

# COVID-19 subject MPCluster2-Seq14

*2021-04-20*

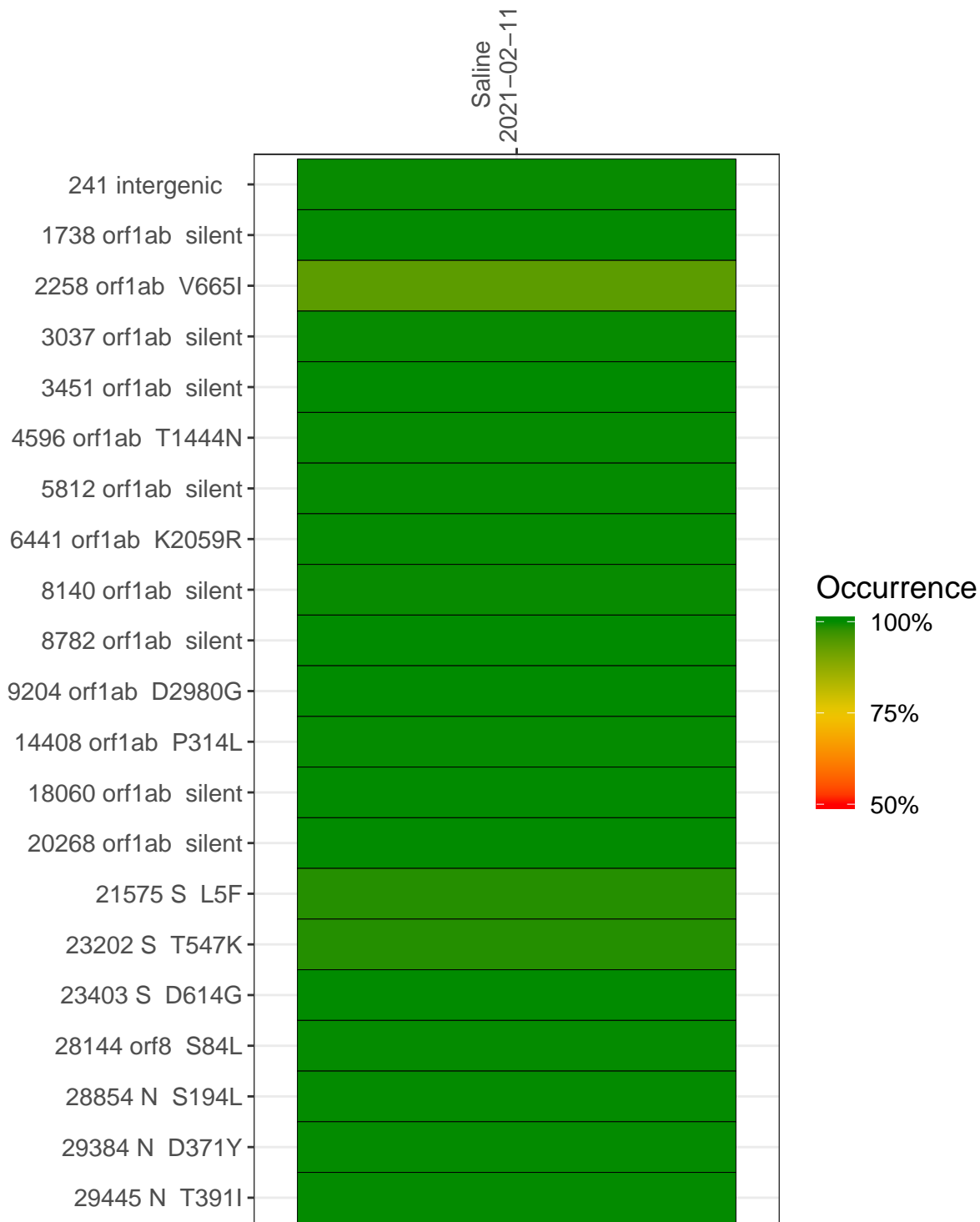
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software 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)
VSP0806	composite	NA	Saline	2021-02-11	25.39	B.1.234	100.0%	99.9%
VSP0806-1	single experiment	NA	Saline	2021-02-11	29.47	B.1.234	100.0%	99.8%
VSP0806-2	single experiment	NA	Saline	2021-02-11	29.85	B.1.234	99.9%	99.9%
VSP0806-3	single experiment	NA	Saline	2021-02-11	29.84	B.1.234	99.8%	99.8%
VSP0806-4	single experiment	NA	Saline	2021-02-11	11.75	B.1.234	99.4%	96.1%
VSP0806-5	single experiment	NA	Saline	2021-02-11	29.91	B.1.234	99.8%	99.8%

