# COVID-19 subject 222-TCE

*2020-10-23*

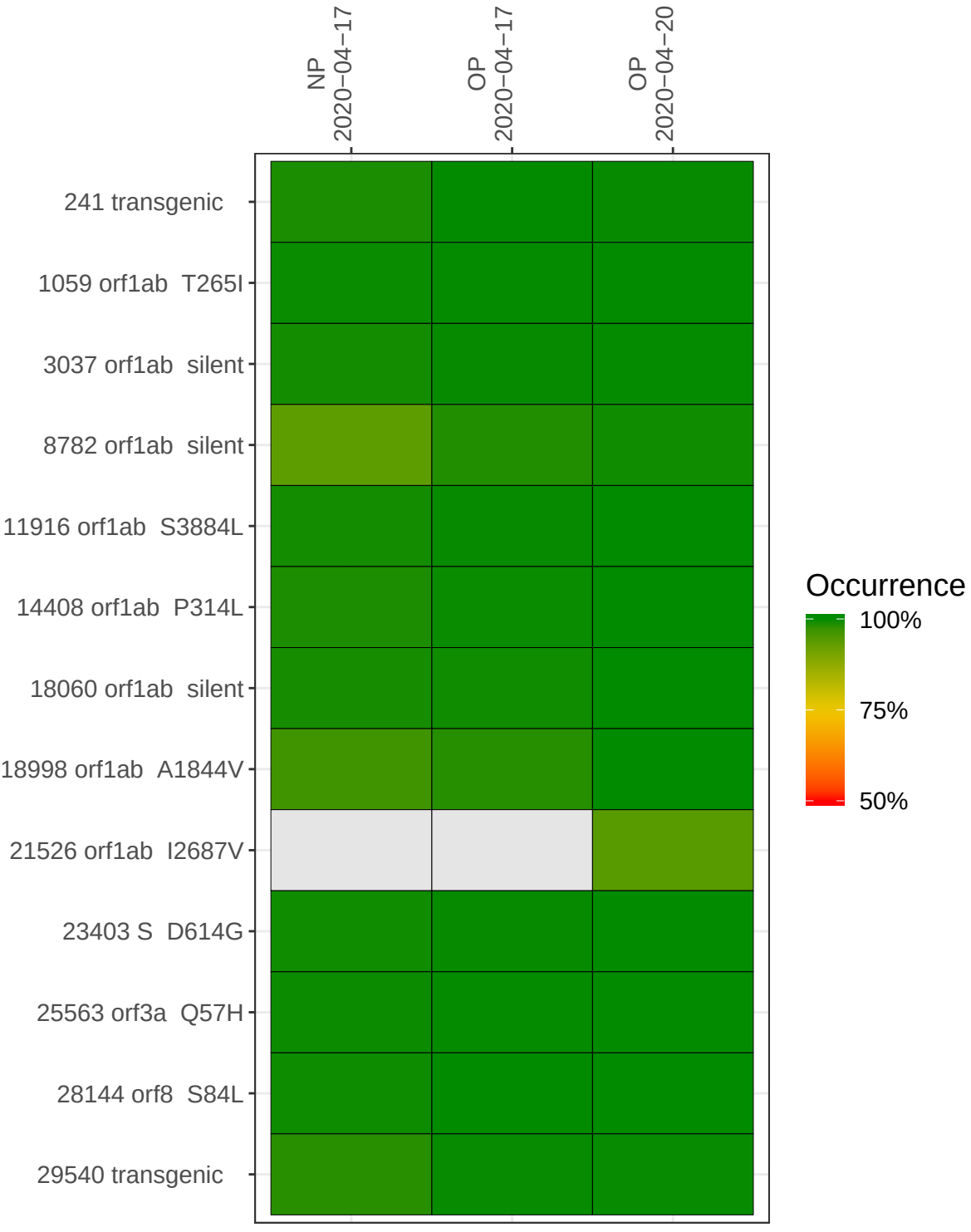
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

