COVID-19 subject 266

2021-06-23

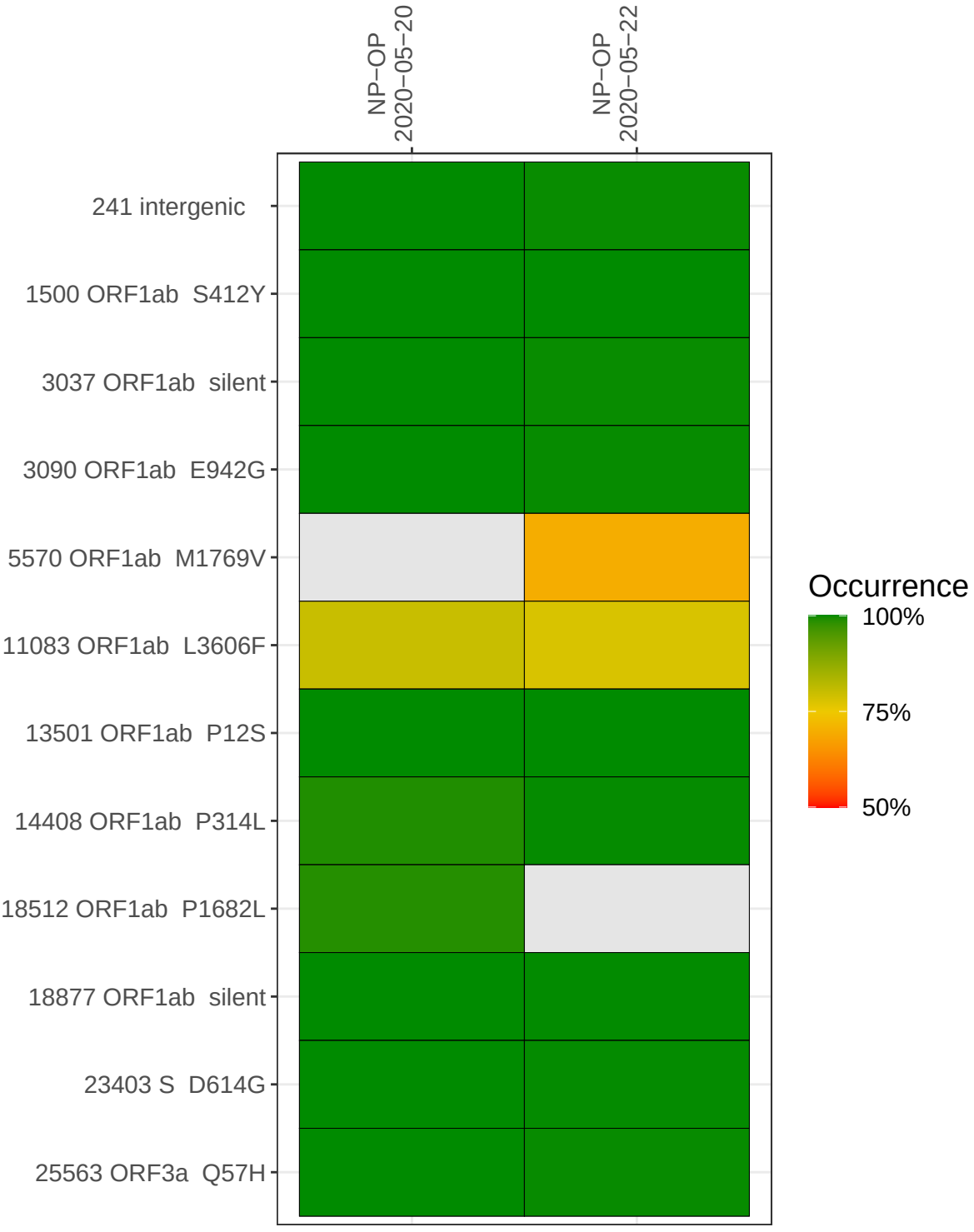
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with > 90% sequence coverage.

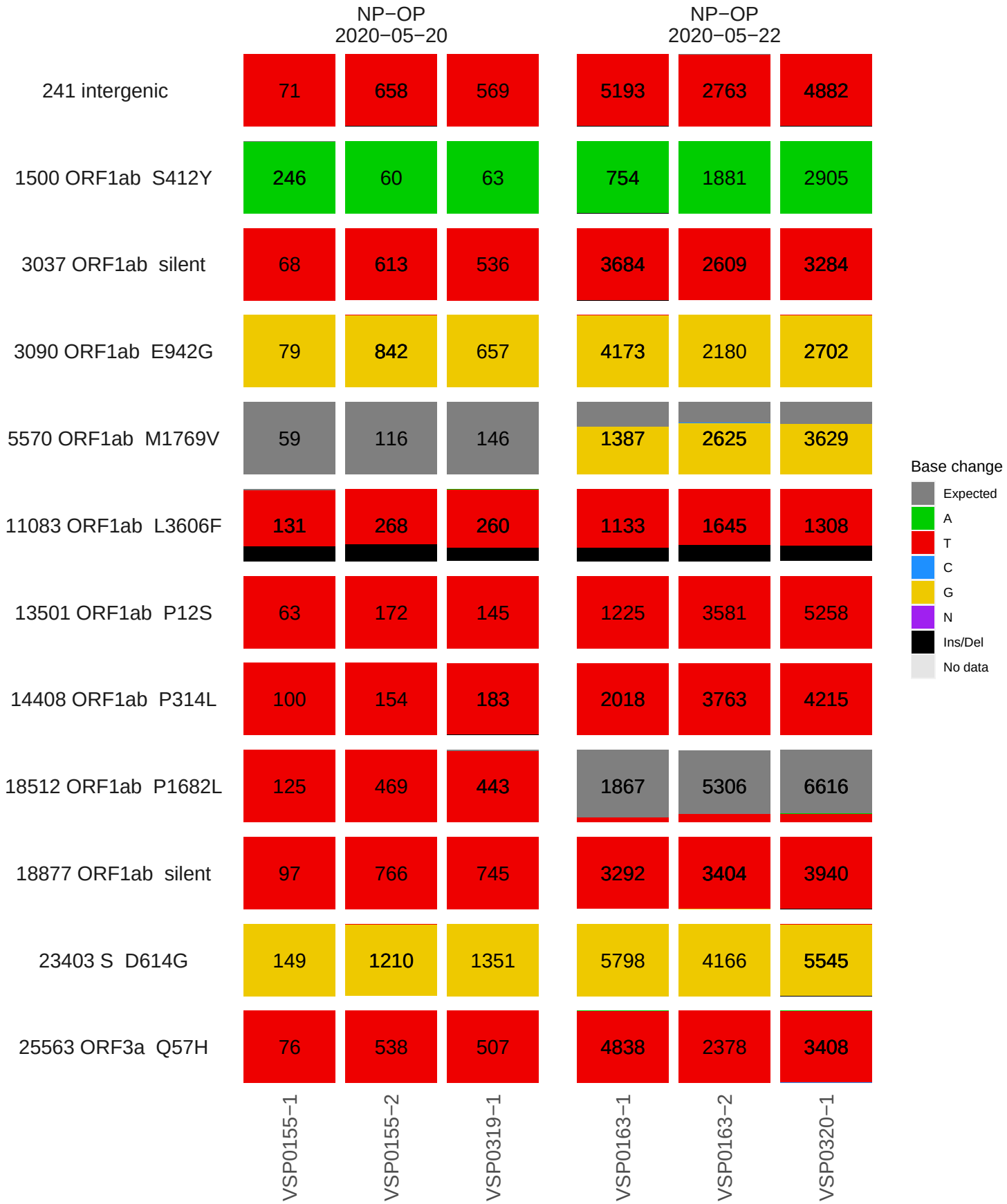
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0155	composite	NA	NP-OP	2020-05-20	22.33	B.1	99.8%	99.3%
VSP0163	composite	NA	NP-OP	2020-05-22	29.75	B.1	100.0%	99.8%
VSP0155-1	single experiment	17000	NP-OP	2020-05-20	21.43	B.1	99.3%	98.7%
VSP0155-2	single experiment	85000	NP-OP	2020-05-20	22.33	B.1	99.7%	98.8%
VSP0163-1	single experiment	1530000	NP-OP	2020-05-22	29.75	B.1	99.9%	99.8%
VSP0163-2	single experiment	7650000	NP-OP	2020-05-22	29.84	B.1	99.9%	99.7%
VSP0319-1	single experiment	143500	NP-OP	2020-05-20	22.25	B.1	99.4%	98.7%
VSP0320-1	single experiment	5750000	NP-OP	2020-05-22	29.86	B.1	99.7%	99.7%

