COVID-19 subject 251

2020-10-23

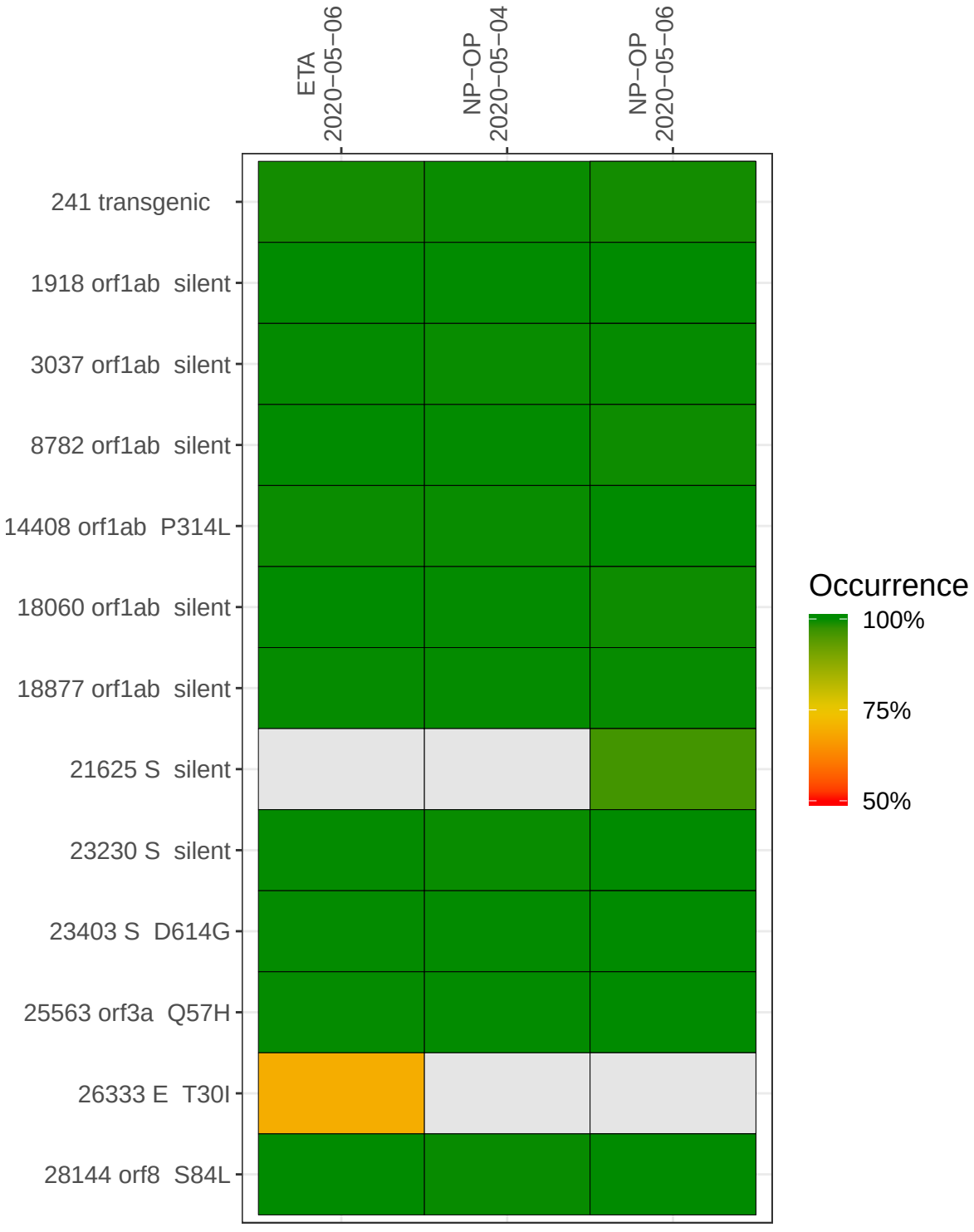
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found (here).

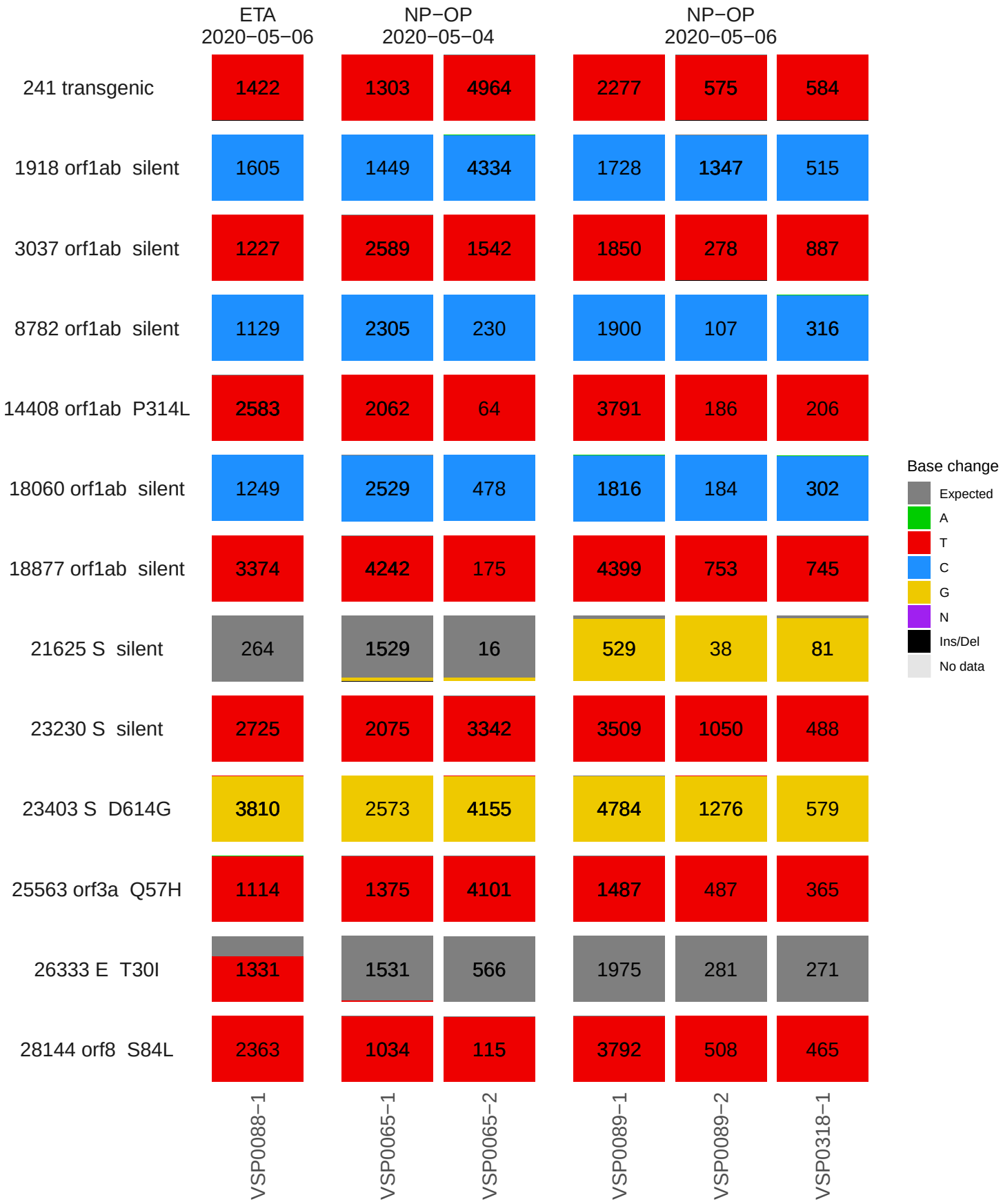
Table 1. Sample summary.

