

COVID-19 subject 247

2021-06-23

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.

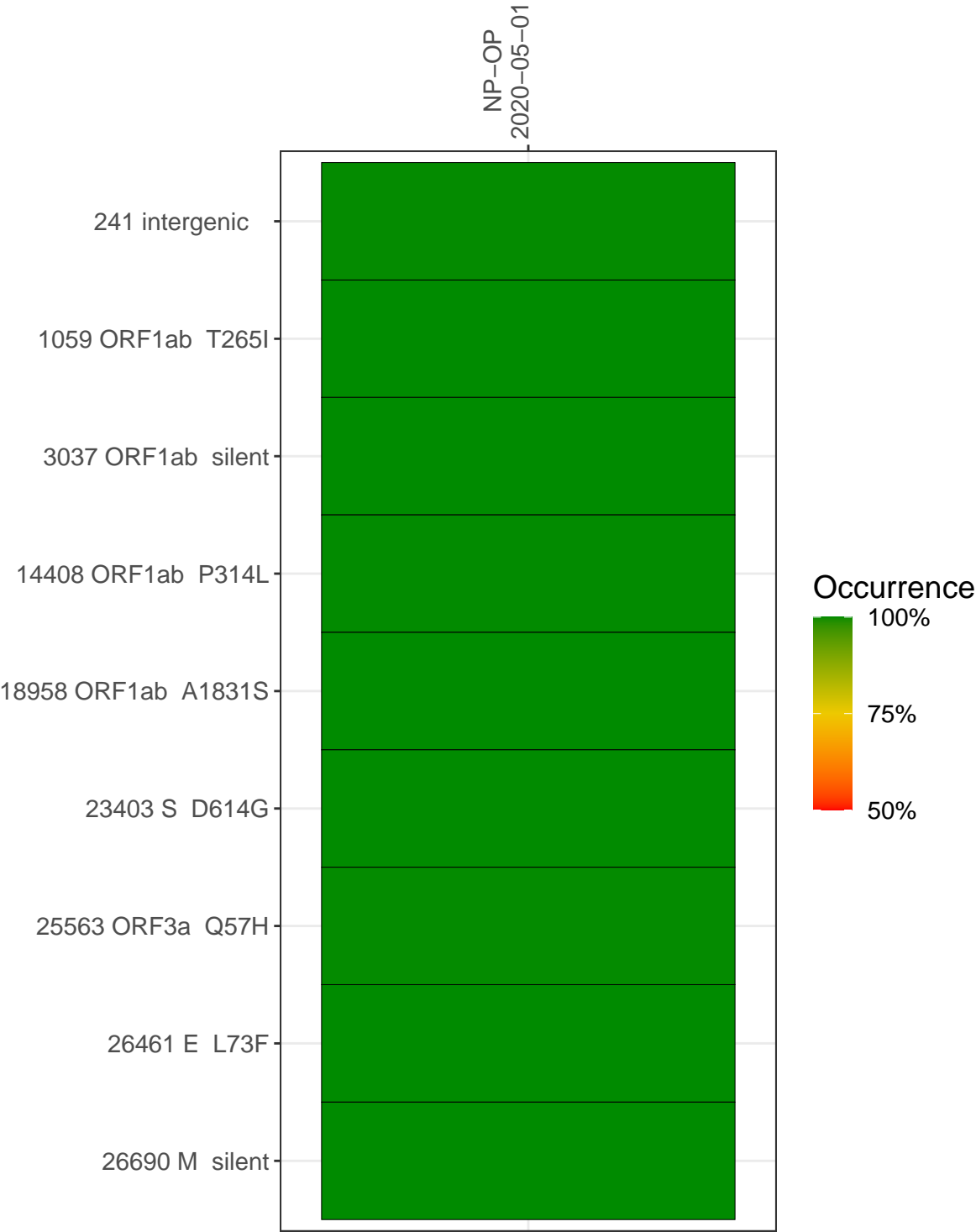
Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with $> 90\%$ sequence coverage.

Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (≥ 5 reads)
VSP0050	composite	NA	NP-OP	2020-05-01	21.42	B.1	99.3%	99.2%
VSP0050-1	single experiment	2190	NP-OP	2020-05-01	4.73	NA	83.3%	82.2%
VSP0050-2	single experiment	2190	NP-OP	2020-05-01	7.49	NA	91.5%	90.7%
VSP0050-3	single experiment	2190	NP-OP	2020-05-01	10.14	B.1	97.8%	96.9%
VSP0050-4	single experiment	2190	NP-OP	2020-05-01	10.21	NA	90.8%	90.3%

Variants shared across samples

The heat map below shows how variants (reference genome /home/common/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) 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.