## 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.



	Saline 2021-02-11				
241 intergenic	21089	5069	623	314	1342
1738 orf1ab silent	13379	4808	966	611	2017
2258 orf1ab V665I	2001	10835	1653	26	2071
3037 orf1ab silent	3494	7327	968	52	2607
3451 orf1ab silent	10582	17213	2331	339	3309
4596 orf1ab T1444N	7204	14460	1605	99	2507
5812 orf1ab silent	19191	19378	1501	198	3668
6441 orf1ab K2059R	5382	20855	3800	36	3428
8140 orf1ab silent	8240	6505	1269	17	1722
8782 orf1ab silent	2105	5757	1117	6	1152
9204 orf1ab D2980G	7115	9788	1679	156	1858
14408 orf1ab P314L	6561	11753	1439	101	3987
18060 orf1ab silent	1710	10999	1349	57	2322
20268 orf1ab silent	368	7050	658	9	1405
21575 S L5F	271	2921	286	2	740
23202 S T547K	12538	16177	2518	870	2605
23403 S D614G	38815	21829	3155	1217	4329
28144 orf8 S84L	11611	16961	3090	287	3298
28854 N S194L	4100	1855	562	295	973
29384 N D371Y	1382	8269	1791	5	1415
29445 N T391I	1735	4591	1060	8	1049
	VSP0806-1	VSP0806-2	VSP0806-3	VSP0806-4	VSP0806-5

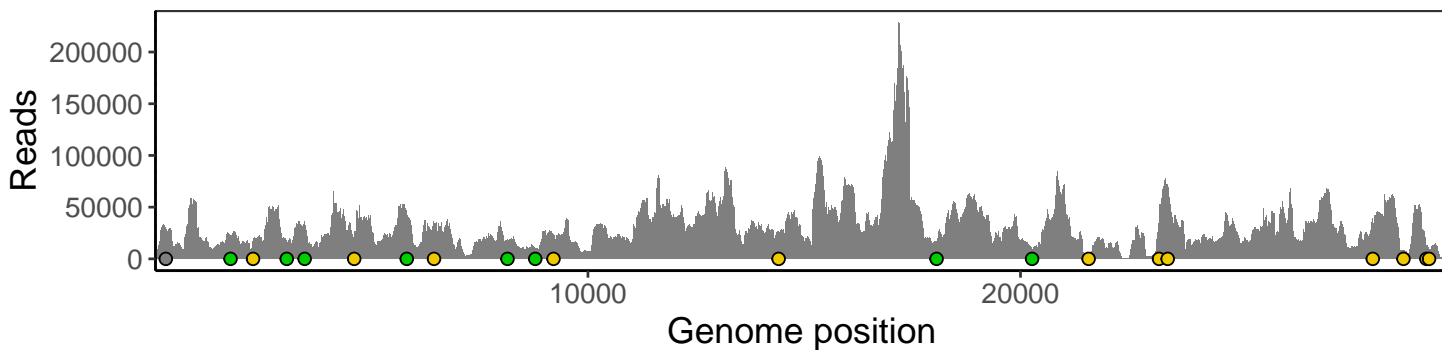
Base change

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

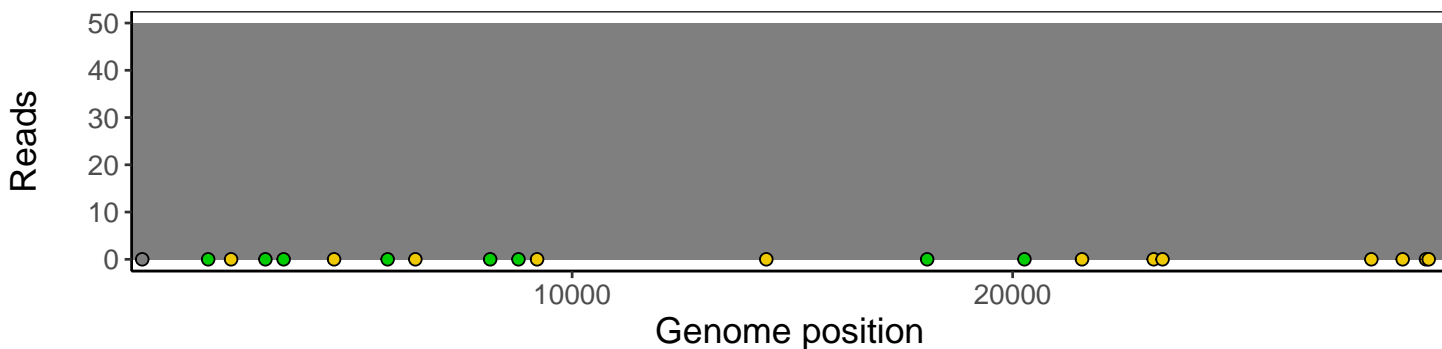
## Analyses of individual experiments and composite results

