

COVID-19 subject 239

2021-06-23

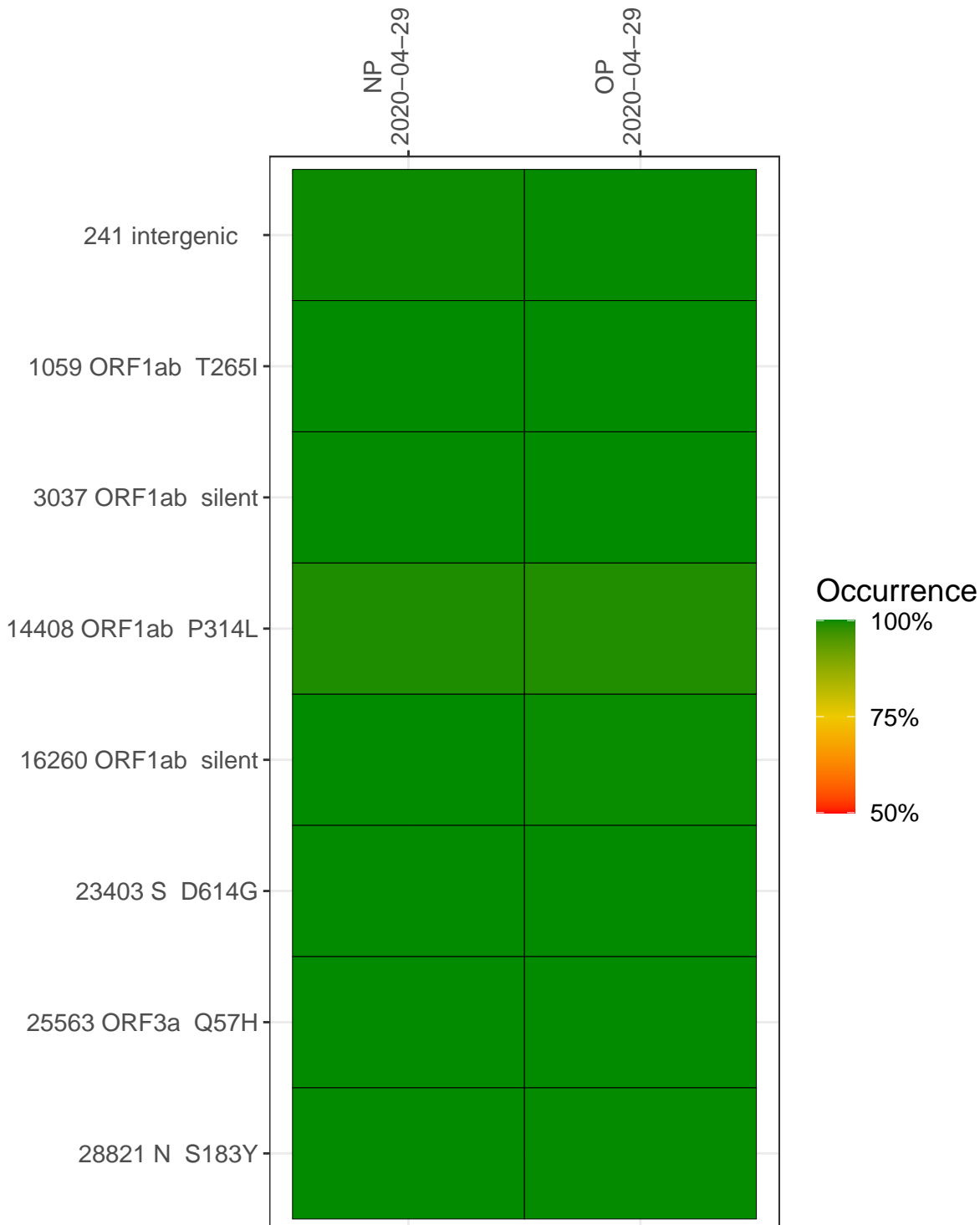
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP0041	composite	NA	NP	2020-04-29	29.84	B.1.369	99.8%	99.8%
VSP0042	composite	NA	OP	2020-04-29	27.48	B.1.369	99.7%	99.7%
VSP0041-1m	single experiment	NA	NP	2020-04-29	29.83	B.1.369	99.8%	99.7%
VSP0041-2	single experiment	NA	NP	2020-04-29	29.84	B.1.369	99.8%	99.8%
VSP0042-1m	single experiment	NA	OP	2020-04-29	1.12	NA	71.5%	63.4%
VSP0042-2	single experiment	6490	OP	2020-04-29	1.18	NA	81.2%	66.0%

