

COVID-19 subject 290

2021-03-01

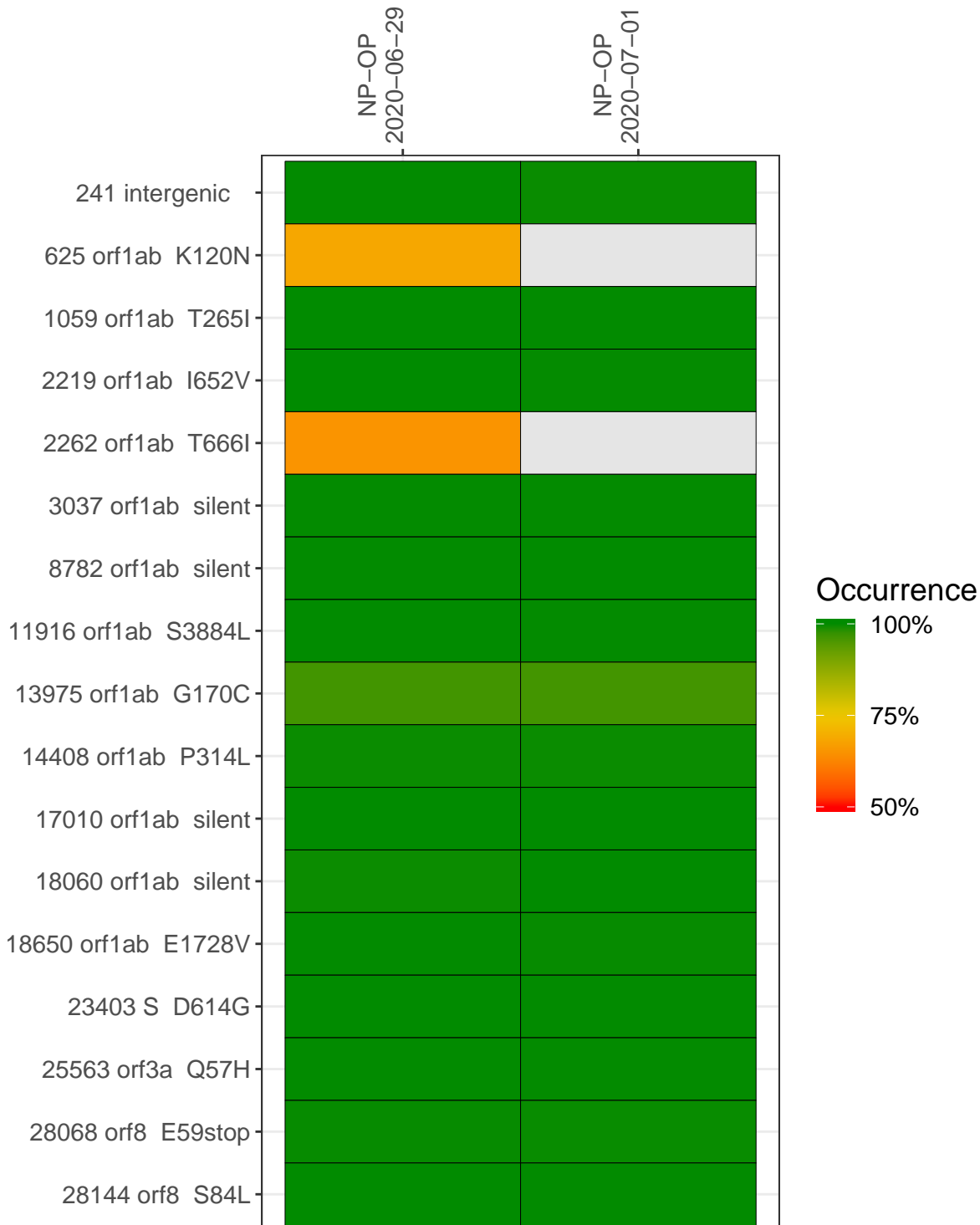
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP0230	composite	NA	NP-OP	2020-06-29	29.80	B.1.291	99.8%	99.8%
VSP0233	composite	NA	NP-OP	2020-07-01	24.18	B.1.291	99.8%	99.8%
VSP0230-1	single experiment	11750	NP-OP	2020-06-29	27.24	B.1.291	99.8%	99.8%
VSP0230-2	single experiment	11750	NP-OP	2020-06-29	29.80	B.1.291	99.8%	99.8%