VSP0806 | 2021-02-11 | Saline | MPCluster2-Seq14 | composite result

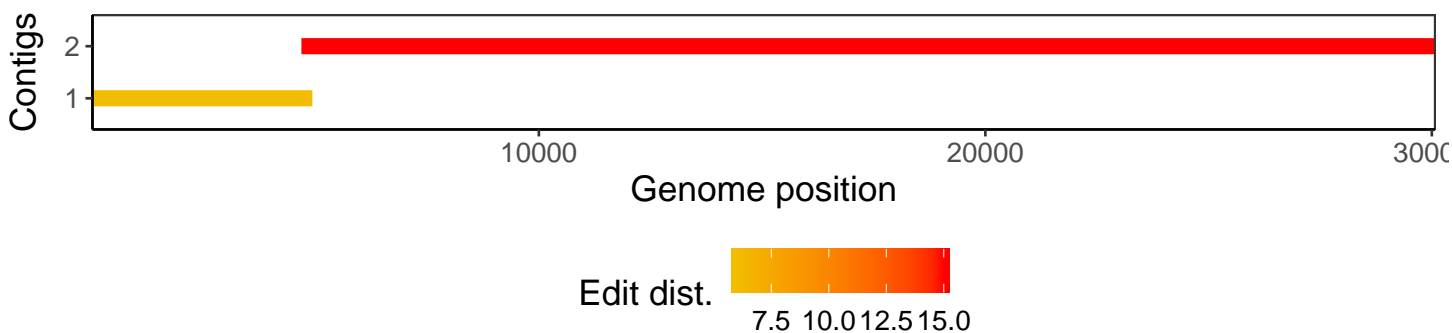
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



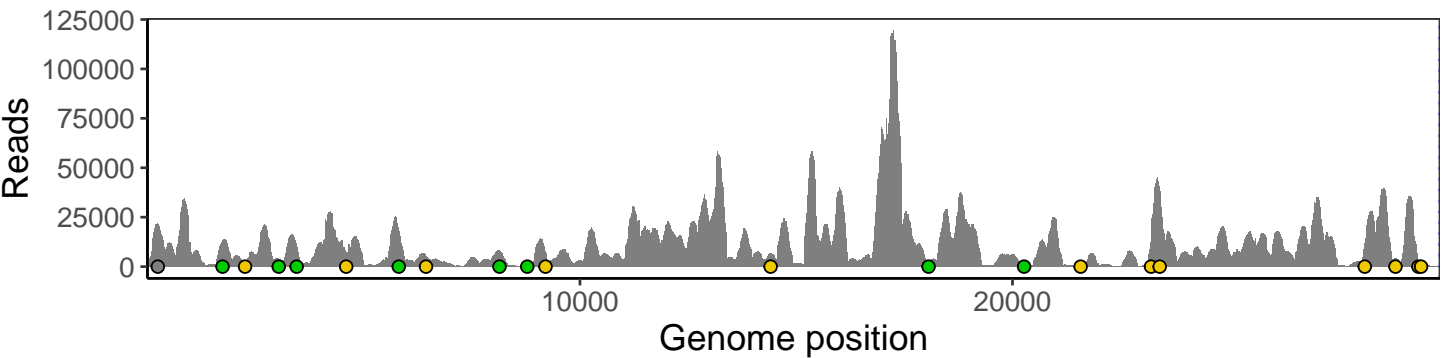
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



