COVID-19 subject 203

2020-10-23

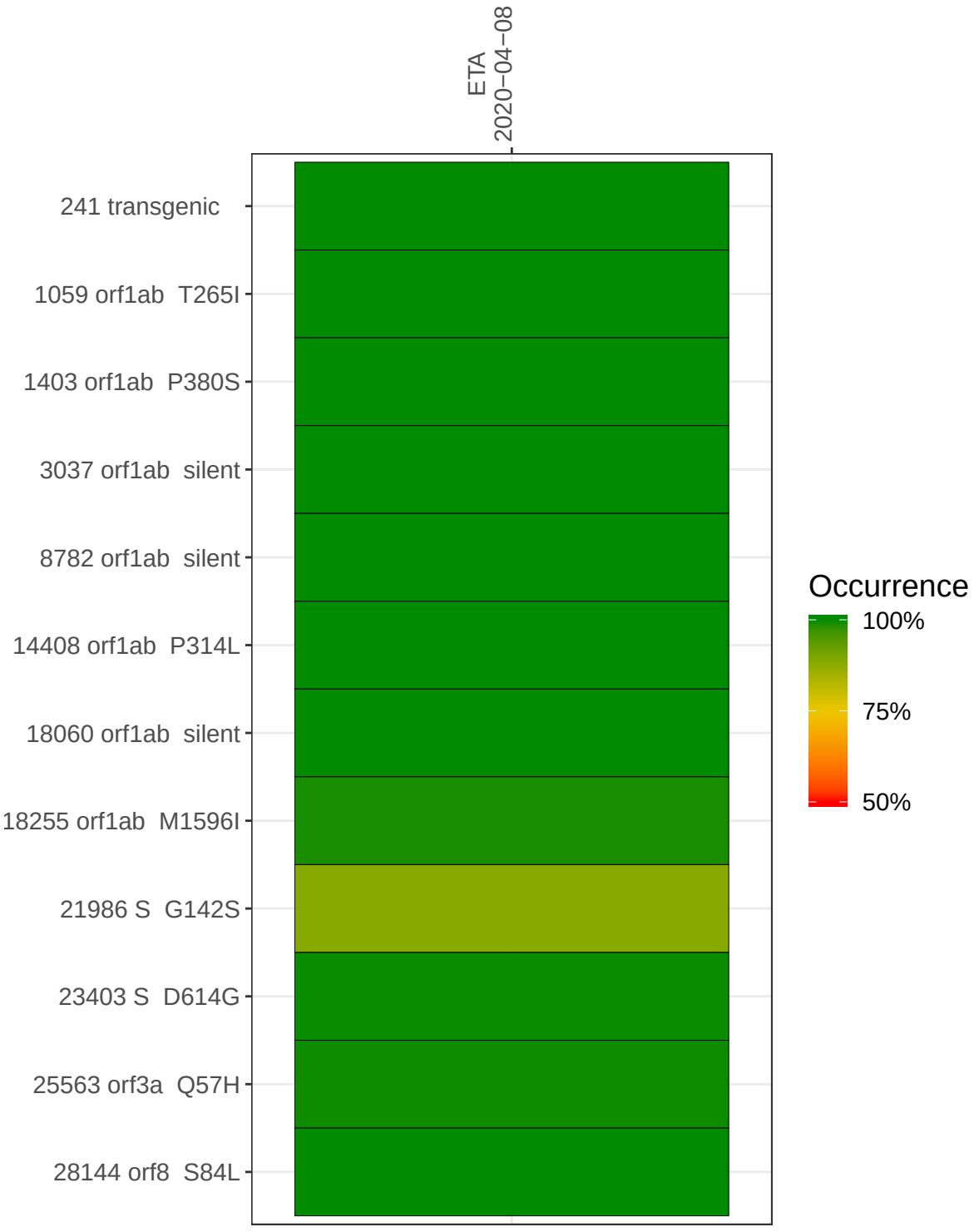
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

