# COVID-19 subject 239

*2021-01-08*

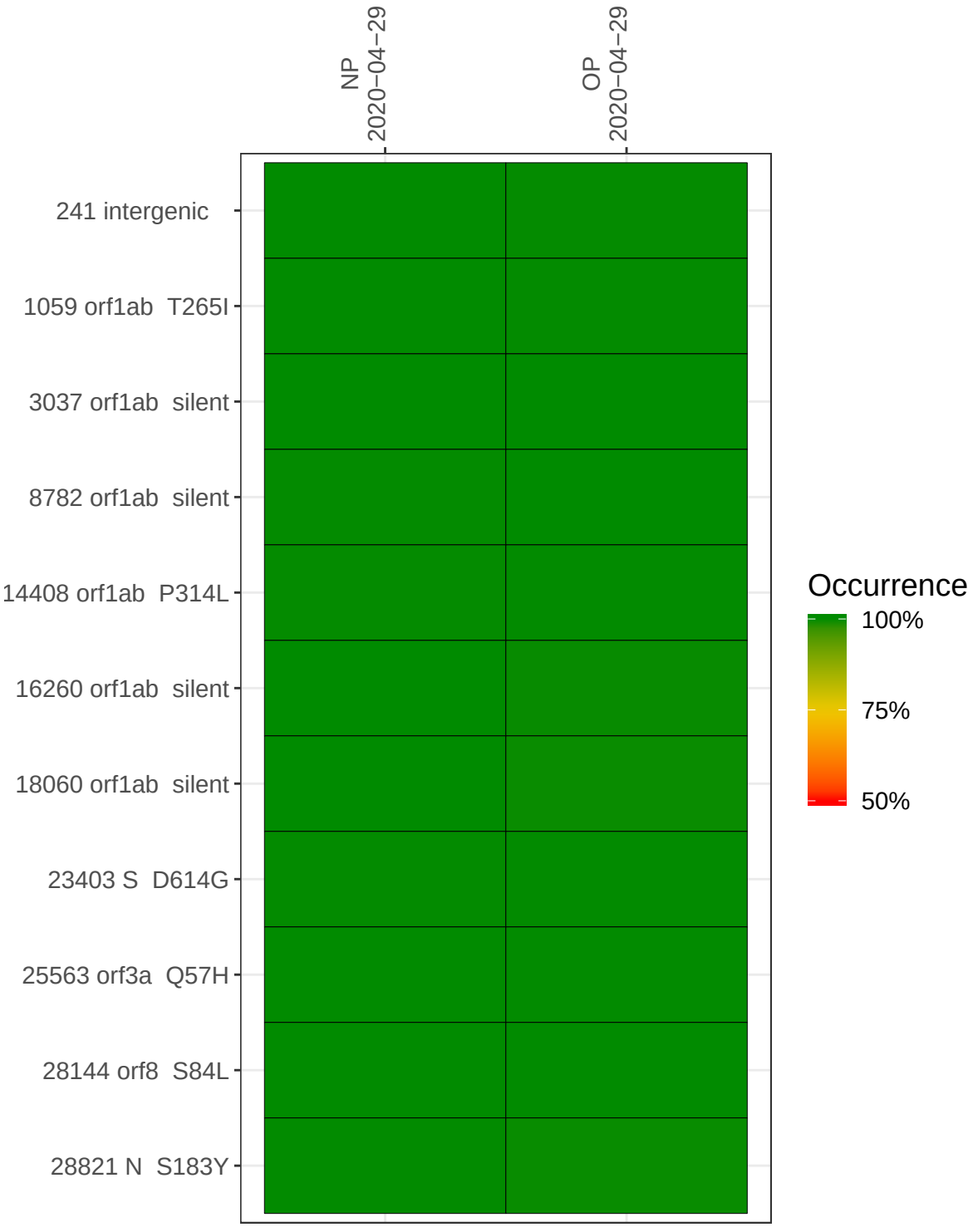
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

