COVID-19 subject 211-TCE

2021-01-10

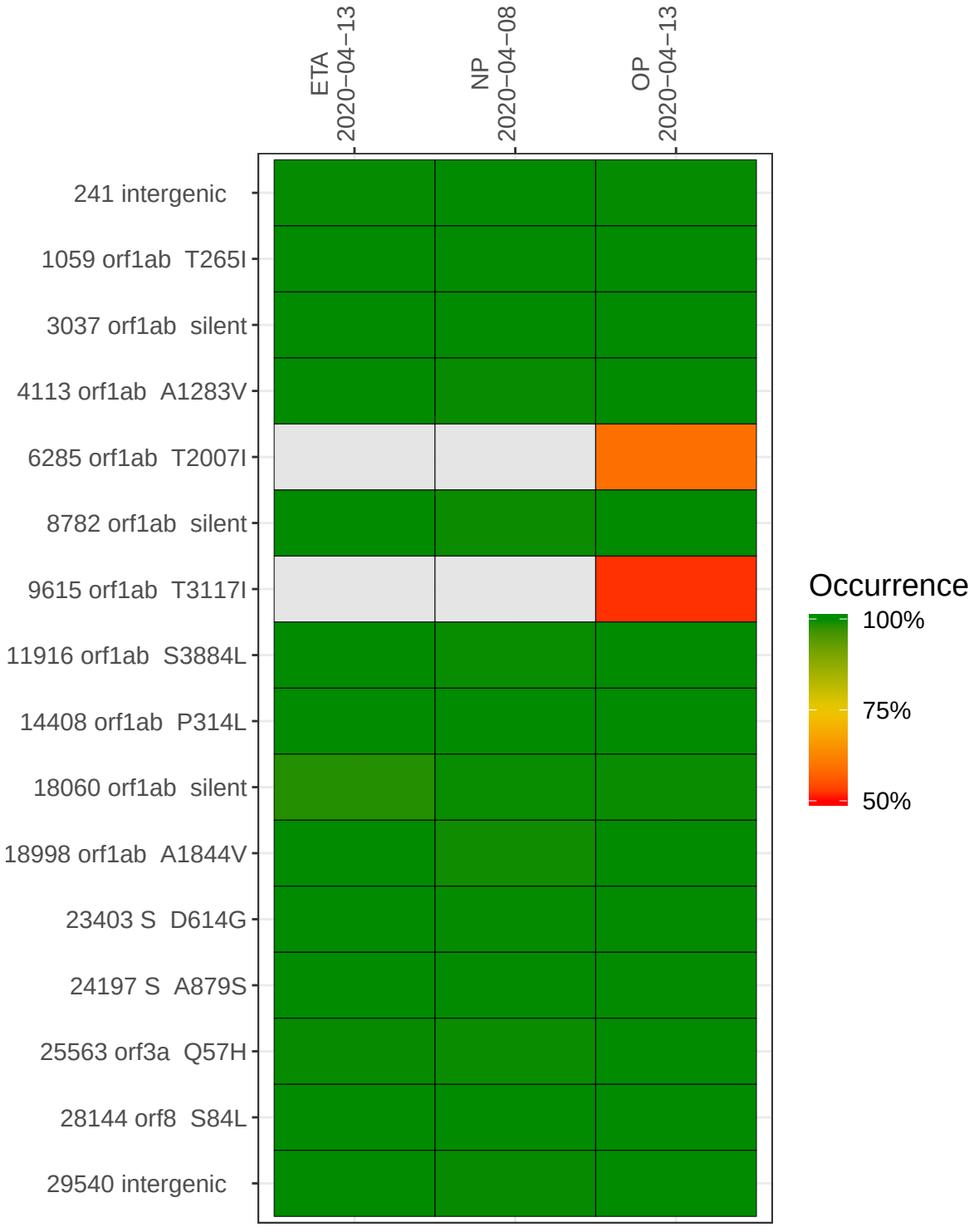
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

