COVID-19 subject H2102030405

2021-03-12

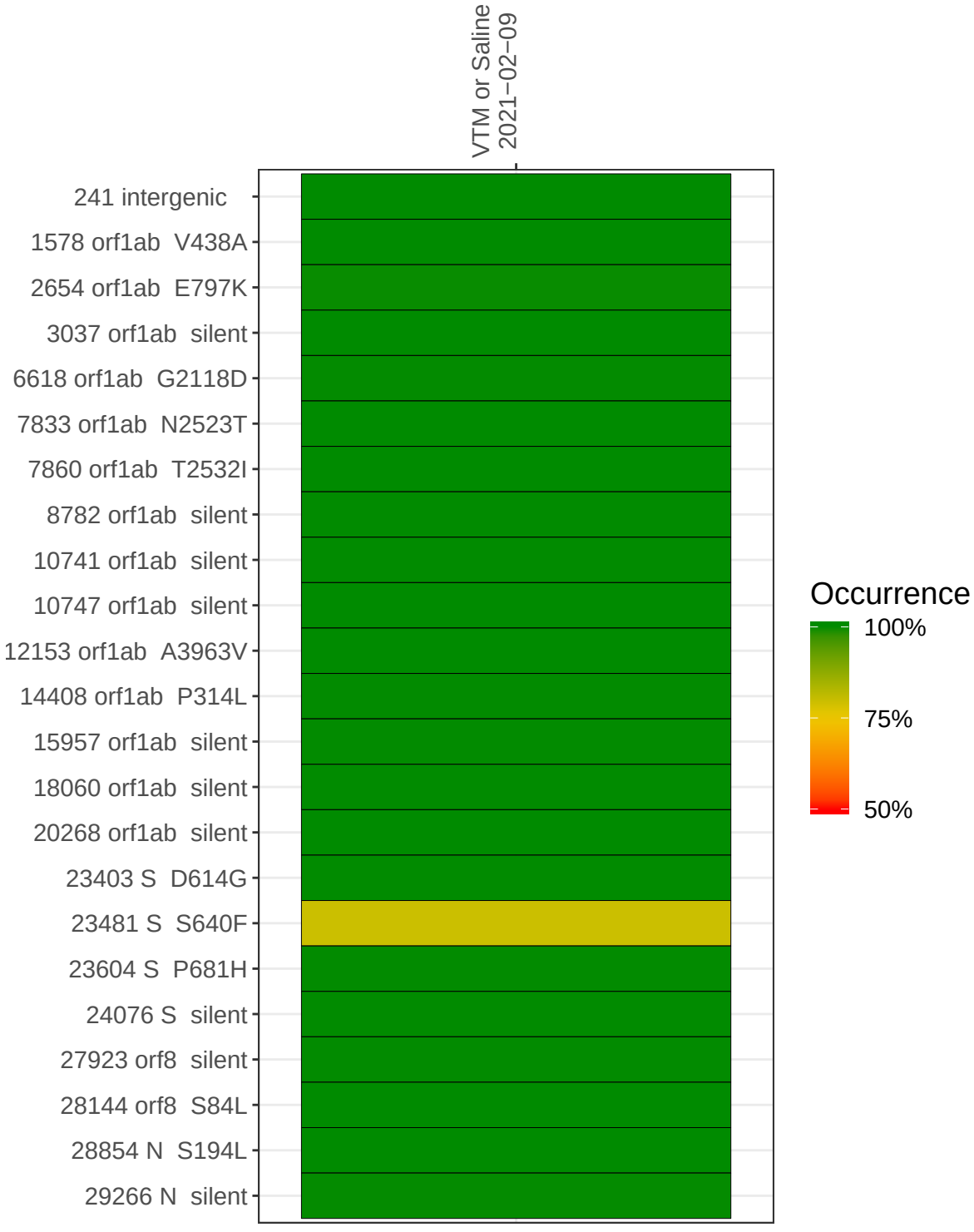
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

