COVID-19 subject 269

2021-06-23

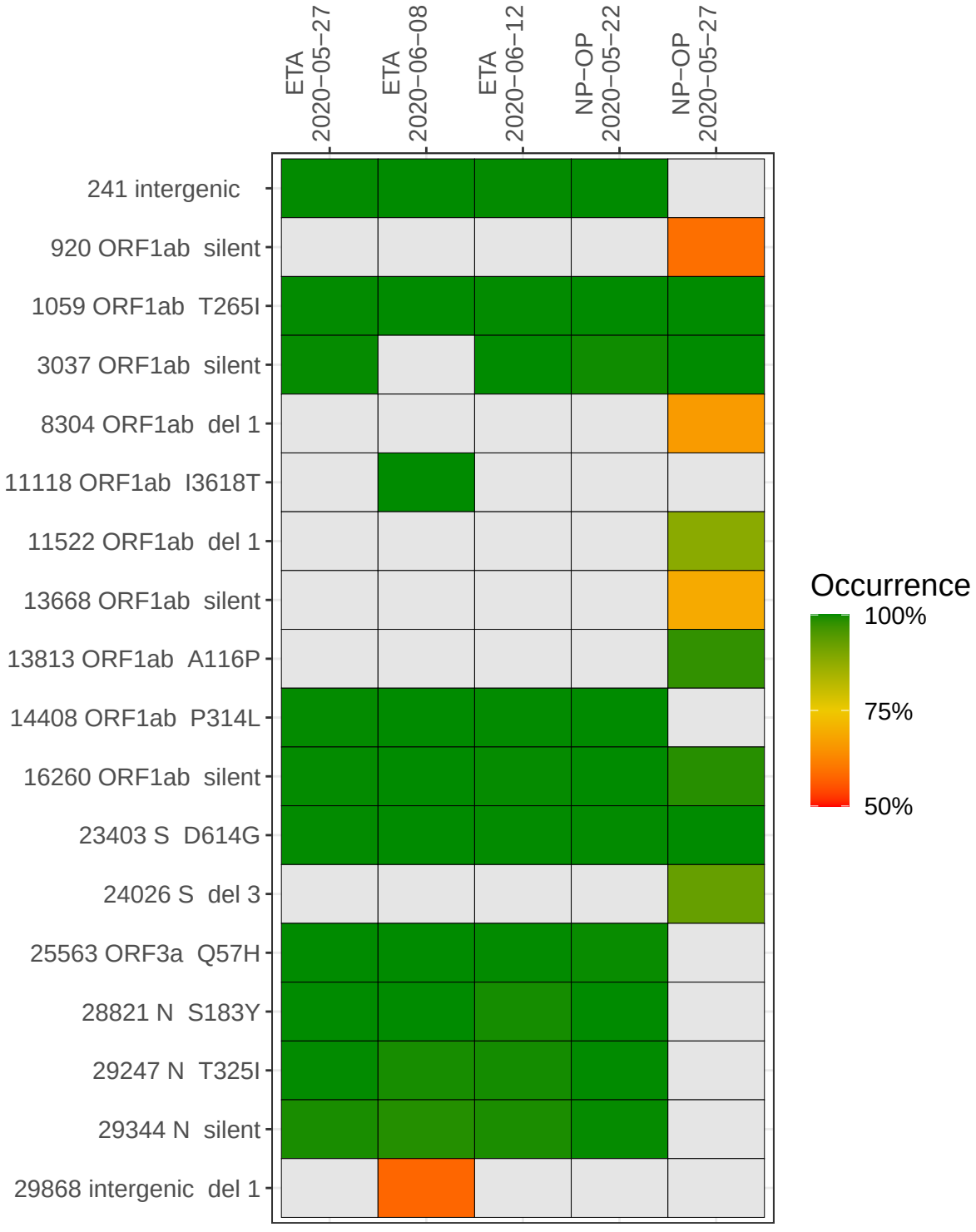
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

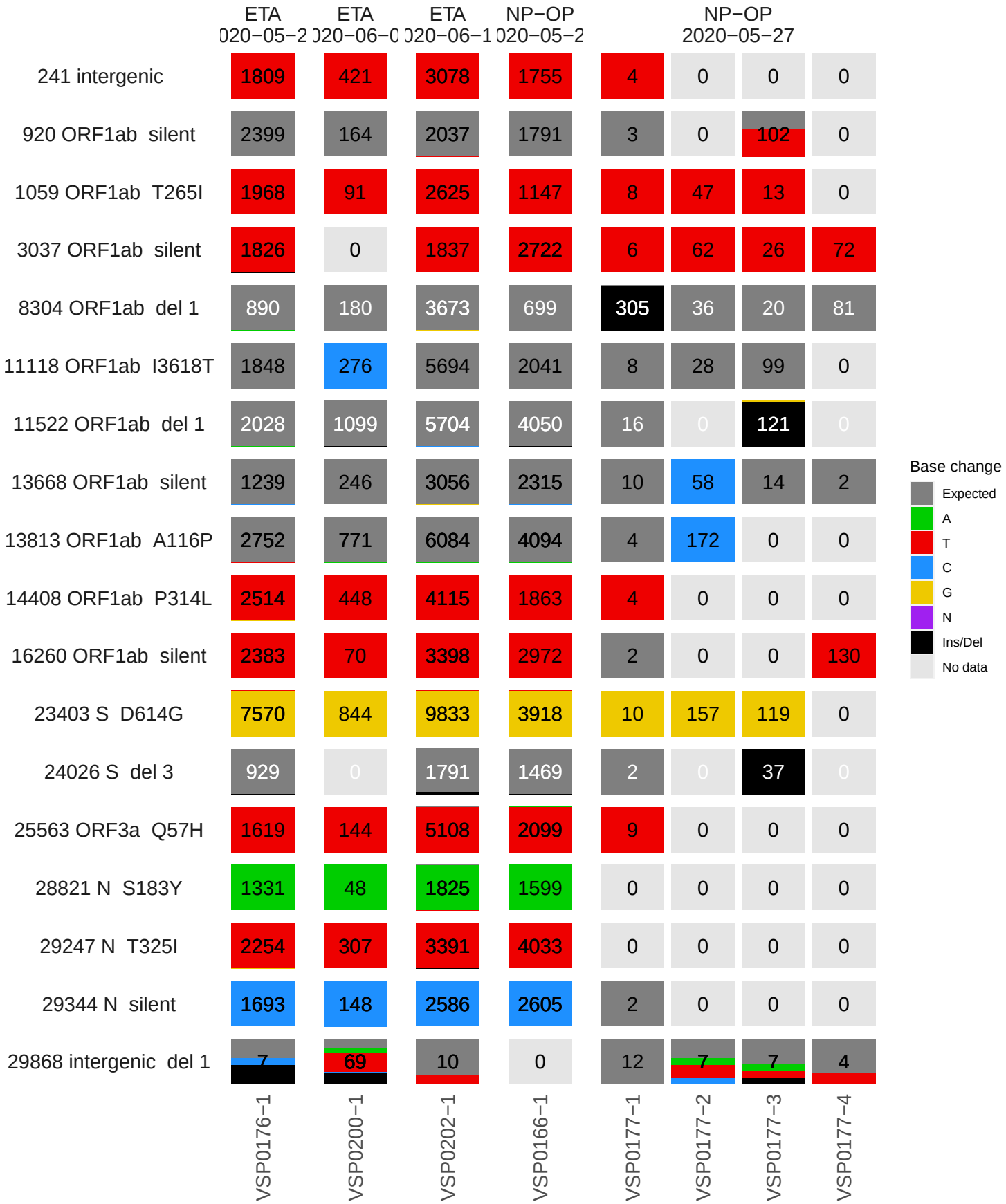
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0177	composite	NA	NP-OP	2020-05-27	4.03	NA	90.1%	79.9%
VSP0166-1	single experiment	NA	NP-OP	2020-05-22	29.84	B.1.369	99.9%	99.7%
VSP0176-1	single experiment	166000.0	ETA	2020-05-27	29.82	B.1.369	99.9%	99.8%
VSP0177-1	single experiment	59.7	NP-OP	2020-05-27	1.03	NA	72.8%	38.6%
VSP0177-2	single experiment	NA	NP-OP	2020-05-27	1.01	NA	31.8%	27.6%
VSP0177-3	single experiment	NA	NP-OP	2020-05-27	1.02	NA	40.9%	38.3%
VSP0177-4	single experiment	NA	NP-OP	2020-05-27	0.93	NA	38.7%	36.3%
VSP0200-1	single experiment	NA	ETA	2020-06-08	5.92	NA	84.7%	82.6%
VSP0202-1	single experiment	16300.0	ETA	2020-06-12	29.83	B.1.369	99.9%	99.8%