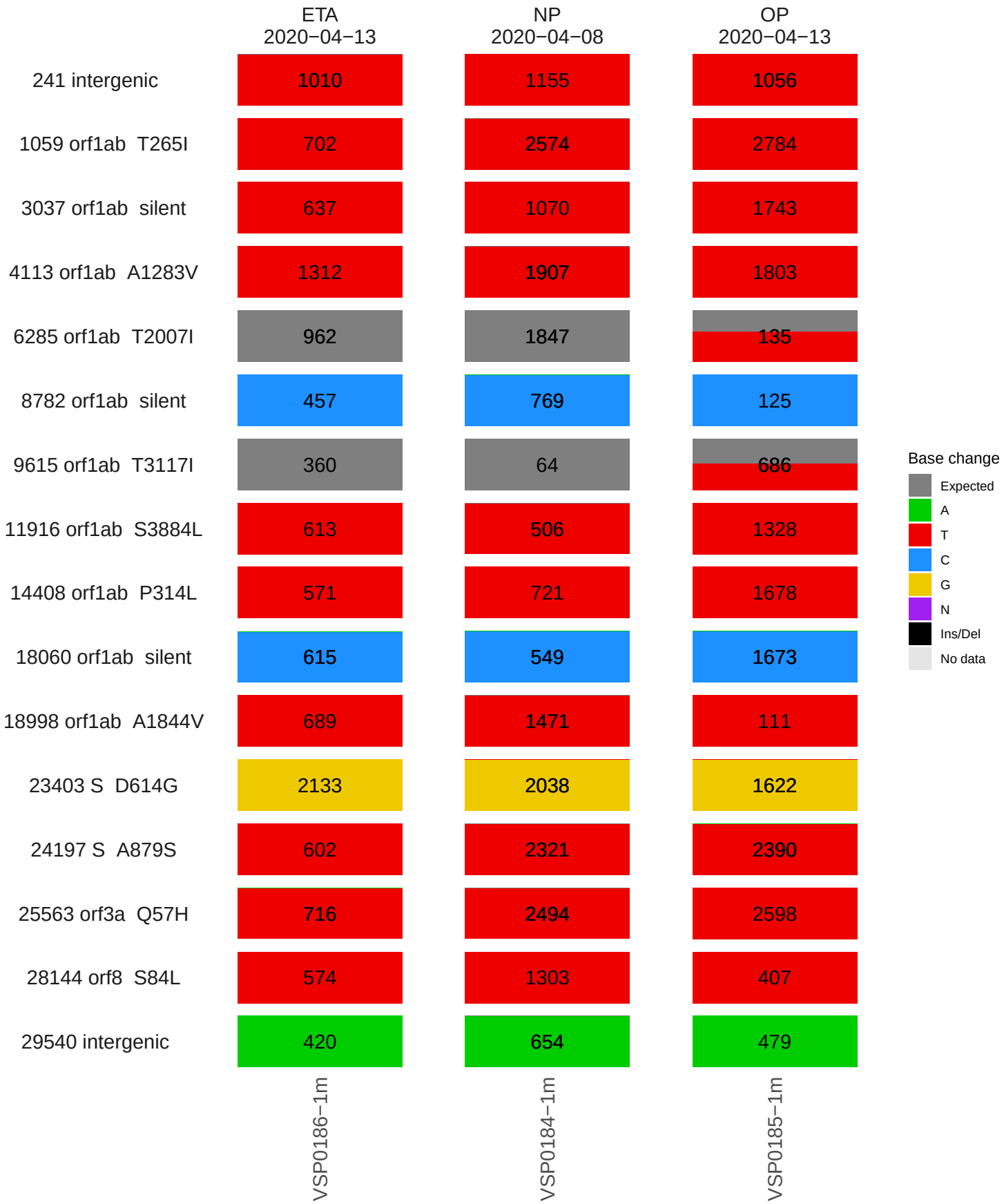
Table 1. Sample summary.

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	29.96	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.

