COVID-19 subject AHS19005093

2021-03-29

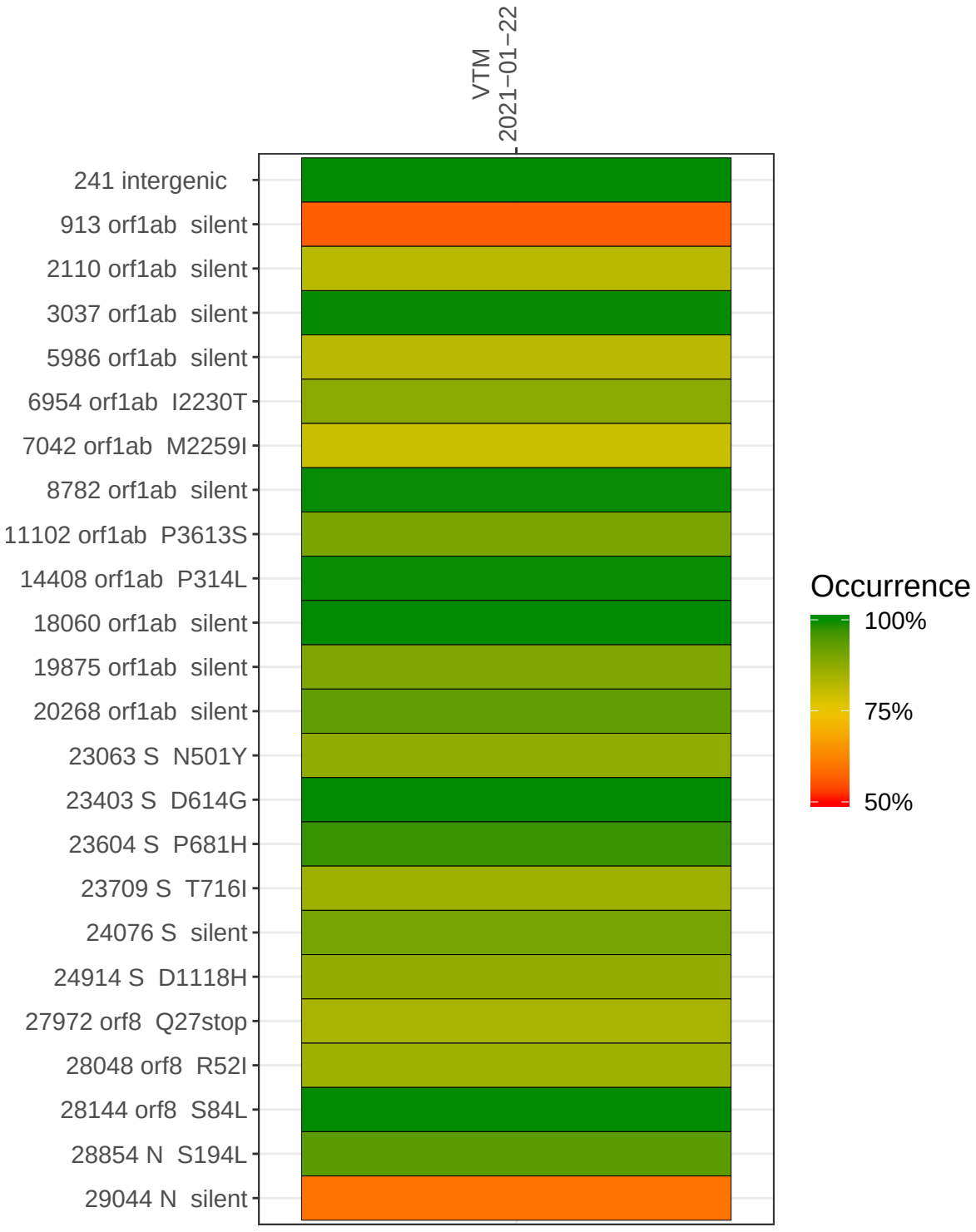
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