Experiment	Type	Input genomes	Sample type	Sample date	Largest contig (KD)	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0065	composite	NA	NP-OP	2020-05-04	29.94	99.9%	99.8%
VSP0089	composite	NA	NP-OP	2020-05-06	30.00	99.9%	99.7%
VSP0065-1	single experiment	7550000	NP-OP	2020-05-04	29.88	99.9%	99.8%
VSP0065-2	single experiment	7550000	NP-OP	2020-05-04	29.85	99.8%	99.3%
VSP0088-1	single experiment	255500	ETA	2020-05-06	29.82	99.8%	99.8%
VSP0089-1	single experiment	570000	NP-OP	2020-05-06	29.91	99.9%	99.7%
VSP0089-2	single experiment	570000	NP-OP	2020-05-06	29.86	99.3%	98.6%
VSP0318-1	single experiment	890000	NP-OP	2020-05-06	24.79	99.8%	99.1%

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.

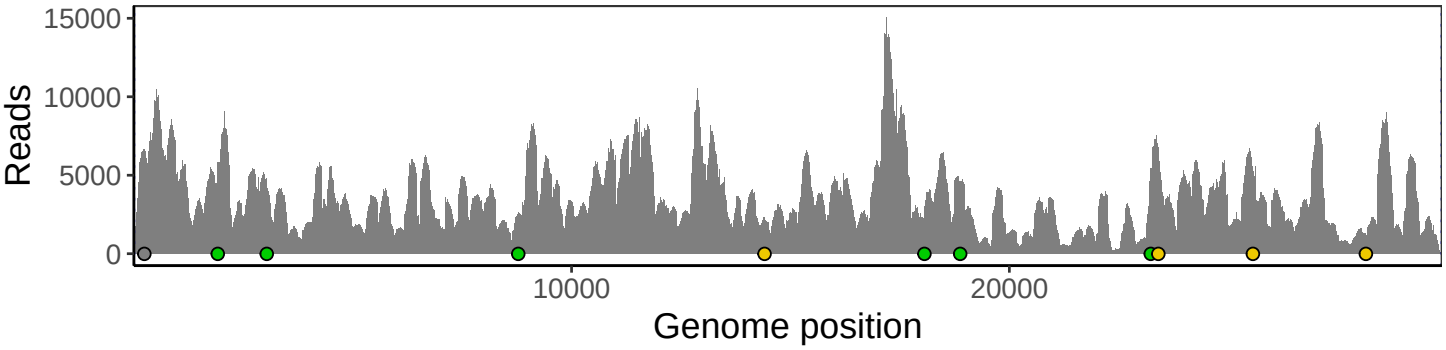



ETA
2020−05−06
NP−OP
2020−05−04
NP−OP
2020−05−06
241 transgenic
1422
1303
4964
2277
575
584
1918 orf1ab silent
1605
1449
4334
1728
1347
515
3037 orf1ab silent
1227
2589
1542
1850
278
887
8782 orf1ab silent
1129
2305
230
1900
107
316
14408 orf1ab P314L
2583
2062
64
3791
186
206
18060 orf1ab silent
1249
2529
478
1816
184
302
18877 orf1ab silent
3374
4242
175
4399
753
745
21625 S silent
264
1529
16
529
38
81
23230 S silent
2725
2075
3342
3509
1050
488
23403 S D614G
3810
2573
4155
4784
1276
579
25563 orf3a Q57H
1114
1375
4101
1487
487
365
26333 E T30I
1331
1531
566
1975
281
271
28144 orf8 S84L
2363
1034
115
3792
508
465
VSP0088−1
VSP0065−1
VSP0065−2
VSP0089−1
VSP0089−2
VSP0318−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

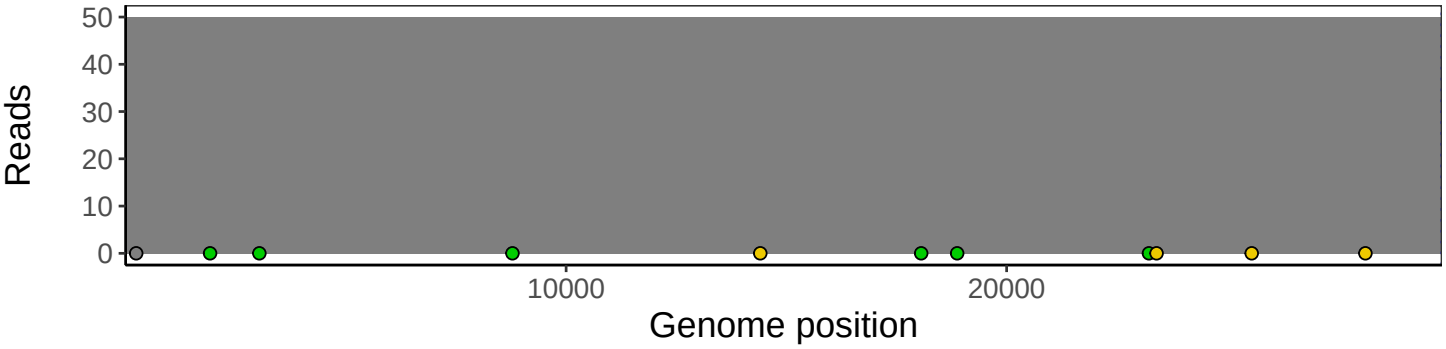
Analyses of individual experiments and composite results.

