

COVID-19 subject 234

2021-01-10

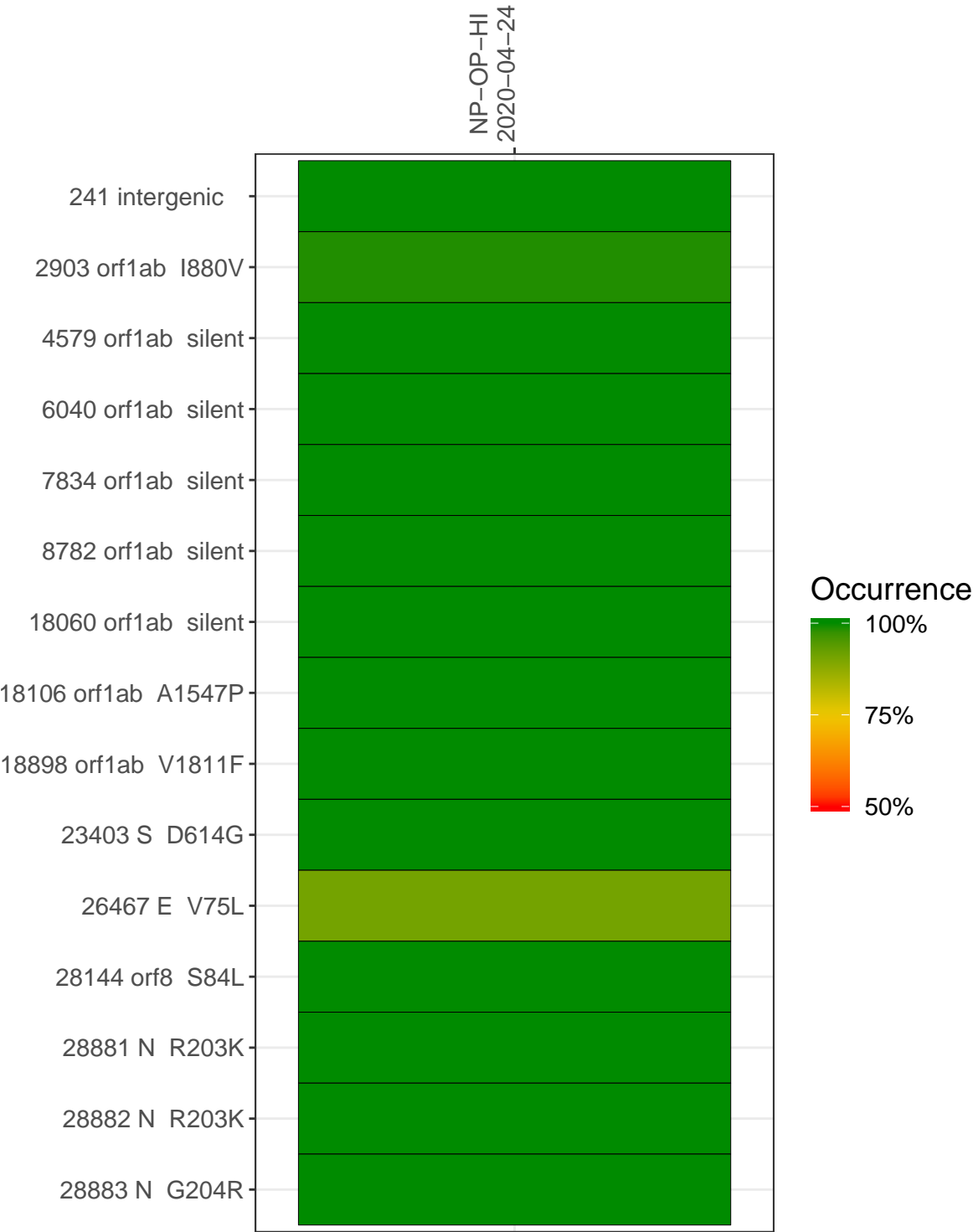
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. The code base for this analysis can be found ([here](#)).

