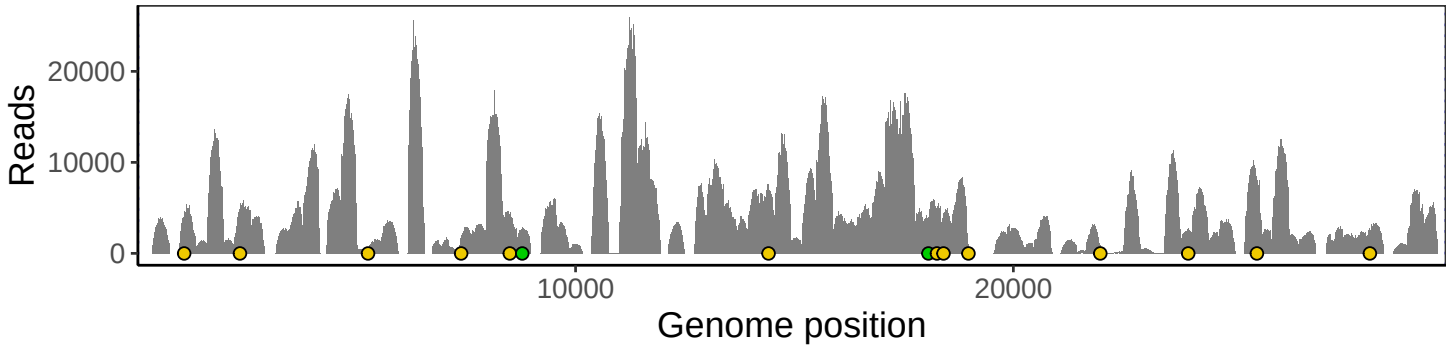


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

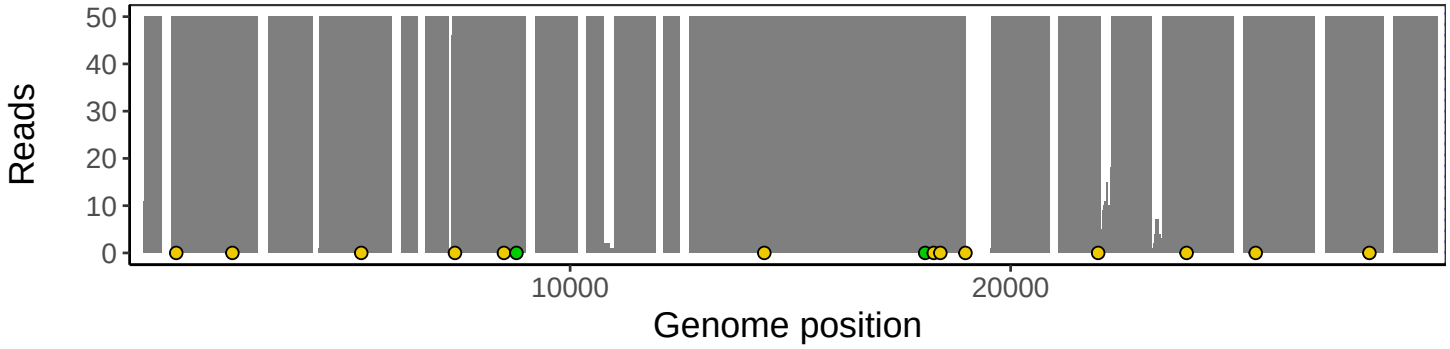


VSP0069-3 | 04/24/2020 | NP-OP | 228no-t | 97.5 genomes | single experiment

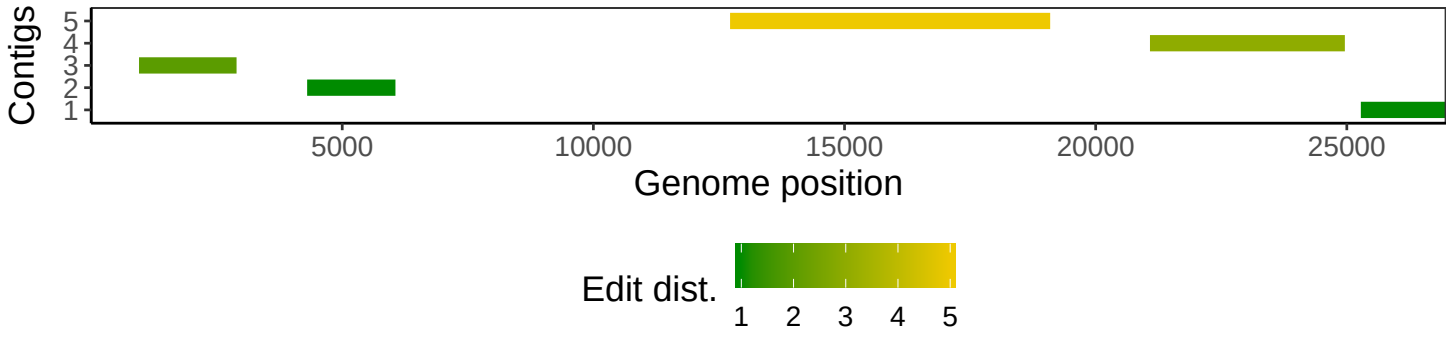
