COVID-19 subject 211-TCE

2020-11-30

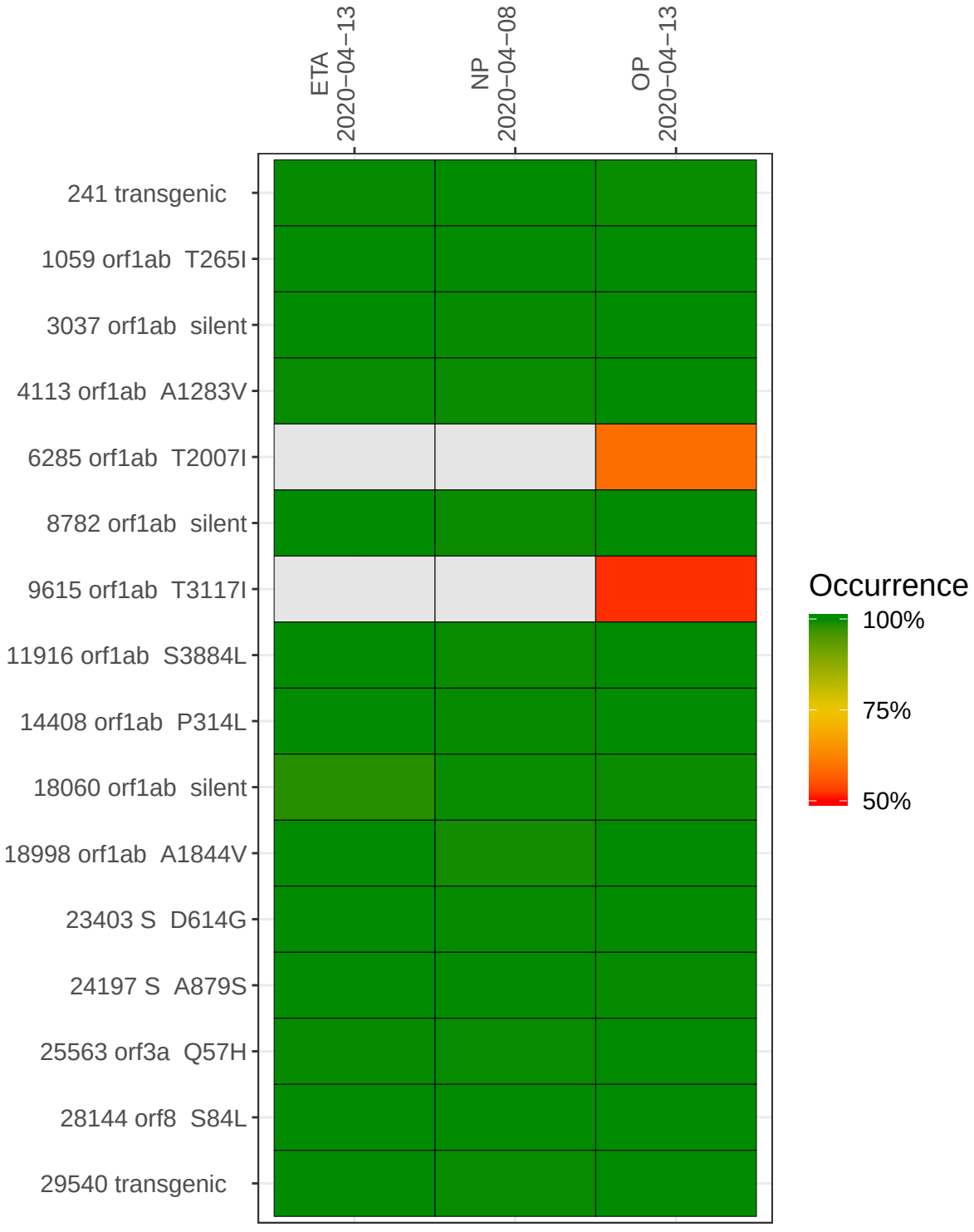
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