NP-OP
2020-05-01

	VSP0050-1	VSP0050-2	VSP0050-3	VSP0050-4
241 intergenic	300	622	1287	978
1059 ORF1ab T265I	116	850	219	476
3037 ORF1ab silent	63	589	1152	195
14408 ORF1ab P314L	407	1321	1163	2126
18958 ORF1ab A1831S	11	771	284	1018
23403 S D614G	1395	3352	5215	3126
25563 ORF3a Q57H	154	647	501	710
26461 E L73F	821	465	993	334
26690 M silent	969	1021	2214	1938

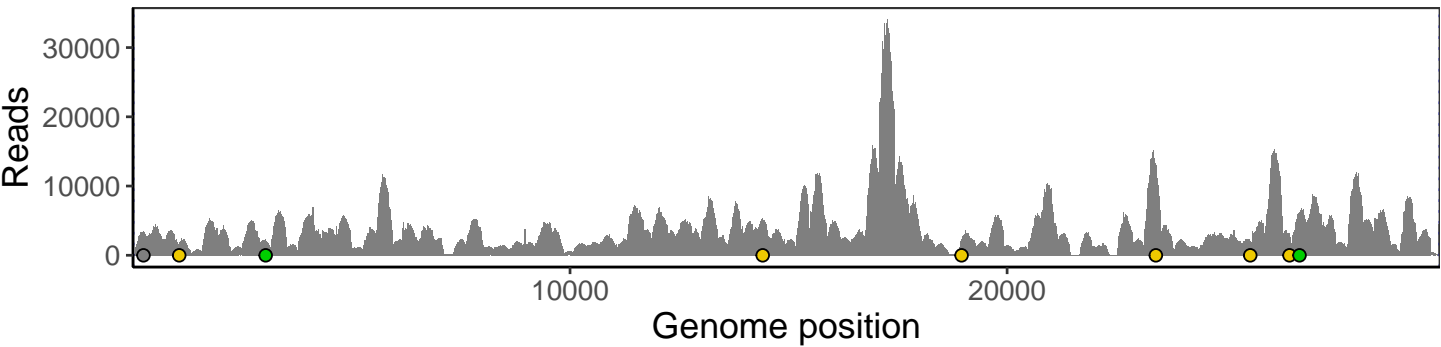
Base change

- Expected
- A
- T
- C
- G
- N
- Ins/Del
- No data

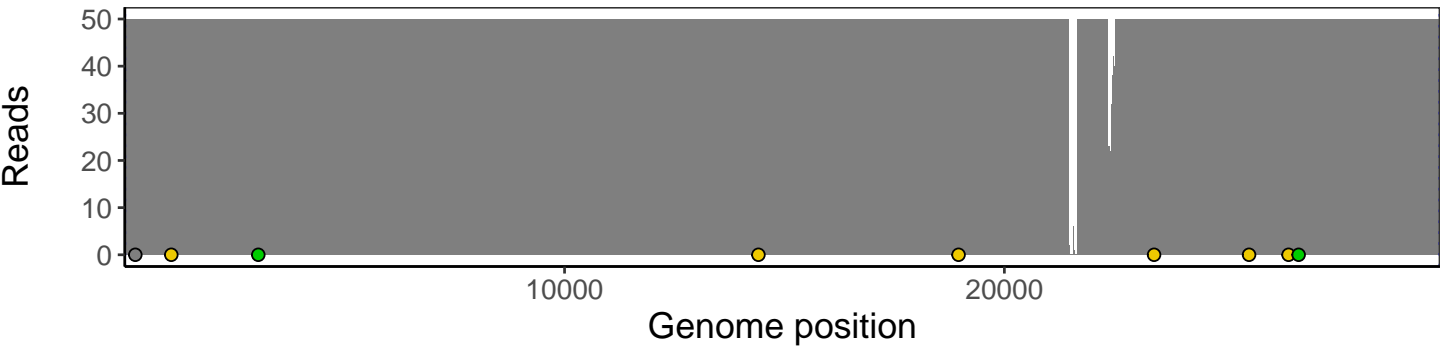
Analyses of individual experiments and composite results

