COVID-19 subject 266

2021-01-10

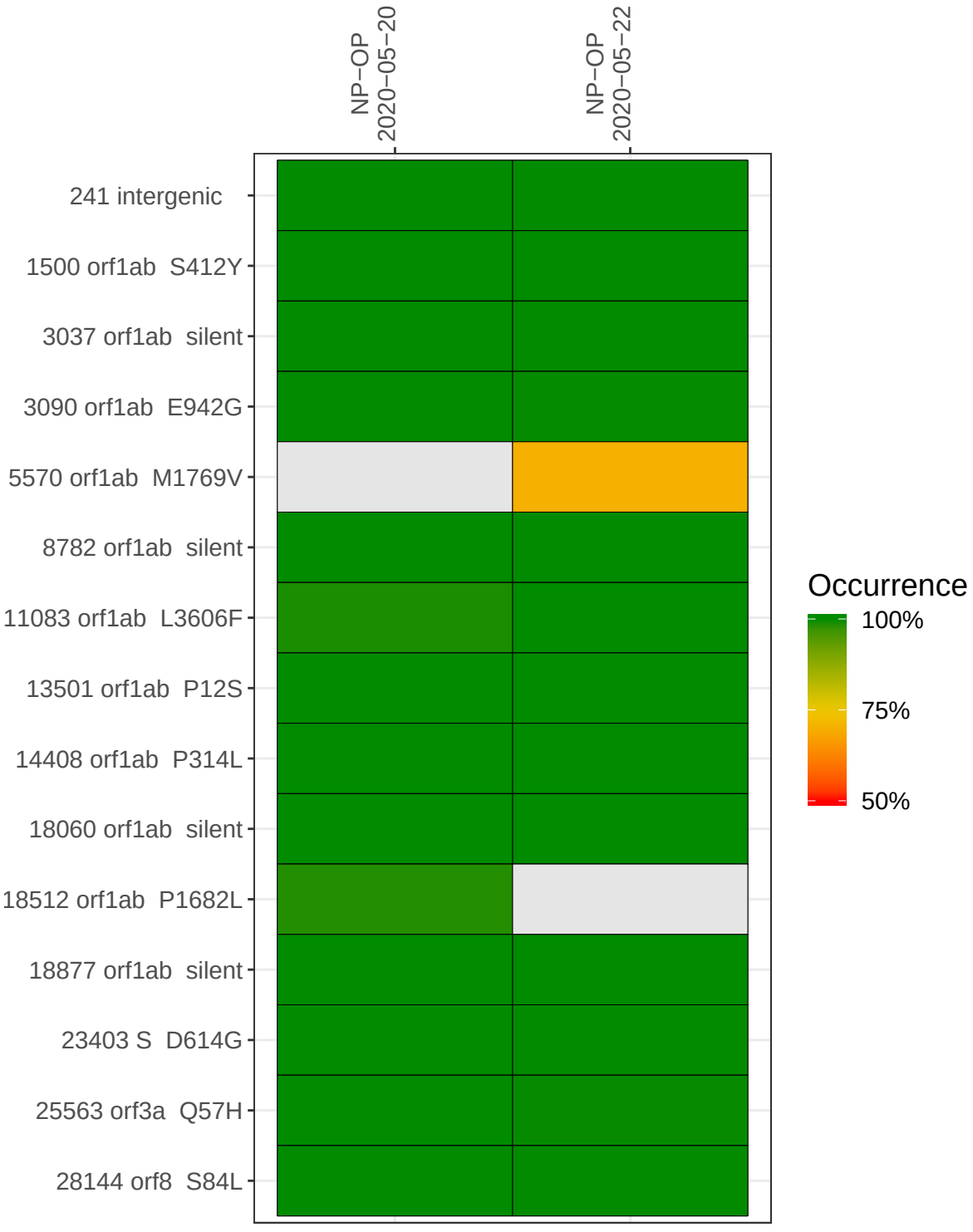
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

