COVID-19 subject 251

2021-04-17

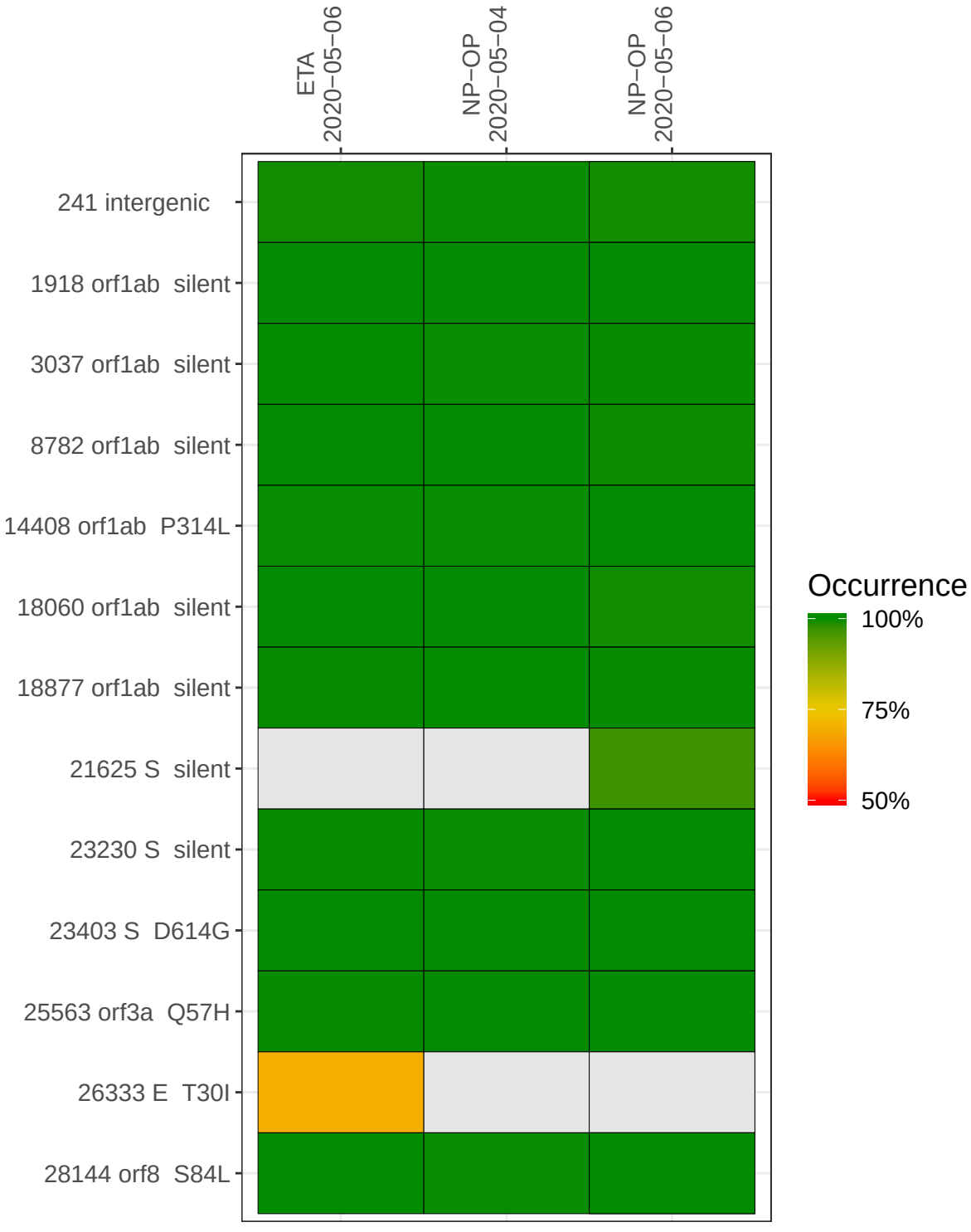
The table below provides a summary of subject samples for which sequencing data is available.
The experiments column shows the number of sequencing experiments performed for each specimen.
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software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

