COVID-19 subject 263

2021-03-01

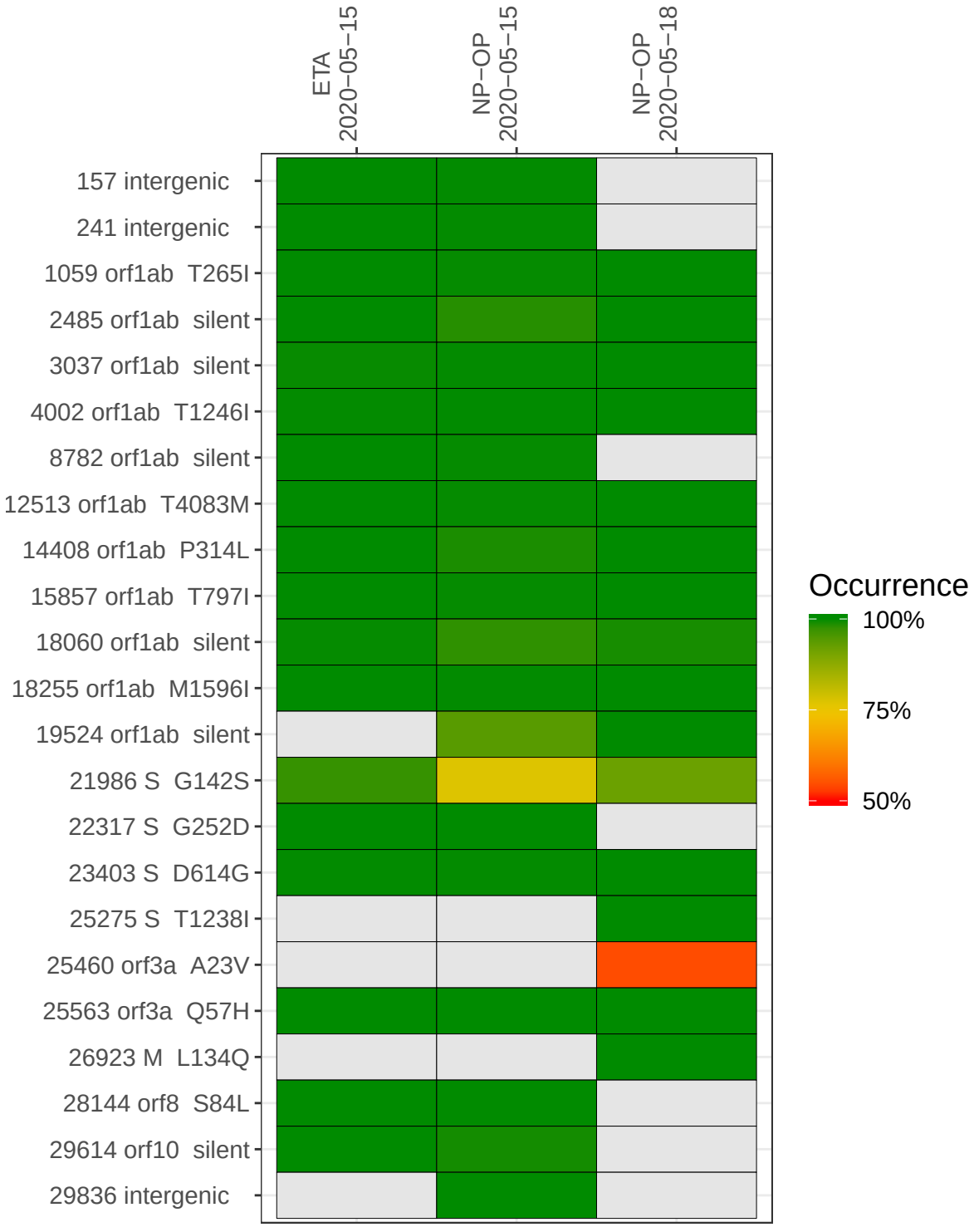
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