VSP0065 | 2020-05-04 | NP-OP | 251-q | composite result

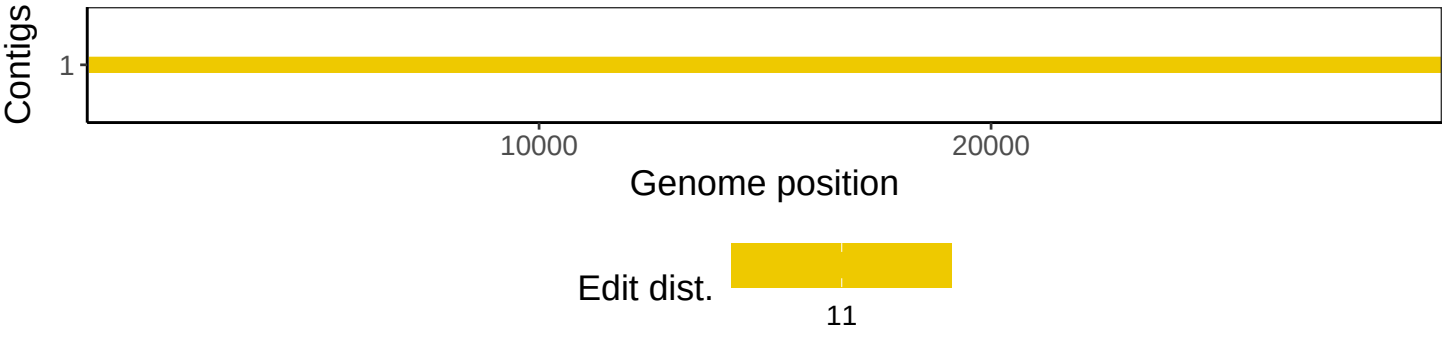
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