VSP0050 | 2020-05-01 | NP-OP | 247-qia | composite result

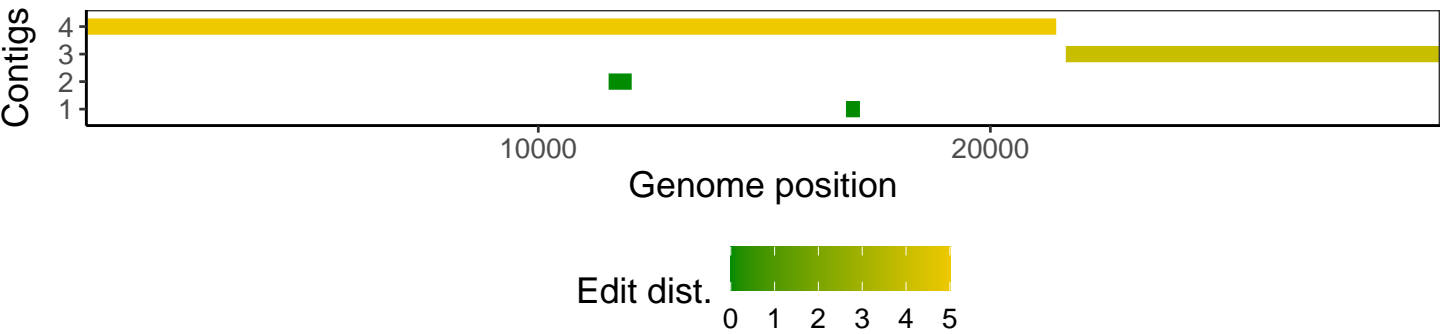
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



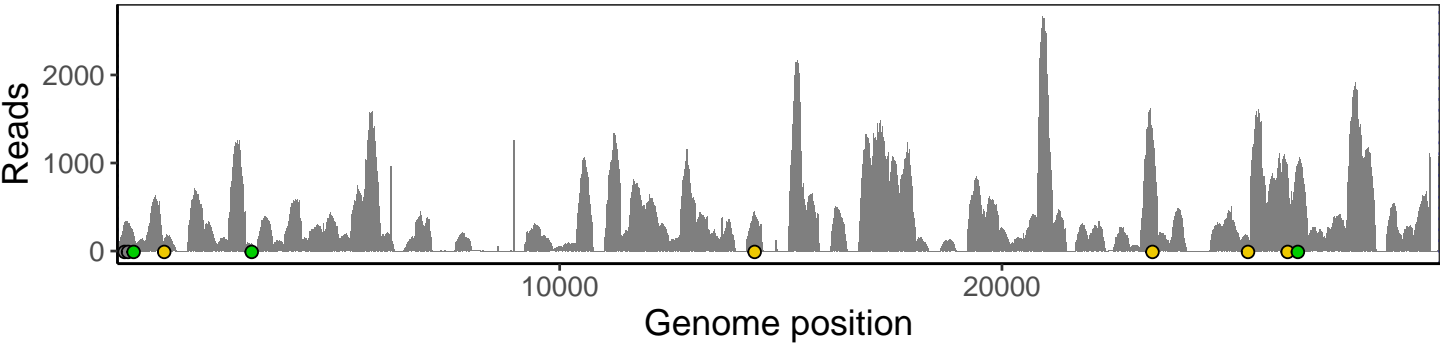
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



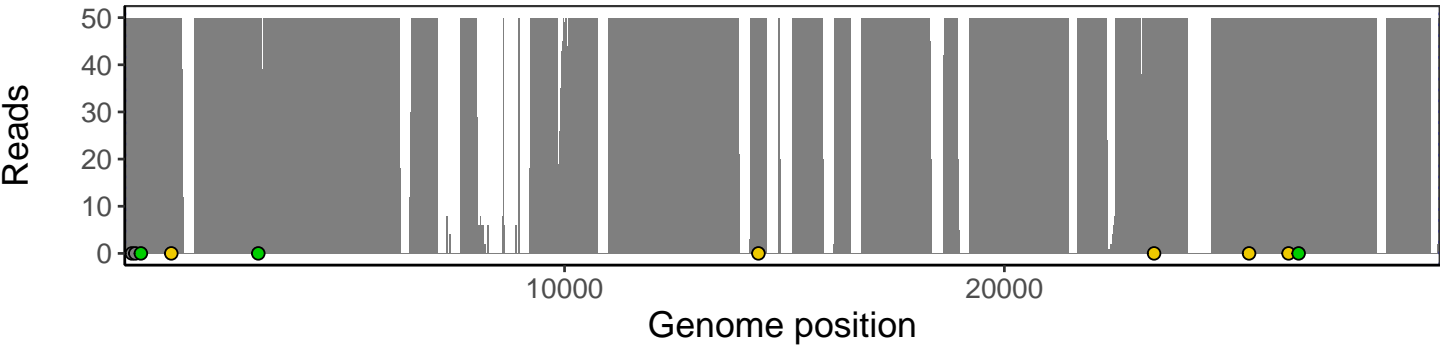
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