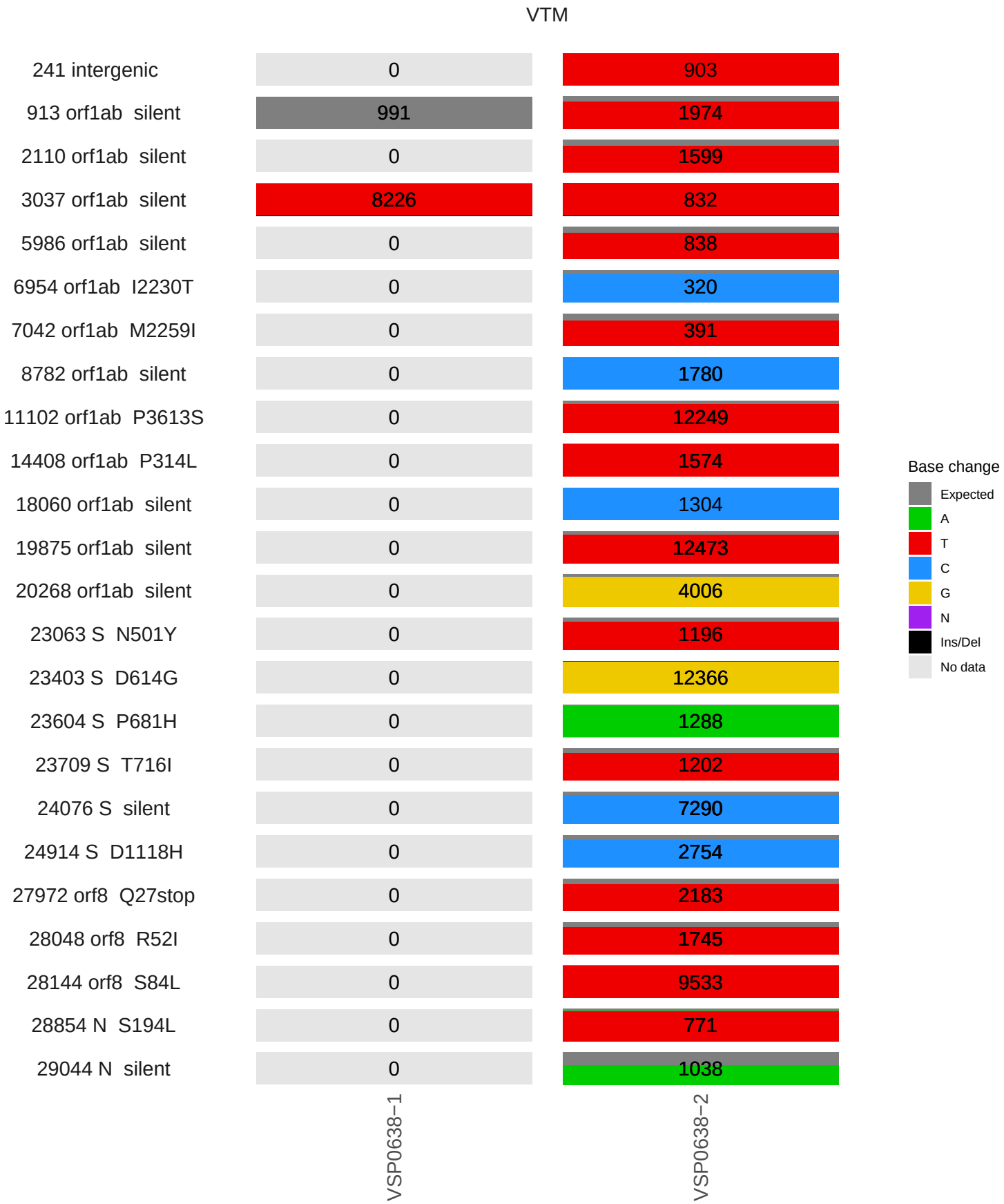
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0638	composite	NA	VTM	2021-01-22	22.30	B.1.243	99.8%	99.2%
VSP0638-1	single experiment	NA	VTM	2021-01-22	1.14	NA	12.9%	11.6%
VSP0638-2	single experiment	NA	VTM	2021-01-22	22.30	B.1.243	99.8%	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.

