

# COVID-19 subject H2102030405

*2021-03-29*

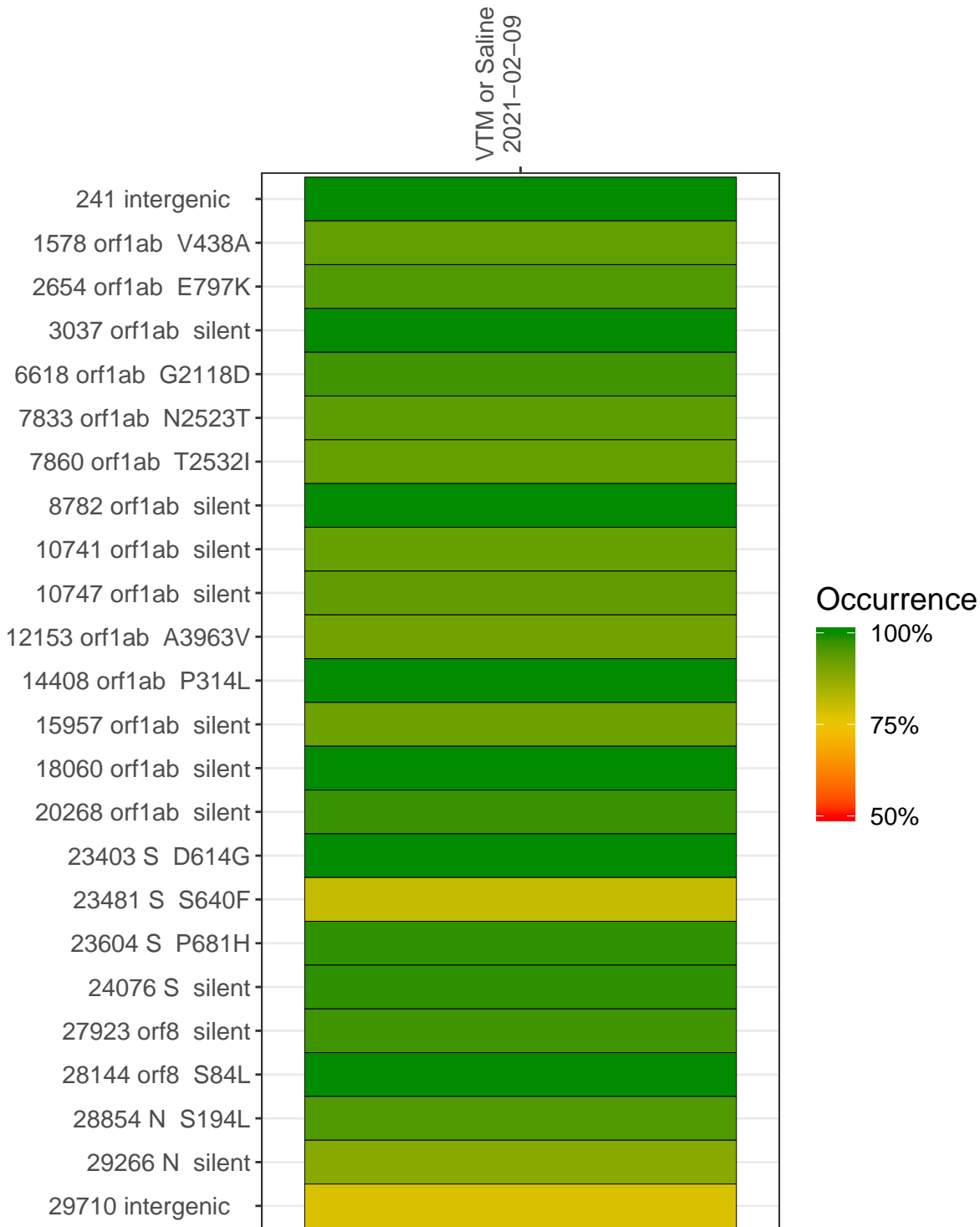
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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 ( $\geq 5$ reads)
VSP0670	composite	NA	VTM or Saline	2021-02-09	29.94	B.1.243	99.8%	99.8%
VSP0670-1	single experiment	NA	VTM or Saline	2021-02-09	12.39	B.1.243	92.6%	91.0%
VSP0670-2	single experiment	NA	VTM or Saline	2021-02-09	12.28	B.1.243	91.7%	91.0%
VSP0670-3	single experiment	NA	VTM or Saline	2021-02-09	22.29	B.1.243	99.4%	99.2%