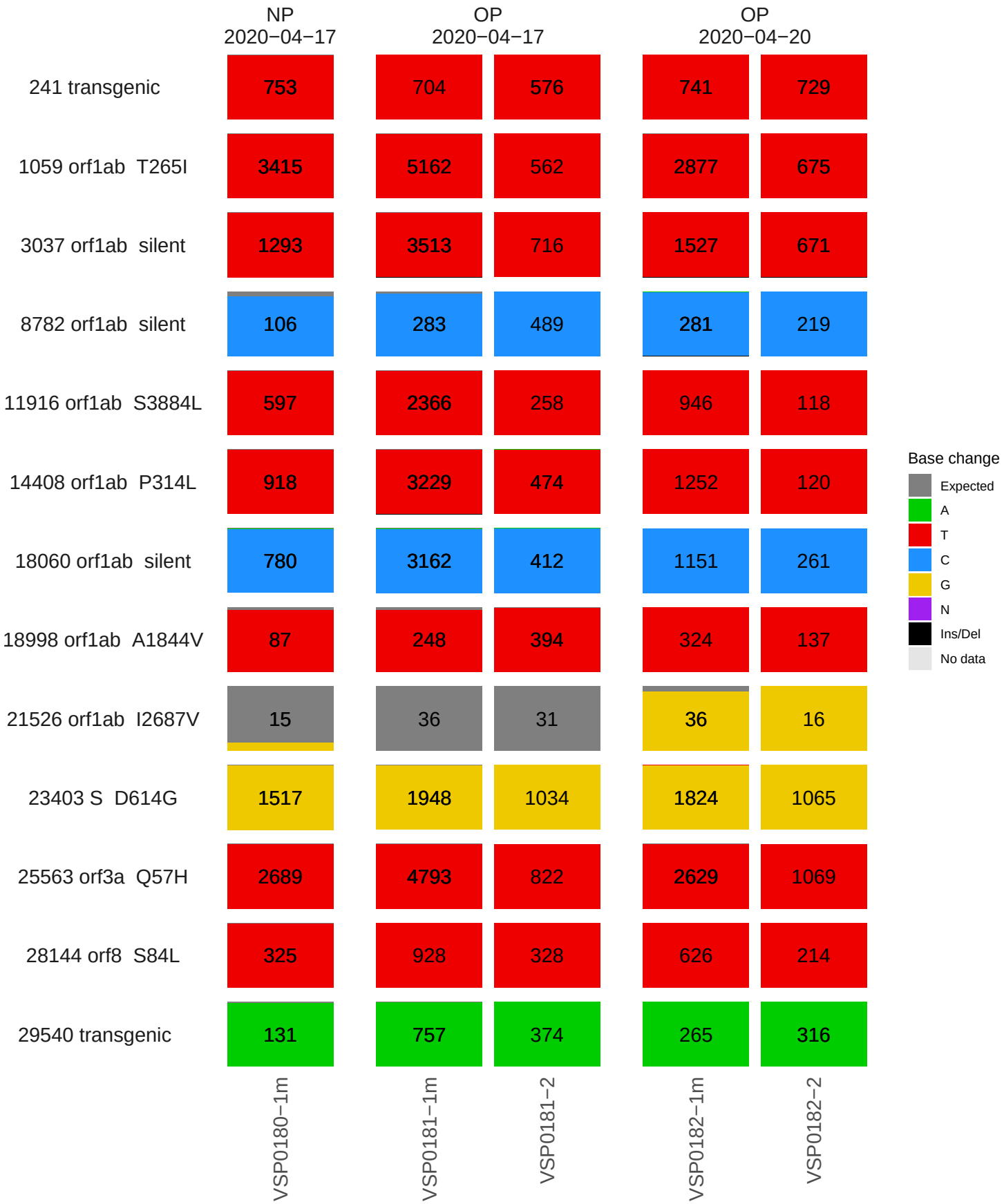
Table 1. Sample summary.

| Experiment | Type | Input genomes | Sample type | Sample date | Largest contig (KD) | Reference read coverage | Reference read coverage (>= 5 reads) |
|---|---|---|---|---|---|---|---|
| VSP0181 | composite | NA | OP | 2020-04-17 | 29.34 | 99.9% | 99.9% |
| VSP0182 | composite | NA | OP | 2020-04-20 | 29.88 | 99.9% | 99.9% |
| VSP0180-1m | single experiment | NA | NP | 2020-04-17 | 29.87 | 99.9% | 99.7% |
| VSP0181-1m | single experiment | NA | OP | 2020-04-17 | 30.04 | 99.9% | 99.9% |
| VSP0181-2 | single experiment | 1.510e+11 | OP | 2020-04-17 | 29.34 | 99.9% | 99.7% |
| VSP0182-1m | single experiment | NA | OP | 2020-04-20 | 29.87 | 99.9% | 99.9% |
| VSP0182-2 | single experiment | 1.325e+11 | OP | 2020-04-20 | 20.33 | 99.9% | 99.4% |

**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.

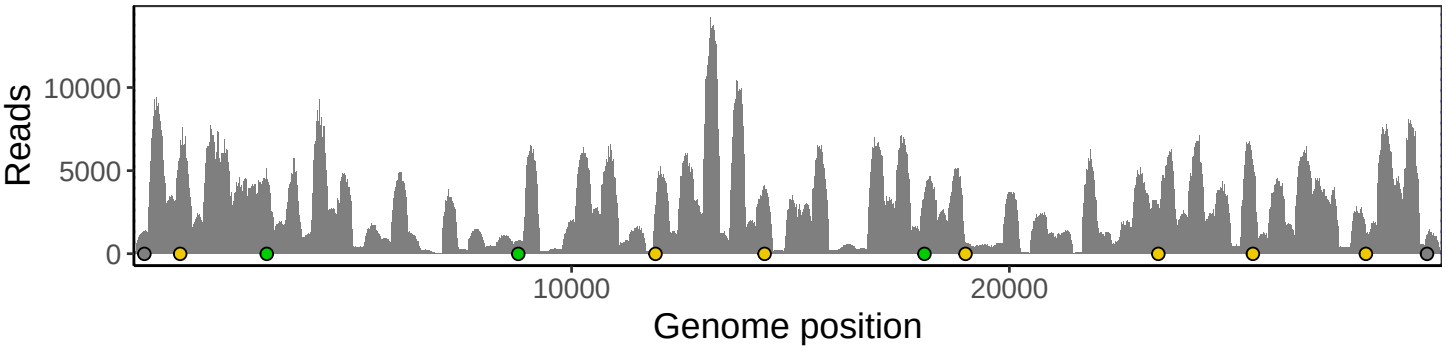



NP
2020−04−17
OP
2020−04−17
OP
2020−04−20
241 transgenic
753
704
576
741
729
1059 orf1ab T265I
3415
5162
562
2877
675
3037 orf1ab silent
1293
3513
716
1527
671
8782 orf1ab silent
106
283
489
281
219
11916 orf1ab S3884L
597
2366
258
946
118
14408 orf1ab P314L
918
3229
474
1252
120
18060 orf1ab silent
780
3162
412
1151
261
18998 orf1ab A1844V
87
248
394
324
137
21526 orf1ab I2687V
15
36
31
36
16
23403 S D614G
1517
1948
1034
1824
1065
25563 orf3a Q57H
2689
4793
822
2629
1069
28144 orf8 S84L
325
928
328
626
214
29540 transgenic
131
757
374
265
316
VSP0180−1m
VSP0181−1m
VSP0181−2
VSP0182−1m
VSP0182−2
Base change
Expected
A
T
C
G
N
Ins/Del
No data