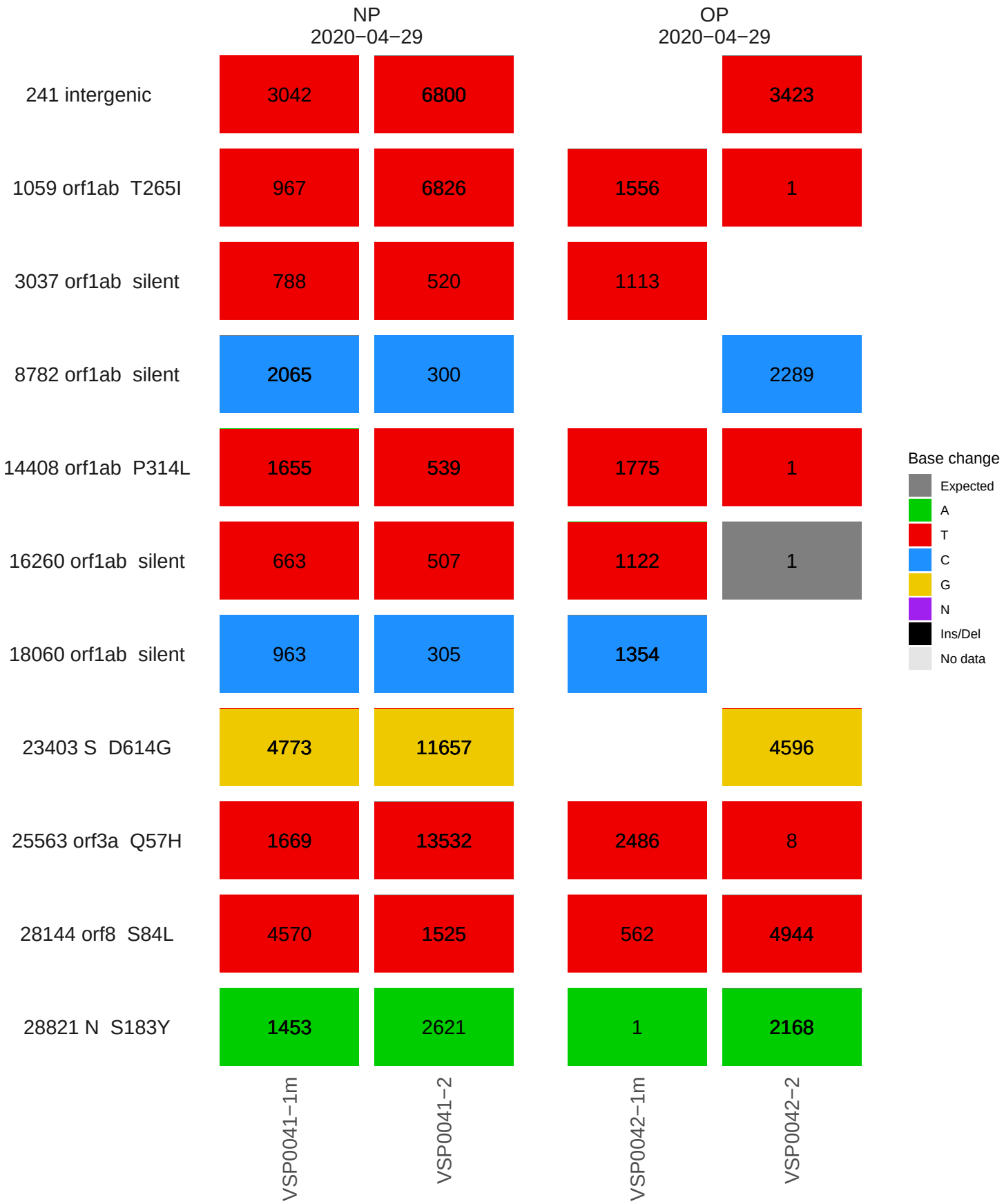
Table 1. Sample summary.

| Experiment | Type | Input genomes | Sample type | Sample date | Largest contig (KD) | Reference read coverage | Reference read coverage (>= 5 reads) |
|---|---|---|---|---|---|---|---|
| VSP0041 | composite | NA | NP | 2020-04-29 | 29.84 | 100.0% | 99.8% |
| VSP0042 | composite | NA | OP | 2020-04-29 | 27.48 | 100.0% | 99.8% |
| VSP0041-1m | single experiment | NA | NP | 2020-04-29 | 29.83 | 100.0% | 99.8% |
| VSP0041-2 | single experiment | NA | NP | 2020-04-29 | 29.84 | 100.0% | 99.5% |
| VSP0042-1m | single experiment | NA | OP | 2020-04-29 | 1.12 | 100.0% | 63.3% |
| VSP0042-2 | single experiment | 6490 | OP | 2020-04-29 | 1.18 | 100.0% | 64.7% |