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 2020-04-29		OP 2020-04-29	
241 intergenic	5842	13426	0	6657
1059 ORF1ab T265I	1847	13114	2967	2
3037 ORF1ab silent	1510	1006	2131	0
14408 ORF1ab P314L	3188	1051	3428	2
16260 ORF1ab silent	1265	985	2151	2
23403 S D614G	9120	22418	0	8907
25563 ORF3a Q57H	3172	25656	4709	16
28821 N S183Y	2751	5130	2	4115
	VSP0041-1m	VSP0041-2	VSP0042-1m	VSP0042-2

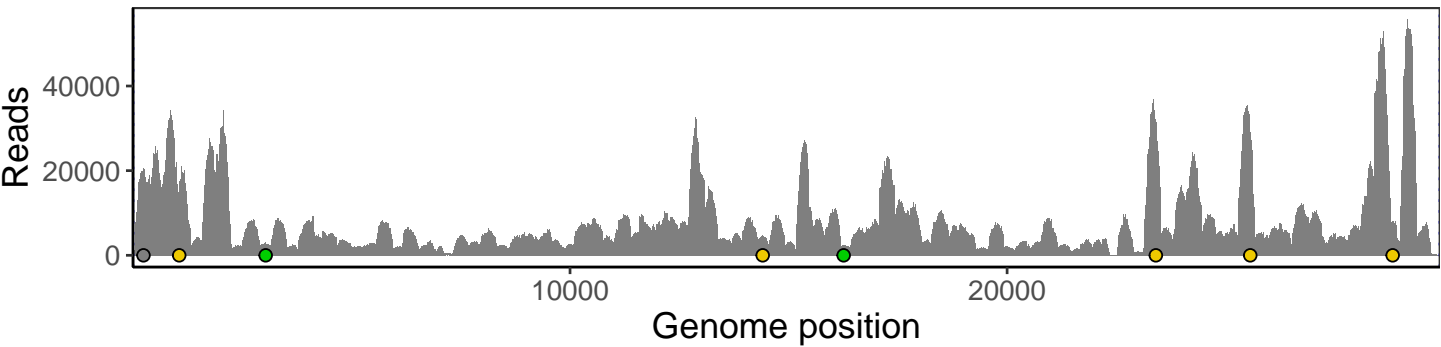
Base change



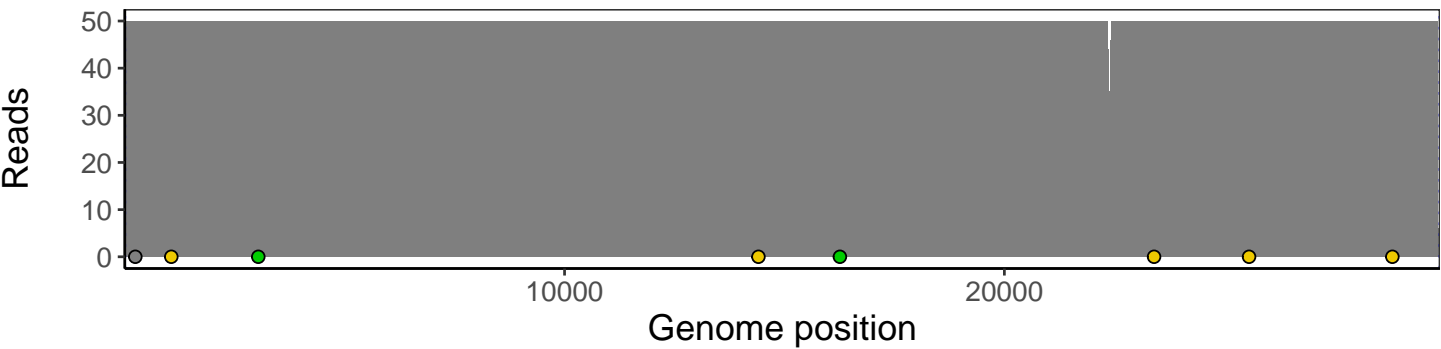
Analyses of individual experiments and composite results

