COVID-19 subject 256

2021-03-01

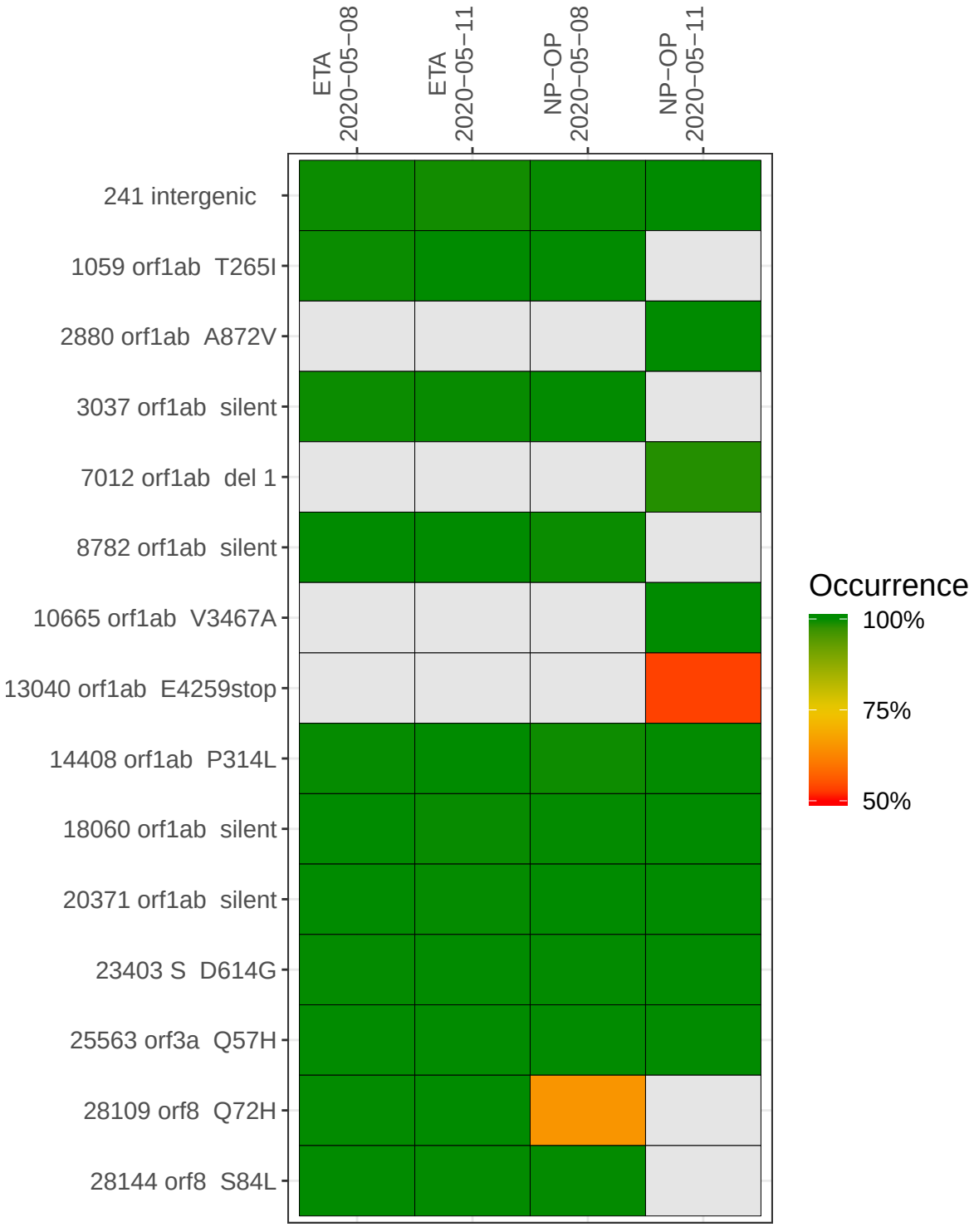
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

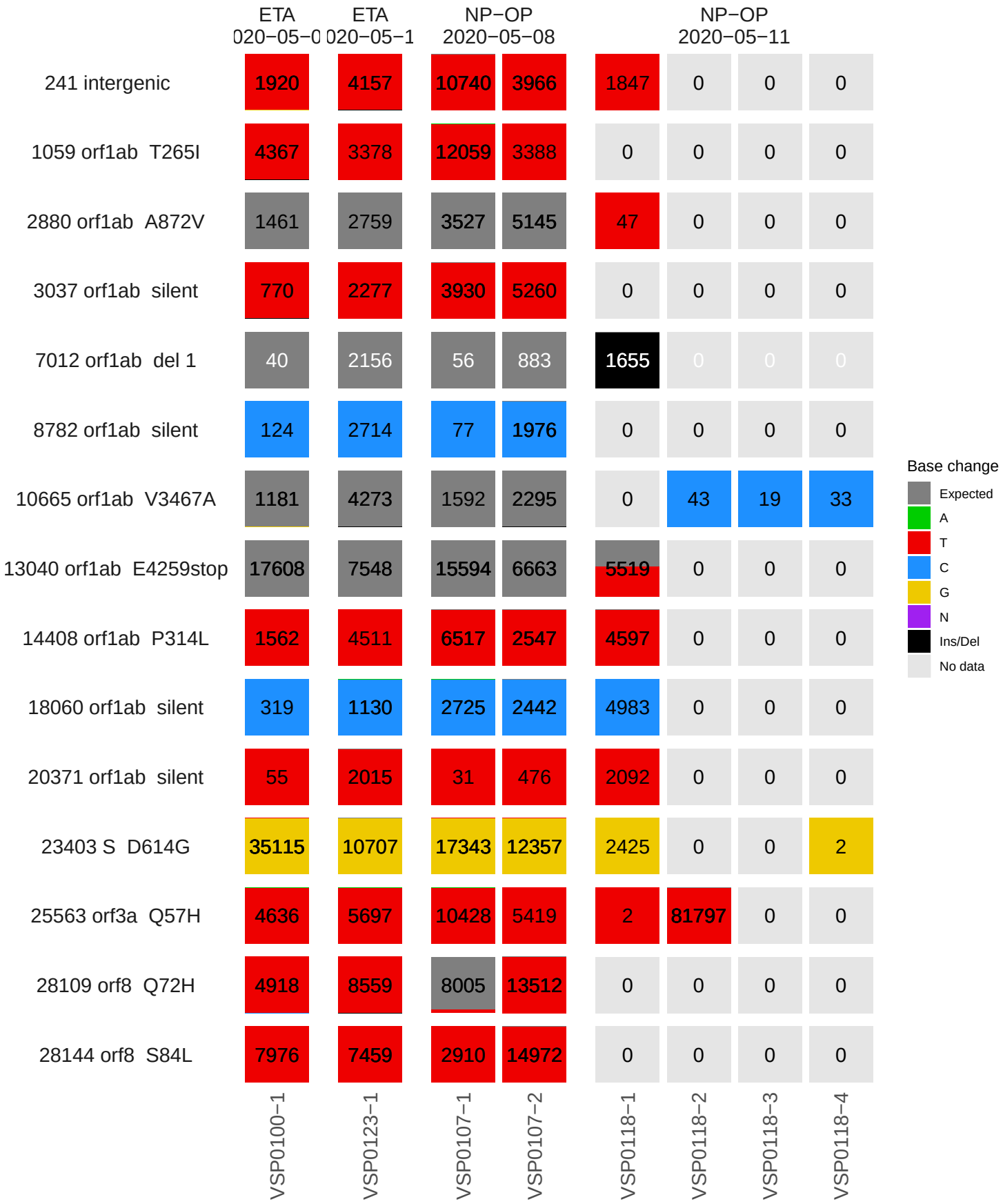
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0107	composite	NA	NP-OP	2020-05-08	29.68	B.1	99.9%	99.9%
VSP0118	composite	NA	NP-OP	2020-05-11	2.63	NA	62.5%	58.8%
VSP0100-1	single experiment	2760000	ETA	2020-05-08	29.82	B.1	99.7%	99.7%
VSP0107-1	single experiment	595000	NP-OP	2020-05-08	29.89	B.1	99.9%	99.9%
VSP0107-2	single experiment	595000	NP-OP	2020-05-08	29.68	B.1	99.9%	99.8%
VSP0118-1	single experiment	269	NP-OP	2020-05-11	2.67	NA	56.6%	54.2%
VSP0118-2	single experiment	1345	NP-OP	2020-05-11	0.60	NA	9.3%	6.1%
VSP0118-3	single experiment	1345	NP-OP	2020-05-11	0.56	NA	11.1%	8.1%
VSP0118-4	single experiment	1345	NP-OP	2020-05-11	0.60	NA	10.9%	7.3%
VSP0123-1	single experiment	123000	ETA	2020-05-11	29.26	B.1	99.9%	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 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.