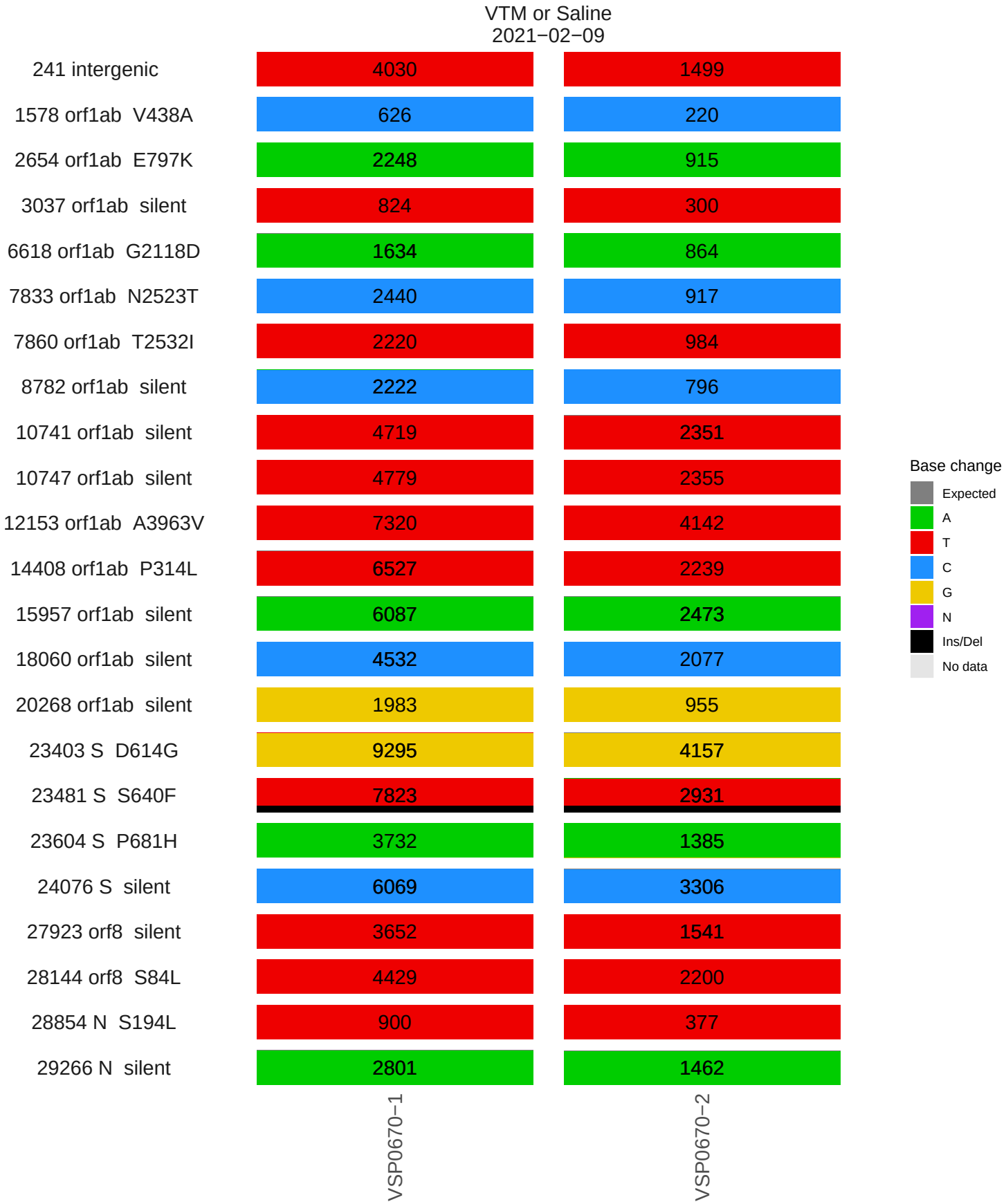
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0670	composite	NA	VTM or Saline	2021-02-09	12.39	B.1.243	92.8%	91.2%
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%

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.