**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.

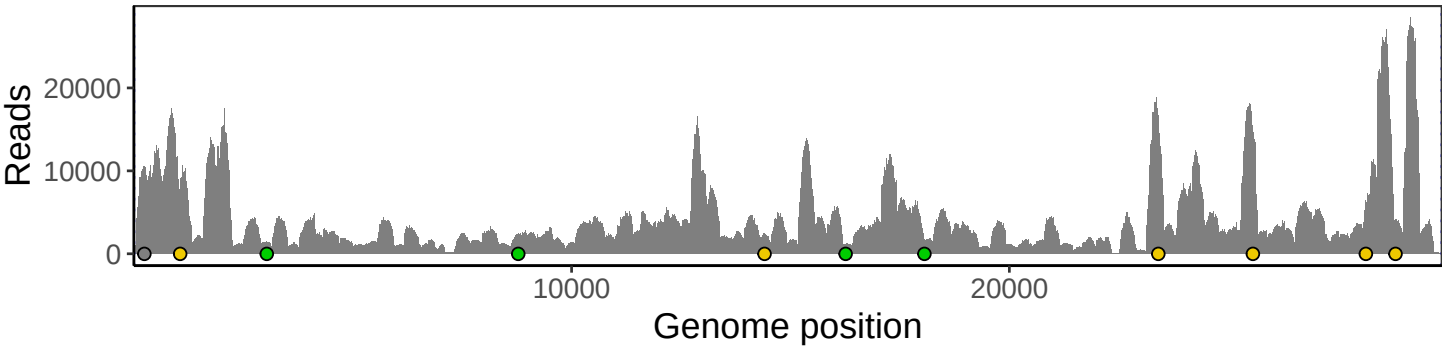



NP
2020−04−29
OP
2020−04−29
241 intergenic
1059 orf1ab T265I
3037 orf1ab silent
8782 orf1ab silent
14408 orf1ab P314L
16260 orf1ab silent
18060 orf1ab silent
23403 S D614G
25563 orf3a Q57H
28144 orf8 S84L
28821 N S183Y
3042
6800
3423
967
6826
1556
1
788
520
1113
2065
300
2289
1655
539
1775
1
663
507
1122
1
963
305
1354
4773
11657
4596
1669
13532
2486
8
4570
1525
562
4944
1453
2621
1
2168
VSP0041−1m
VSP0041−2
VSP0042−1m
VSP0042−2
Base change
Expected
A
T
C
G
N
Ins/Del
No data

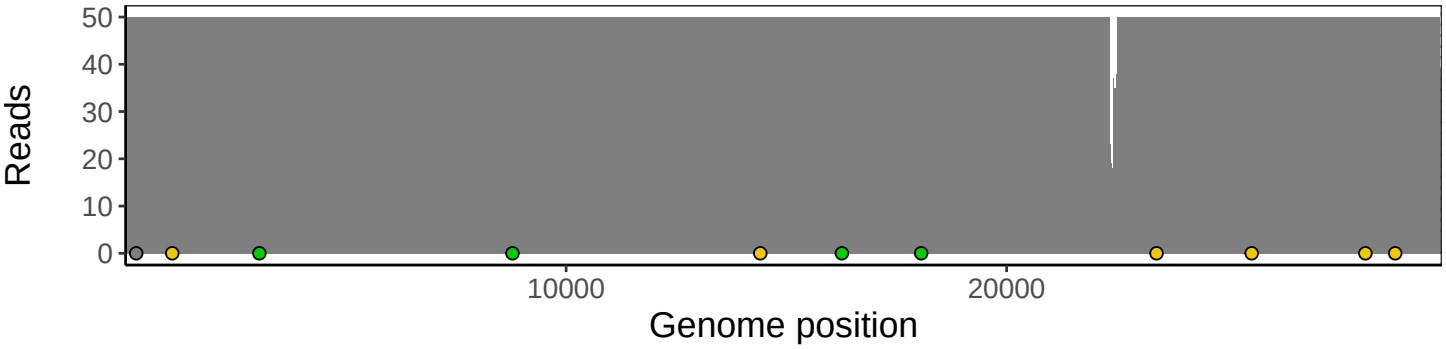
## Analyses of individual experiments and composite results.

### VSP0041 | 2020-04-29 | NP | 239n-tri | composite result

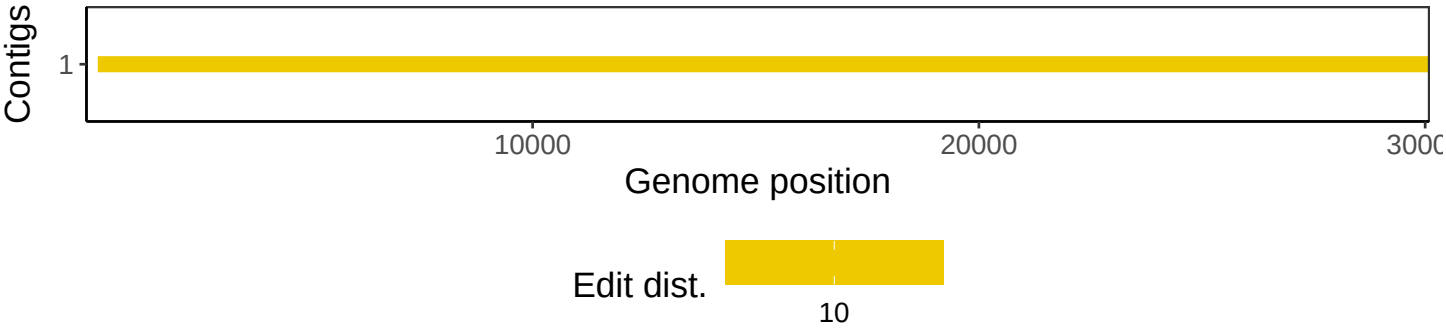
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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