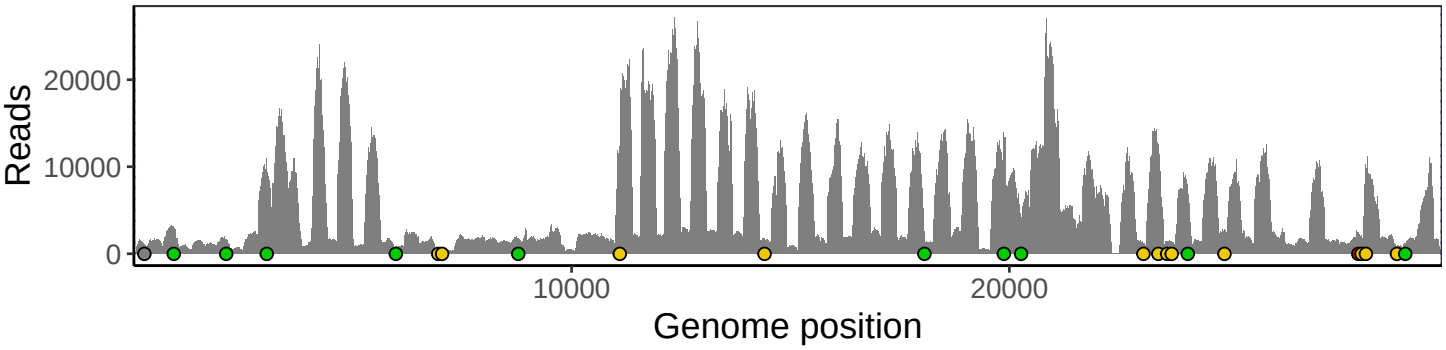



VTM
241 intergenic
913 orf1ab silent
2110 orf1ab silent
3037 orf1ab silent
5986 orf1ab silent
6954 orf1ab I2230T
7042 orf1ab M2259I
8782 orf1ab silent
11102 orf1ab P3613S
14408 orf1ab P314L
18060 orf1ab silent
19875 orf1ab silent
20268 orf1ab silent
23063 S N501Y
23403 S D614G
23604 S P681H
23709 S T716I
24076 S silent
24914 S D1118H
27972 orf8 Q27stop
28048 orf8 R52I
28144 orf8 S84L
28854 N S194L
29044 N silent
0
991
0
8226
0
0
0
0
0
0
0
0
0
0
0
0
0
0
0
0
0
0
0
903
1974
1599
832
838
320
391
1780
12249
1574
1304
12473
4006
1196
12366
1288
1202
7290
2754
2183
1745
9533
771
1038
VSP0638−1
VSP0638−2
Base change
Expected
A
T
C
G
N
Ins/Del
No data

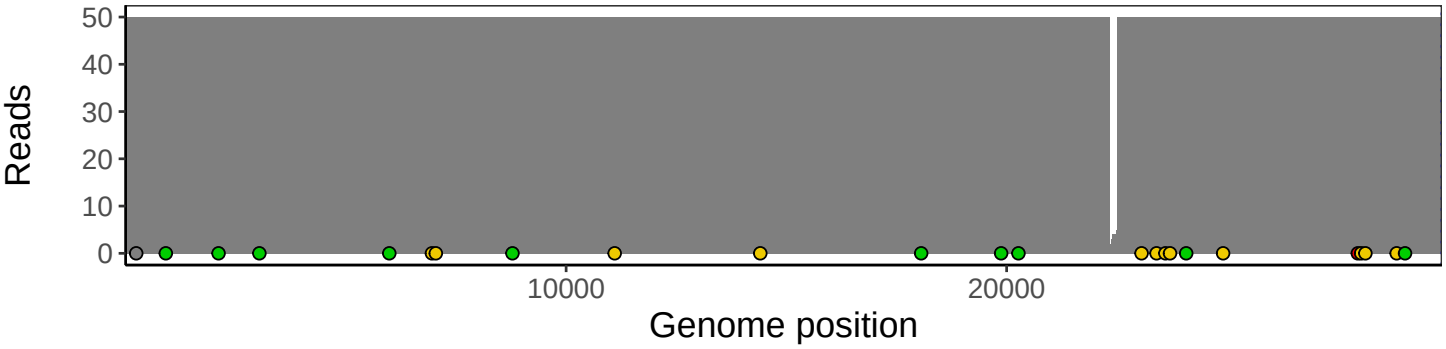
Analyses of individual experiments and composite results