VSP0233-1	single experiment	27900	NP-OP	2020-07-01	29.86	B.1.291	99.8%	99.8%
VSP0233-2	single experiment	27900	NP-OP	2020-07-01	28.54	B.1.291	99.8%	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 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 2020-06-29		NP-OP 2020-07-01	
241 intergenic	7852	9657	5860	7834
625 orf1ab K120N	3398	4916	2705	4535
1059 orf1ab T265I	2568	3824	2096	3469
2219 orf1ab I652V	1713	1886	1428	1996
2262 orf1ab T666I	1584	1635	1227	1545
3037 orf1ab silent	4438	3468	3984	2570
8782 orf1ab silent	5186	3894	4240	2185
11916 orf1ab S3884L	4077	3551	4181	3318
13975 orf1ab G170C	2965	2752	3651	2416
14408 orf1ab P314L	6090	5410	5521	3996
17010 orf1ab silent	10618	9854	11662	9782
18060 orf1ab silent	2811	1695	2683	1506
18650 orf1ab E1728V	4668	3975	5283	4775
23403 S D614G	5244	6066	6850	9528
25563 orf3a Q57H	2947	3752	3171	4503
28068 orf8 E59stop	3845	3424	4924	4321
28144 orf8 S84L	3345	3760	4874	5420
	VSP0230-1	VSP0230-2	VSP0233-1	VSP0233-2

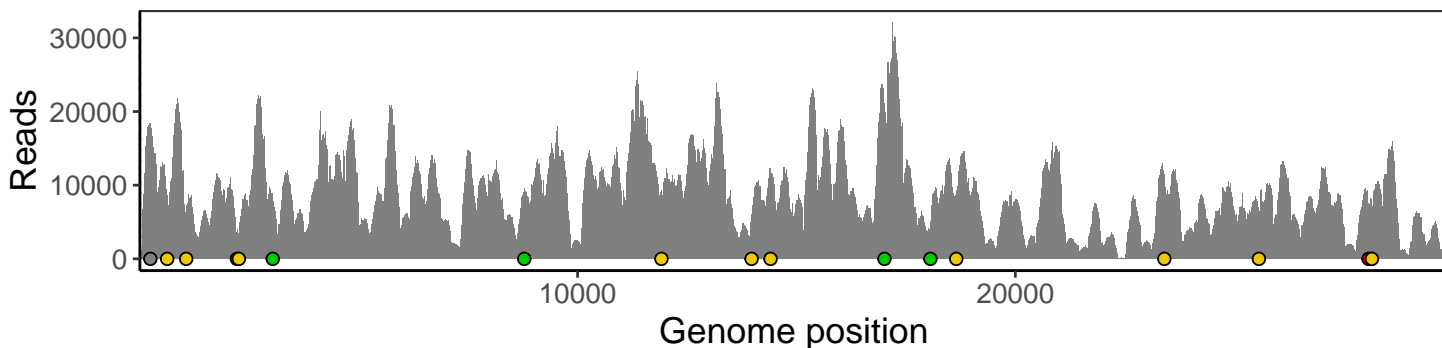
Base change

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

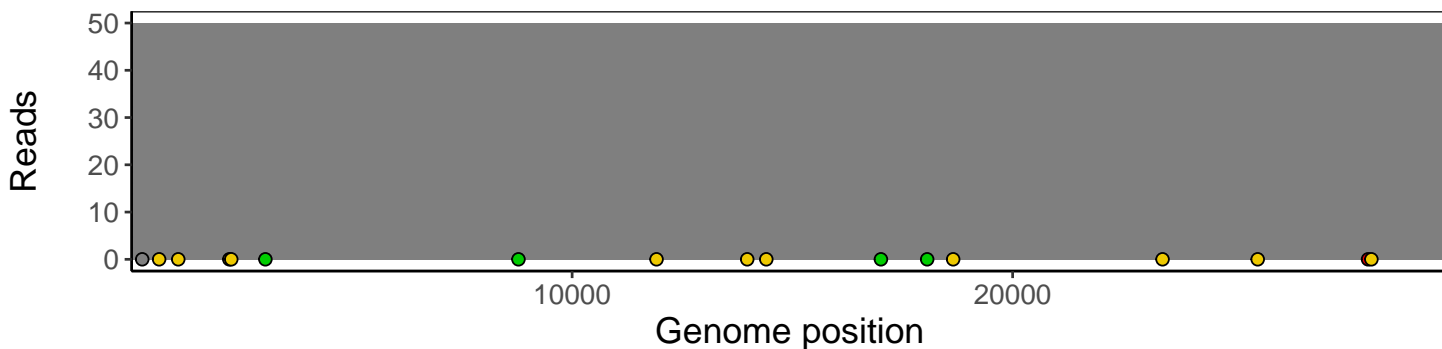
Analyses of individual experiments and composite results

VSP0230 | 2020-06-29 | NP-OP | 290no-q | composite result

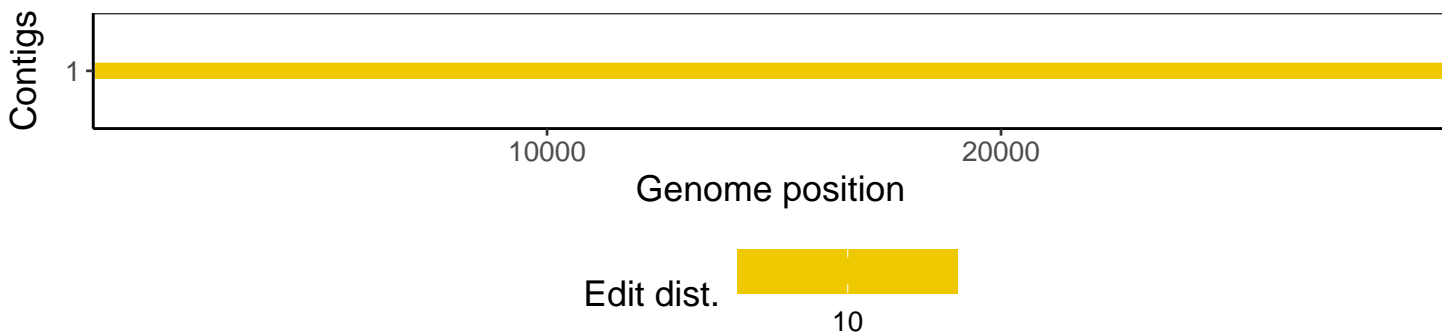
