# COVID-19 subject MPCluster2-Seq7

*2021-06-23*

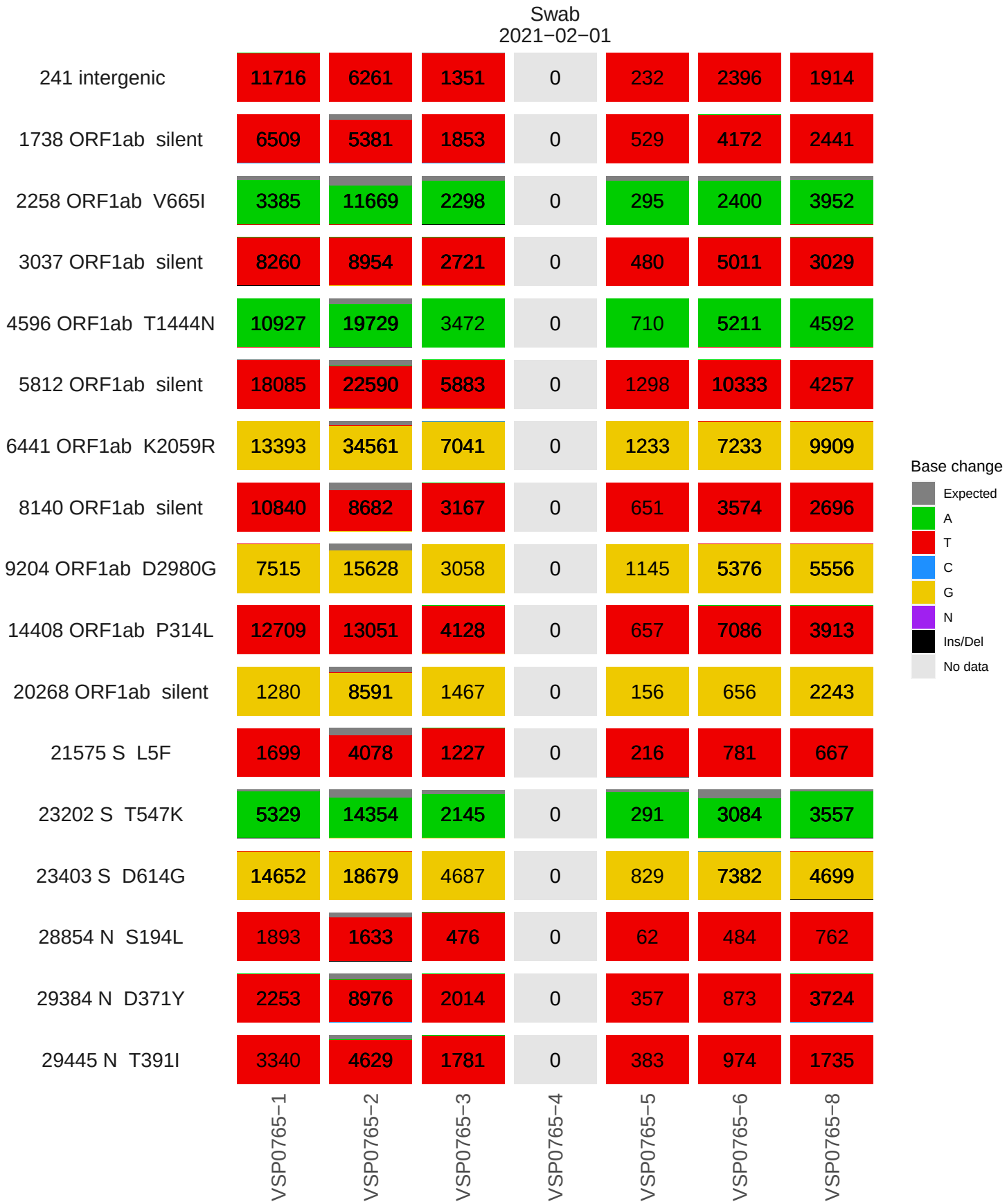
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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) |
|---|---|---|---|---|---|---|---|---|
| VSP0765 | composite | NA | Swab | 2021-02-01 | 29.89 | B.1.234 | 100.0% | 99.8% |
| VSP0765-1 | single experiment | NA | Swab | 2021-02-01 | 29.89 | B.1.234 | 99.8% | 99.8% |
| VSP0765-2 | single experiment | NA | Swab | 2021-02-01 | 29.88 | B.1.234 | 99.8% | 99.7% |
| VSP0765-3 | single experiment | NA | Swab | 2021-02-01 | 29.85 | B.1.234 | 99.8% | 99.7% |
| VSP0765-4 | single experiment | NA | Swab | 2021-02-01 | NA | NA | 3.3% | 0.9% |
| VSP0765-5 | single experiment | NA | Swab | 2021-02-01 | 29.91 | B.1.234 | 99.7% | 99.6% |
| VSP0765-6 | single experiment | NA | Swab | 2021-02-01 | 29.81 | B.1.234 | 99.7% | 99.7% |
| VSP0765-8 | single experiment | NA | Swab | 2021-02-01 | 29.88 | B.1.234 | 99.8% | 99.7% |