## 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.



VTM or Saline

241 intergenic	4030	1499	2576
1578 orf1ab V438A	626	220	3272
2654 orf1ab E797K	2248	915	15423
3037 orf1ab silent	824	300	4816
6618 orf1ab G2118D	1634	864	11545
7833 orf1ab N2523T	2440	917	5925
7860 orf1ab T2532I	2220	984	5399
8782 orf1ab silent	2222	796	10502
10741 orf1ab silent	4719	2351	558
10747 orf1ab silent	4779	2355	526
12153 orf1ab A3963V	7320	4142	1096
14408 orf1ab P314L	6527	2239	510
15957 orf1ab silent	6087	2473	775
18060 orf1ab silent	4532	2077	434
20268 orf1ab silent	1983	955	2324
23403 S D614G	9295	4157	6494
23481 S S640F	7823	2931	3082
23604 S P681H	3732	1385	405
24076 S silent	6069	3306	5332
27923 orf8 silent	3652	1541	14731
28144 orf8 S84L	4429	2200	12118
28854 N S194L	900	377	774
29266 N silent	2801	1462	553
29710 intergenic	0	0	2603
	VSP0670-1	VSP0670-2	VSP0670-3

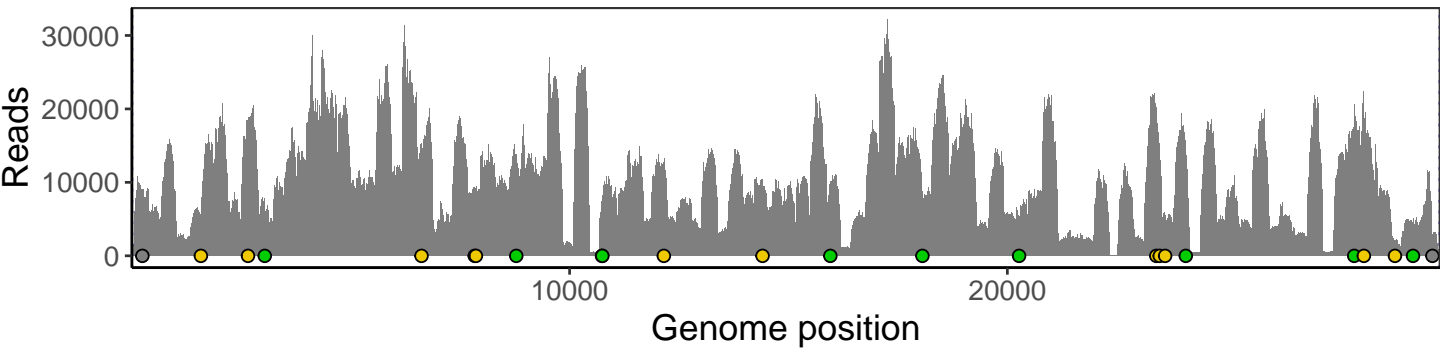
Base change

- Expected
- A
- T
- C
- G
- N
- Ins/Del
- No data

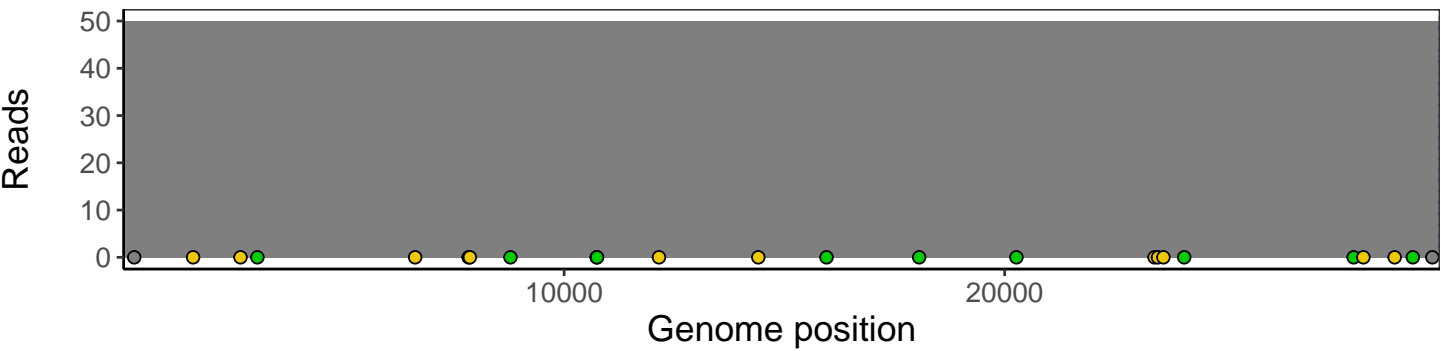
# Analyses of individual experiments and composite results