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



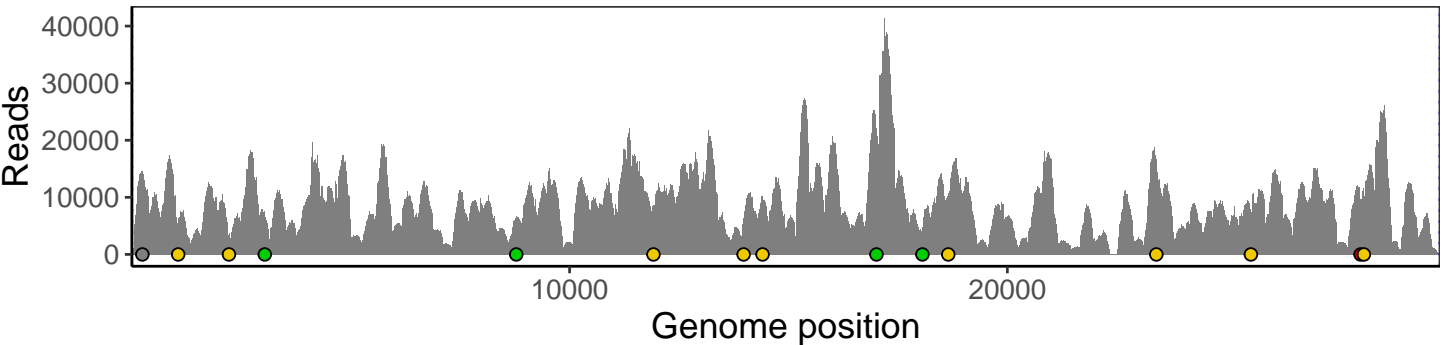
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



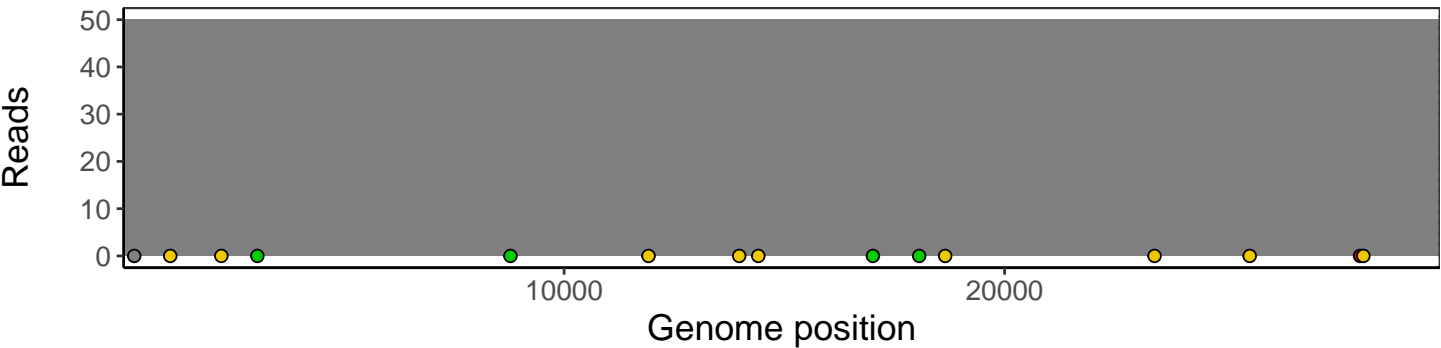
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



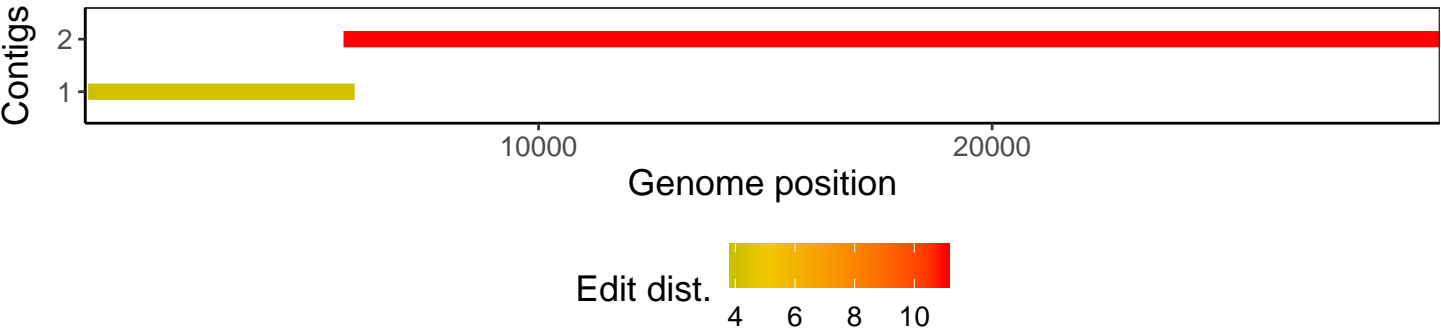
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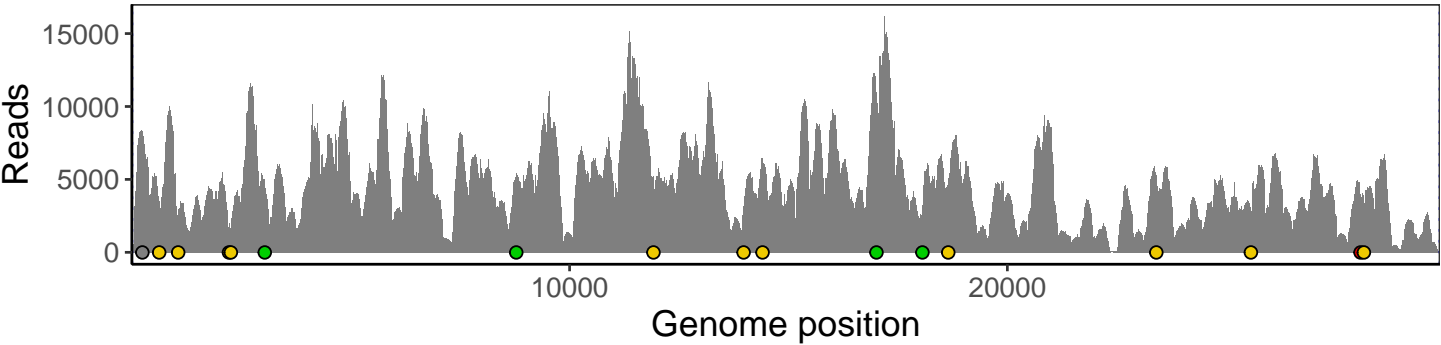
