# COVID-19 subject 434

*2021-03-01*

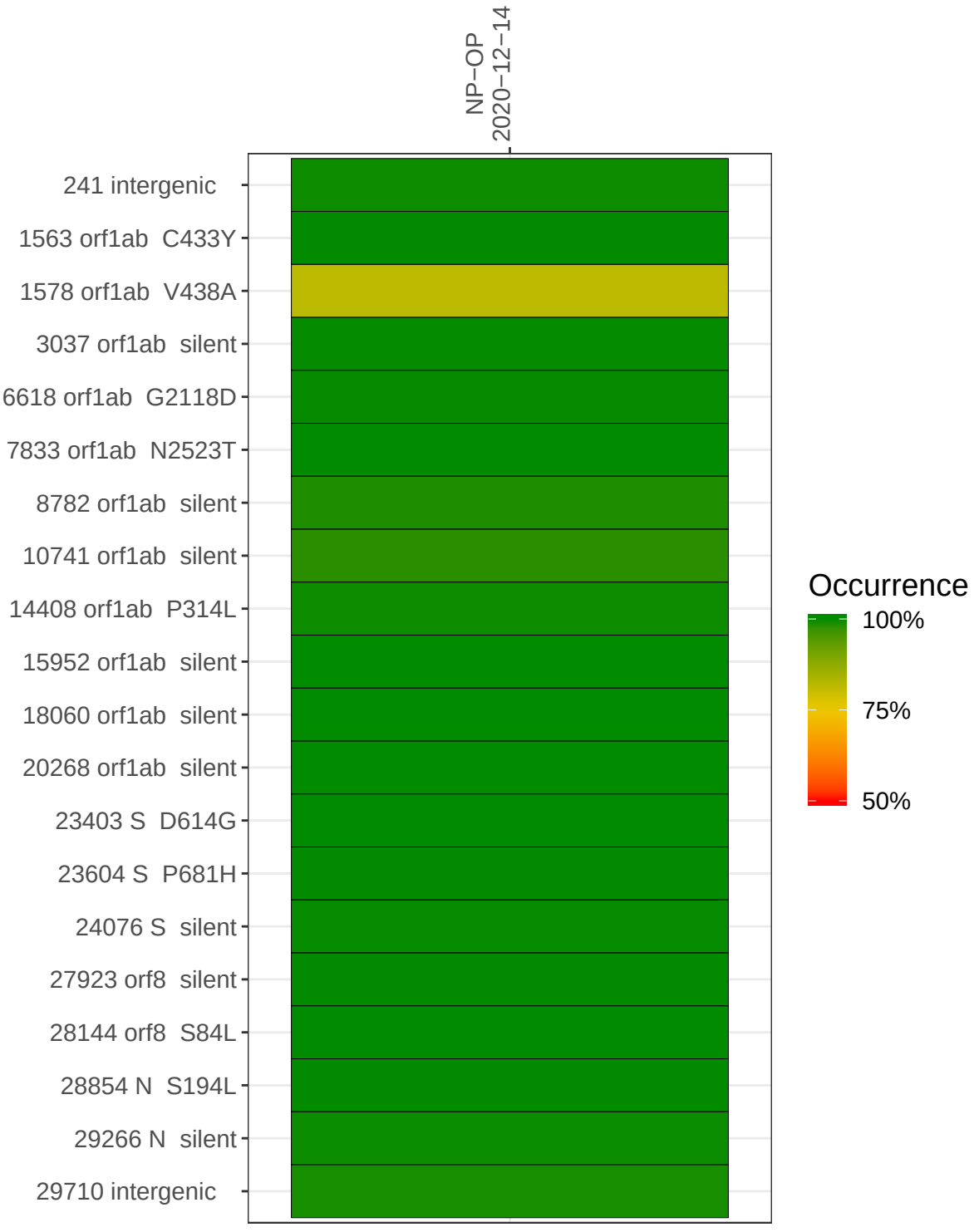
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