**Variants shared across samples**

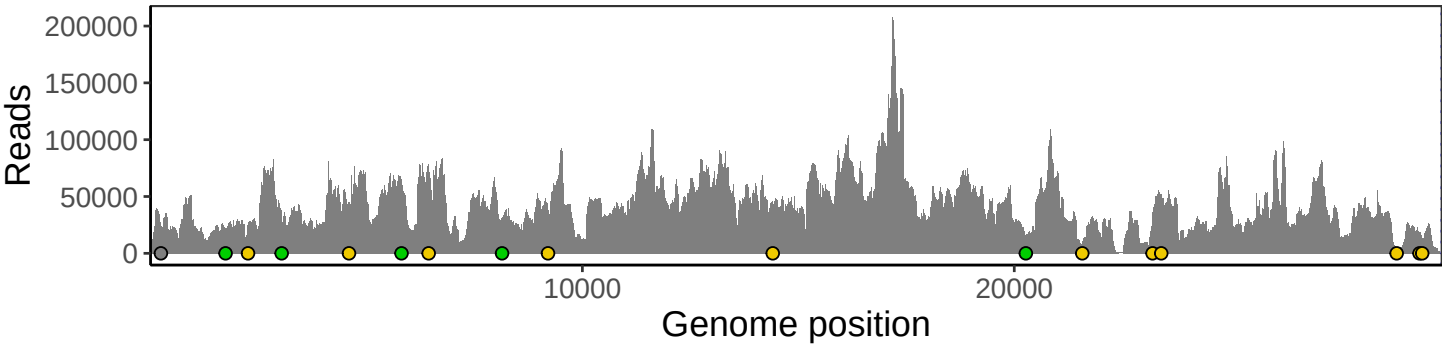
The heat map below shows how variants (reference genome /home/common/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) are shared across subject samples where the percent variance is colored. Variants are called if a variant position is covered by 5 or more reads, the alternative base is found in $> 50\%$ of read 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.


Swab
2021−02−01
241 intergenic
1738 ORF1ab silent
2258 ORF1ab V665I
3037 ORF1ab silent
4596 ORF1ab T1444N
5812 ORF1ab silent
6441 ORF1ab K2059R
8140 ORF1ab silent
9204 ORF1ab D2980G
14408 ORF1ab P314L
20268 ORF1ab silent
21575 S L5F
23202 S T547K
23403 S D614G
28854 N S194L
29384 N D371Y
29445 N T391I
11716 6261 1351 0 232 2396 1914
6509 5381 1853 0 529 4172 2441
3385 11669 2298 0 295 2400 3952
8260 8954 2721 0 480 5011 3029
10927 19729 3472 0 710 5211 4592
18085 22590 5883 0 1298 10333 4257
13393 34561 7041 0 1233 7233 9909
10840 8682 3167 0 651 3574 2696
7515 15628 3058 0 1145 5376 5556
12709 13051 4128 0 657 7086 3913
1280 8591 1467 0 156 656 2243
1699 4078 1227 0 216 781 667
5329 14354 2145 0 291 3084 3557
14652 18679 4687 0 829 7382 4699
1893 1633 476 0 62 484 762
2253 8976 2014 0 357 873 3724
3340 4629 1781 0 383 974 1735
VSP0765−1
VSP0765−2
VSP0765−3
VSP0765−4
VSP0765−5
VSP0765−6
VSP0765−8
Base change
Expected
A
T
C
G
N
Ins/Del
No data

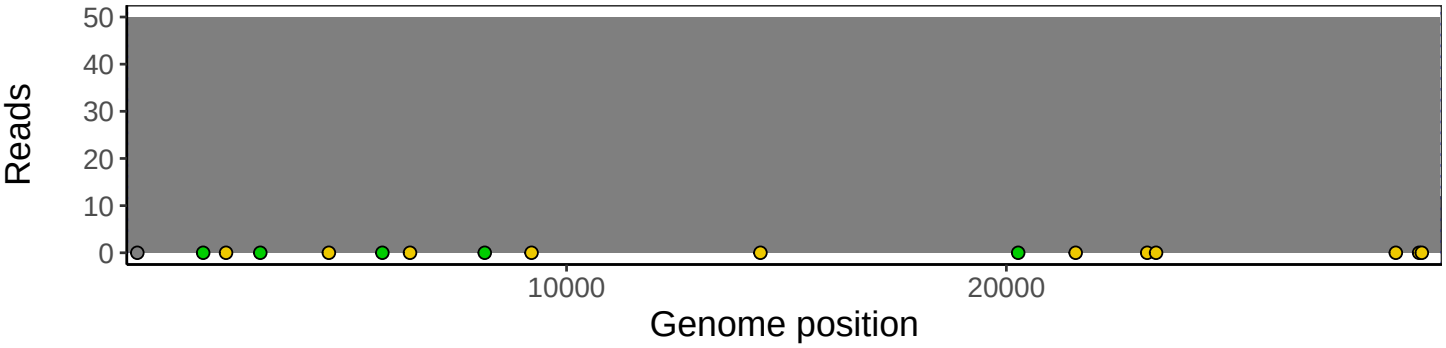
## Analyses of individual experiments and composite results

### VSP0765 | 2021-02-01 | Swab | MPCluster2-Seq7 | composite result

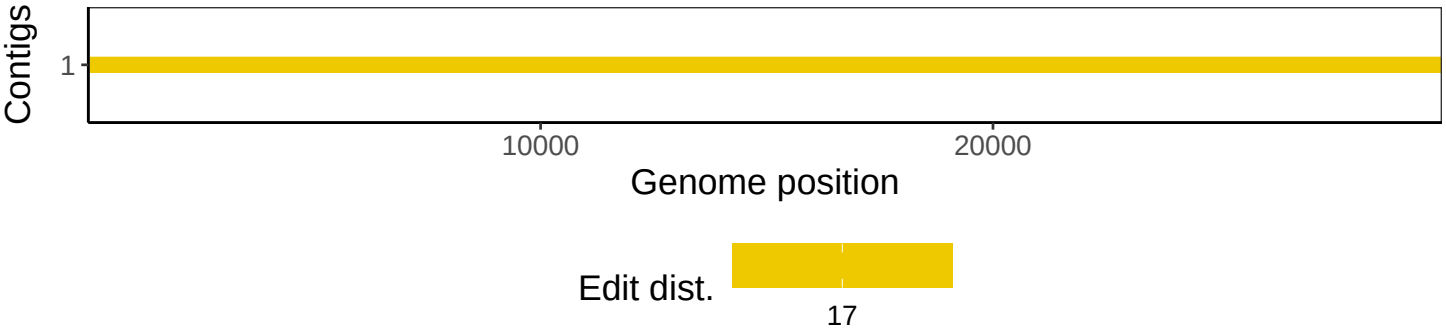
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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