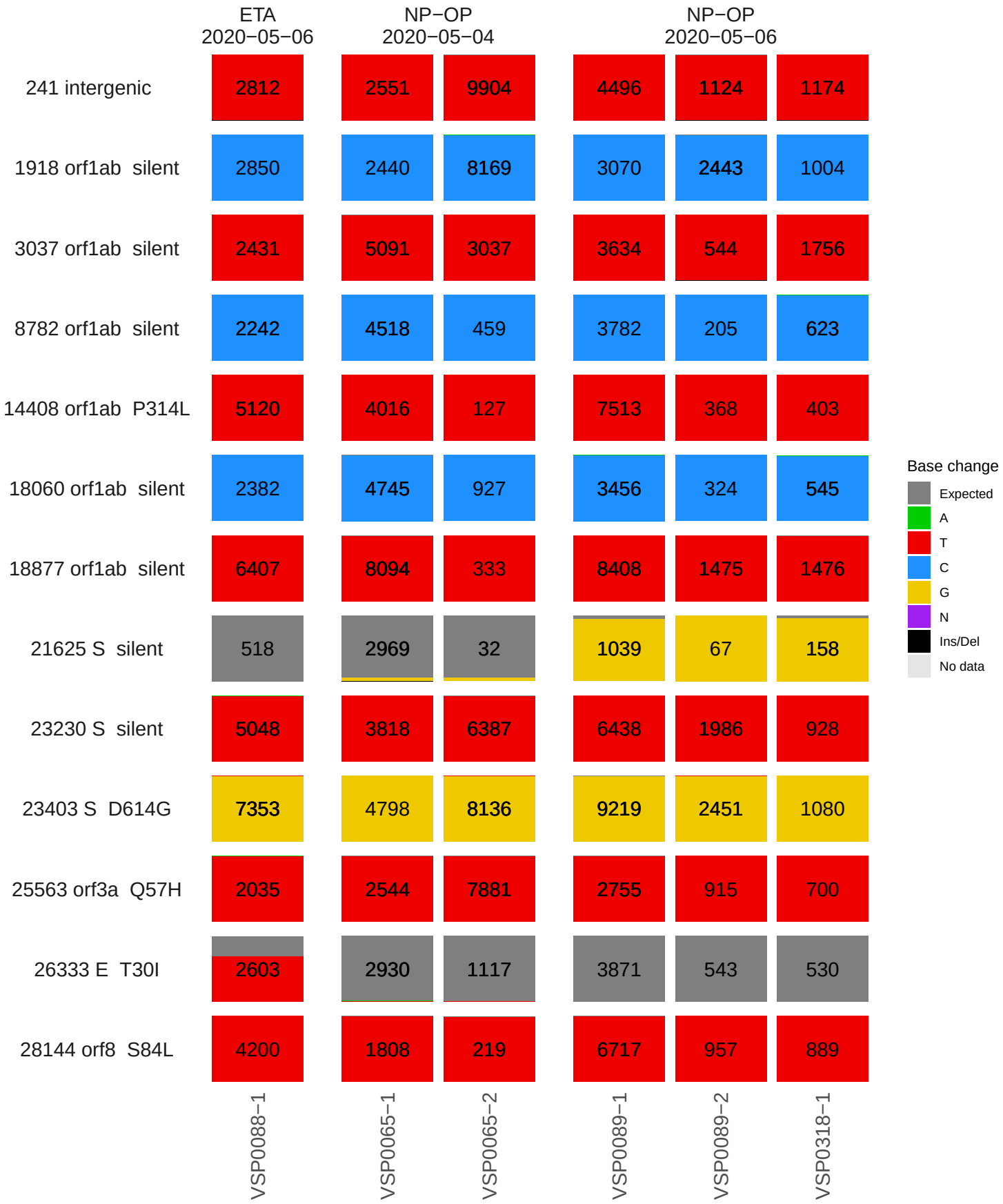
Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (>= 5 reads)
VSP0065	composite	NA	NP-OP	2020-05-04	16.53	B.1.439	99.9%	99.8%
VSP0089	composite	NA	NP-OP	2020-05-06	30.00	B.1.439	99.9%	99.7%
VSP0065-1	single experiment	7550000	NP-OP	2020-05-04	16.47	B.1.439	99.9%	99.8%
VSP0065-2	single experiment	7550000	NP-OP	2020-05-04	29.85	B.1.439	99.8%	99.6%
VSP0088-1	single experiment	255500	ETA	2020-05-06	29.82	B.1.439	99.8%	99.8%
VSP0089-1	single experiment	570000	NP-OP	2020-05-06	29.91	B.1.439	99.9%	99.7%
VSP0089-2	single experiment	570000	NP-OP	2020-05-06	29.45	B.1.439	99.4%	99.1%
VSP0318-1	single experiment	890000	NP-OP	2020-05-06	24.51	B.1.439	99.8%	99.7%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/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.

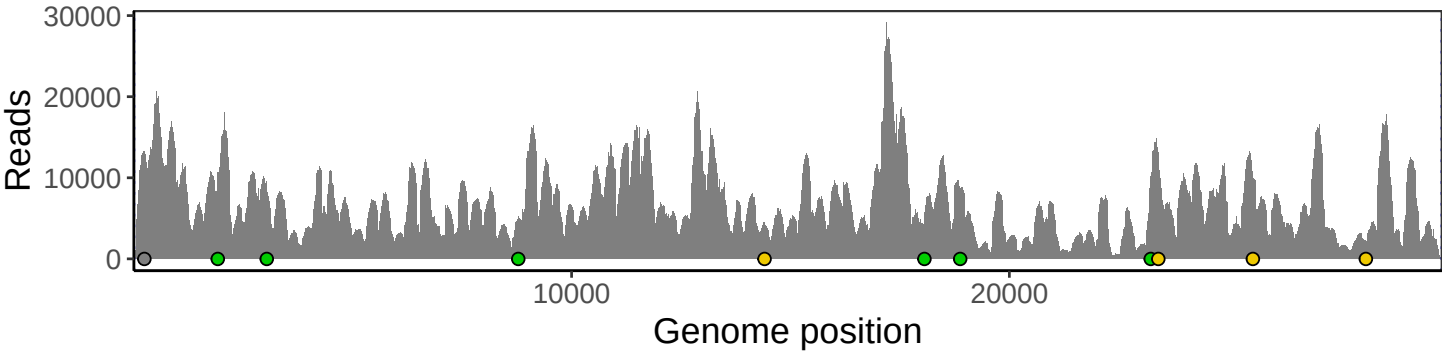



ETA
2020−05−06
NP−OP
2020−05−04
NP−OP
2020−05−06
241 intergenic
2812
2551
9904
4496
1124
1174
1918 orf1ab silent
2850
2440
8169
3070
2443
1004
3037 orf1ab silent
2431
5091
3037
3634
544
1756
8782 orf1ab silent
2242
4518
459
3782
205
623
14408 orf1ab P314L
5120
4016
127
7513
368
403
18060 orf1ab silent
2382
4745
927
3456
324
545
18877 orf1ab silent
6407
8094
333
8408
1475
1476
21625 S silent
518
2969
32
1039
67
158
23230 S silent
5048
3818
6387
6438
1986
928
23403 S D614G
7353
4798
8136
9219
2451
1080
25563 orf3a Q57H
2035
2544
7881
2755
915
700
26333 E T30I
2603
2930
1117
3871
543
530
28144 orf8 S84L
4200
1808
219
6717
957
889
VSP0088−1
VSP0065−1
VSP0065−2
VSP0089−1
VSP0089−2
VSP0318−1
Base change
Expected
A
T
C
G
N
Ins/Del
No data

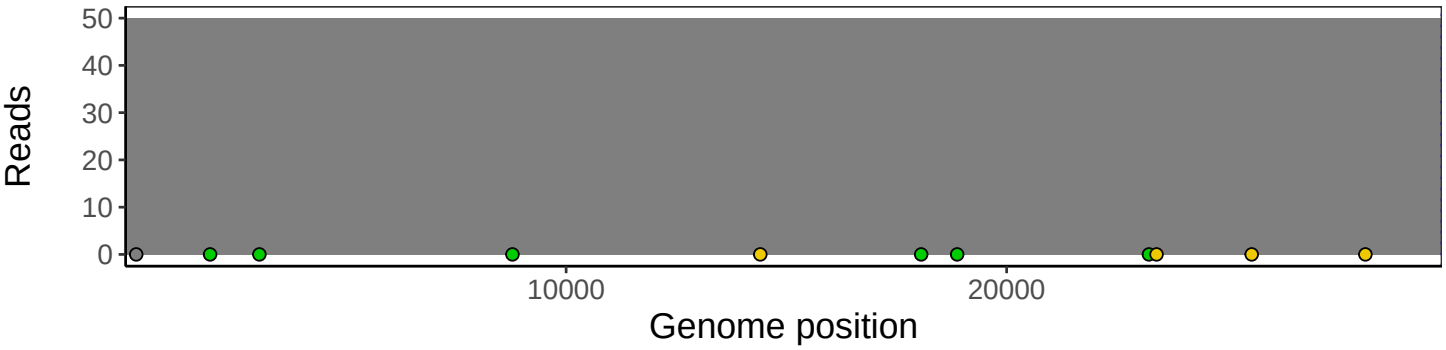
Analyses of individual experiments and composite results

