COVID-19 subject 228

2020-10-23

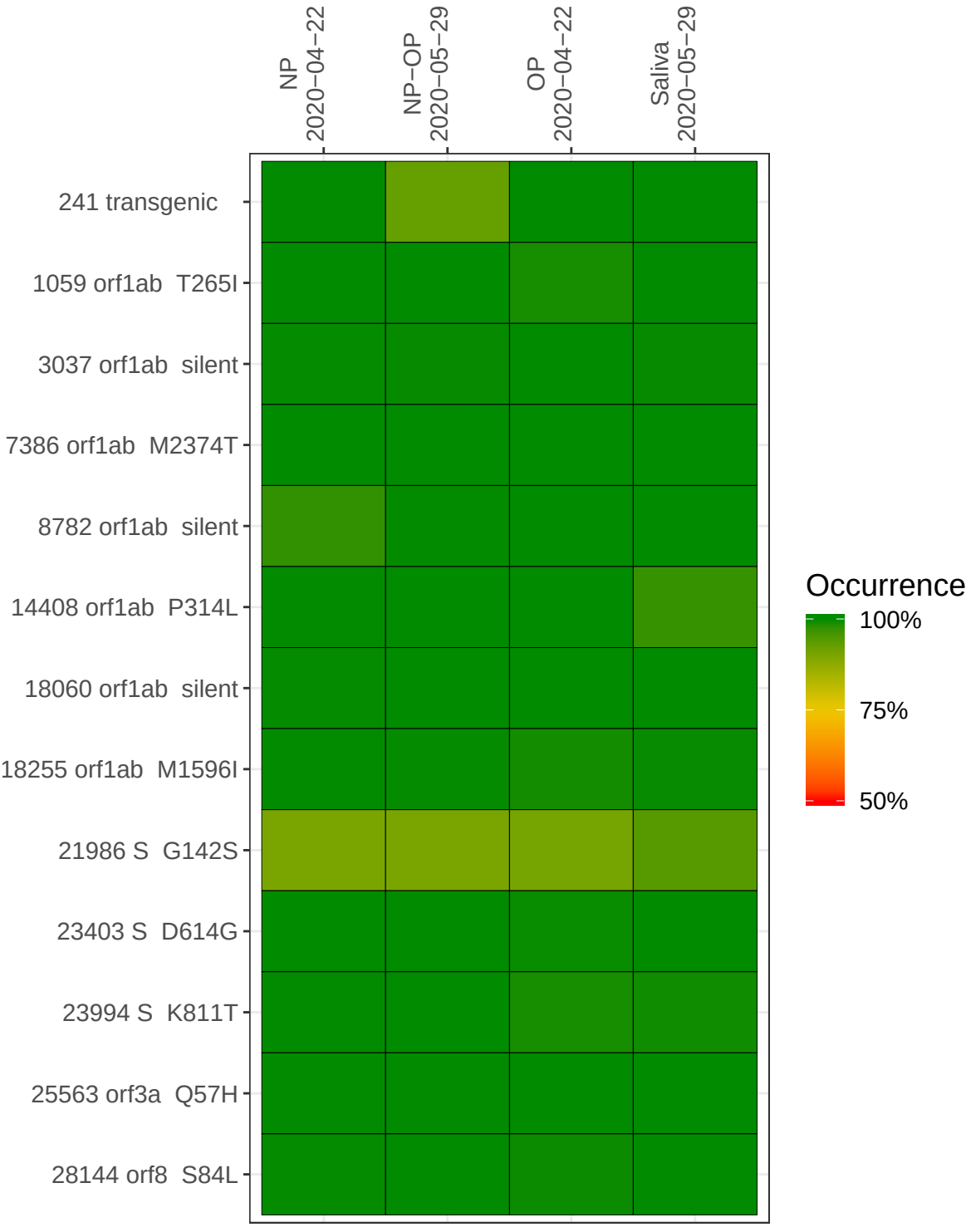
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

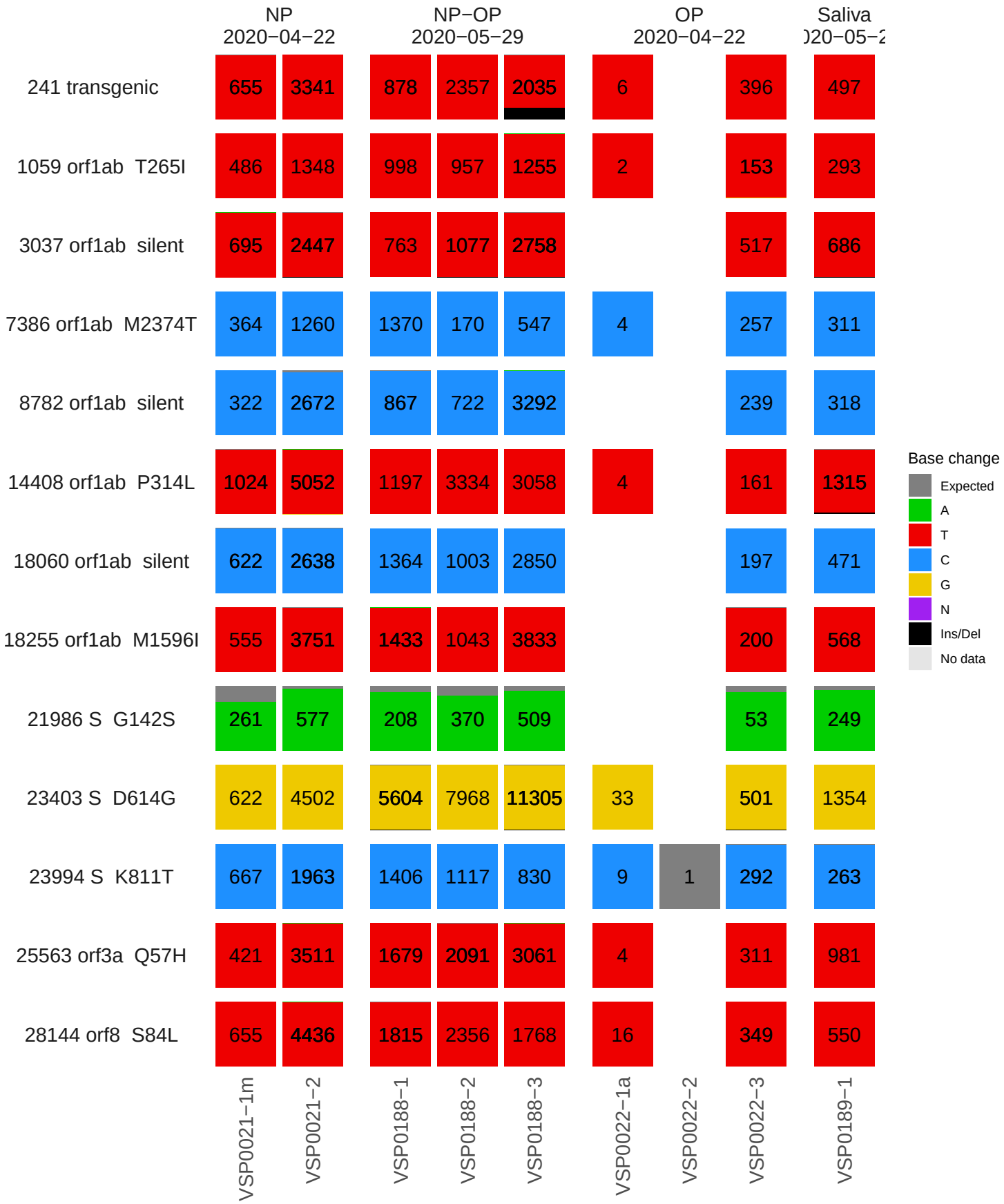
Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0021	composite	NA	NP	2020-04-22	29.82	99.8%	99.8%
VSP0022	composite	NA	OP	2020-04-22	29.68	99.8%	98.8%
VSP0187	composite	NA	ETA	2020-05-29	NA	NA	NA
VSP0188	composite	NA	NP-OP	2020-05-29	29.90	99.8%	99.8%
VSP0021-1m	single experiment	NA	NP	2020-04-22	29.82	99.8%	99.7%
VSP0021-2	single experiment	1.10e+04	NP	2020-04-22	29.82	99.8%	99.8%
VSP0022-1a	single experiment	2.68e+05	OP	2020-04-22	1.75	78.3%	37.7%
VSP0022-2	single experiment	1.34e+06	OP	2020-04-22	0.24	6.2%	0.0%
VSP0022-3	single experiment	1.34e+06	OP	2020-04-22	29.68	99.8%	98.8%
VSP0187-1	single experiment	6.02e+01	ETA	2020-05-29	NA	NA	NA
VSP0187-2	single experiment	3.01e+02	ETA	2020-05-29	NA	NA	NA
VSP0188-1	single experiment	2.04e+03	NP-OP	2020-05-29	9.60	93.7%	93.5%
VSP0188-2	single experiment	1.02e+04	NP-OP	2020-05-29	22.61	99.1%	99.1%
VSP0188-3	single experiment	1.02e+04	NP-OP	2020-05-29	29.87	99.8%	99.8%
VSP0189-1	single experiment	8.51e+04	Saliva	2020-05-29	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.