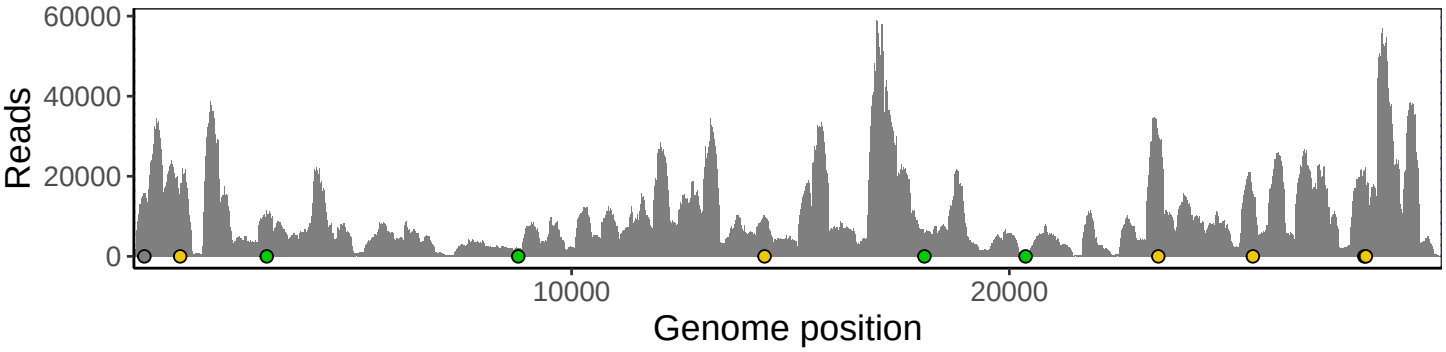



ETA 020−05−0
ETA 020−05−1
NP−OP 2020−05−08
NP−OP 2020−05−11
241 intergenic
1059 orf1ab T265I
2880 orf1ab A872V
3037 orf1ab silent
7012 orf1ab del 1
8782 orf1ab silent
10665 orf1ab V3467A
13040 orf1ab E4259stop
14408 orf1ab P314L
18060 orf1ab silent
20371 orf1ab silent
23403 S D614G
25563 orf3a Q57H
28109 orf8 Q72H
28144 orf8 S84L
1920 4157 10740 3966 1847 0 0 0
4367 3378 12059 3388 0 0 0 0
1461 2759 3527 5145 47 0 0 0
770 2277 3930 5260 0 0 0 0
40 2156 56 883 1655 0 0 0
124 2714 77 1976 0 0 0 0
1181 4273 1592 2295 0 43 19 33
17608 7548 15594 6663 5519 0 0 0
1562 4511 6517 2547 4597 0 0 0
319 1130 2725 2442 4983 0 0 0
55 2015 31 476 2092 0 0 0
35115 10707 17343 12357 2425 0 0 2
4636 5697 10428 5419 2 81797 0 0
4918 8559 8005 13512 0 0 0 0
7976 7459 2910 14972 0 0 0 0
VSP0100−1
VSP0123−1
VSP0107−1
VSP0107−2
VSP0118−1
VSP0118−2
VSP0118−3
VSP0118−4
Base change
Expected
A
T
C
G
N
Ins/Del
No data

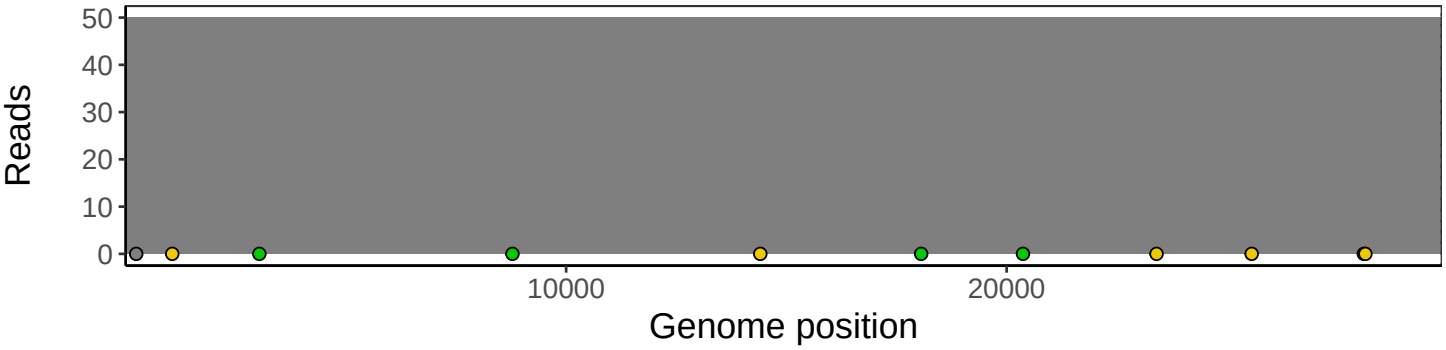
Analyses of individual experiments and composite results

VSP0107 | 2020-05-08 | NP-OP | 256no-t | composite result

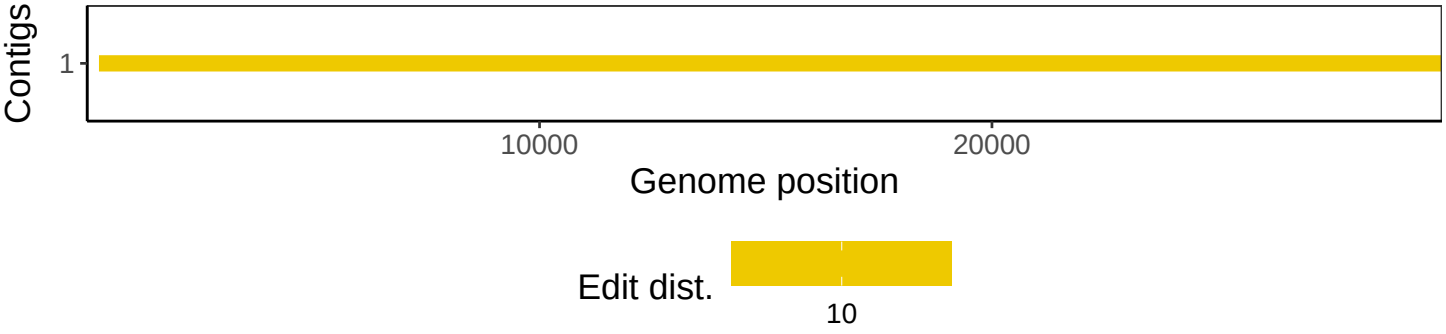
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