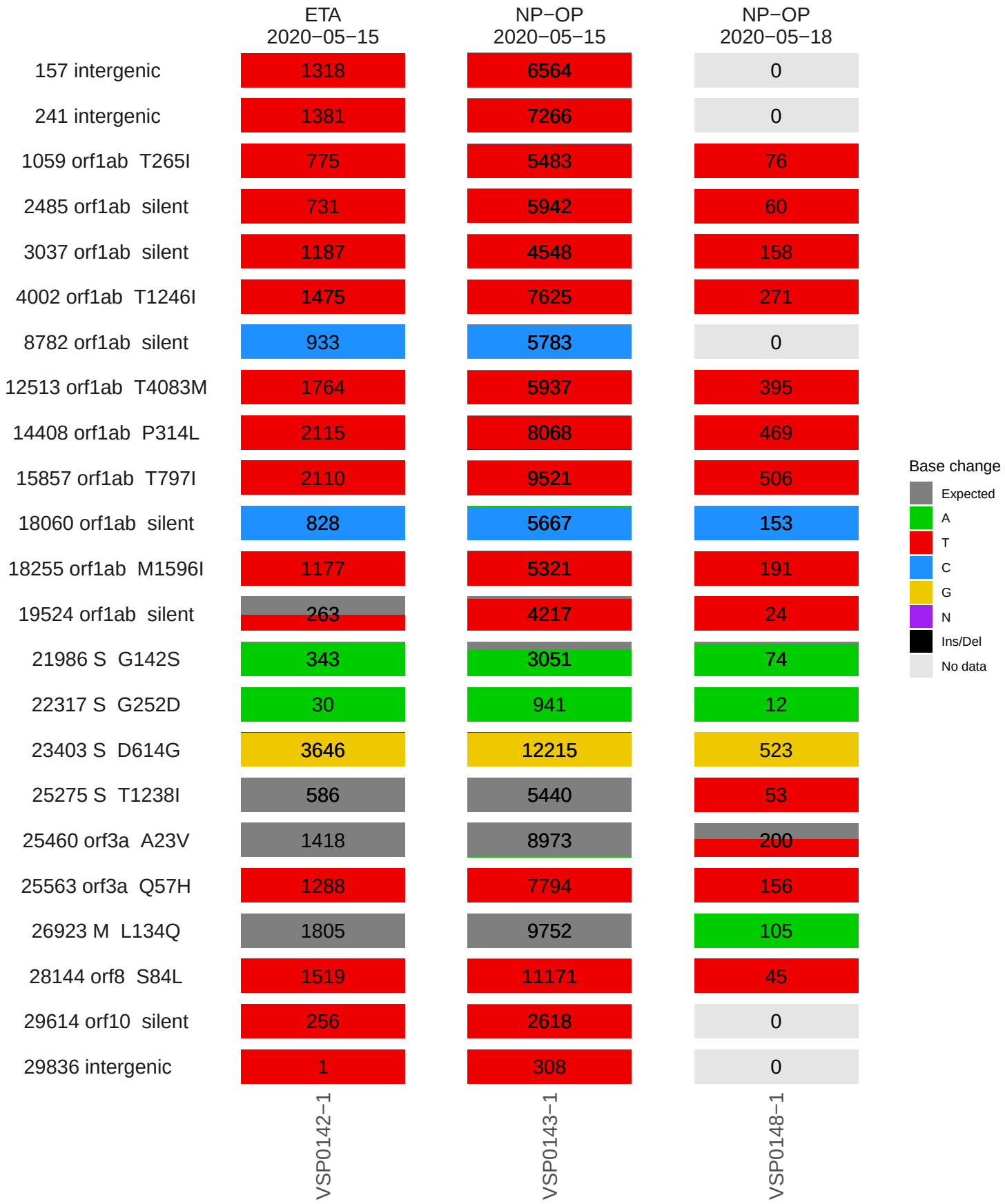
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0142-1	single experiment	NA	ETA	2020-05-15	29.81	B.1.350	99.7%	99.7%
VSP0143-1	single experiment	172000	NP-OP	2020-05-15	29.87	B.1.350	99.8%	99.8%
VSP0148-1	single experiment	NA	NP-OP	2020-05-18	8.68	B.1.350	90.7%	90.2%

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.