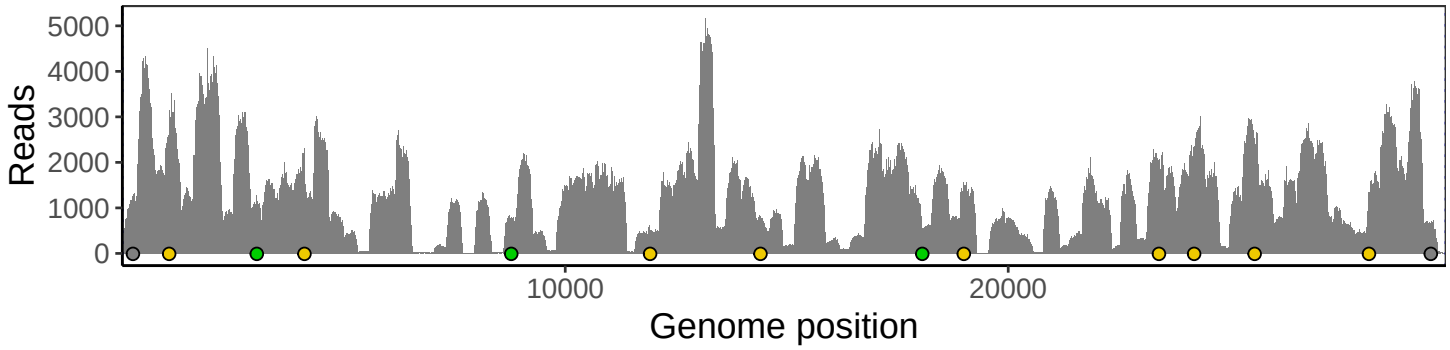



ETA
2020−04−13
NP
2020−04−08
OP
2020−04−13
241 intergenic
1059 orf1ab T265I
3037 orf1ab silent
4113 orf1ab A1283V
6285 orf1ab T2007I
8782 orf1ab silent
9615 orf1ab T3117I
11916 orf1ab S3884L
14408 orf1ab P314L
18060 orf1ab silent
18998 orf1ab A1844V
23403 S D614G
24197 S A879S
25563 orf3a Q57H
28144 orf8 S84L
29540 intergenic
1010
1155
1056
702
2574
2784
637
1070
1743
1312
1907
1803
962
1847
135
457
769
125
360
64
686
613
506
1328
571
721
1678
615
549
1673
689
1471
111
2133
2038
1622
602
2321
2390
716
2494
2598
574
1303
407
420
654
479
Base change
Expected
A
T
C
G
N
Ins/Del
No data
VSP0186−1m
VSP0184−1m
VSP0185−1m

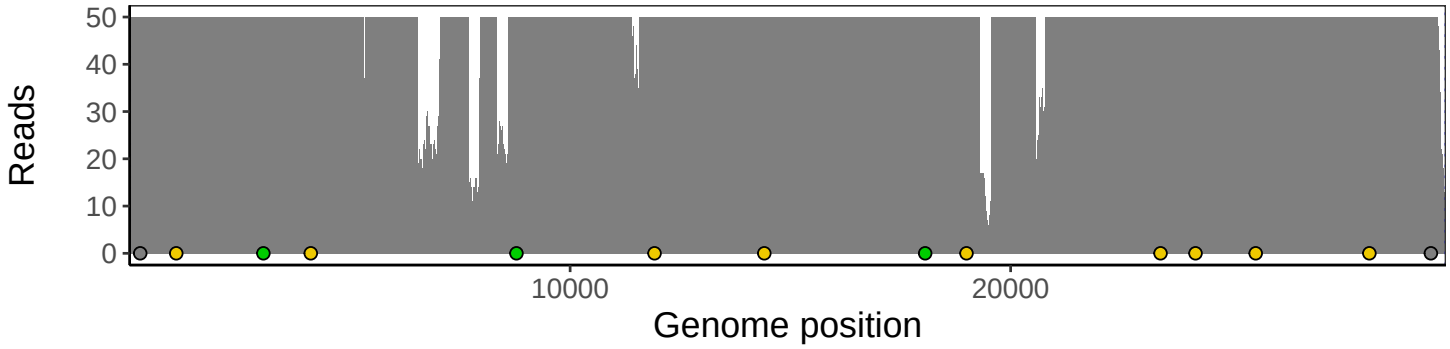
Analyses of individual experiments and composite results.

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

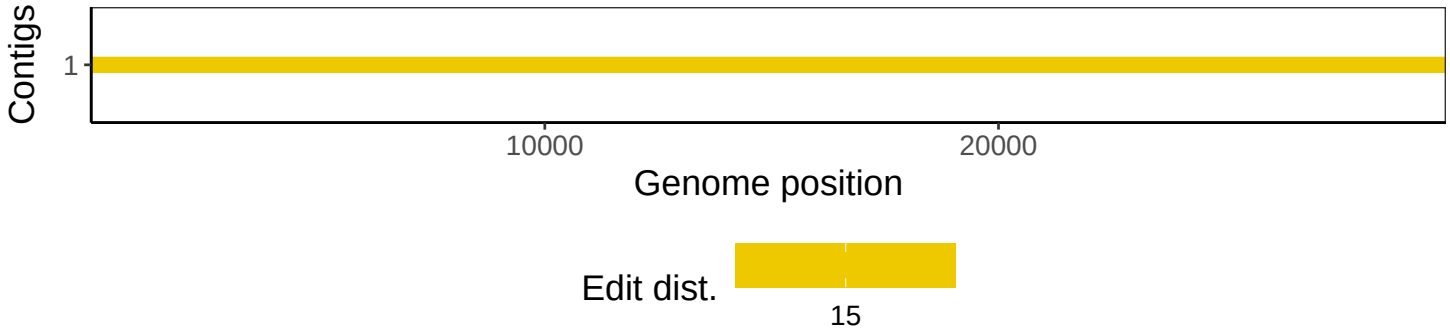
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