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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.



No pileup data available.

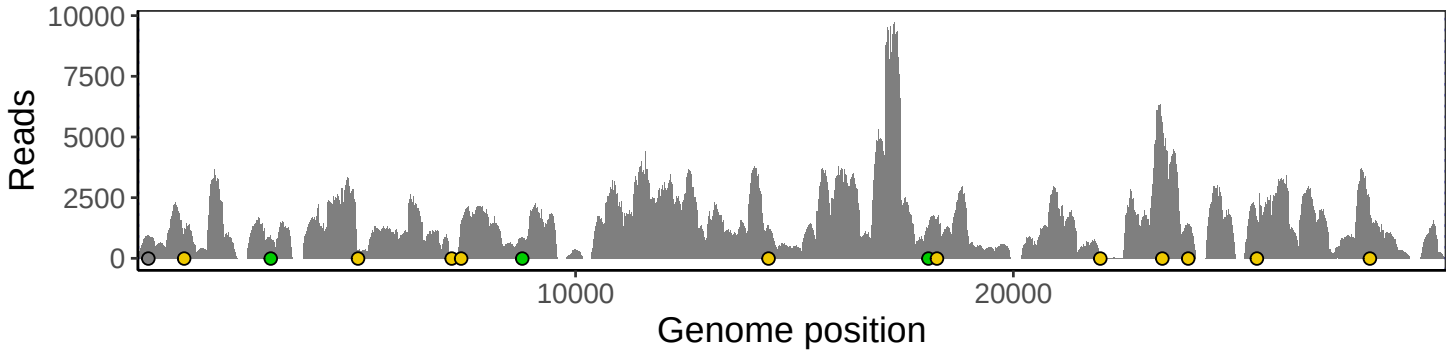
No contig data available.

No pileup data available.

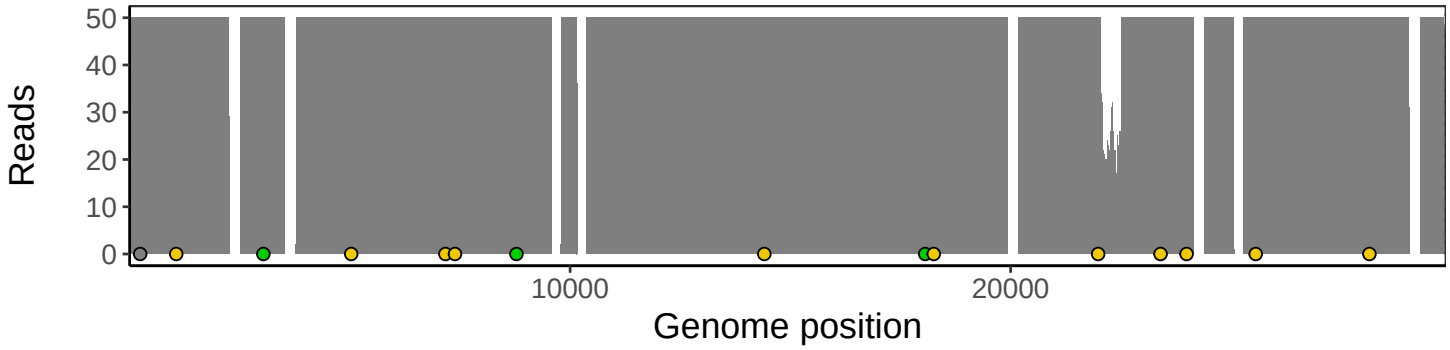
No contig data available.