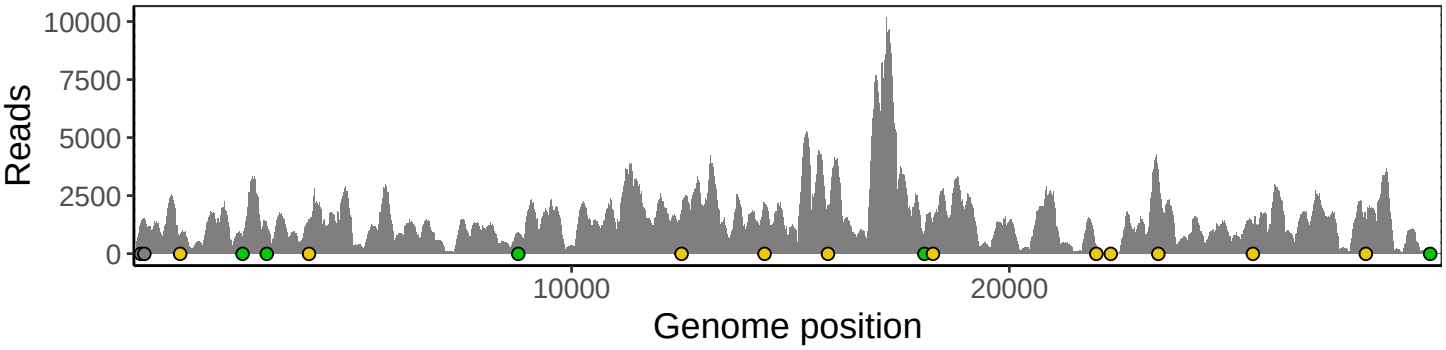



ETA
2020−05−15
NP−OP
2020−05−15
NP−OP
2020−05−18
157 intergenic
1318
6564
0
241 intergenic
1381
7266
0
1059 orf1ab T265I
775
5483
76
2485 orf1ab silent
731
5942
60
3037 orf1ab silent
1187
4548
158
4002 orf1ab T1246I
1475
7625
271
8782 orf1ab silent
933
5783
0
12513 orf1ab T4083M
1764
5937
395
14408 orf1ab P314L
2115
8068
469
15857 orf1ab T797I
2110
9521
506
18060 orf1ab silent
828
5667
153
18255 orf1ab M1596I
1177
5321
191
19524 orf1ab silent
263
4217
24
21986 S G142S
343
3051
74
22317 S G252D
30
941
12
23403 S D614G
3646
12215
523
25275 S T1238I
586
5440
53
25460 orf3a A23V
1418
8973
200
25563 orf3a Q57H
1288
7794
156
26923 M L134Q
1805
9752
105
28144 orf8 S84L
1519
11171
45
29614 orf10 silent
256
2618
0
29836 intergenic
1
308
0
VSP0142−1
VSP0143−1
VSP0148−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

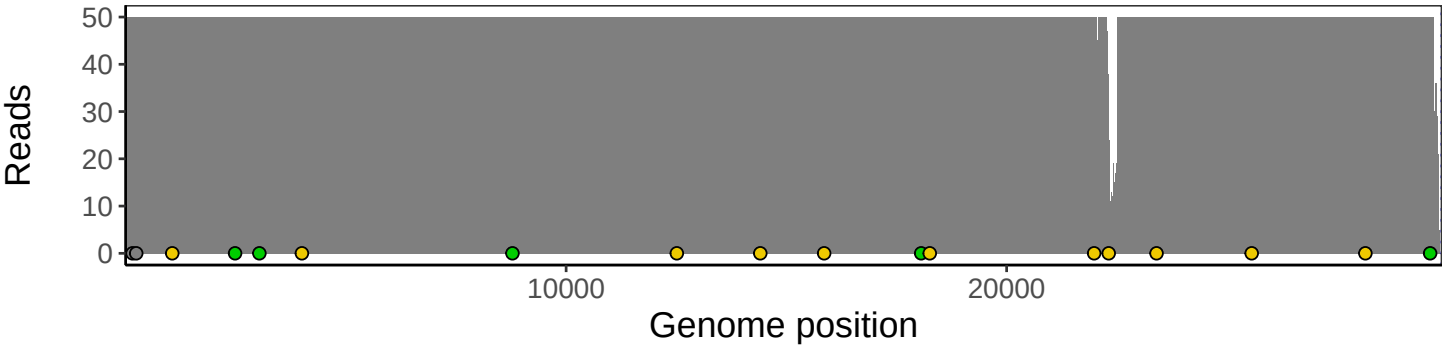
Analyses of individual experiments and composite results