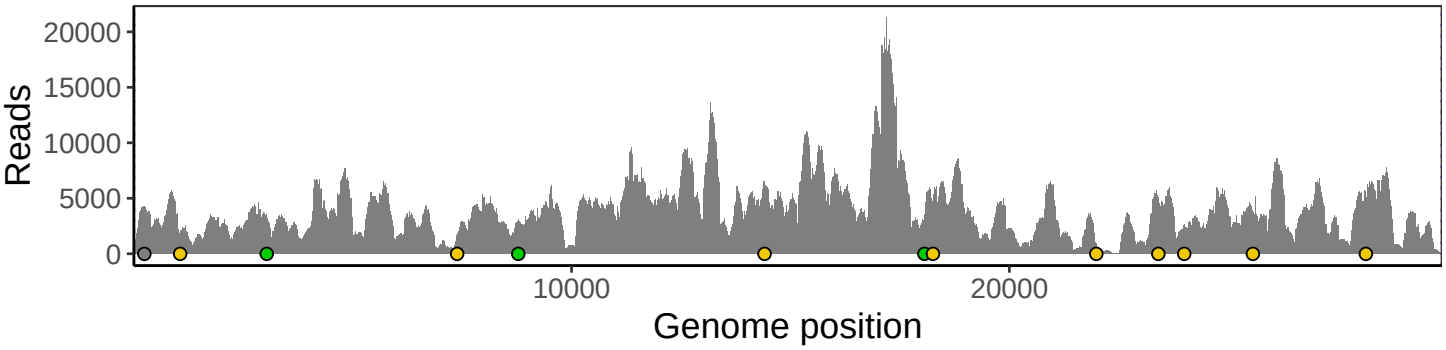



NP
2020−04−22
NP−OP
2020−05−29
OP
2020−04−22
Saliva
)20−05−2
241 transgenic
1059 orf1ab T265I
3037 orf1ab silent
7386 orf1ab M2374T
8782 orf1ab silent
14408 orf1ab P314L
18060 orf1ab silent
18255 orf1ab M1596I
21986 S G142S
23403 S D614G
23994 S K811T
25563 orf3a Q57H
28144 orf8 S84L
655 3341 878 2357 2035 6 396 497
486 1348 998 957 1255 2 153 293
695 2447 763 1077 2758 517 686
364 1260 1370 170 547 4 257 311
322 2672 867 722 3292 239 318
1024 5052 1197 3334 3058 4 161 1315
622 2638 1364 1003 2850 197 471
555 3751 1433 1043 3833 200 568
261 577 208 370 509 53 249
622 4502 5604 7968 11305 33 501 1354
667 1963 1406 1117 830 9 1 292 263
421 3511 1679 2091 3061 4 311 981
655 4436 1815 2356 1768 16 349 550
Base change
Expected
A
T
C
G
N
Ins/Del
No data
VSP0021−1m
VSP0021−2
VSP0188−1
VSP0188−2
VSP0188−3
VSP0022−1a
VSP0022−2
VSP0022−3
VSP0189−1

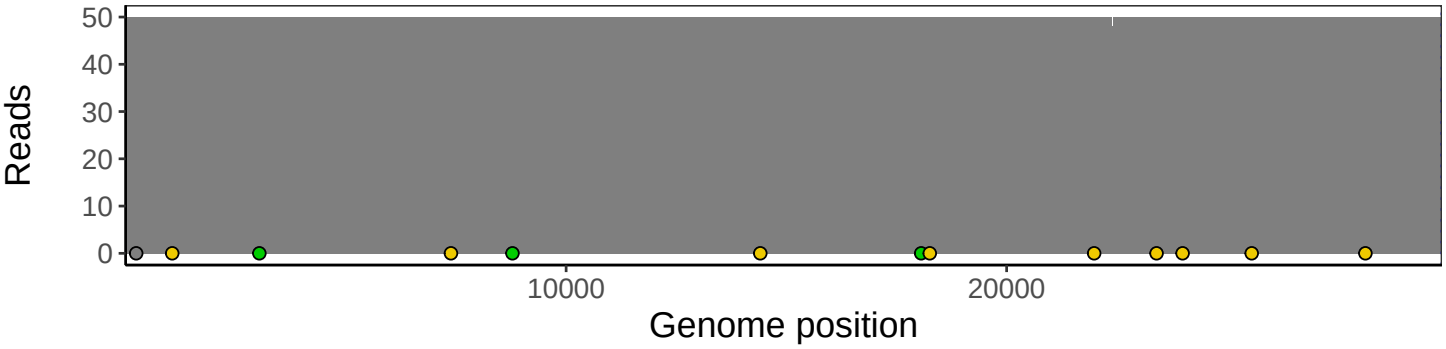
Analyses of individual experiments and composite results.

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

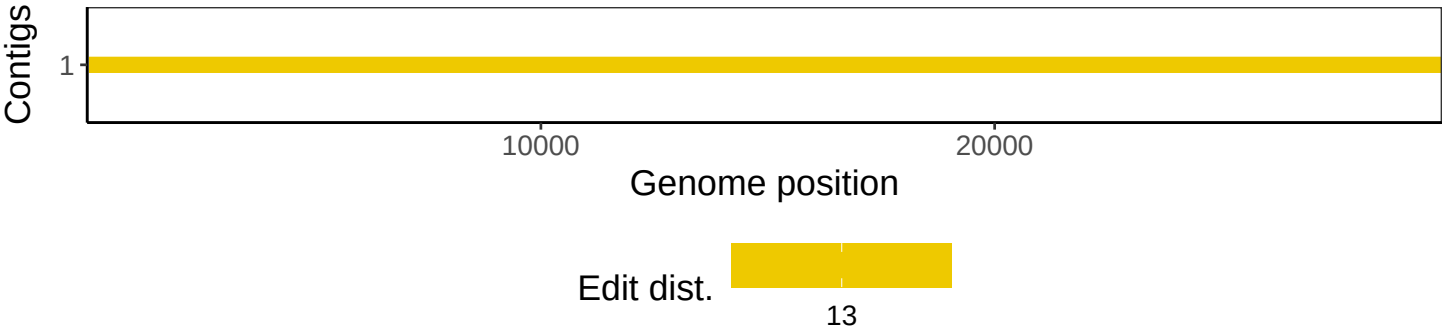
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