VSP0041 | 2020-04-29 | NP | 239n-tri | composite result

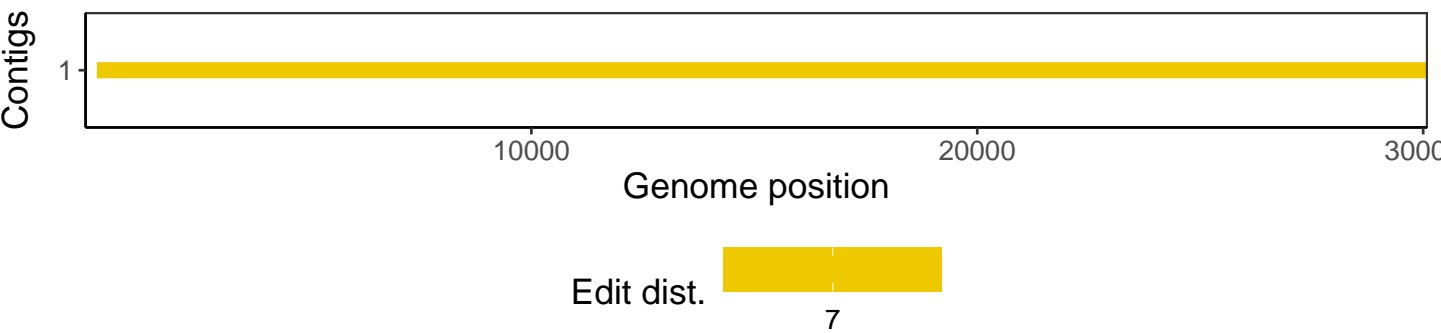
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



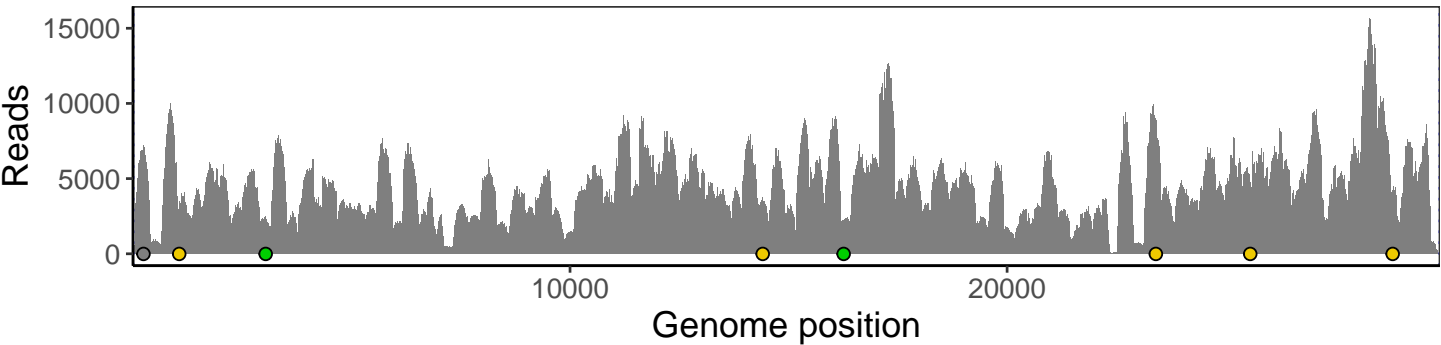
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