Variants shared across samples

The heat map below shows how variants (reference genome /home/common/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) are shared across subject samples where the percent variance is colored. Variants are called if a variant position is covered by 5 or 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.

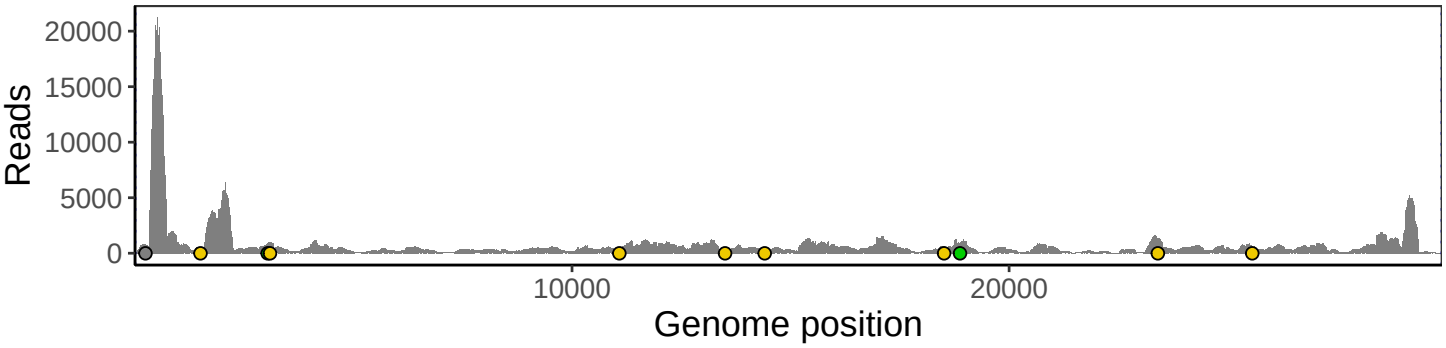



NP−OP
2020−05−20
NP−OP
2020−05−22
241 intergenic
71
658
569
5193
2763
4882
1500 ORF1ab S412Y
246
60
63
754
1881
2905
3037 ORF1ab silent
68
613
536
3684
2609
3284
3090 ORF1ab E942G
79
842
657
4173
2180
2702
5570 ORF1ab M1769V
59
116
146
1387
2625
3629
11083 ORF1ab L3606F
131
268
260
1133
1645
1308
13501 ORF1ab P12S
63
172
145
1225
3581
5258
14408 ORF1ab P314L
100
154
183
2018
3763
4215
18512 ORF1ab P1682L
125
469
443
1867
5306
6616
18877 ORF1ab silent
97
766
745
3292
3404
3940
23403 S D614G
149
1210
1351
5798
4166
5545
25563 ORF3a Q57H
76
538
507
4838
2378
3408
VSP0155−1
VSP0155−2
VSP0319−1
VSP0163−1
VSP0163−2
VSP0320−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

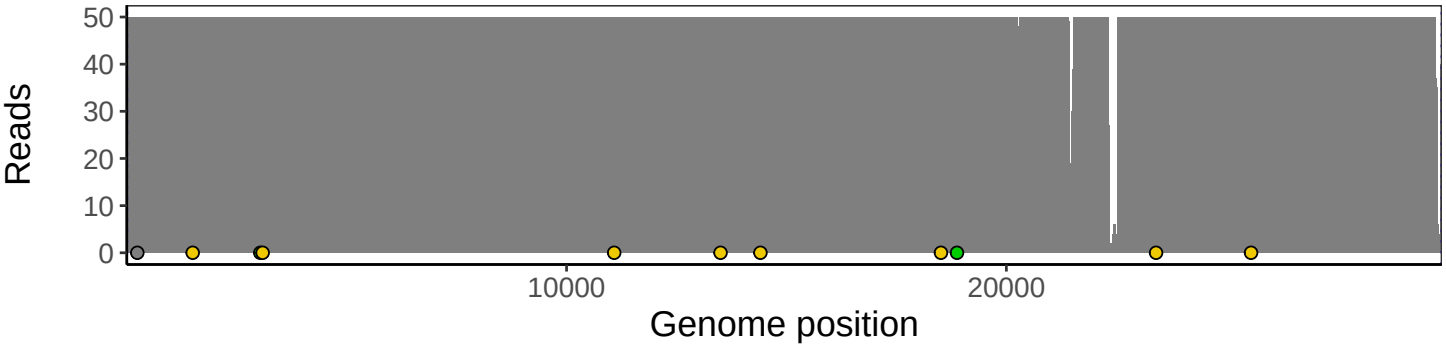
Analyses of individual experiments and composite results