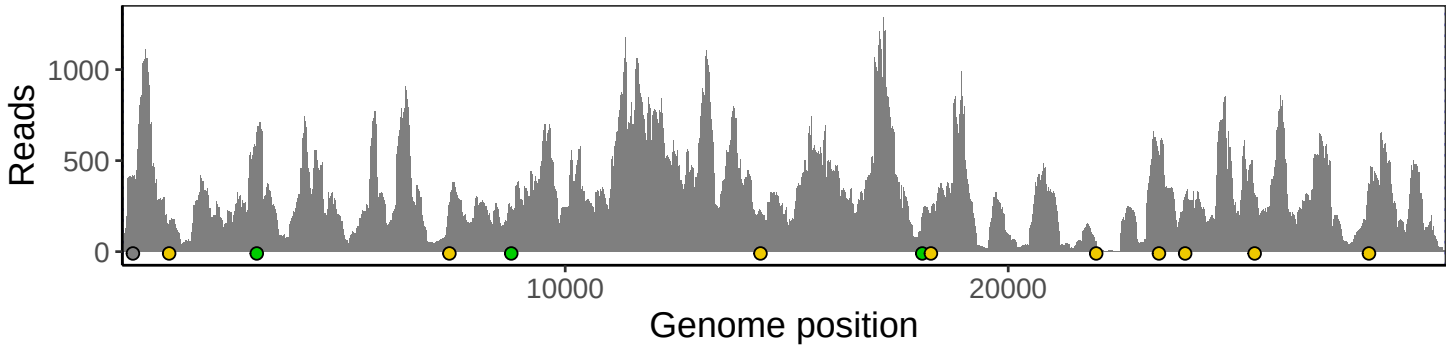


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

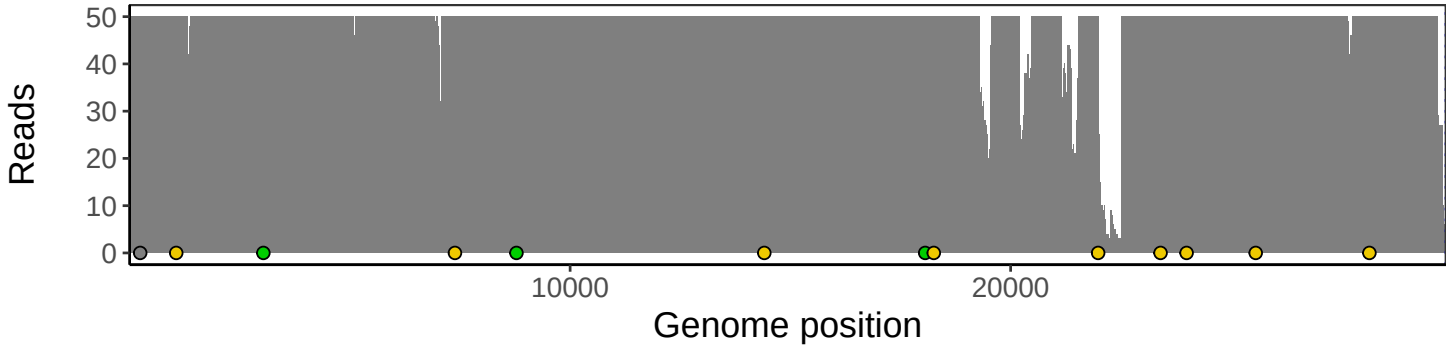


VSP0022 | 2020-04-22 | OP | 228o | composite result

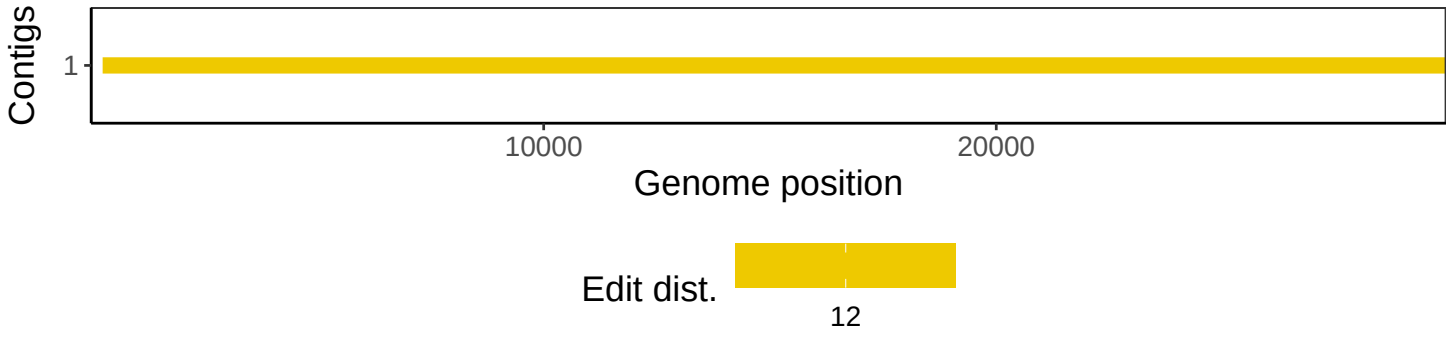
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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.

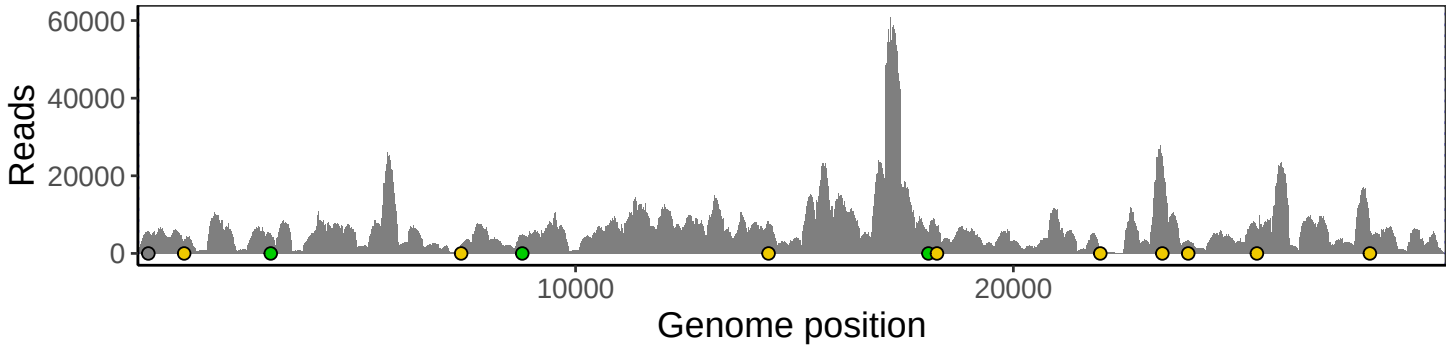


No pileup data available.

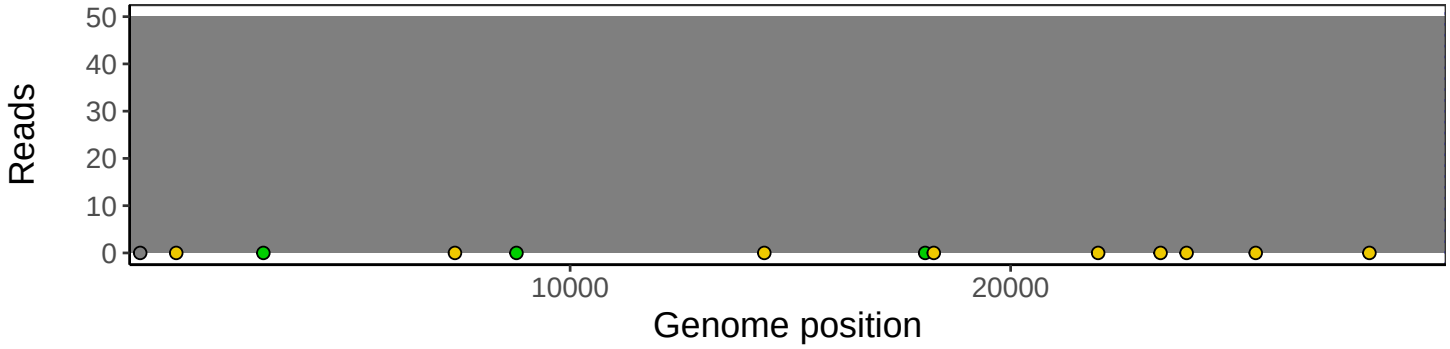
No contig data available.

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

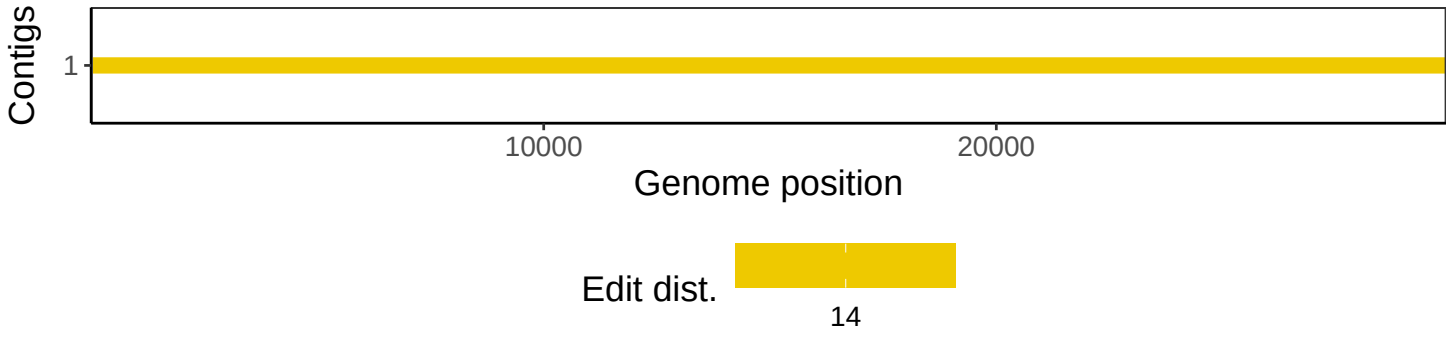
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