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

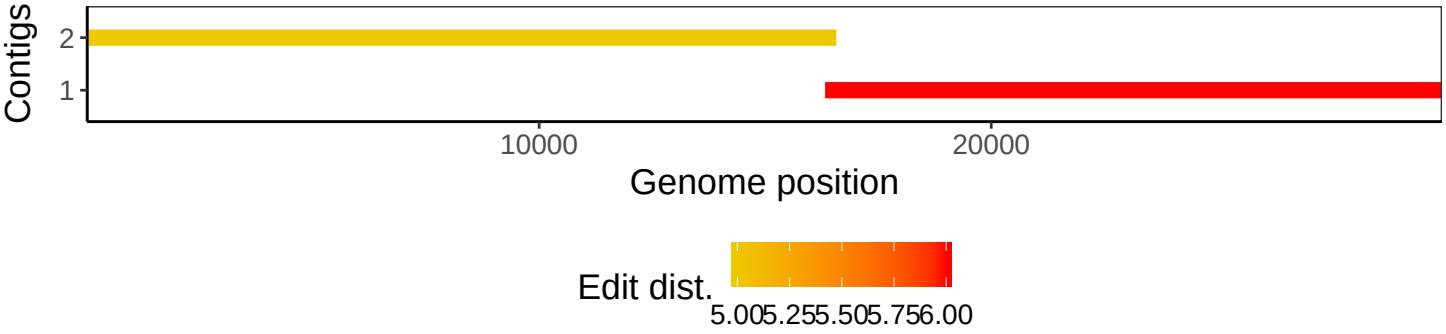
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

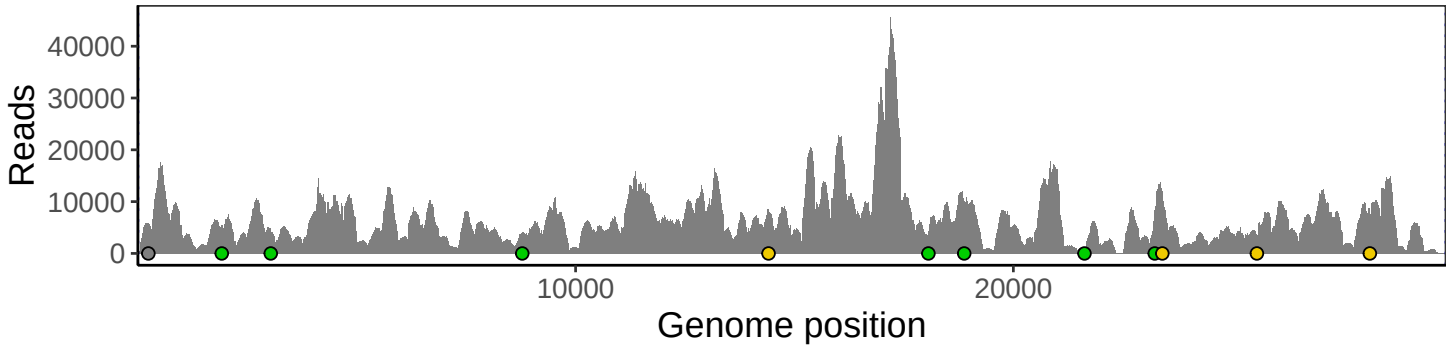


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

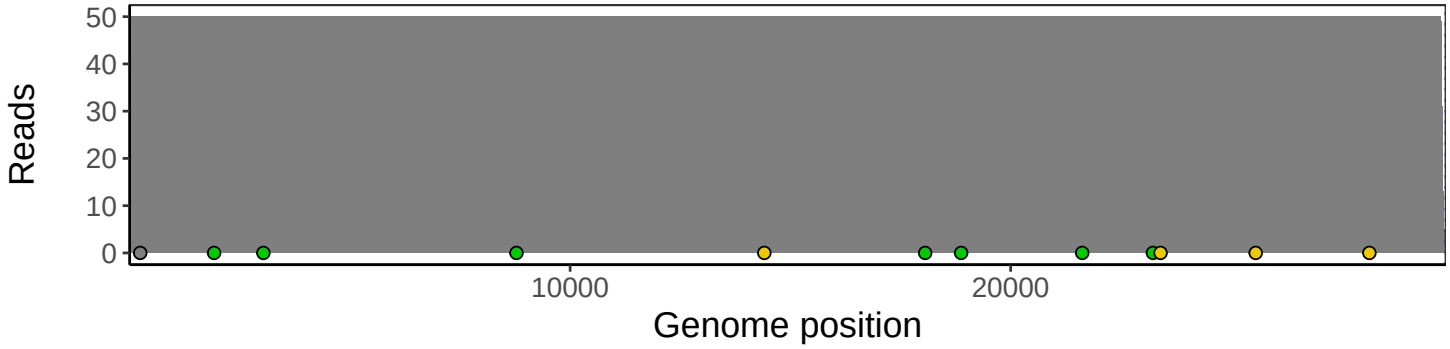


VSP0089 | 2020-05-06 | NP-OP | 251no-q | composite result

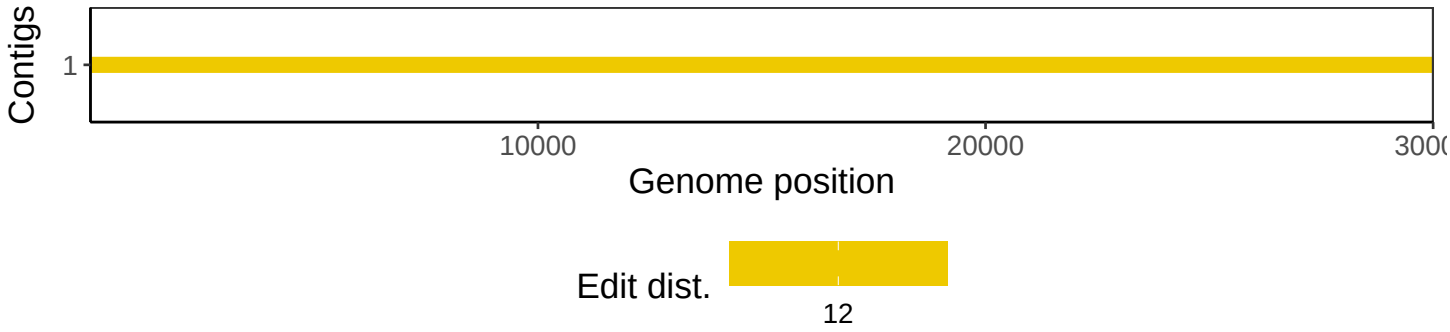
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