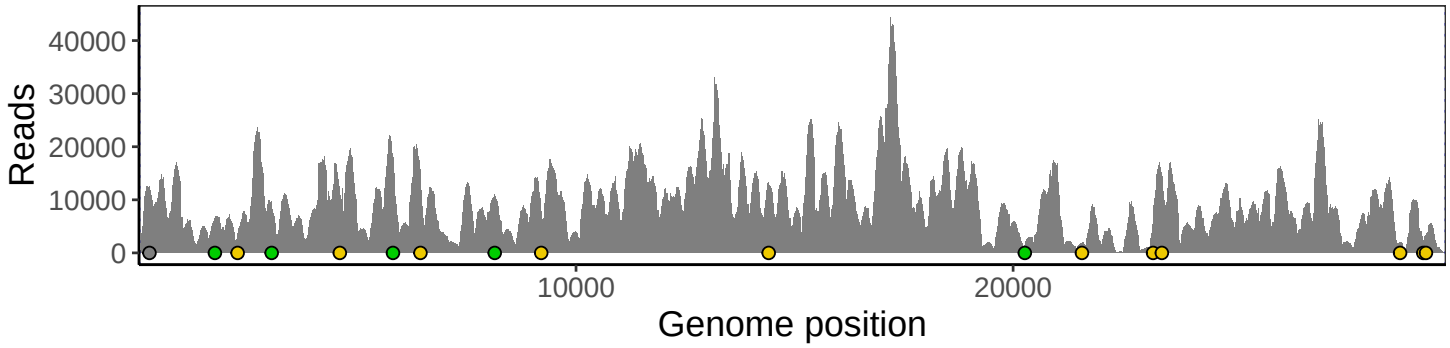



The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

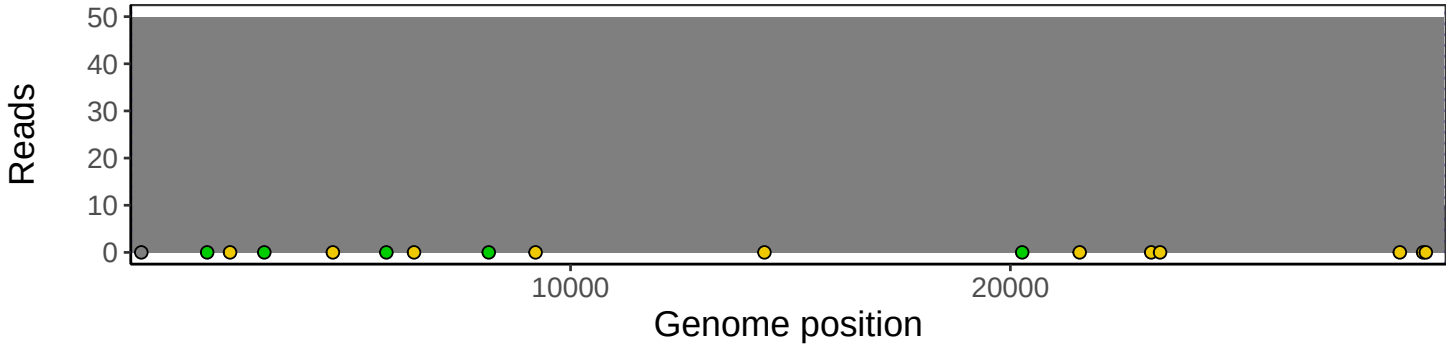


**VSP0765-1 | 2021-02-01 | Swab | MPCluster2-Seq7 | genomes | single experiment**

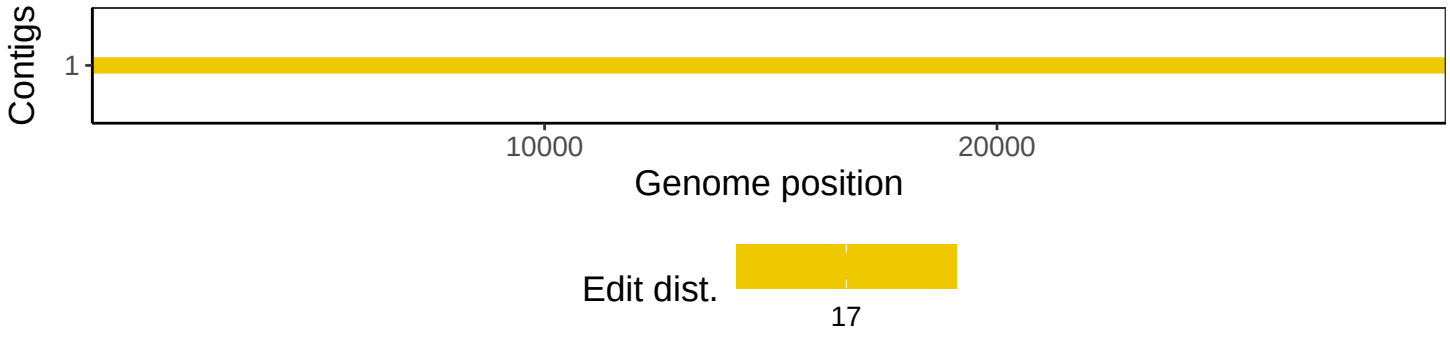
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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