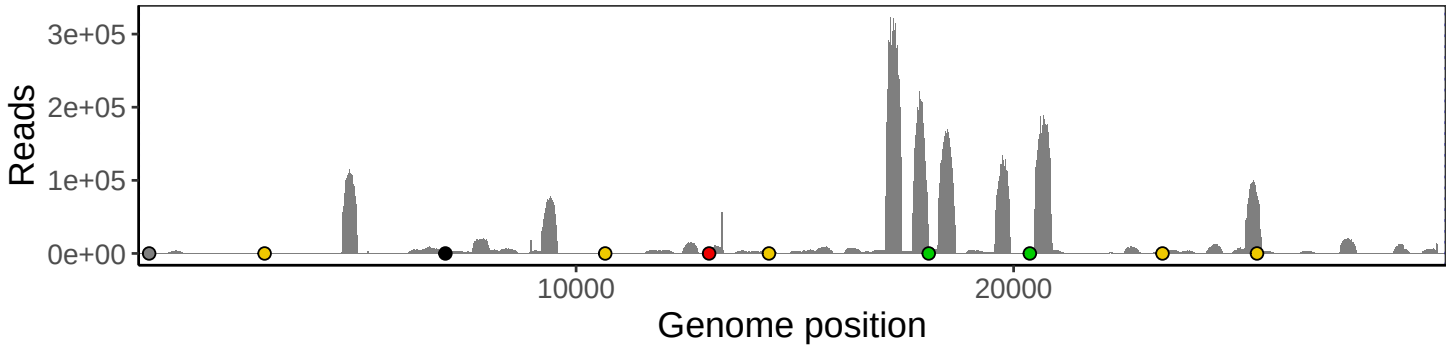


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

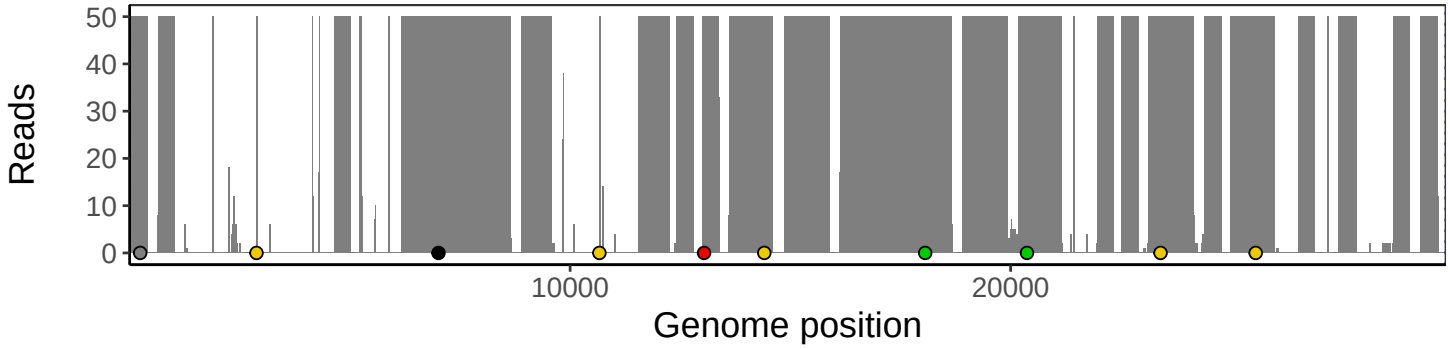


VSP0118 | 2020-05-11 | NP-OP | 256no-t2 | composite result

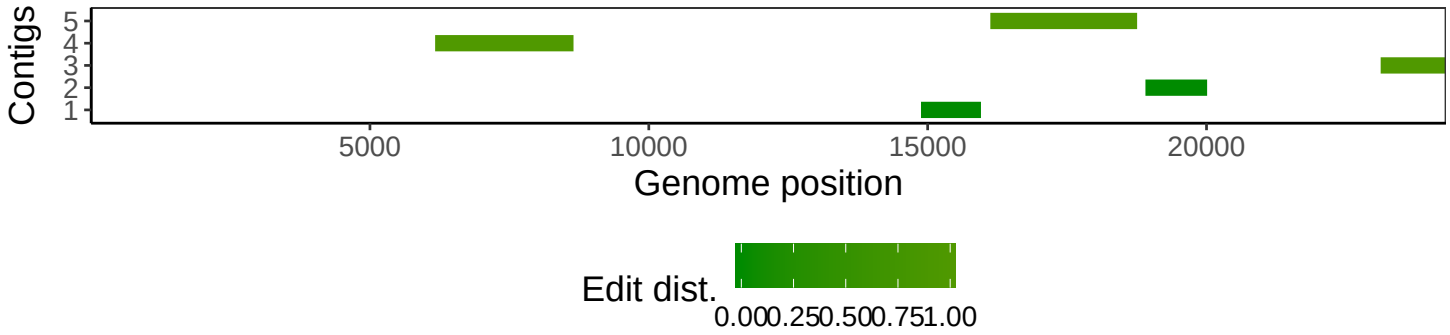
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