VSP0142-1 | 2020-05-15 | ETA | 263e-q1 | genomes | single experiment

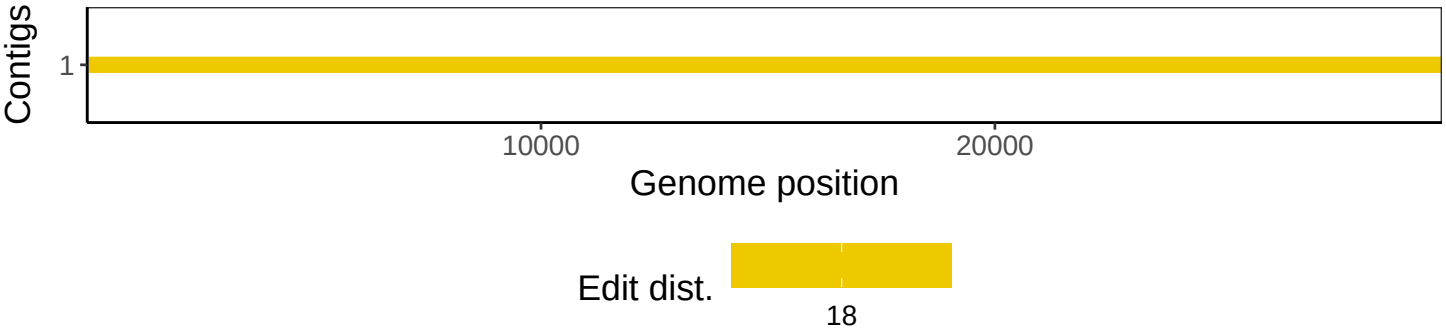
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

