COVID-19 subject H2102030405

2021-04-01

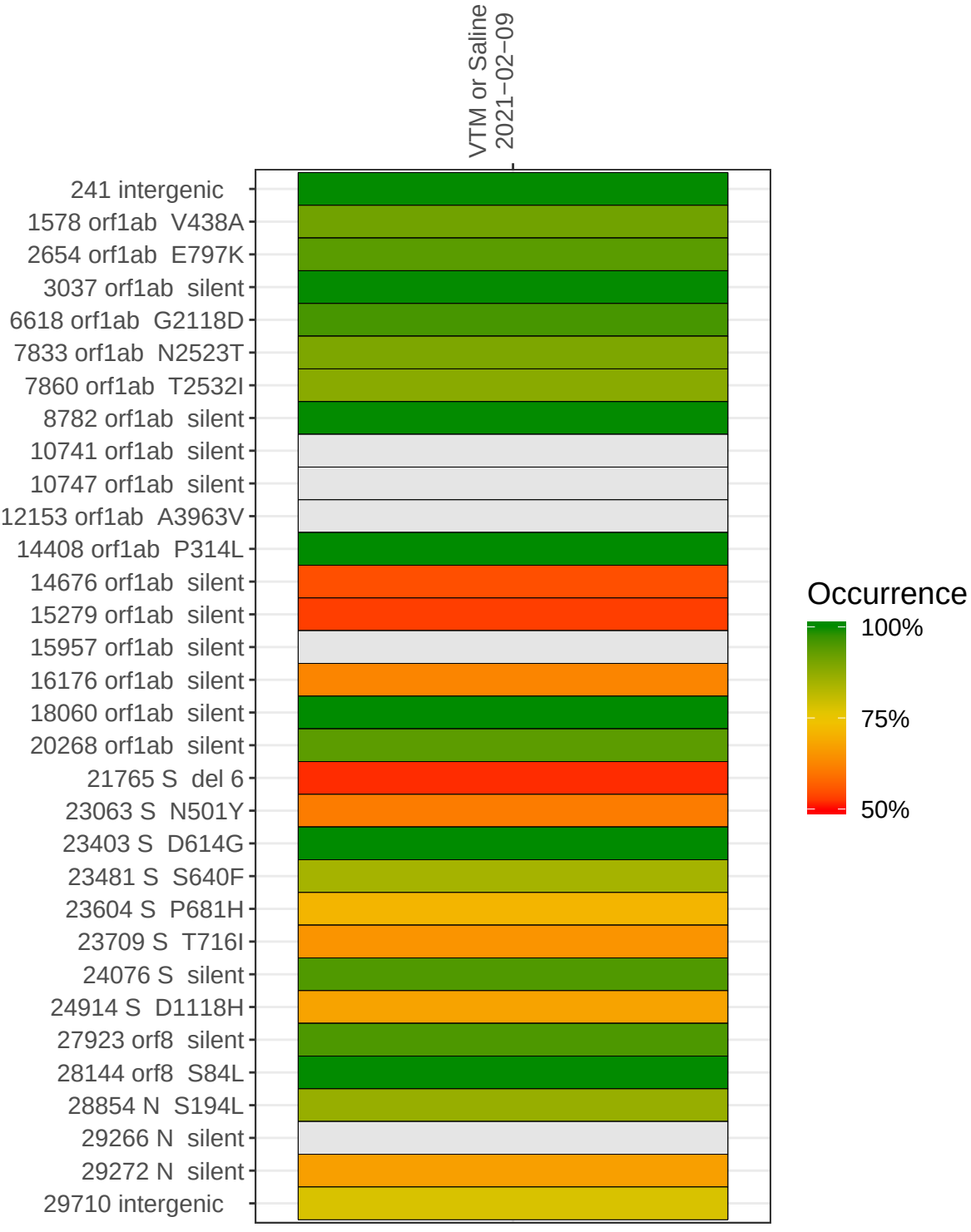
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