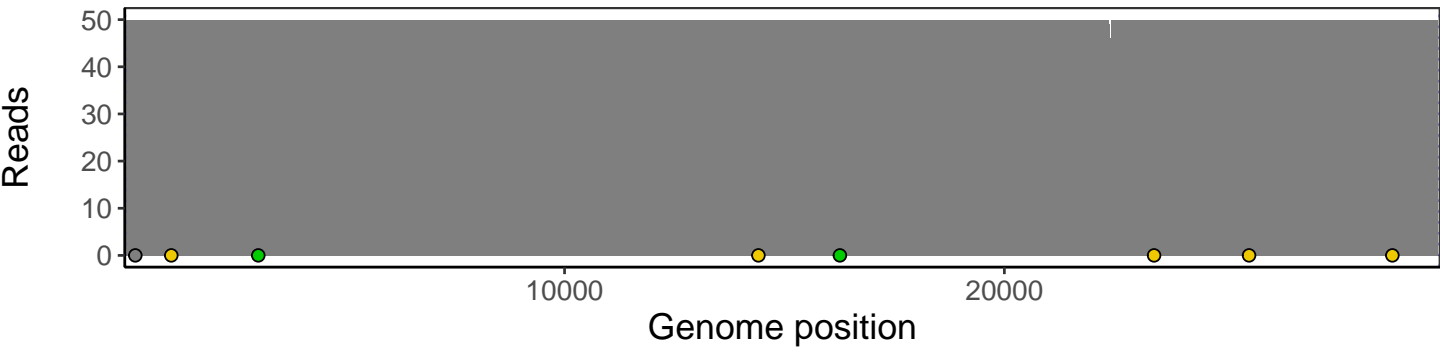
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



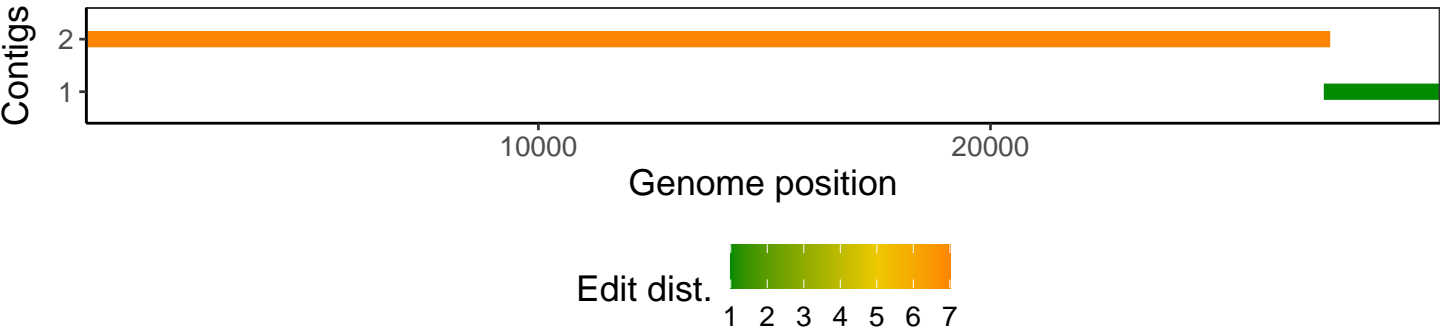
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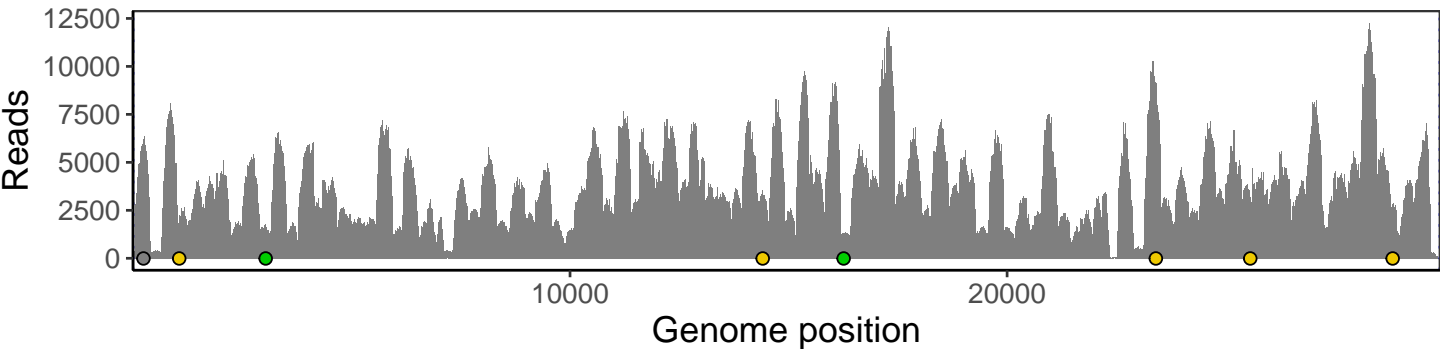
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