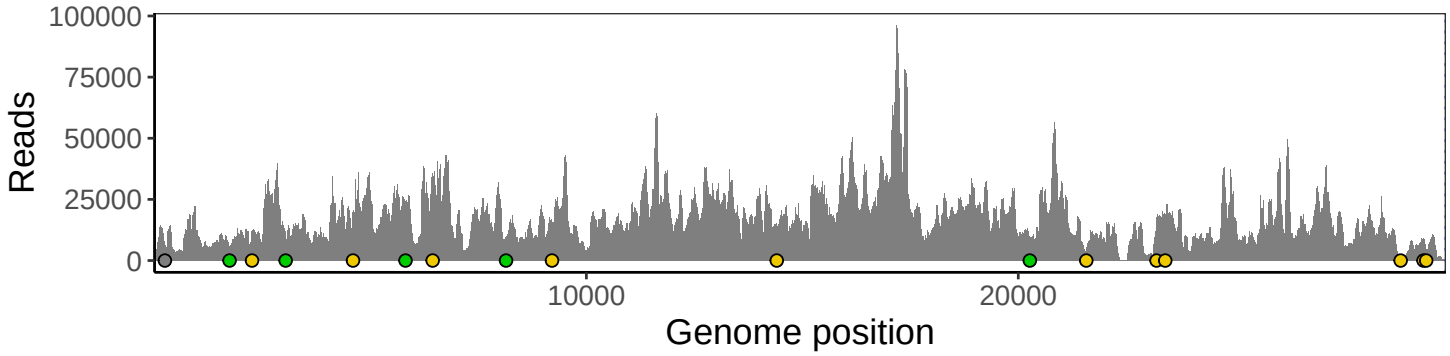



The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

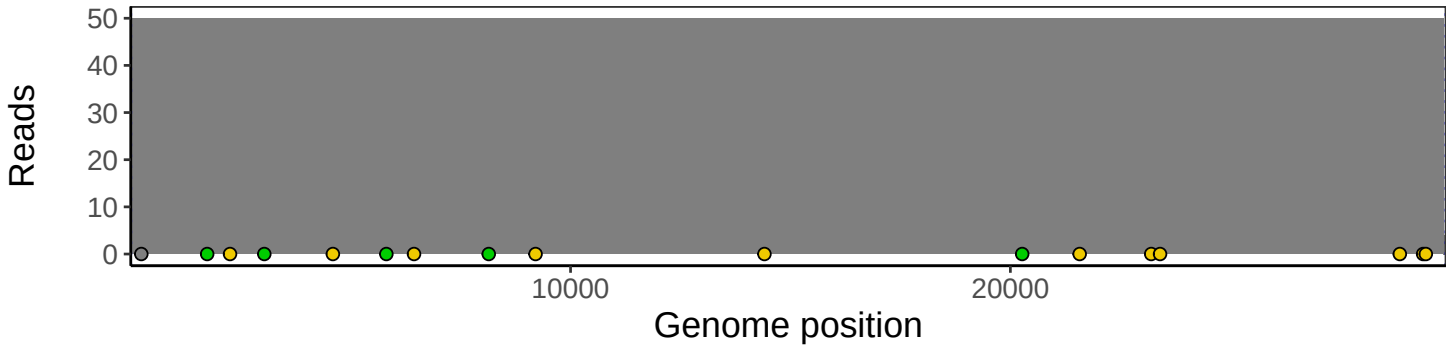


**VSP0765-2 | 2021-02-01 | Swab | MPCluster2-Seq7 | genomes | single experiment**

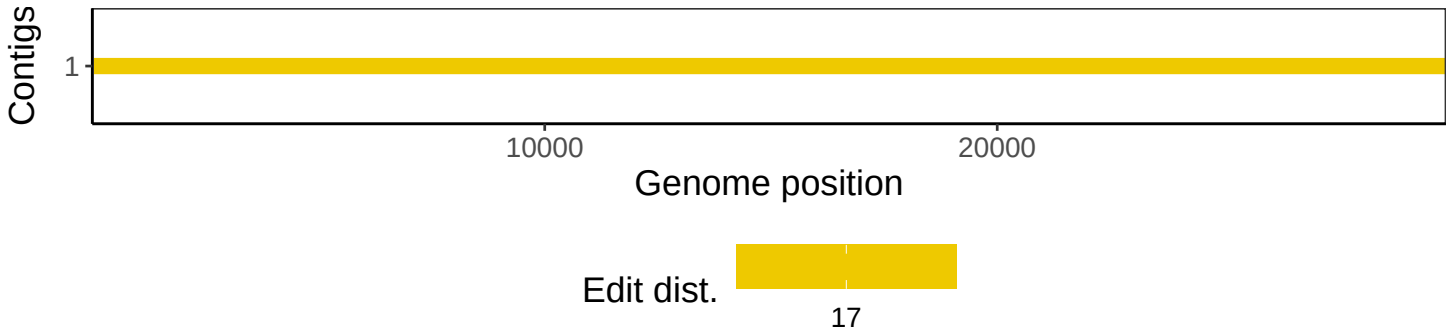
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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