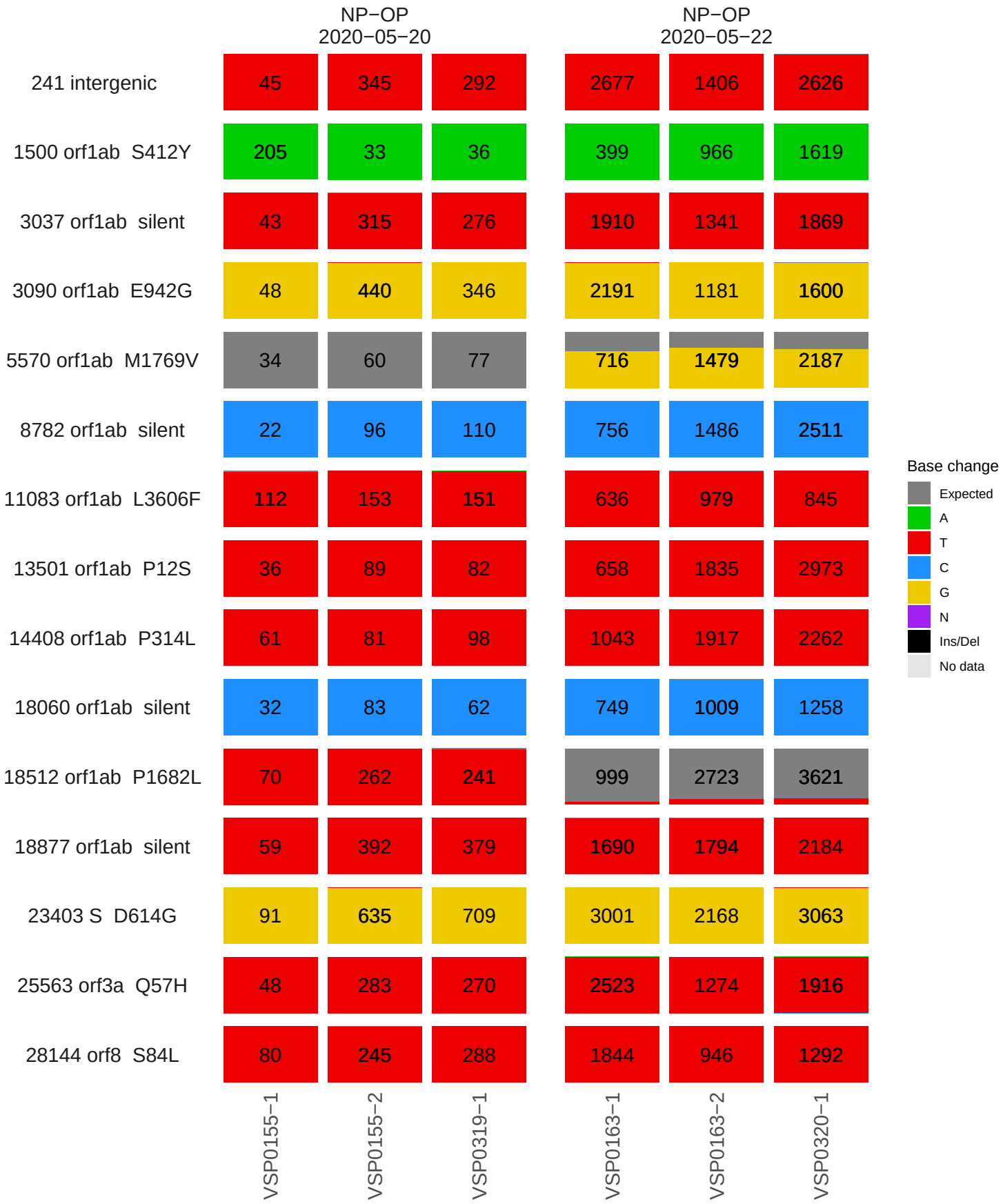
Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0155	composite	NA	NP-OP	2020-05-20	22.33	99.8%	99.0%
VSP0163	composite	NA	NP-OP	2020-05-22	29.75	99.9%	99.8%
VSP0155-1	single experiment	17000	NP-OP	2020-05-20	21.43	99.4%	98.5%
VSP0155-2	single experiment	85000	NP-OP	2020-05-20	22.33	99.7%	98.6%
VSP0163-1	single experiment	1530000	NP-OP	2020-05-22	29.75	99.9%	99.8%
VSP0163-2	single experiment	7650000	NP-OP	2020-05-22	29.84	99.9%	99.8%
VSP0319-1	single experiment	143500	NP-OP	2020-05-20	22.25	99.3%	98.5%
VSP0320-1	single experiment	5750000	NP-OP	2020-05-22	29.86	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.

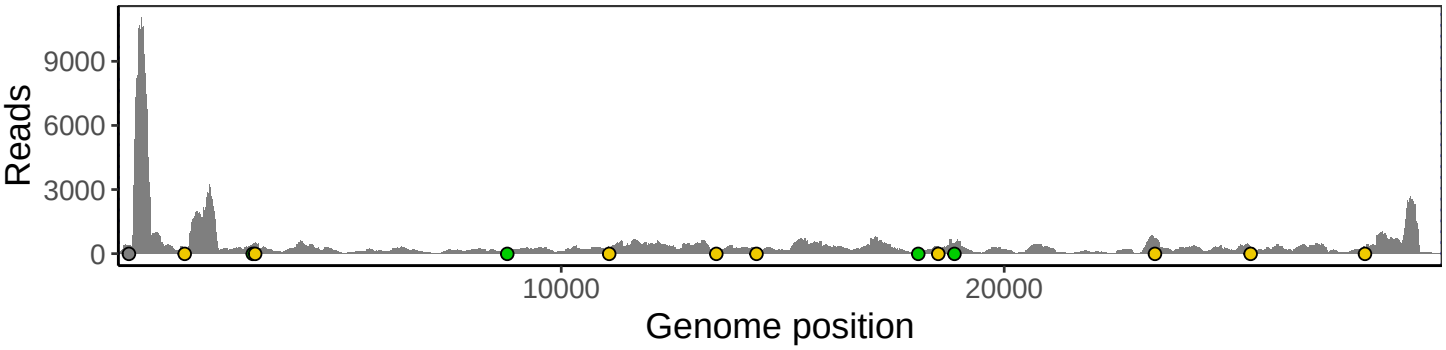



NP−OP
2020−05−20
NP−OP
2020−05−22
241 intergenic
1500 orf1ab S412Y
3037 orf1ab silent
3090 orf1ab E942G
5570 orf1ab M1769V
8782 orf1ab silent
11083 orf1ab L3606F
13501 orf1ab P12S
14408 orf1ab P314L
18060 orf1ab silent
18512 orf1ab P1682L
18877 orf1ab silent
23403 S D614G
25563 orf3a Q57H
28144 orf8 S84L
45 345 292 2677 1406 2626
205 33 36 399 966 1619
43 315 276 1910 1341 1869
48 440 346 2191 1181 1600
34 60 77 716 1479 2187
22 96 110 756 1486 2511
112 153 151 636 979 845
36 89 82 658 1835 2973
61 81 98 1043 1917 2262
32 83 62 749 1009 1258
70 262 241 999 2723 3621
59 392 379 1690 1794 2184
91 635 709 3001 2168 3063
48 283 270 2523 1274 1916
80 245 288 1844 946 1292
VSP0155−1
VSP0155−2
VSP0319−1
VSP0163−1
VSP0163−2
VSP0320−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

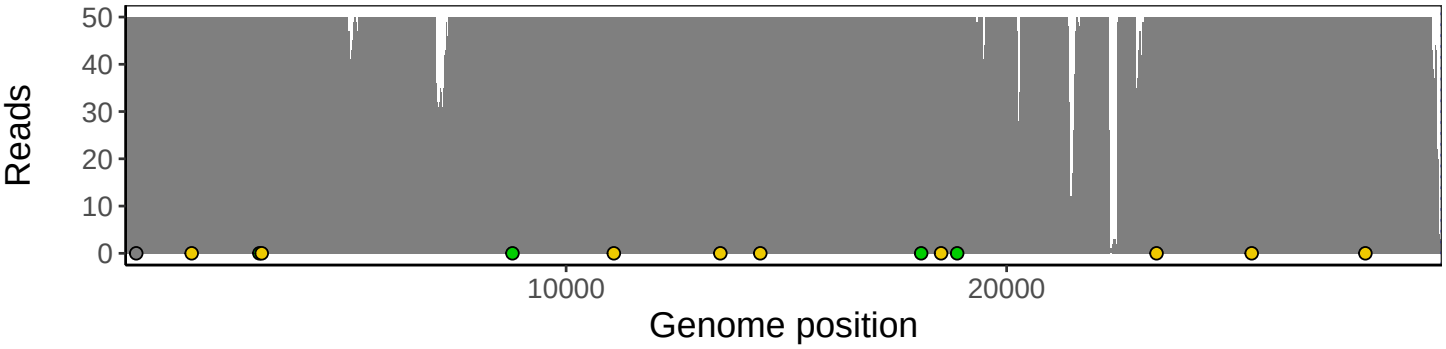
Analyses of individual experiments and composite results.