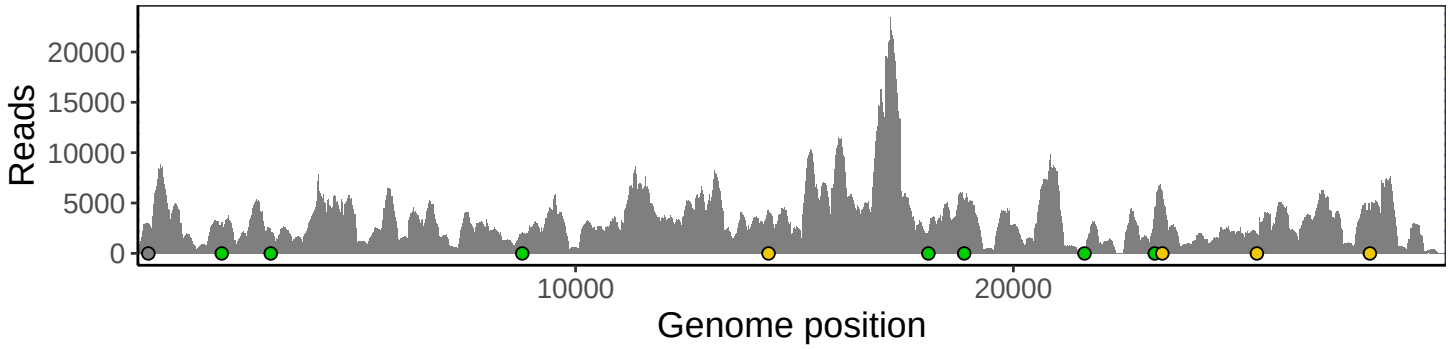


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

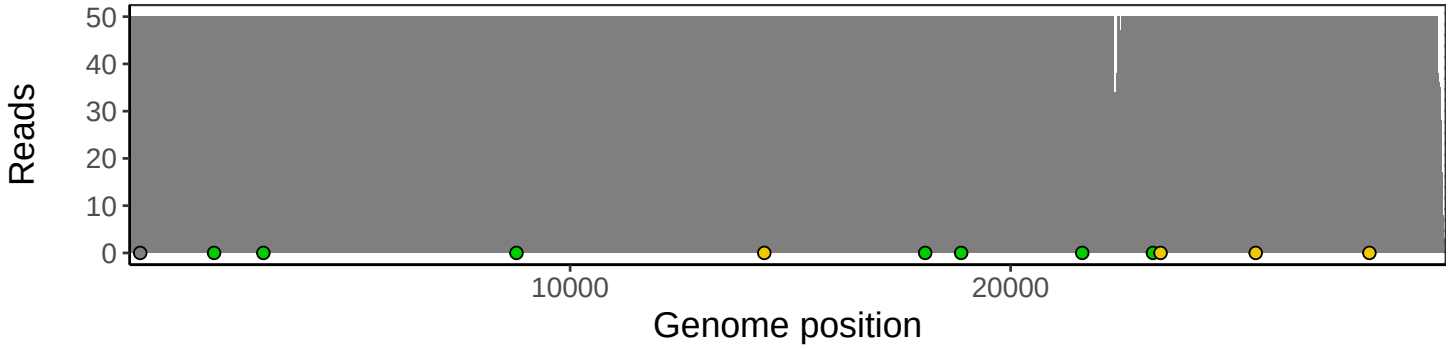


VSP0089 | 2020-05-06 | NP-OP | 251no-q | composite result

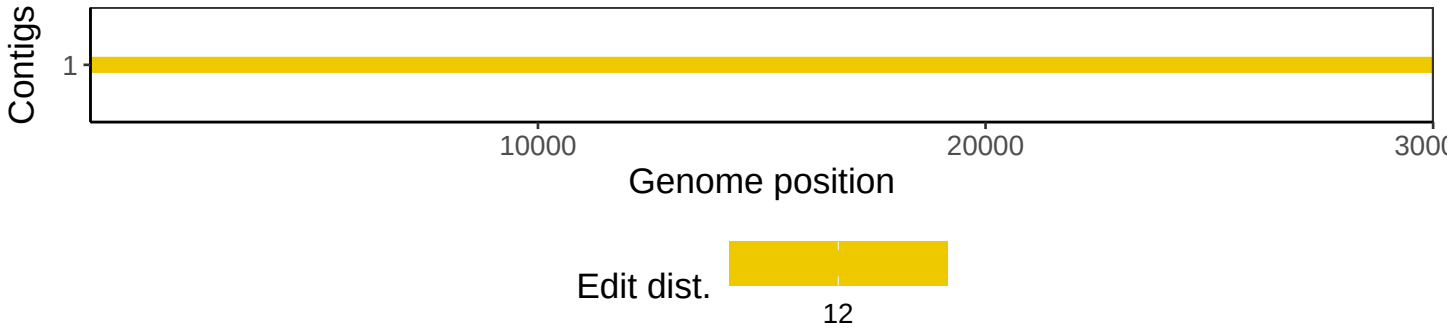
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

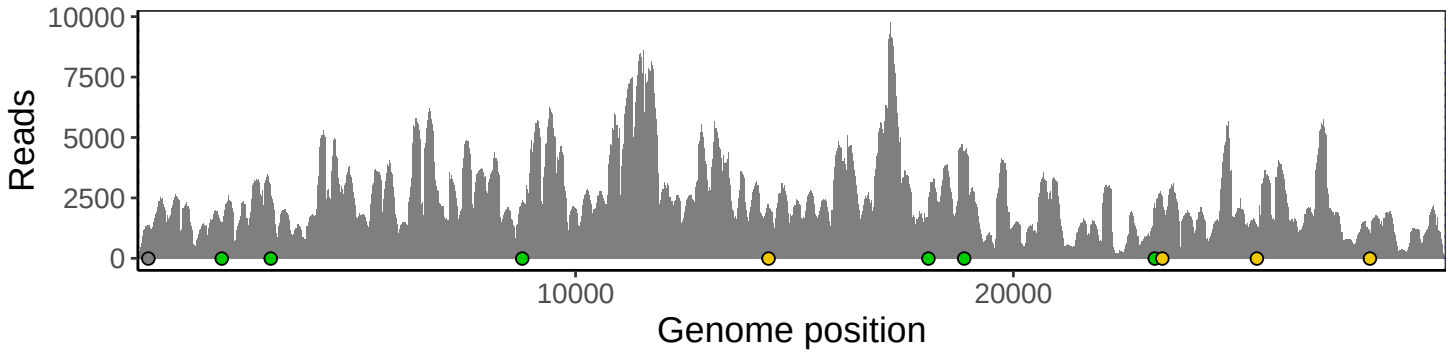


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

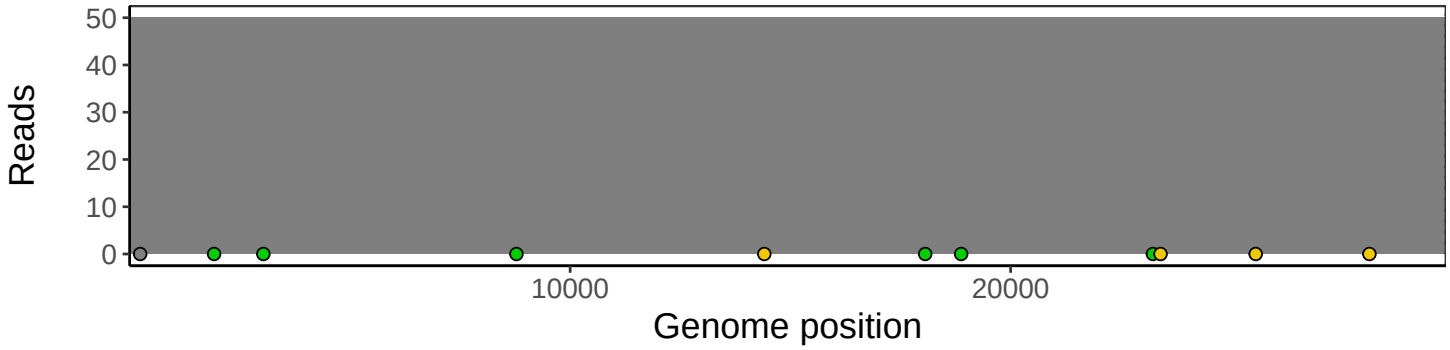


VSP0065-1 | 2020-05-04 | NP-OP | 251-q | 7550000 genomes | single experiment

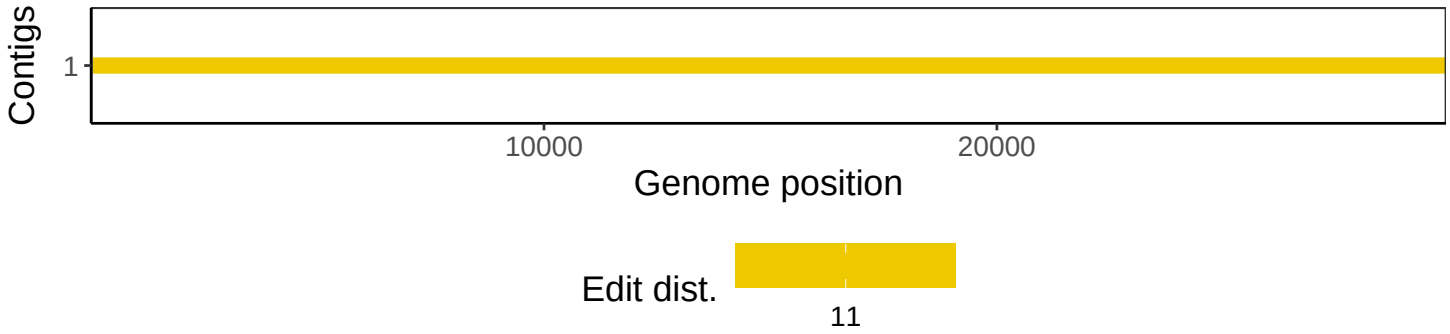
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