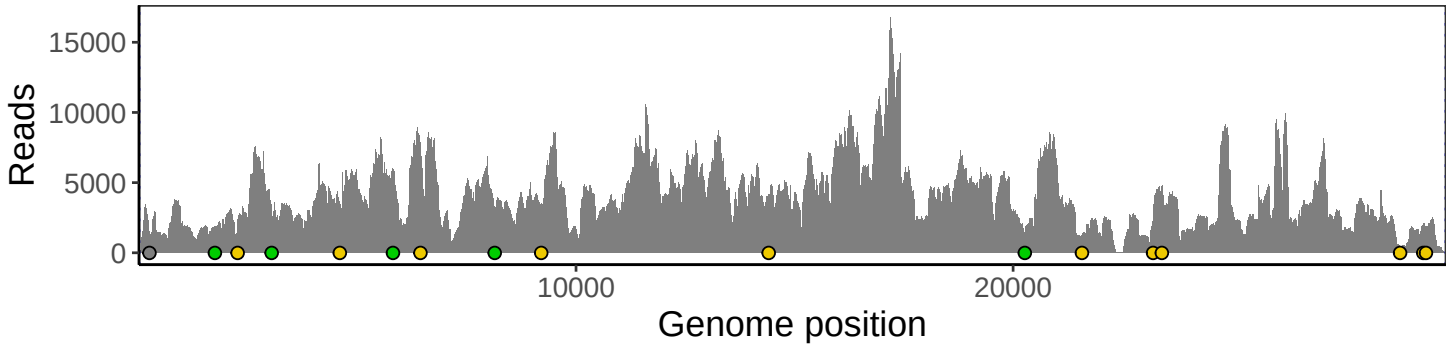



The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

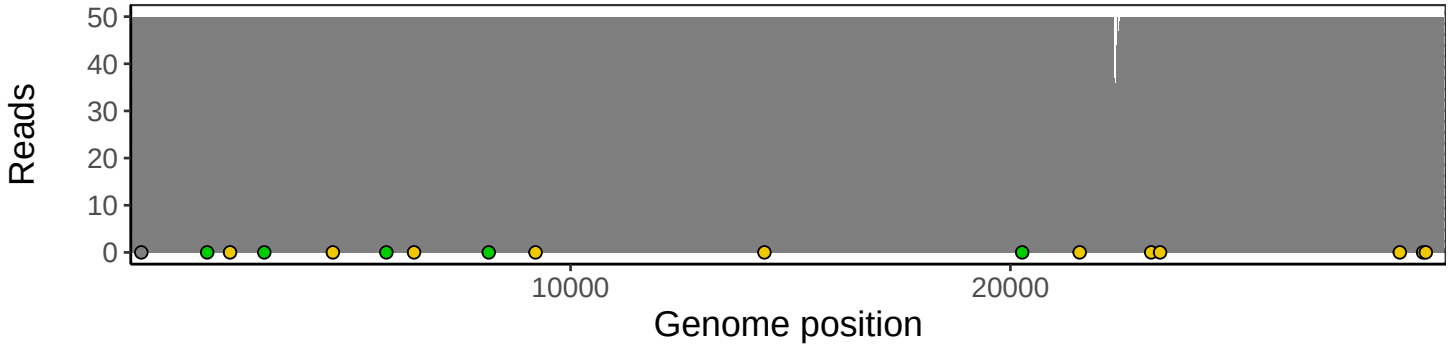


**VSP0765-3 | 2021-02-01 | Swab | MPCluster2-Seq7 | genomes | single experiment**

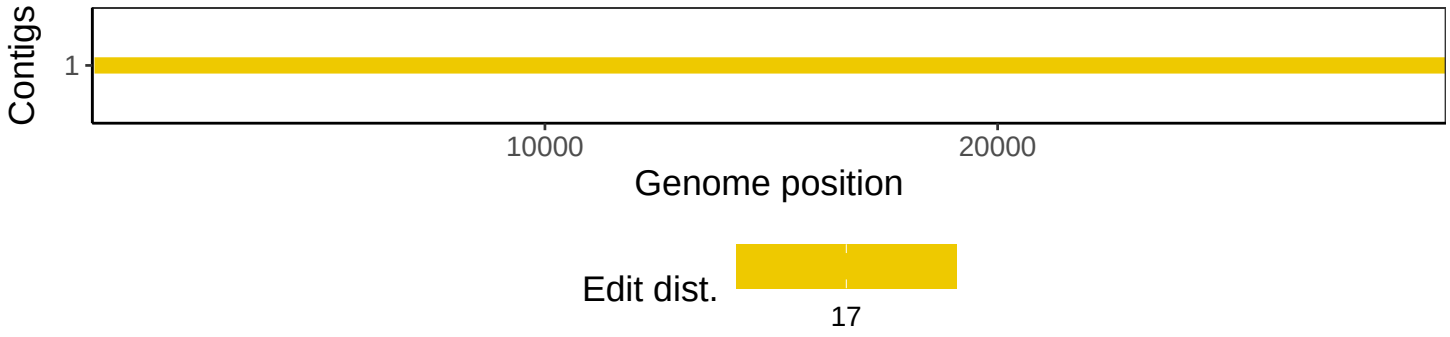
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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