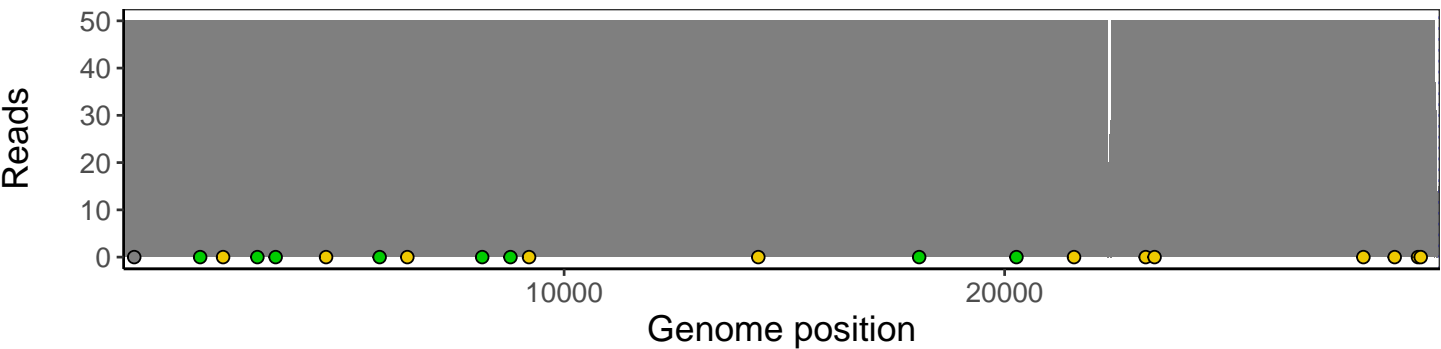
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