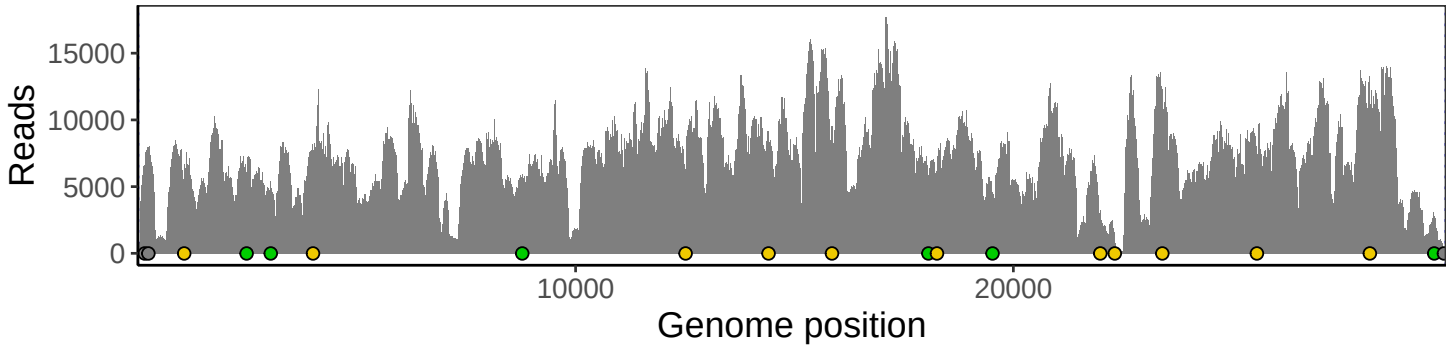


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

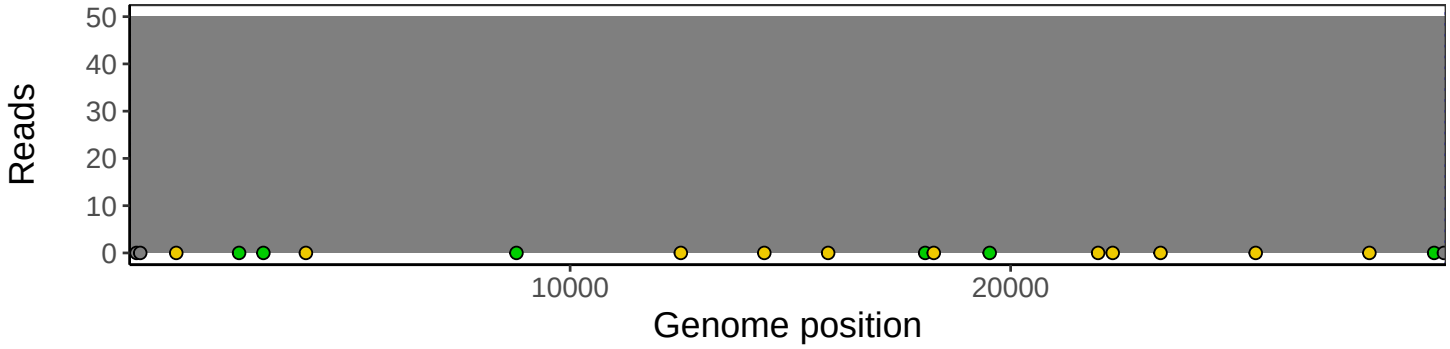


VSP0143-1 | 2020-05-15 | NP-OP | 263no-q1 | 172000 genomes | single experiment

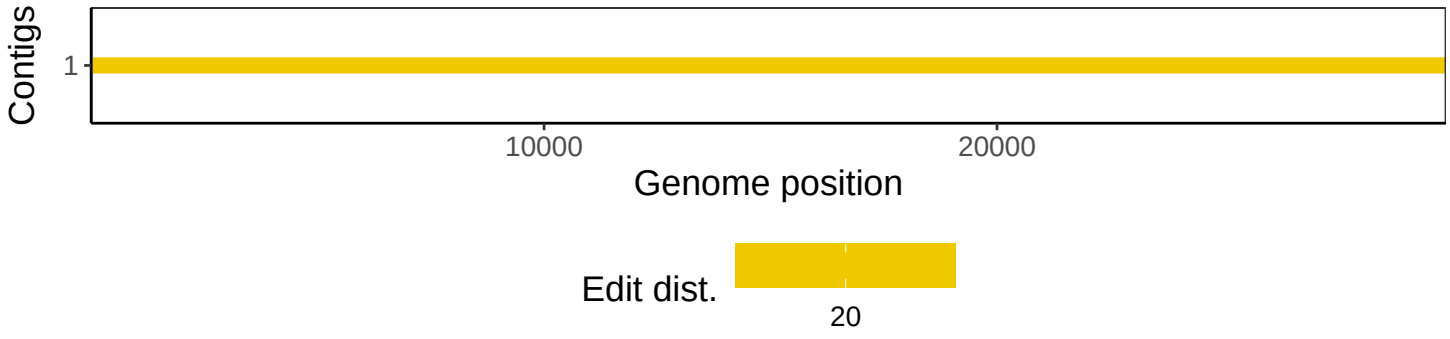
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