VSP0188-1 | 05/29/2020 | NP-OP | 228no-q | 2040 genomes | single experiment

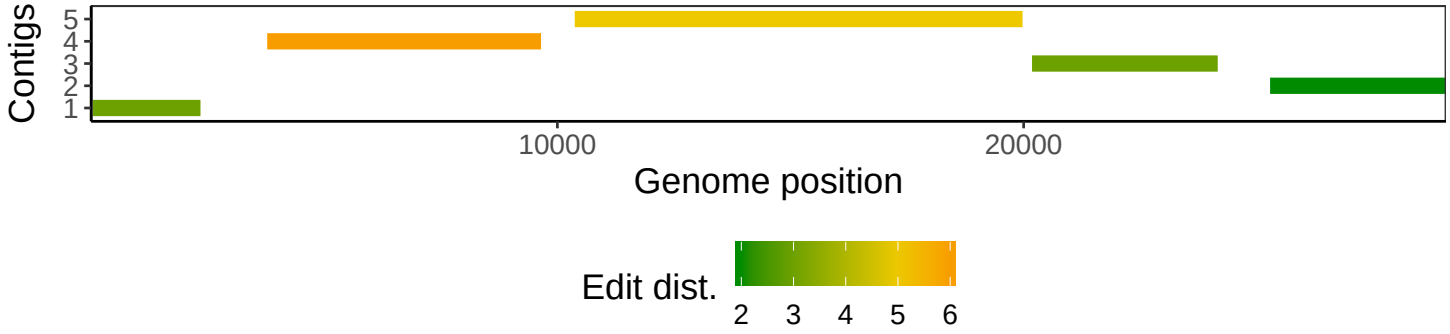
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