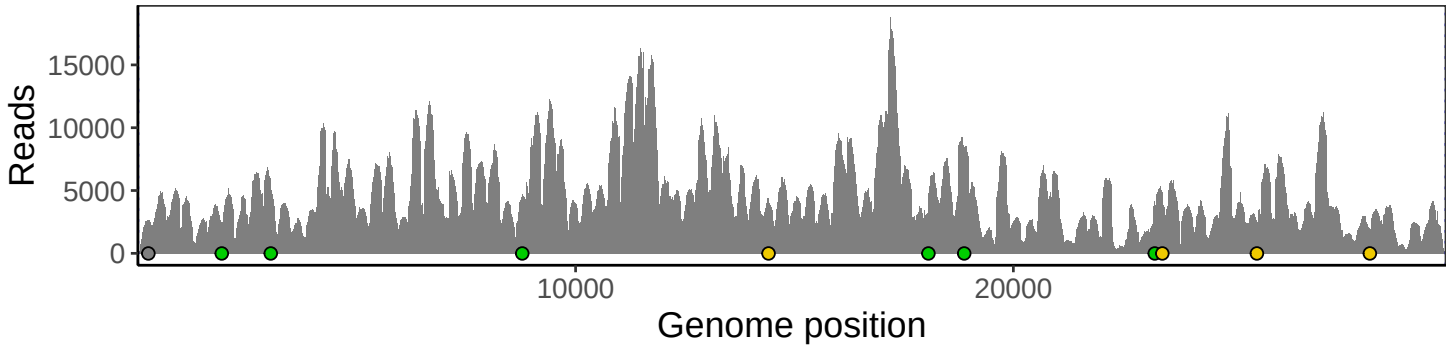


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

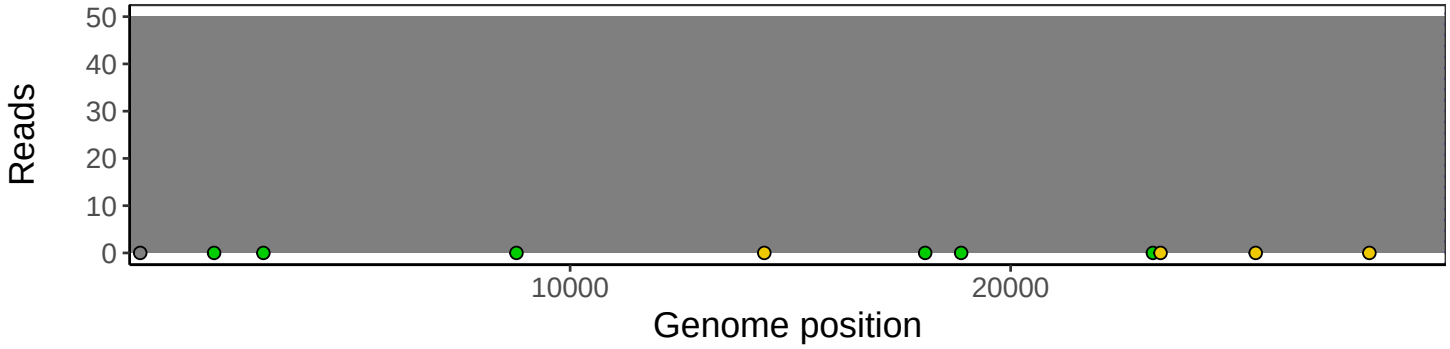


VSP0065-1 | 2020-05-04 | NP-OP | 251-q | 7550000 genomes | single experiment

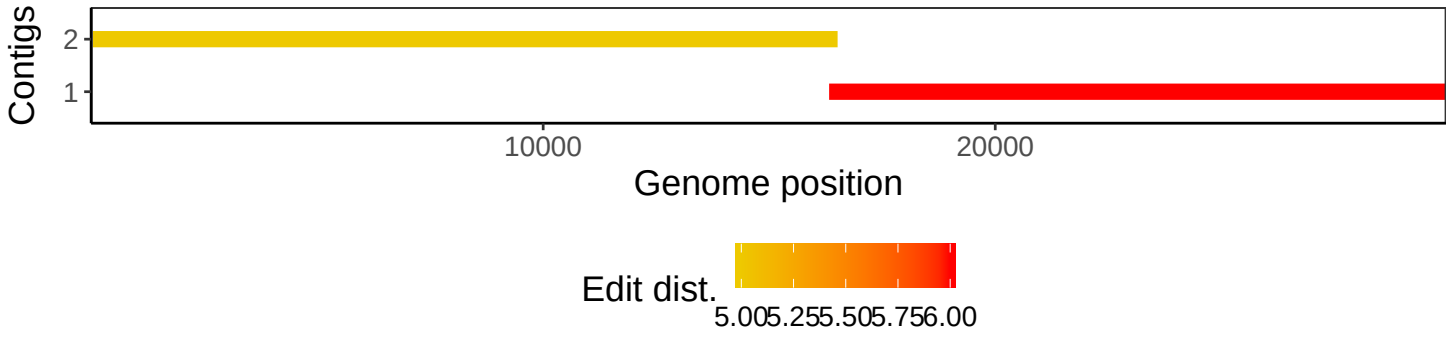
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