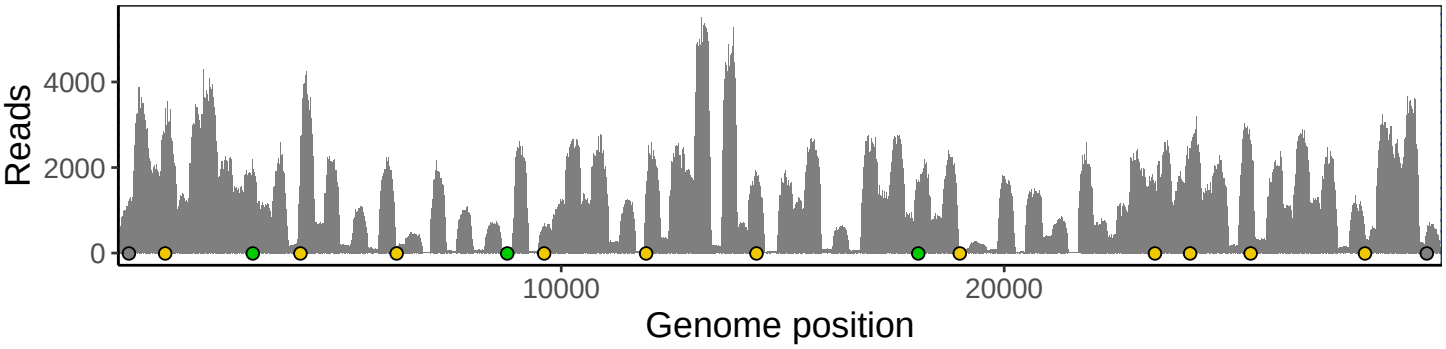


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

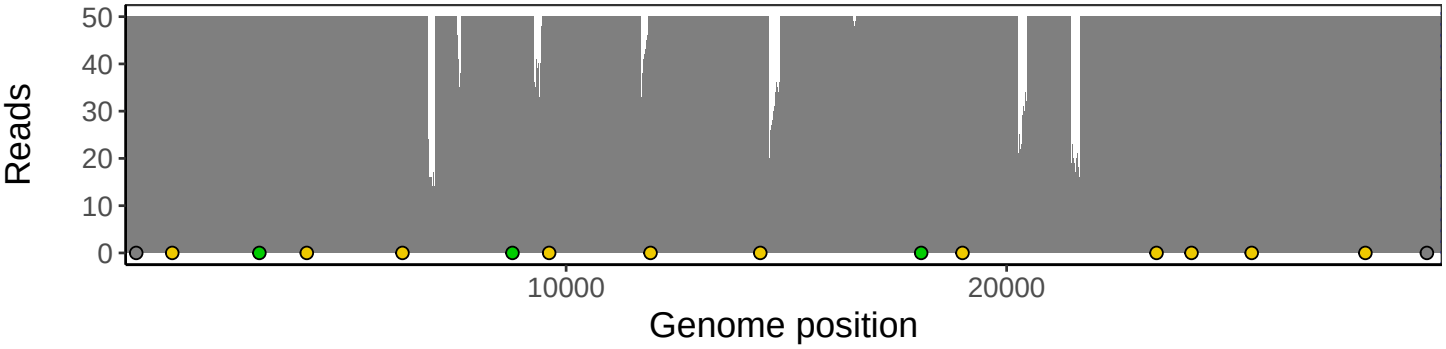


VSP0185-1m | 2020-04-13 | OP | 6 | genomes | single experiment

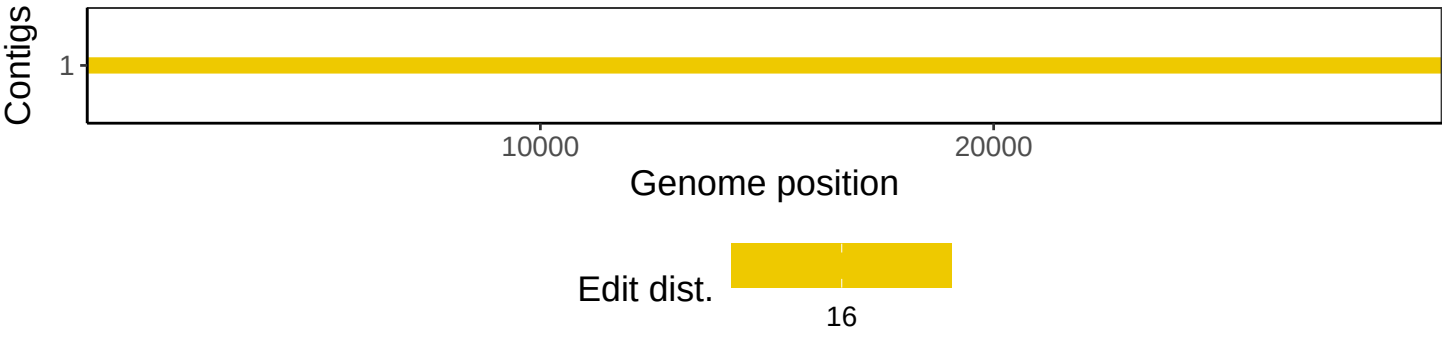
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