VSP0155 | 2020-05-20 | NP-OP | 266no-q | composite result

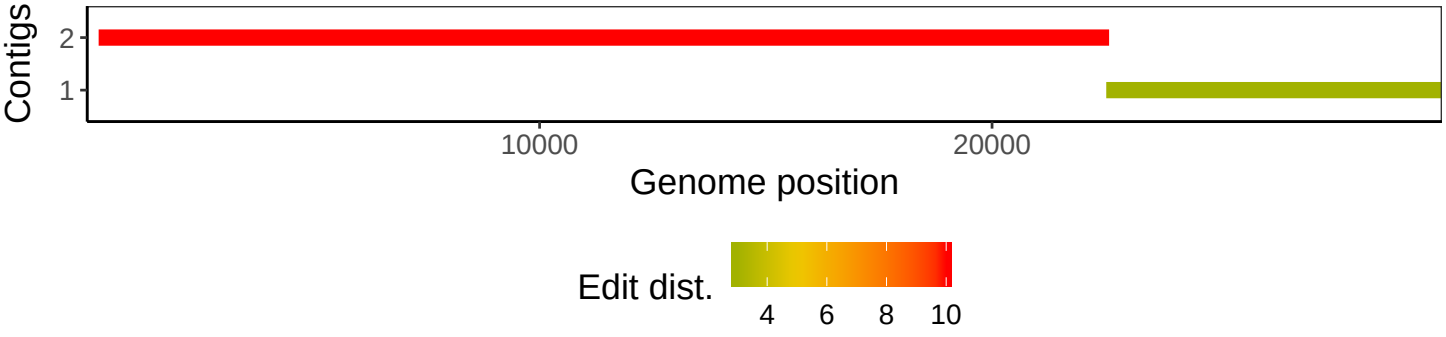
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