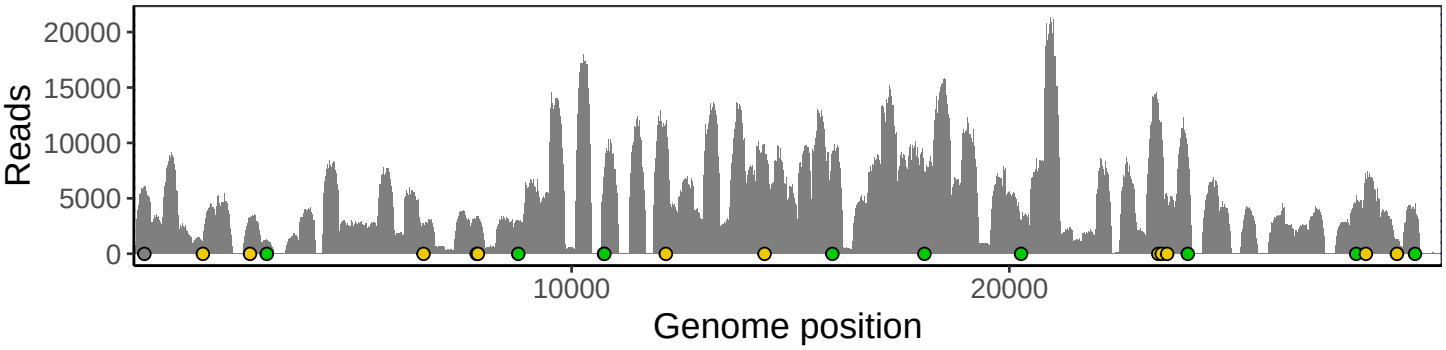



VTM or Saline
2021−02−09
241 intergenic
1578 orf1ab V438A
2654 orf1ab E797K
3037 orf1ab silent
6618 orf1ab G2118D
7833 orf1ab N2523T
7860 orf1ab T2532I
8782 orf1ab silent
10741 orf1ab silent
10747 orf1ab silent
12153 orf1ab A3963V
14408 orf1ab P314L
15957 orf1ab silent
18060 orf1ab silent
20268 orf1ab silent
23403 S D614G
23481 S S640F
23604 S P681H
24076 S silent
27923 orf8 silent
28144 orf8 S84L
28854 N S194L
29266 N silent
4030
626
2248
824
1634
2440
2220
2222
4719
4779
7320
6527
6087
4532
1983
9295
7823
3732
6069
3652
4429
900
2801
1499
220
915
300
864
917
984
796
2351
2355
4142
2239
2473
2077
955
4157
2931
1385
3306
1541
2200
377
1462
VSP0670−1
VSP0670−2
Base change
Expected
A
T
C
G
N
Ins/Del
No data

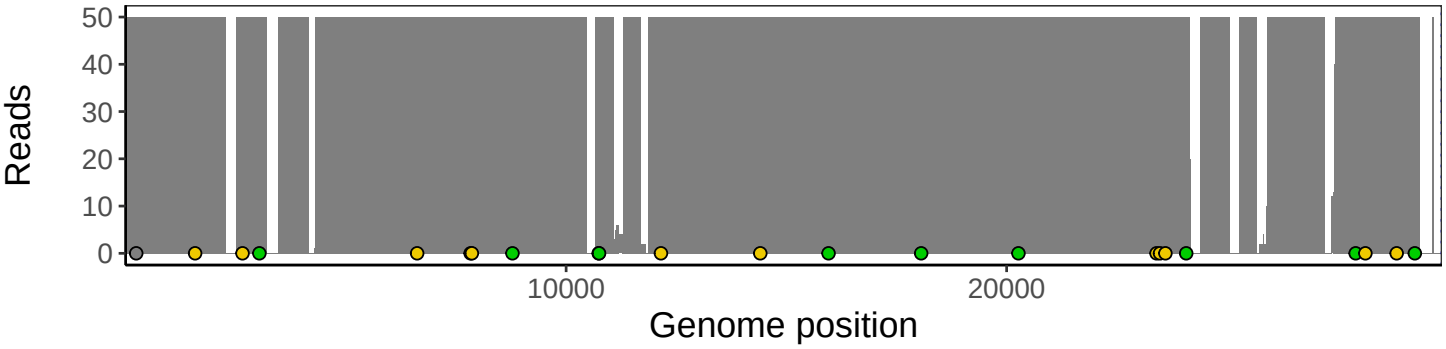
Analyses of individual experiments and composite results