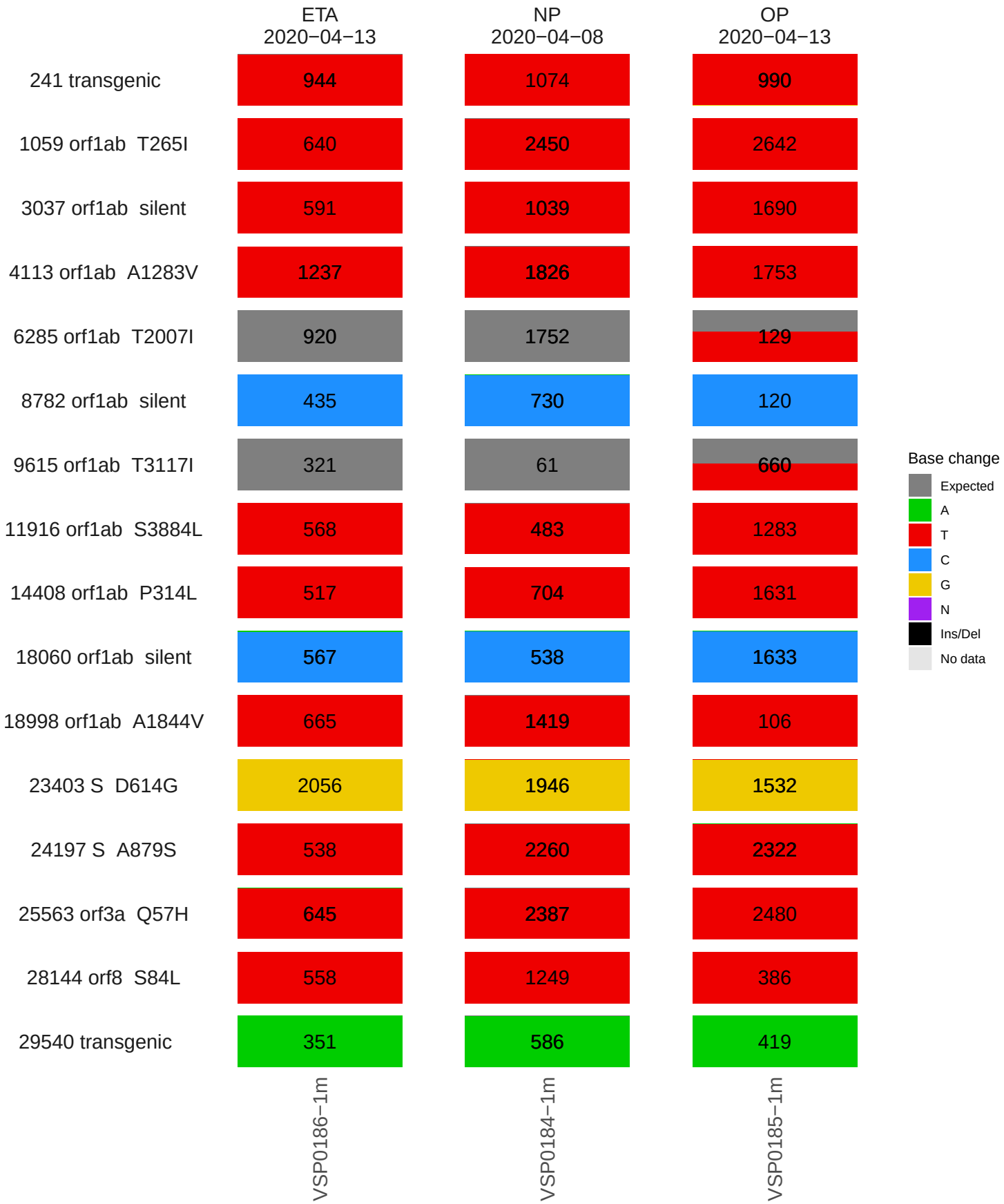
Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0184-1m	single experiment	NA	NP	2020-04-08	29.86	99.9%	99.8%
VSP0185-1m	single experiment	NA	OP	2020-04-13	29.88	99.9%	99.8%
VSP0186-1m	single experiment	NA	ETA	2020-04-13	29.80	99.9%	99.8%

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 for 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.