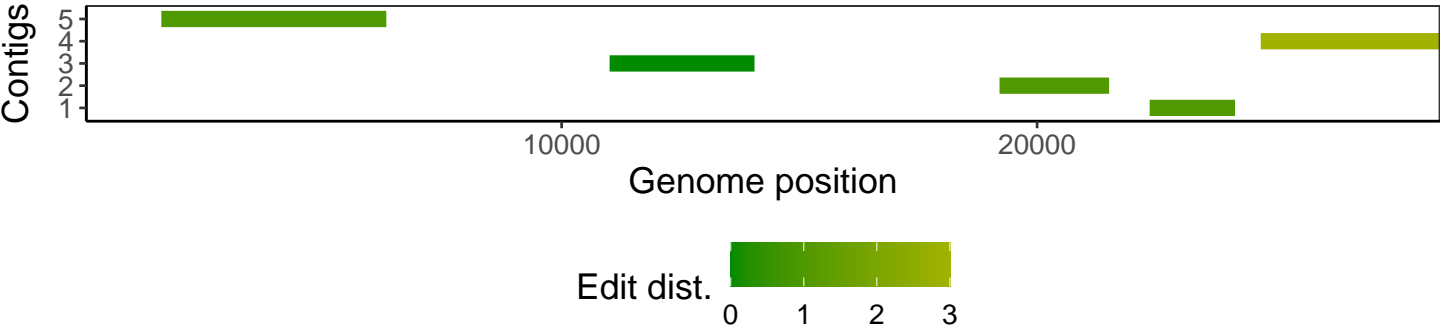
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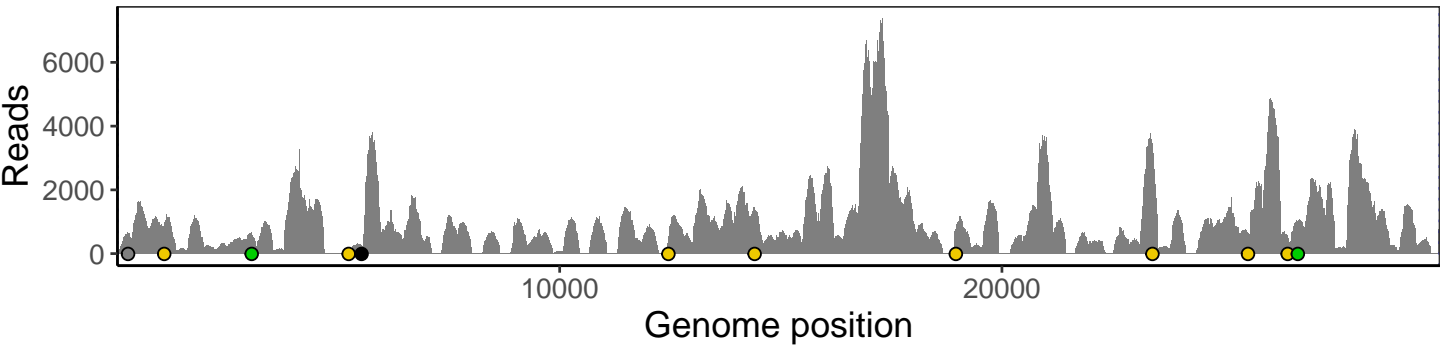
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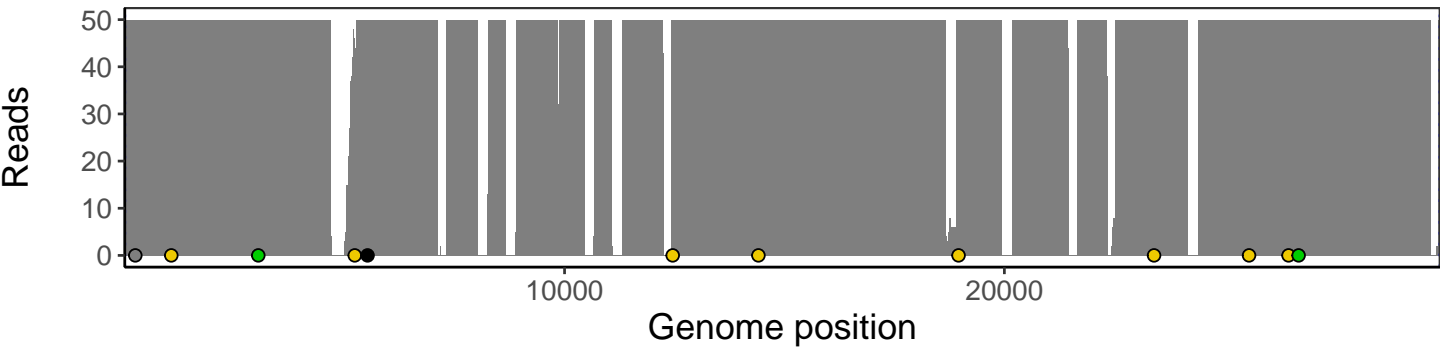