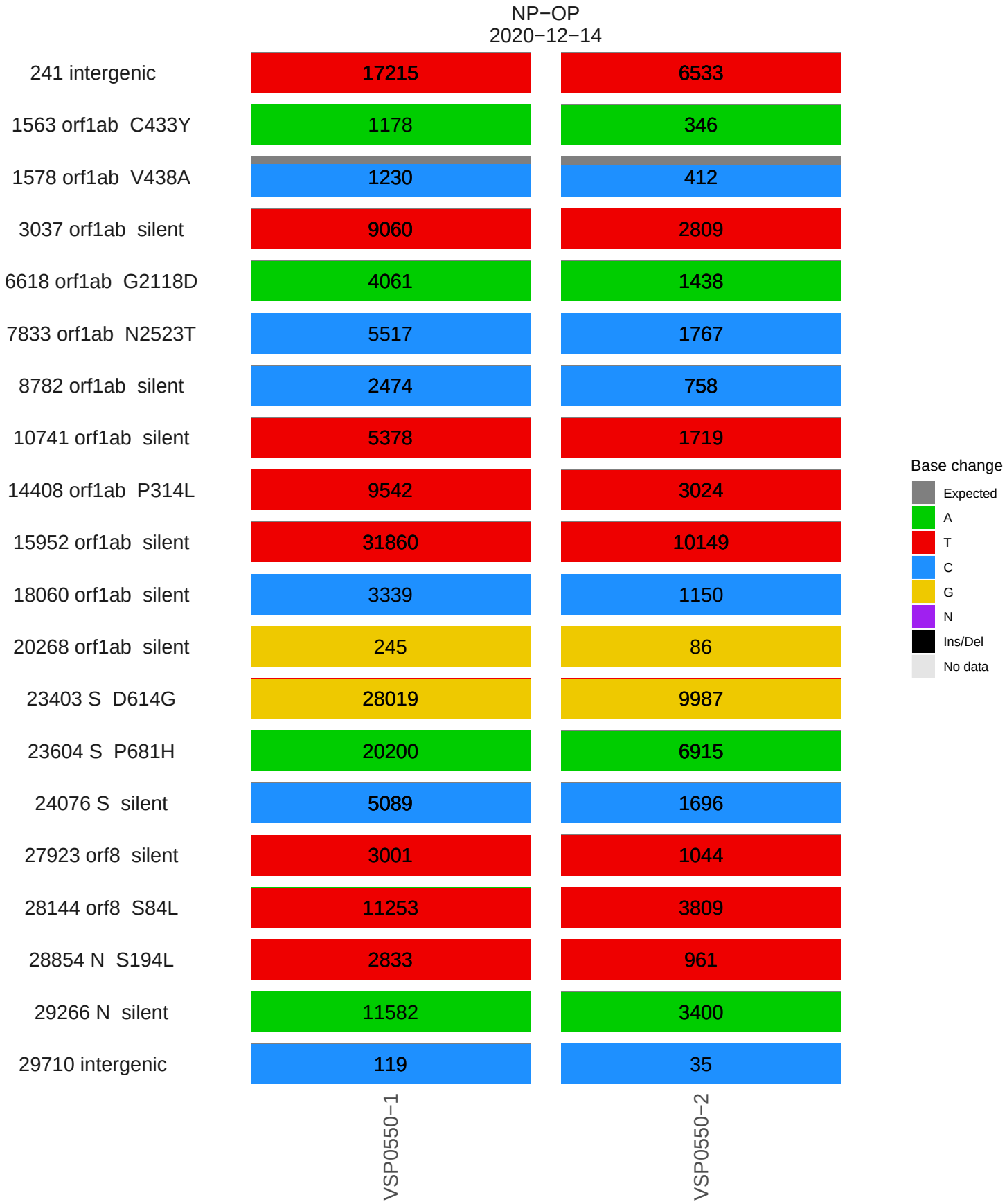
Table 1. Sample summary.

| Experiment | Type | Genomes | Sample type | Sample date | Largest contig (KD) | Lineage | Reference read coverage | Reference read coverage (>= 5 reads) |
|---|---|---|---|---|---|---|---|---|
| VSP0550 | composite | NA | NP-OP | 2020-12-14 | 21.37 | B.1.243 | 99.9% | 99.7% |
| VSP0550-1 | single experiment | NA | NP-OP | 2020-12-14 | 29.07 | B.1.243 | 99.7% | 99.7% |
| VSP0550-2 | single experiment | NA | NP-OP | 2020-12-14 | 29.91 | B.1.243 | 99.9% | 99.6% |