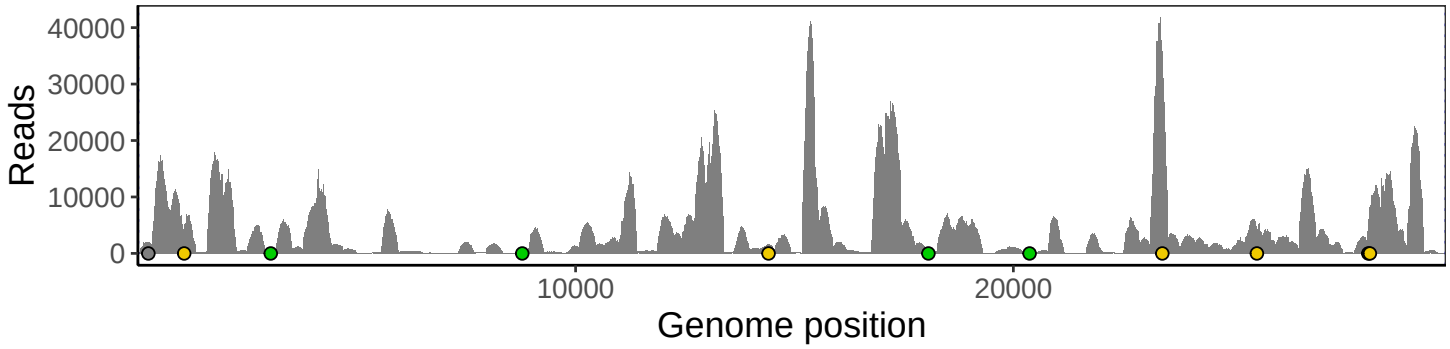


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

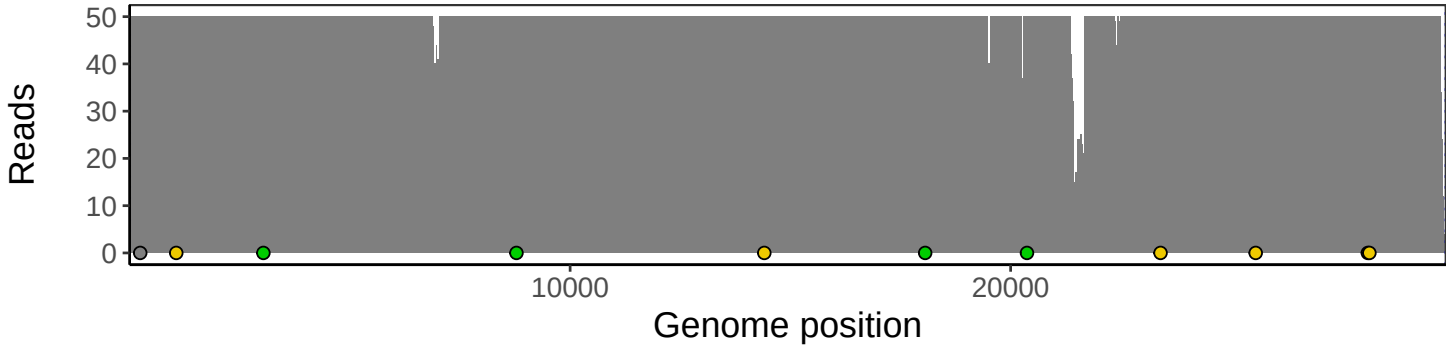


VSP0100-1 | 2020-05-08 | ETA | 256e-q | 2760000 genomes | single experiment

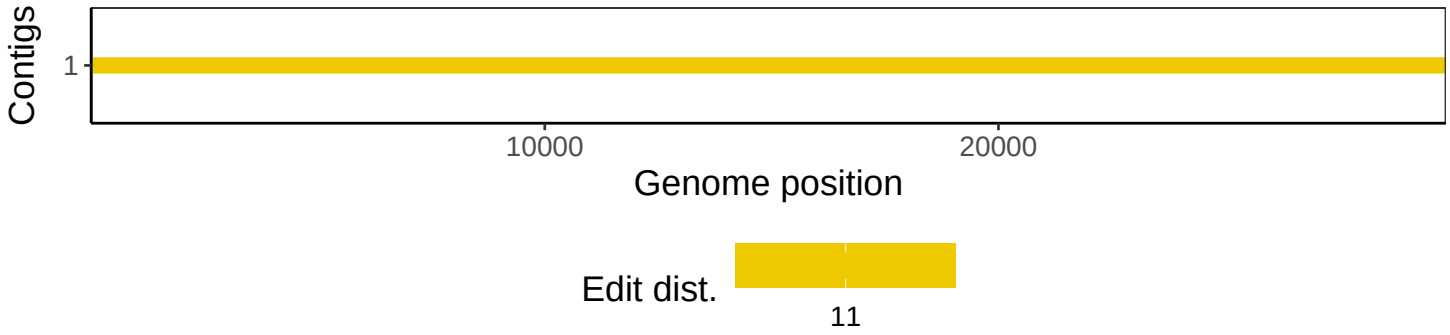
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

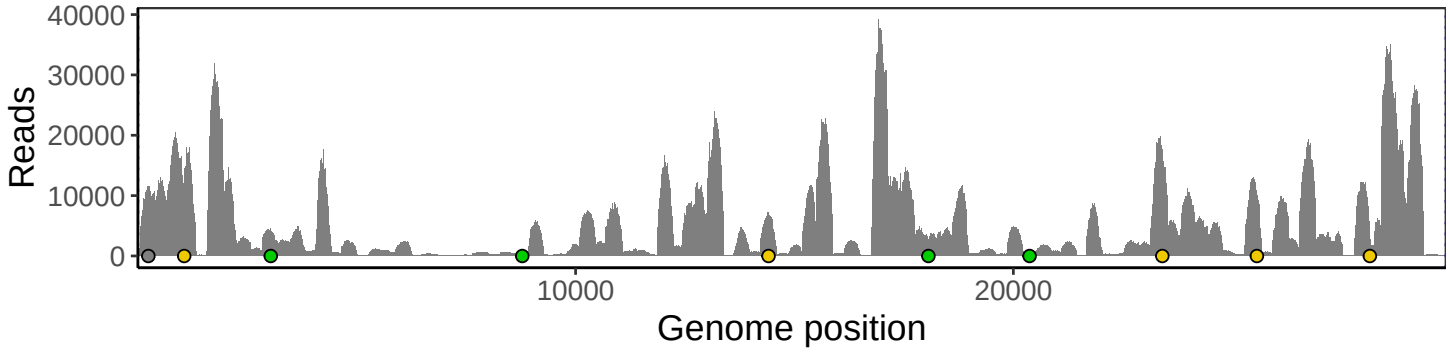


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

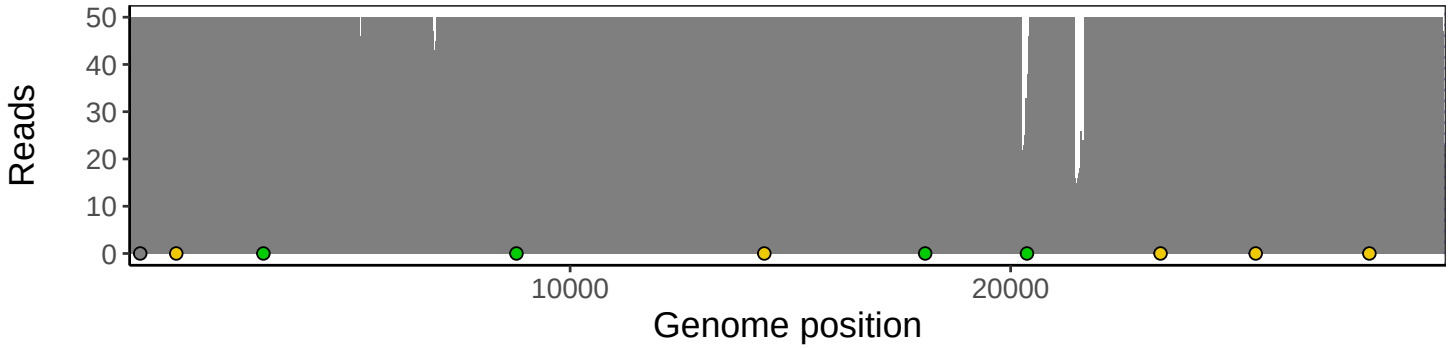


VSP0107-1 | 2020-05-08 | NP-OP | 256no-t | 595000 genomes | single experiment

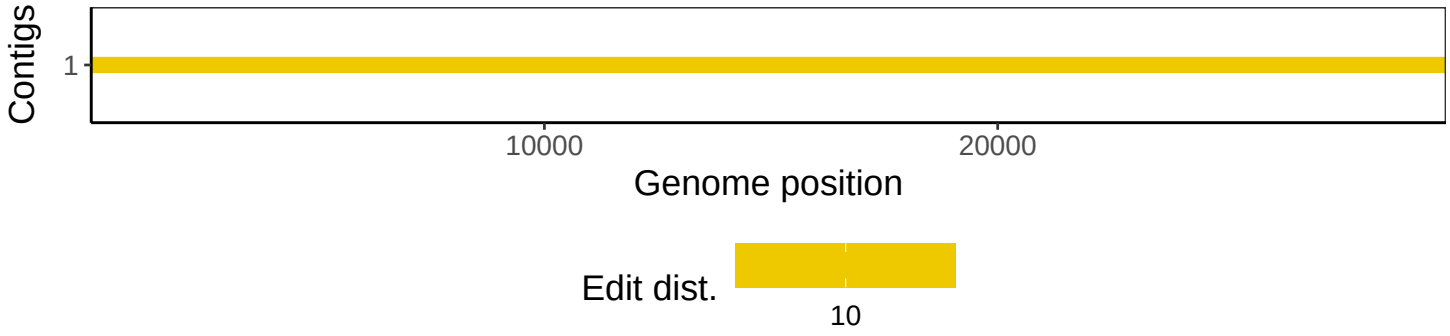
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