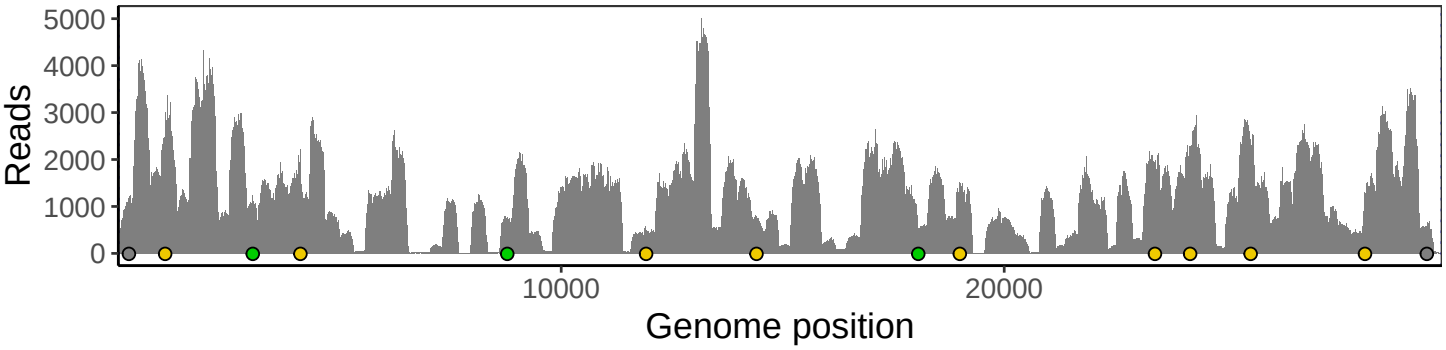



ETA
2020−04−13
NP
2020−04−08
OP
2020−04−13
241 transgenic
944
1074
990
1059 orf1ab T265I
640
2450
2642
3037 orf1ab silent
591
1039
1690
4113 orf1ab A1283V
1237
1826
1753
6285 orf1ab T2007I
920
1752
129
8782 orf1ab silent
435
730
120
9615 orf1ab T3117I
321
61
660
11916 orf1ab S3884L
568
483
1283
14408 orf1ab P314L
517
704
1631
18060 orf1ab silent
567
538
1633
18998 orf1ab A1844V
665
1419
106
23403 S D614G
2056
1946
1532
24197 S A879S
538
2260
2322
25563 orf3a Q57H
645
2387
2480
28144 orf8 S84L
558
1249
386
29540 transgenic
351
586
419
VSP0186−1m
VSP0184−1m
VSP0185−1m
Base change
Expected
A
T
C
G
N
Ins/Del
No data

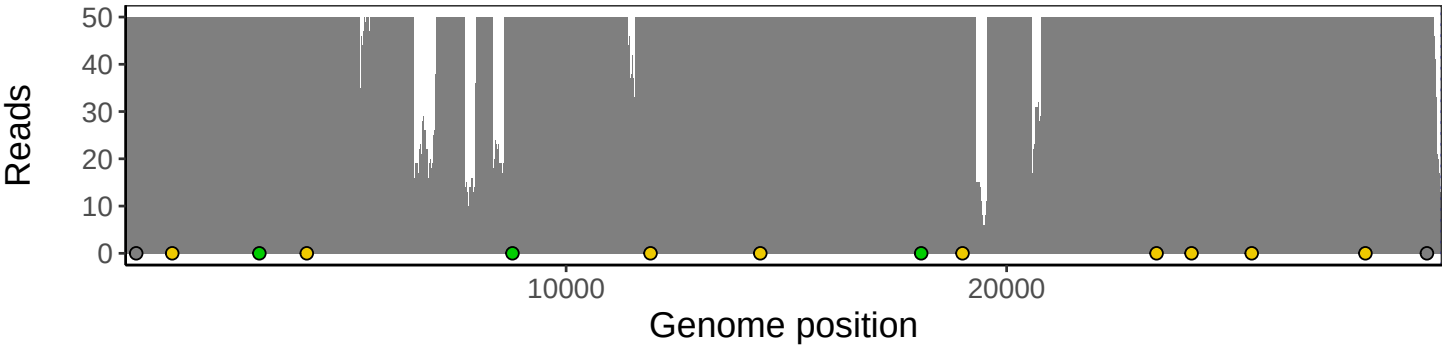
Analyses of individual experiments and composite results.