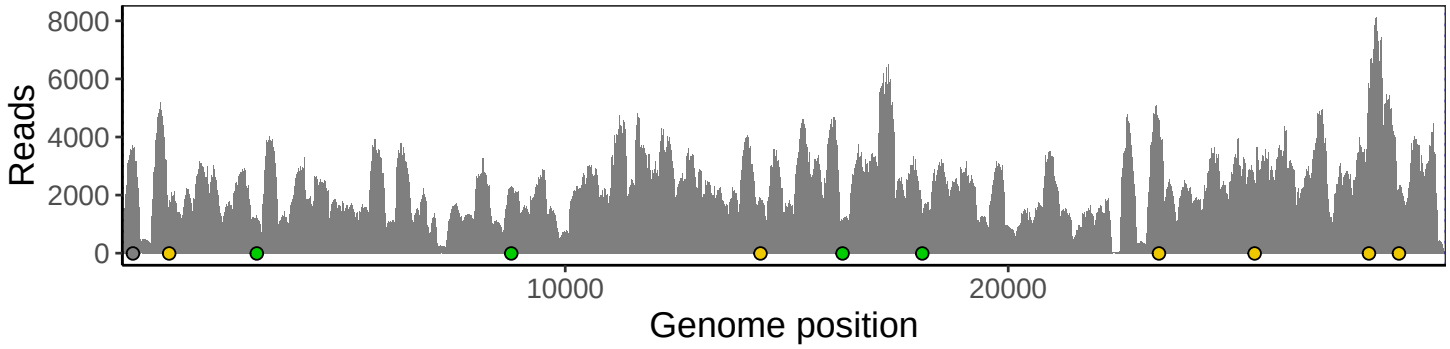



The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

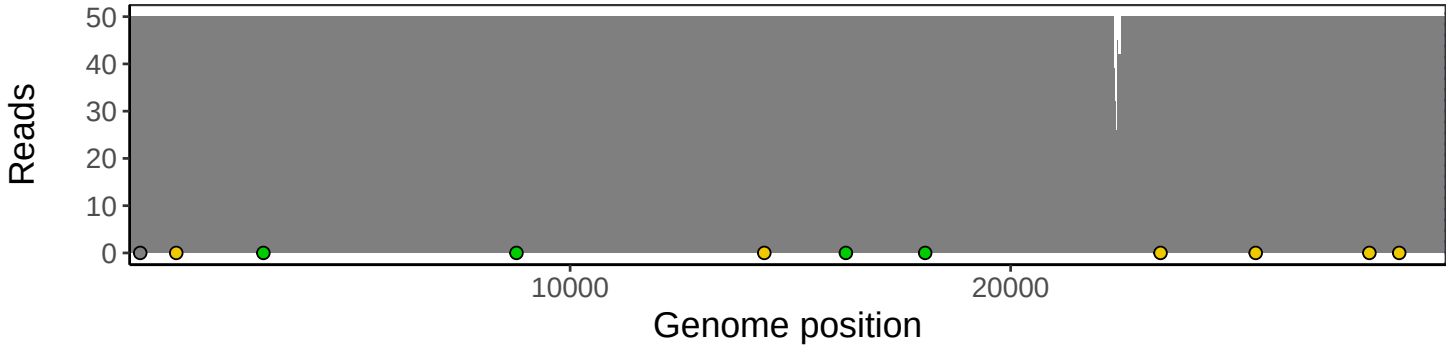


**VSP0042 | 2020-04-29 | OP | 239o-tri | composite result**

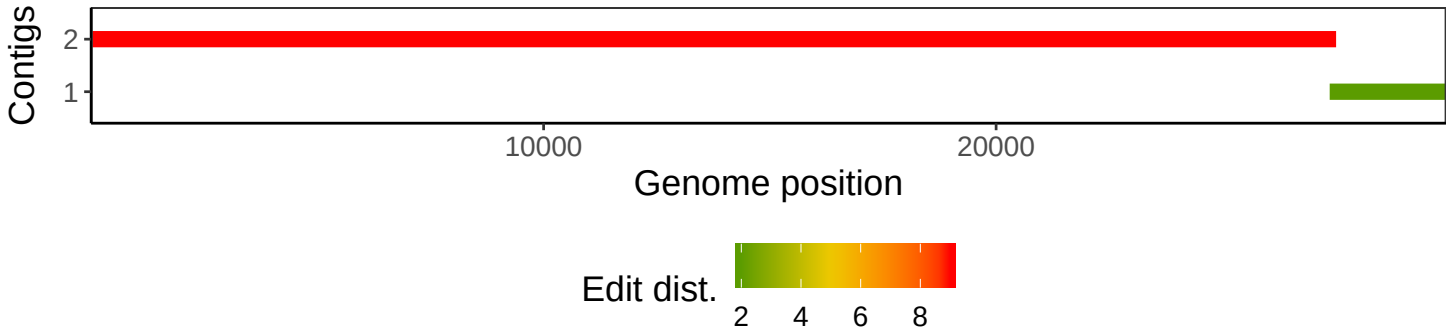
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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