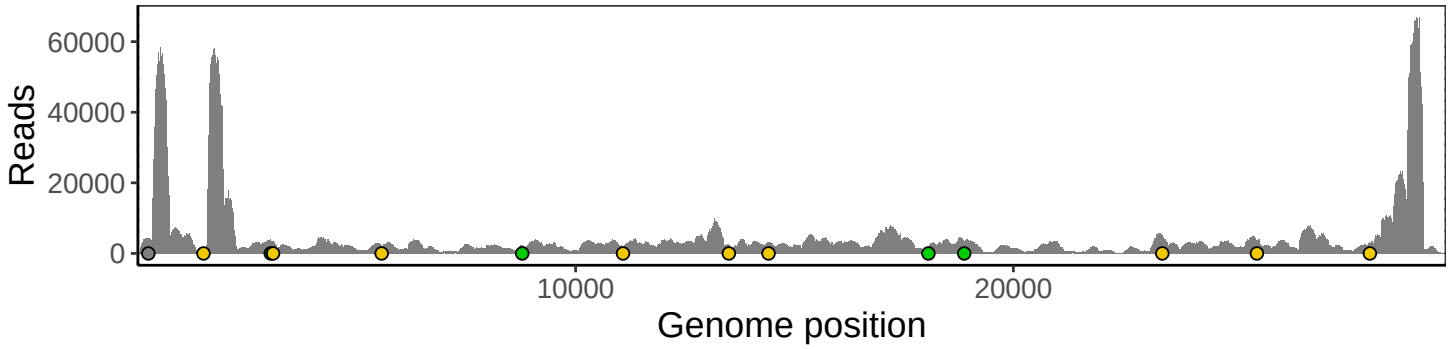


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

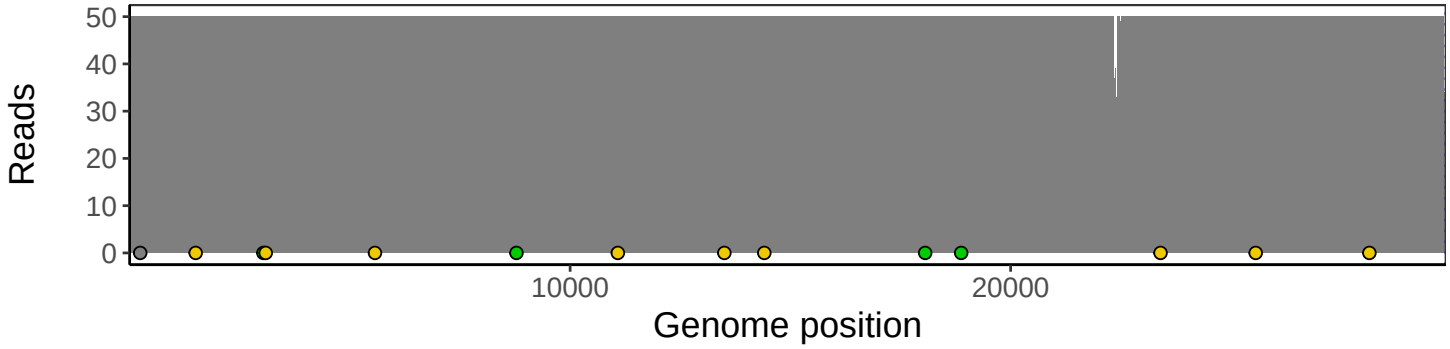


VSP0163 | 2020-05-22 | NP-OP | 266no-q | composite result

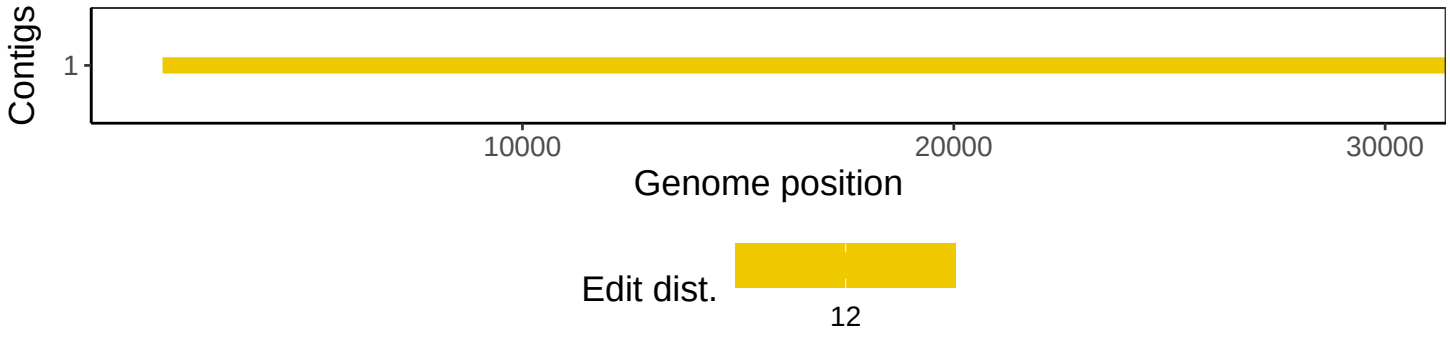
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

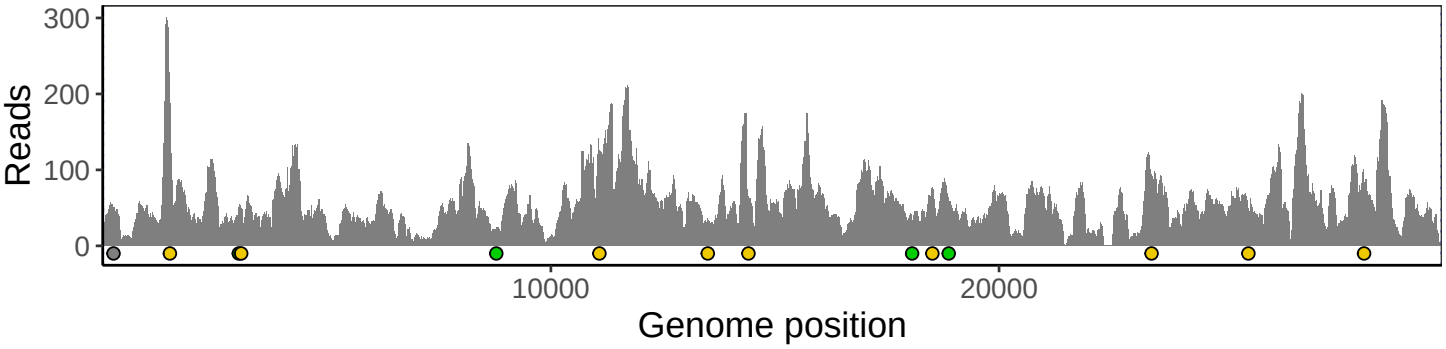


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

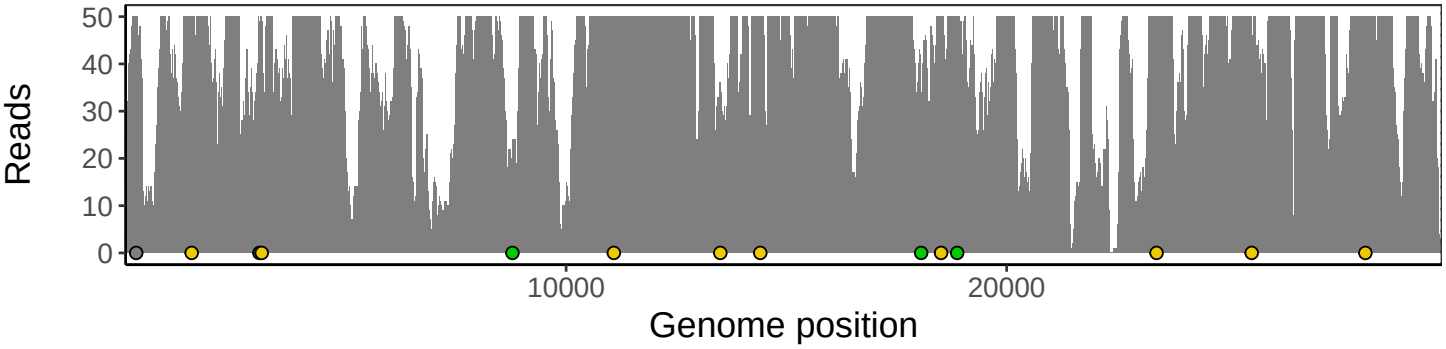


VSP0155-1 | 2020-05-20 | NP-OP | 266no-q | 17000 genomes | single experiment

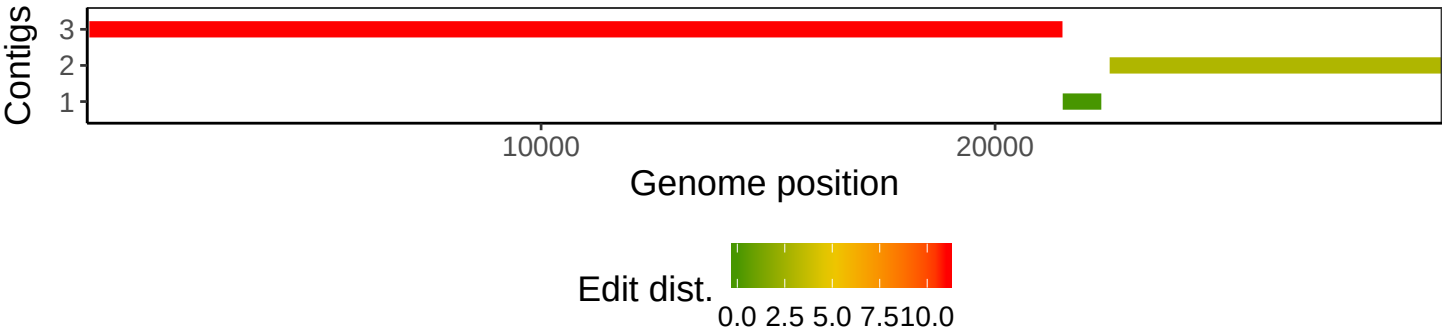
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