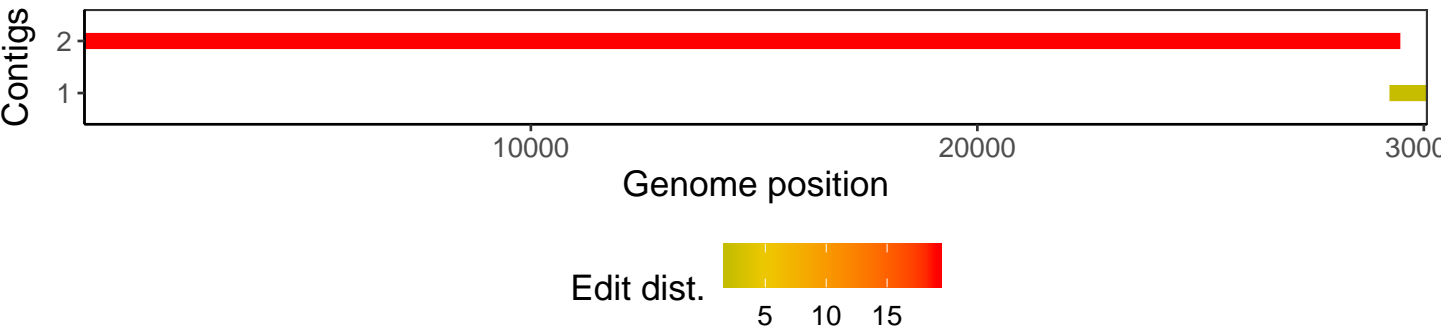
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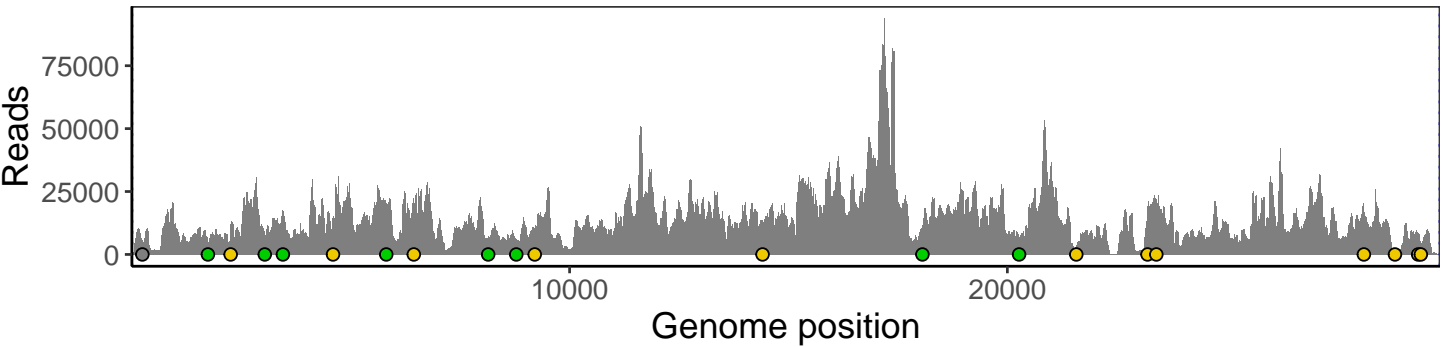
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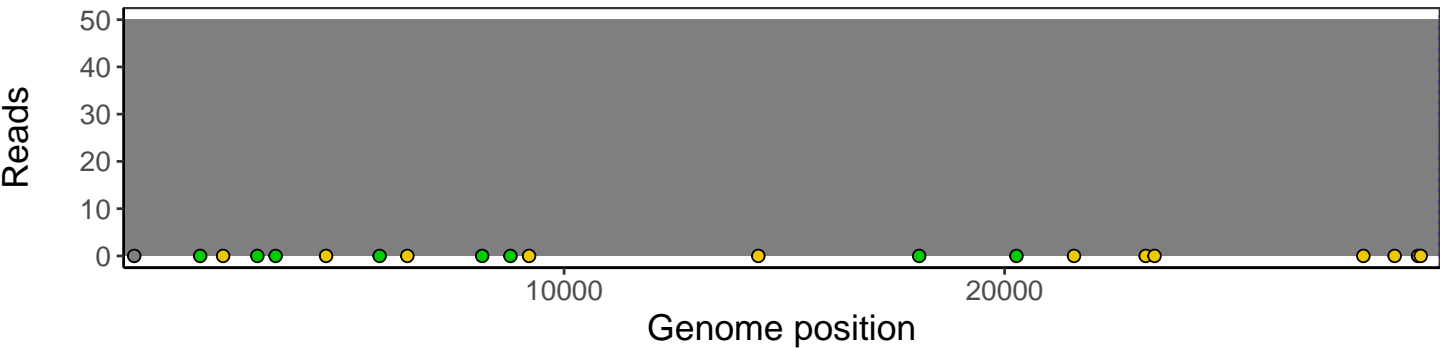
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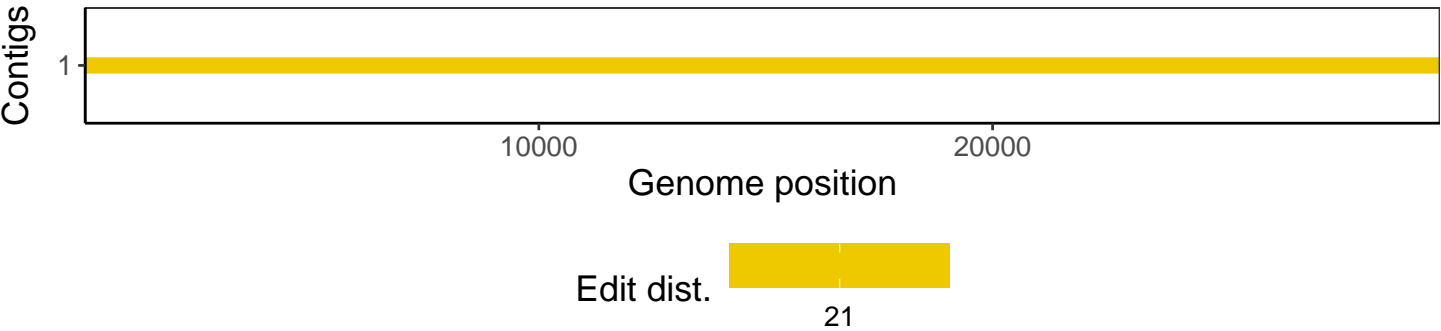
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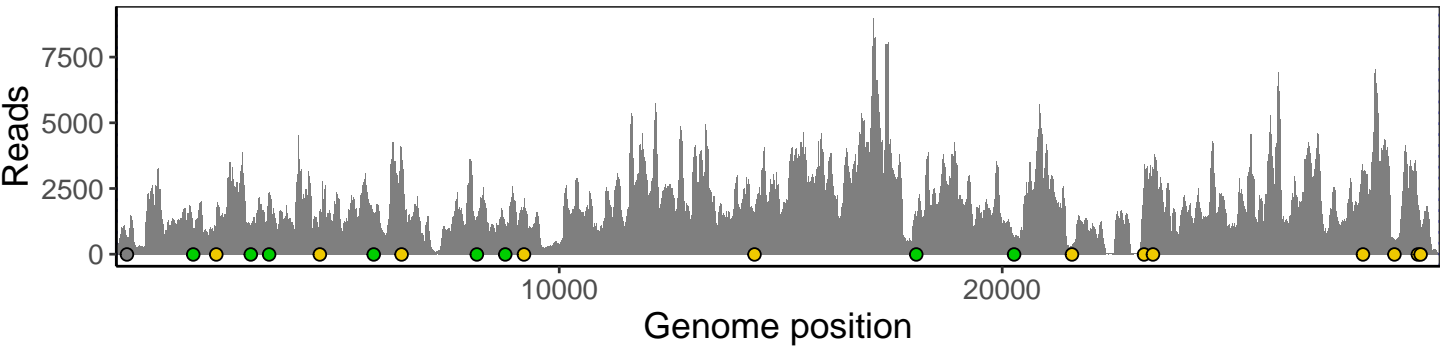
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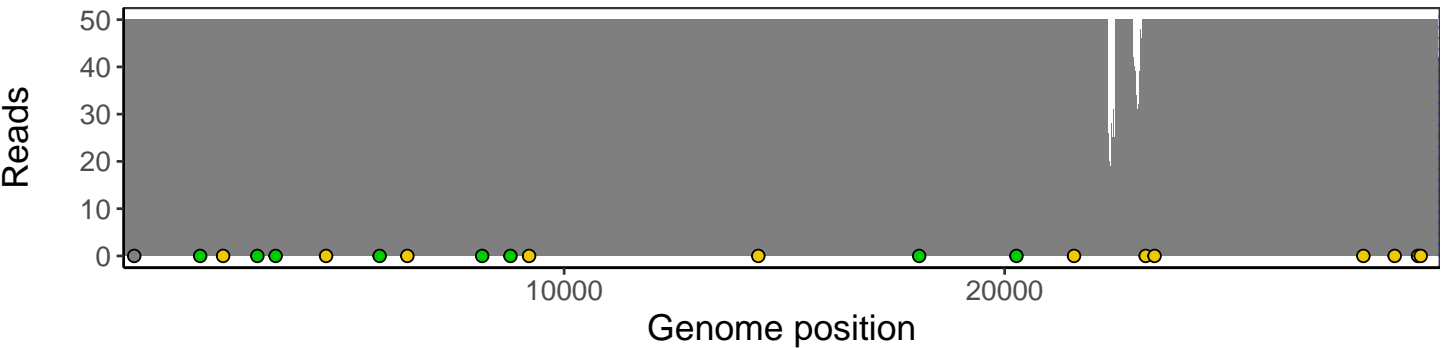