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

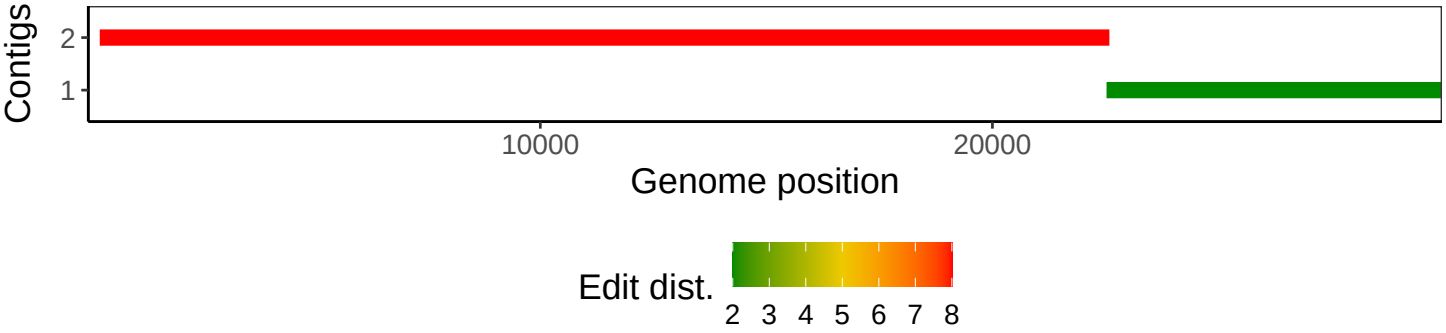
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

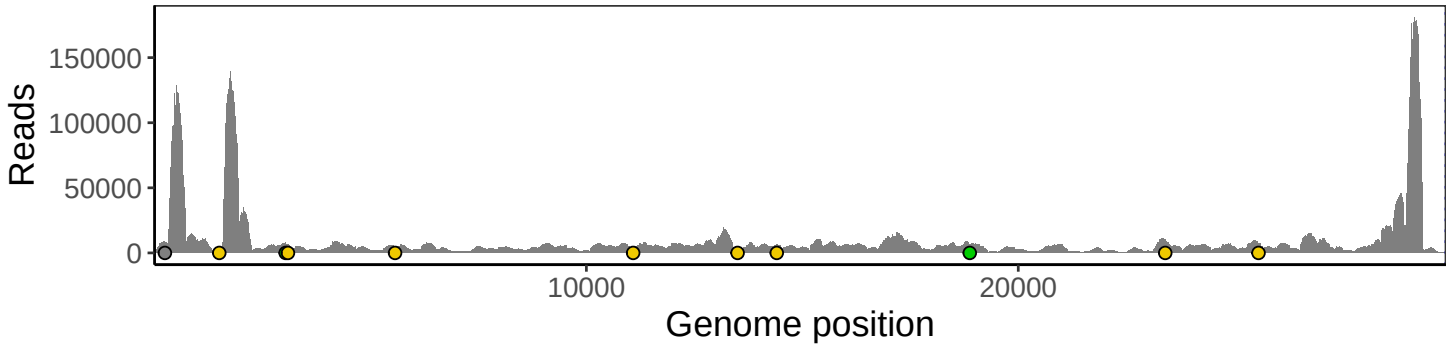


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

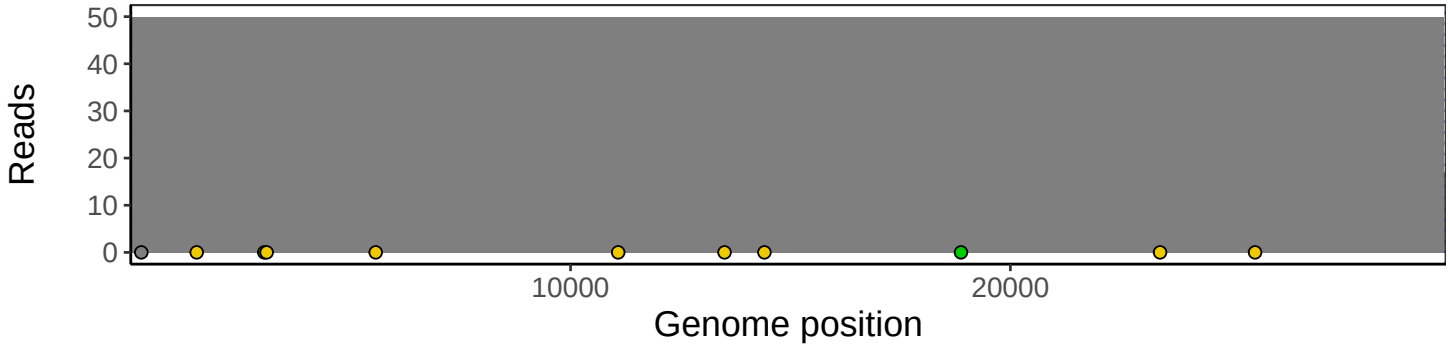


VSP0163 | 2020-05-22 | NP-OP | 266no-q | composite result

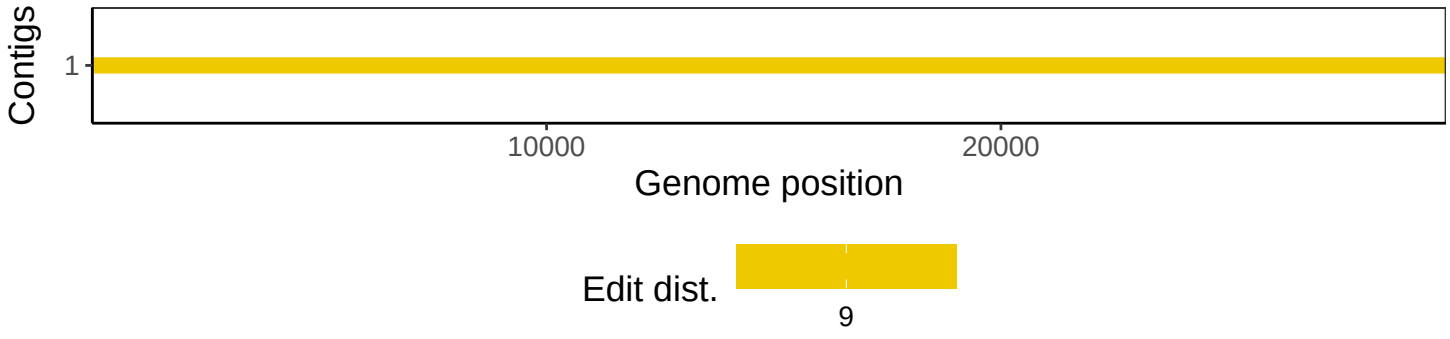
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