**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.

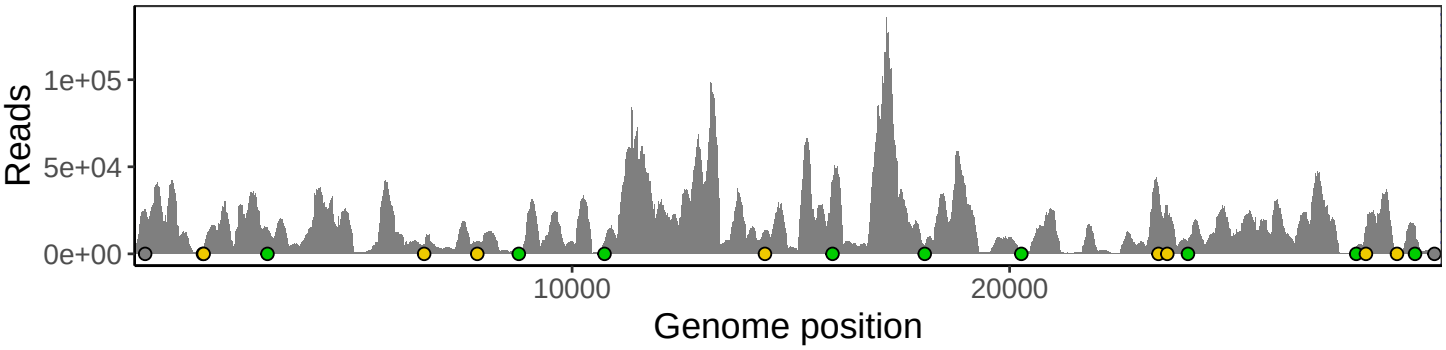



NP−OP
2020−12−14
241 intergenic
1563 orf1ab C433Y
1578 orf1ab V438A
3037 orf1ab silent
6618 orf1ab G2118D
7833 orf1ab N2523T
8782 orf1ab silent
10741 orf1ab silent
14408 orf1ab P314L
15952 orf1ab silent
18060 orf1ab silent
20268 orf1ab silent
23403 S D614G
23604 S P681H
24076 S silent
27923 orf8 silent
28144 orf8 S84L
28854 N S194L
29266 N silent
29710 intergenic
17215
6533
1178
346
1230
412
9060
2809
4061
1438
5517
1767
2474
758
5378
1719
9542
3024
31860
10149
3339
1150
245
86
28019
9987
20200
6915
5089
1696
3001
1044
11253
3809
2833
961
11582
3400
119
35
VSP0550−1
VSP0550−2
Base change
Expected
A
T
C
G
N
Ins/Del
No data

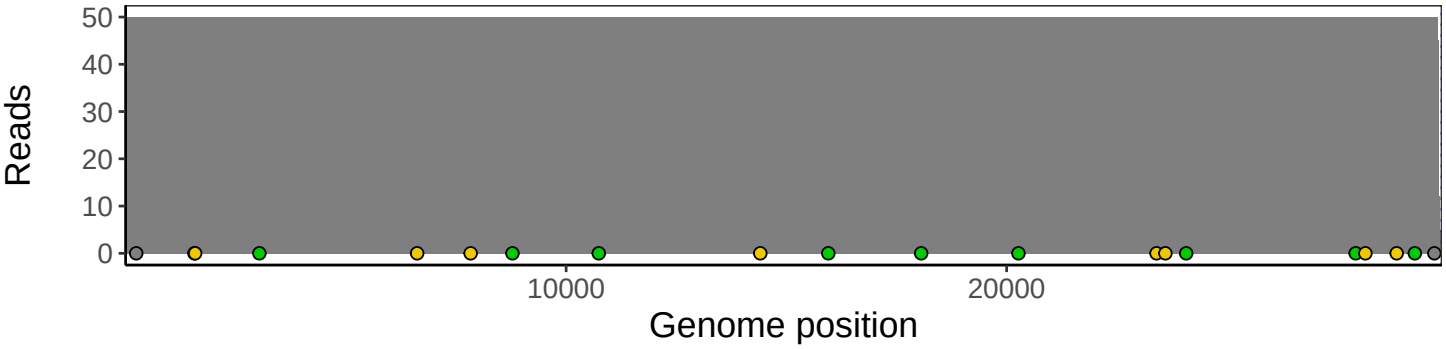
## Analyses of individual experiments and composite results