VSP0638 | 2021-01-22 | VTM | H2101191203 | composite result

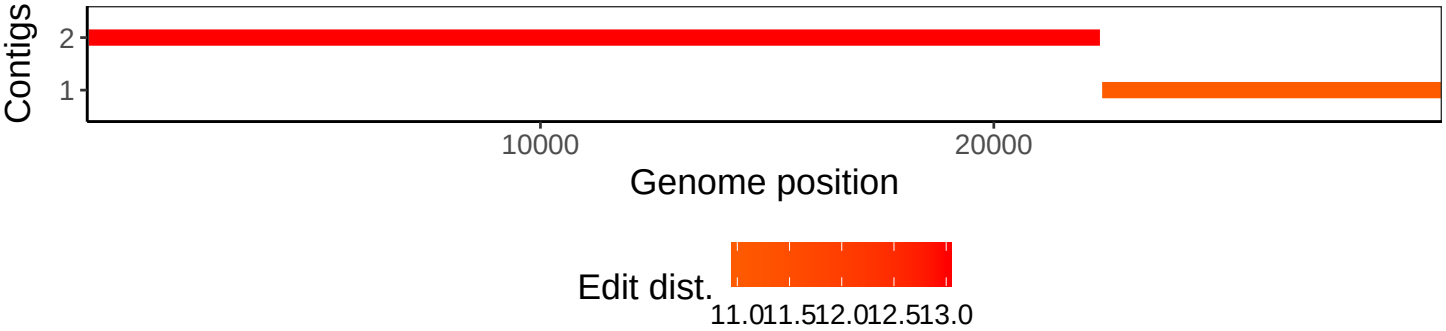
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