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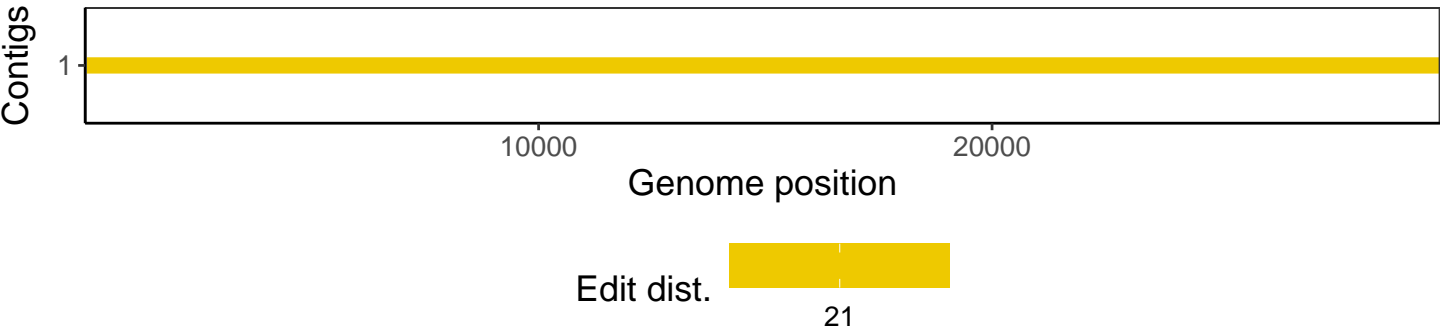
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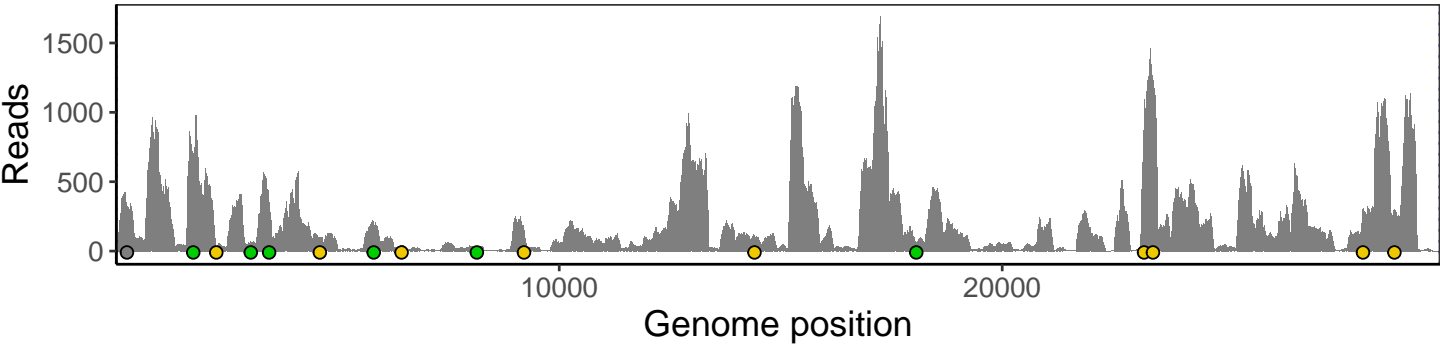
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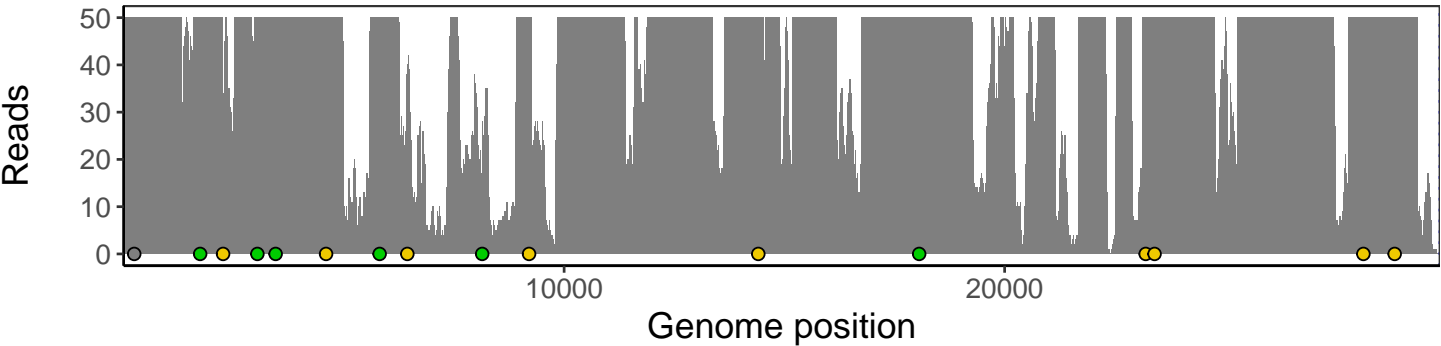
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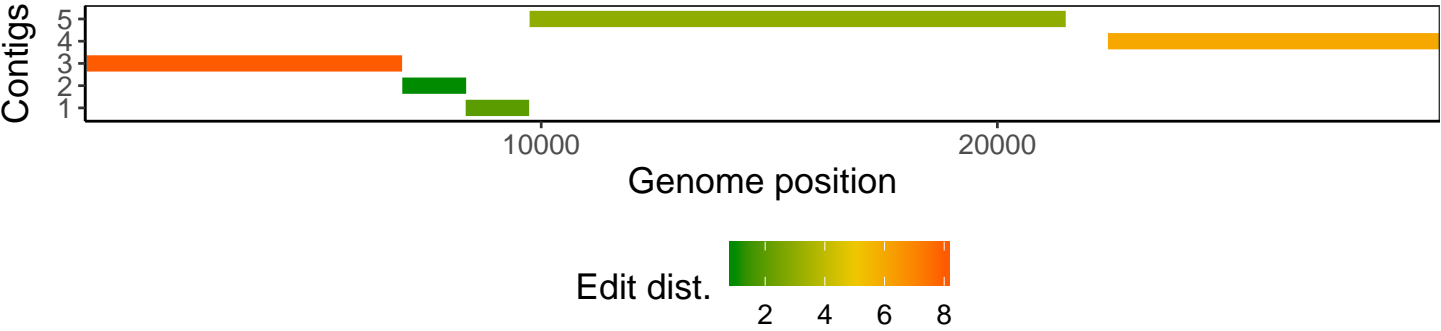
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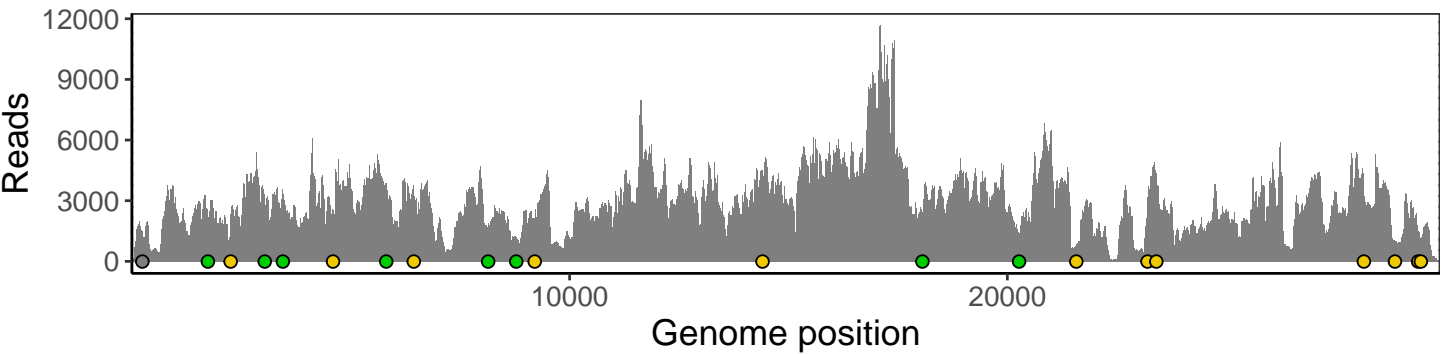