VSP0670 | 2021-02-09 | VTM or Saline | H2102030405 | composite result

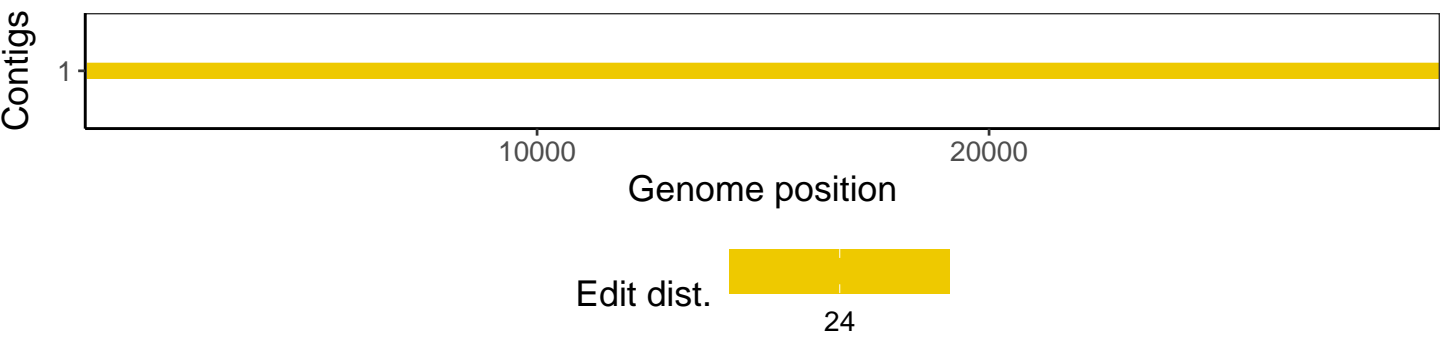
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



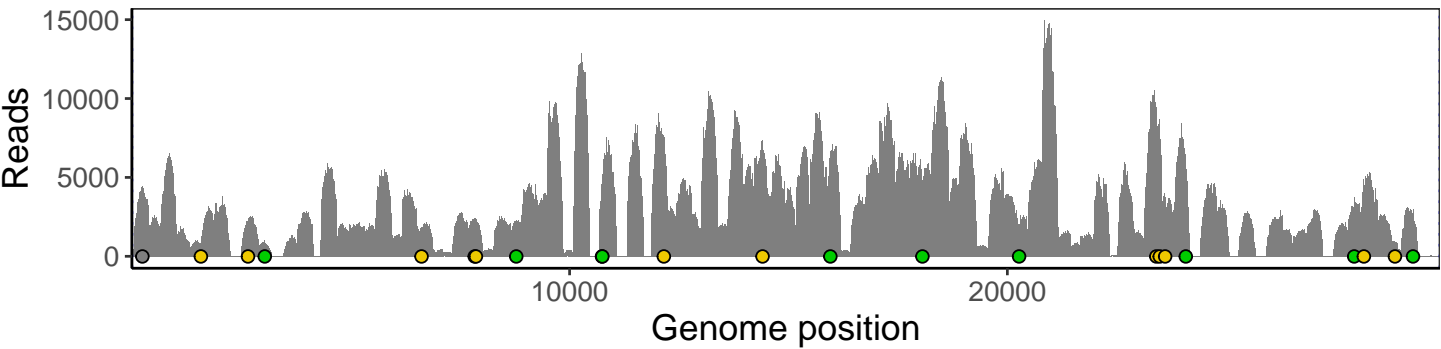
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



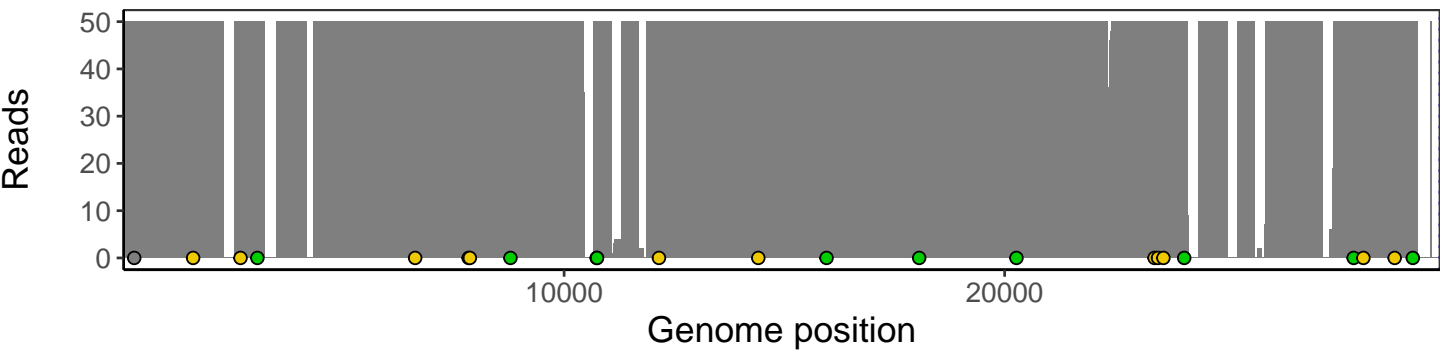
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



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.