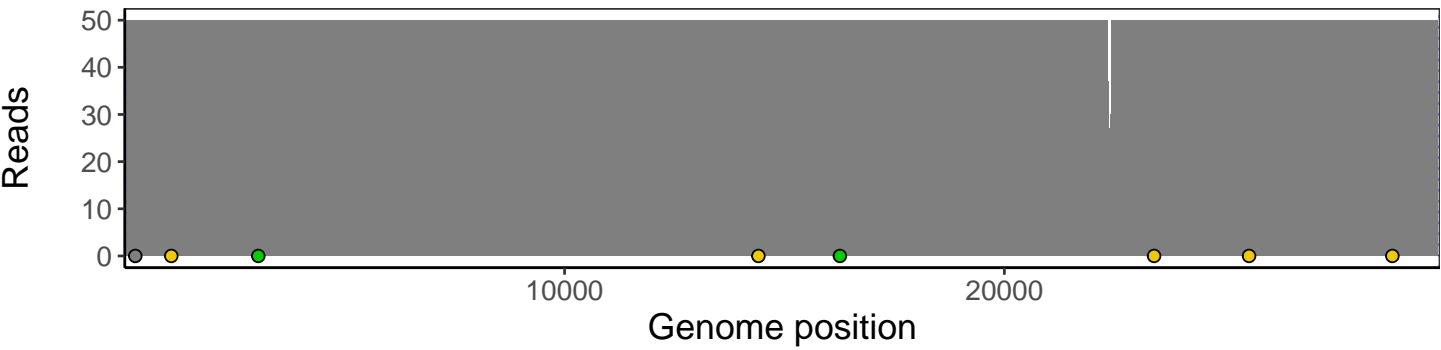
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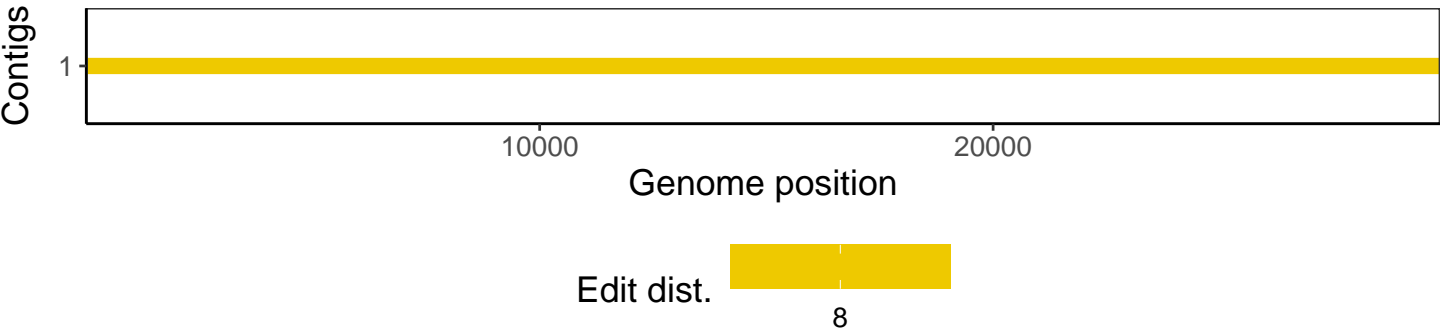
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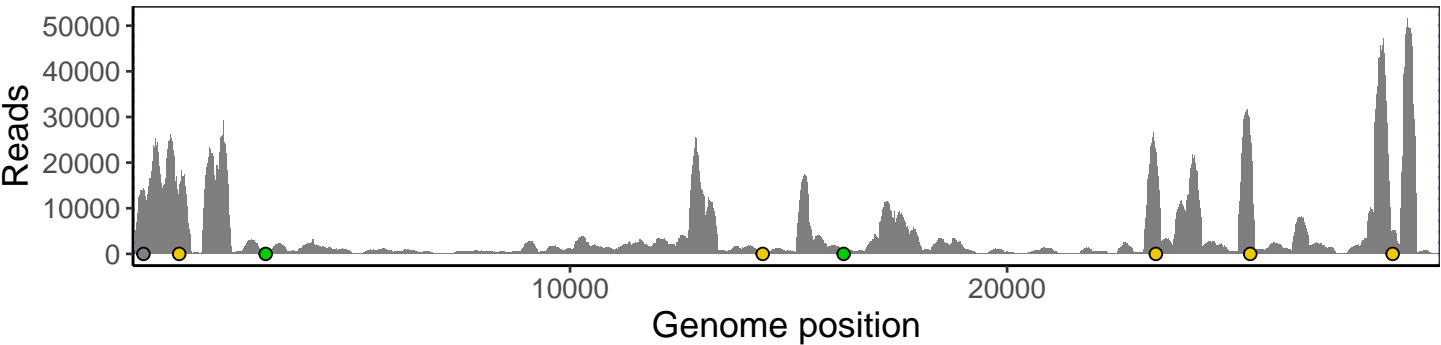
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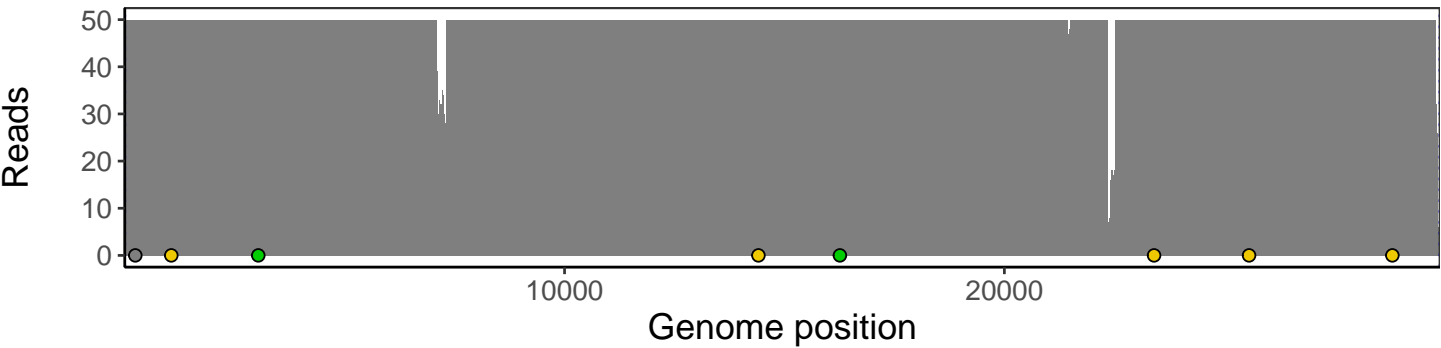