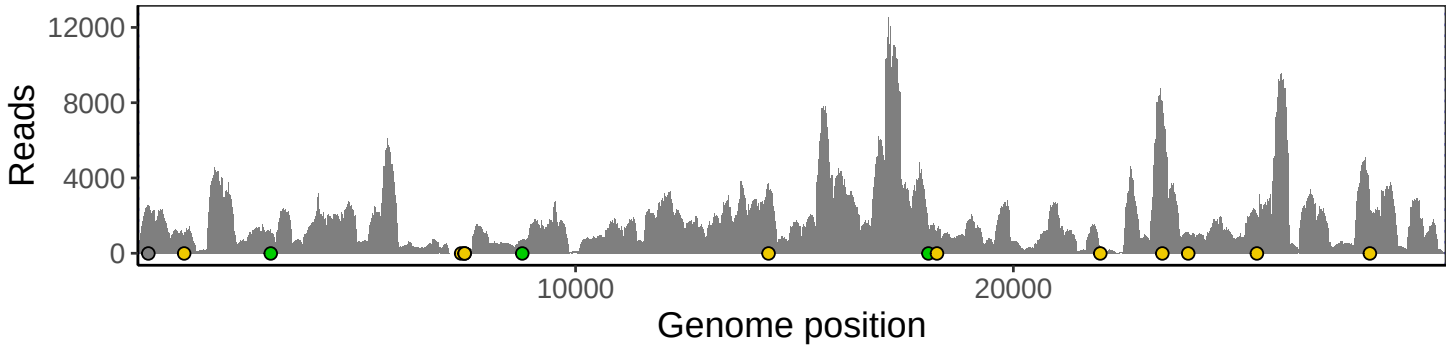


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

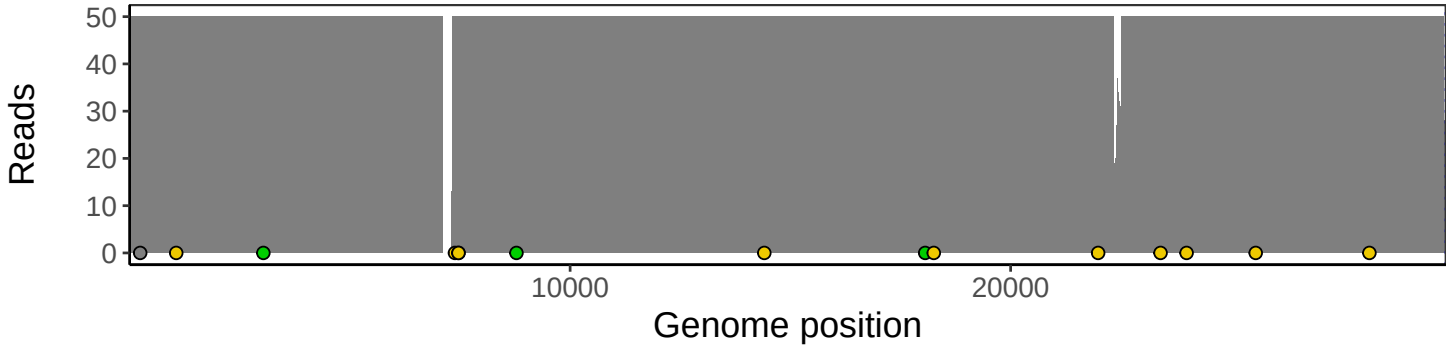


VSP0188-2 | 05/29/2020 | NP-OP | 228no-q | 10200 genomes | single experiment

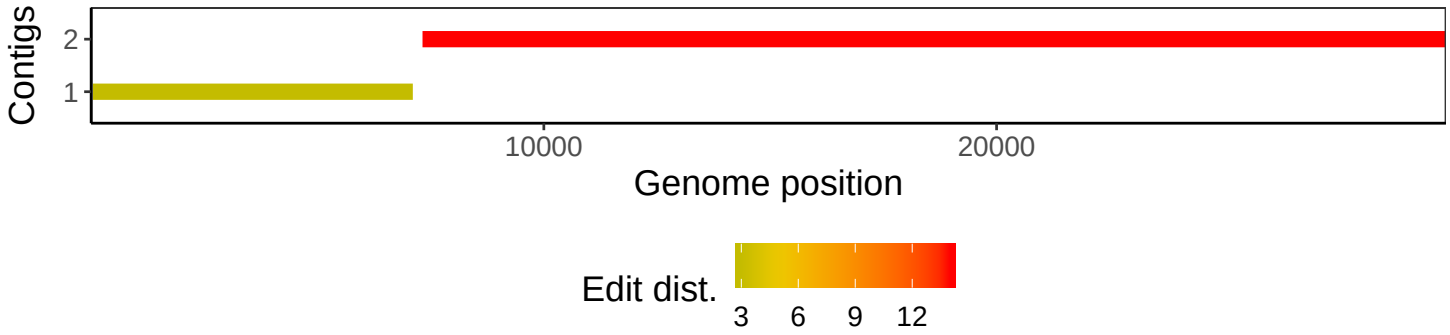
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