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



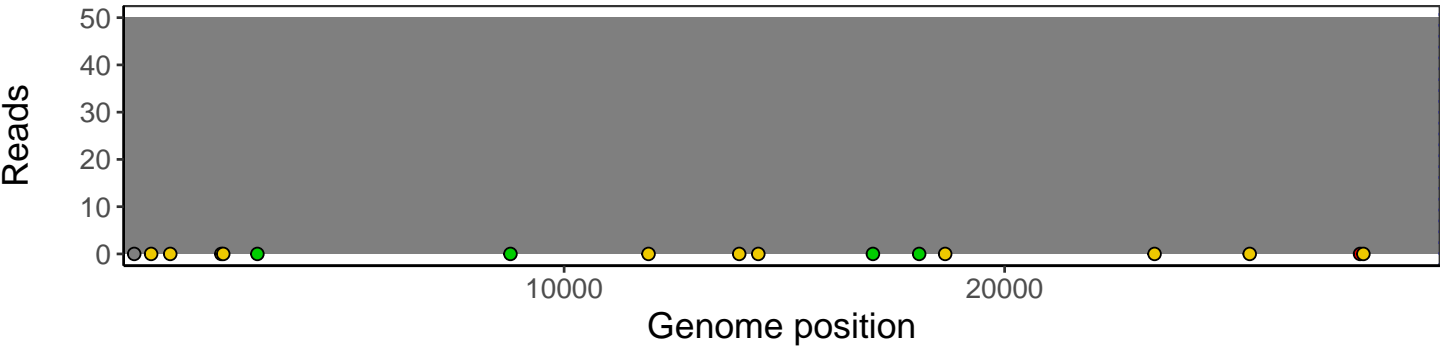
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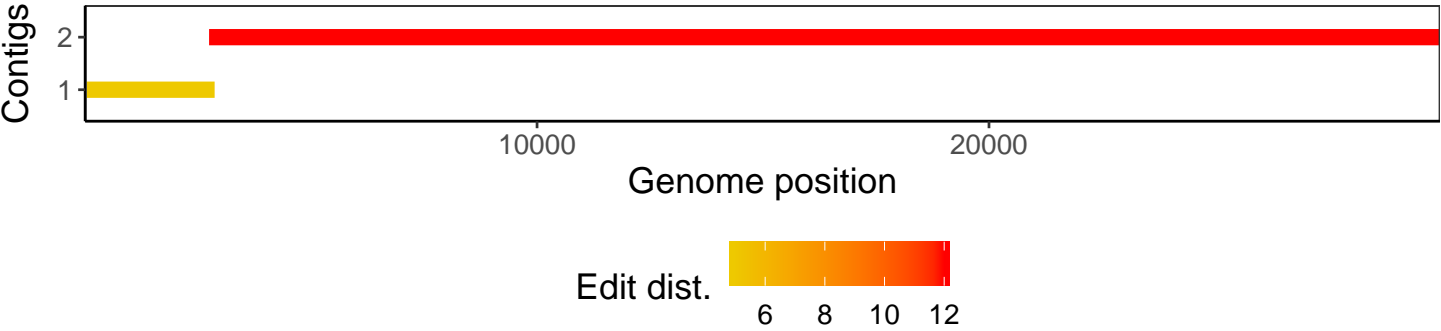
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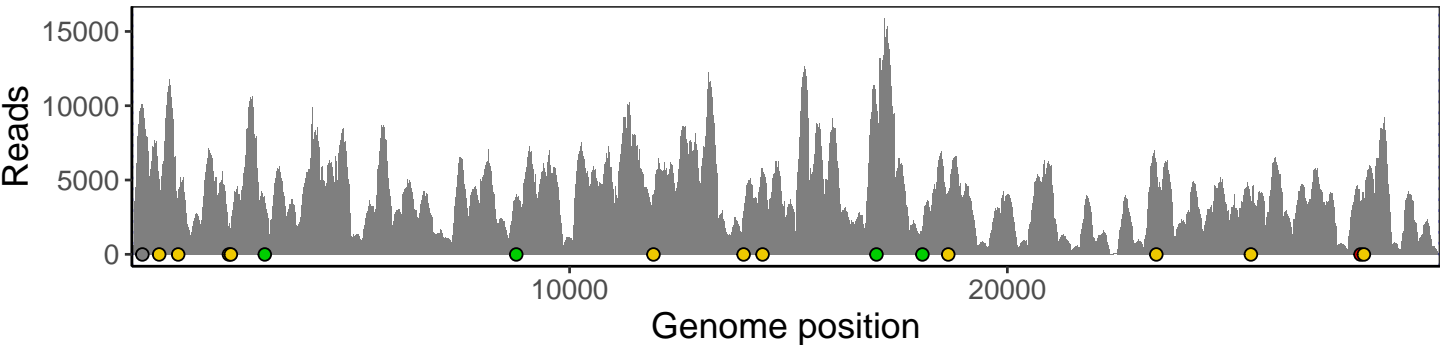
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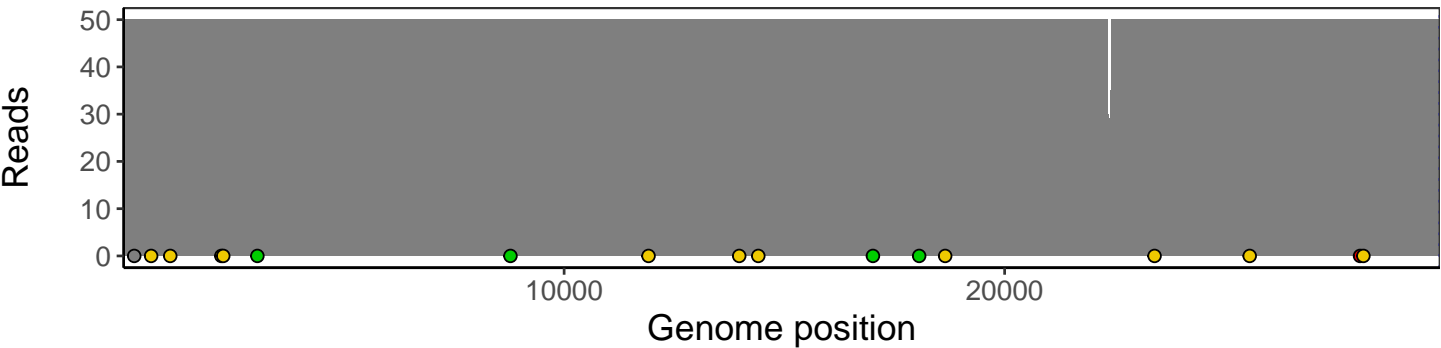
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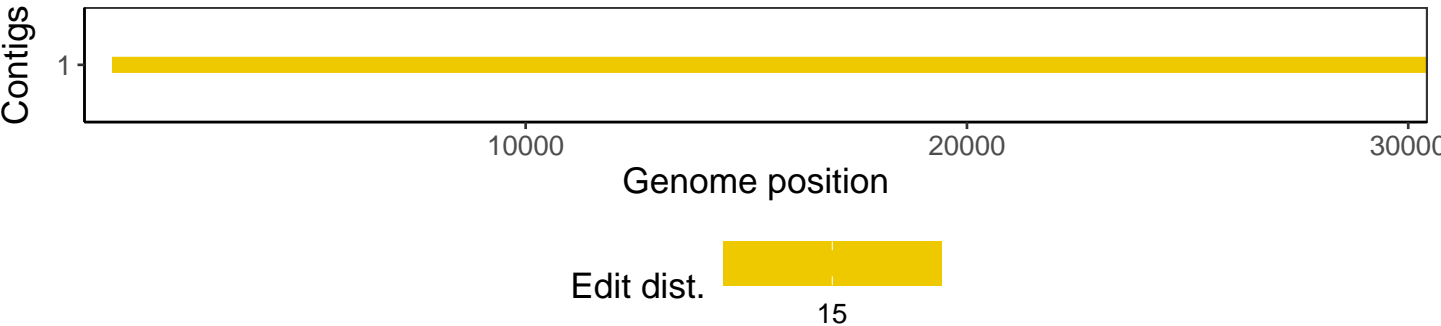