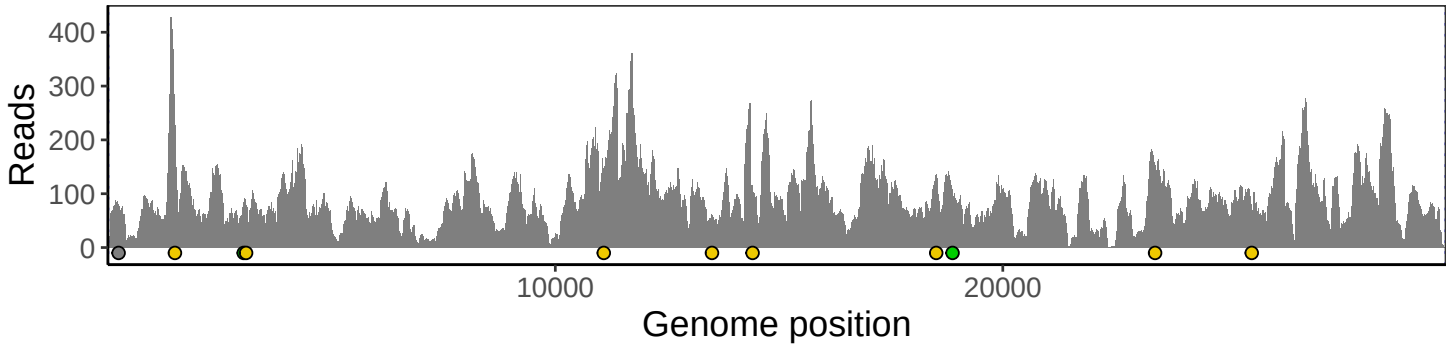


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

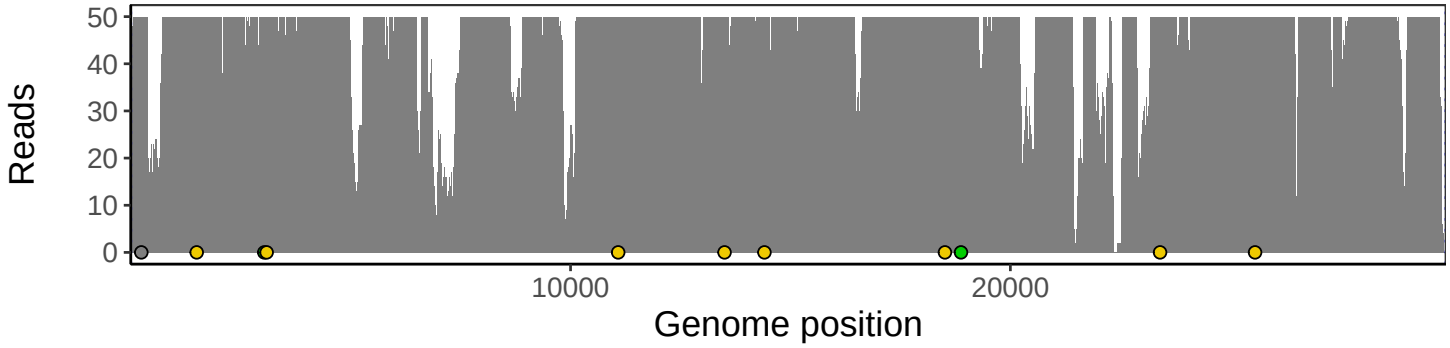


VSP0155-1 | 2020-05-20 | NP-OP | 266no-q | 17000 genomes | single experiment

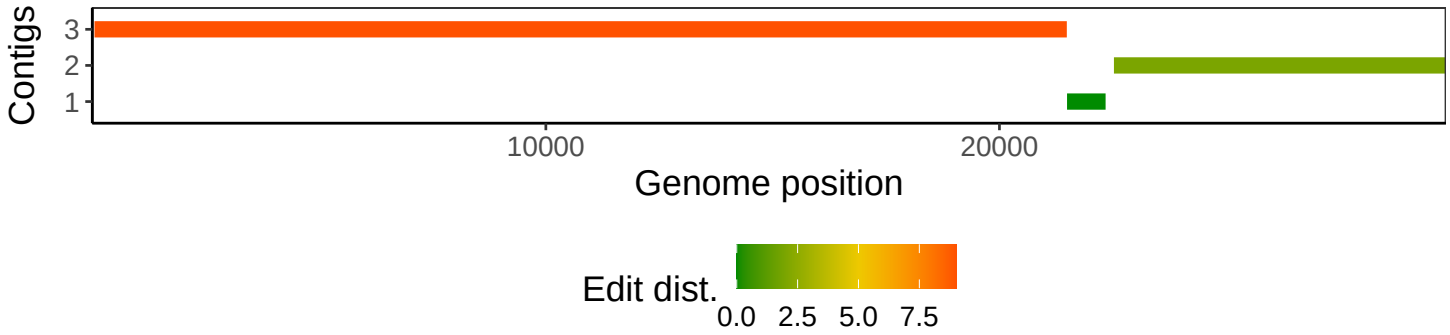
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