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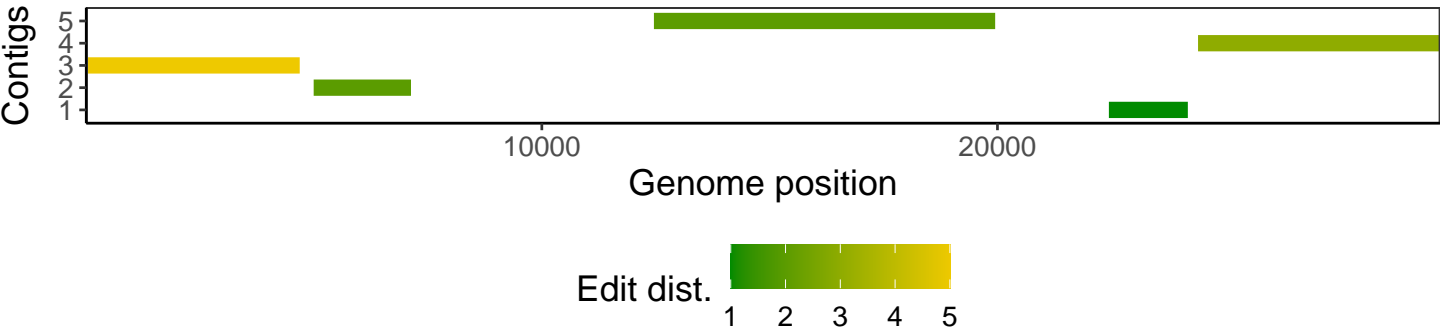
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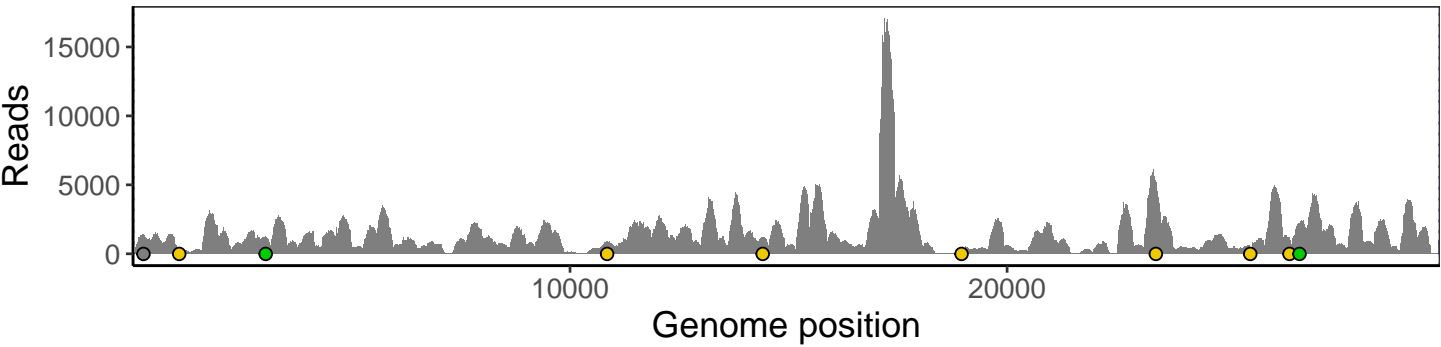
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