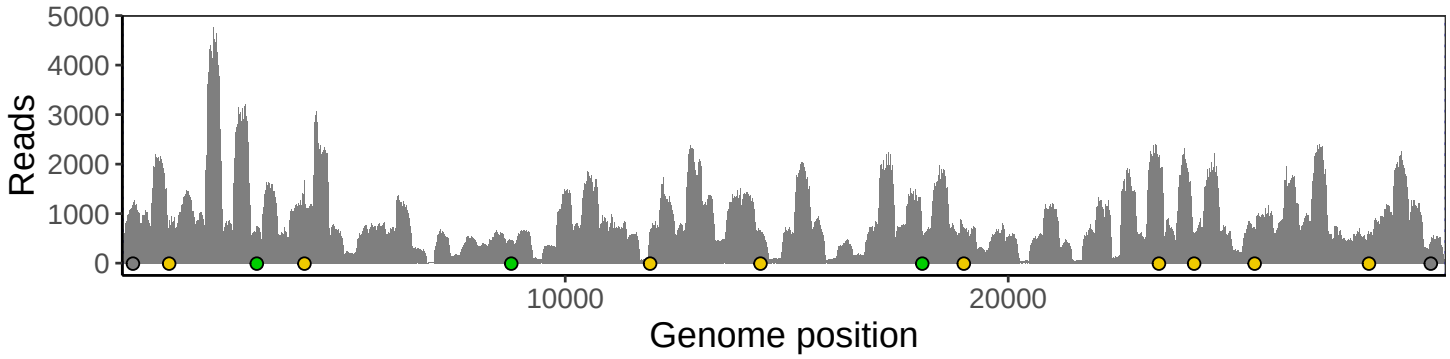


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

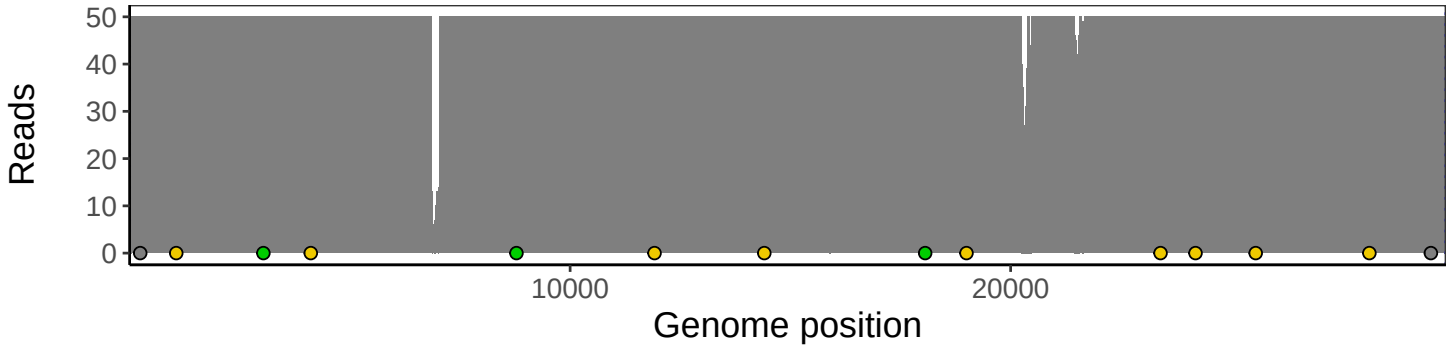


VSP0186-1m | 2020-04-13 | ETA | 7 | genomes | single experiment

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.