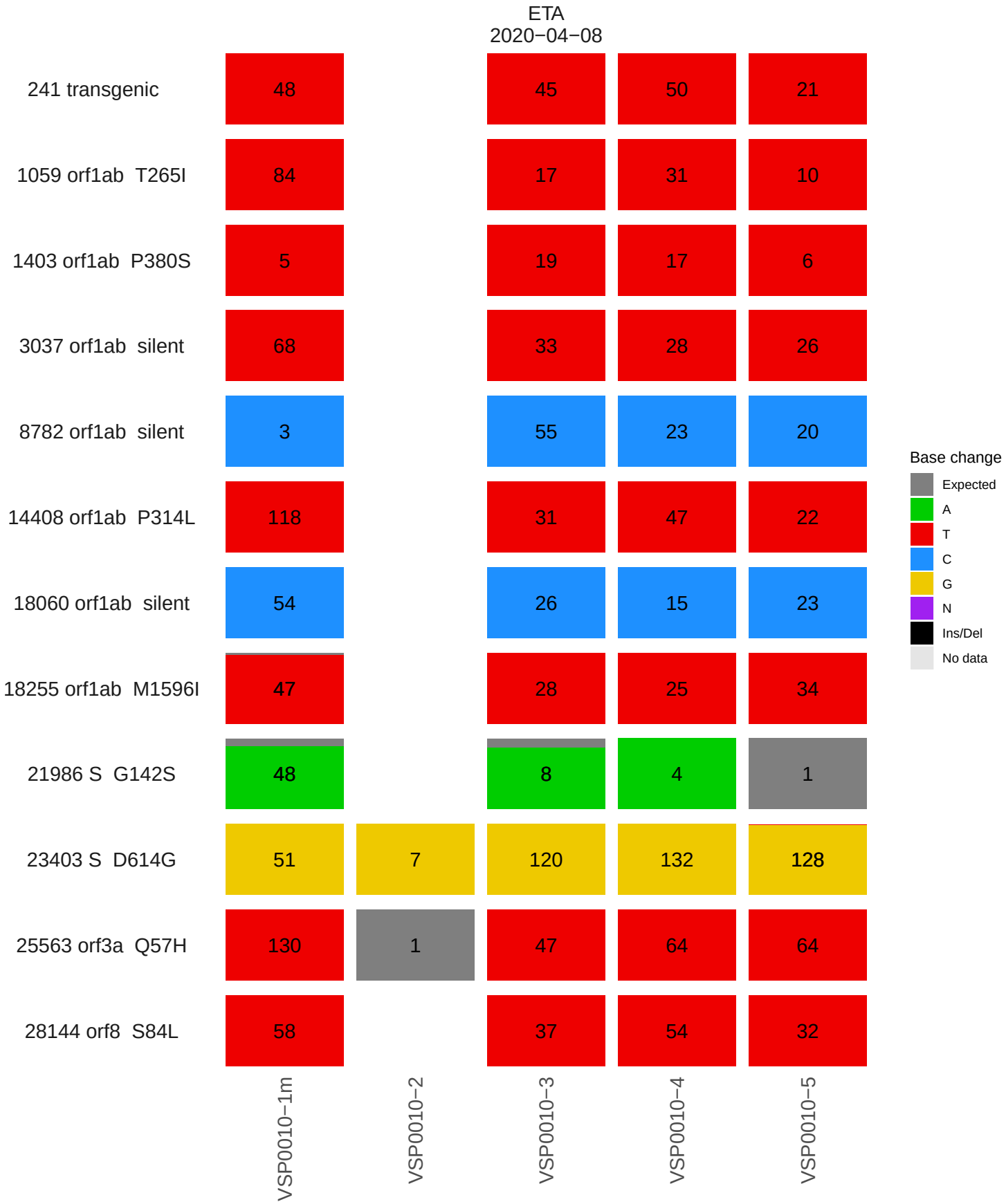
Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0010	composite	NA	ETA	2020-04-08	29.84	99.8%	99.4%
VSP0010-1m	single experiment	NA	ETA	2020-04-08	4.43	93.1%	79.2%
VSP0010-2	single experiment	14750	ETA	2020-04-08	0.60	39.1%	4.8%
VSP0010-3	single experiment	2950	ETA	2020-04-08	9.76	96.9%	91.8%
VSP0010-4	single experiment	2950	ETA	2020-04-08	10.36	97.4%	93.6%
VSP0010-5	single experiment	2950	ETA	2020-04-08	17.66	98.5%	91.3%

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.