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

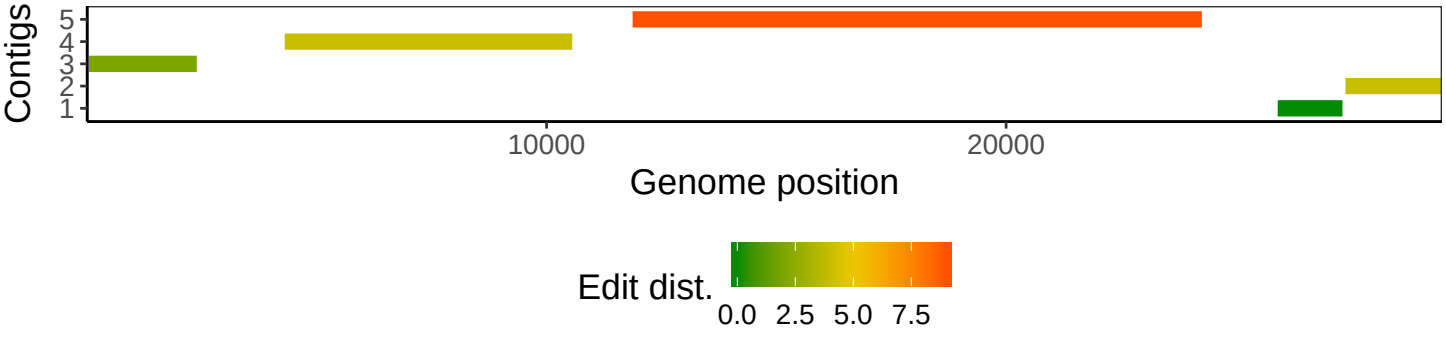
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