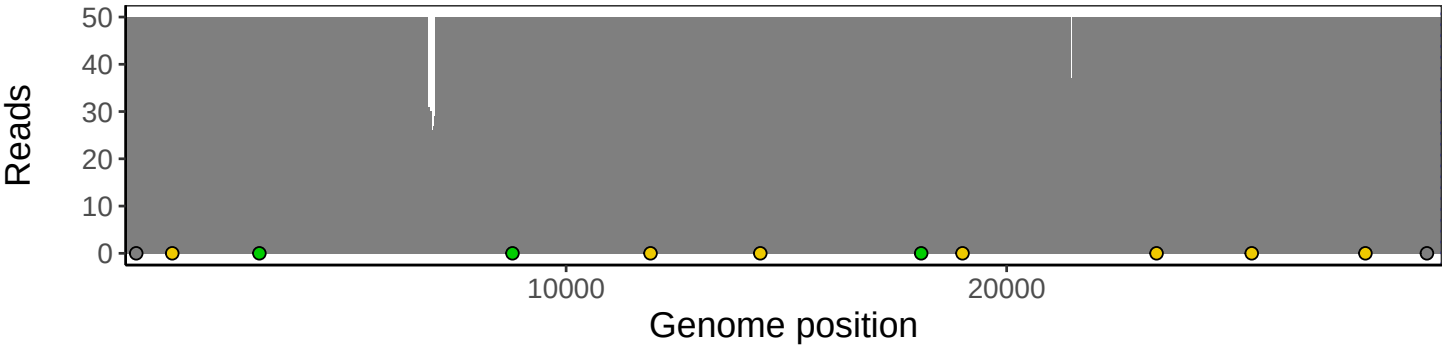
## Analyses of individual experiments and composite results.

### VSP0181 | 2020-04-17 | OP | 2 | composite result

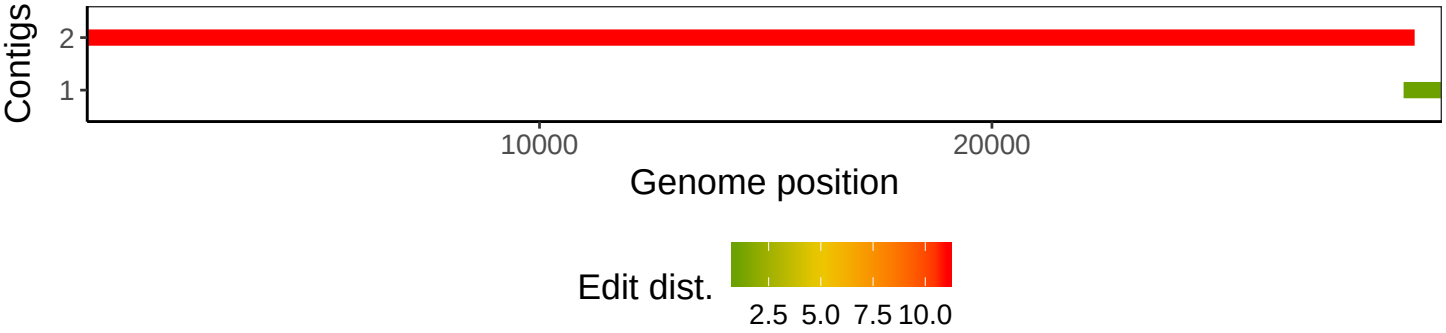
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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