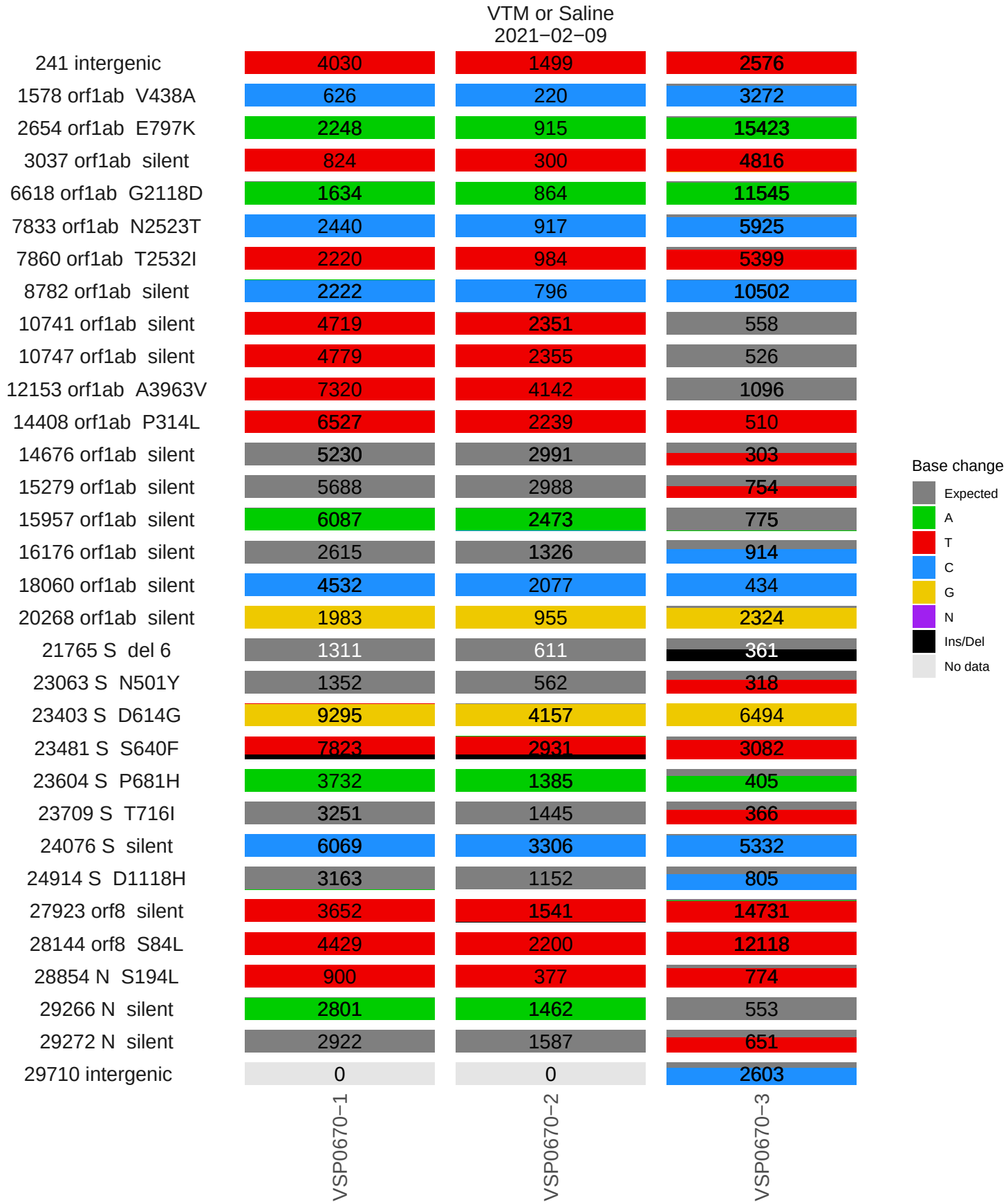
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
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.