### VSP0550 | 2020-12-14 | NP-OP | 434no | composite result

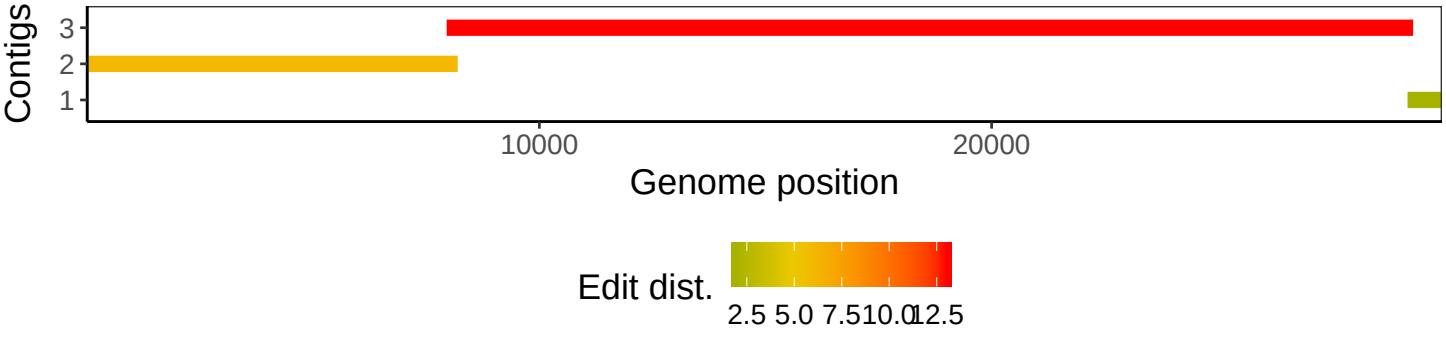
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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