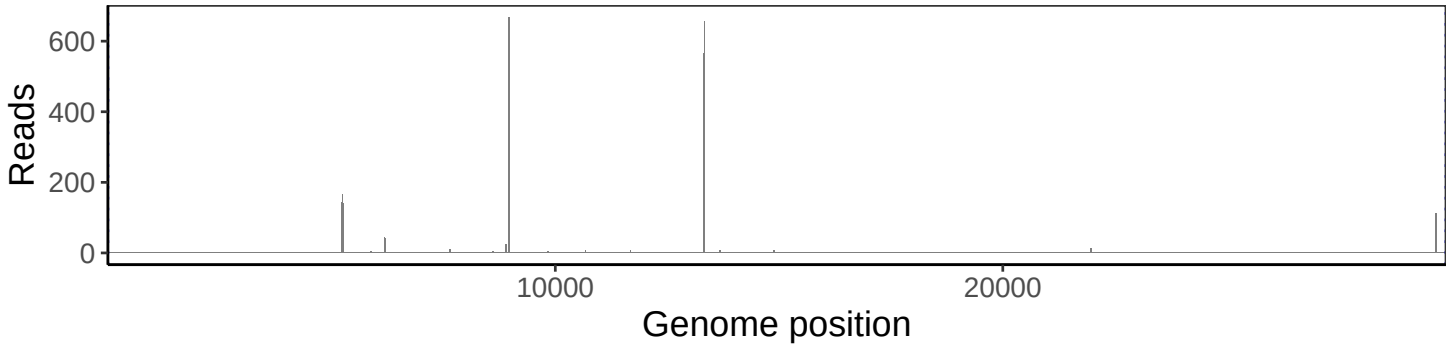



The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

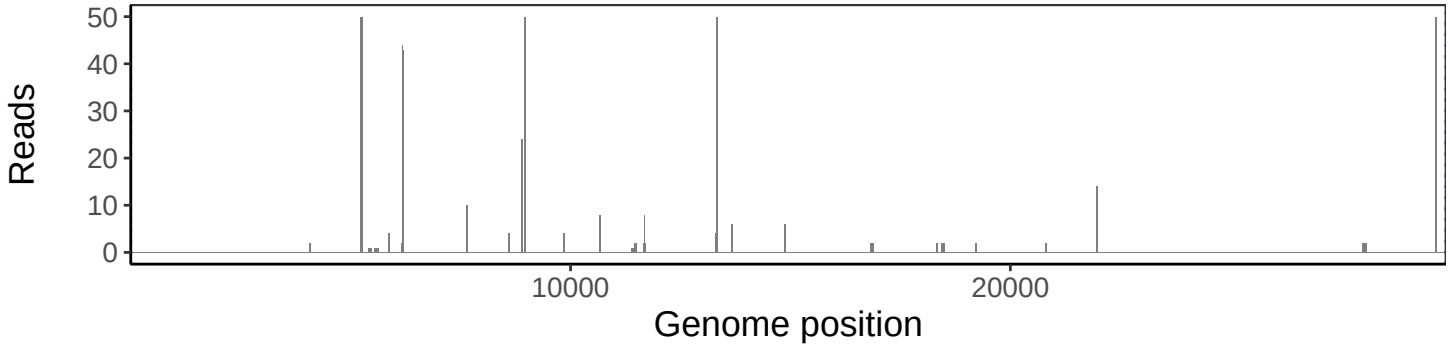


**VSP0765-4 | 2021-02-01 | Swab | MPCluster2-Seq7 | genomes | single experiment**

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.