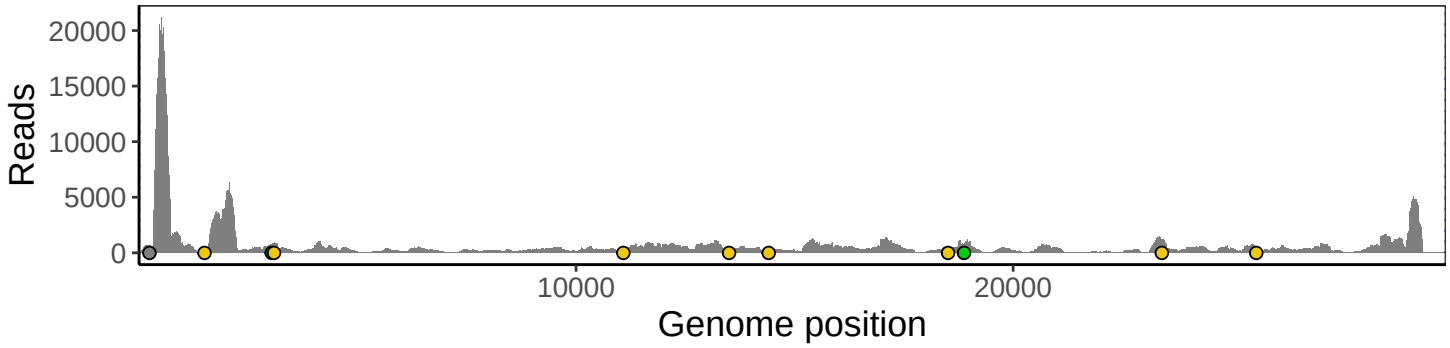


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

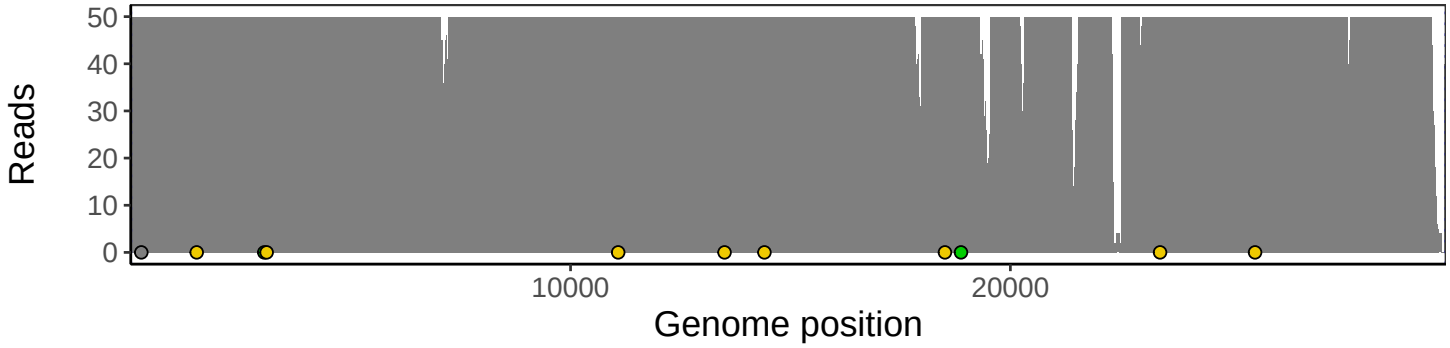


VSP0155-2 | 2020-05-20 | NP-OP | 266no-q | 85000 genomes | single experiment

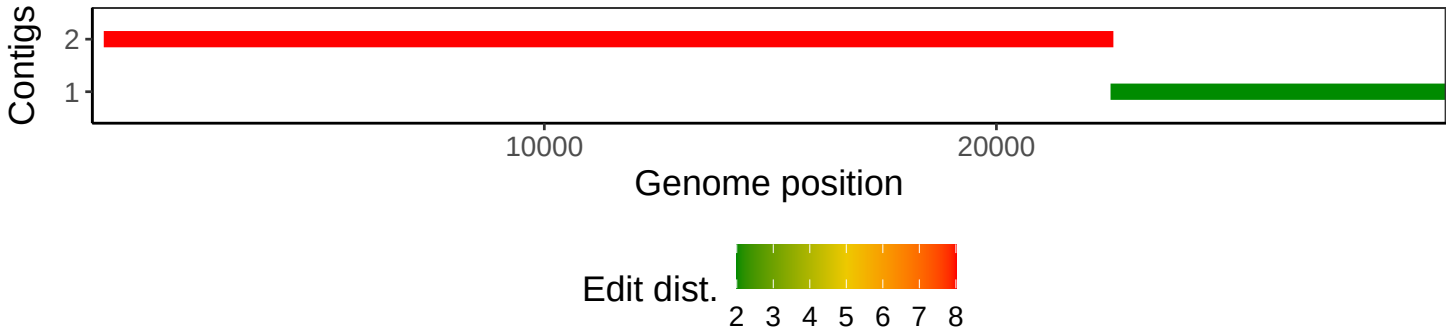
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