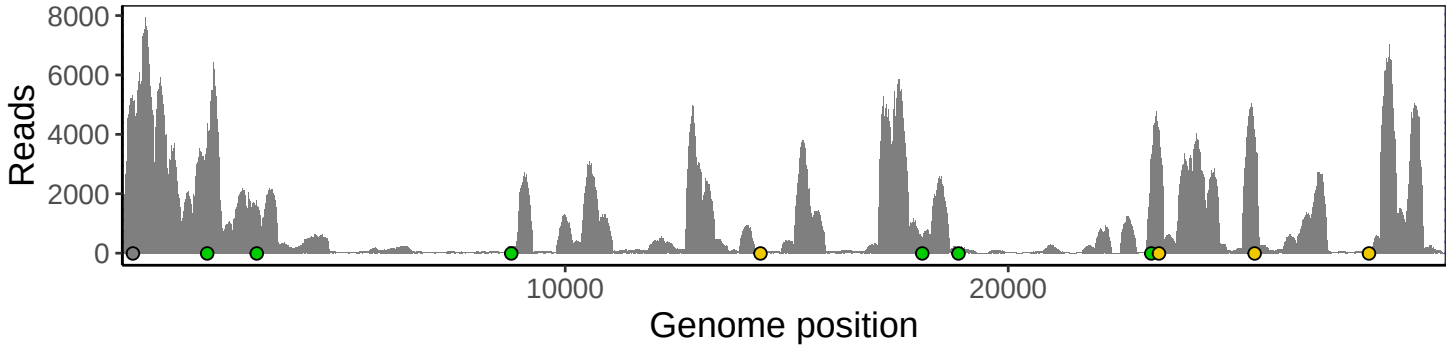


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

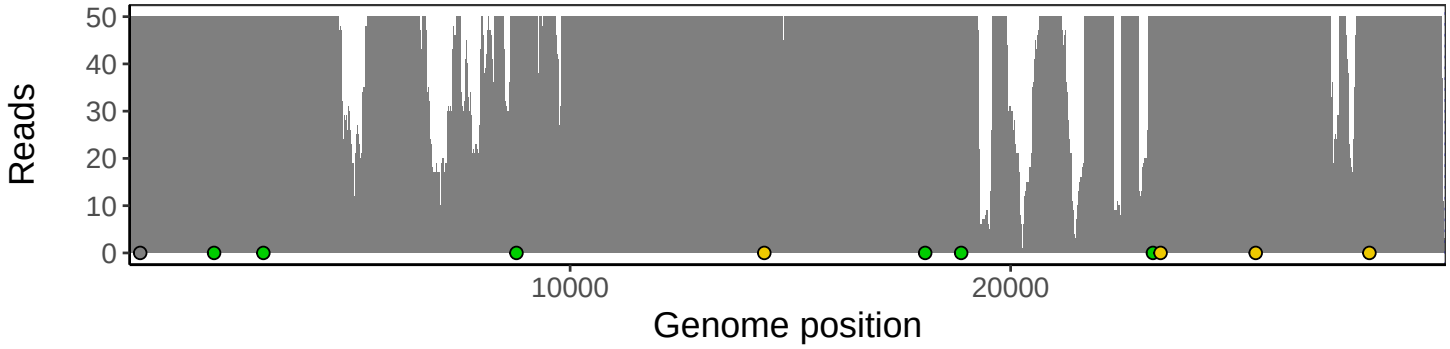


VSP0065-2 | 2020-05-04 | NP-OP | 251-q | 7550000 genomes | single experiment

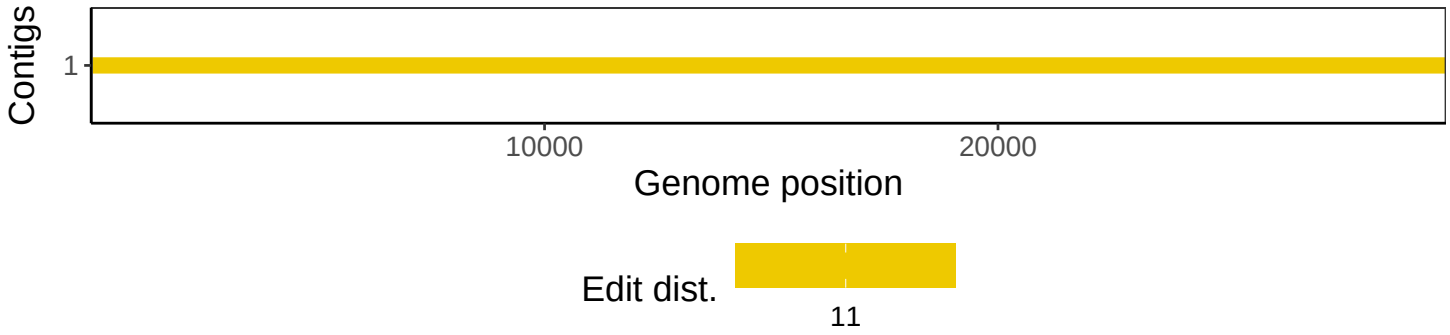
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