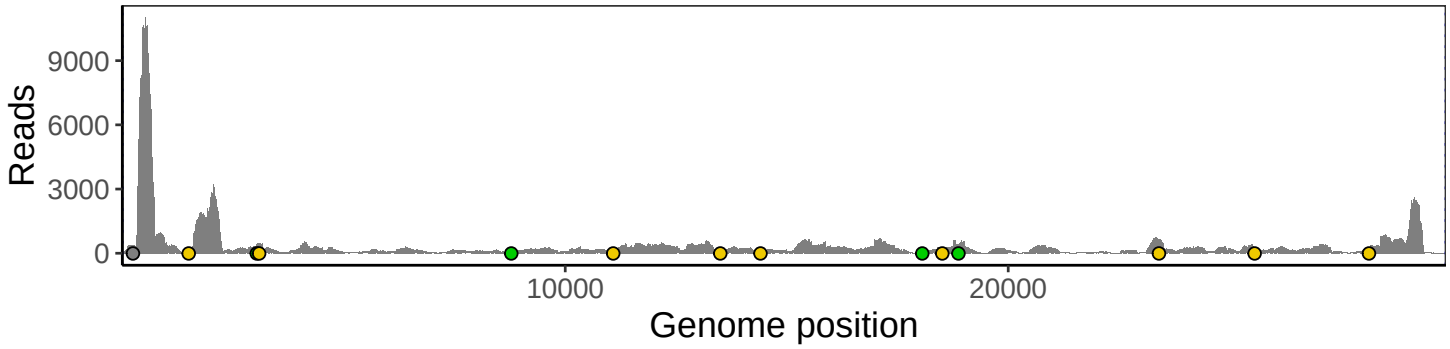


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

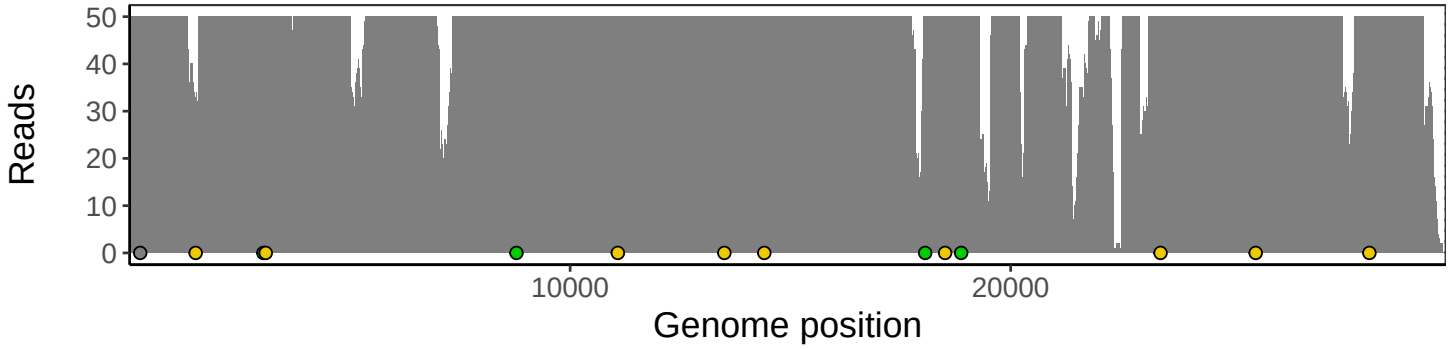


VSP0155-2 | 2020-05-20 | NP-OP | 266no-q | 85000 genomes | single experiment

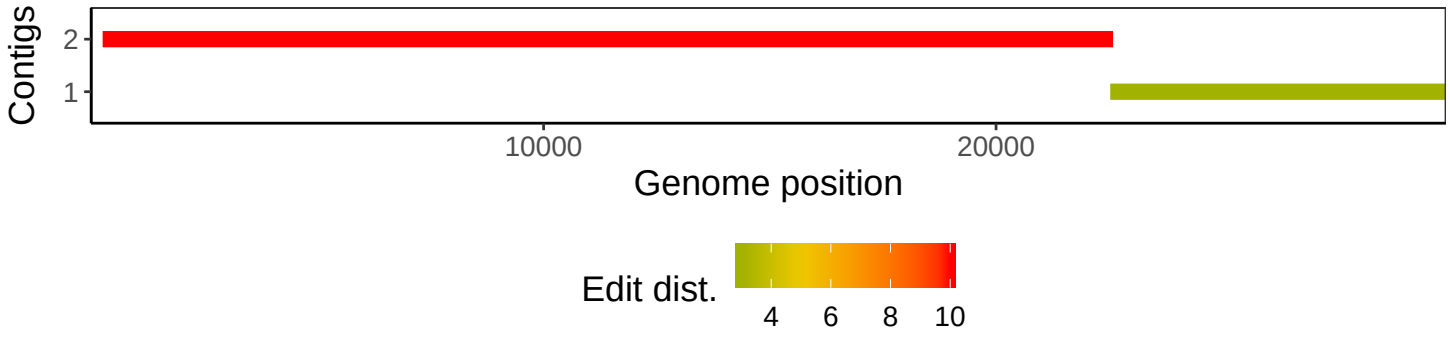
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