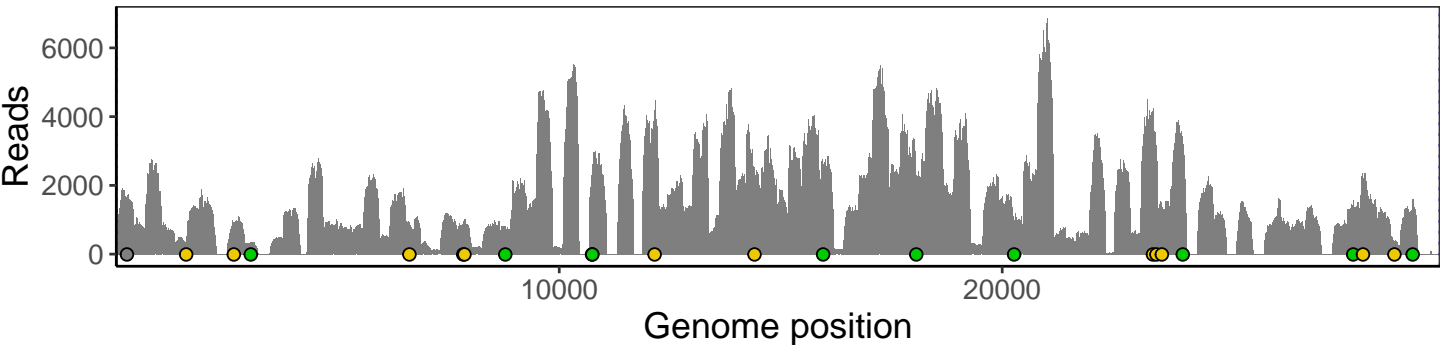
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



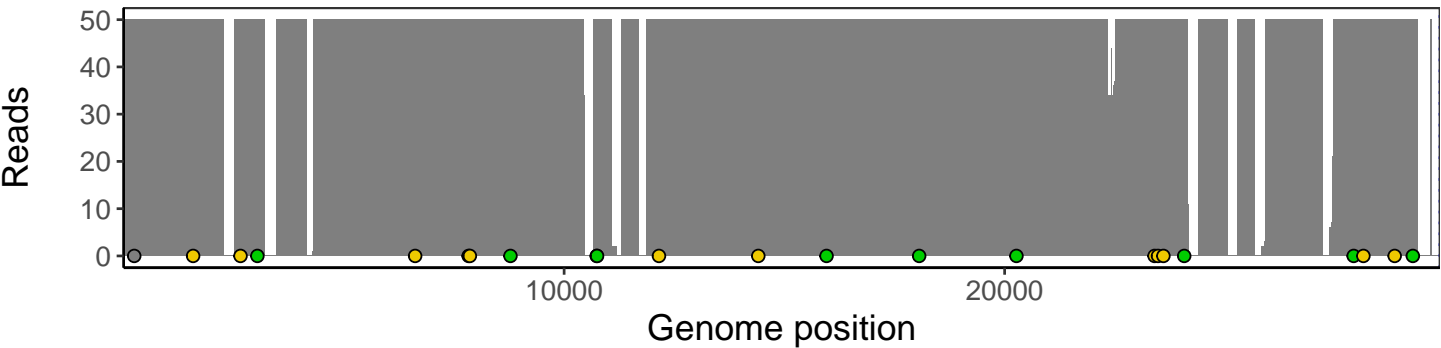
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The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold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