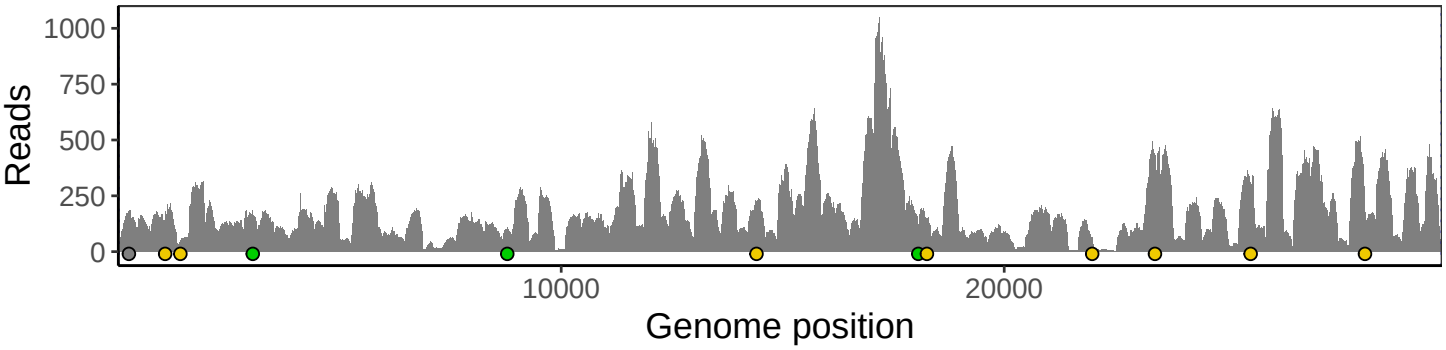



ETA
2020−04−08
241 transgenic
1059 orf1ab T265I
1403 orf1ab P380S
3037 orf1ab silent
8782 orf1ab silent
14408 orf1ab P314L
18060 orf1ab silent
18255 orf1ab M1596I
21986 S G142S
23403 S D614G
25563 orf3a Q57H
28144 orf8 S84L
48 45 50 21
84 17 31 10
5 19 17 6
68 33 28 26
3 55 23 20
118 31 47 22
54 26 15 23
47 28 25 34
48 8 4 1
51 7 120 132 128
130 1 47 64 64
58 37 54 32
VSP0010−1m
VSP0010−2
VSP0010−3
VSP0010−4
VSP0010−5
Base change
Expected
A
T
C
G
N
Ins/Del
No data

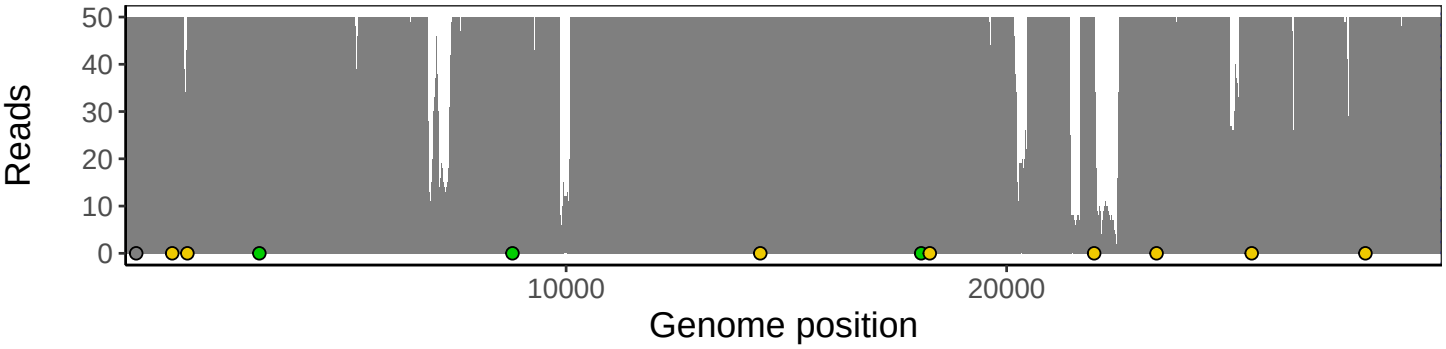
Analyses of individual experiments and composite results.

VSP0010 | 2020-04-08 | ETA | 203-tri | composite result

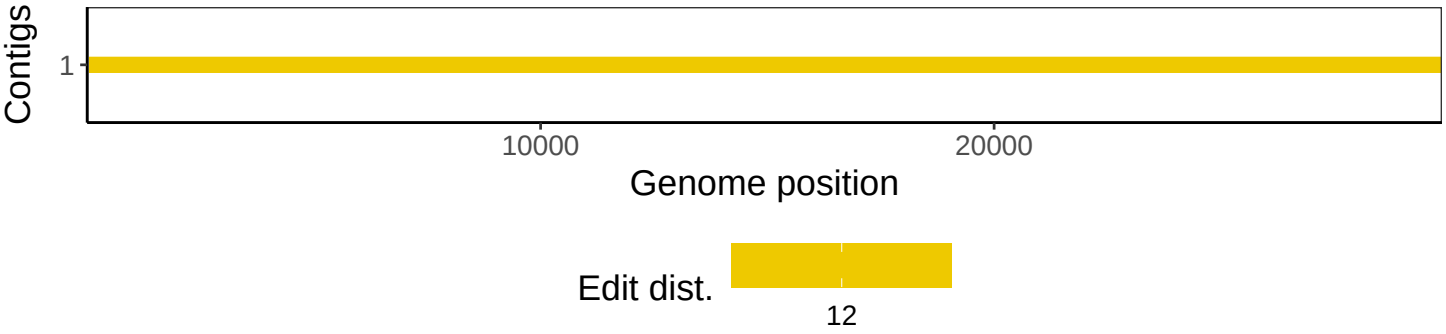
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