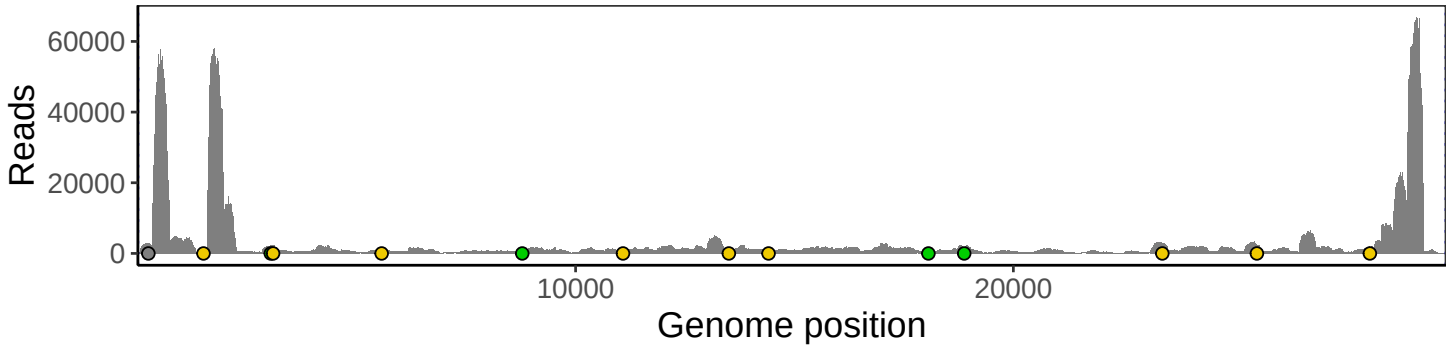


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

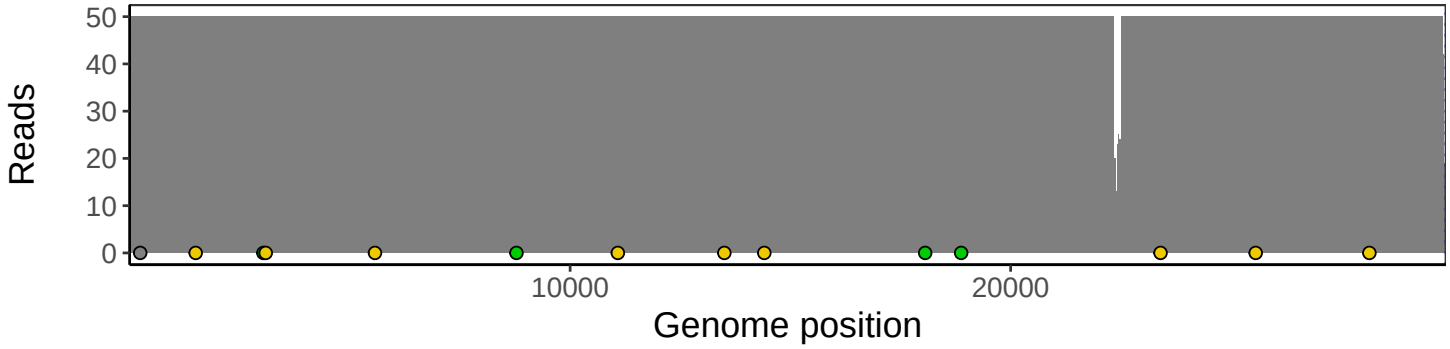


VSP0163-1 | 2020-05-22 | NP-OP | 266no-q | 1530000 genomes | single experiment

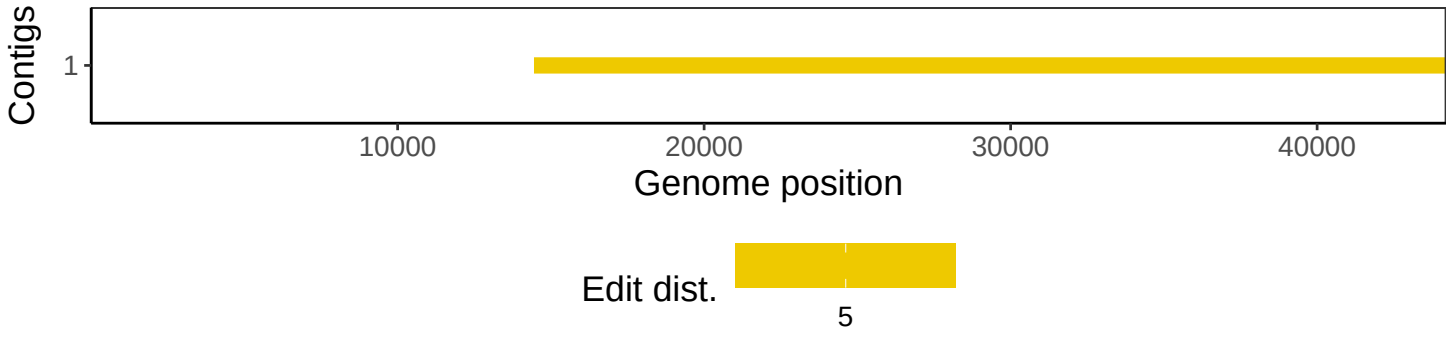
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