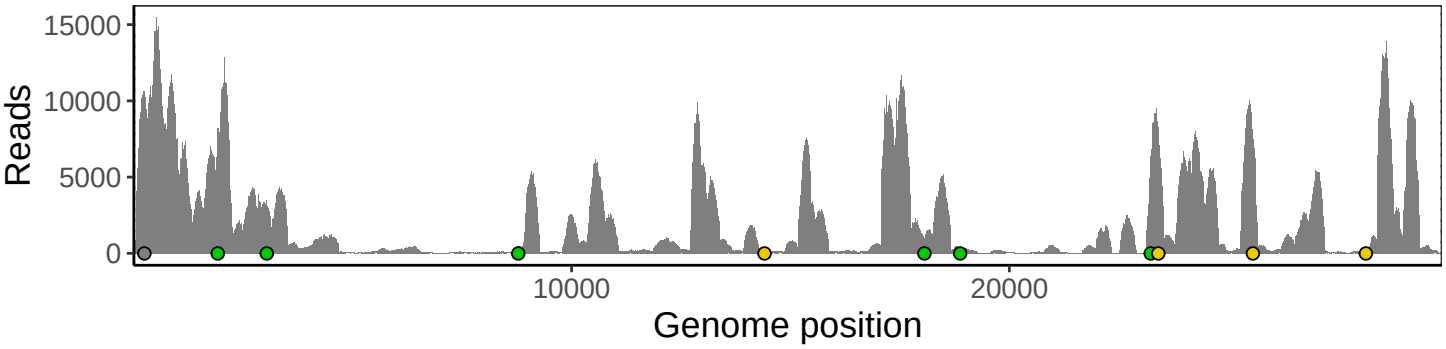


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

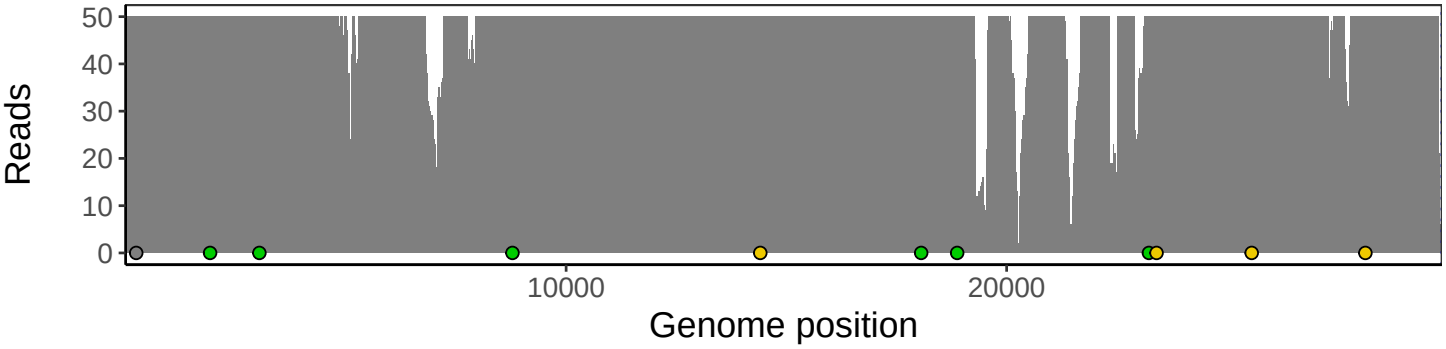


VSP0065-2 | 2020-05-04 | NP-OP | 251-q | 7550000 genomes | single experiment

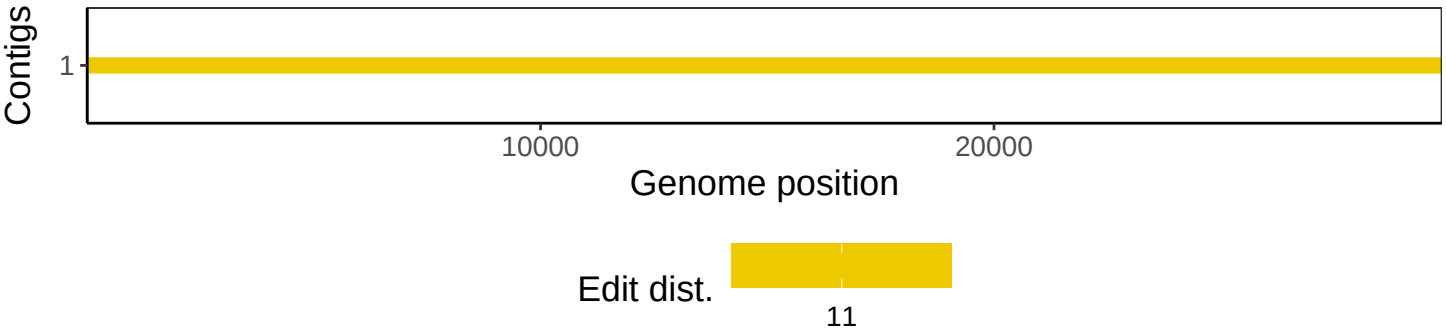
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