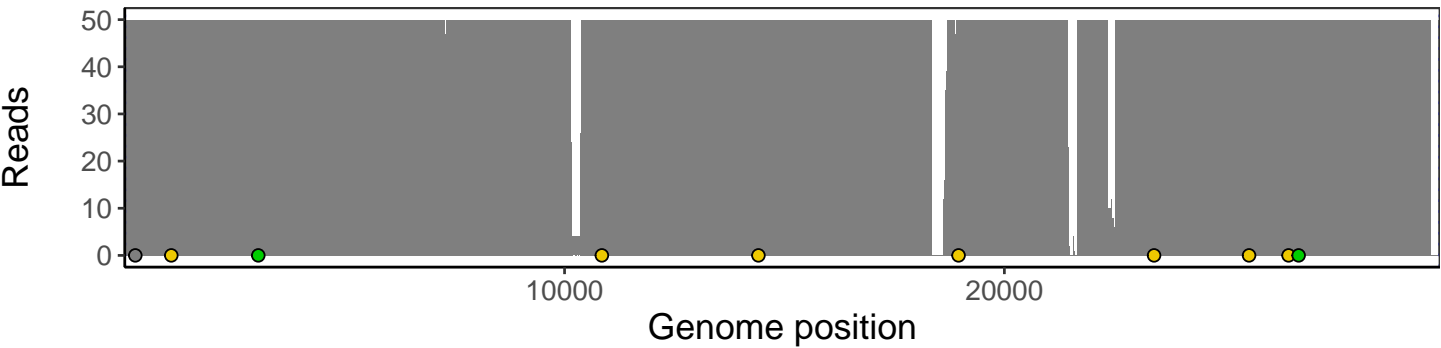
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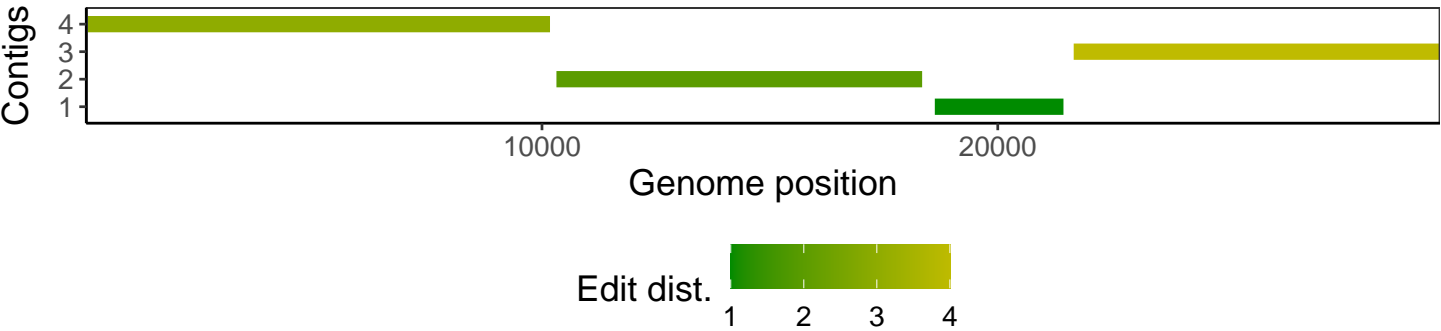
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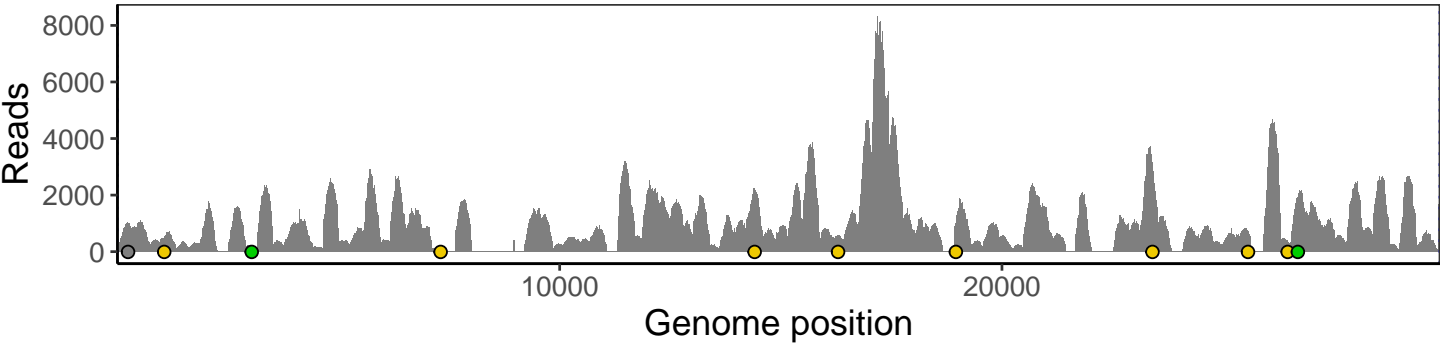
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