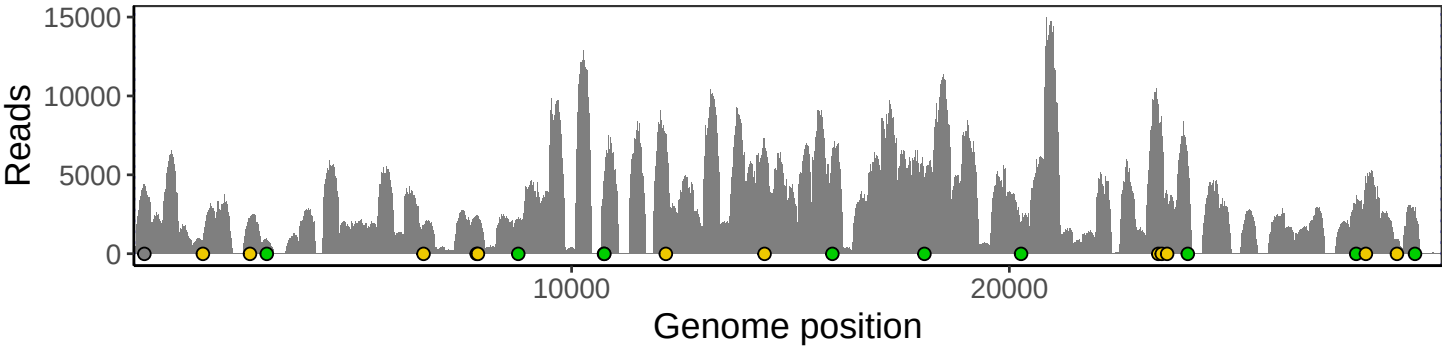



VTM or Saline
2021−02−09
241 intergenic
1578 orf1ab V438A
2654 orf1ab E797K
3037 orf1ab silent
6618 orf1ab G2118D
7833 orf1ab N2523T
7860 orf1ab T2532I
8782 orf1ab silent
10741 orf1ab silent
10747 orf1ab silent
12153 orf1ab A3963V
14408 orf1ab P314L
14676 orf1ab silent
15279 orf1ab silent
15957 orf1ab silent
16176 orf1ab silent
18060 orf1ab silent
20268 orf1ab silent
21765 S del 6
23063 S N501Y
23403 S D614G
23481 S S640F
23604 S P681H
23709 S T716I
24076 S silent
24914 S D1118H
27923 orf8 silent
28144 orf8 S84L
28854 N S194L
29266 N silent
29272 N silent
29710 intergenic
4030 1499 2576
626 220 3272
2248 915 15423
824 300 4816
1634 864 11545
2440 917 5925
2220 984 5399
2222 796 10502
4719 2351 558
4779 2355 526
7320 4142 1096
6527 2239 510
5230 2991 303
5688 2988 754
6087 2473 775
2615 1326 914
4532 2077 434
1983 955 2324
1311 611 361
1352 562 318
9295 4157 6494
7823 2931 3082
3732 1385 405
3251 1445 366
6069 3306 5332
3163 1152 805
3652 1541 14731
4429 2200 12118
900 377 774
2801 1462 553
2922 1587 651
0 0 2603
VSP0670−1
VSP0670−2
VSP0670−3
Base change
Expected
A
T
C
G
N
Ins/Del
No data

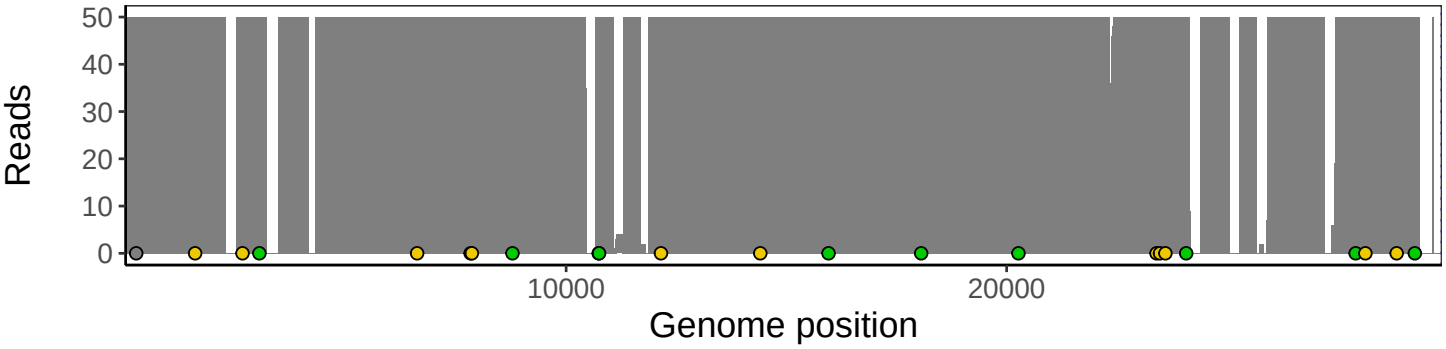
Analyses of individual experiments and composite results