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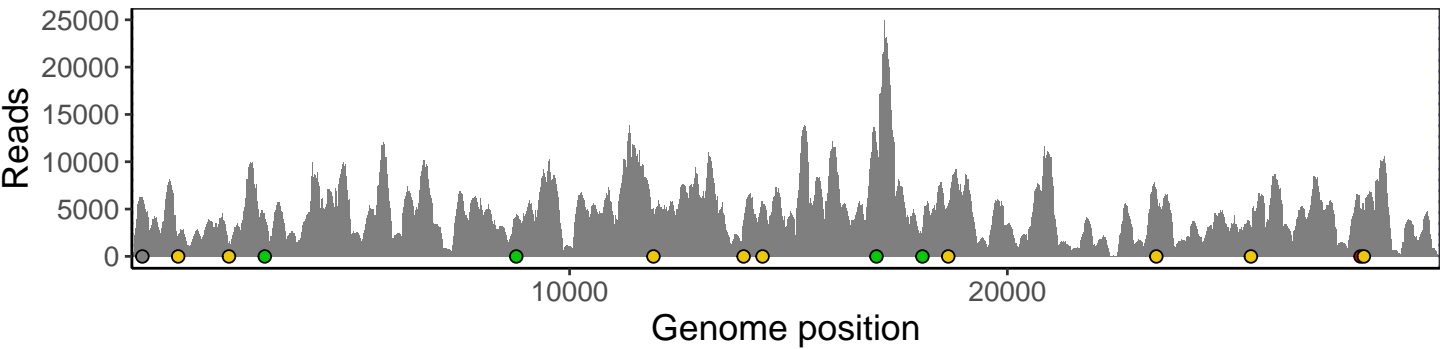
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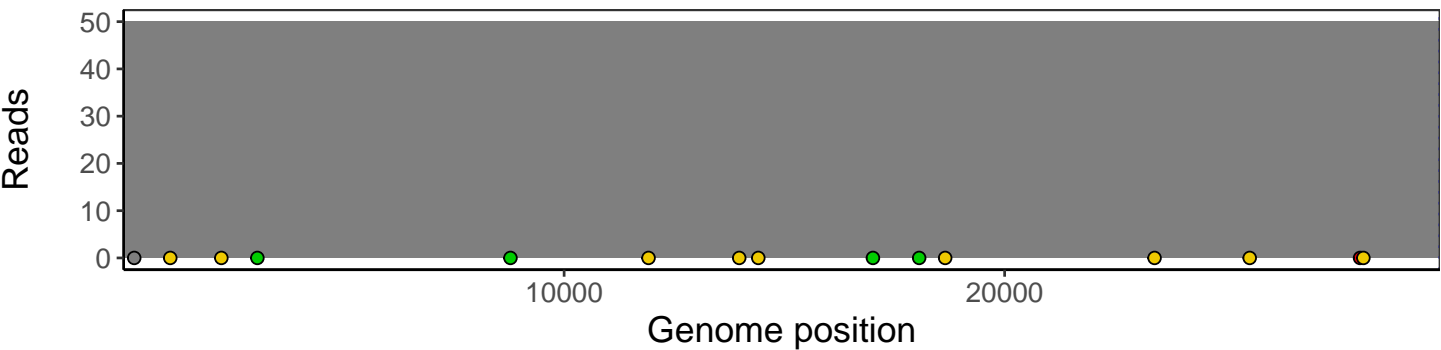
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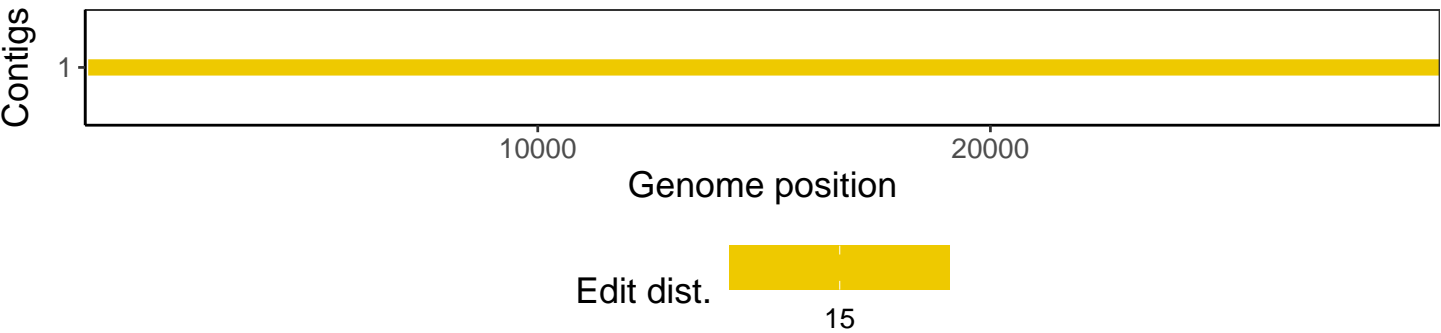
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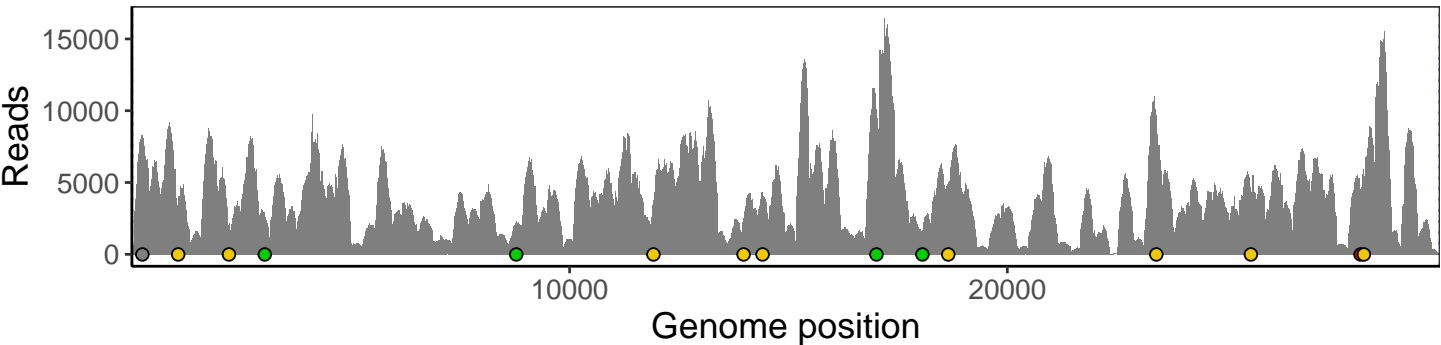