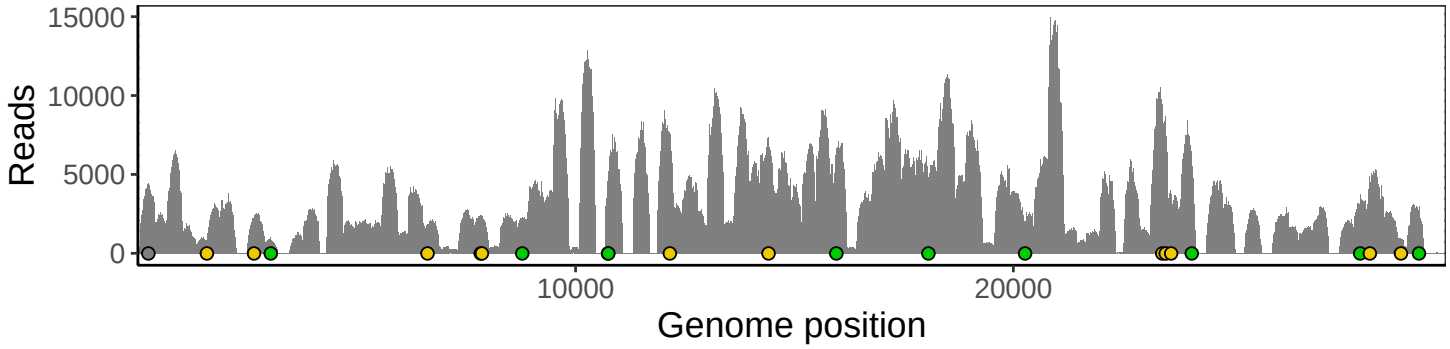


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

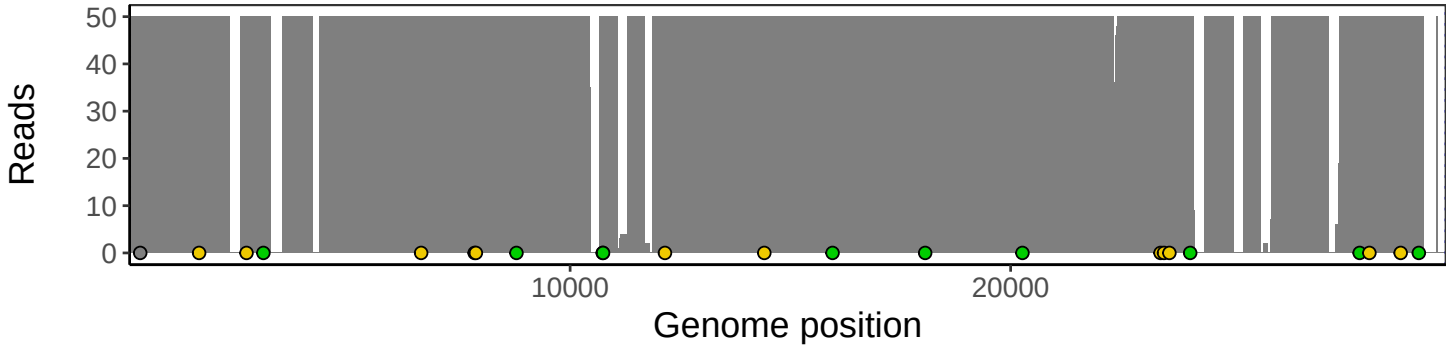


VSP0670-1 | 2021-02-09 | VTM or Saline | H2102030405 | genomes | single experiment

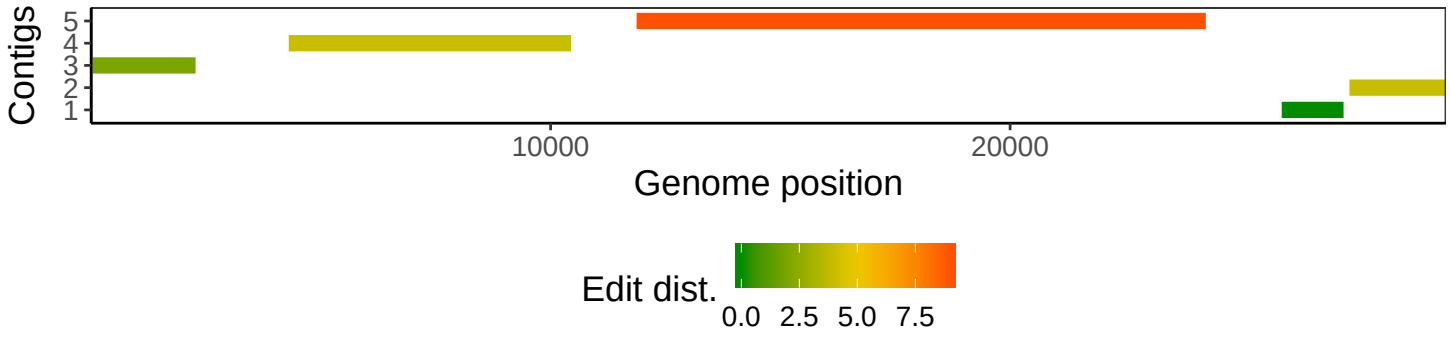
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