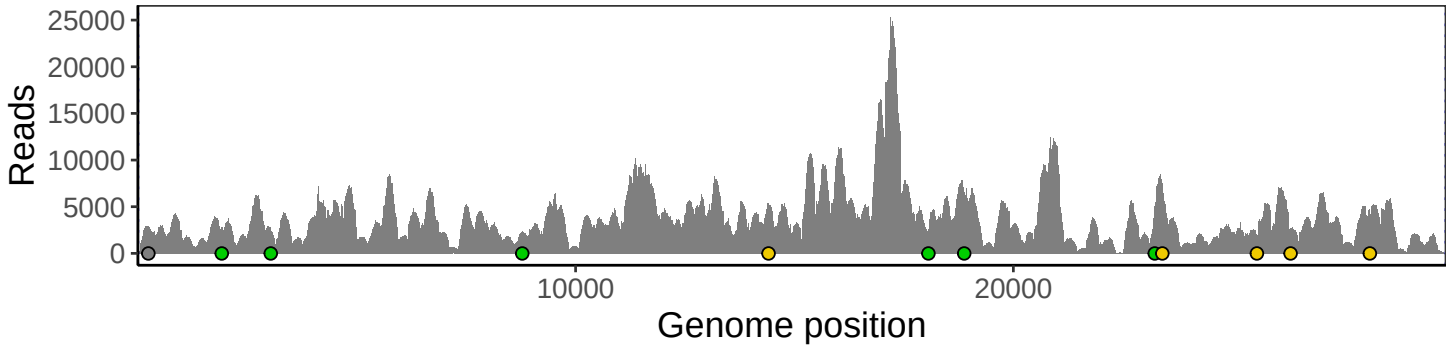


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

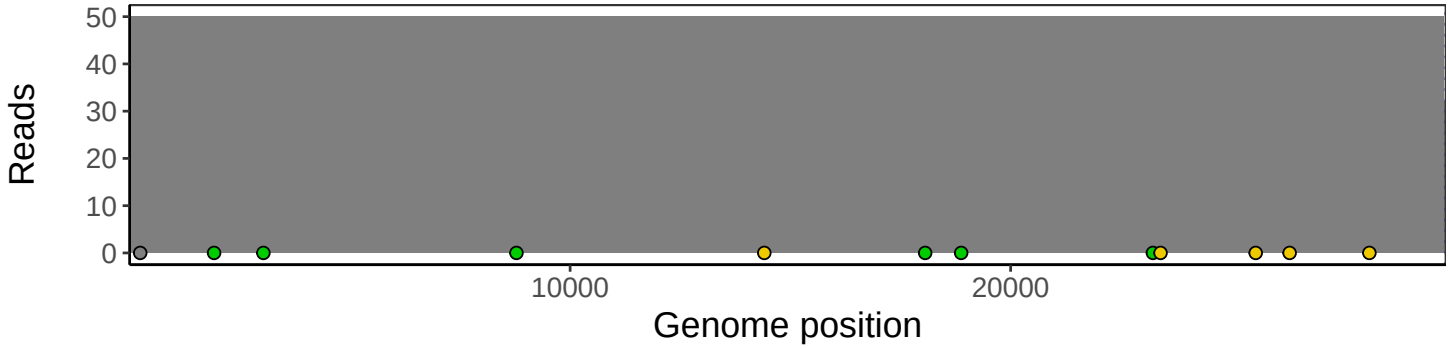


VSP0088-1 | 2020-05-06 | ETA | 251e-q | 255500 genomes | single experiment

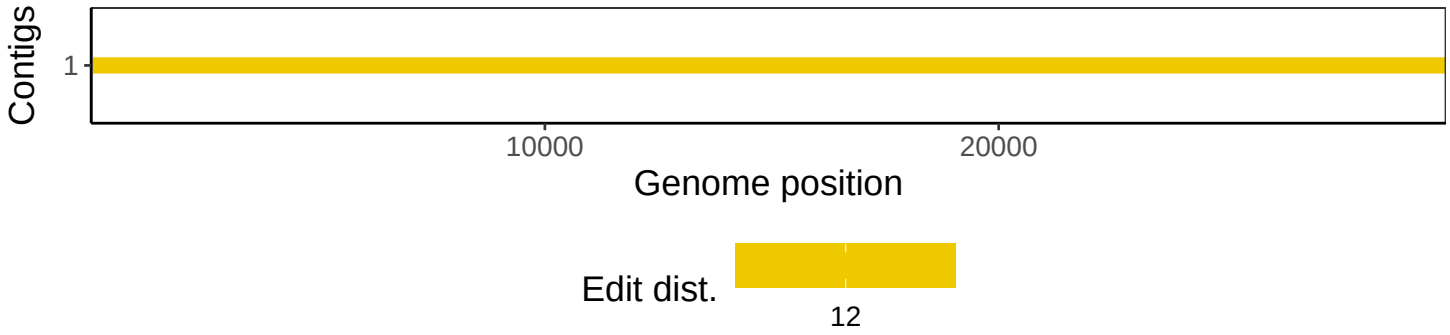
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