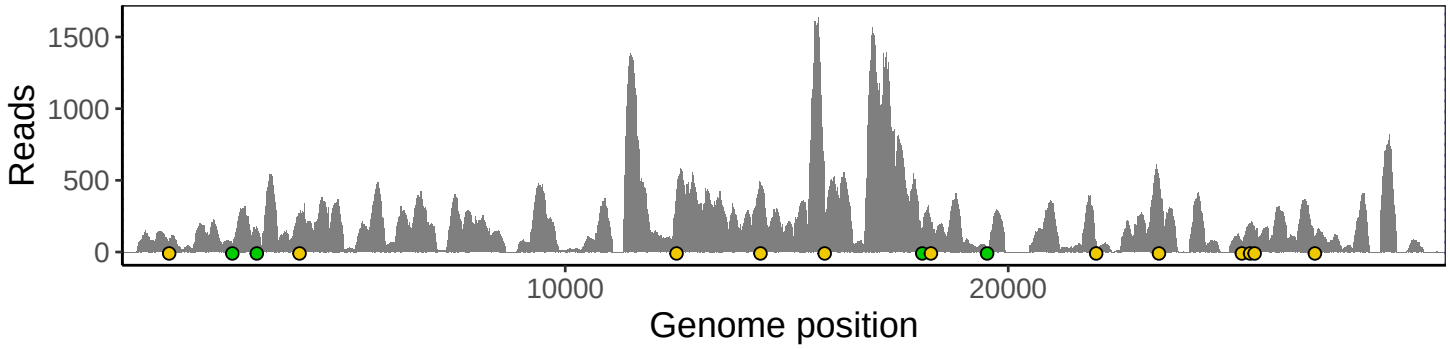


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

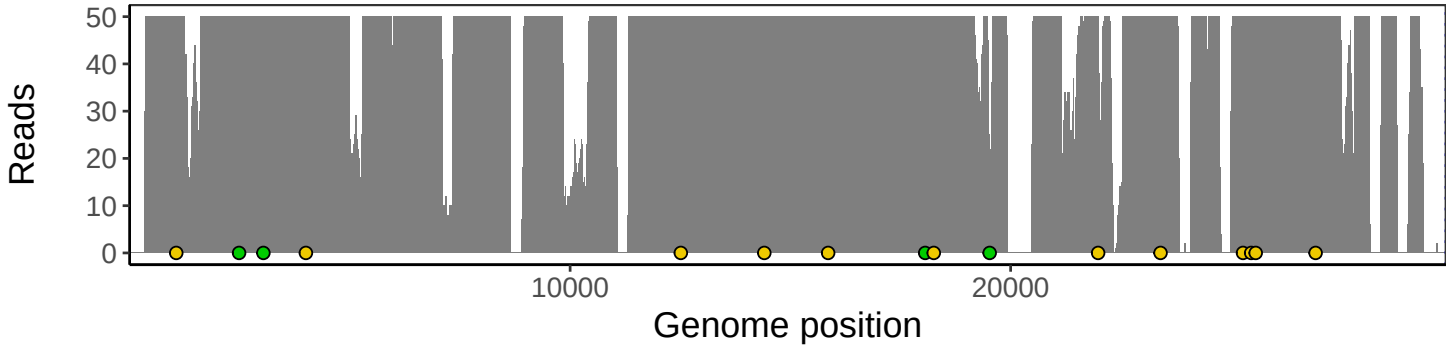


VSP0148-1 | 2020-05-18 | NP-OP | 263no-q2 | genomes | single experiment

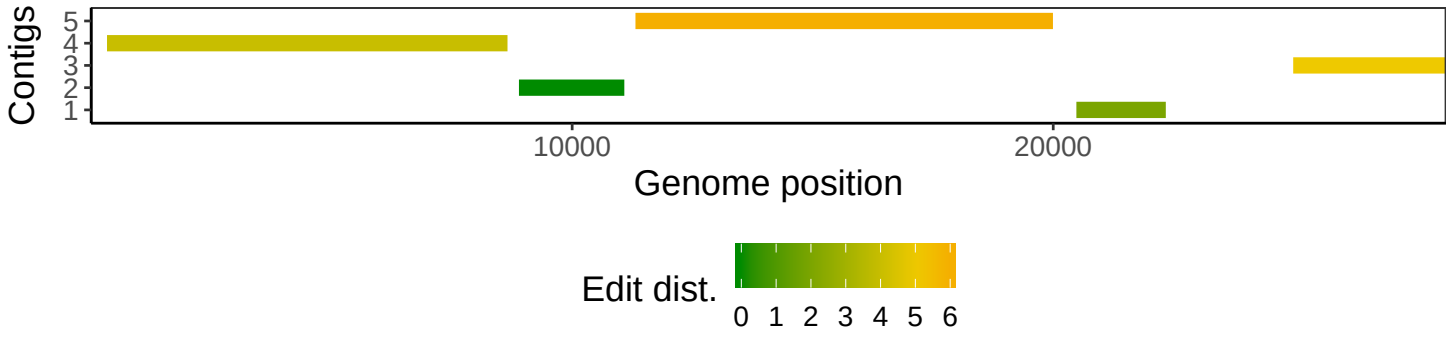
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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