VSP0184-1m | 2020-04-08 | NP | 5 | genomes | single experiment

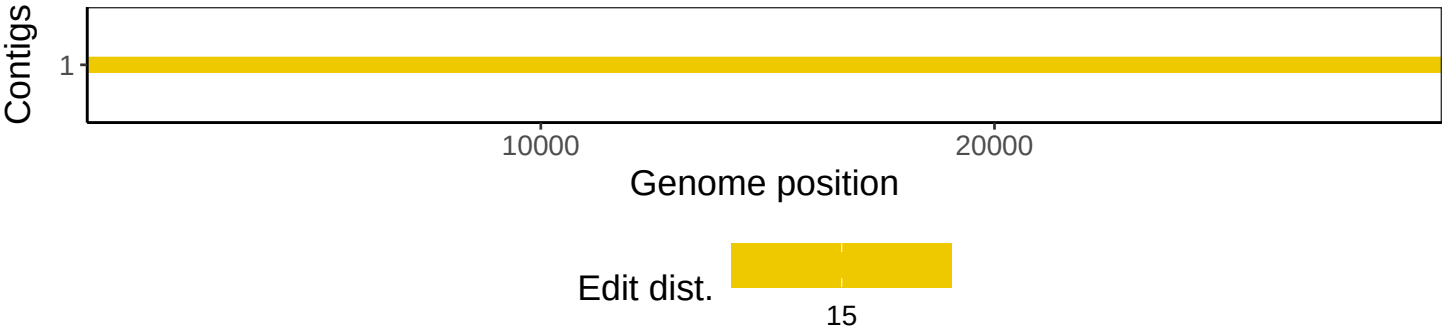
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