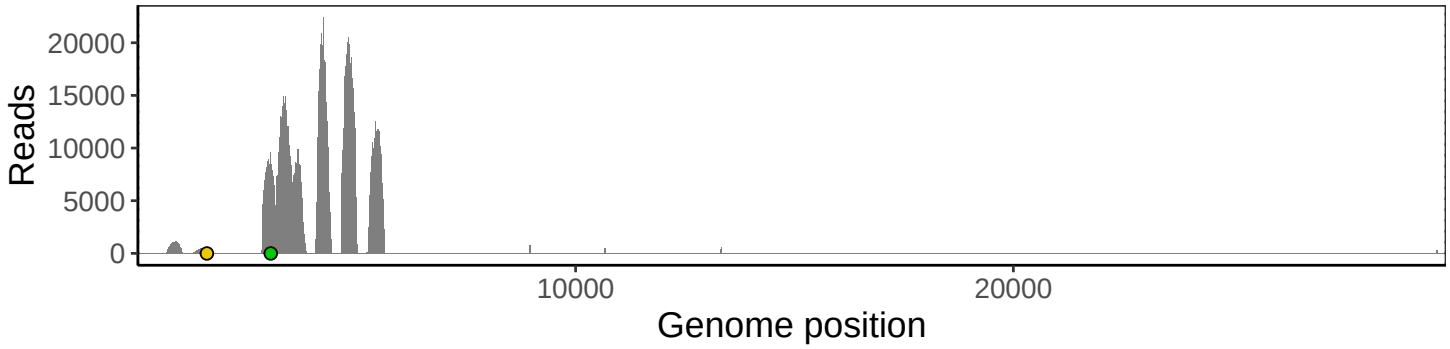


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

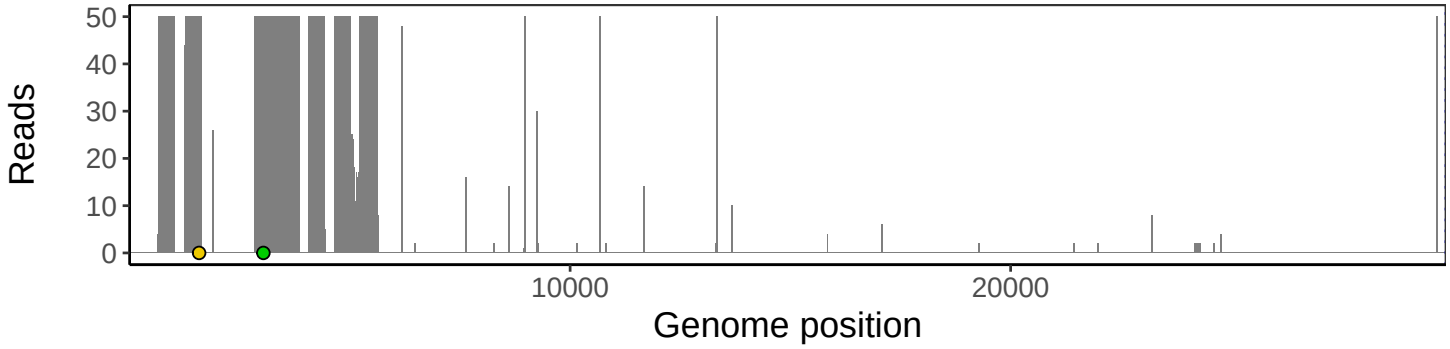


VSP0638-1 | 2021-01-22 | VTM | H2101191203 | genomes | single experiment

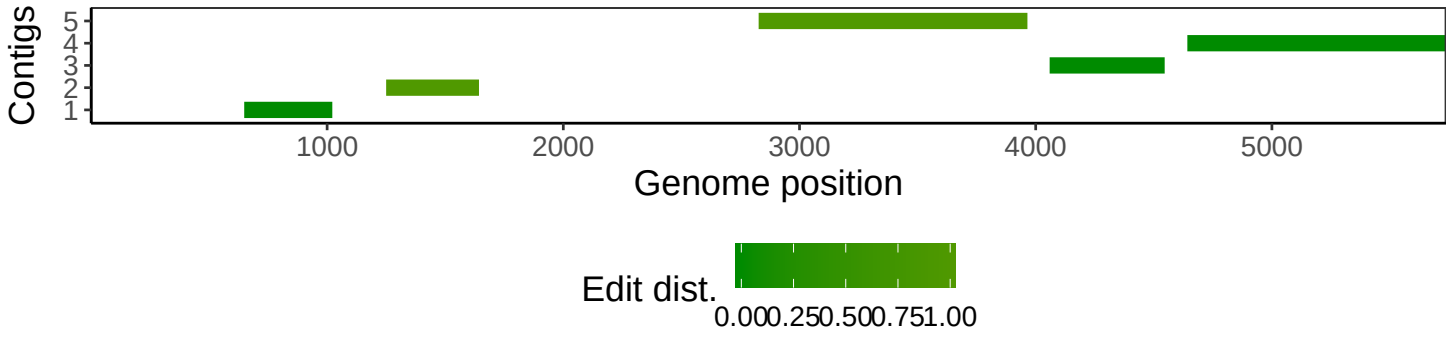
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