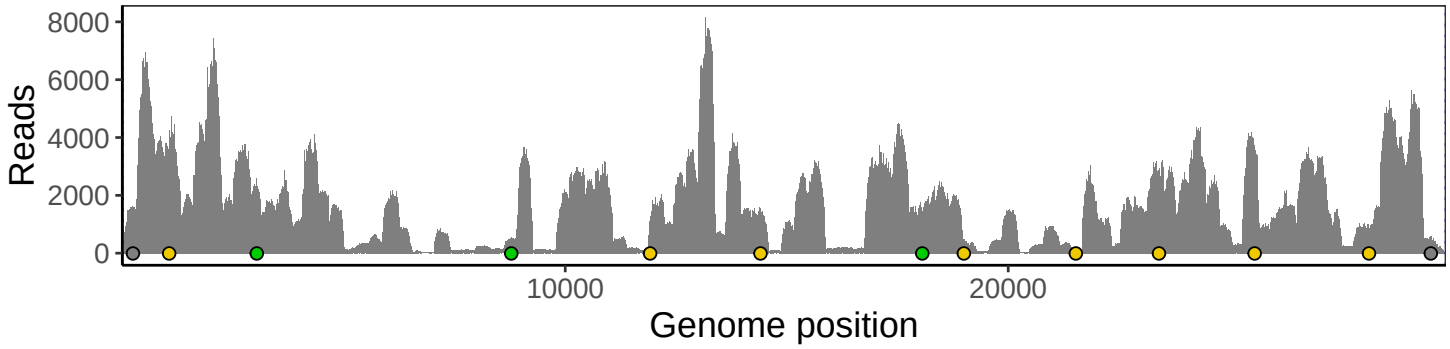



The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

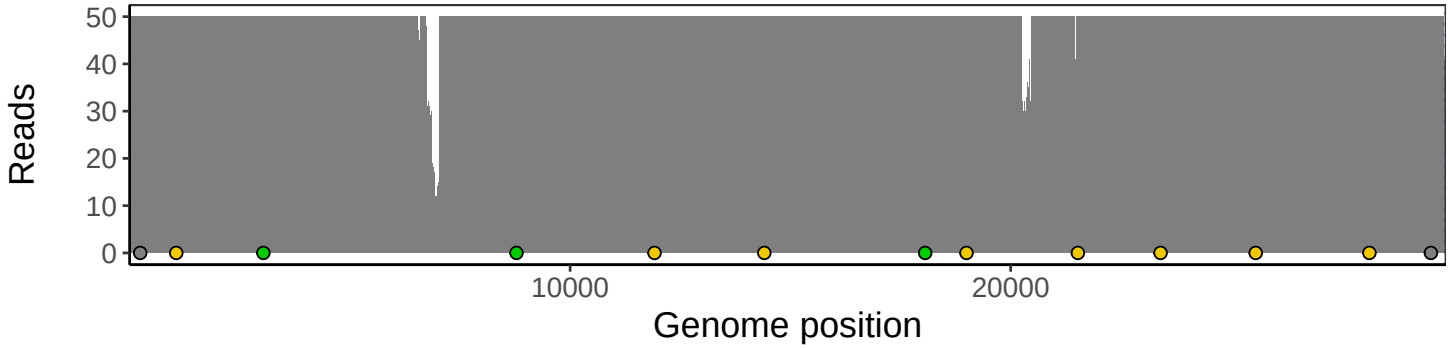


**VSP0182 | 2020-04-20 | OP | 3 | composite result**

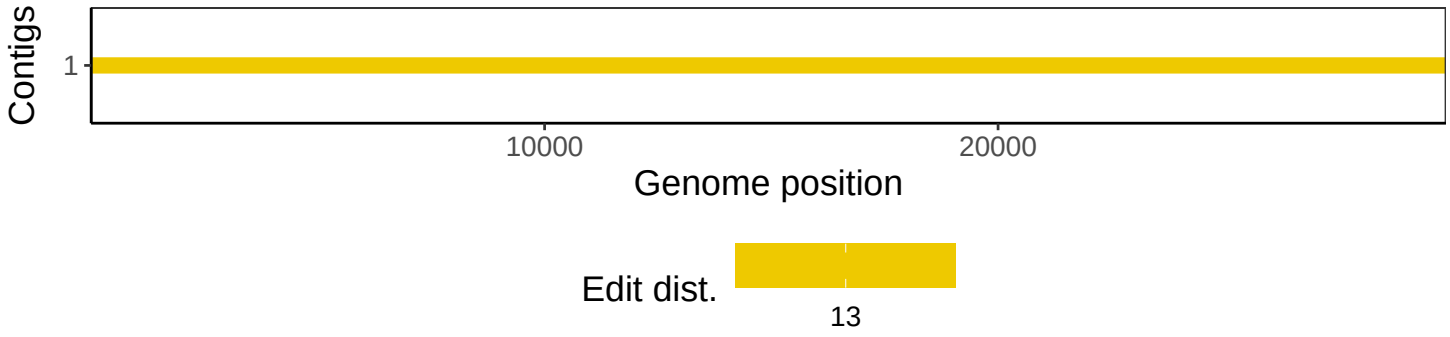
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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