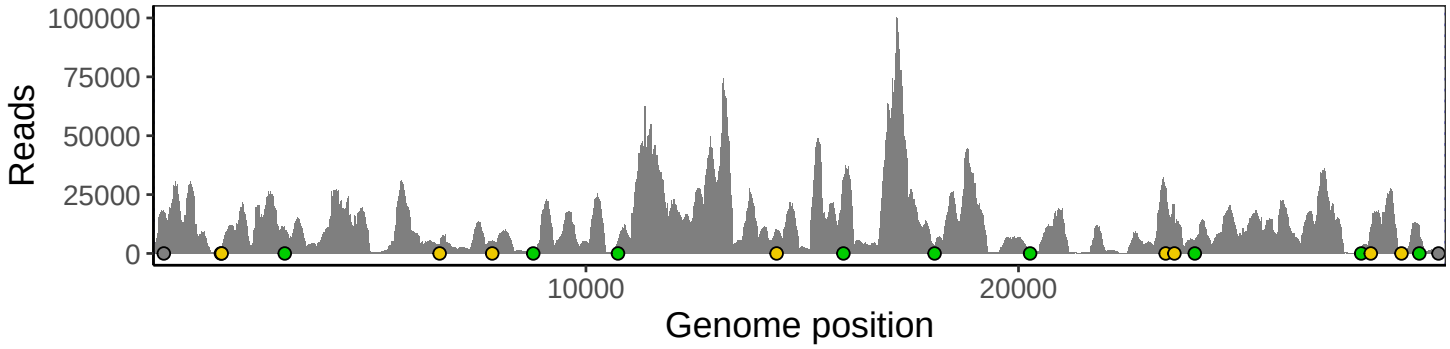



The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

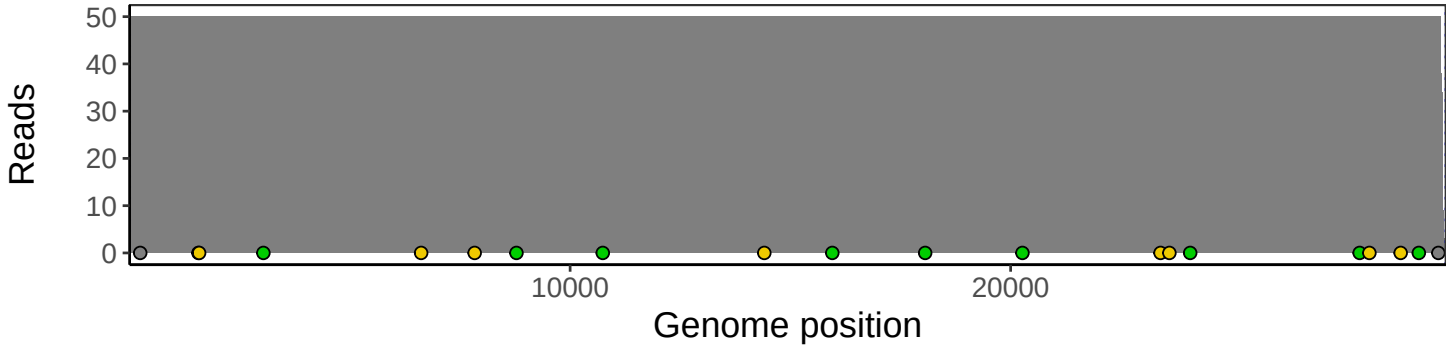


**VSP0550-1 | 2020-12-14 | NP-OP | 434no | genomes | single experiment**

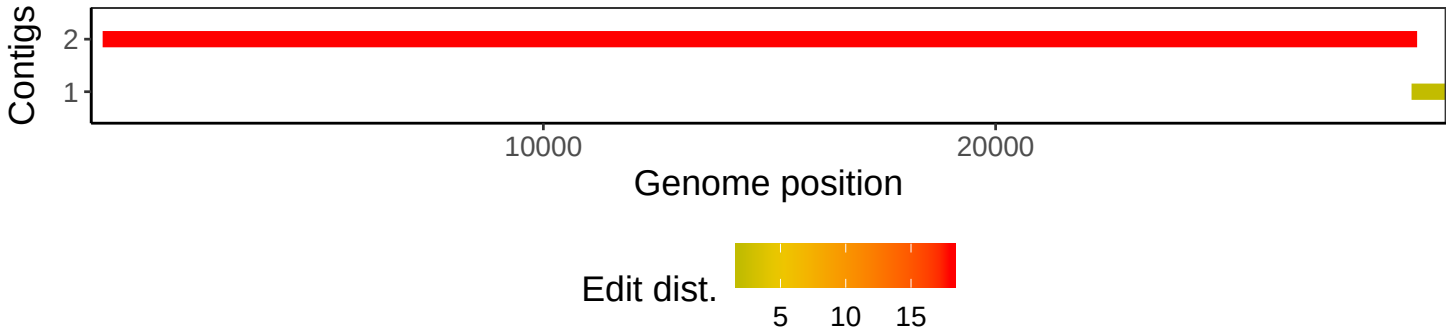
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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