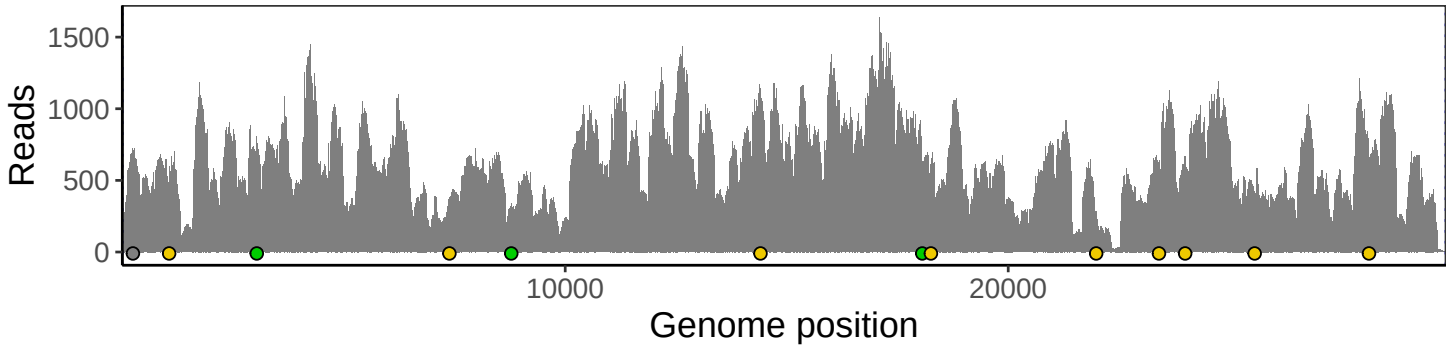


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

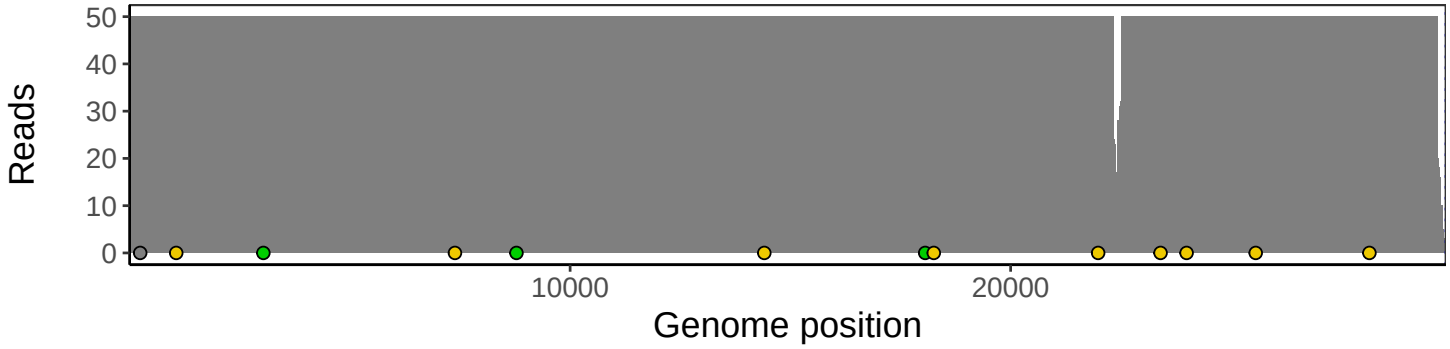


VSP0021-1m | 2020-04-22 | NP | 228n | genomes | single experiment

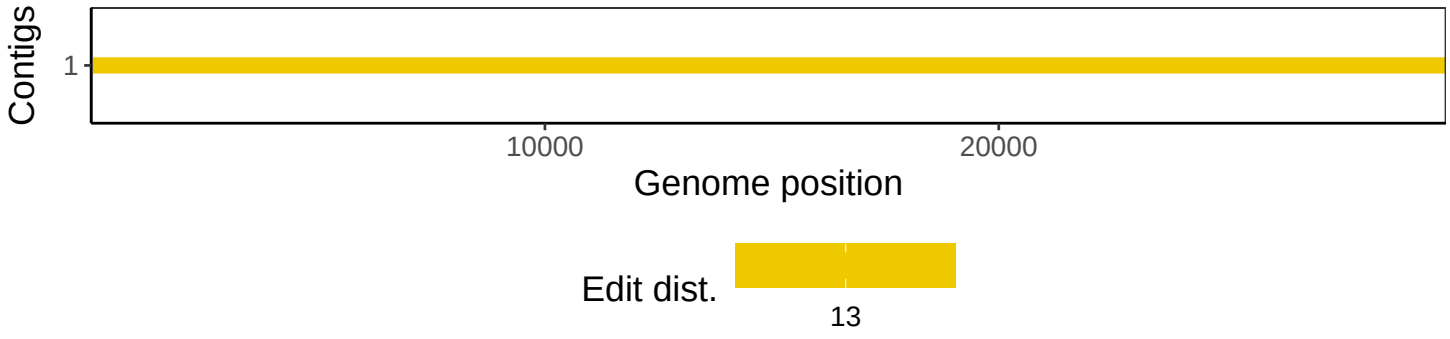
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

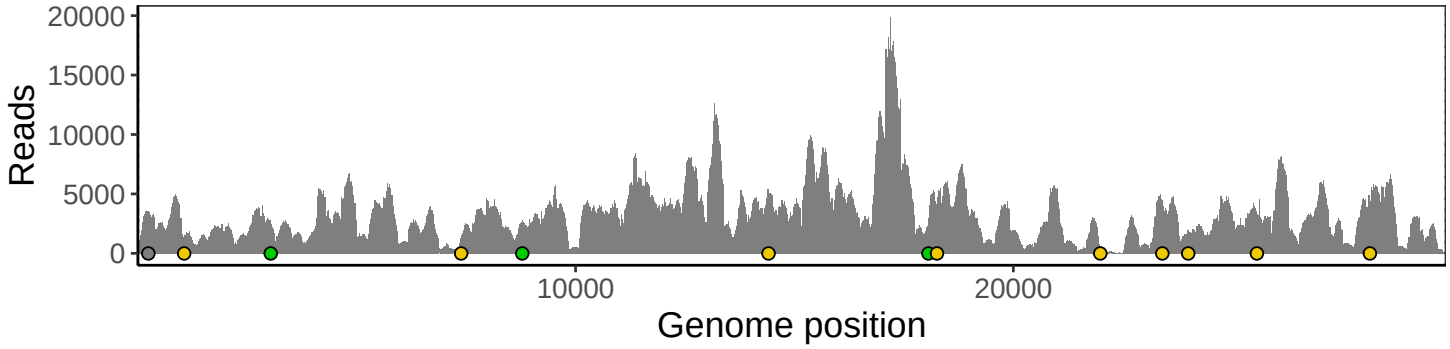


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

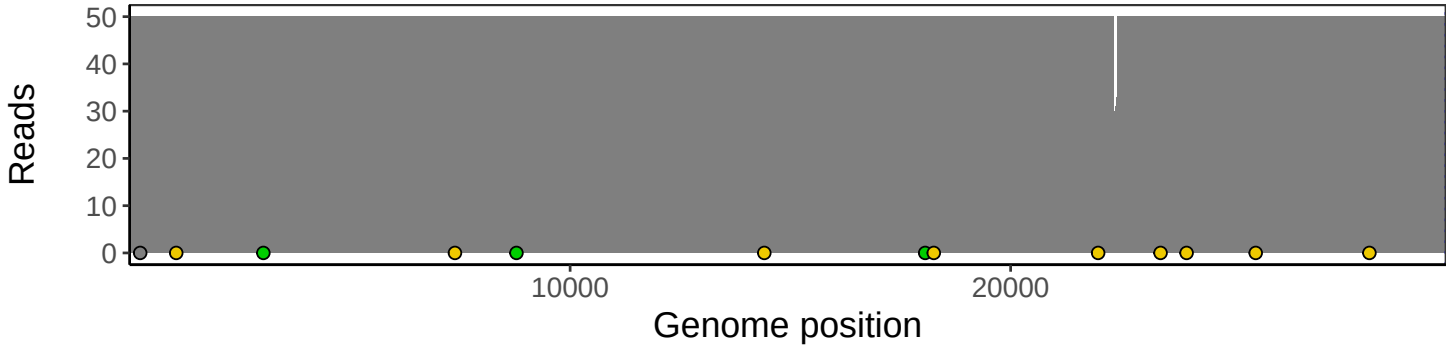


VSP0021-2 | 2020-04-22 | NP | 228n | 11000 genomes | single experiment

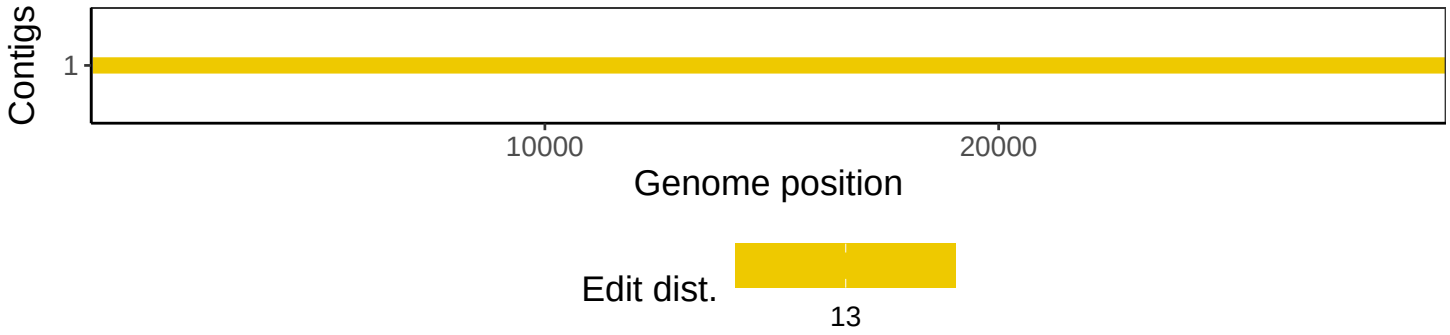
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