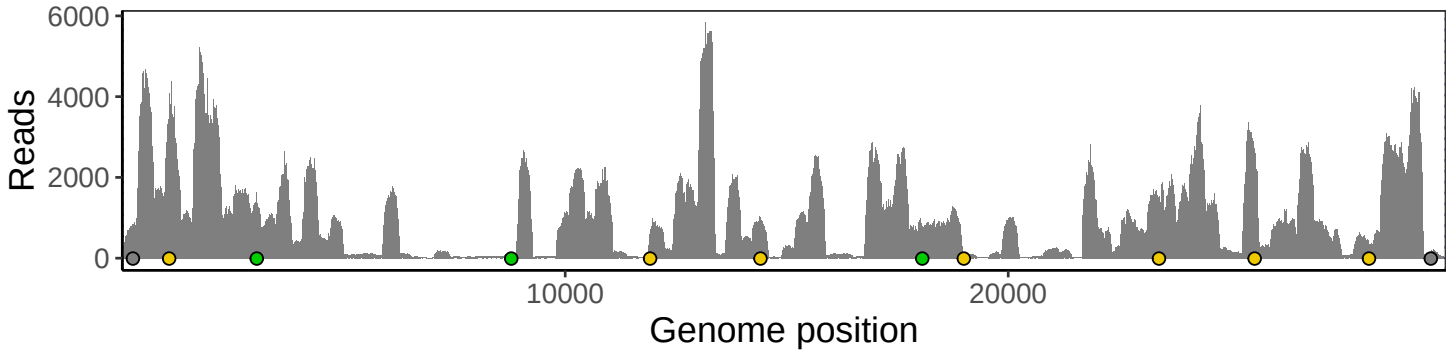



The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

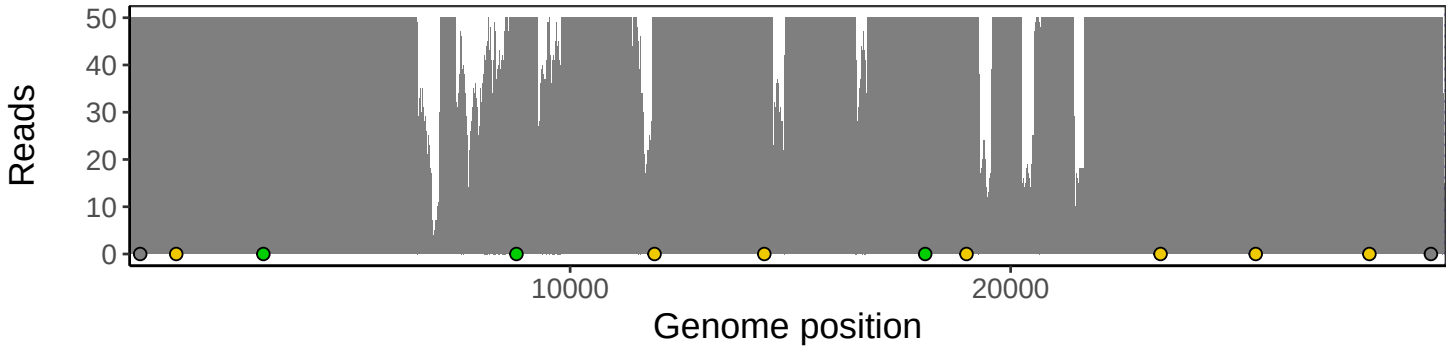


**VSP0180-1m | 2020-04-17 | NP | 1 | genomes | single experiment**

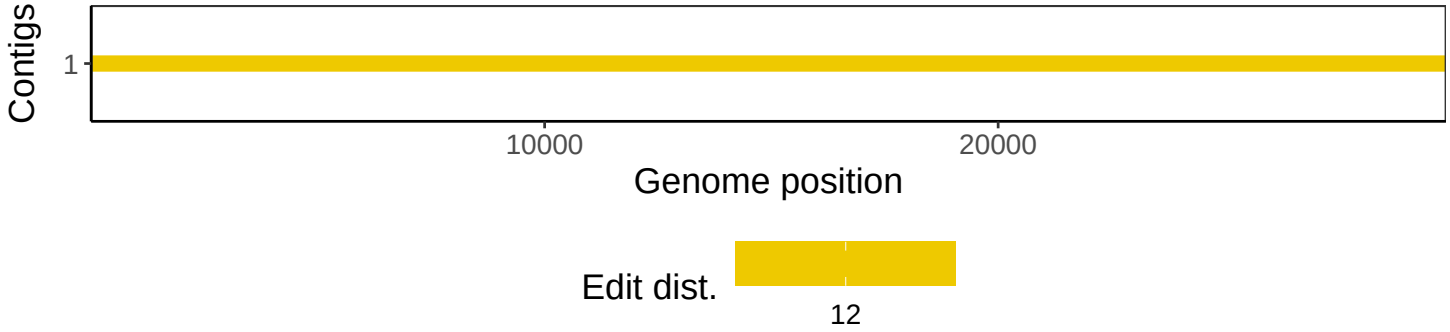
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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