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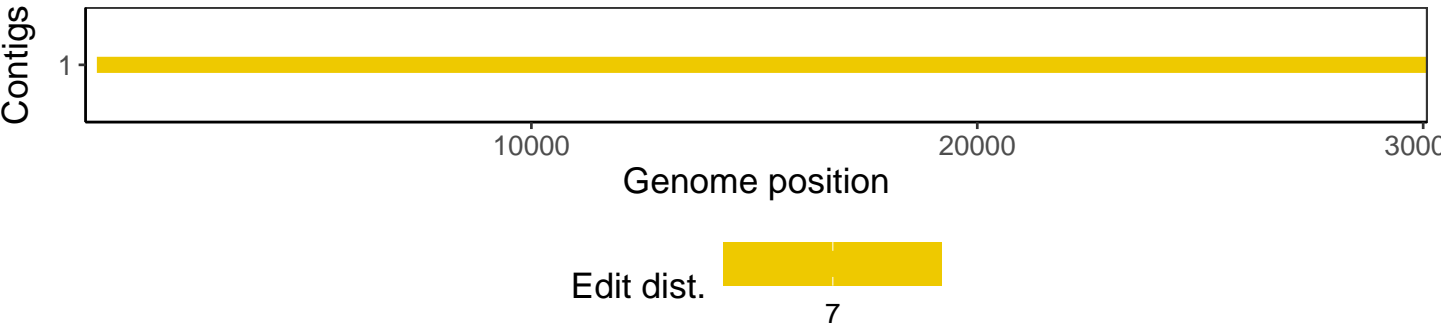
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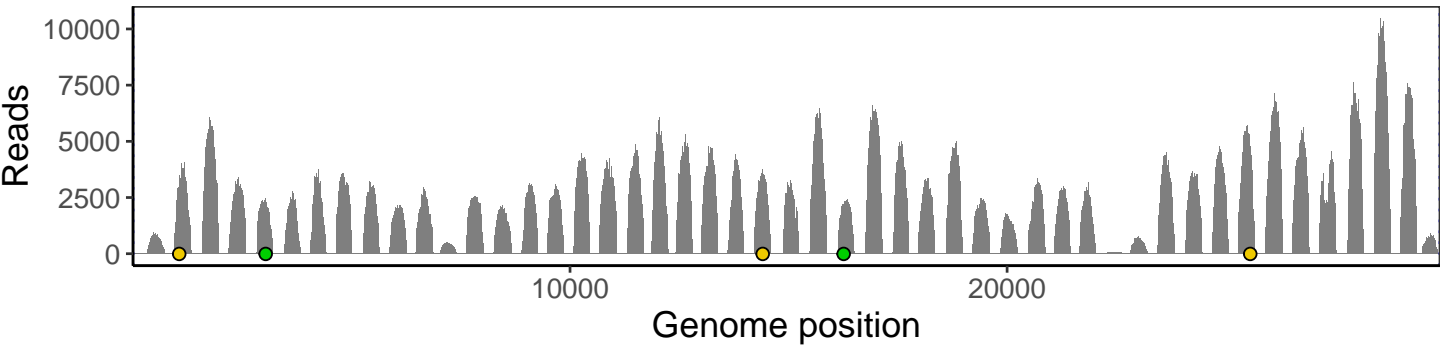
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