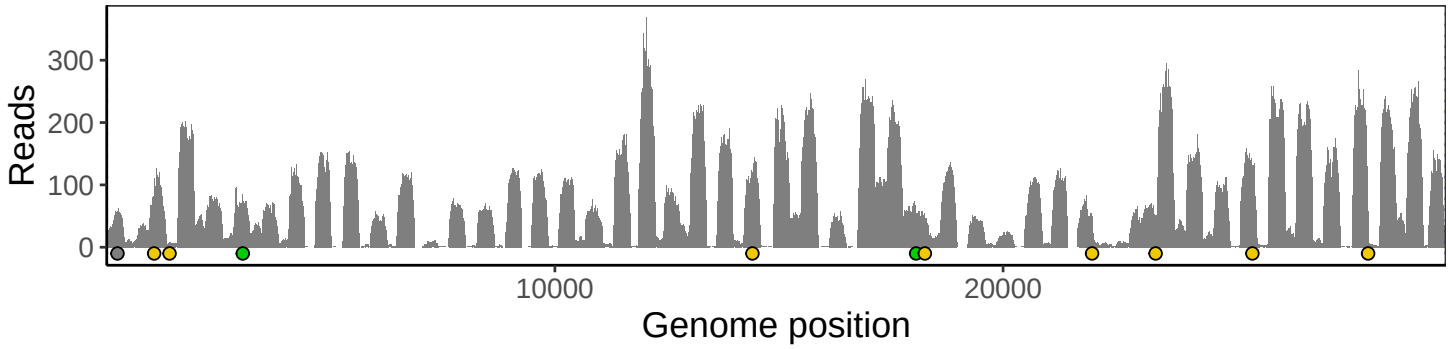


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

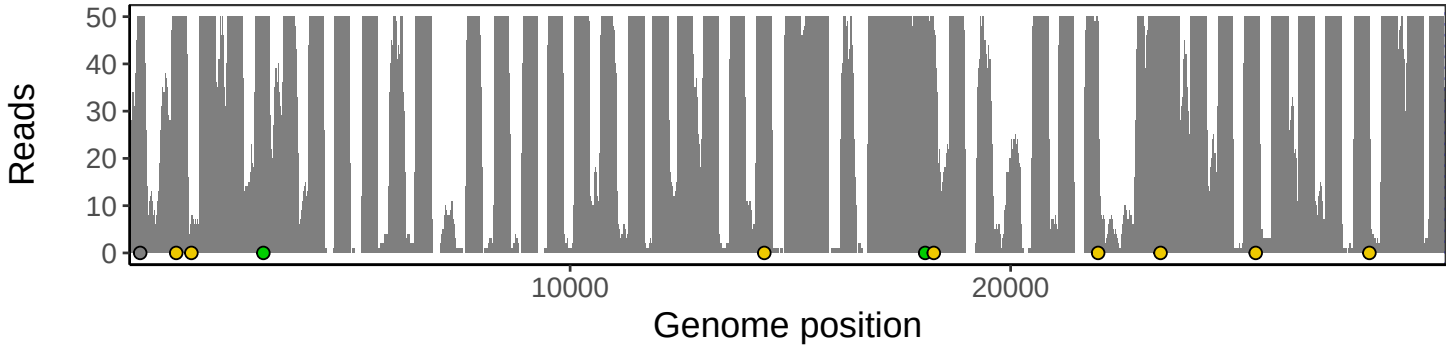


VSP0010-1m | 2020-04-08 | ETA | 203-tri | genomes | single experiment

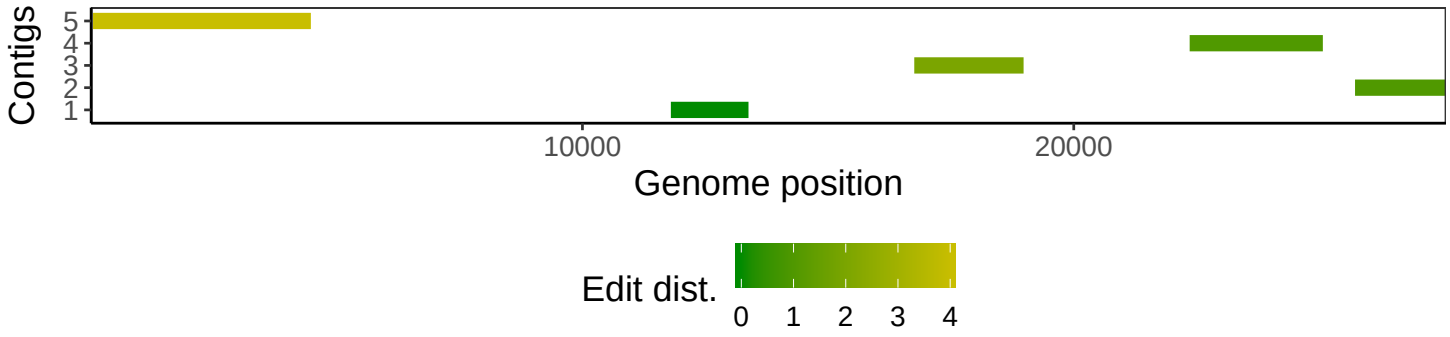
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