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.

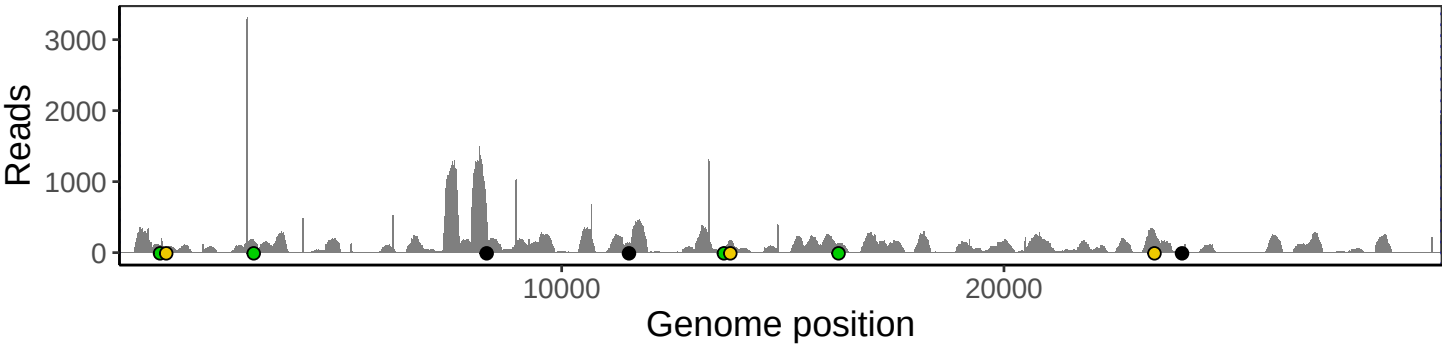



ETA 020−05−2
ETA 020−06−0
ETA 020−06−1
NP−OP 020−05−2
NP−OP 2020−05−27
241 intergenic
920 ORF1ab silent
1059 ORF1ab T265I
3037 ORF1ab silent
8304 ORF1ab del 1
11118 ORF1ab I3618T
11522 ORF1ab del 1
13668 ORF1ab silent
13813 ORF1ab A116P
14408 ORF1ab P314L
16260 ORF1ab silent
23403 S D614G
24026 S del 3
25563 ORF3a Q57H
28821 N S183Y
29247 N T325I
29344 N silent
29868 intergenic del 1
1809 421 3078 1755 4 0 0 0
2399 164 2037 1791 3 0 102 0
1968 91 2625 1147 8 47 13 0
1826 0 1837 2722 6 62 26 72
890 180 3673 699 305 36 20 81
1848 276 5694 2041 8 28 99 0
2028 1099 5704 4050 16 0 121 0
1239 246 3056 2315 10 58 14 2
2752 771 6084 4094 4 172 0 0
2514 448 4115 1863 4 0 0 0
2383 70 3398 2972 2 0 0 130
7570 844 9833 3918 10 157 119 0
929 0 1791 1469 2 0 37 0
1619 144 5108 2099 9 0 0 0
1331 48 1825 1599 0 0 0 0
2254 307 3391 4033 0 0 0 0
1693 148 2586 2605 2 0 0 0
7 69 10 0 12 7 7 4
VSP0176−1
VSP0200−1
VSP0202−1
VSP0166−1
VSP0177−1
VSP0177−2
VSP0177−3
VSP0177−4
Base change
Expected
A
T
C
G
N
Ins/Del
No data

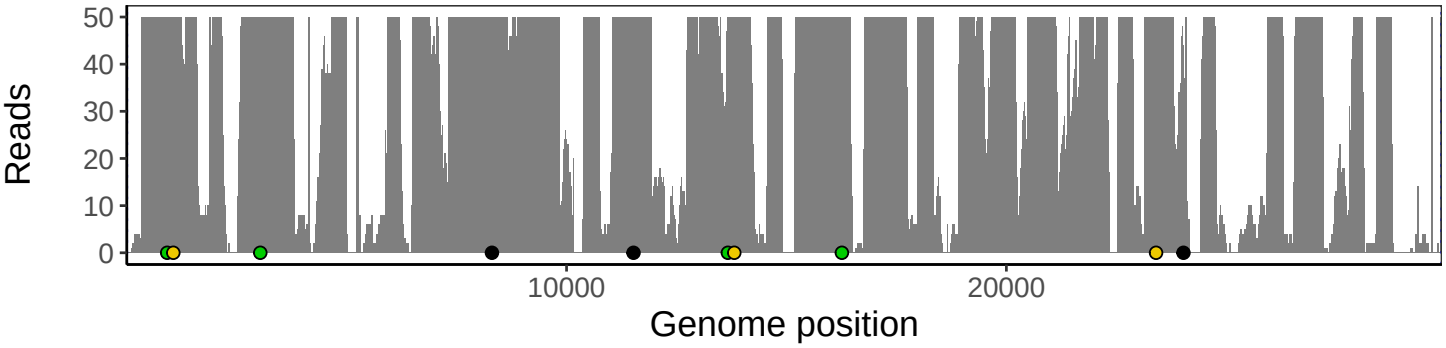
Analyses of individual experiments and composite results