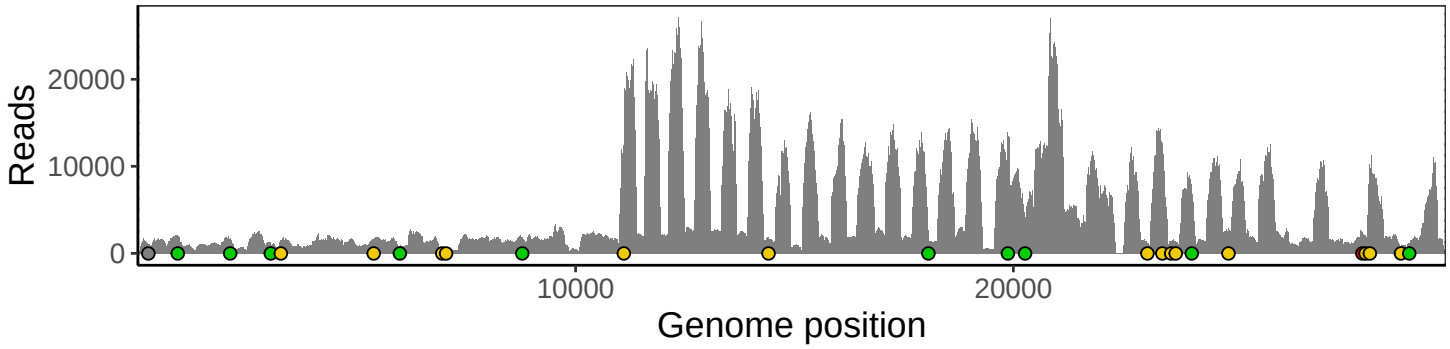


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

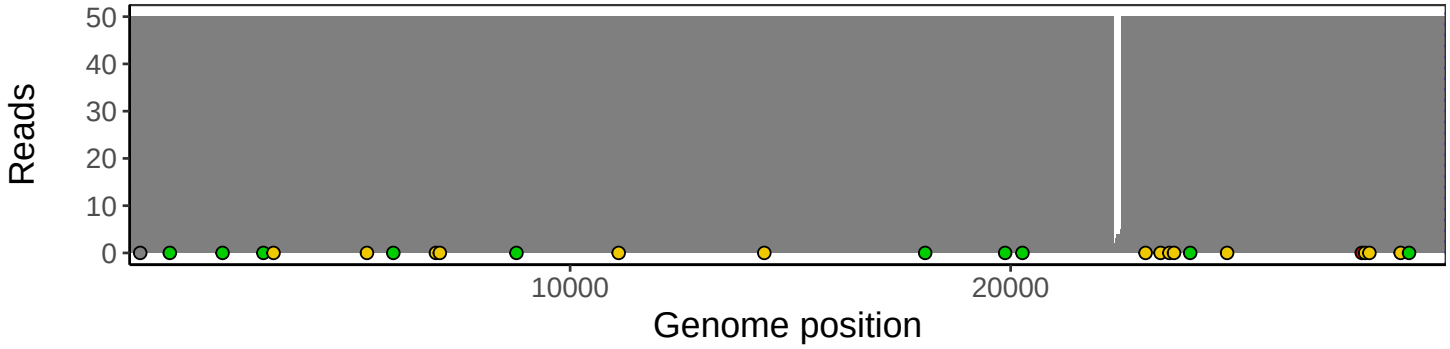


VSP0638-2 | 2021-01-22 | VTM | H2101191203 | genomes | single experiment

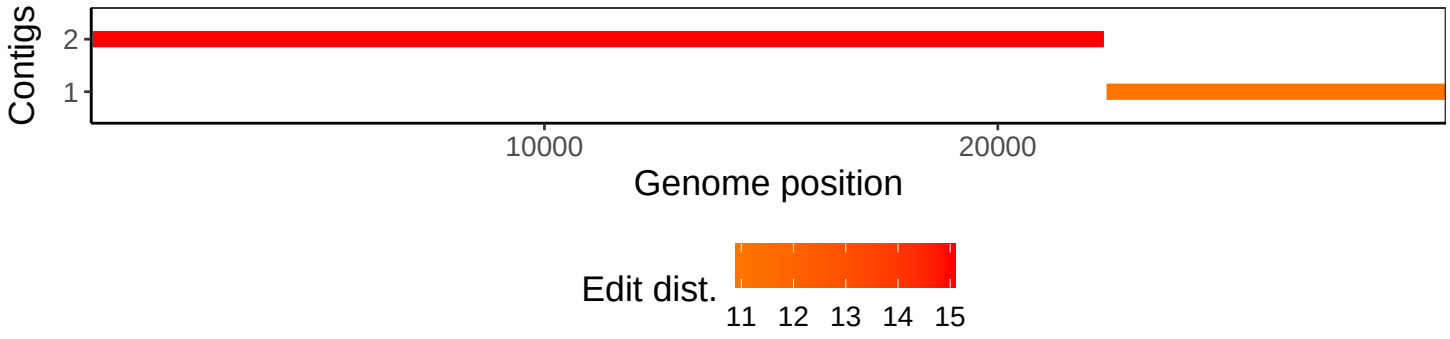
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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