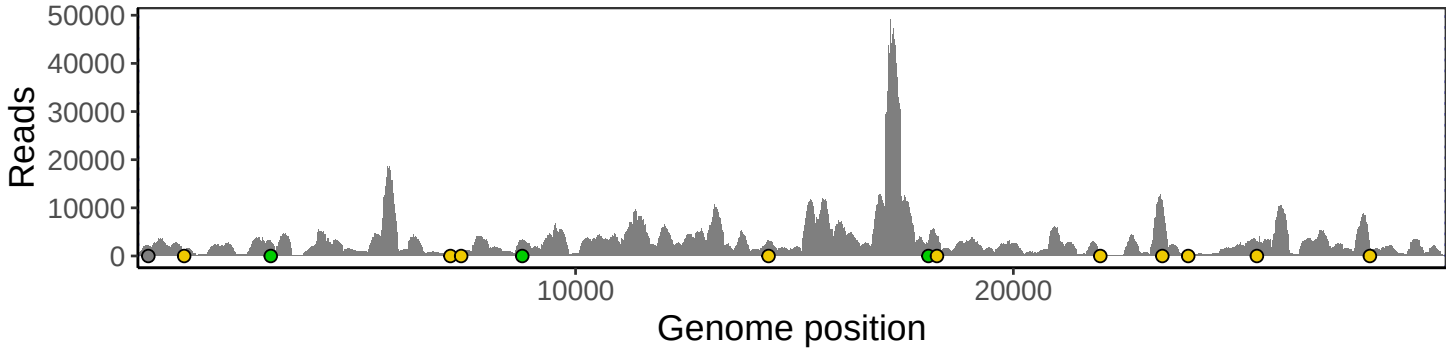


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

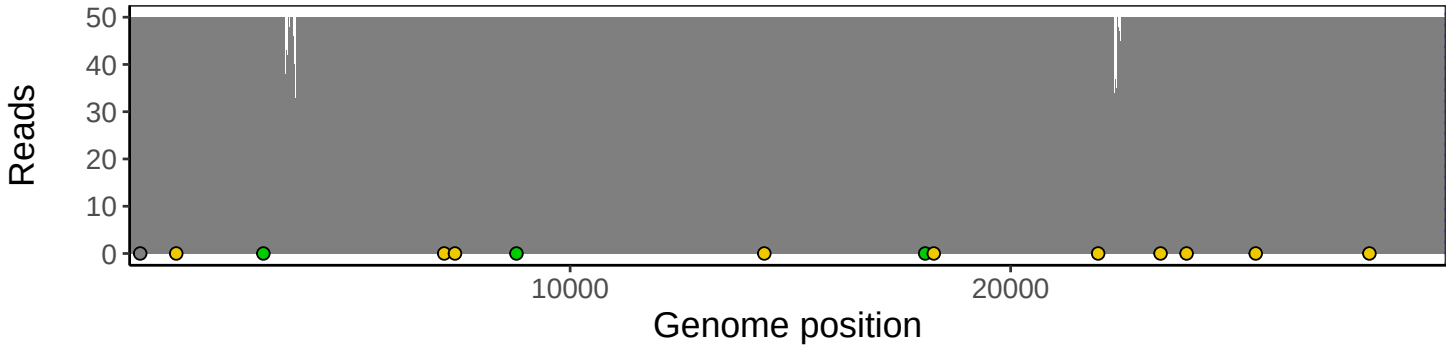


VSP0188-3 | 05/29/2020 | NP-OP | 228no-q | 10200 genomes | single experiment

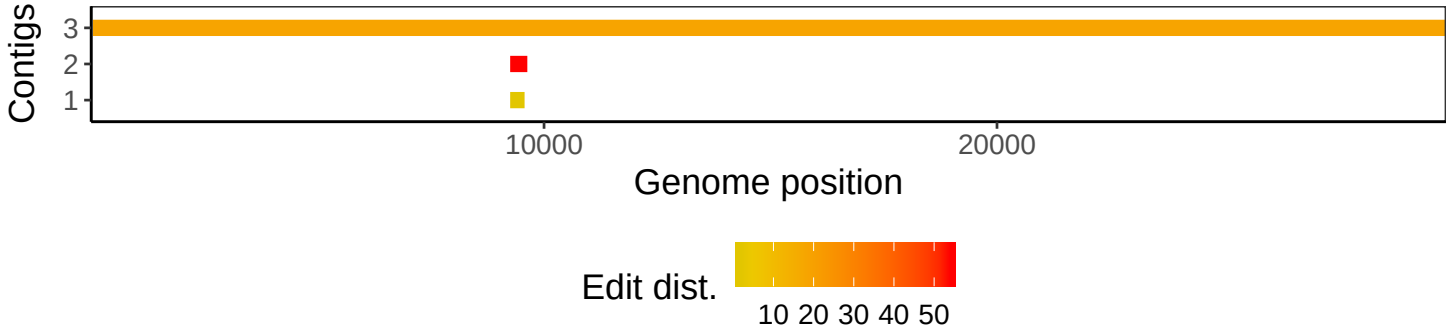
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