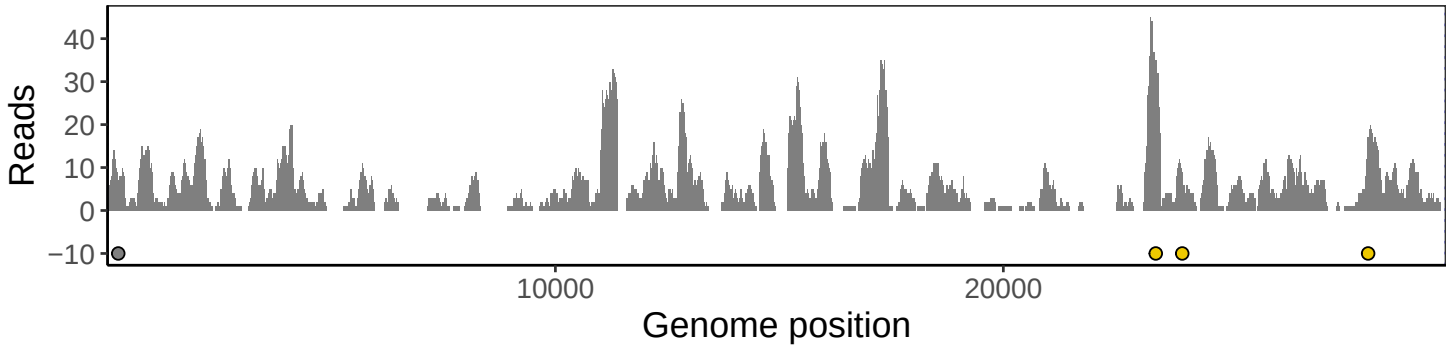


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

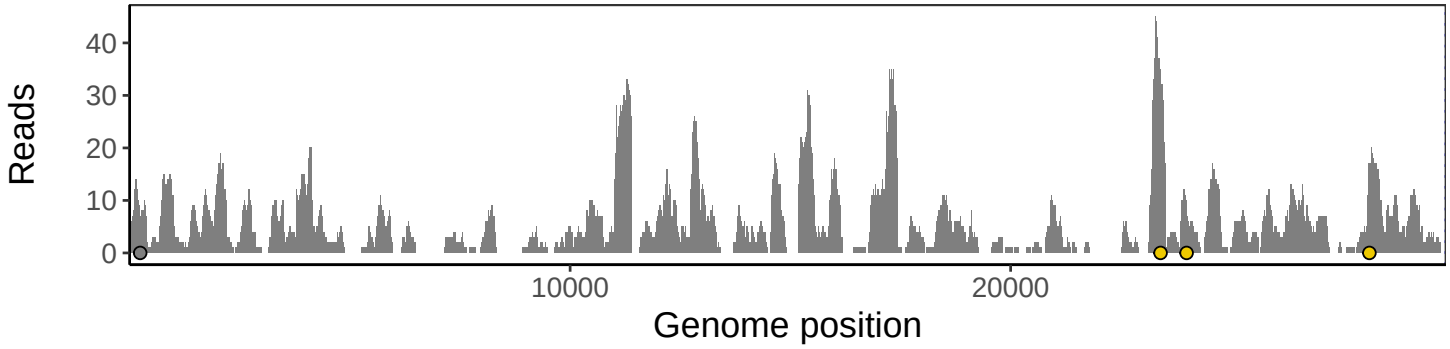


VSP0022-1a | 2020-04-22 | OP | 228o | 268000 genomes | single experiment

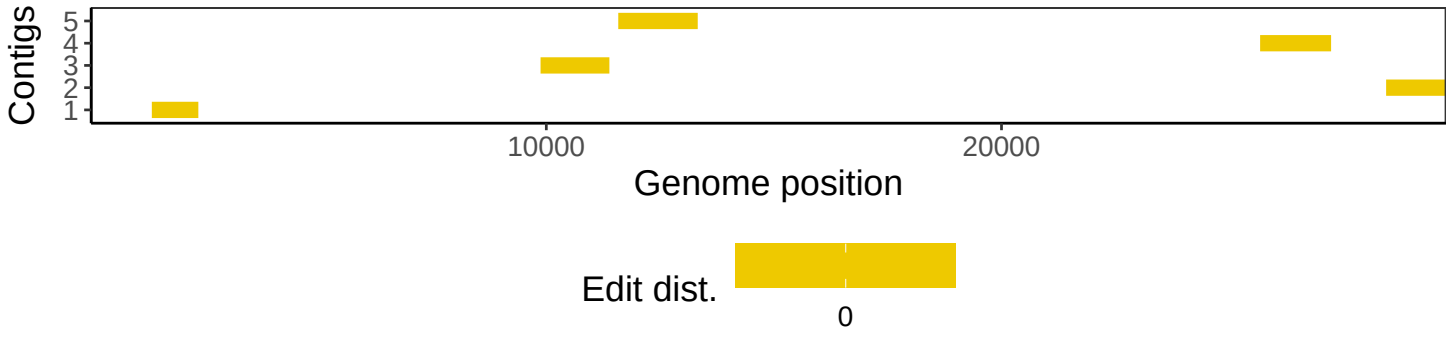
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