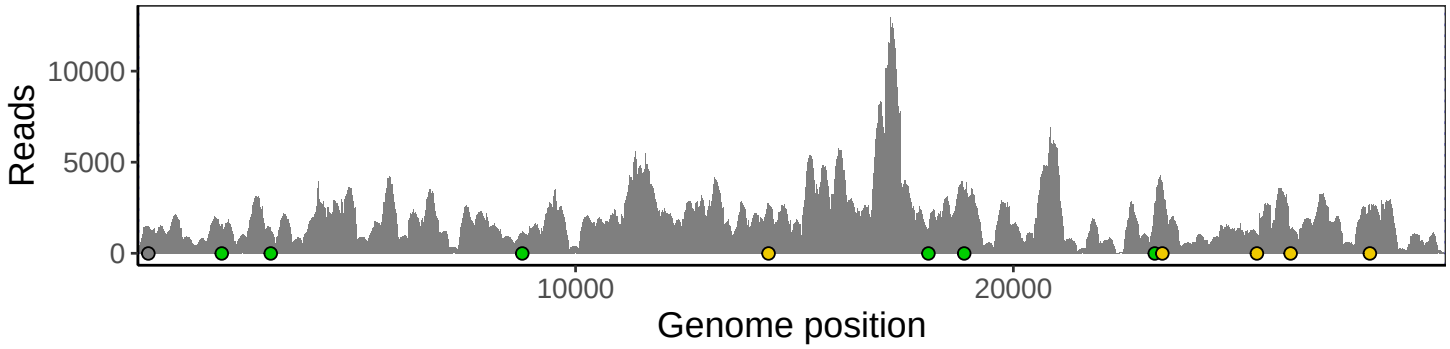


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

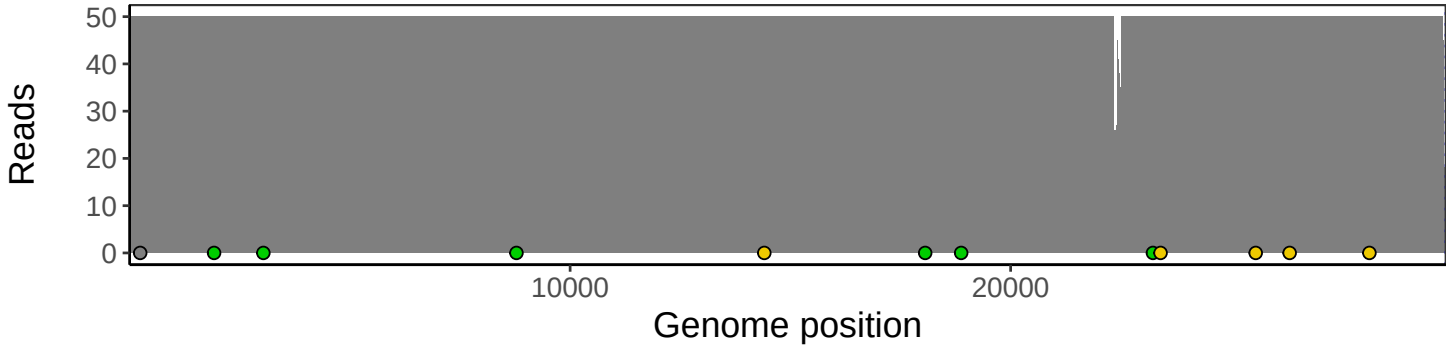


VSP0088-1 | 2020-05-06 | ETA | 251e-q | 255500 genomes | single experiment

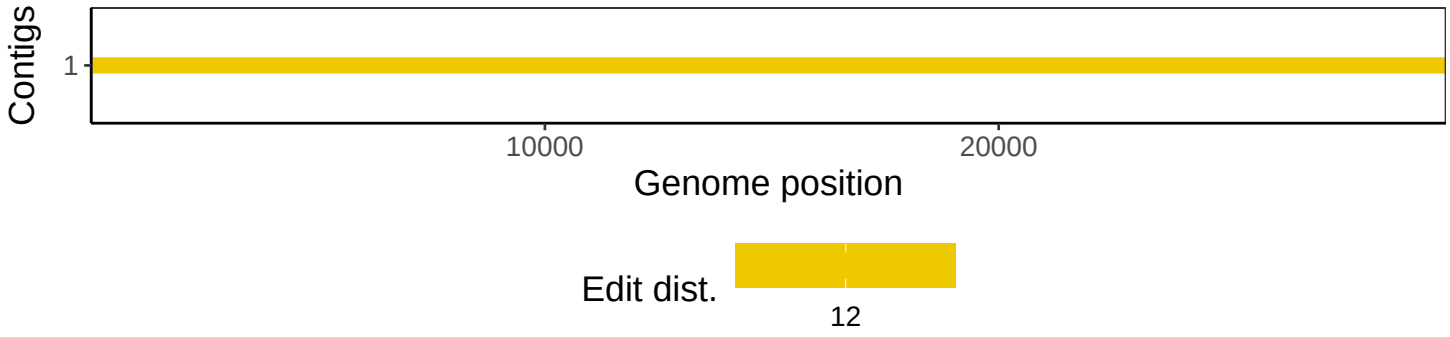
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