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

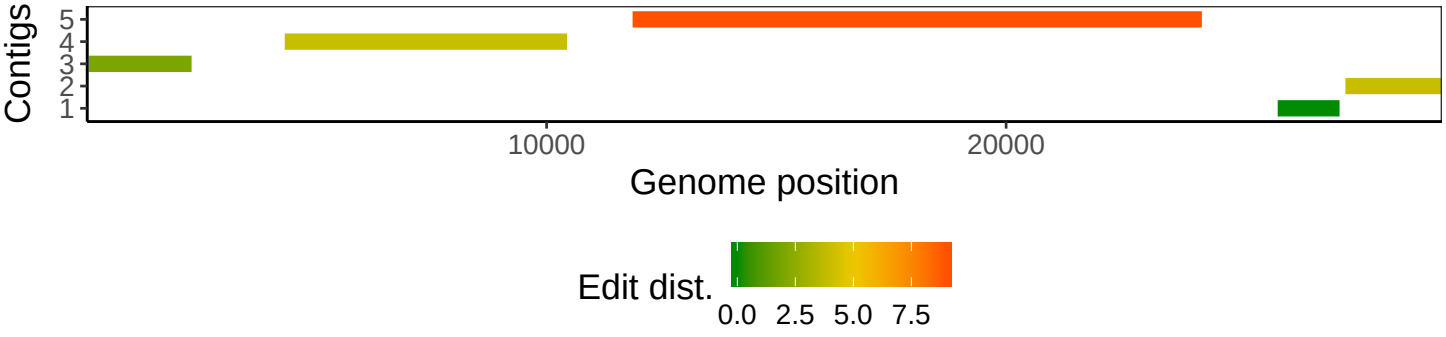
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