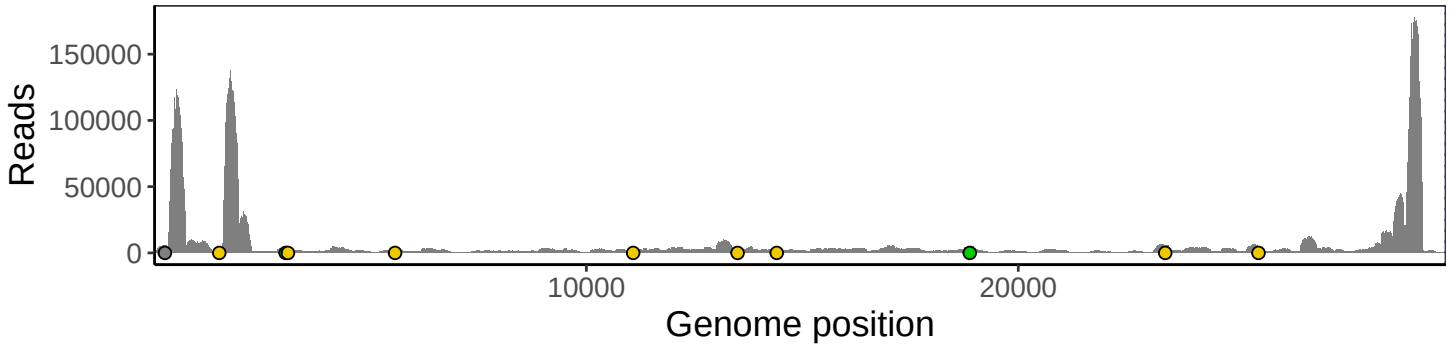


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

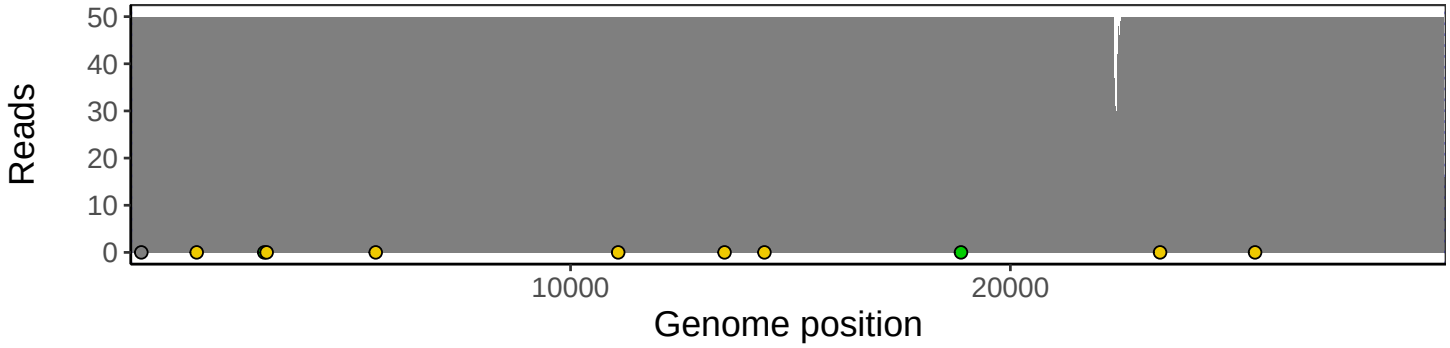


VSP0163-1 | 2020-05-22 | NP-OP | 266no-q | 1530000 genomes | single experiment

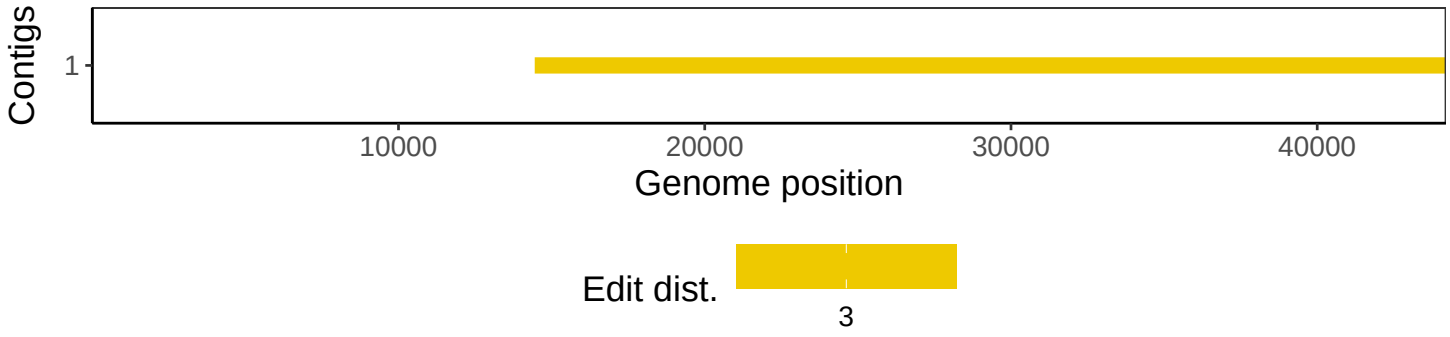
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