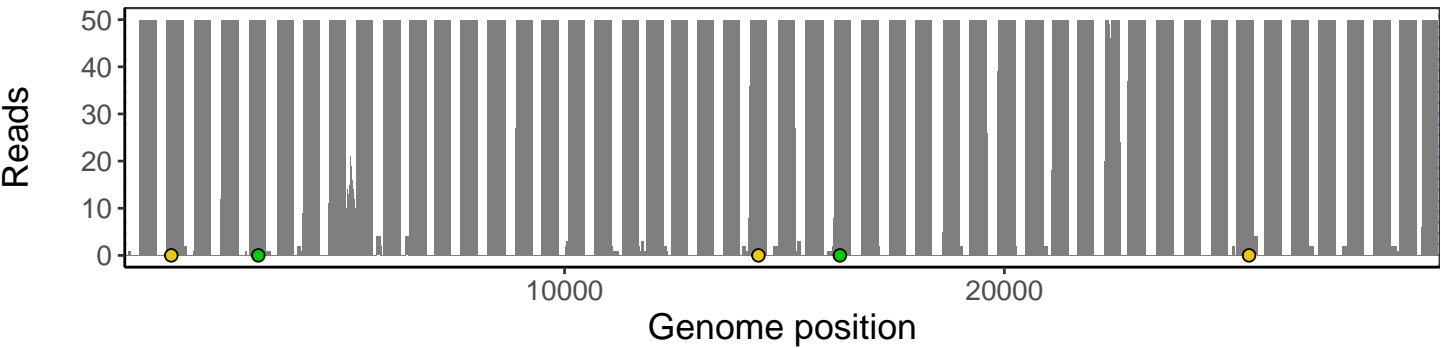
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