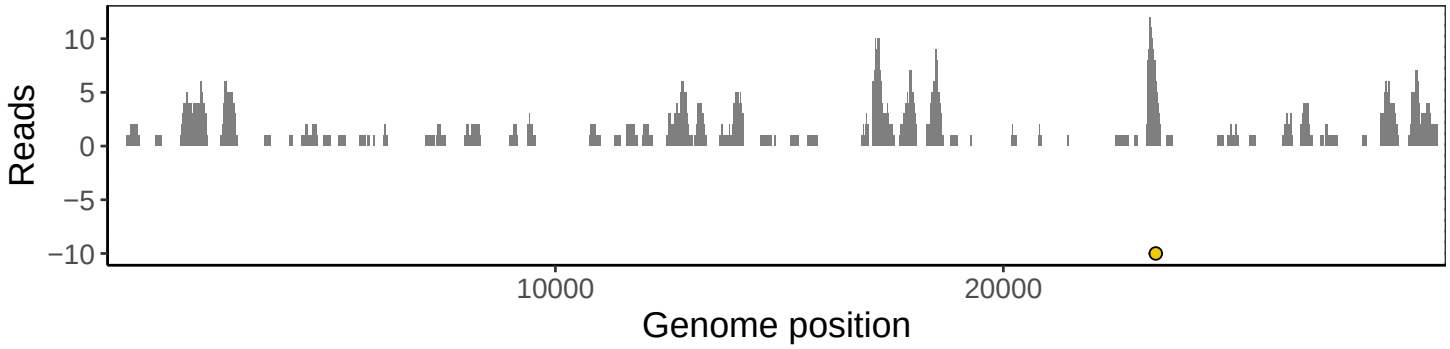


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

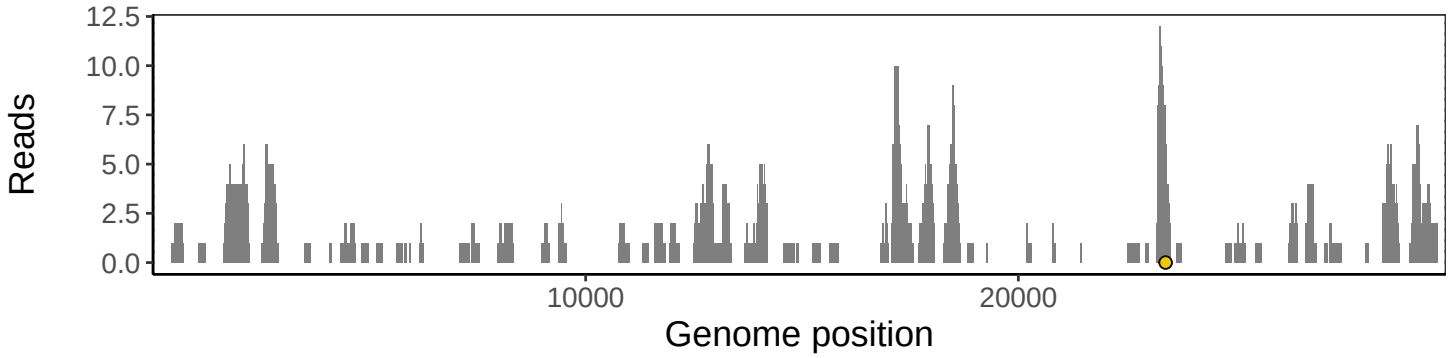


VSP0010-2 | 2020-04-08 | ETA | 203-tri | 14750 genomes | single experiment

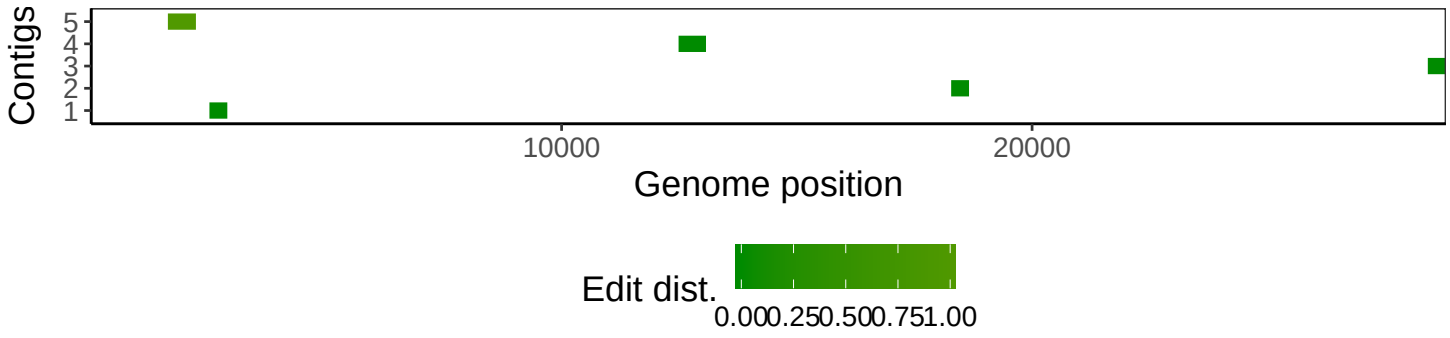
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