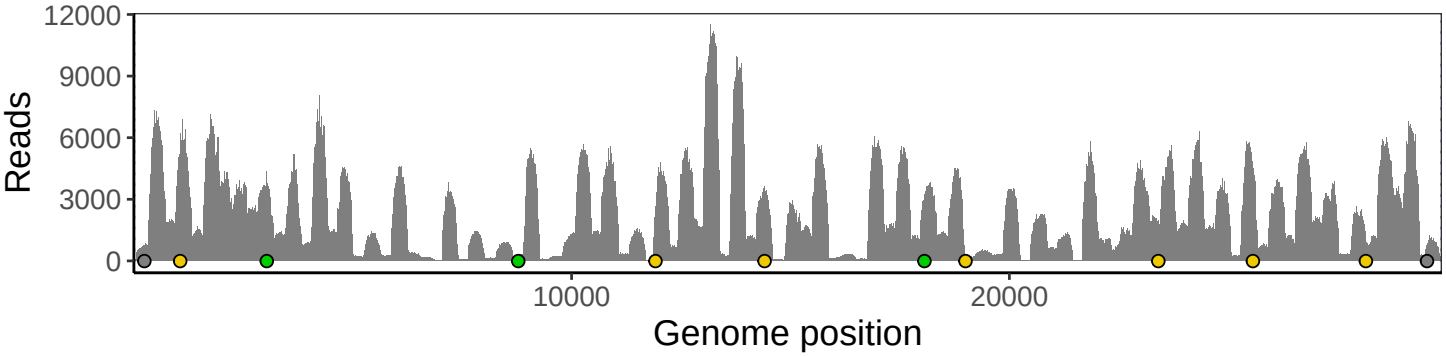



The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

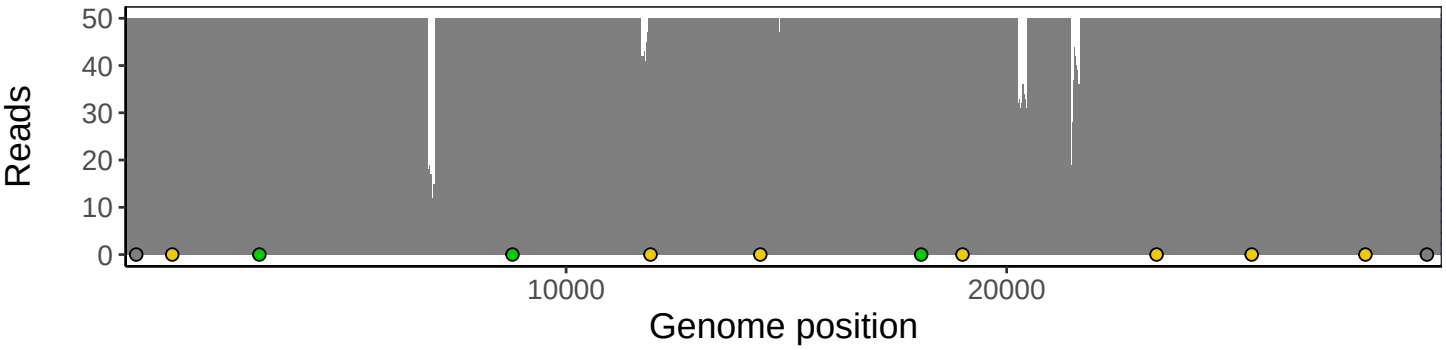


**VSP0181-1m | 2020-04-17 | OP | 2 | genomes | single experiment**

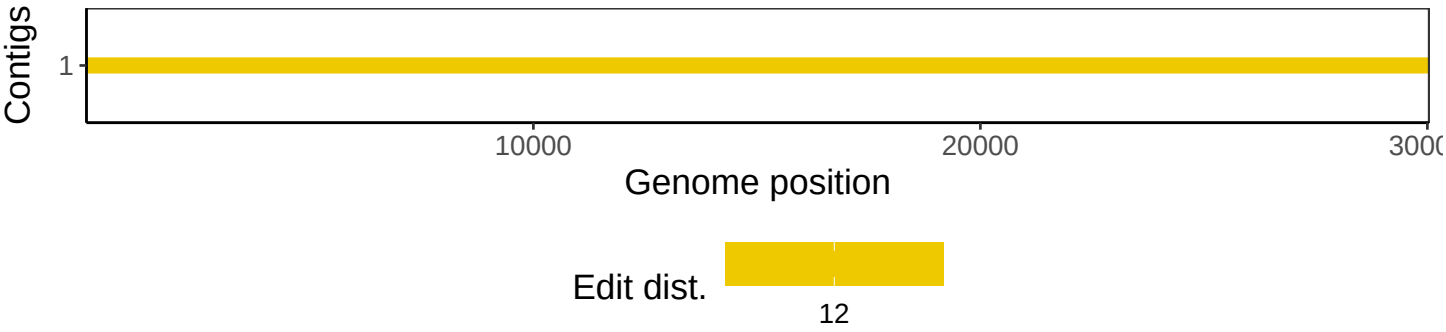
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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