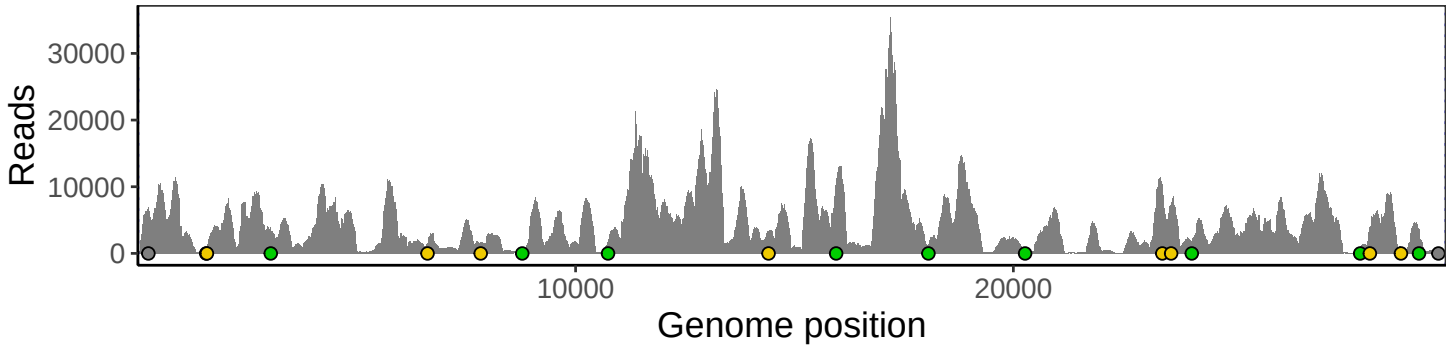



The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

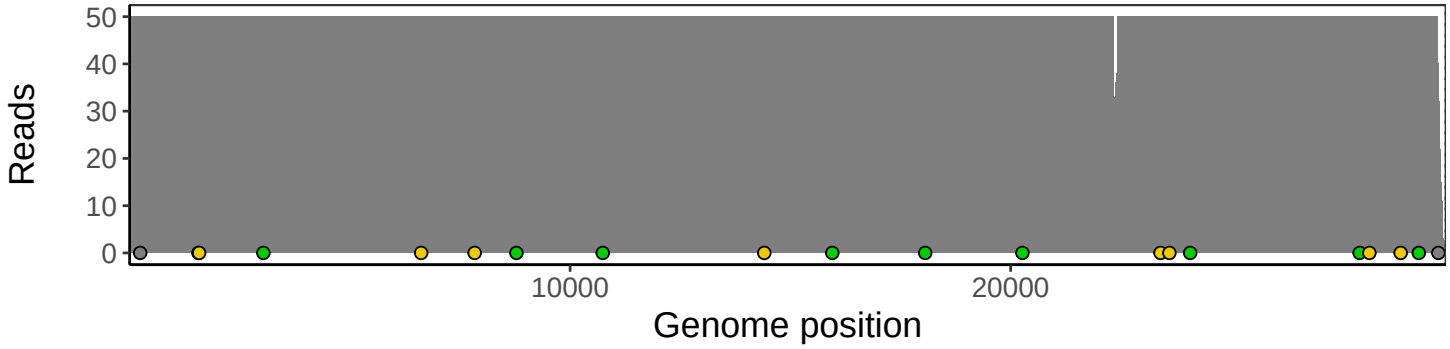


**VSP0550-2 | 2020-12-14 | NP-OP | 434no | genomes | single experiment**

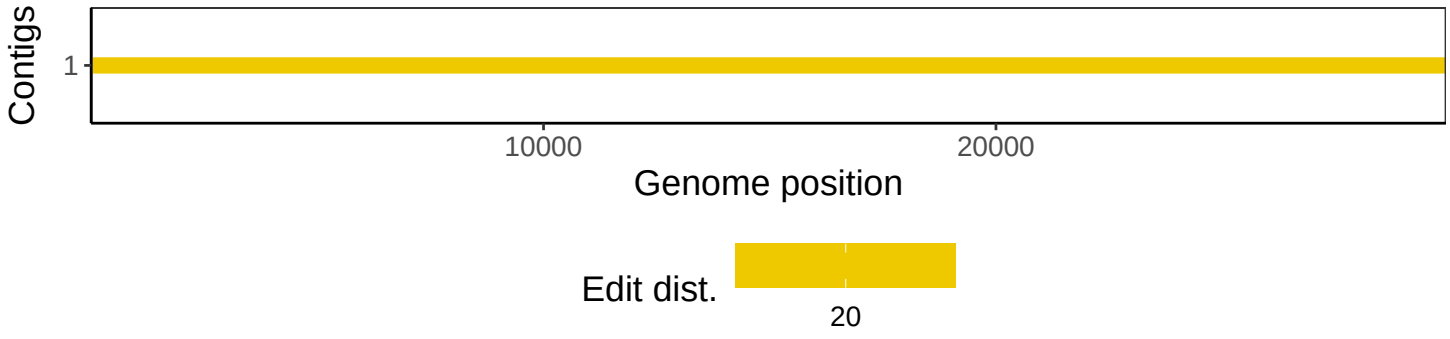
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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 |