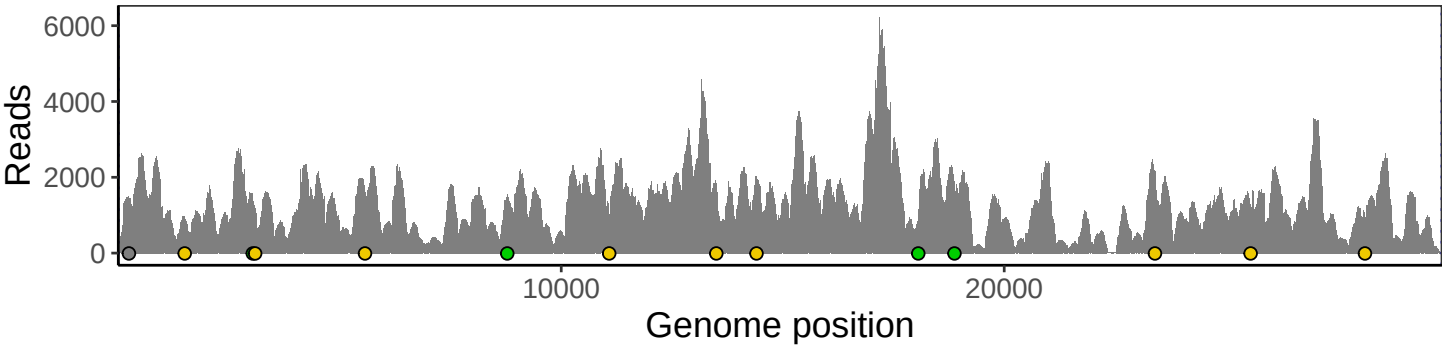


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

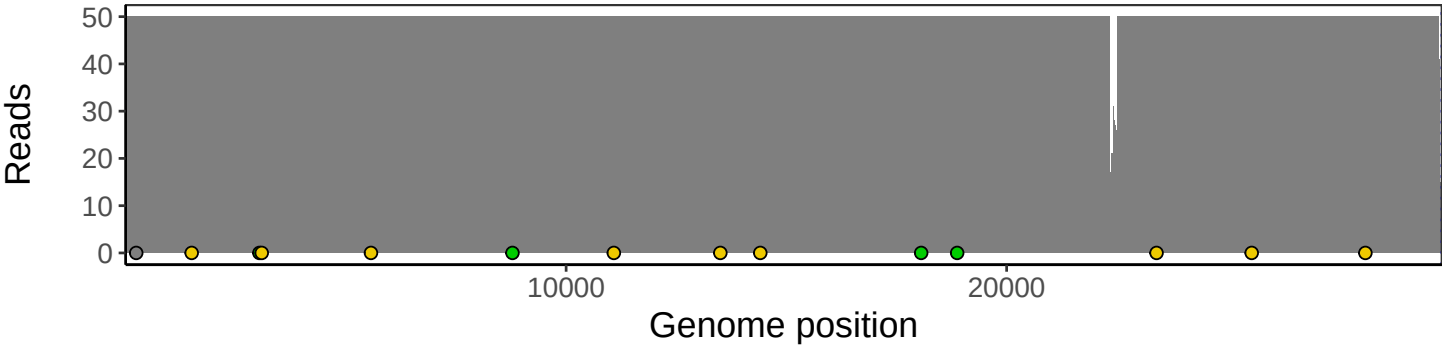


VSP0163-2 | 2020-05-22 | NP-OP | 266no-q | 7650000 genomes | single experiment

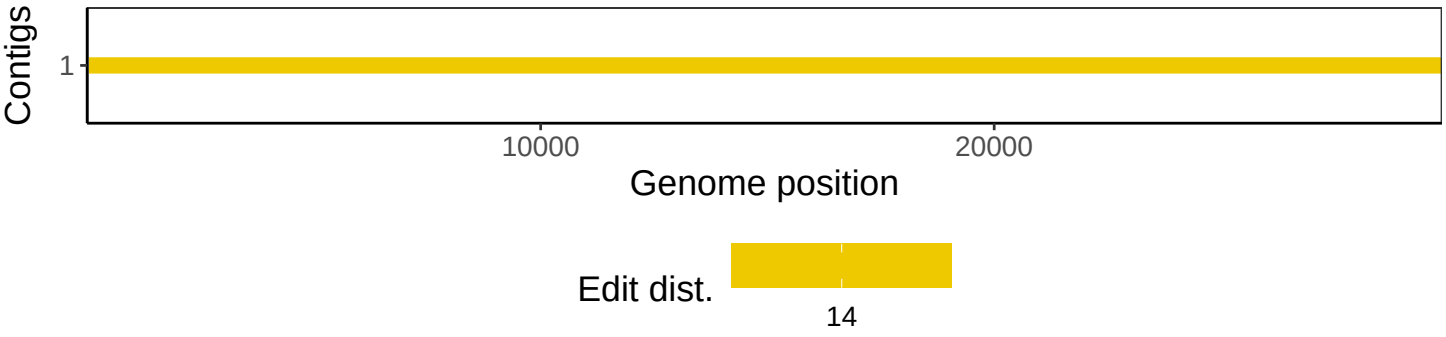
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