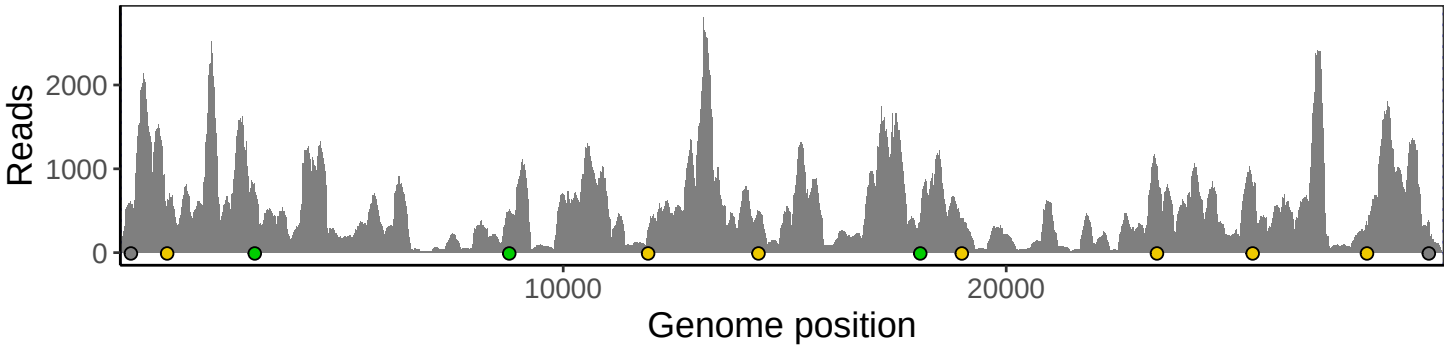



The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

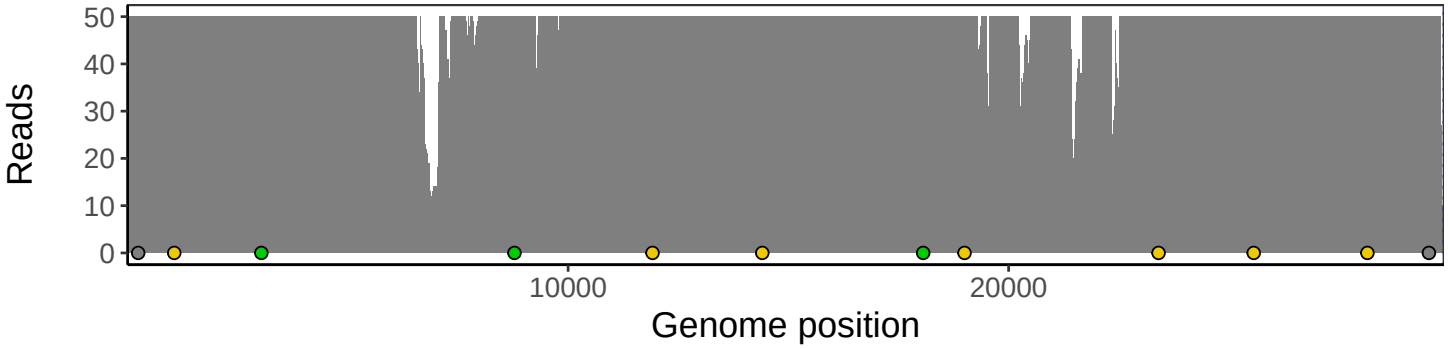


**VSP0181-2 | 2020-04-17 | OP | 2 | 1.51e+11 genomes | single experiment**

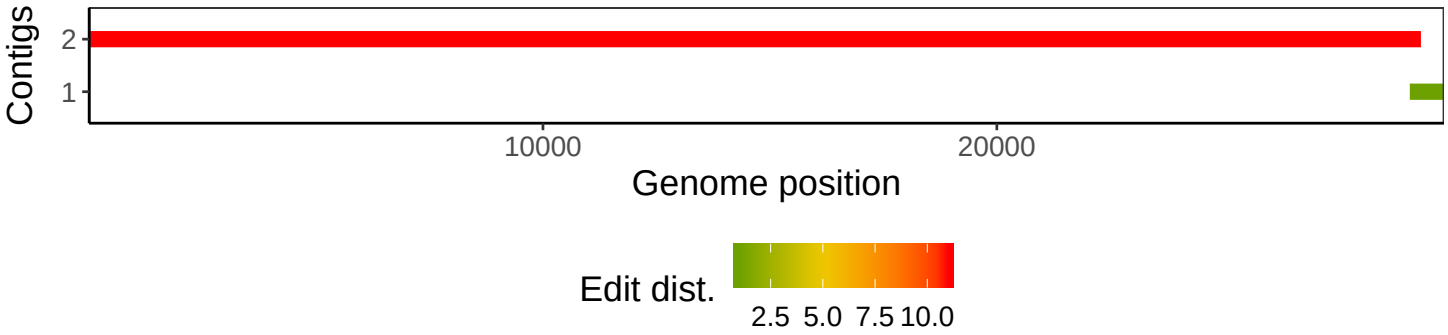
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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

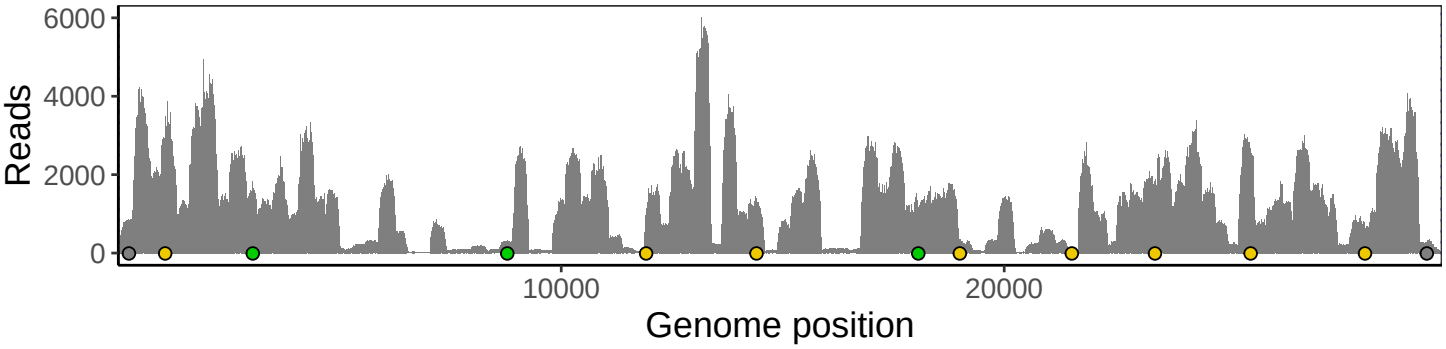



The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

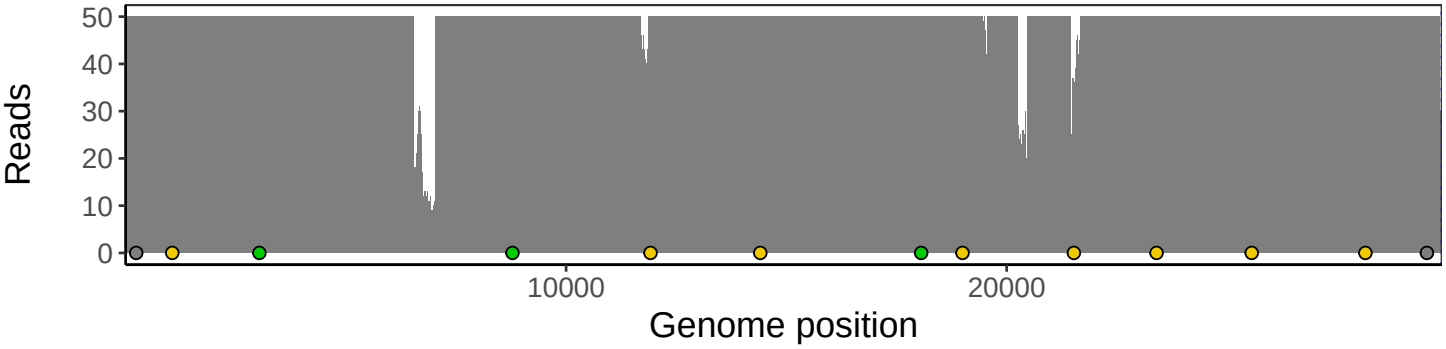


**VSP0182-1m | 2020-04-20 | OP | 3 | genomes | single experiment**

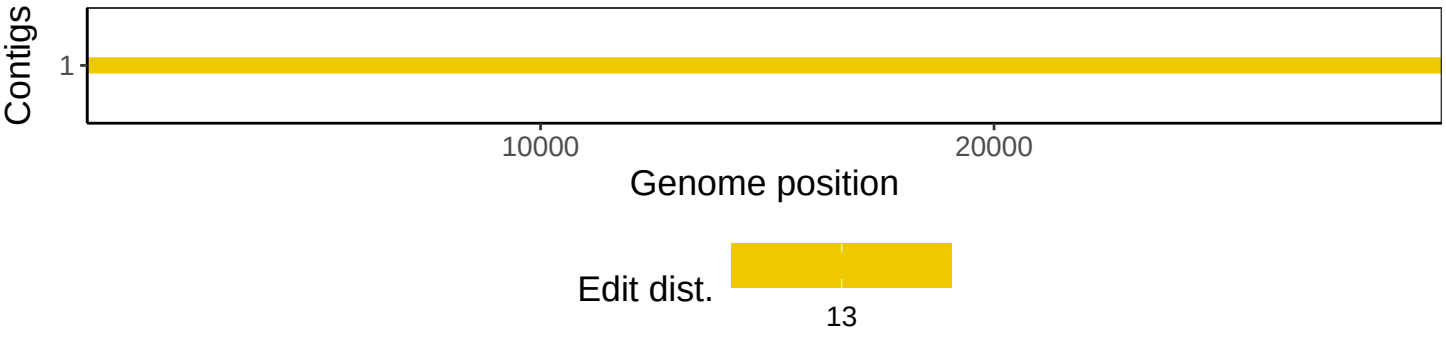
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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