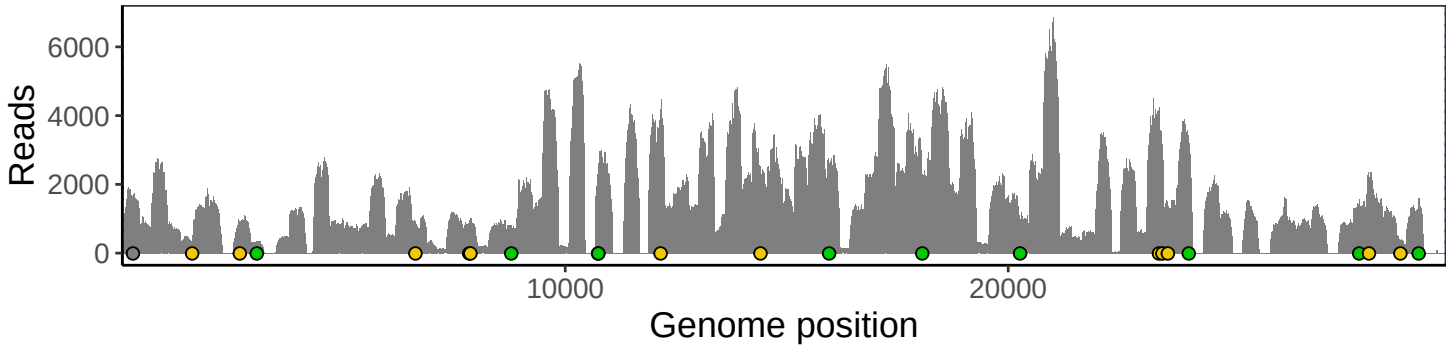


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

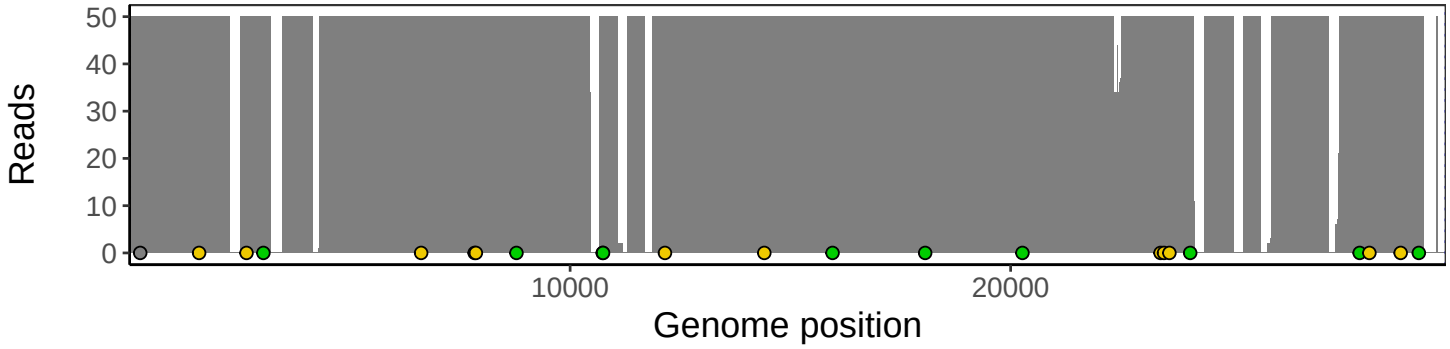


VSP0670-2 | 2021-02-09 | VTM or Saline | H2102030405 | genomes | single experiment

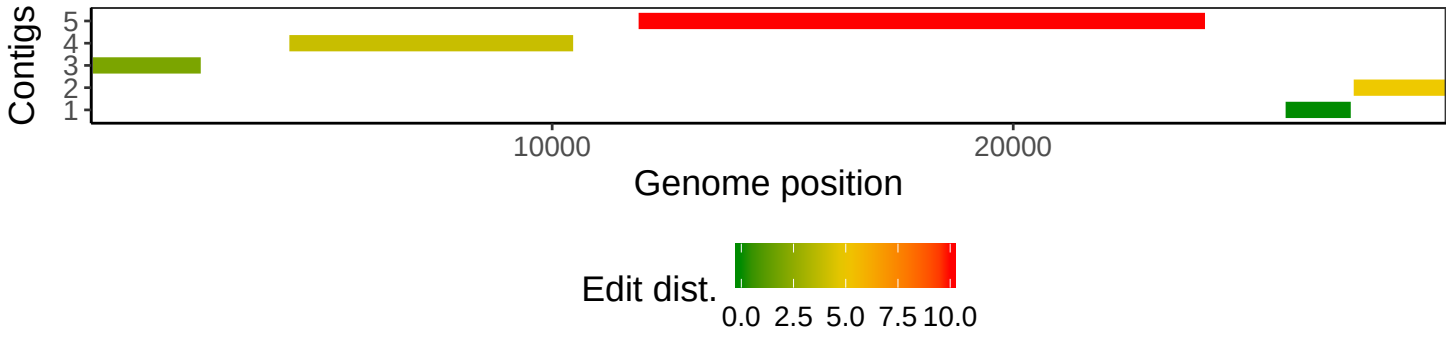
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