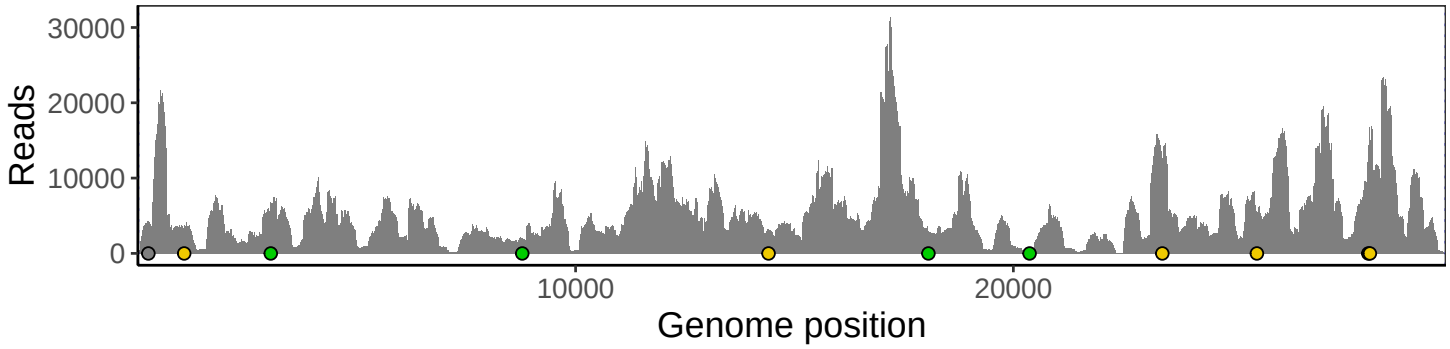


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

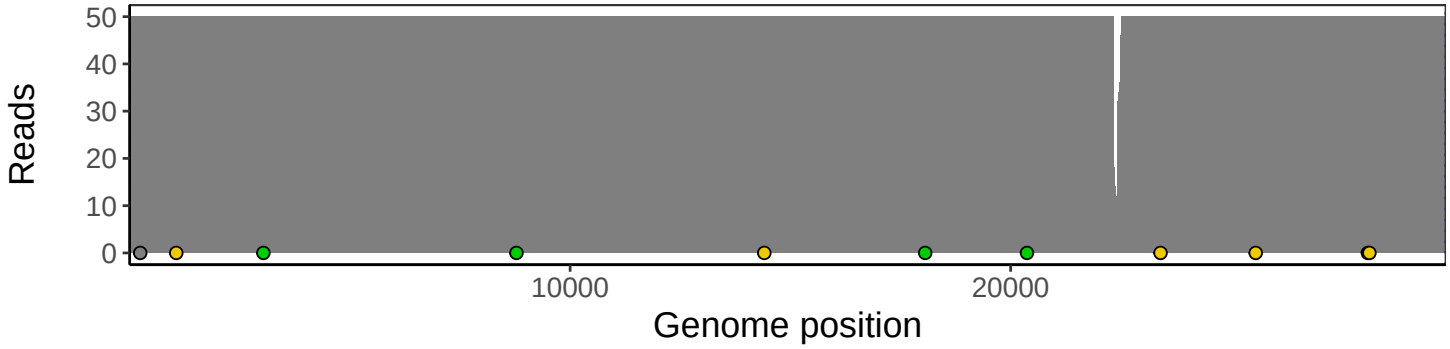


VSP0107-2 | 2020-05-08 | NP-OP | 256no-t | 595000 genomes | single experiment

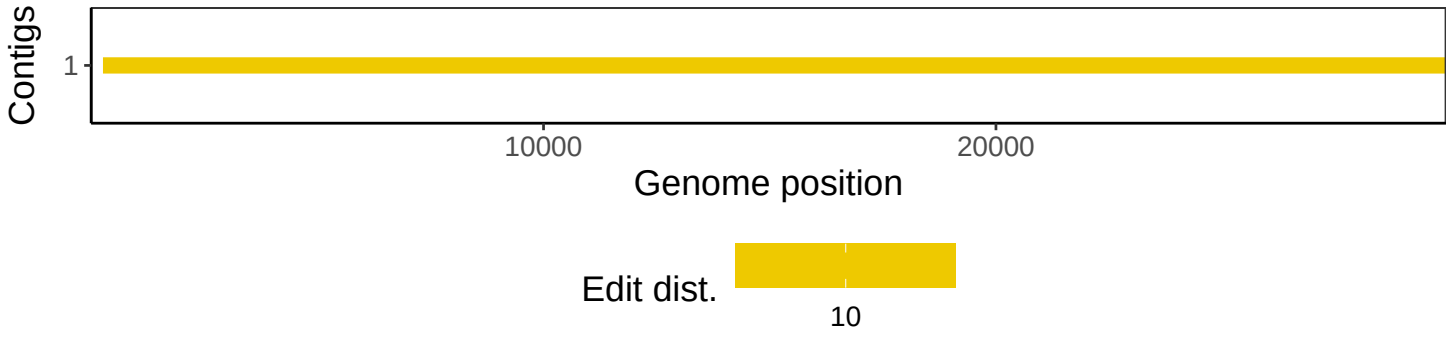
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