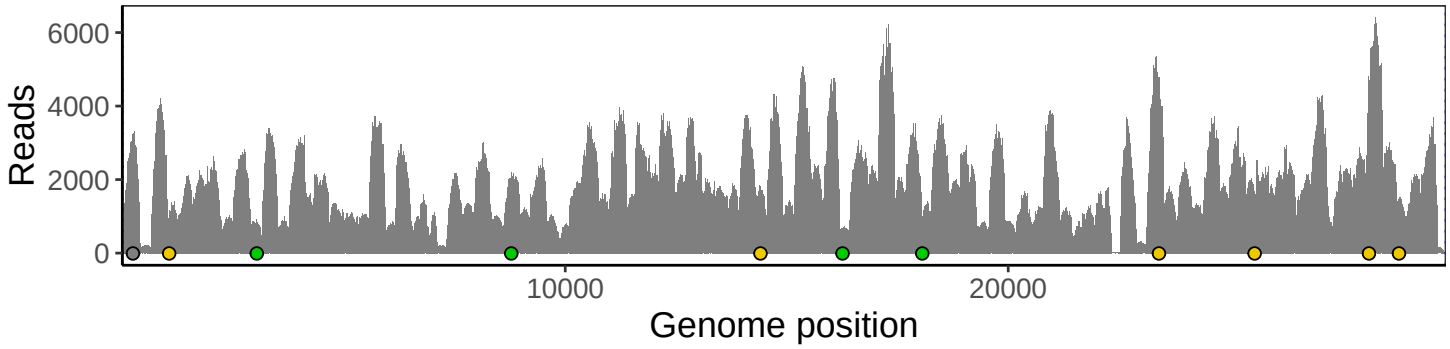



The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

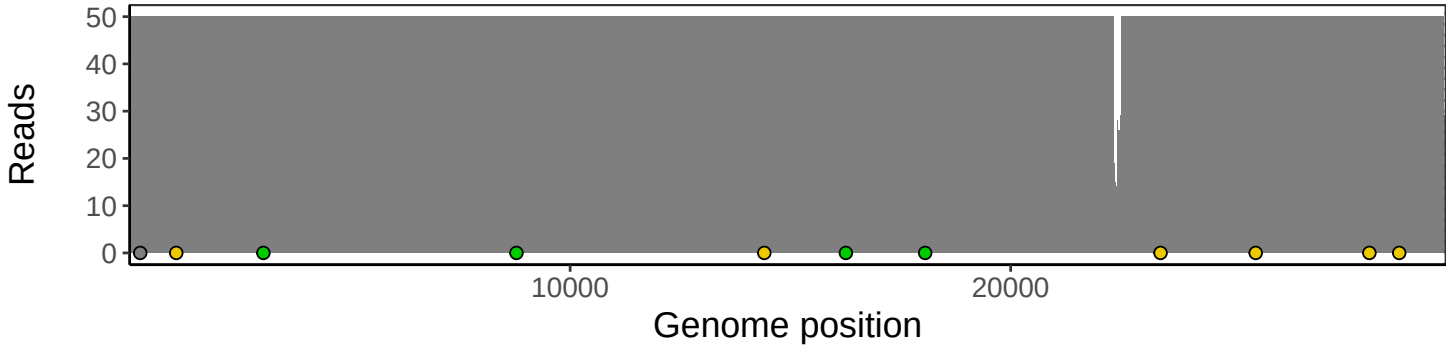


**VSP0041-1m | 2020-04-29 | NP | 239n-tri | genomes | single experiment**

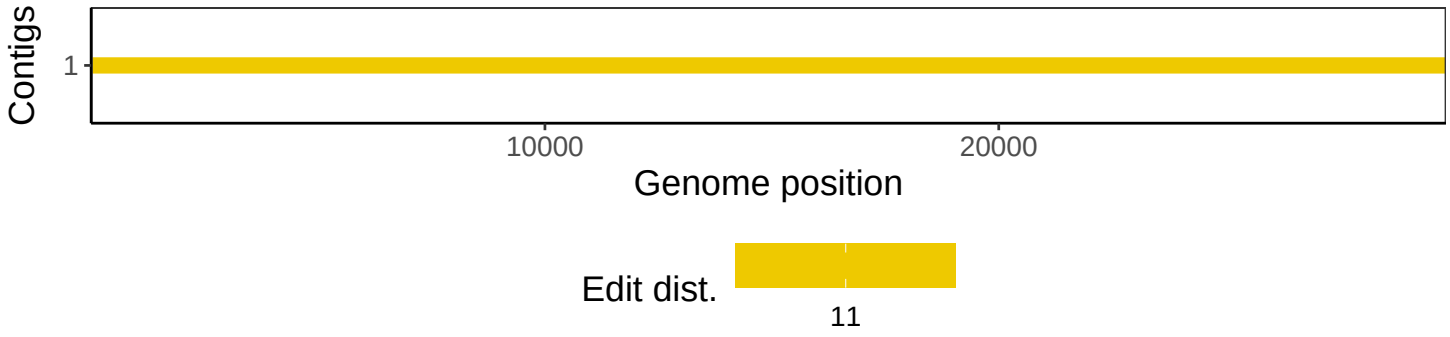
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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