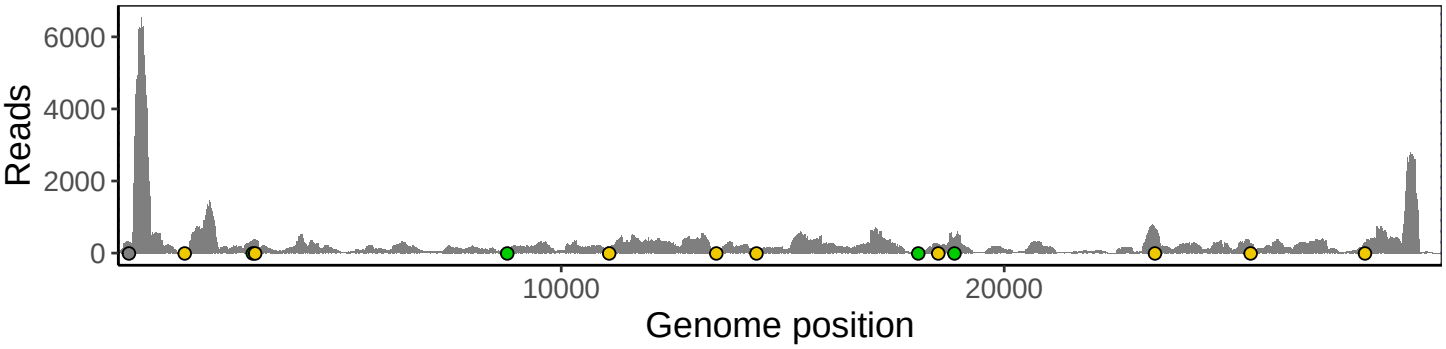


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

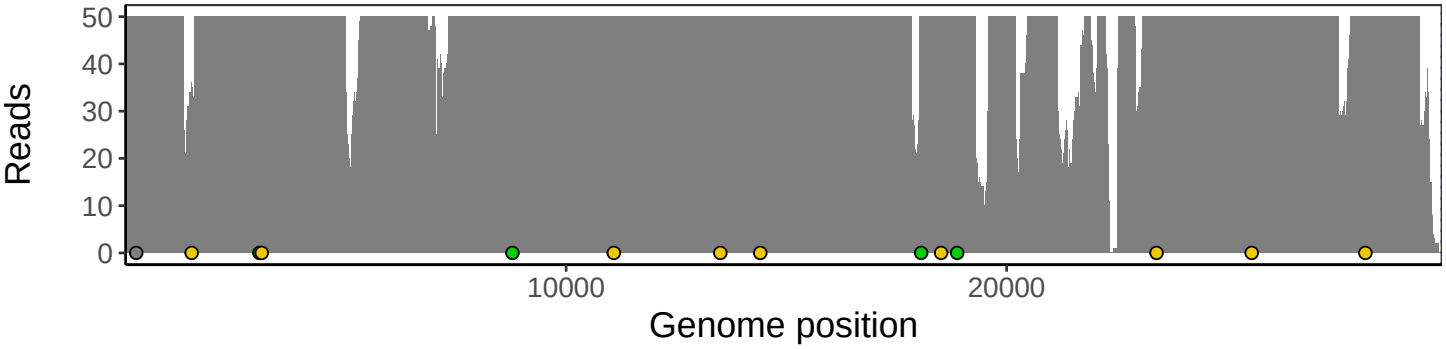


VSP0319-1 | 2020-05-20 | NP-OP | 266no-q | 143500 genomes | single experiment

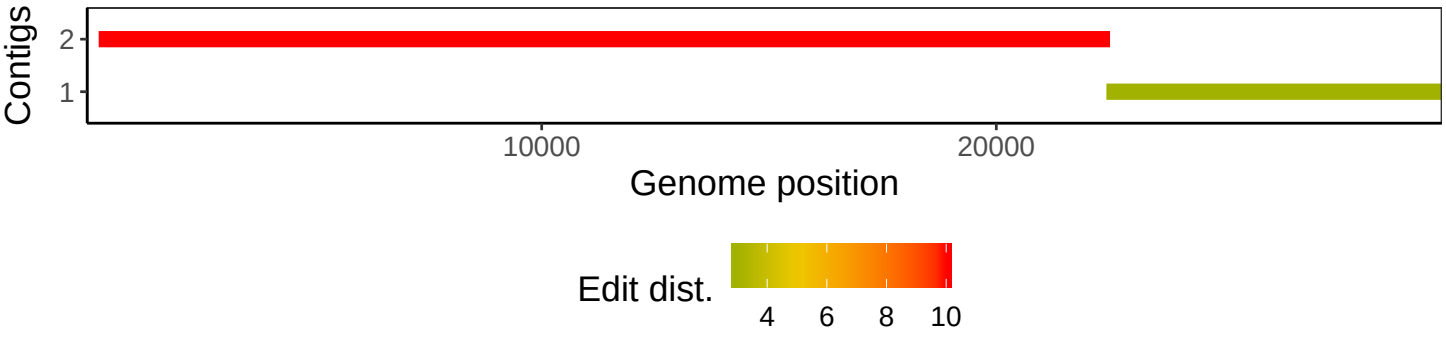
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

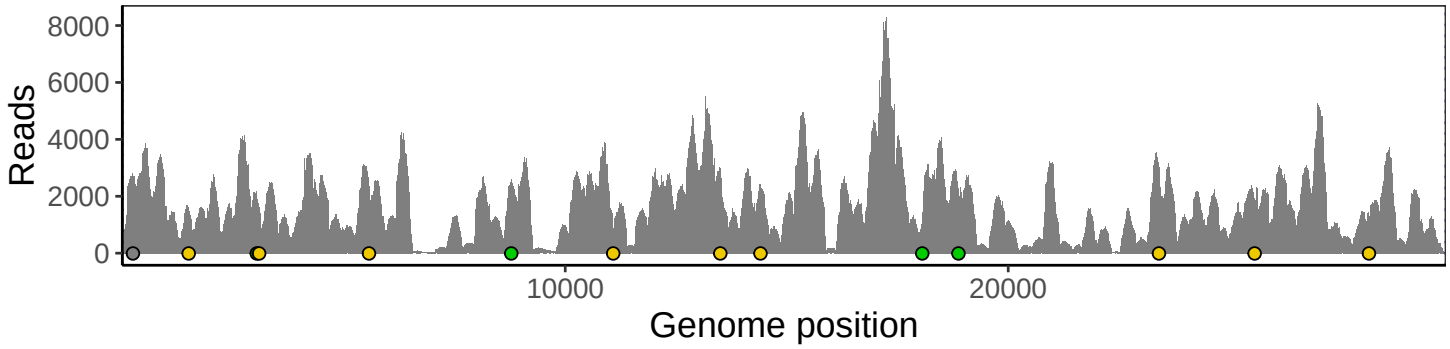


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

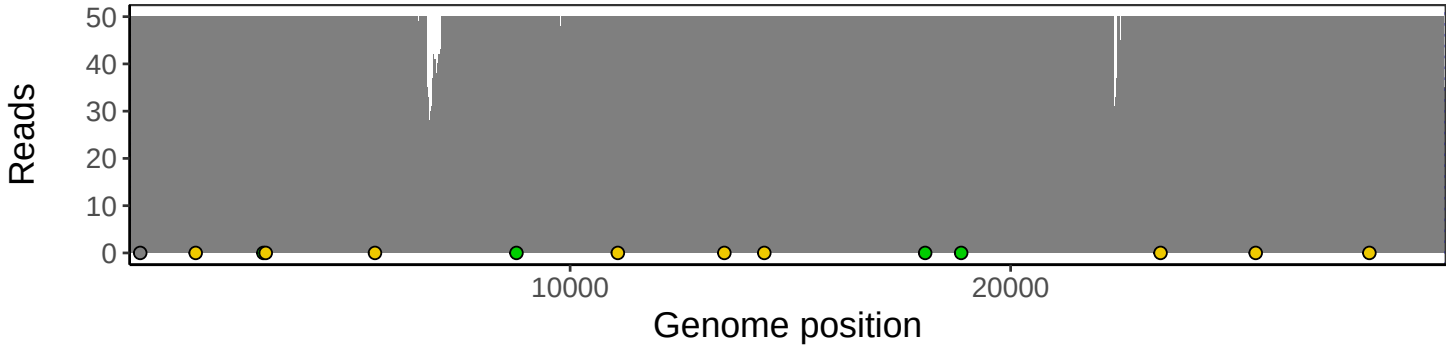


VSP0320-1 | 2020-05-22 | NP-OP | 266no-q | 5750000 genomes | single experiment

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.