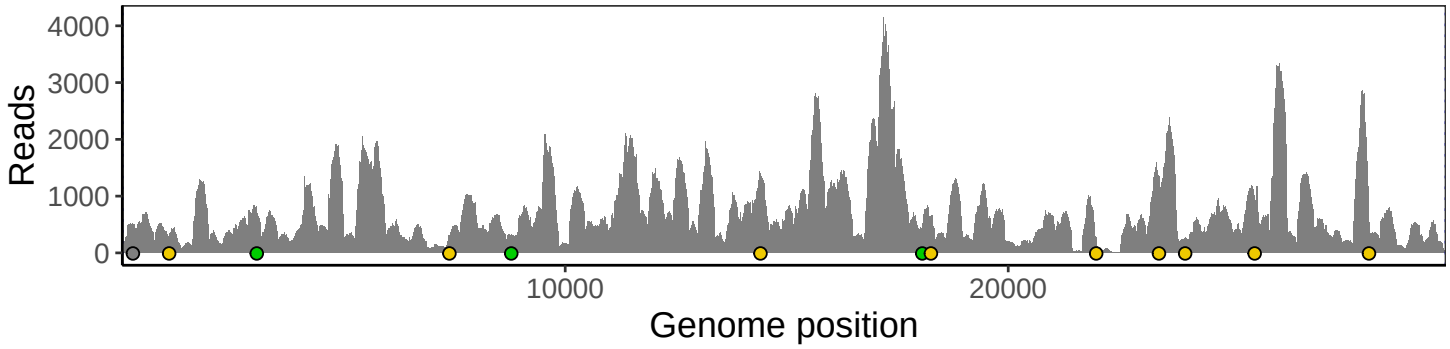


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

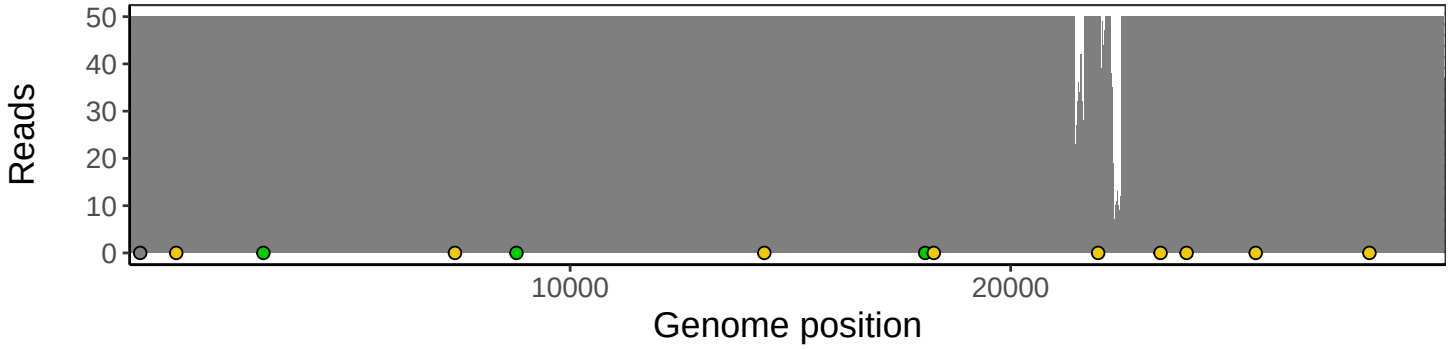


VSP0189-1 | 05/29/2020 | Saliva | 228s-q | 85100 genomes | single experiment

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.