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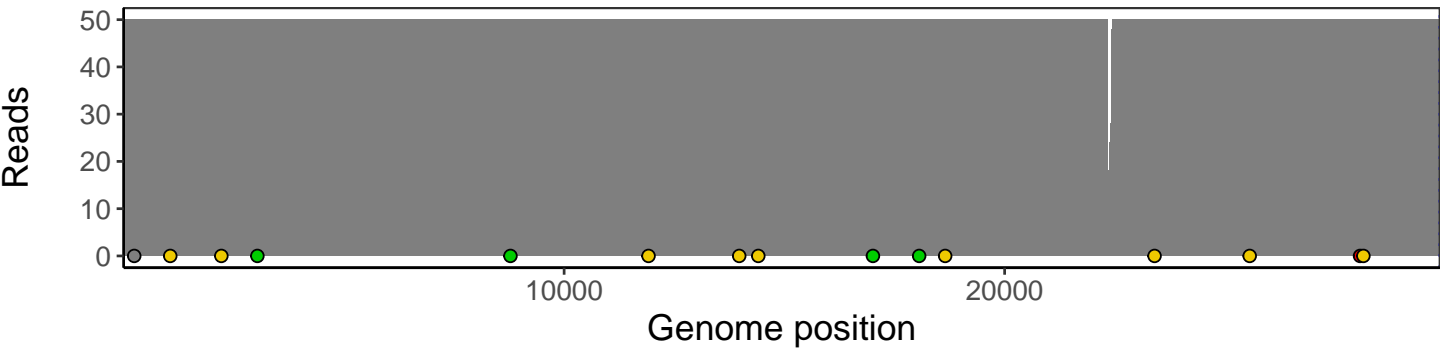
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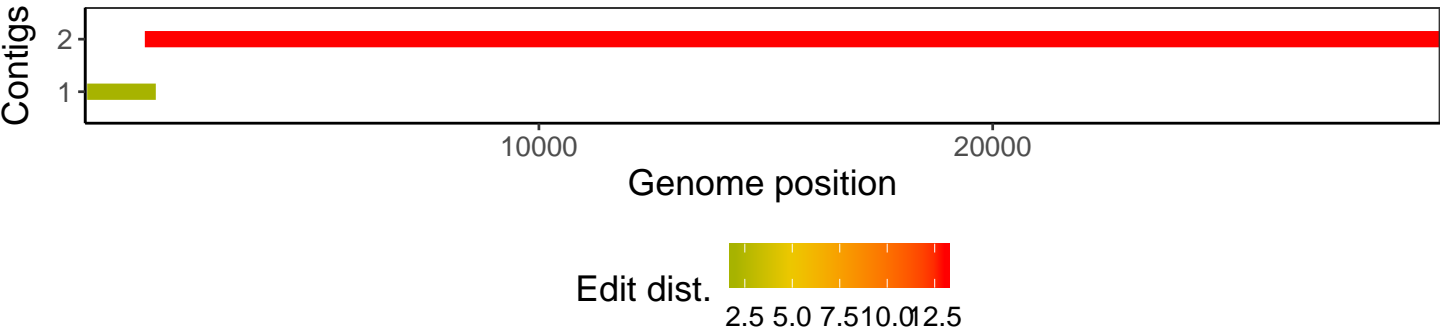
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Software environment

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	2.3.3
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	3.0.0
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