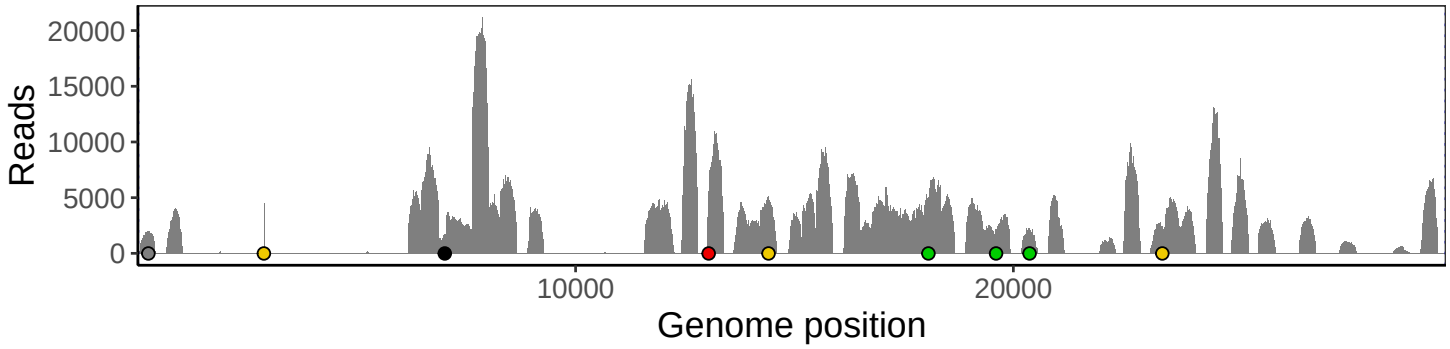


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

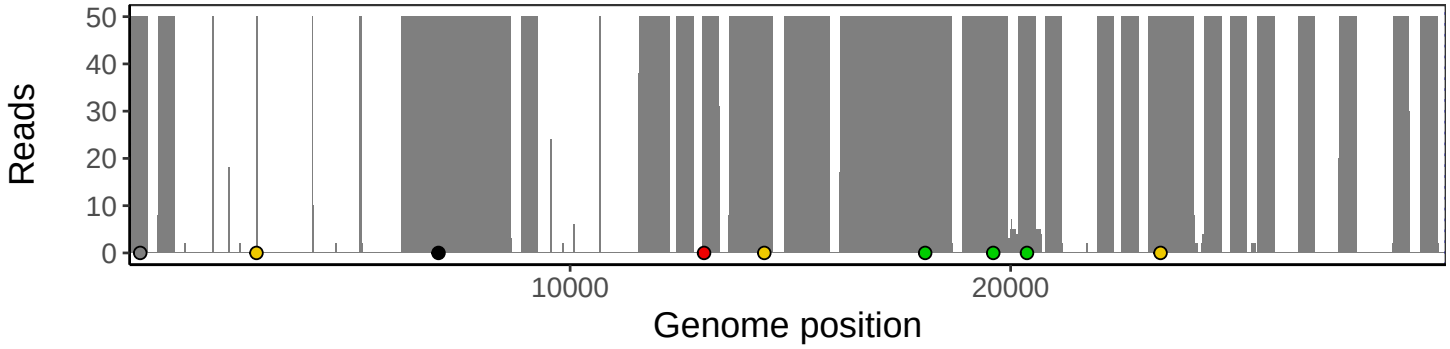


VSP0118-1 | 2020-05-11 | NP-OP | 256no-t2 | 269 genomes | single experiment

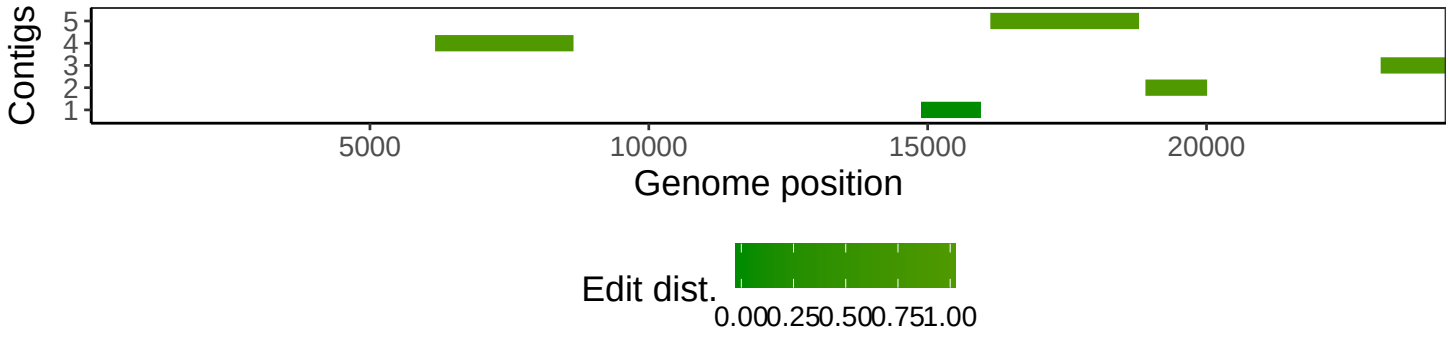
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

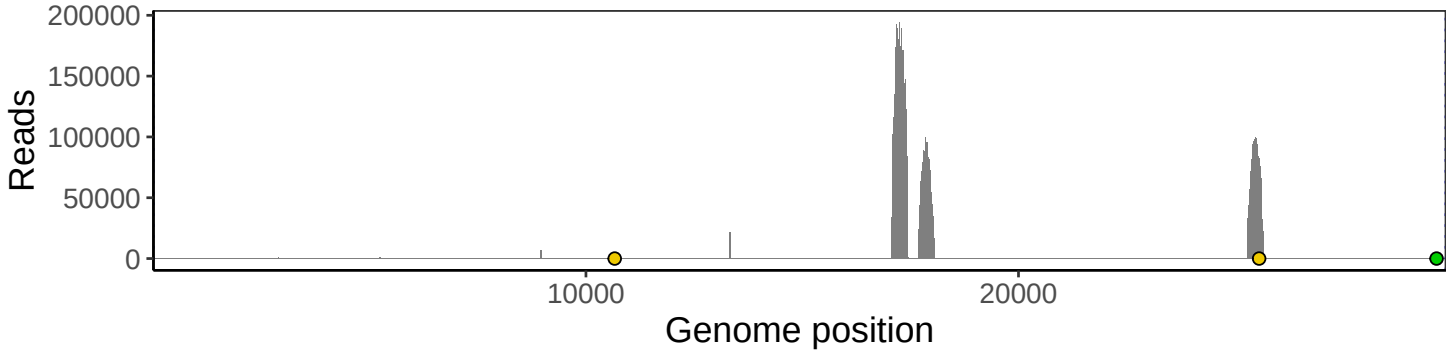


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

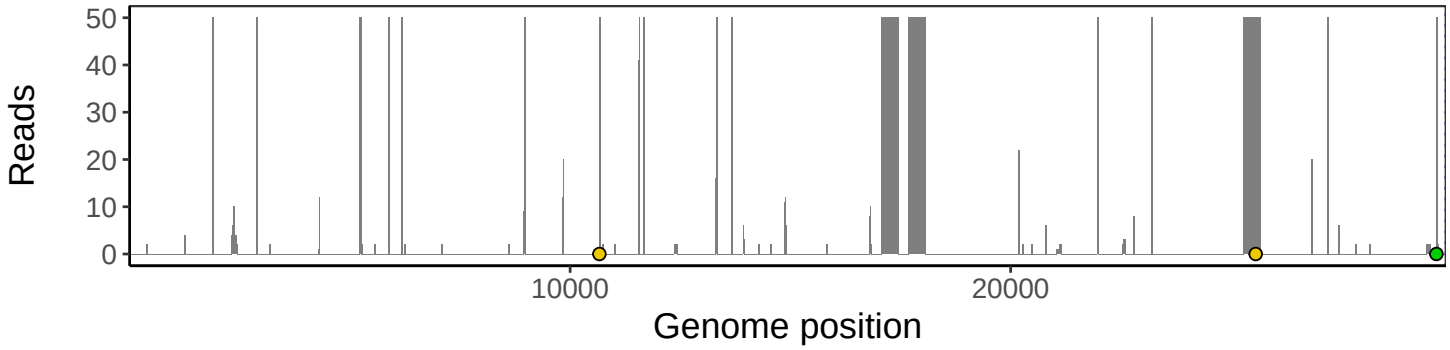


VSP0118-2 | 2020-05-11 | NP-OP | 256no-t2 | 1345 genomes | single experiment

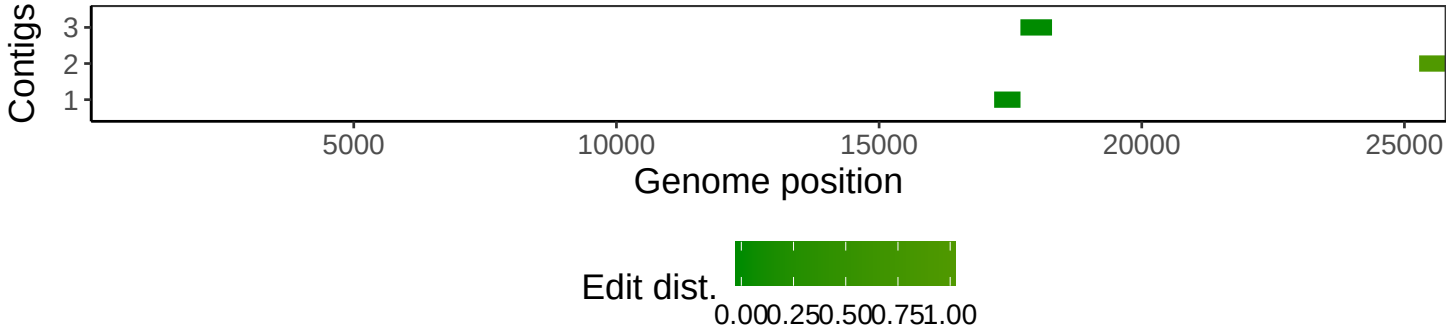
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