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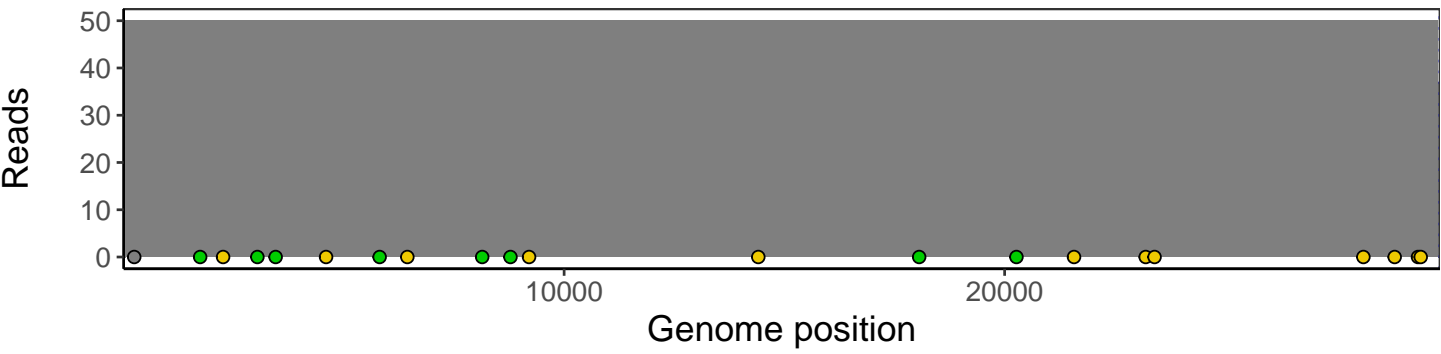