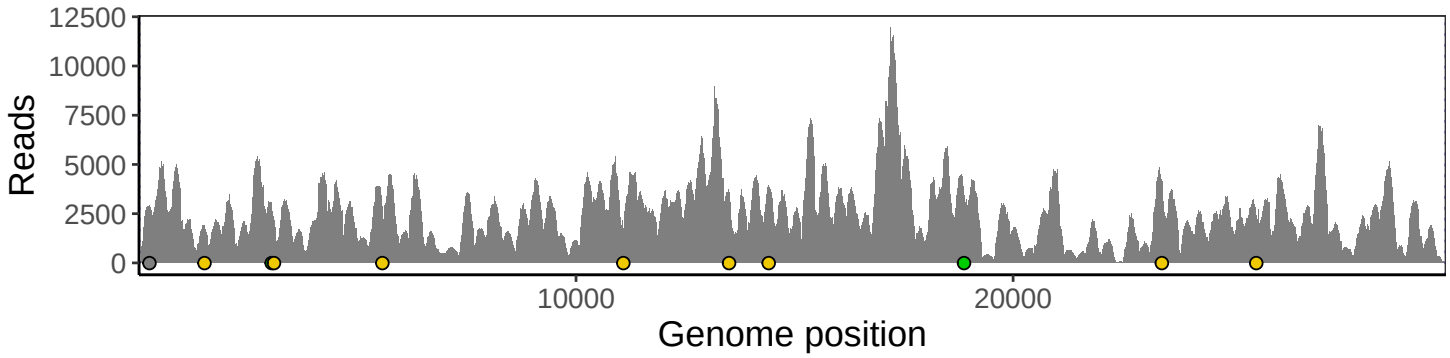


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

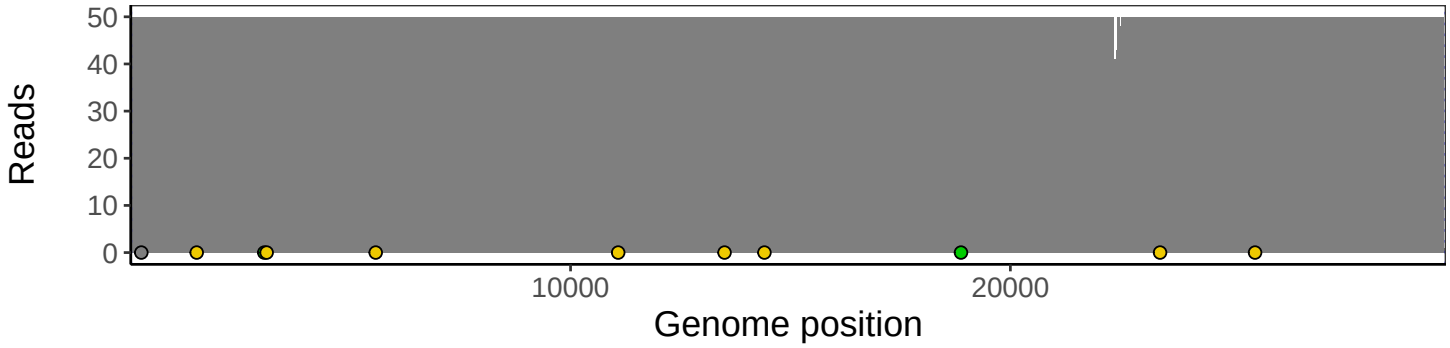


VSP0163-2 | 2020-05-22 | NP-OP | 266no-q | 7650000 genomes | single experiment

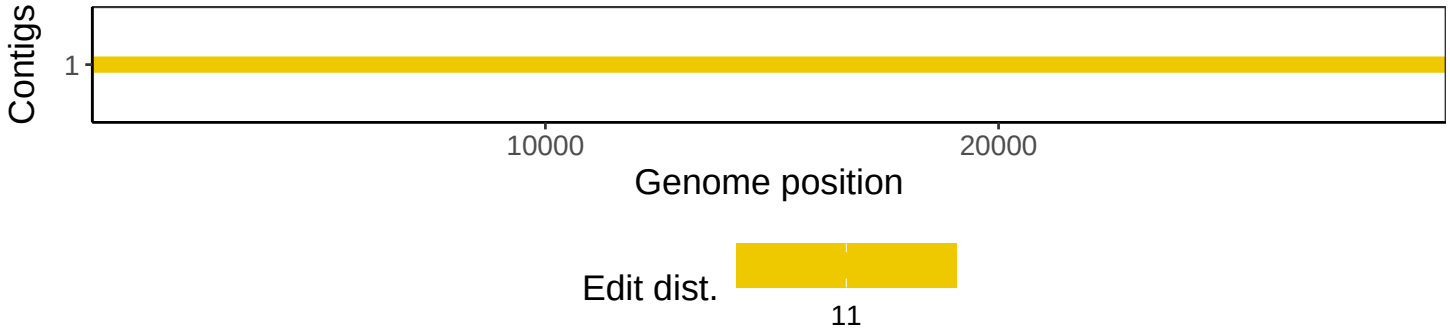
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

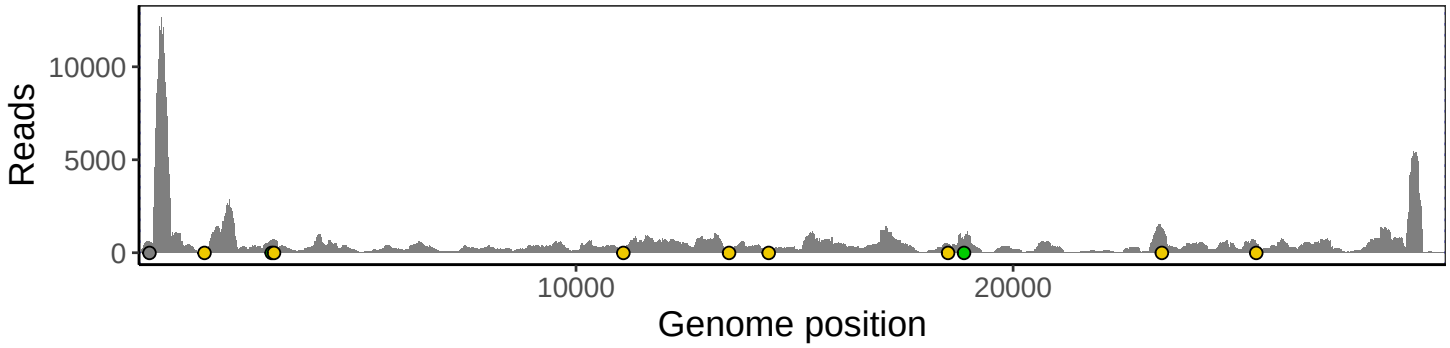


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

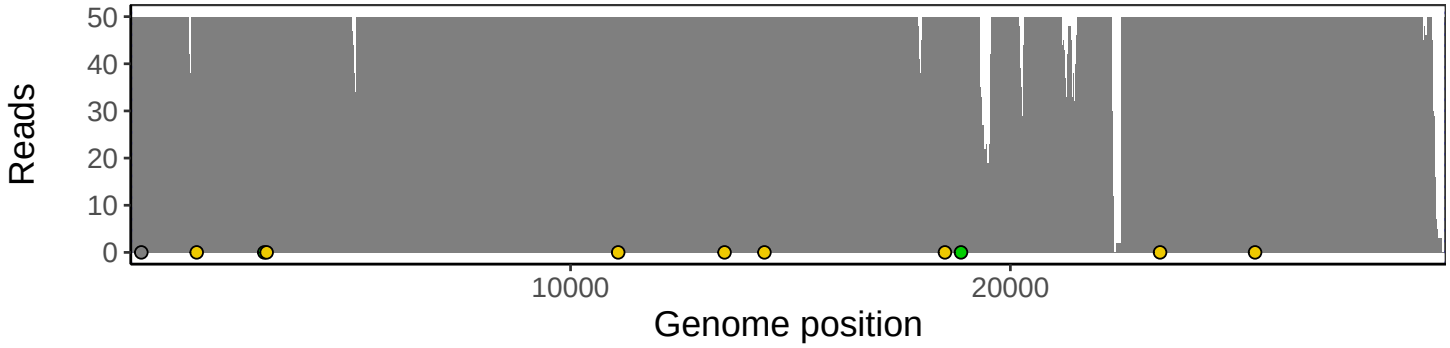


VSP0319-1 | 2020-05-20 | NP-OP | 266no-q | 143500 genomes | single experiment

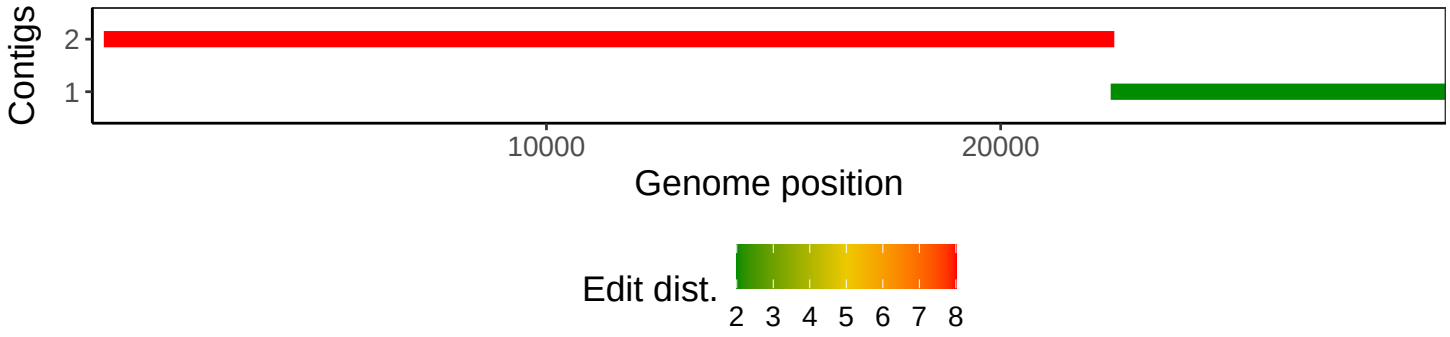
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