VSP0177 | 2020-05-27 | NP-OP | 269no-q | composite result

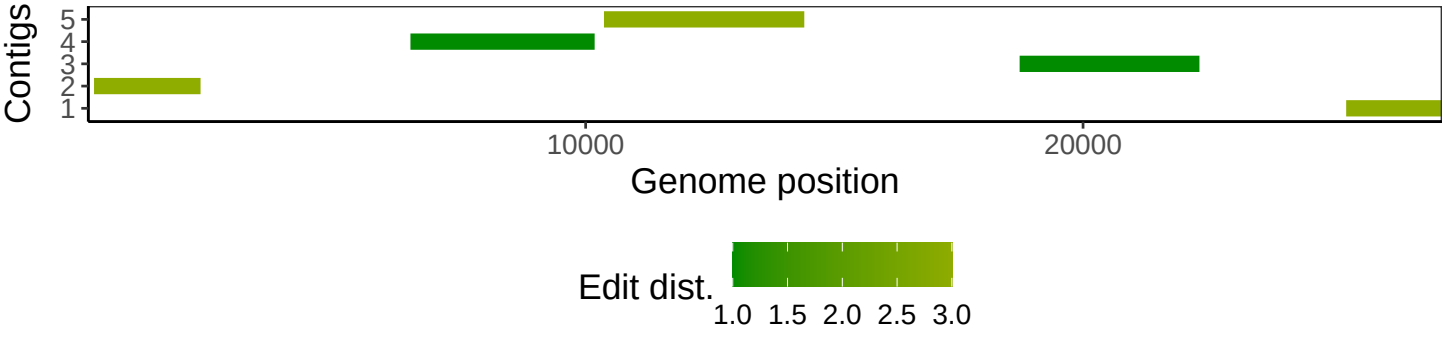
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

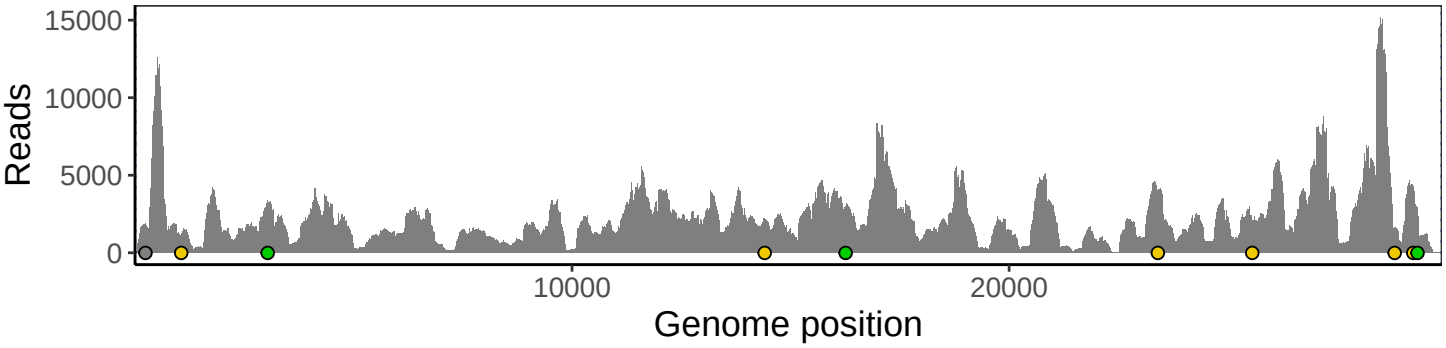


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

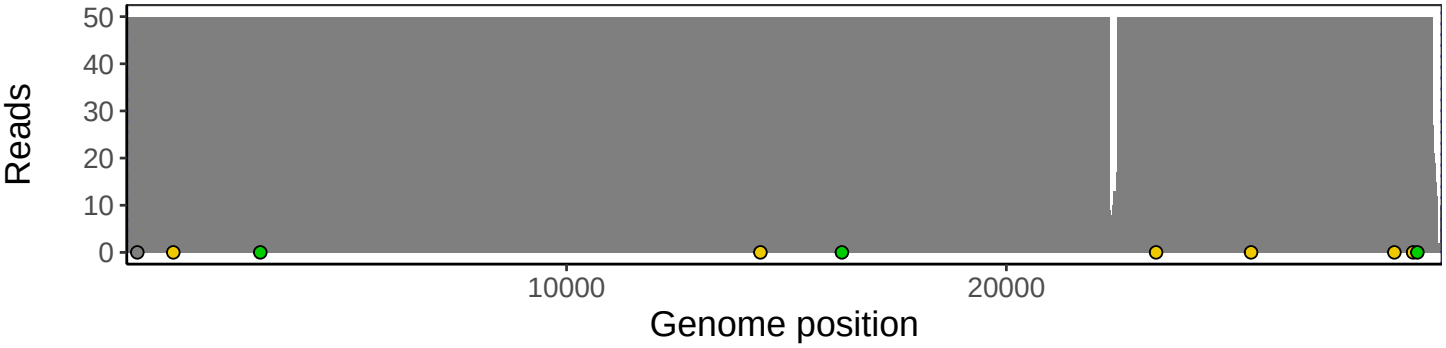


VSP0166-1 | 2020-05-22 | NP-OP | 269no-q | genomes | single experiment

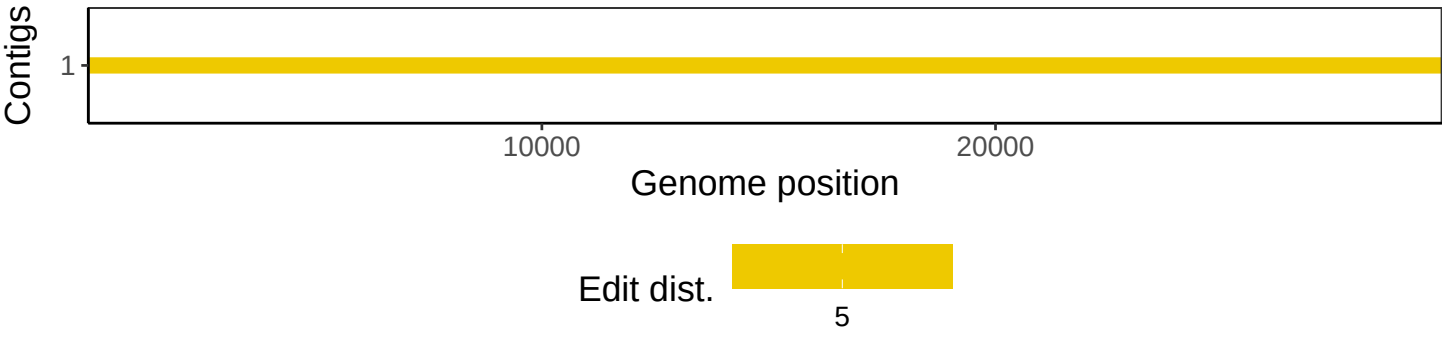
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