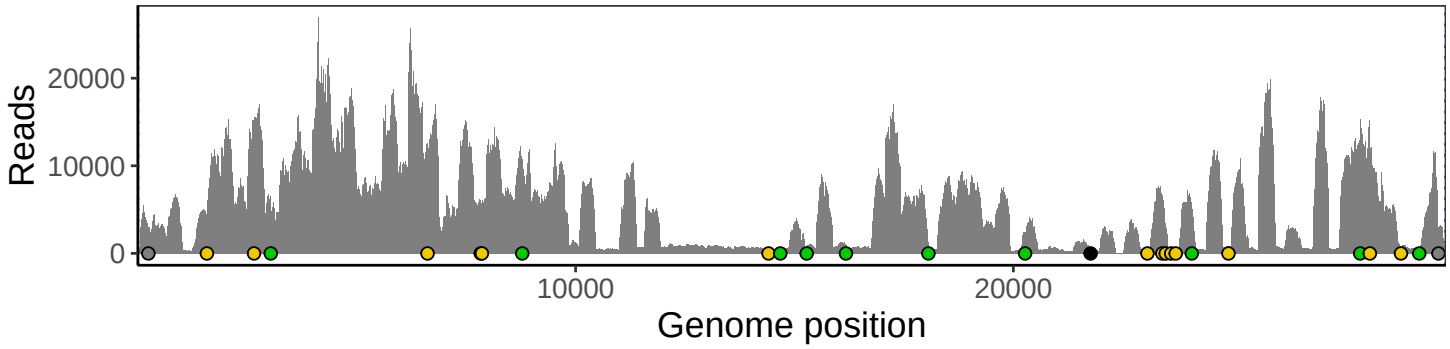


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

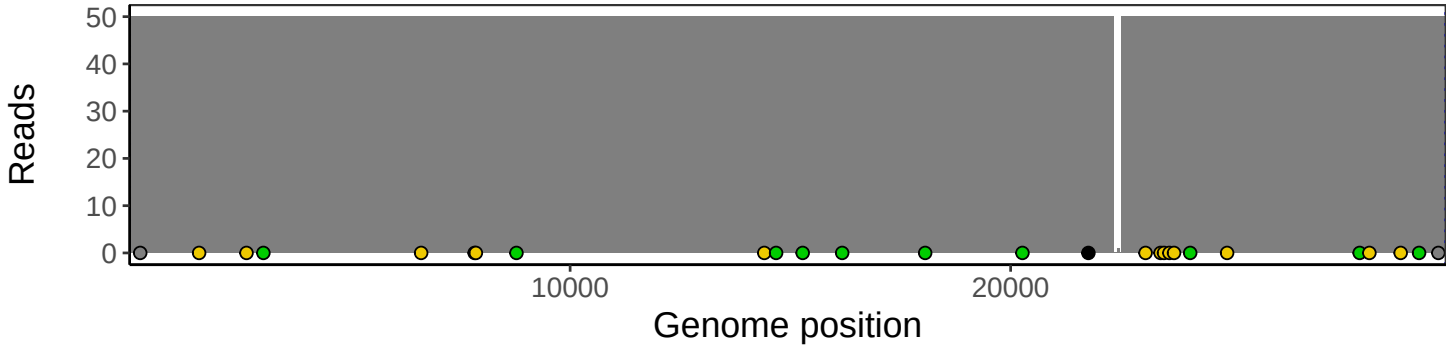


VSP0670-3 | 2021-02-09 | VTM or Saline | H2102030405 | genomes | single experiment

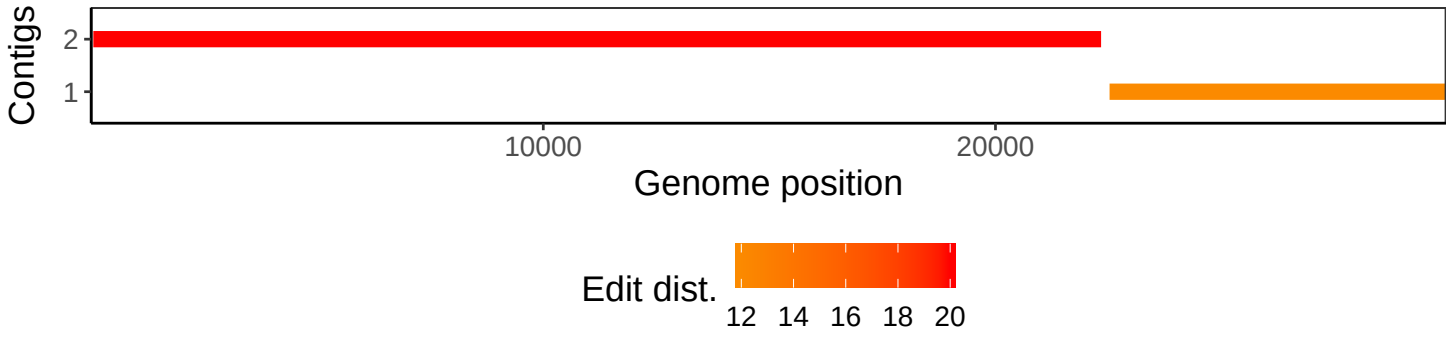
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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