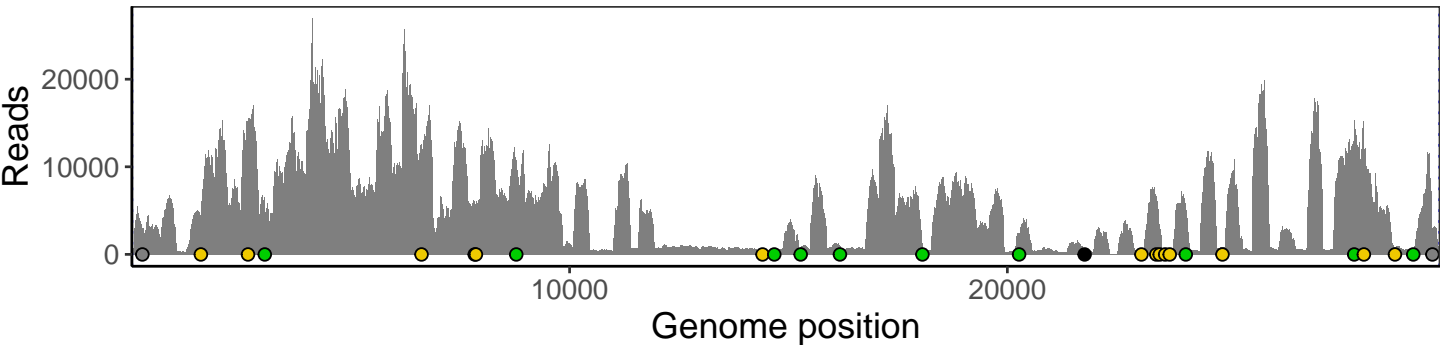
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



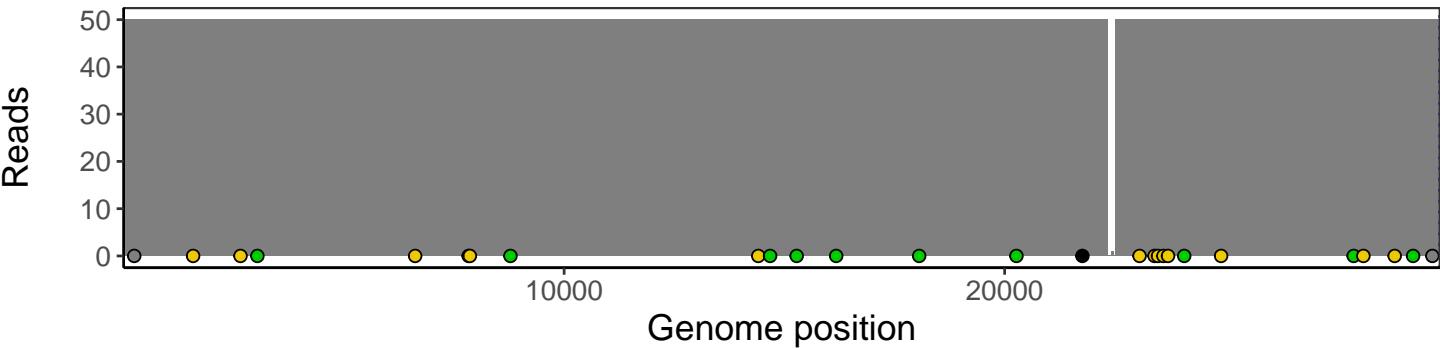
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



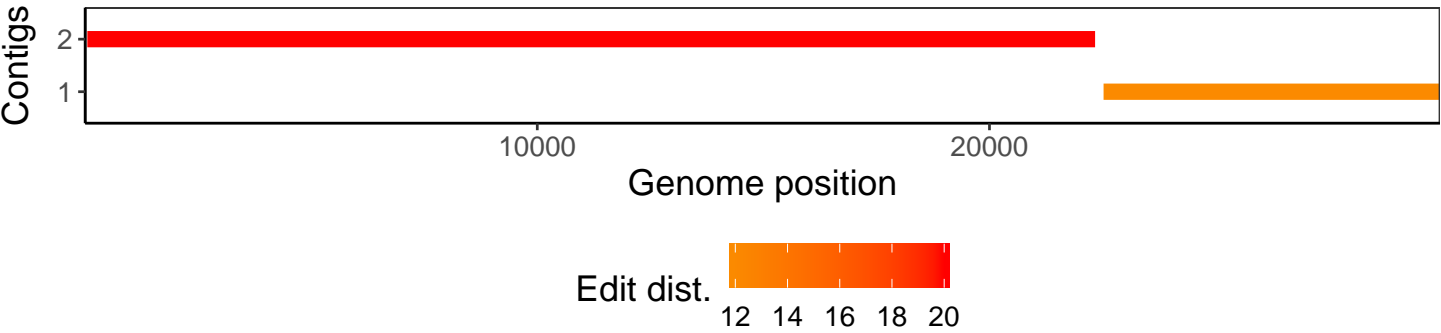
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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 htlib 1.10
bcftools	1.10.2-34-g1a12af0-dirty Using htlib 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