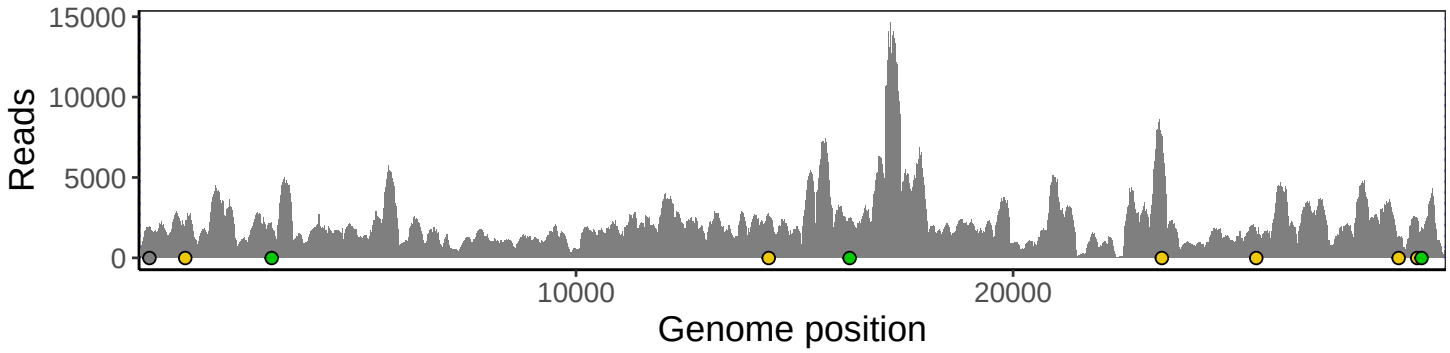


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

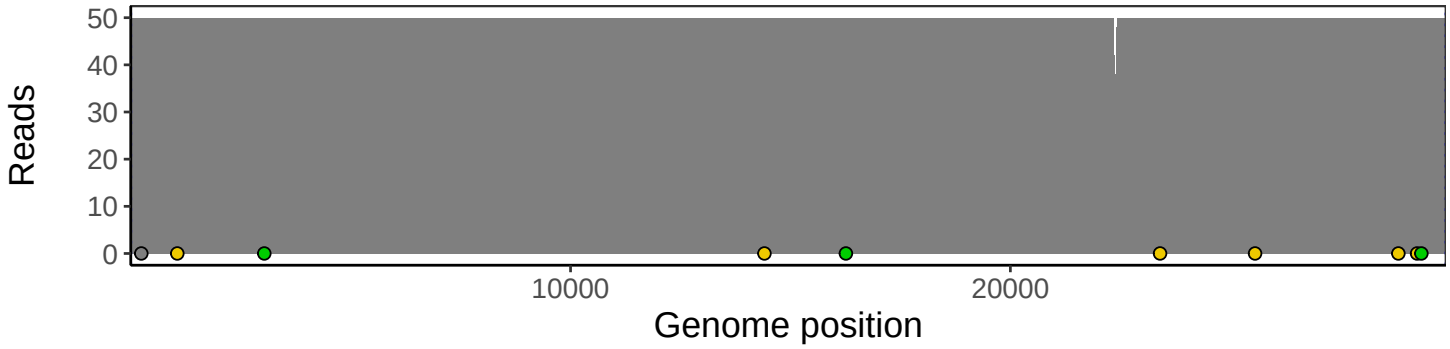


VSP0176-1 | 2020-05-27 | ETA | 269e-q | 166000 genomes | single experiment

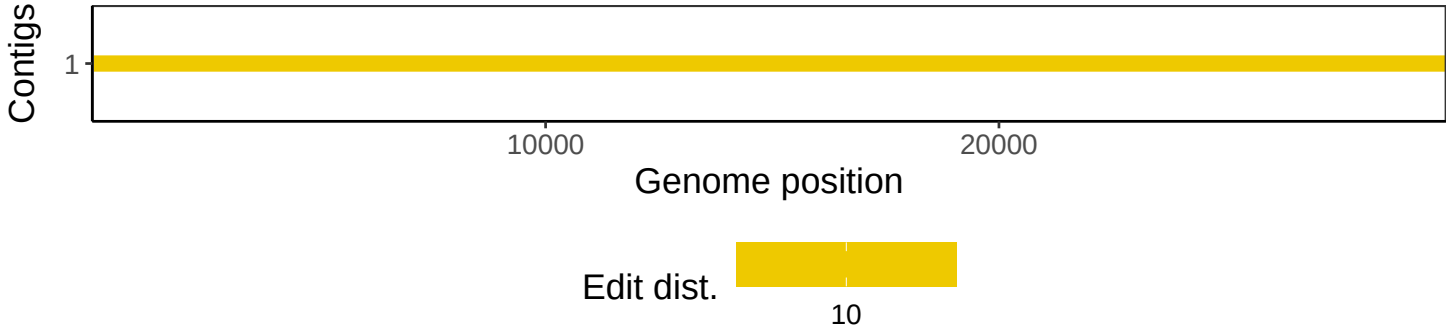
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