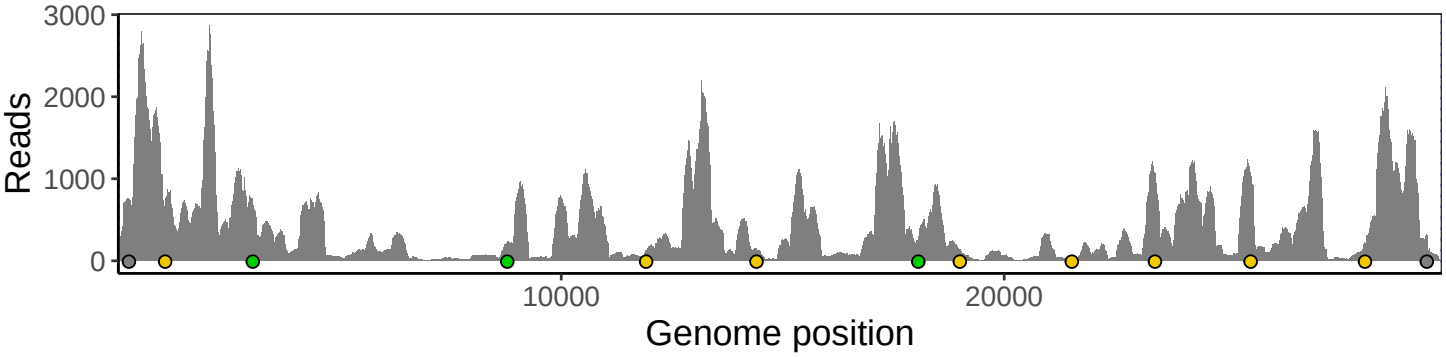



The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

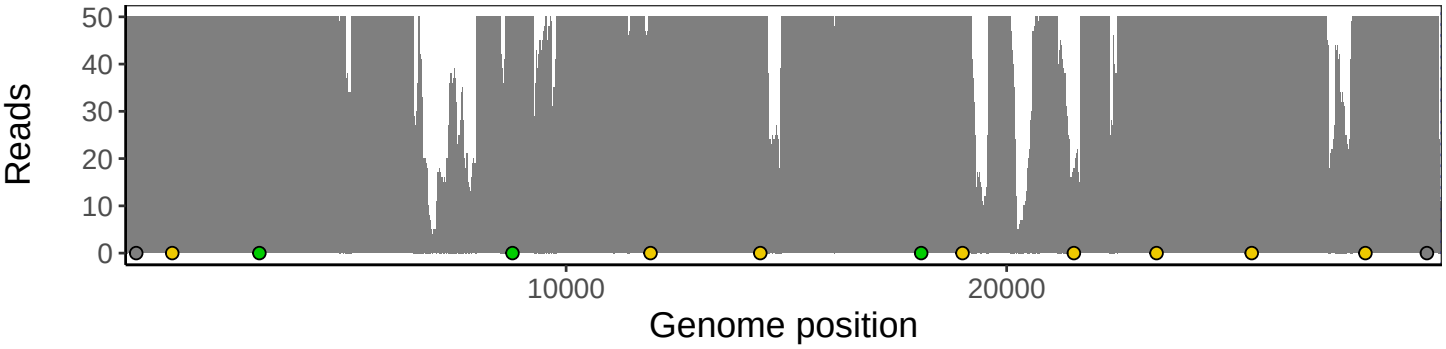


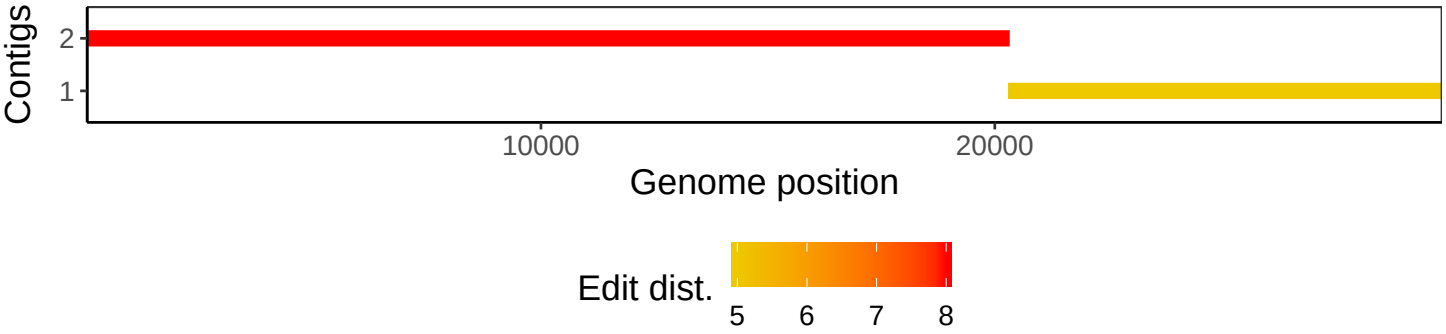
**VSP0182-2 | 2020-04-20 | OP | 3 | 1.325e+11 genomes | single experiment**

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.