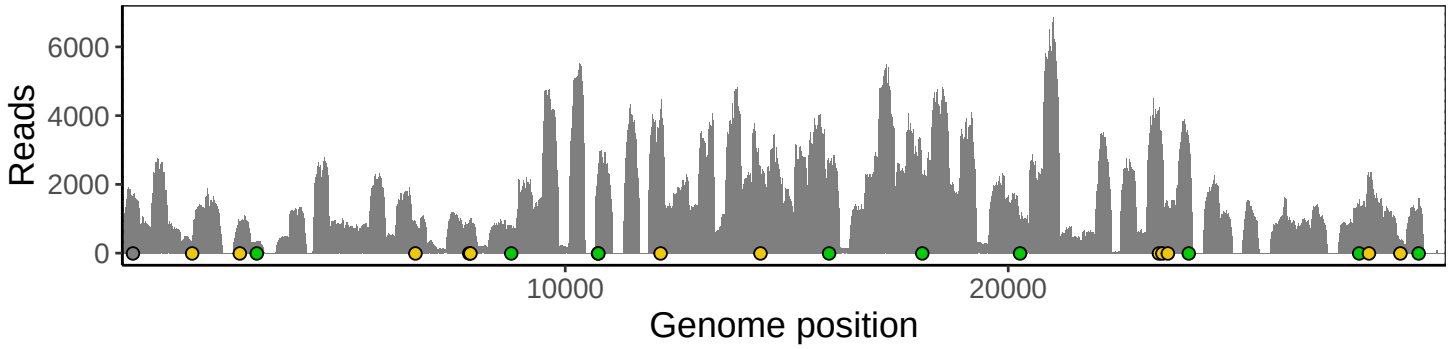


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

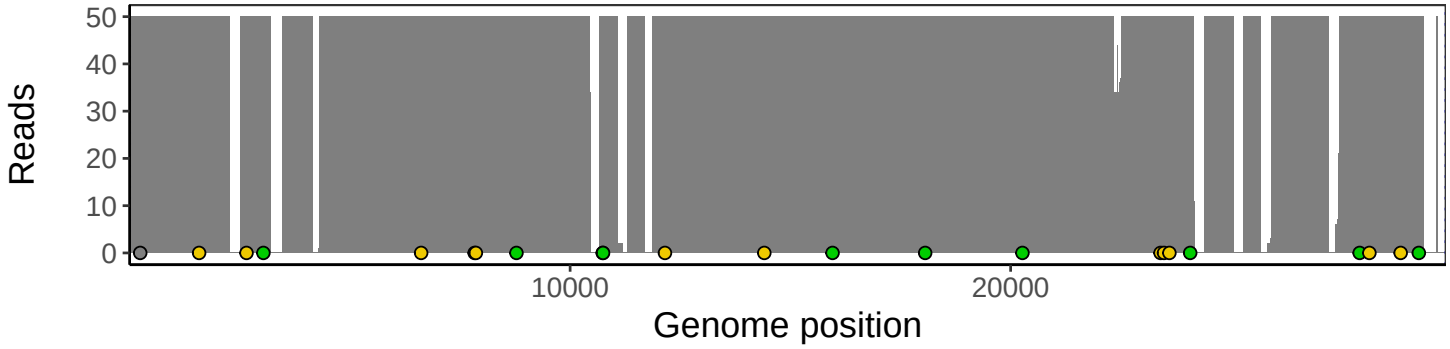


VSP0670-2 | 2021-02-09 | VTM or Saline | H2102030405 | genomes | single experiment

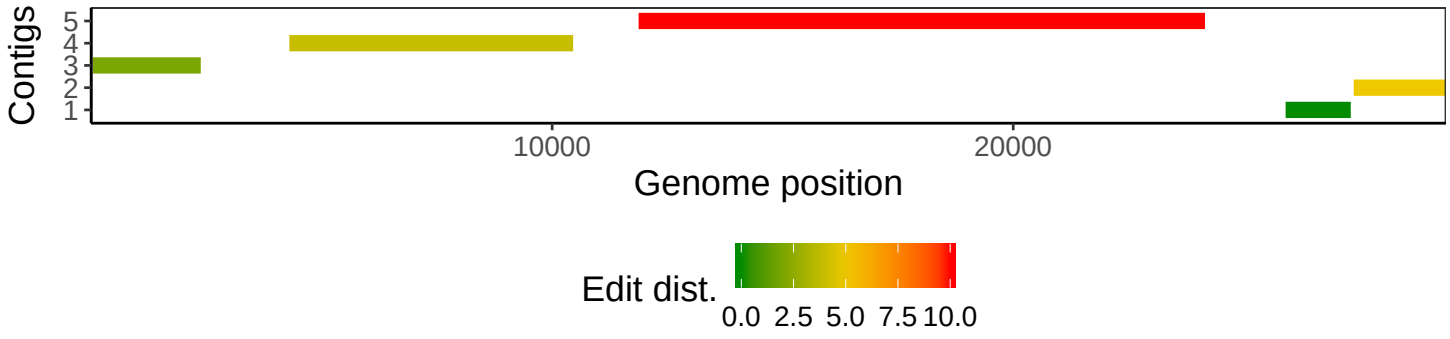
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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