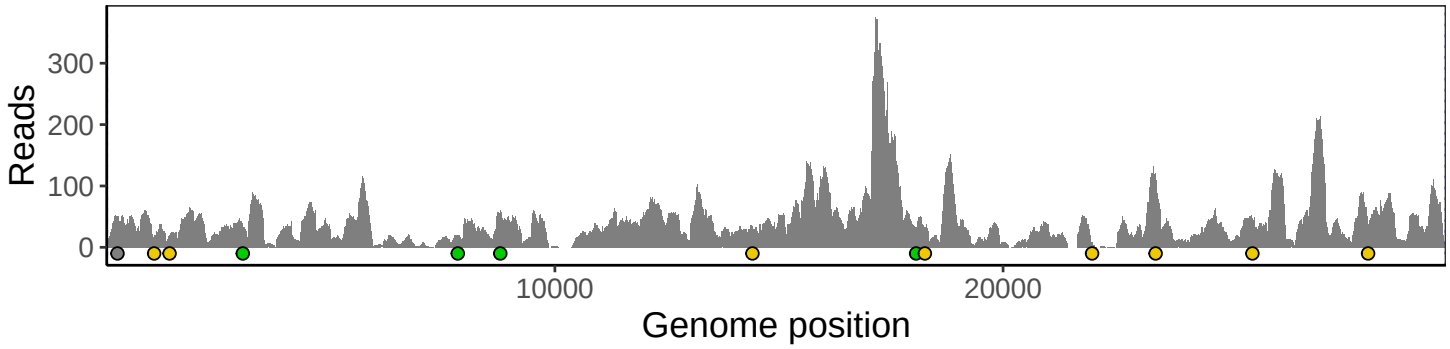


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

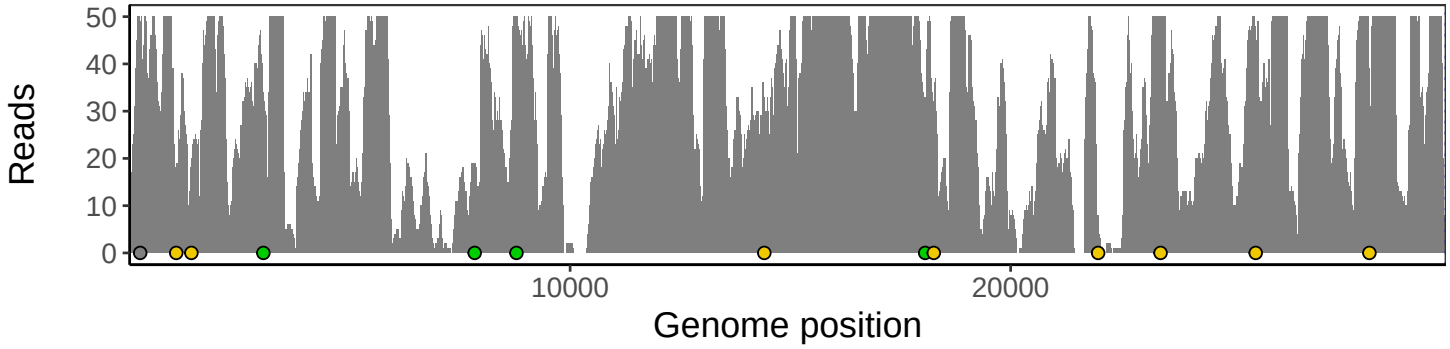


VSP0010-3 | 2020-04-08 | ETA | 203-tri | 2950 genomes | single experiment

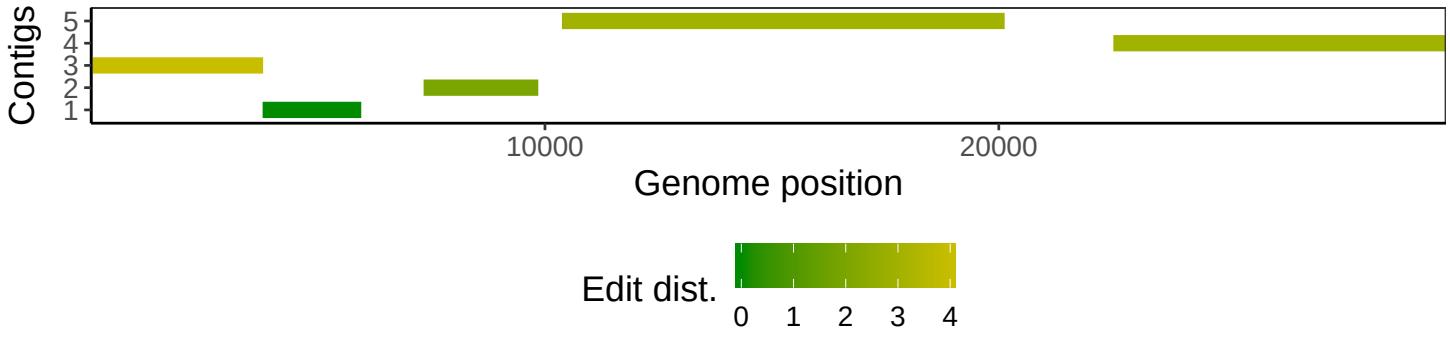
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