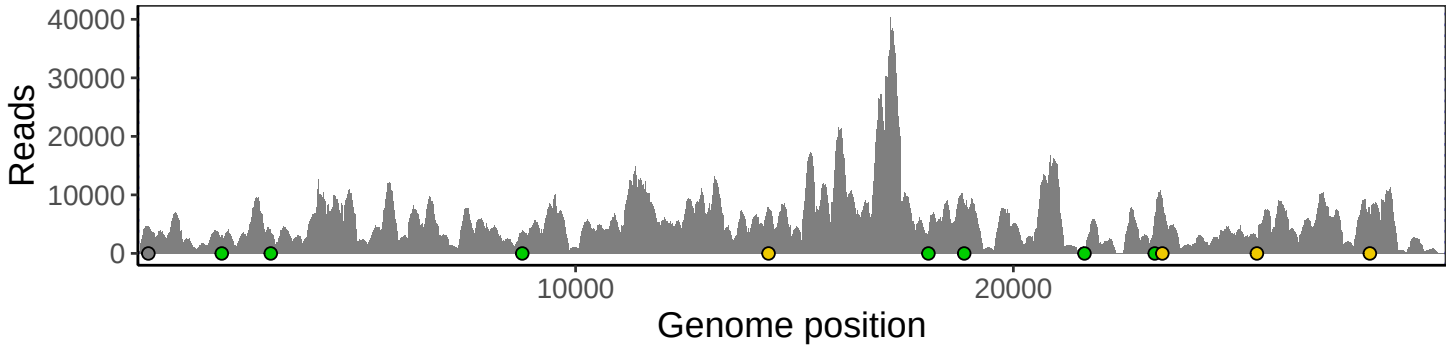


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

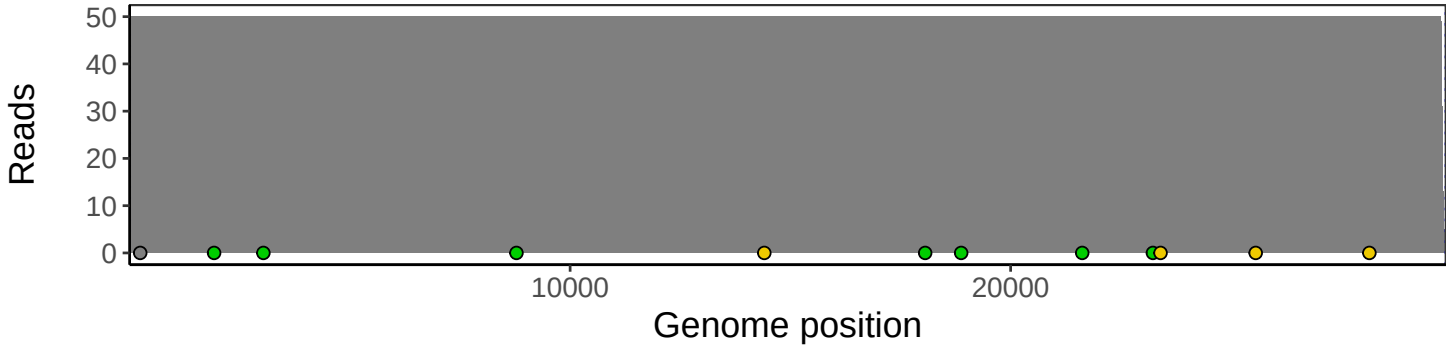


VSP0089-1 | 2020-05-06 | NP-OP | 251no-q | 570000 genomes | single experiment

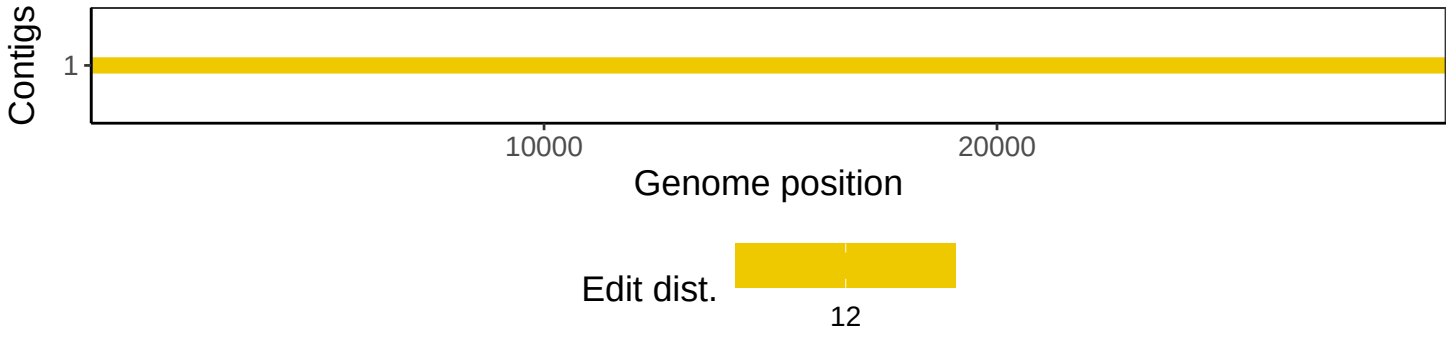
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