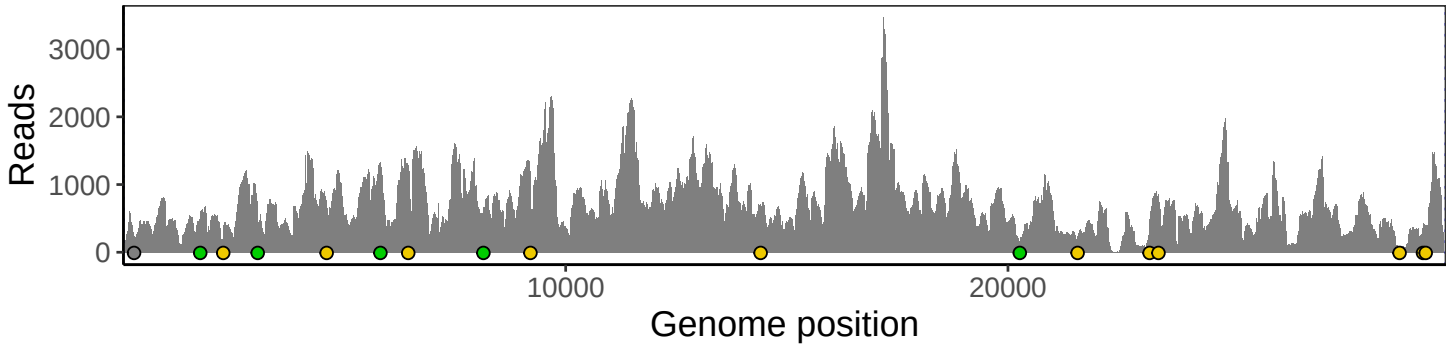

Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



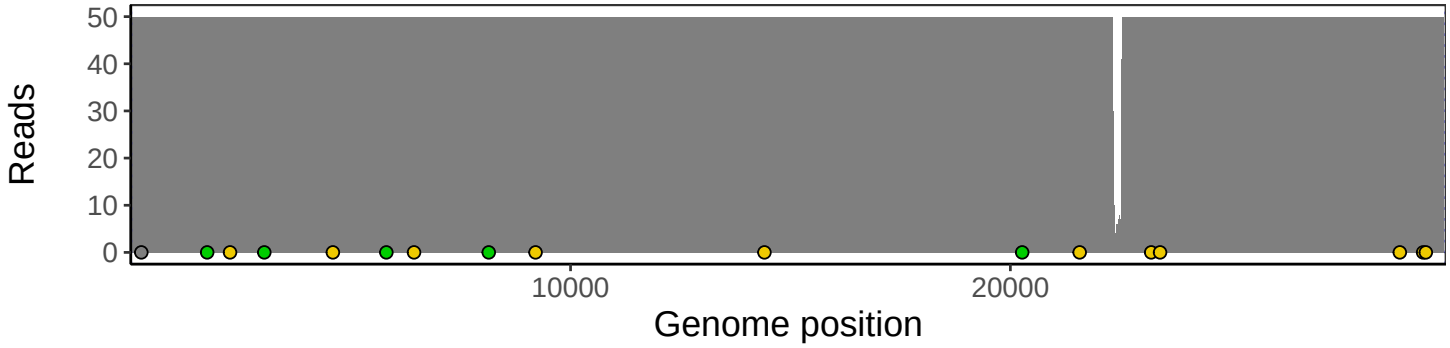

## No contig data available.

**VSP0765-5 | 2021-02-01 | Swab | MPCluster2-Seq7 | genomes | single experiment**

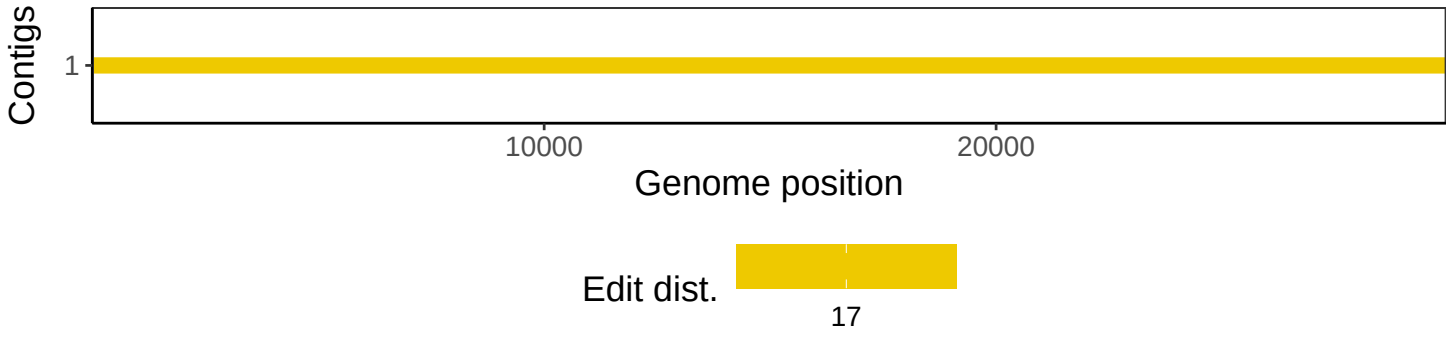
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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

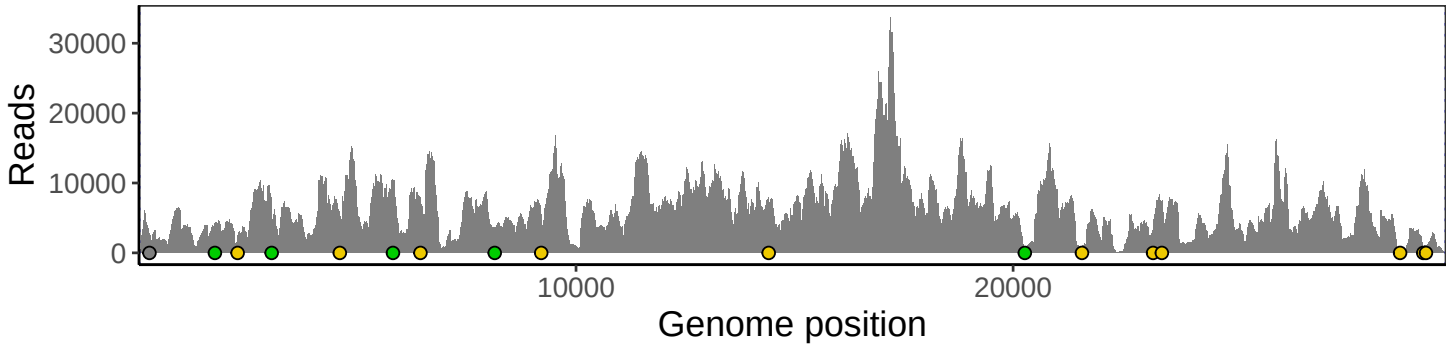



The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

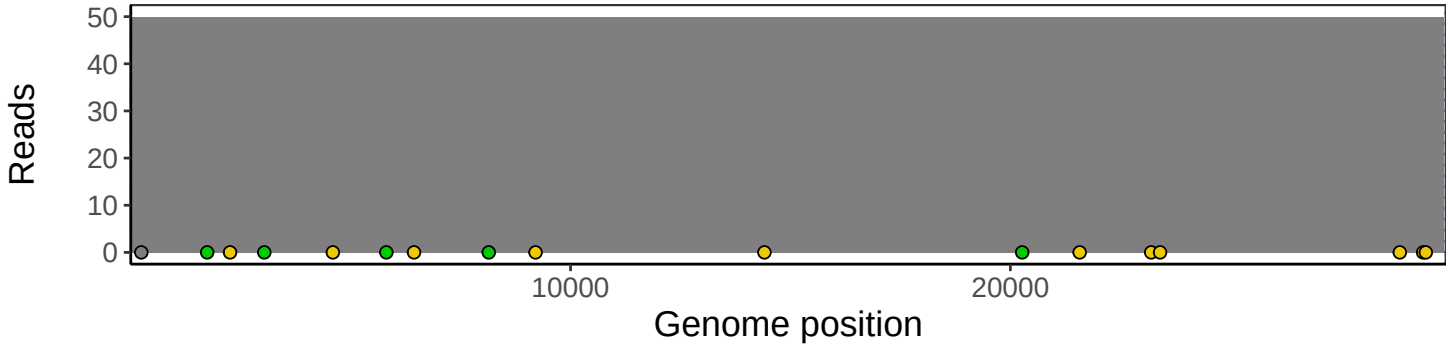


**VSP0765-6 | 2021-02-01 | Swab | MPCluster2-Seq7 | genomes | single experiment**

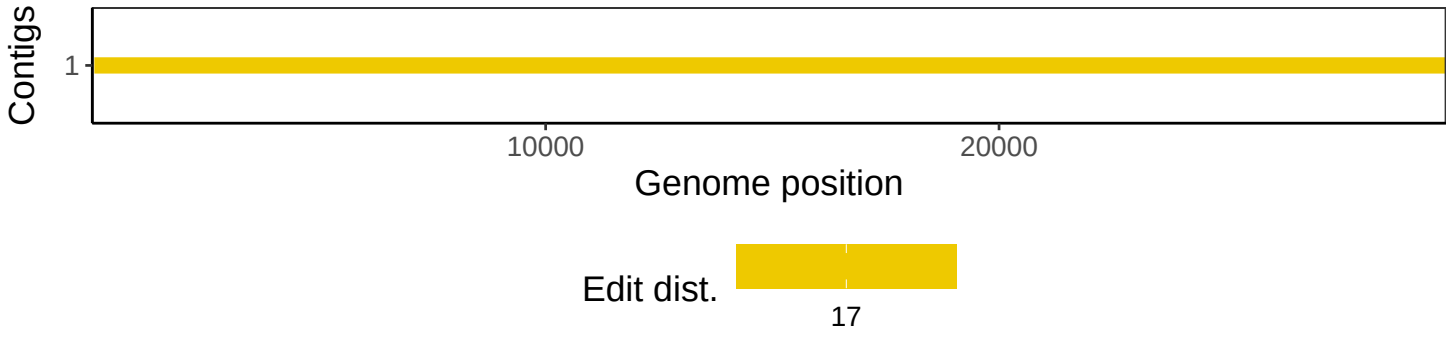
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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