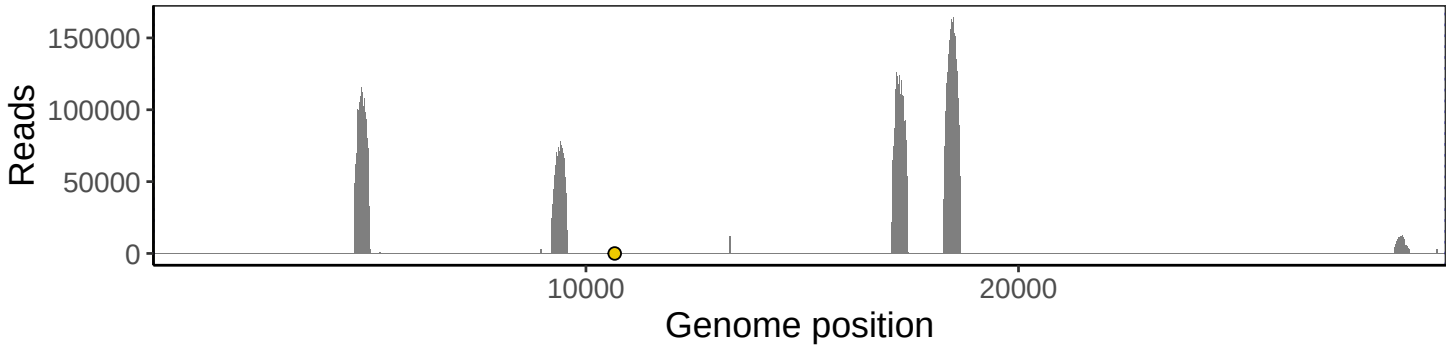


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

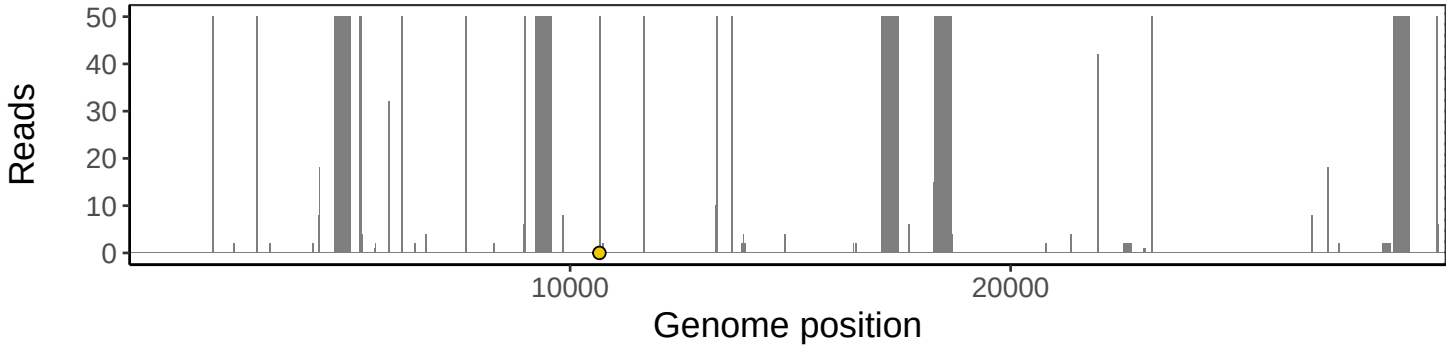


VSP0118-3 | 2020-05-11 | NP-OP | 256no-t2 | 1345 genomes | single experiment

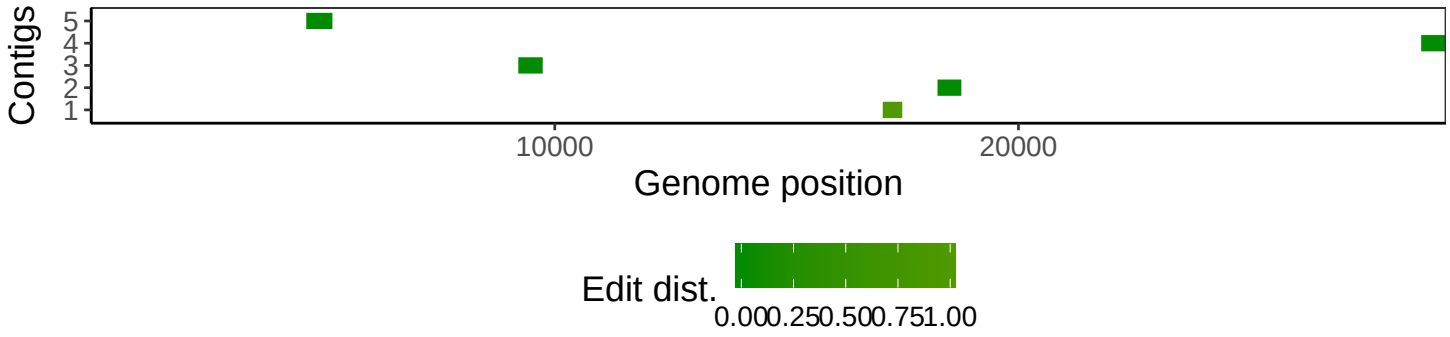
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