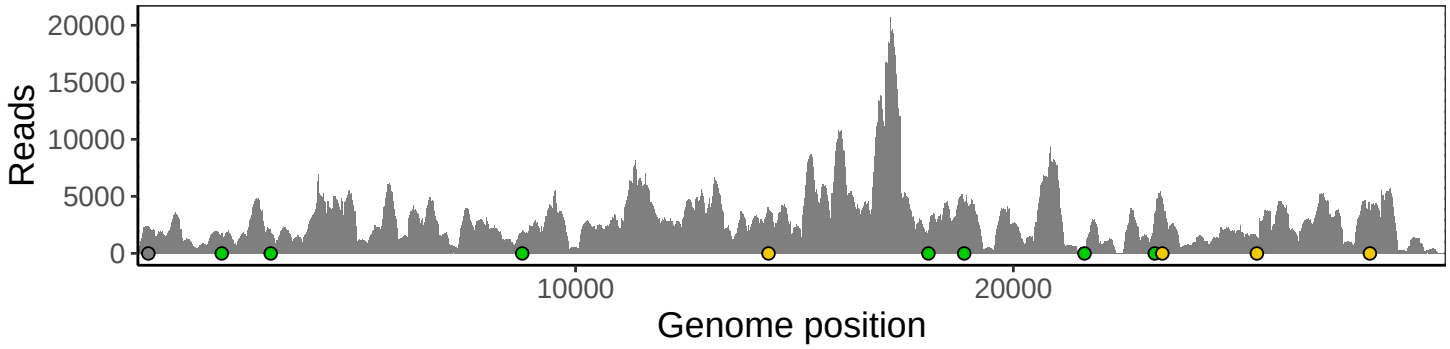


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

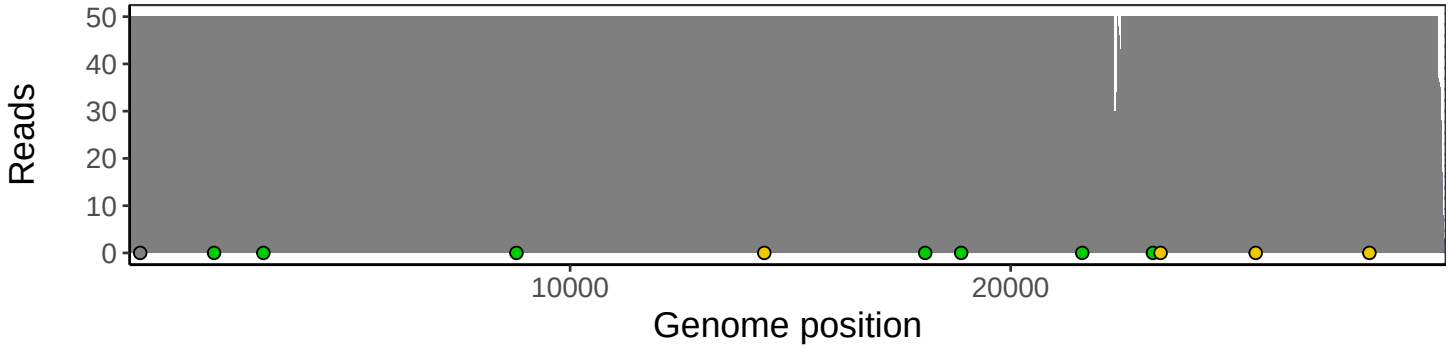


VSP0089-1 | 2020-05-06 | NP-OP | 251no-q | 570000 genomes | single experiment

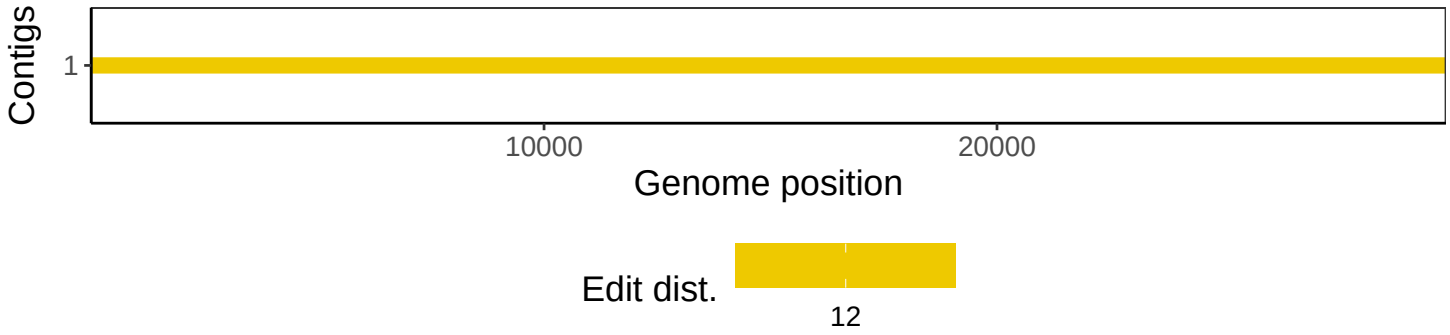
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