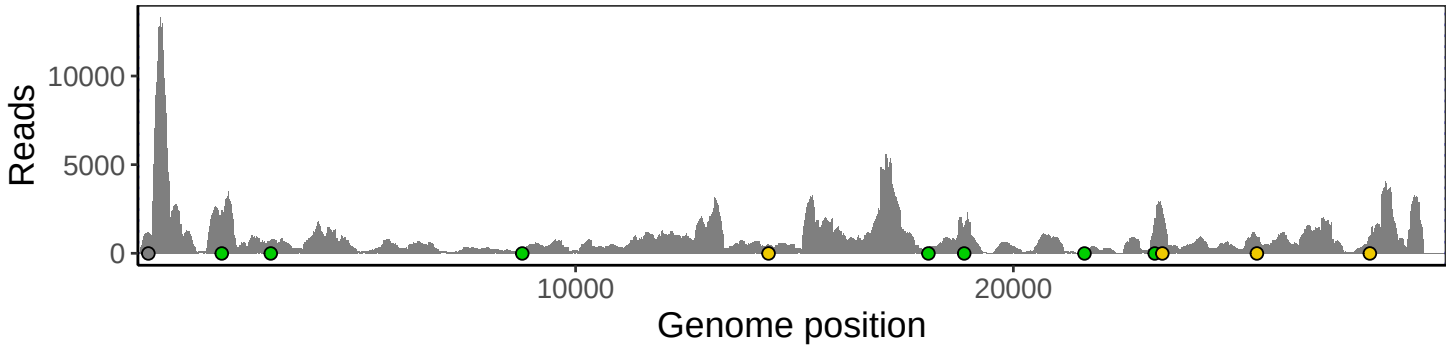


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

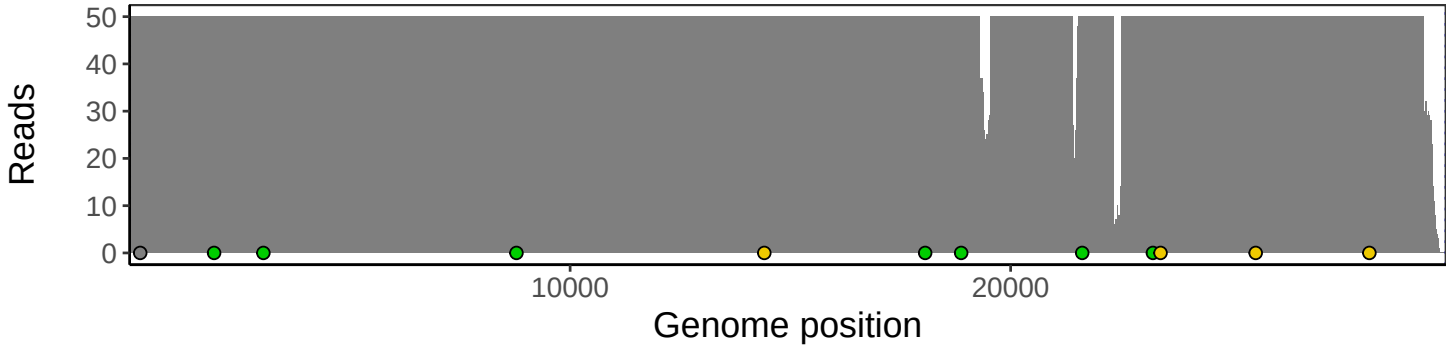


VSP0089-2 | 2020-05-06 | NP-OP | 251no-q | 570000 genomes | single experiment

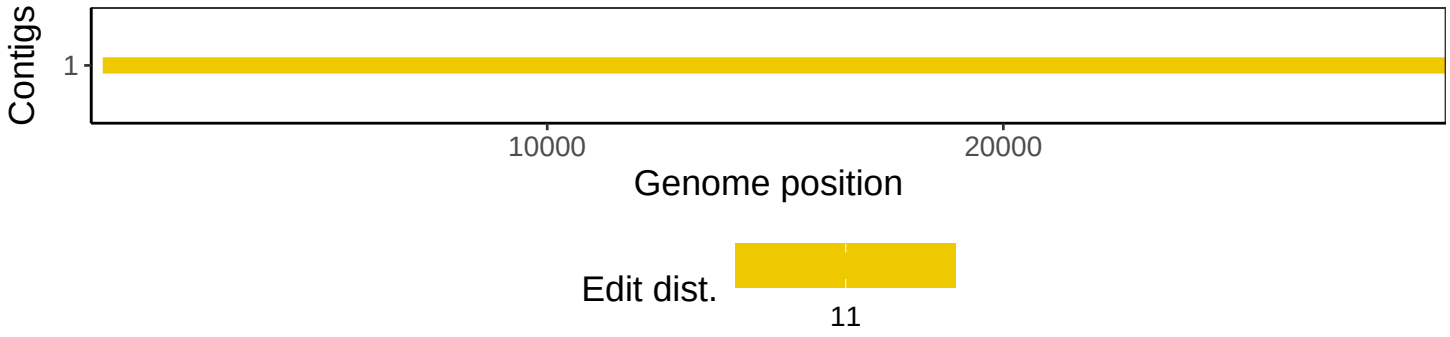
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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

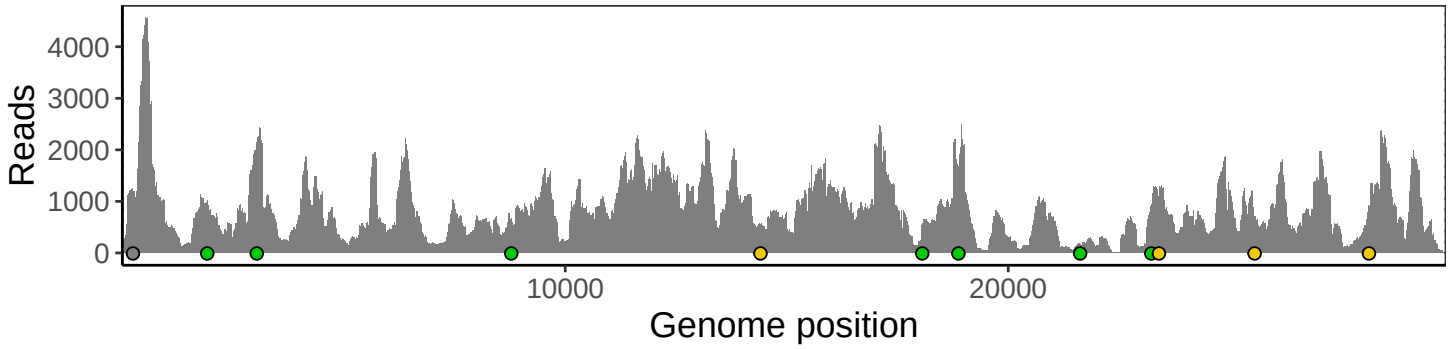


The longest five assembled contigs are shown below colored by their edit distance to the reference genome.

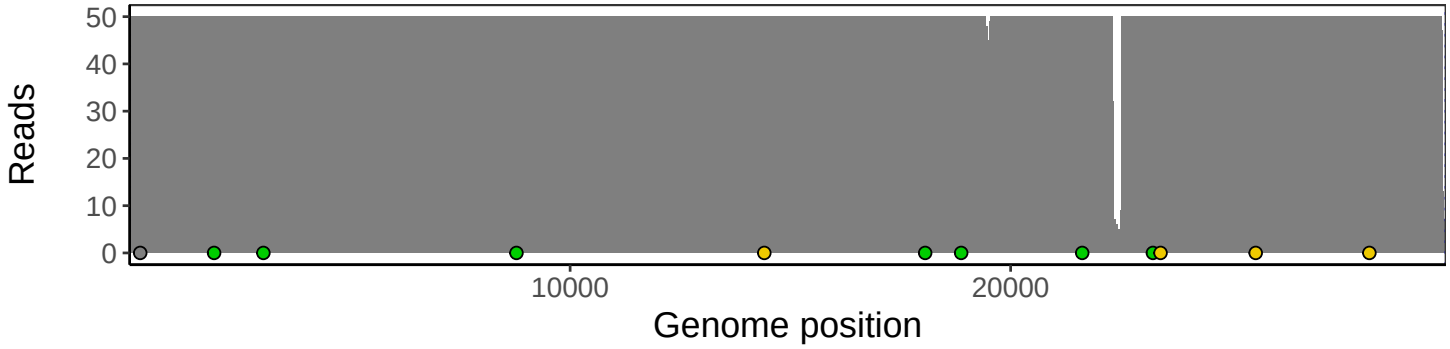


VSP0318-1 | 2020-05-06 | NP-OP | 251no-q | 890000 genomes | single experiment

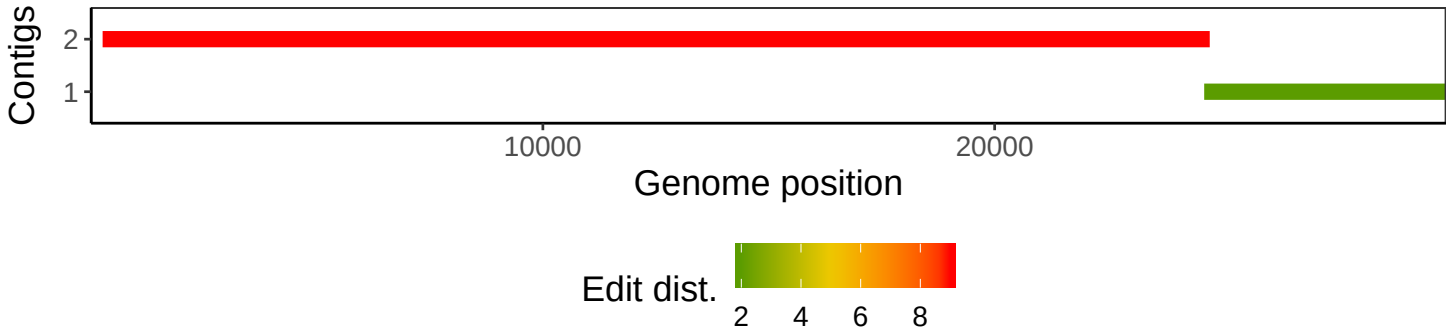
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



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.



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	2.3.8
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