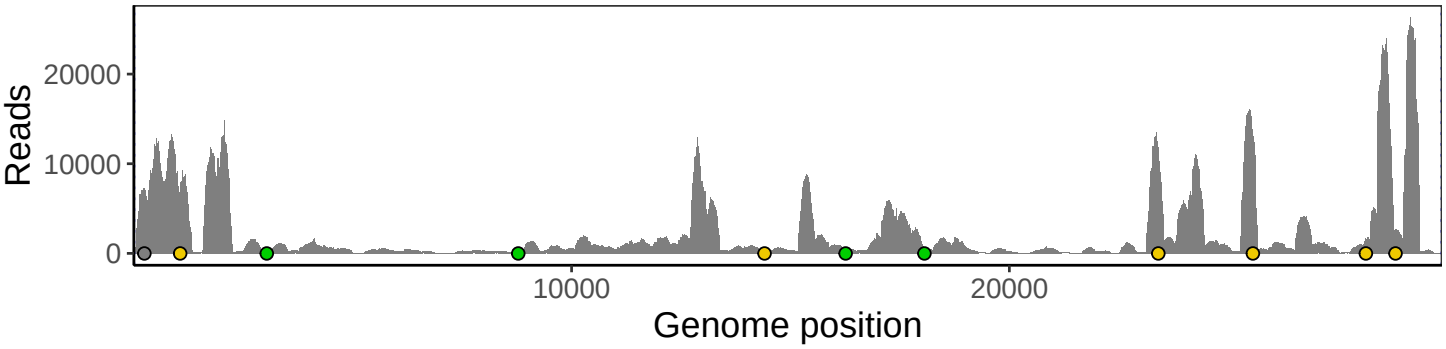



The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

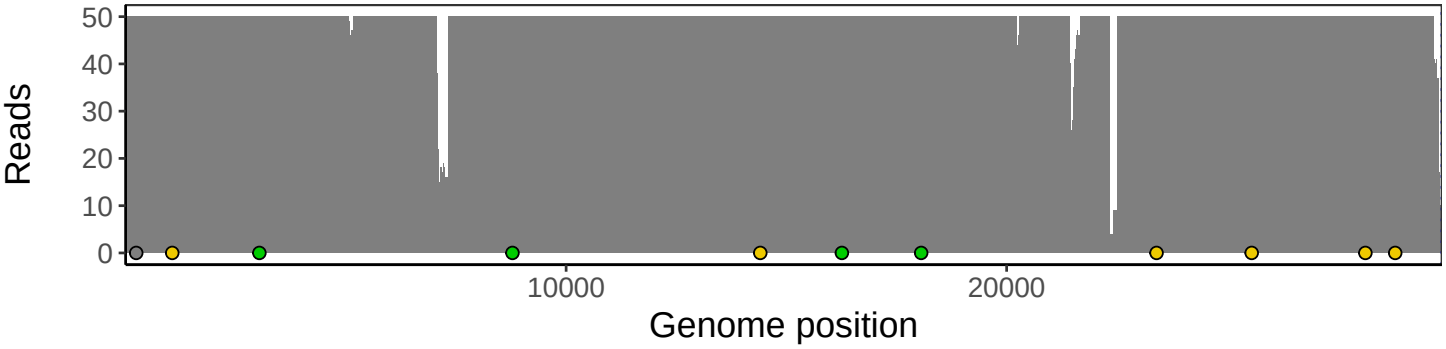


**VSP0041-2 | 2020-04-29 | NP | 239n-tri | genomes | single experiment**

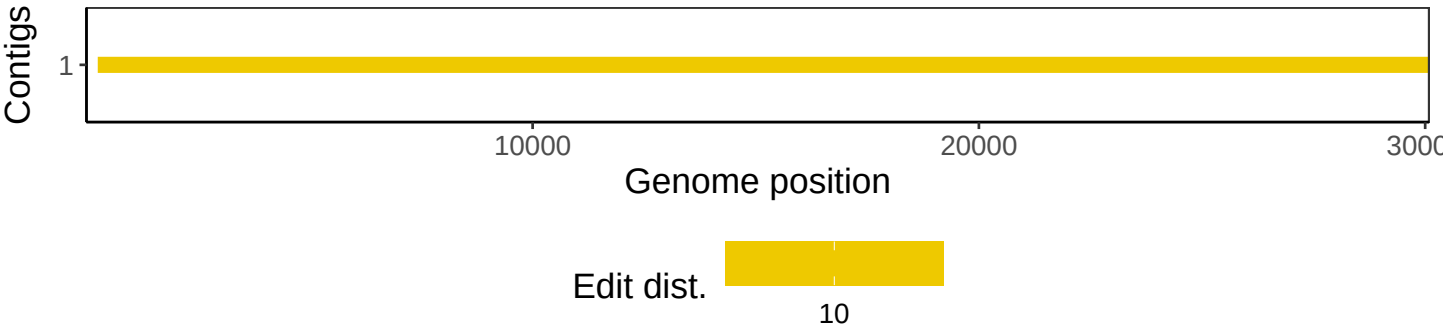
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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