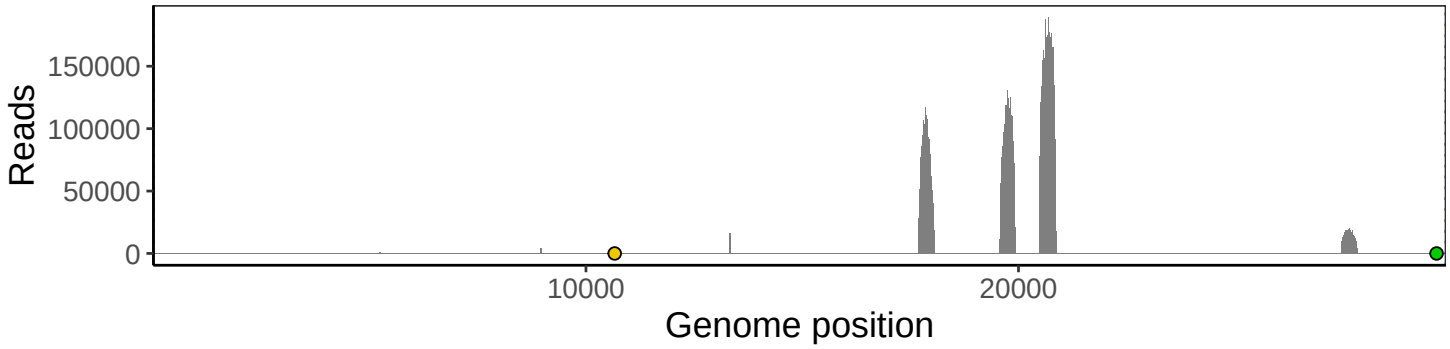


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

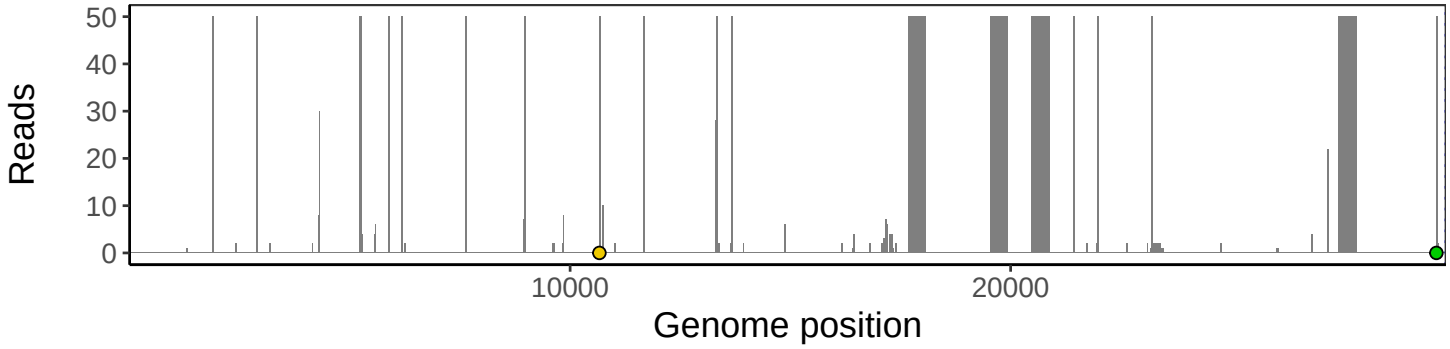


VSP0118-4 | 2020-05-11 | NP-OP | 256no-t2 | 1345 genomes | single experiment

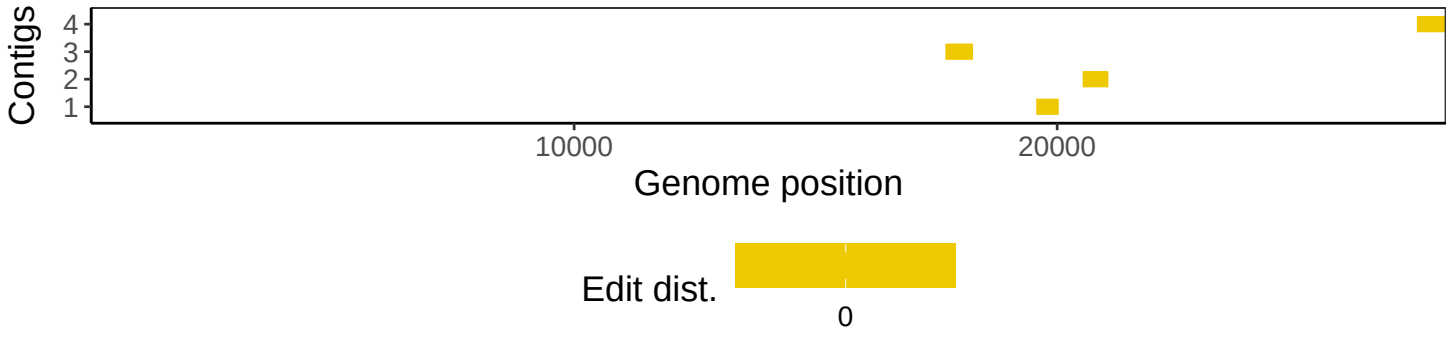
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

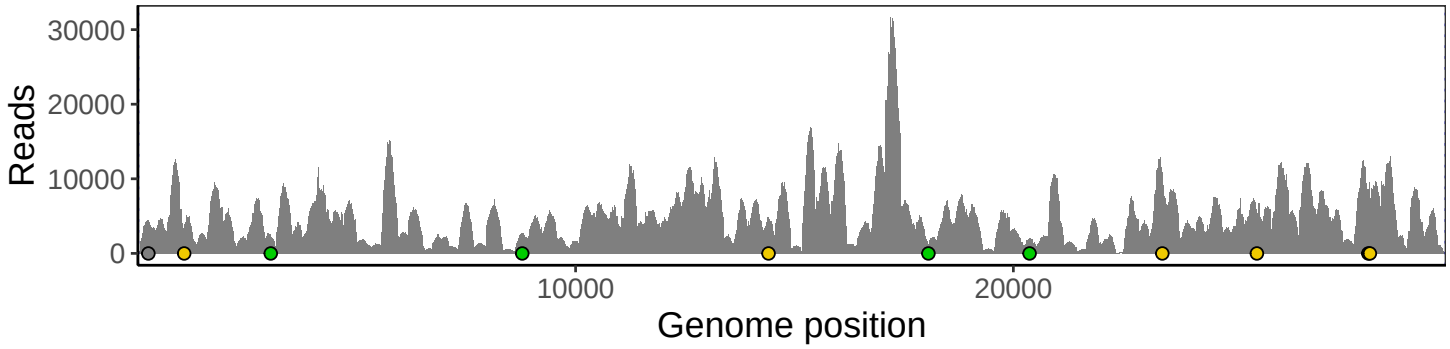


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

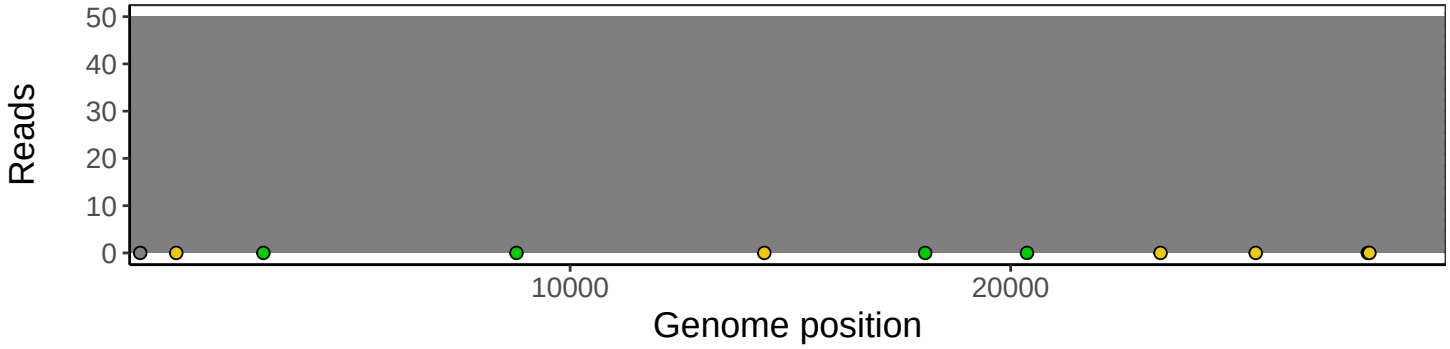


VSP0123-1 | 2020-05-11 | ETA | 256e-q | 123000 genomes | single experiment

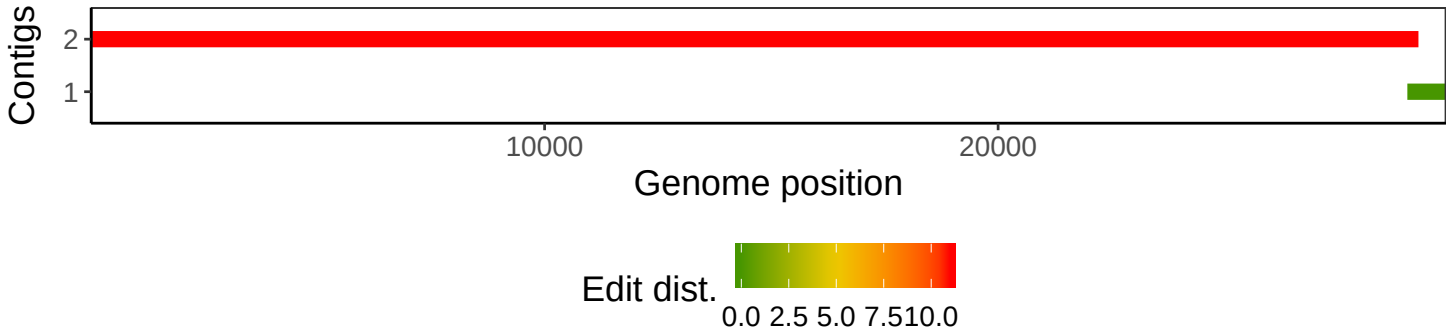
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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	2.3.3
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	3.0.0
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