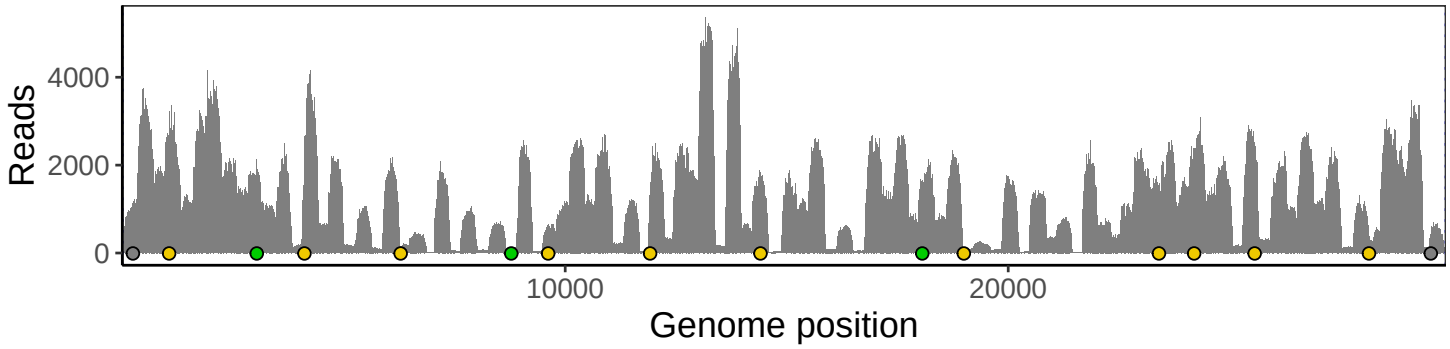


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

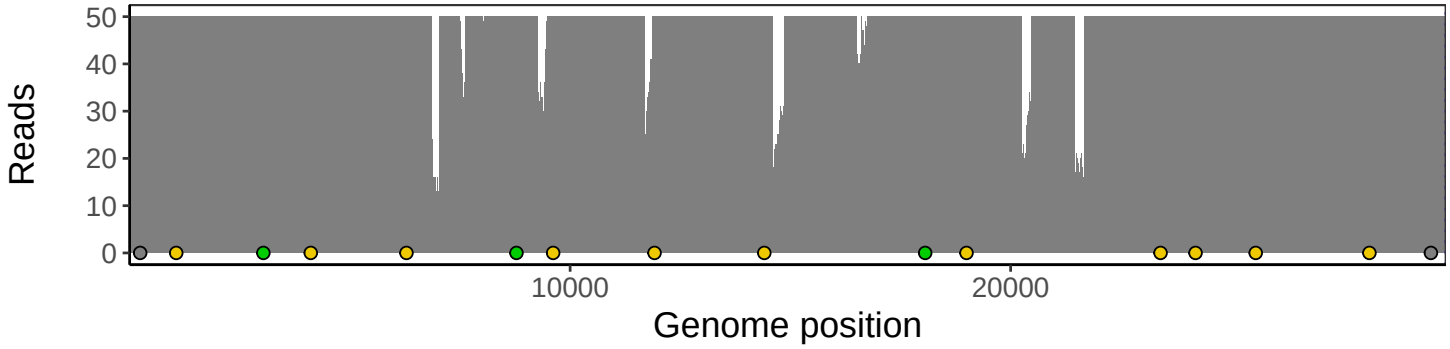


VSP0185-1m | 2020-04-13 | OP | 6 | genomes | single experiment

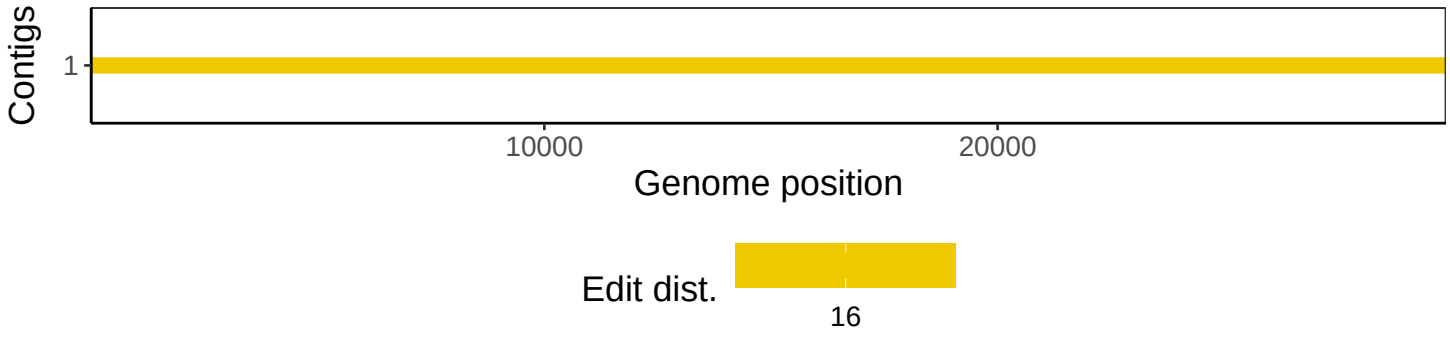
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