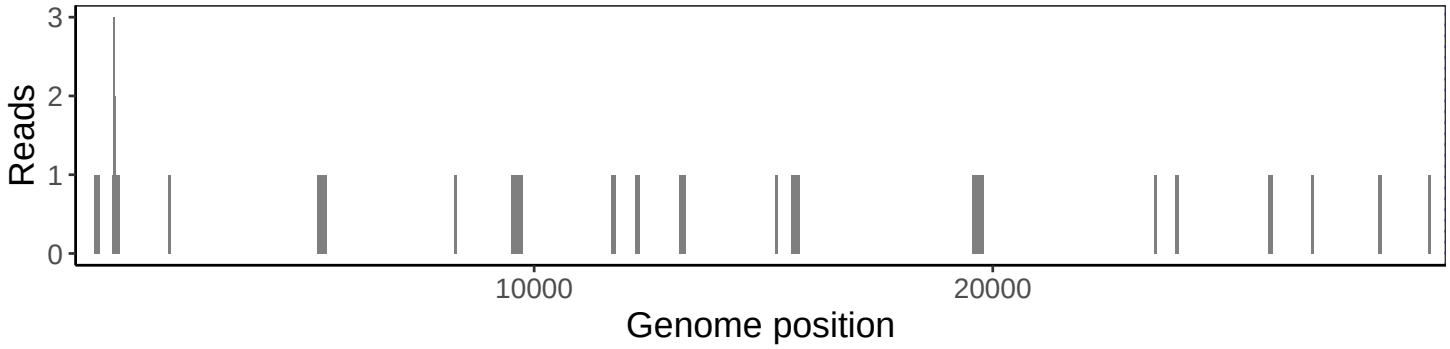


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

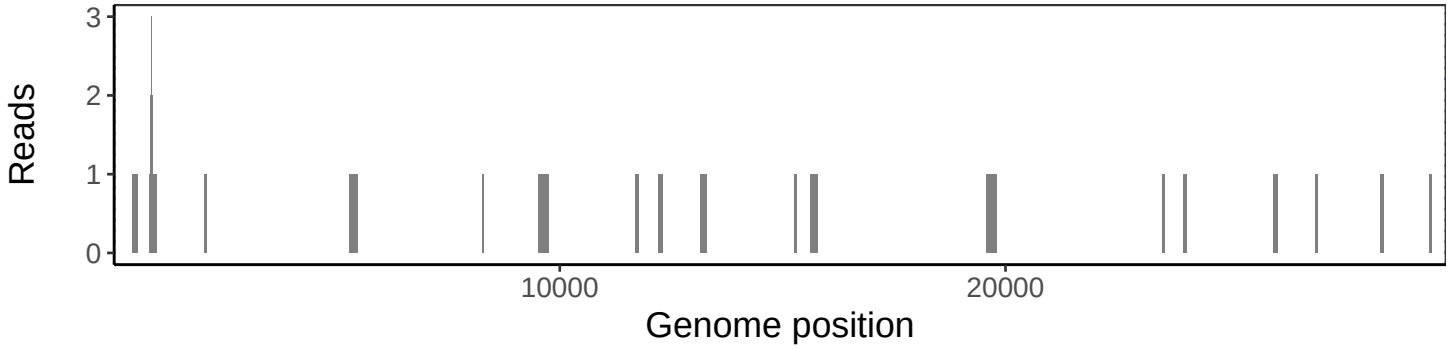


VSP0022-2 | 2020-04-22 | OP | 228o | 1340000 genomes | single experiment

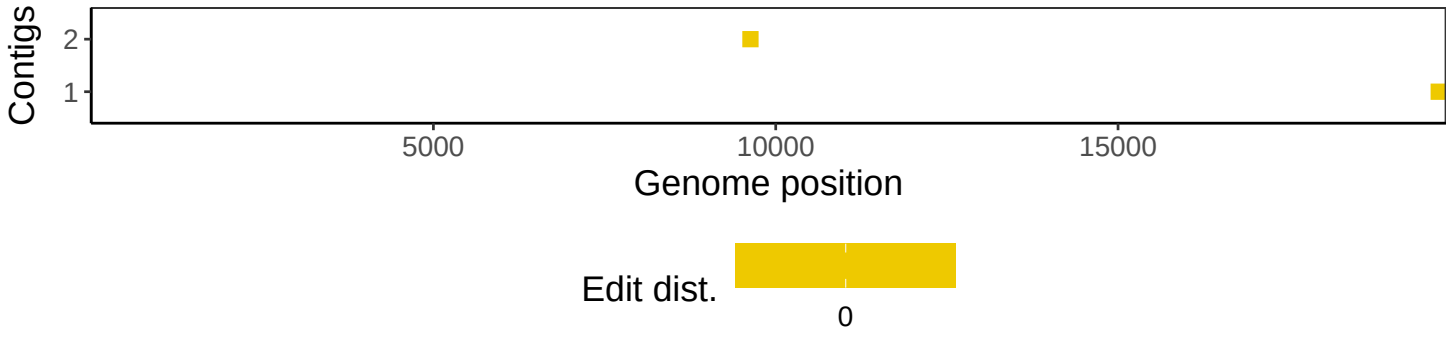
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

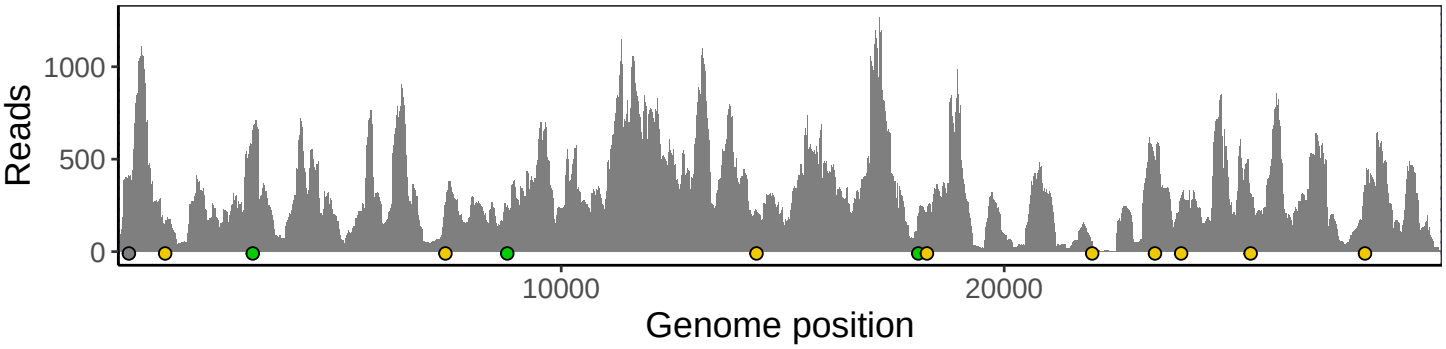


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

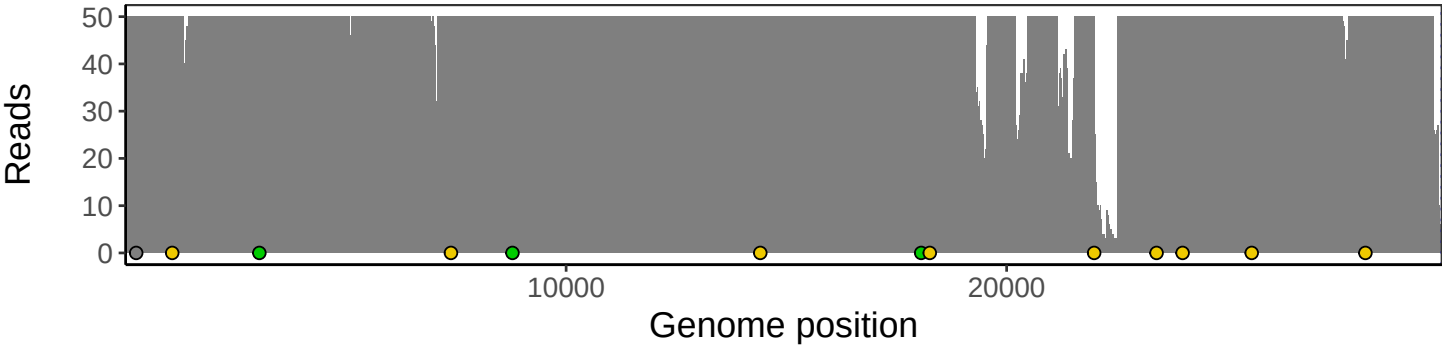


VSP0022-3 | 2020-04-22 | OP | 228o | 1340000 genomes | single experiment

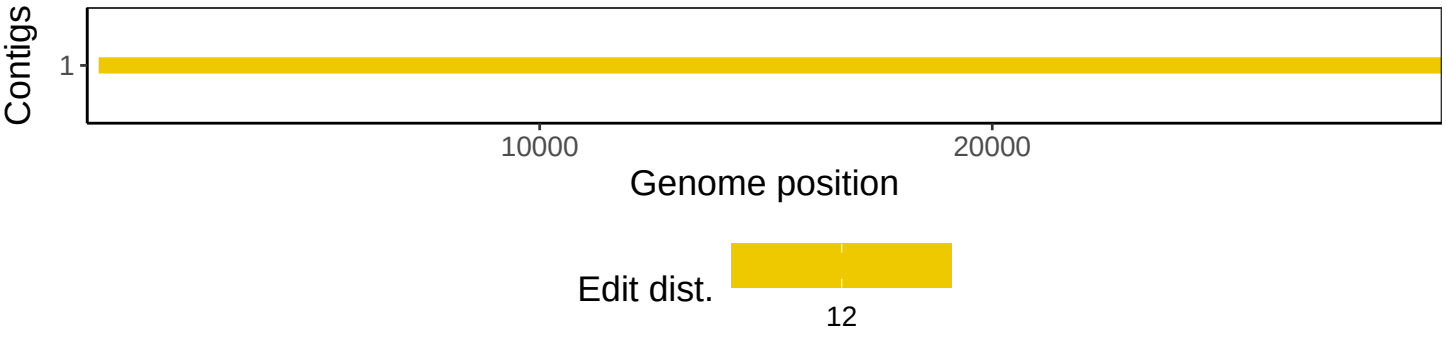
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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.



No pileup data available.

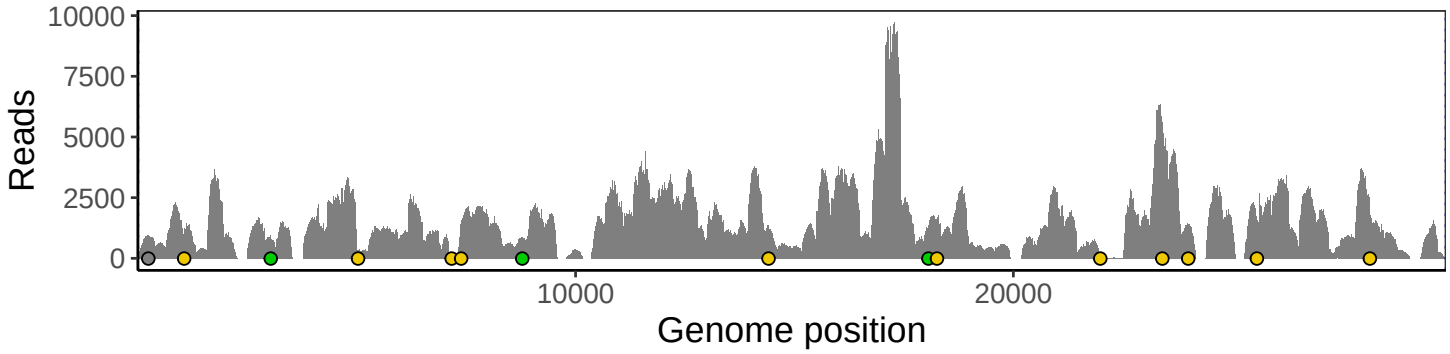
No contig data available.