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.



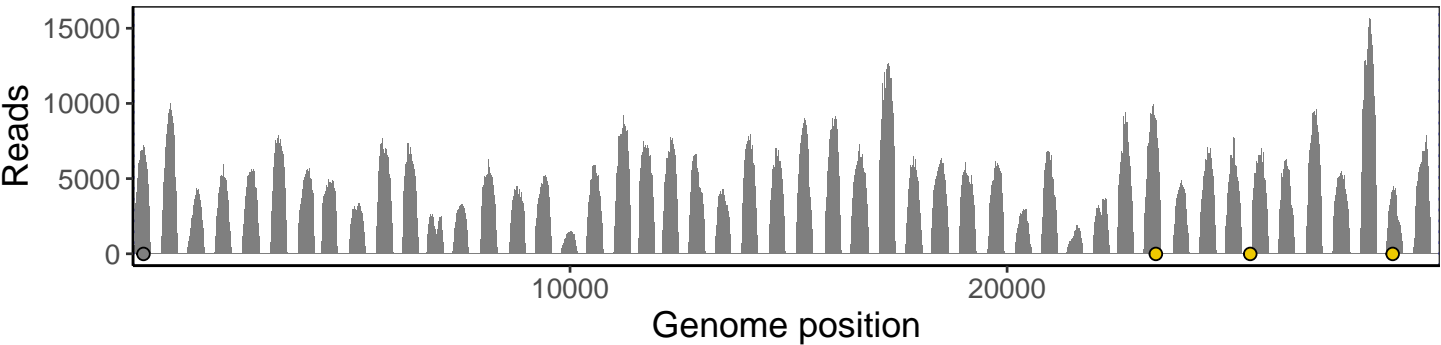
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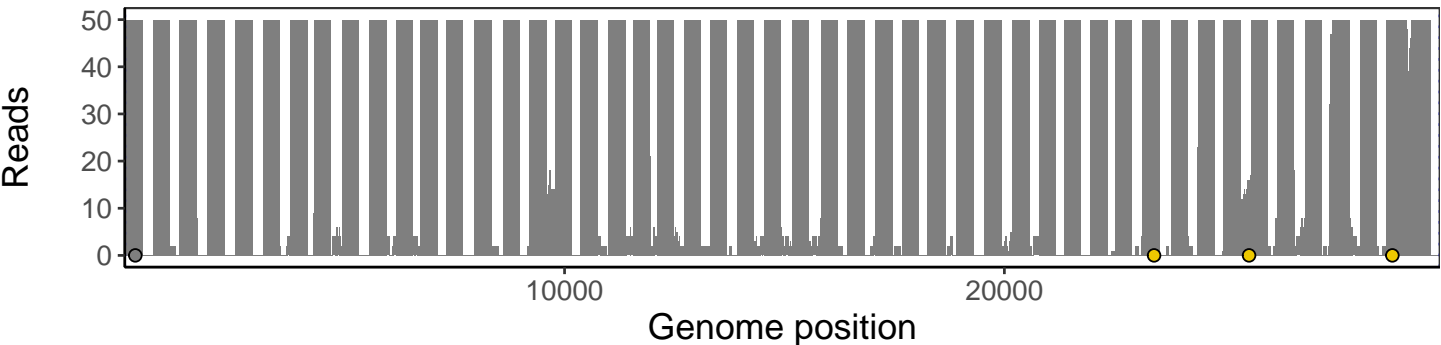
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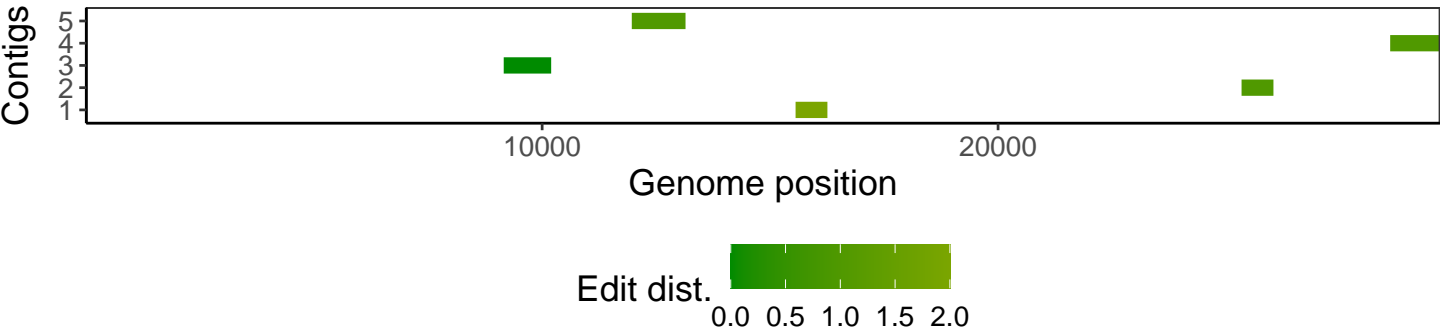
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Software environment

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