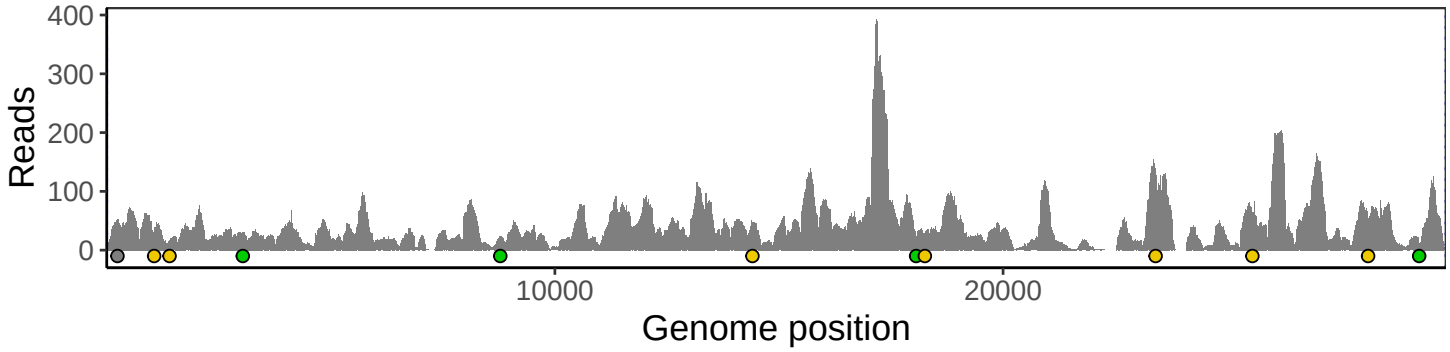


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

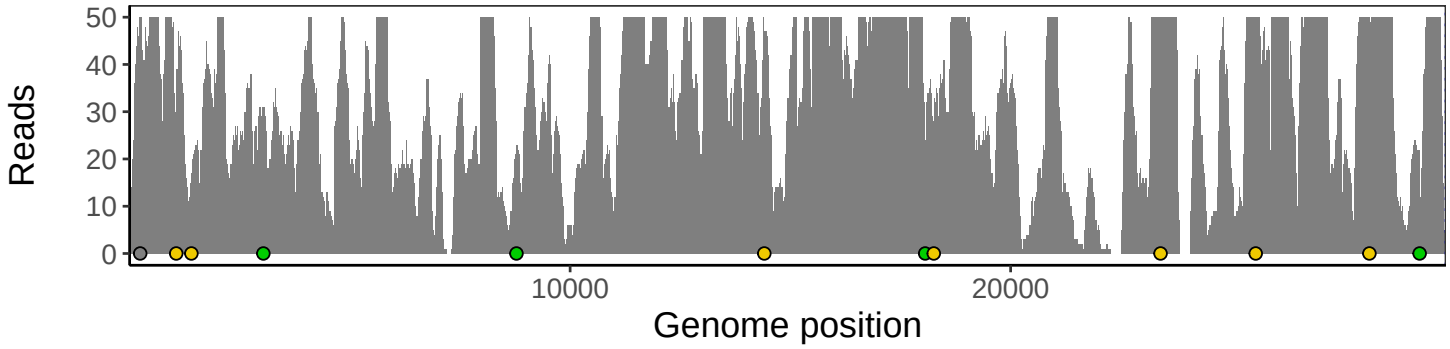


VSP0010-4 | 2020-04-08 | ETA | 203-tri | 2950 genomes | single experiment

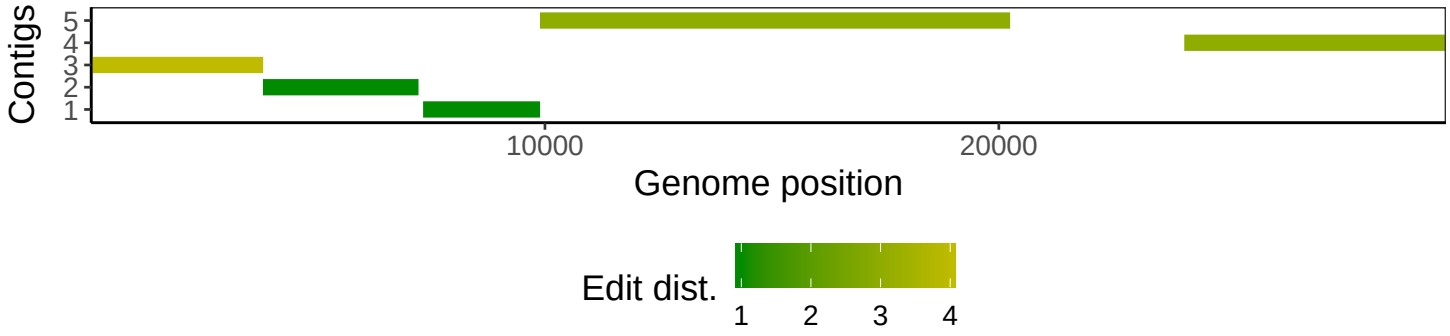
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