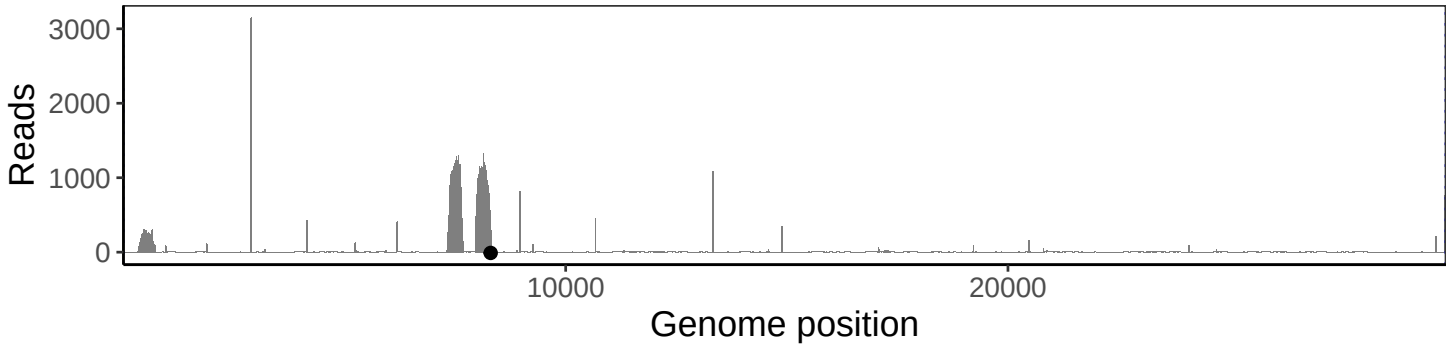


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

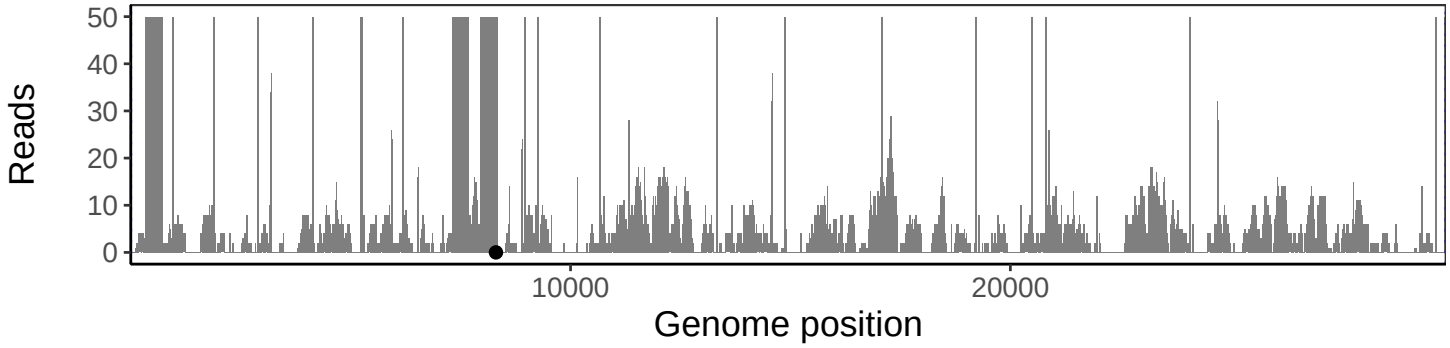


VSP0177-1 | 2020-05-27 | NP-OP | 269no-q | 59.7 genomes | single experiment

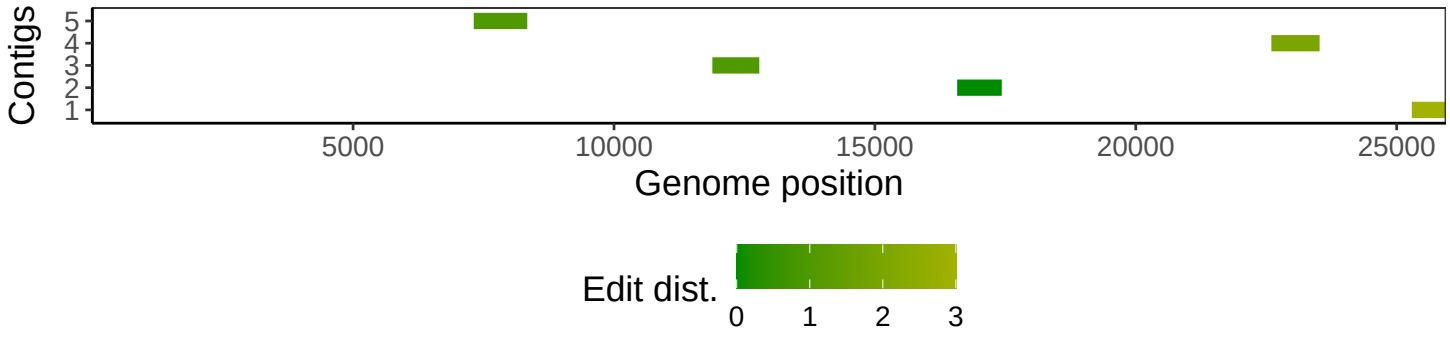
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

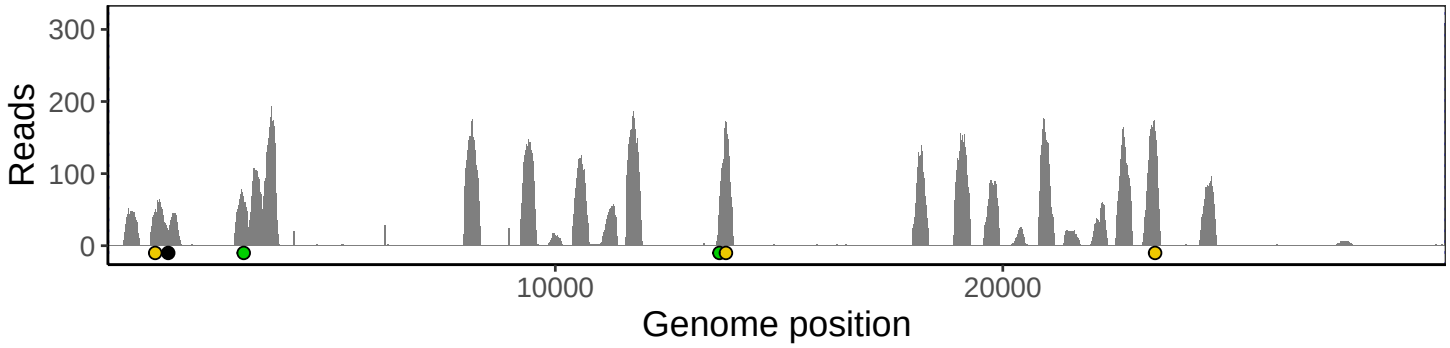


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

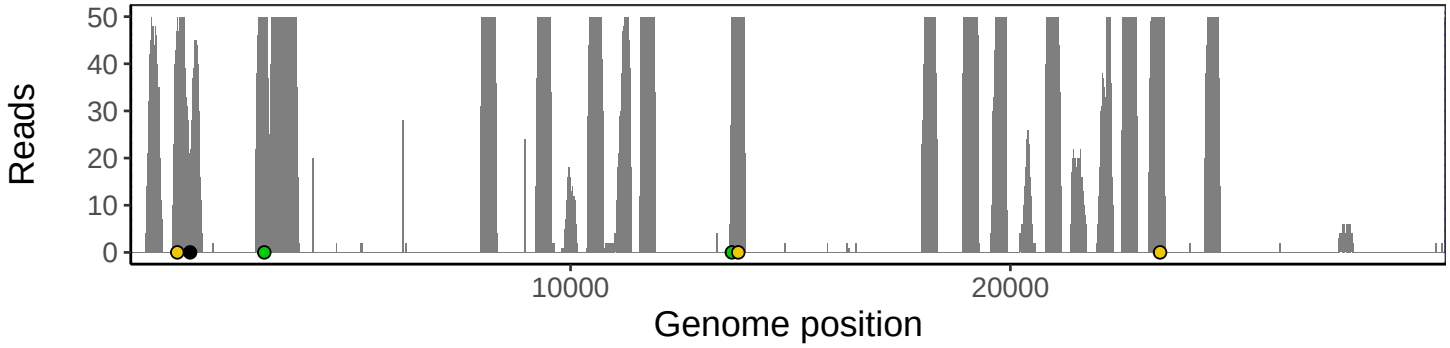


VSP0177-2 | 2020-05-27 | NP-OP | 269no-q | genomes | single experiment

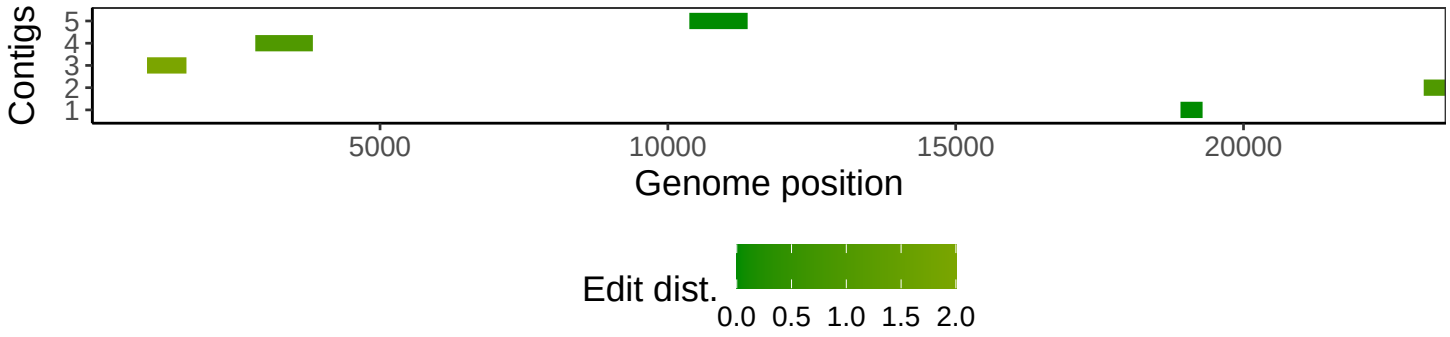
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