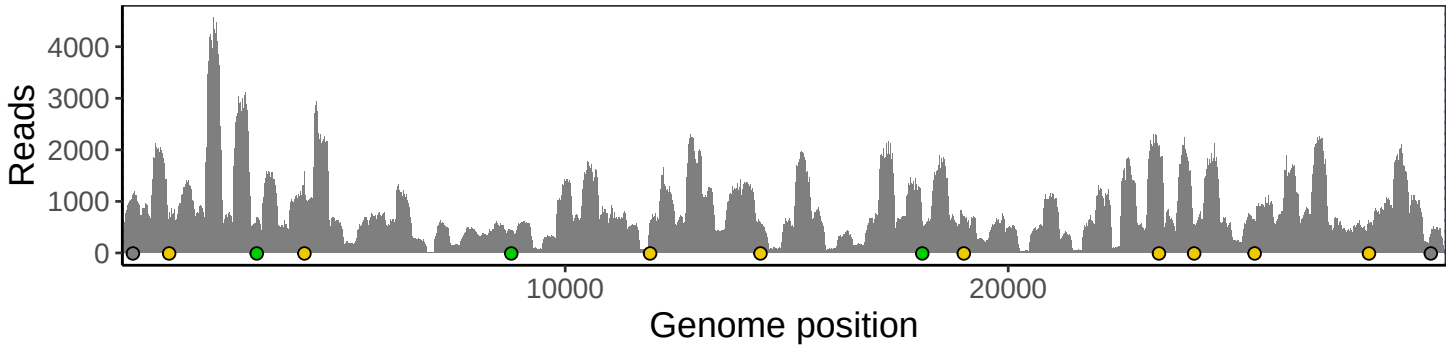


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

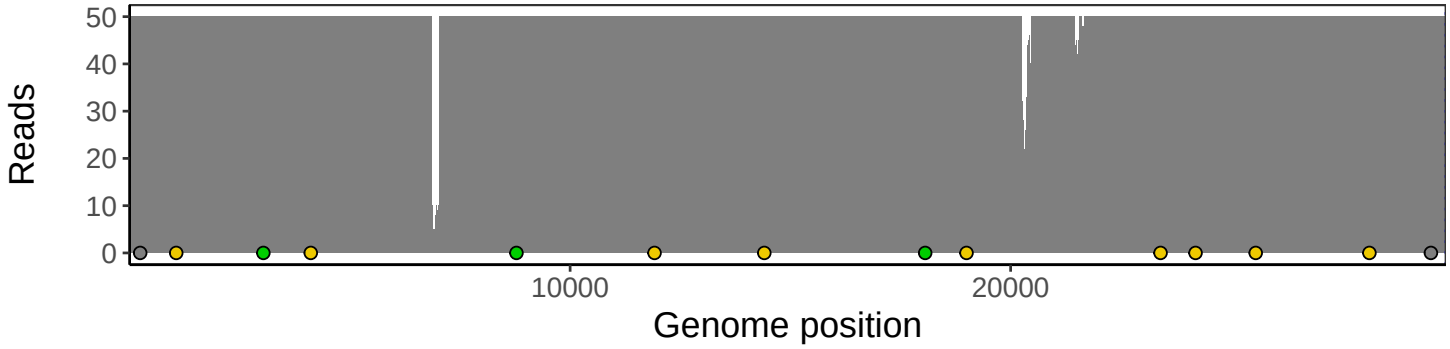
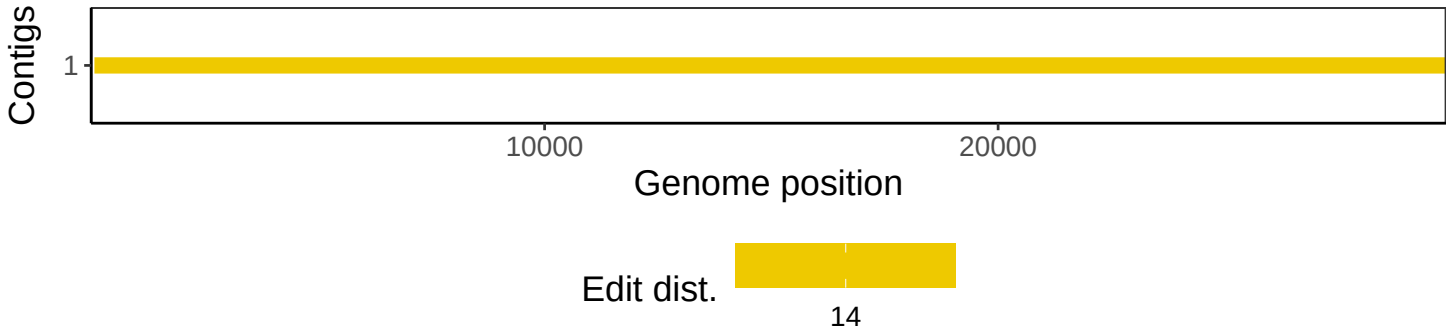


VSP0186-1m | 2020-04-13 | ETA | 7 | genomes | single experiment

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.