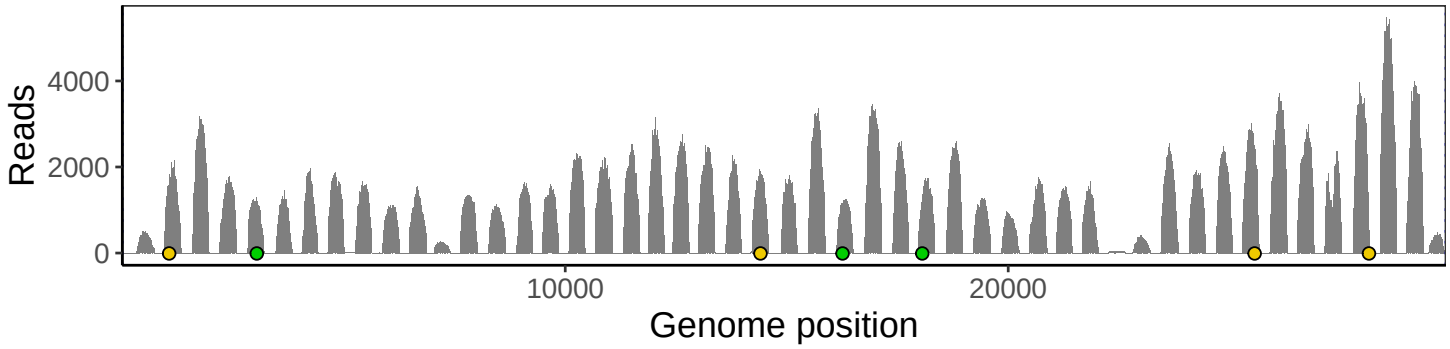



The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

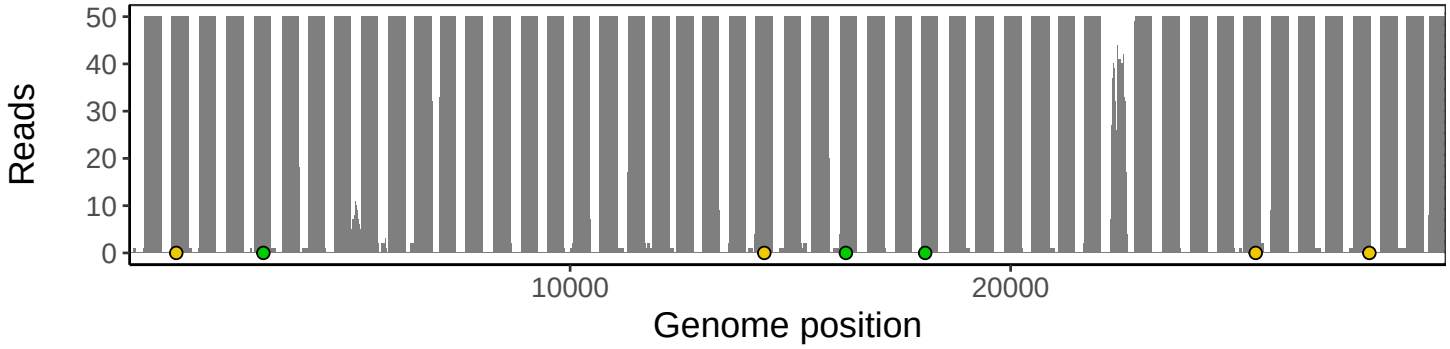


**VSP0042-1m | 2020-04-29 | OP | 239o-tri | genomes | single experiment**

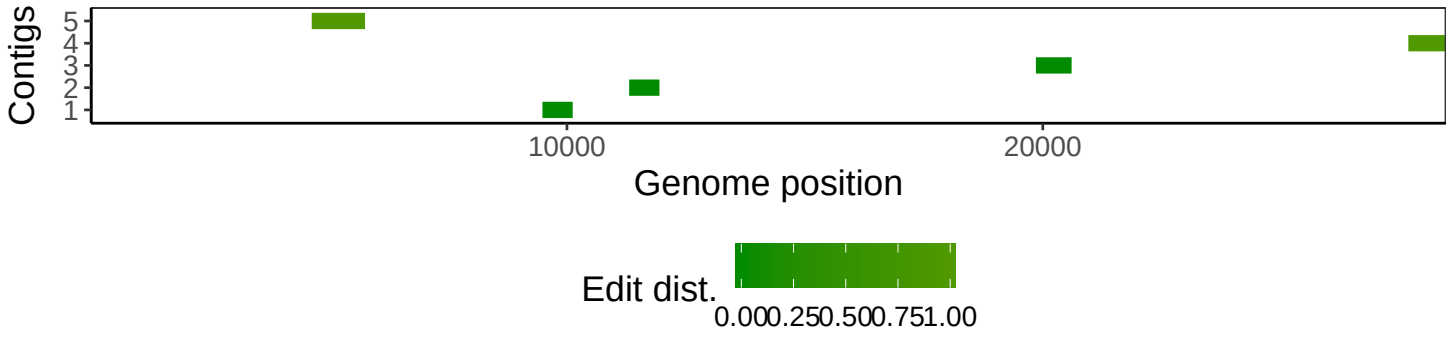
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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