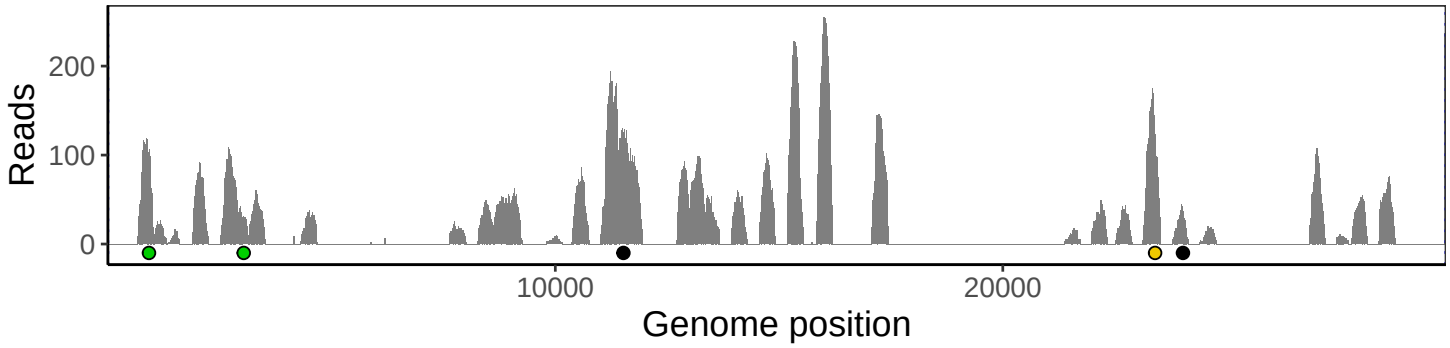


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

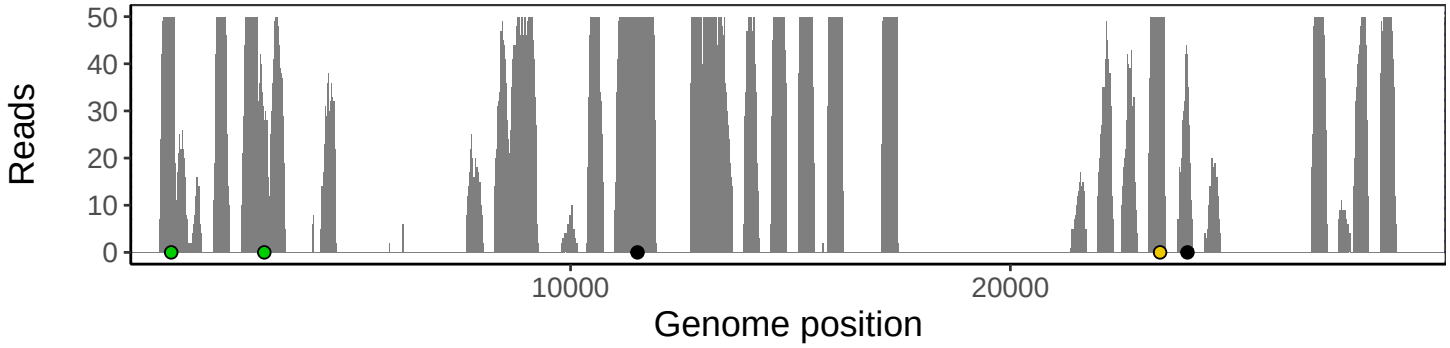


VSP0177-3 | 2020-05-27 | NP-OP | 269no-q | genomes | single experiment

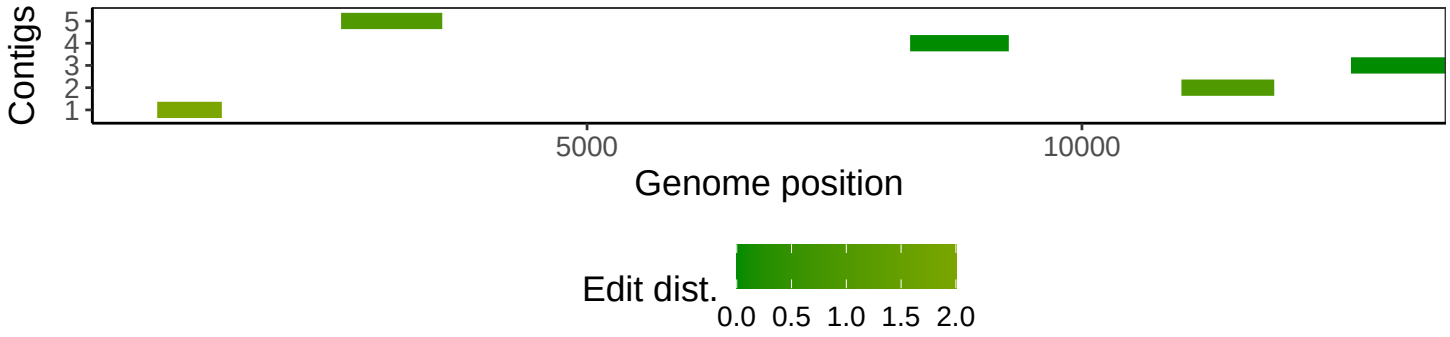
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