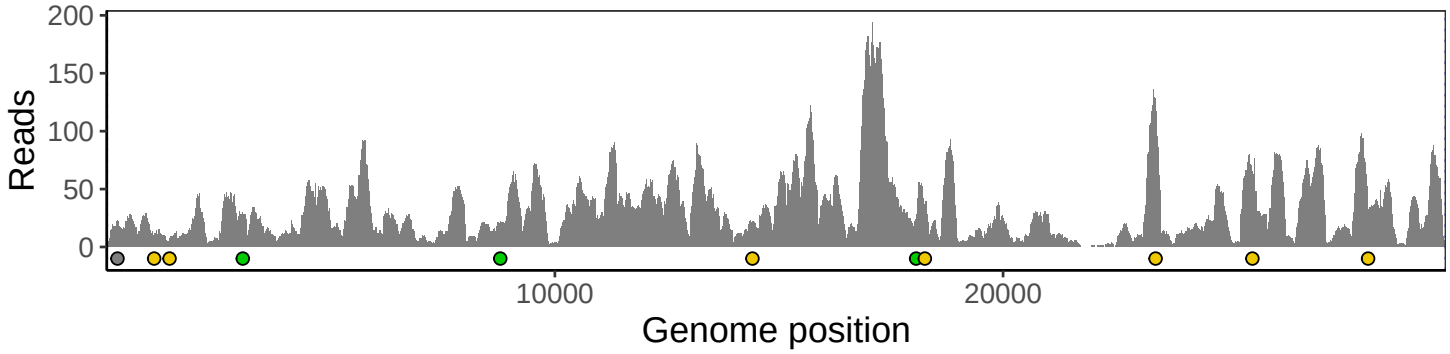


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

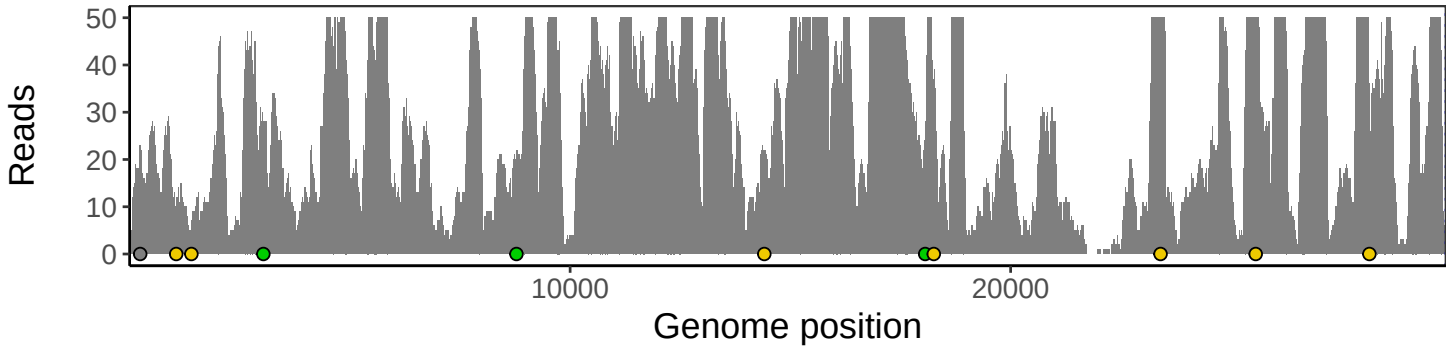


VSP0010-5 | 2020-04-08 | ETA | 203-tri | 2950 genomes | single experiment

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.