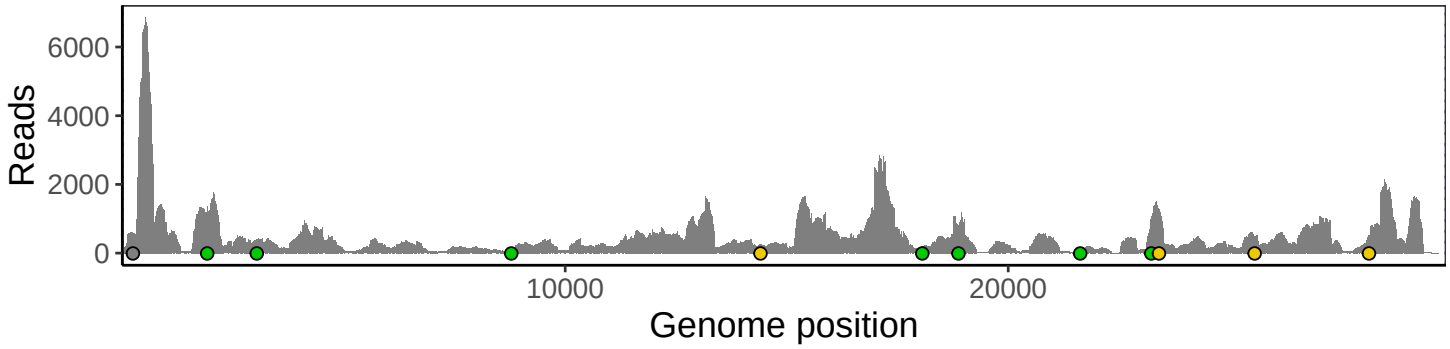


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

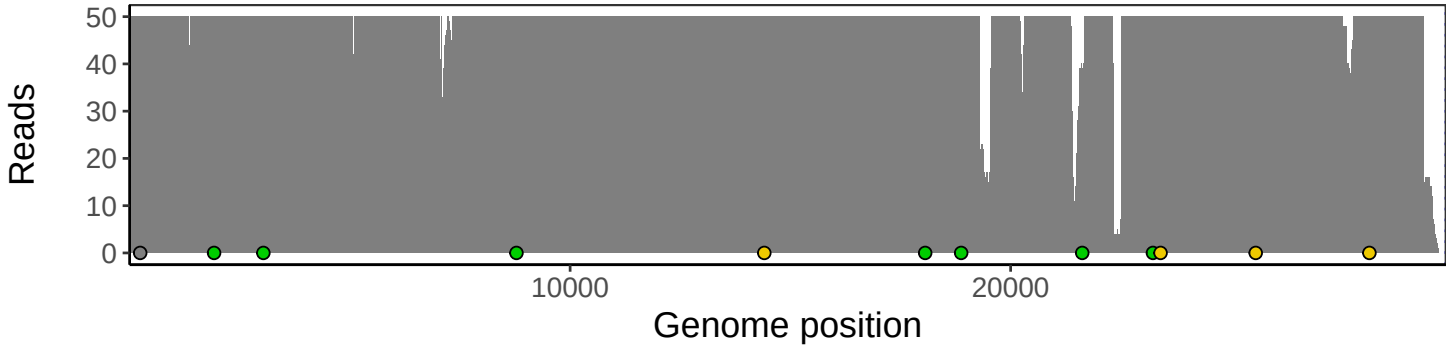


VSP0089-2 | 2020-05-06 | NP-OP | 251no-q | 570000 genomes | single experiment

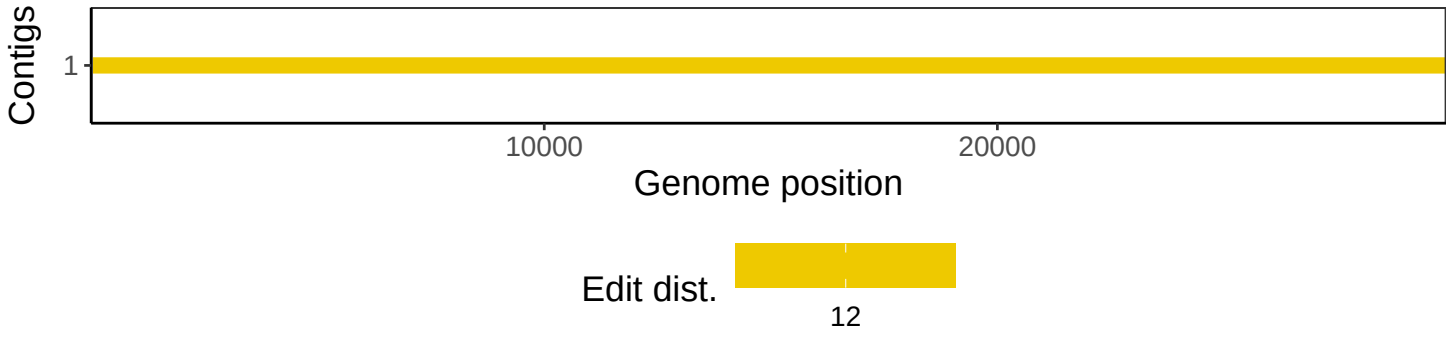
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

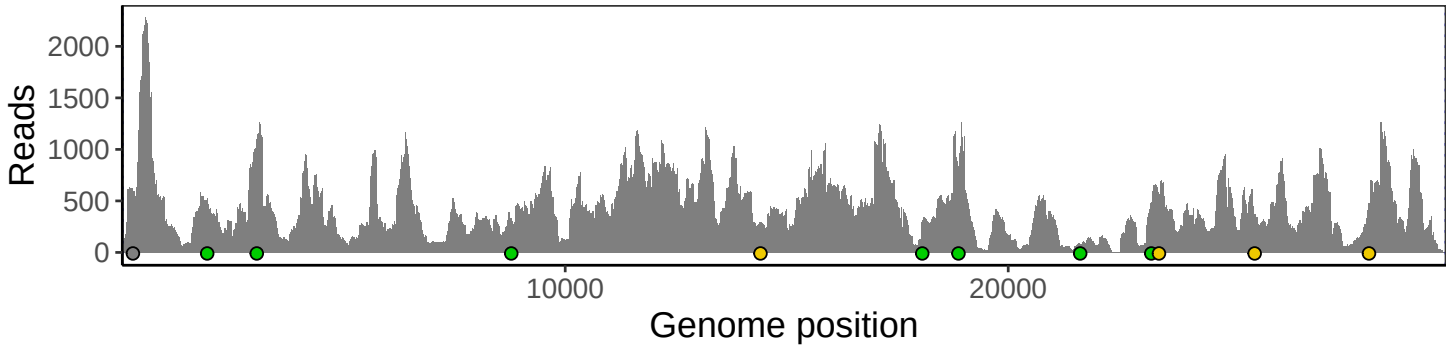


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

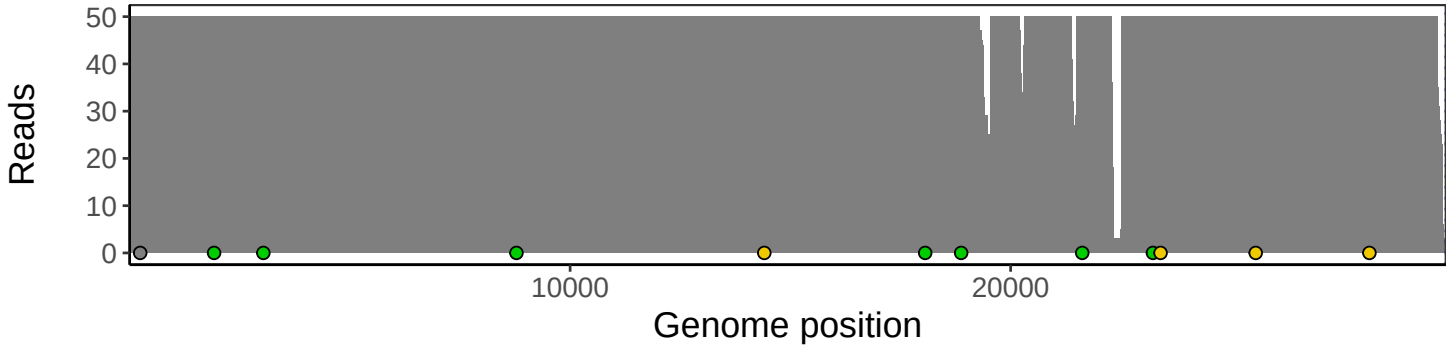


VSP0318-1 | 2020-05-06 | NP-OP | 251no-q | 890000 genomes | single experiment

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.