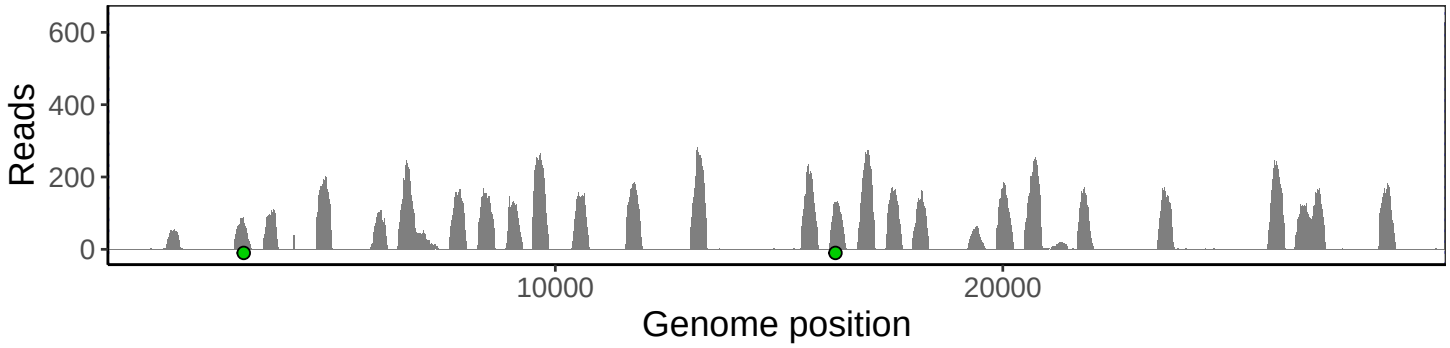


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

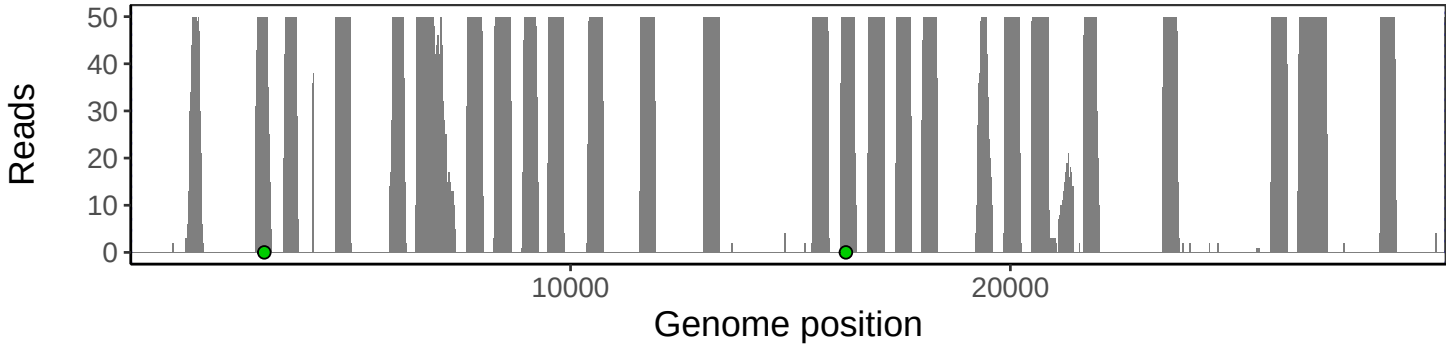


VSP0177-4 | 2020-05-27 | NP-OP | 269no-q | genomes | single experiment

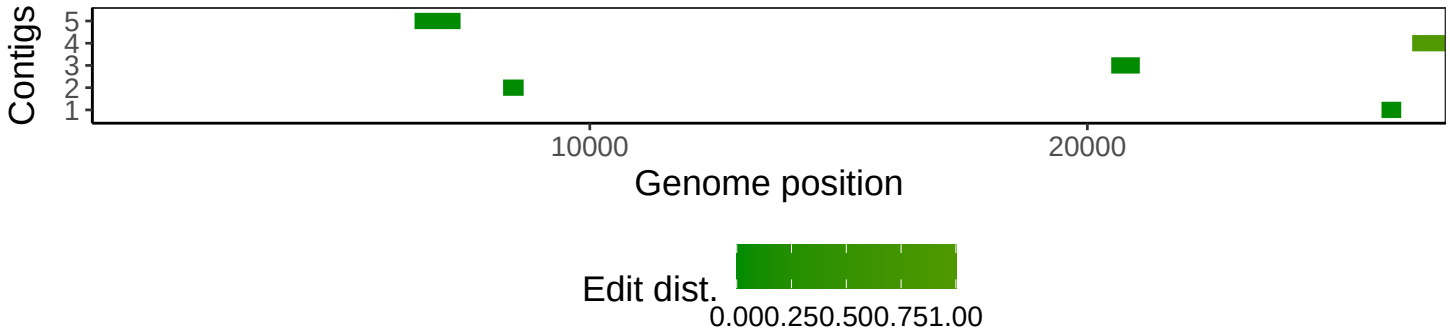
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