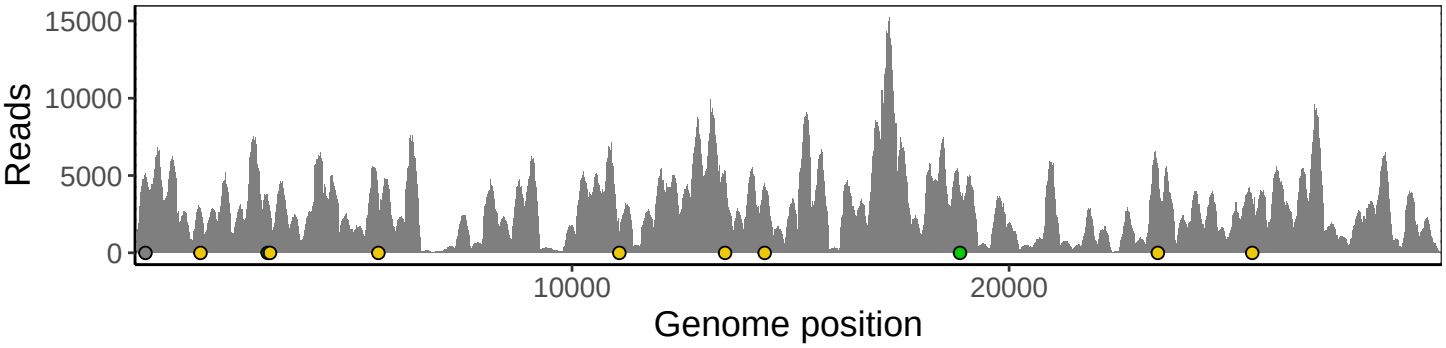


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

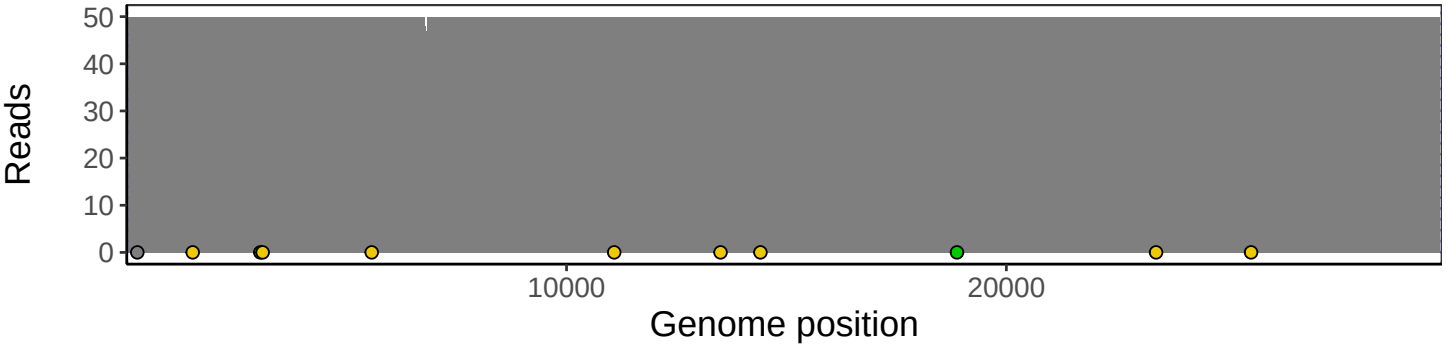


VSP0320-1 | 2020-05-22 | NP-OP | 266no-q | 5750000 genomes | single experiment

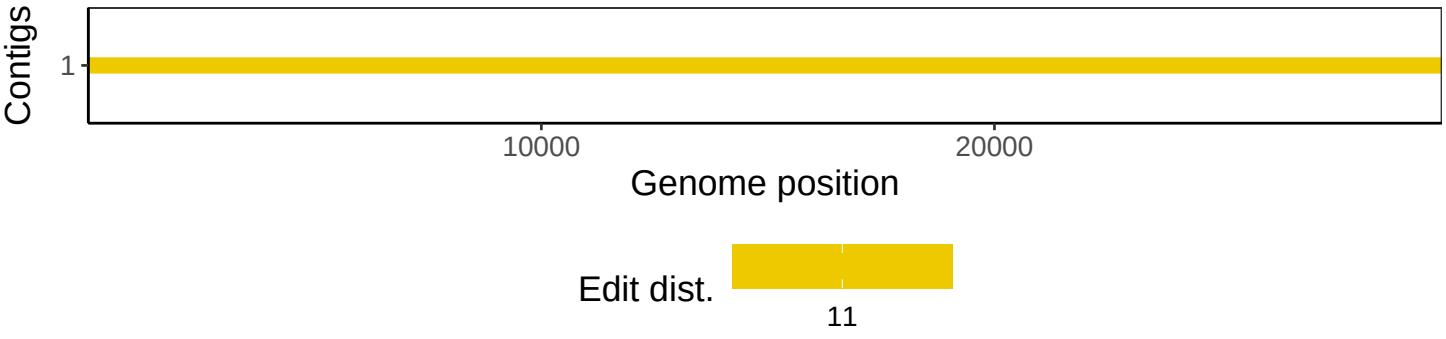
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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.



Software environment

Software/R package	Version
R	3.4.0
bwa	0.7.17-r1198-dirty
samtools	1.10 Using htslib 1.10
bcftools	1.10.2-34-g1a12af0-dirty Using htslib 1.10.2-57-gf58a6f3
pangolin	3.1.3
genbankr	1.4.0
optparse	1.6.0
forcats	0.3.0
stringr	1.4.0
dplyr	0.8.1
purrr	0.2.5
readr	1.1.1
tidyr	0.8.1
tibble	2.1.2
ggplot2	3.3.3
tidyverse	1.2.1
ShortRead	1.34.2
GenomicAlignments	1.12.2
SummarizedExperiment	1.6.5
DelayedArray	0.2.7
matrixStats	0.54.0
Biobase	2.36.2
Rsamtools	1.28.0
GenomicRanges	1.28.6
GenomeInfoDb	1.12.3
Biostrings	2.44.2
XVector	0.16.0
IRanges	2.10.5
S4Vectors	0.14.7
BiocParallel	1.10.1
BiocGenerics	0.22.1