No pileup data available.

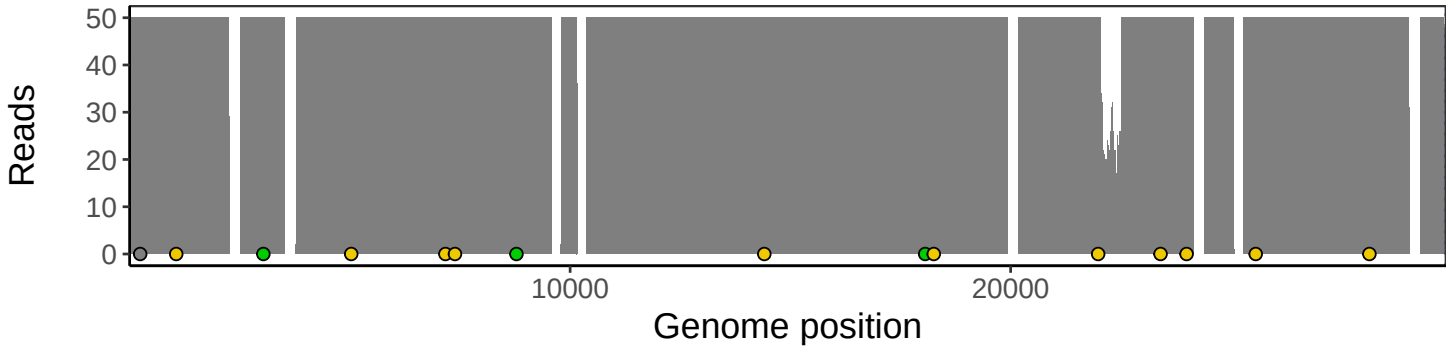
No contig data available.

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

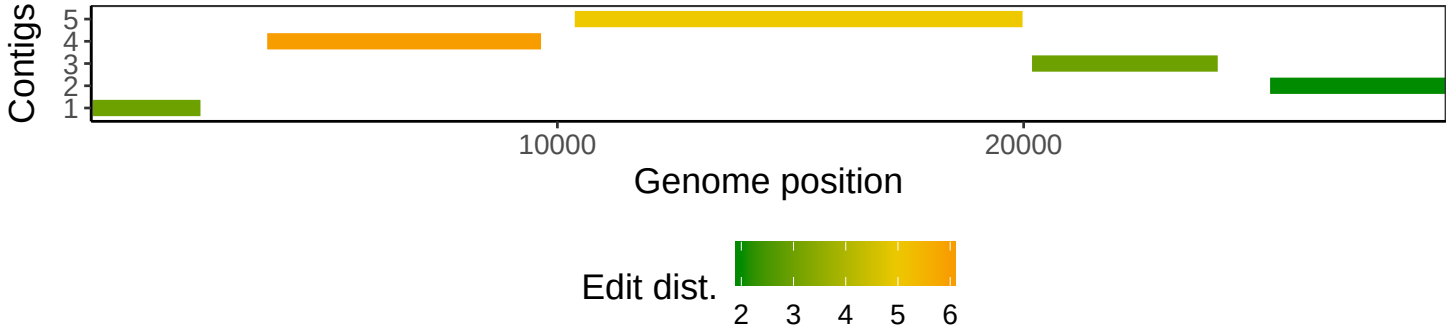
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

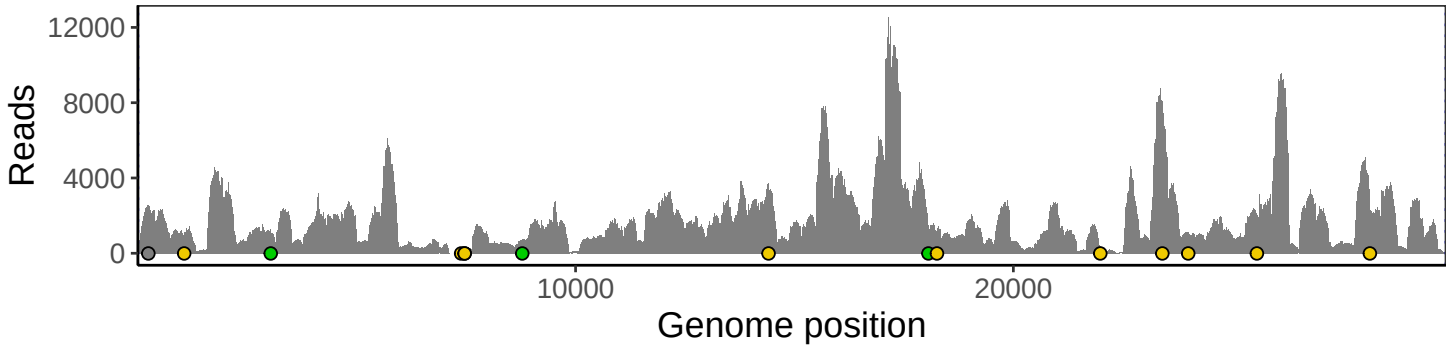


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

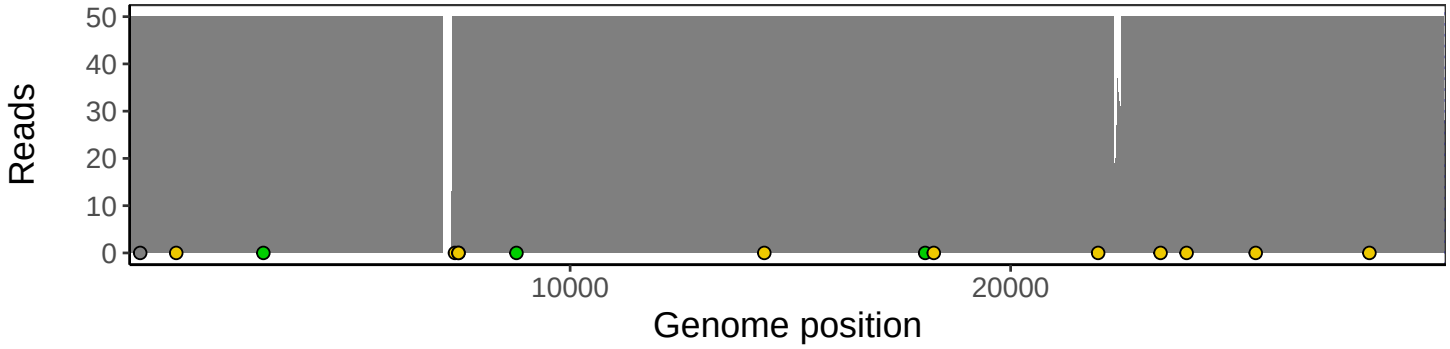


VSP0188-2 | 2020-05-29 | NP-OP | 228no-q | 10200 genomes | single experiment

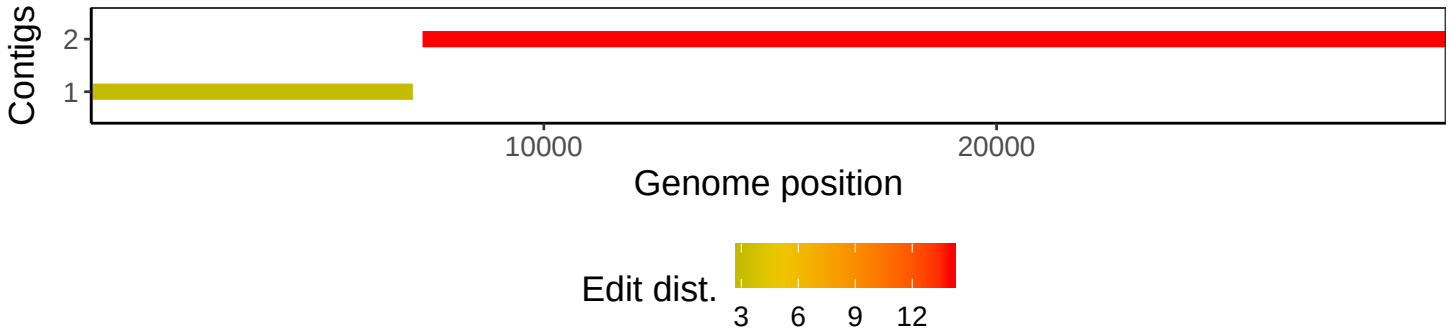
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