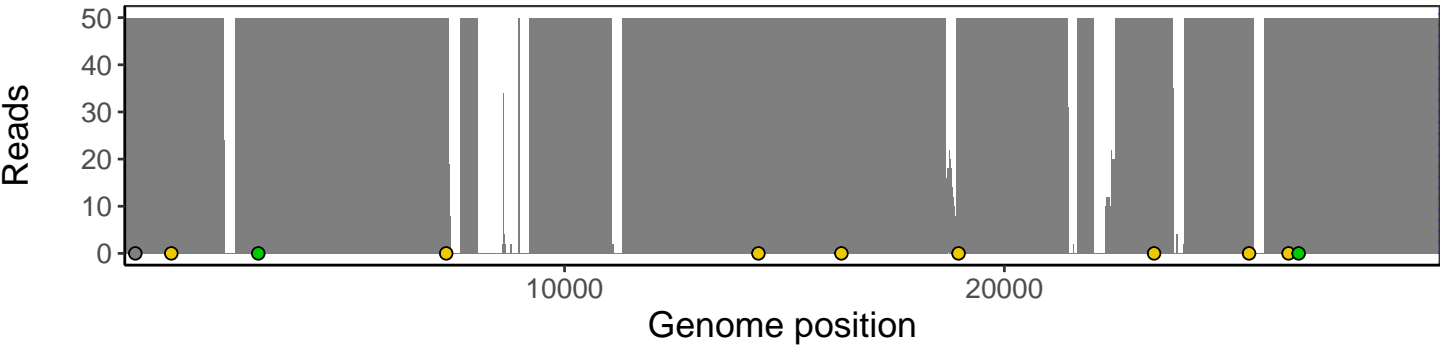
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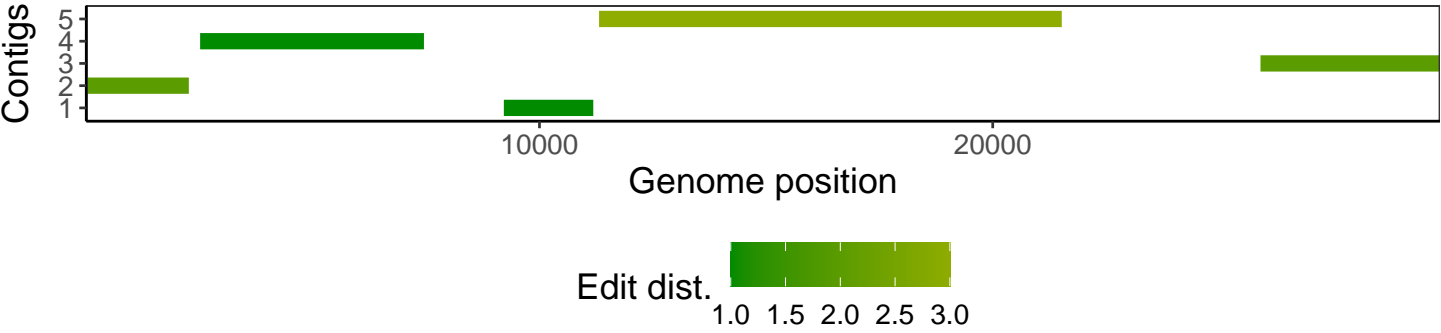
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Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



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Software environment

Software/R package	Version
R	3.4.0
bwa	0.7.17-r1198-dirty
samtools	1.10 Using htlib 1.10
bcftools	1.10.2-34-g1a12af0-dirty Using htlib 1.10.2-57-gf58a6f3
pangolin	3.1.3
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	3.3.3
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