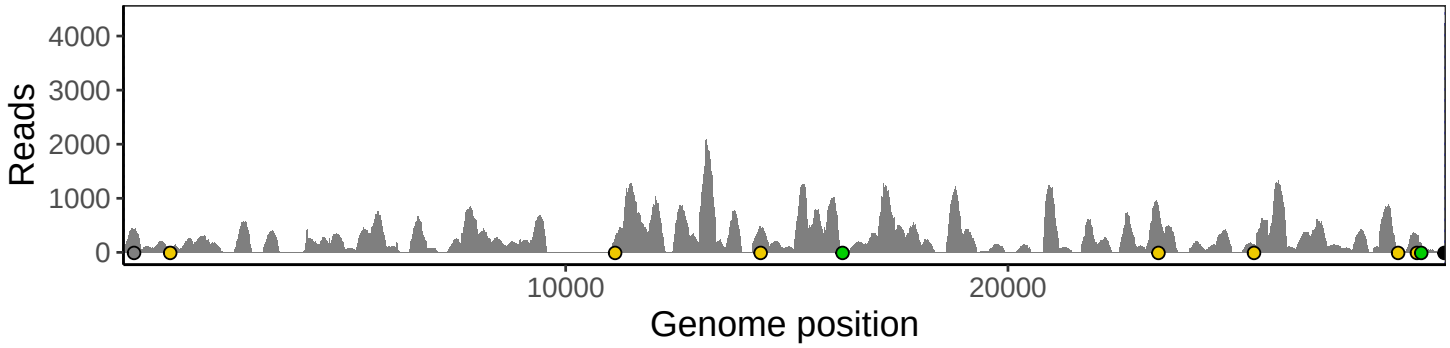


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

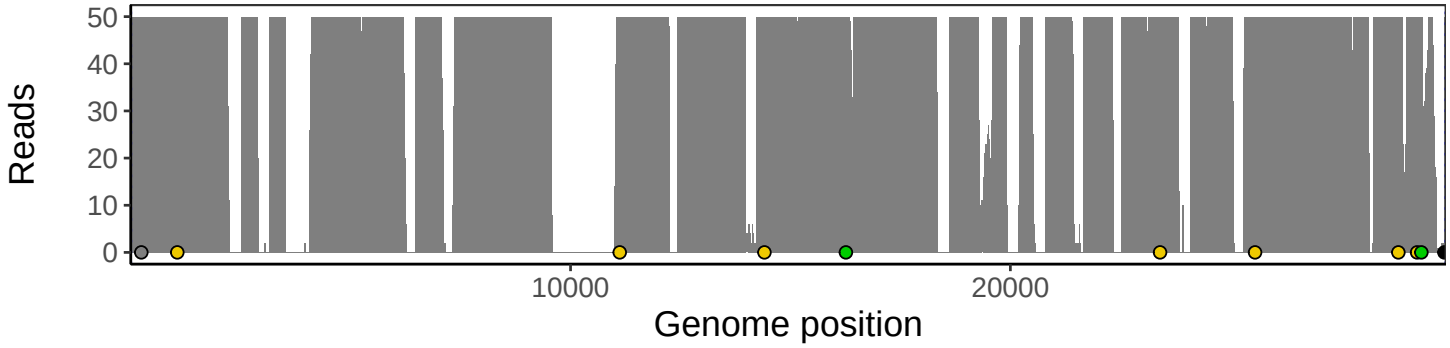


VSP0200-1 | 2020-06-08 | ETA | 269e-q | genomes | single experiment

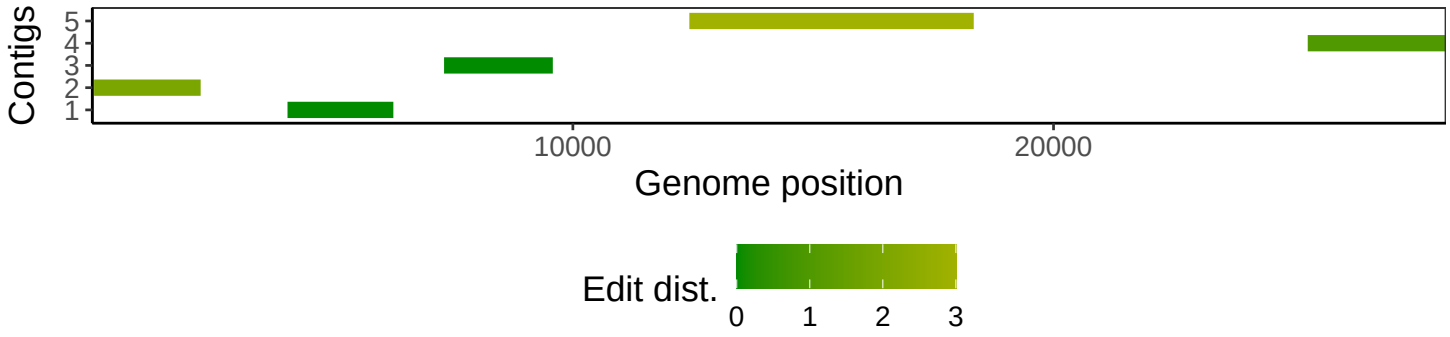
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

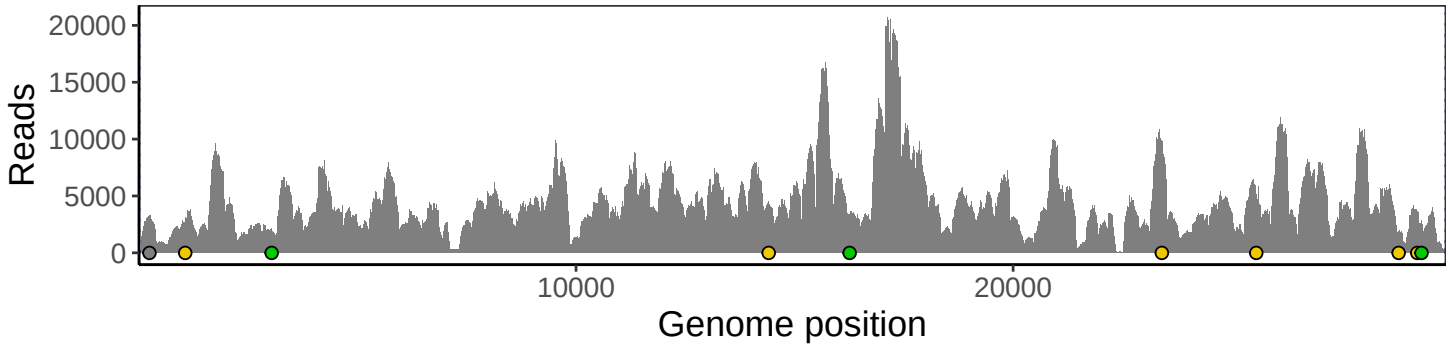


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

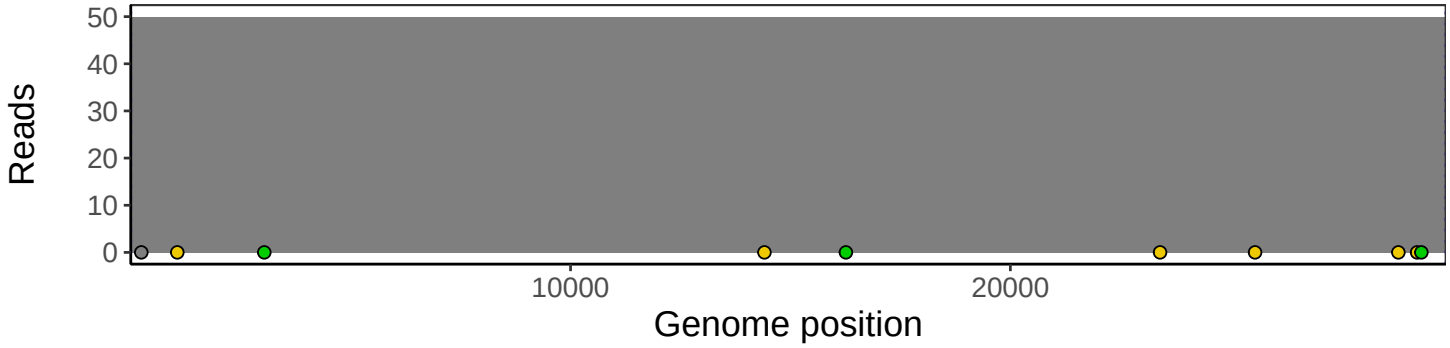


VSP0202-1 | 2020-06-12 | ETA | 269e-q | 16300 genomes | single experiment

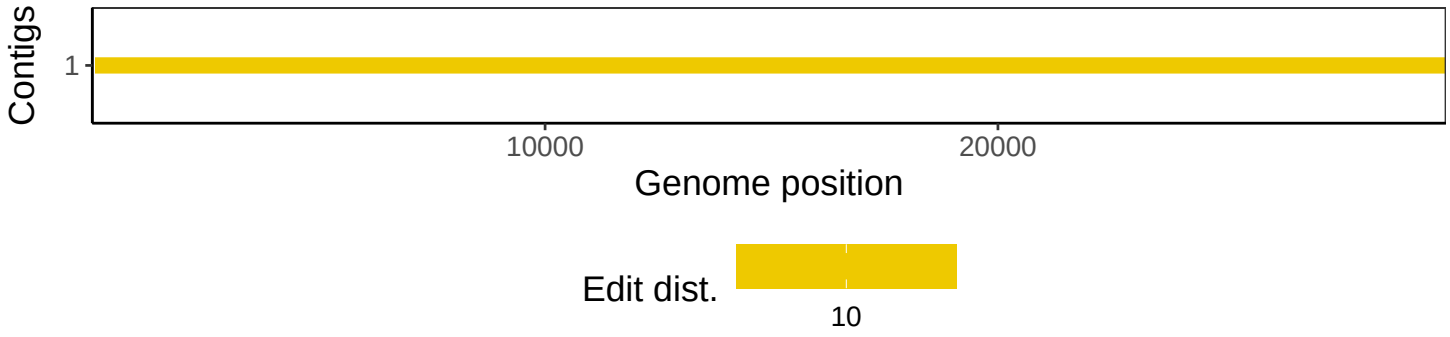
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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