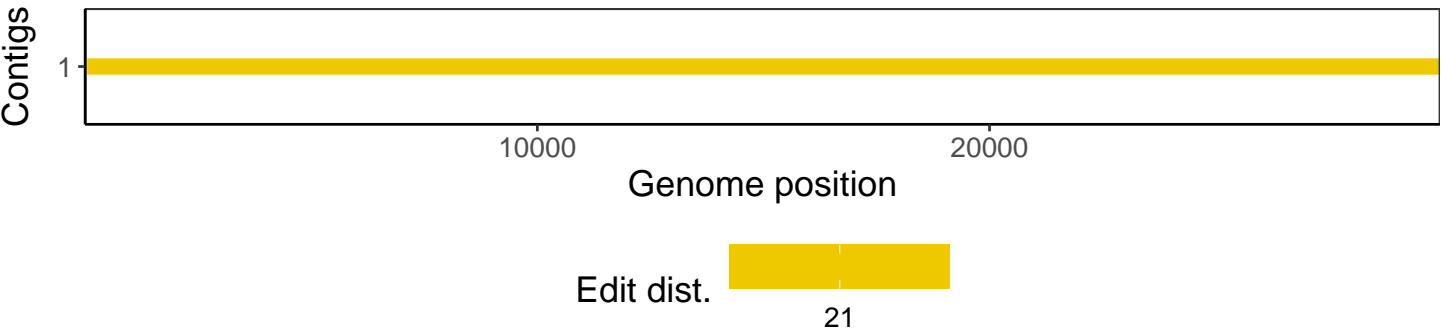
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## Software environment

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	2.3.8
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