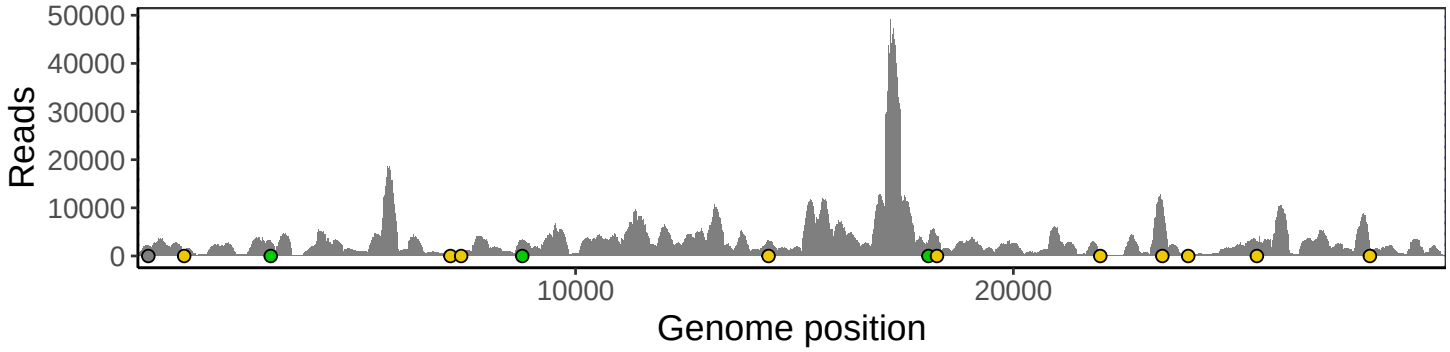


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

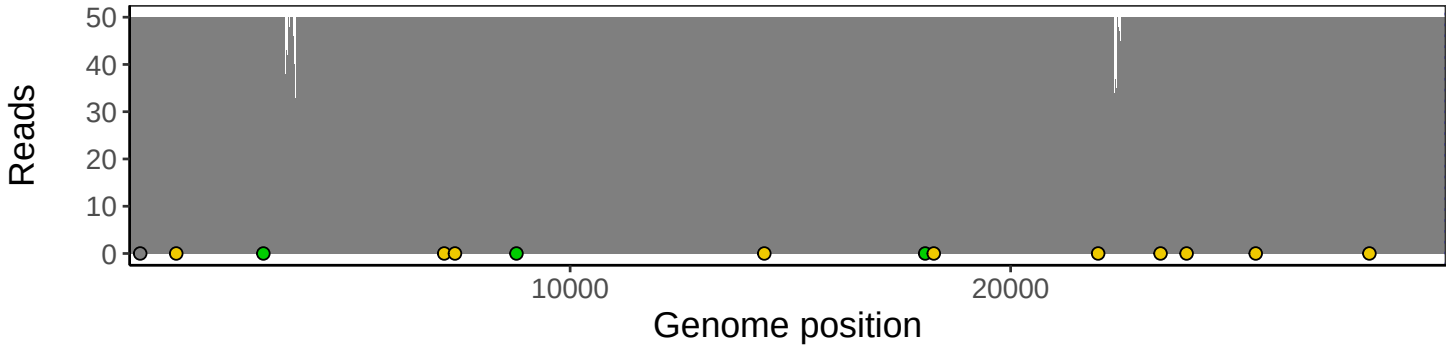


VSP0188-3 | 2020-05-29 | NP-OP | 228no-q | 10200 genomes | single experiment

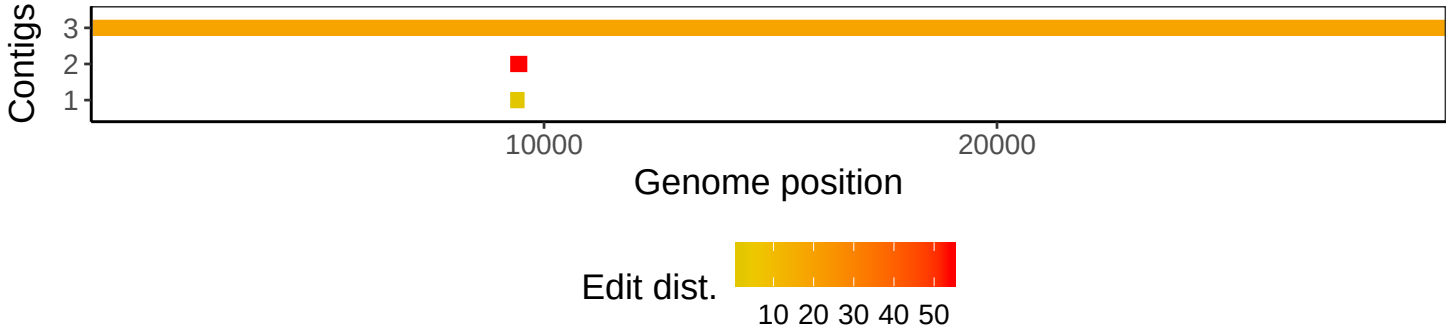
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

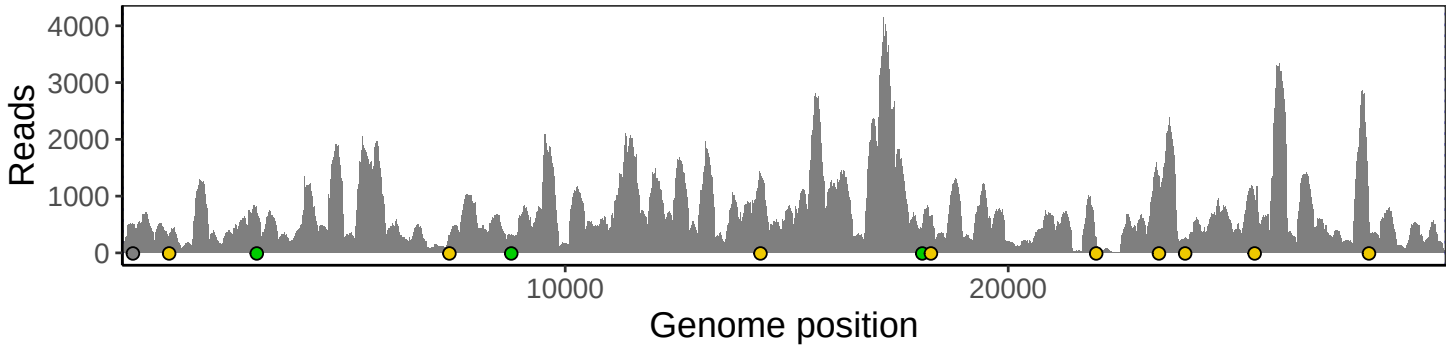


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

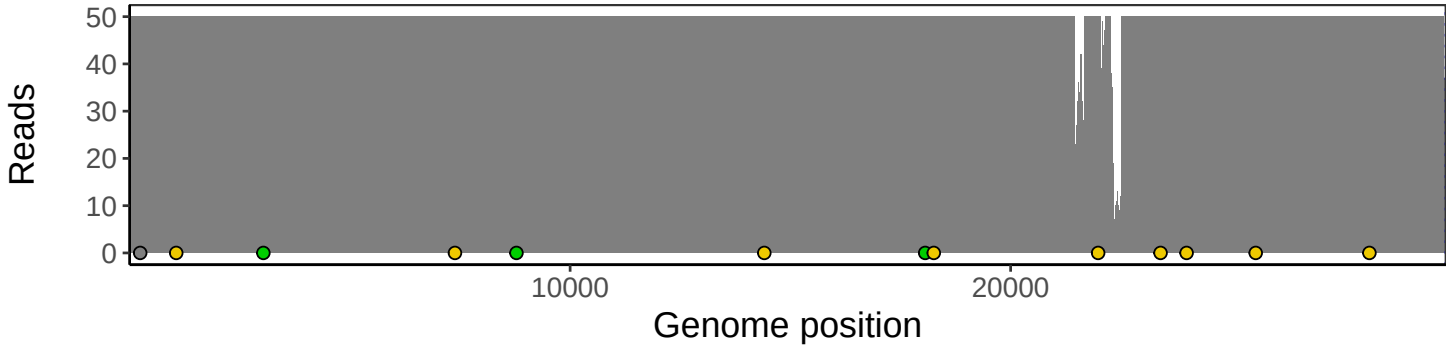


VSP0189-1 | 2020-05-29 | Saliva | 228s-q | 85100 genomes | single experiment

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.