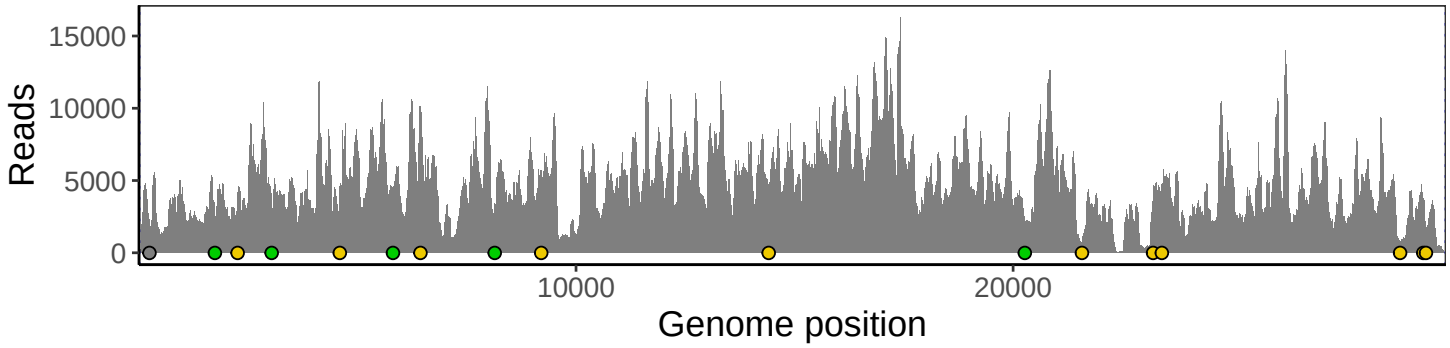



The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

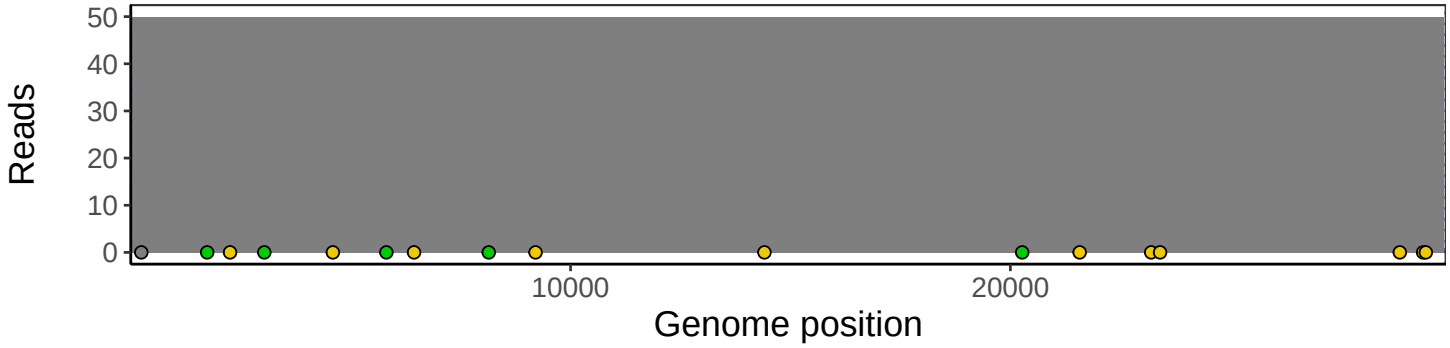


**VSP0765-8 | 2021-02-01 | Swab | MPCluster2-Seq7 | genomes | single experiment**

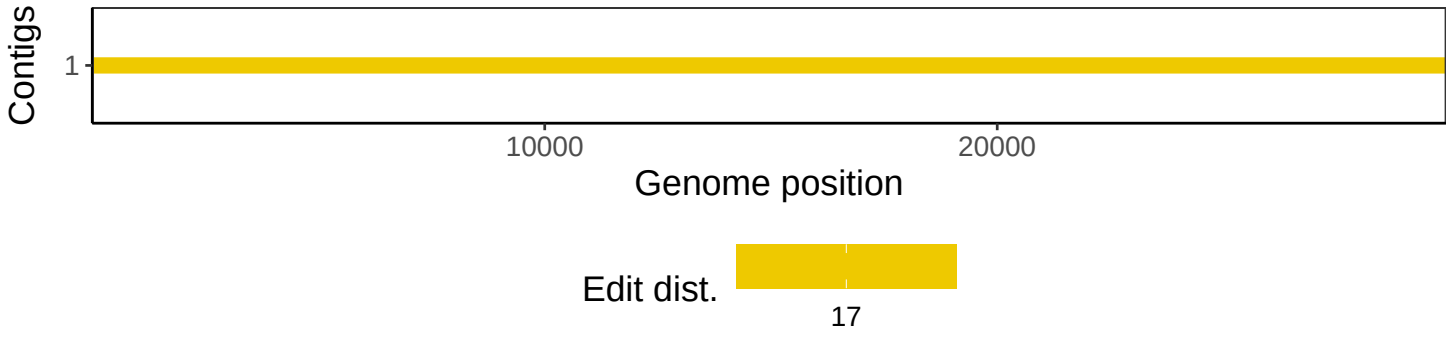
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.




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 | 3.1.3 |
| 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 | 3.3.3 |
| 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 |