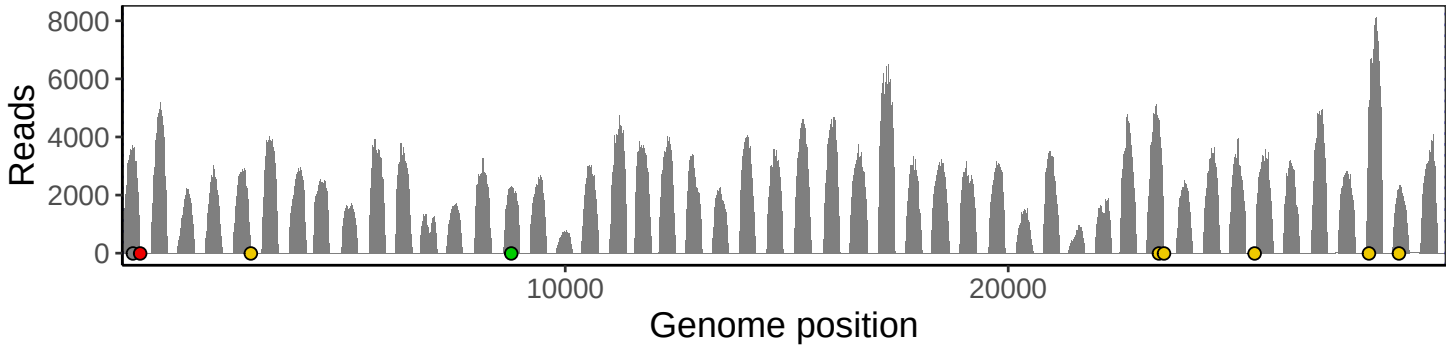



The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

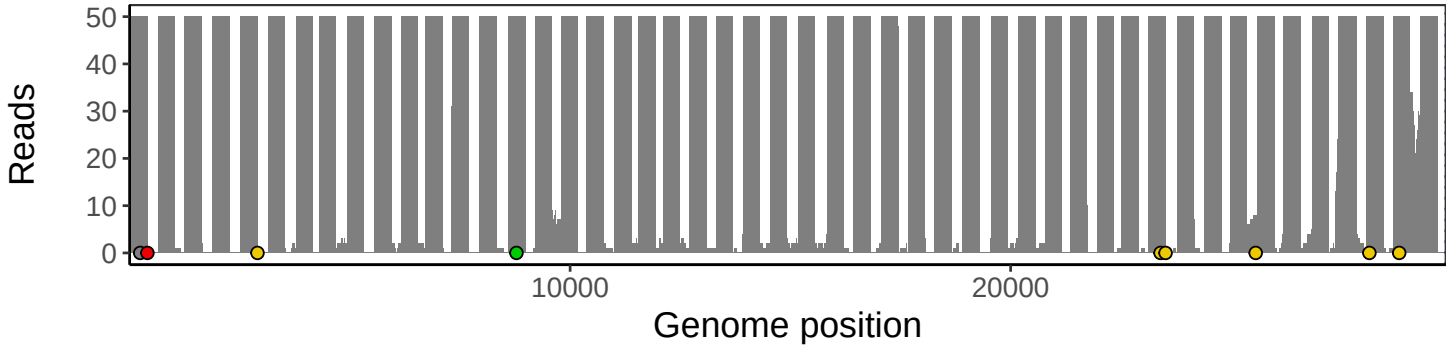


**VSP0042-2 | 2020-04-29 | OP | 239o-tri | 6490 genomes | single experiment**

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.