Table 1. Sample summary.

| Experiment | Type | Input genomes | Sample type | Sample date | Largest contig (KD) | Reference read coverage | Reference read coverage (>= 5 reads) |
|------------|-------------------|---------------|-------------|-------------|---------------------|-------------------------|--------------------------------------|
| VSP0079 | composite | NA | NP-OP-HI | 2020-04-24 | 10.39 | 94.4% | 92.9% |
| VSP0079-1 | single experiment | 147.5 | NP-OP-HI | 2020-04-24 | 2.11 | 58.1% | 46.9% |
| VSP0079-2 | single experiment | 147.5 | NP-OP-HI | 2020-04-24 | 1.96 | 58.2% | 55.2% |
| VSP0079-3 | single experiment | 147.5 | NP-OP-HI | 2020-04-24 | 2.93 | 74.0% | 71.9% |
| VSP0079-4 | single experiment | 147.5 | NP-OP-HI | 2020-04-24 | 3.21 | 56.3% | 53.7% |

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 for 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-HI
2020-04-24

| | | | | |
|---------------------|-----------|-----------|-----------|-----------|
| 241 intergenic | 688 | | 10065 | |
| 2903 orf1ab I880V | 608 | 6 | 3 | 4 |
| 4579 orf1ab silent | 1 | | 2012 | |
| 6040 orf1ab silent | | 1538 | | |
| 7834 orf1ab silent | | | 898 | |
| 8782 orf1ab silent | 2 | 2365 | 6861 | 2160 |
| 18060 orf1ab silent | | | | 405 |
| 18106 orf1ab A1547P | | | | 507 |
| 18898 orf1ab V1811F | | 2589 | 4145 | 1147 |
| 23403 S D614G | 1 | 6680 | 2361 | 14417 |
| 26467 E V75L | 1 | | 10 | |
| 28144 orf8 S84L | 1 | 326 | 11407 | 7285 |
| 28881 N R203K | 211 | 206 | 386 | 1 |
| 28882 N R203K | 210 | 206 | 386 | 1 |
| 28883 N G204R | 210 | 207 | 387 | 1 |
| | VSP0079-1 | VSP0079-2 | VSP0079-3 | VSP0079-4 |

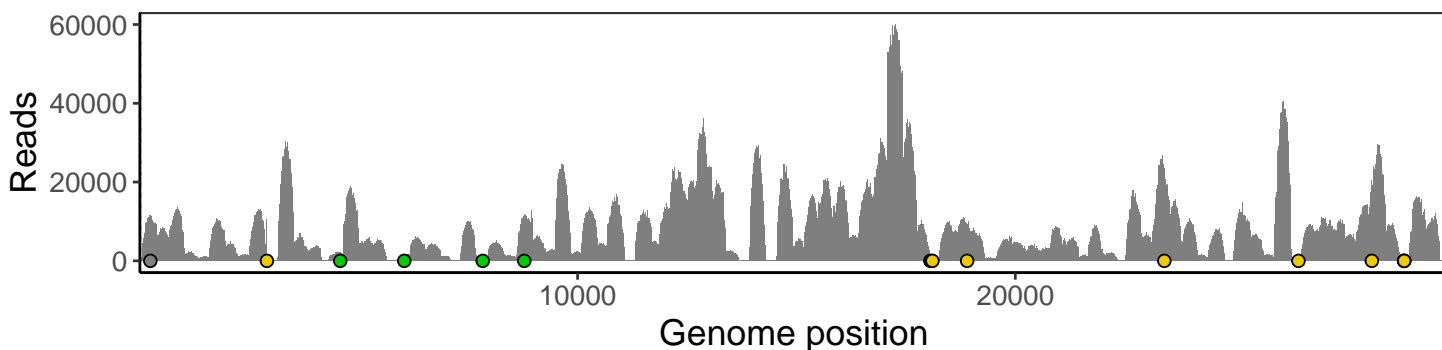
Base change

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

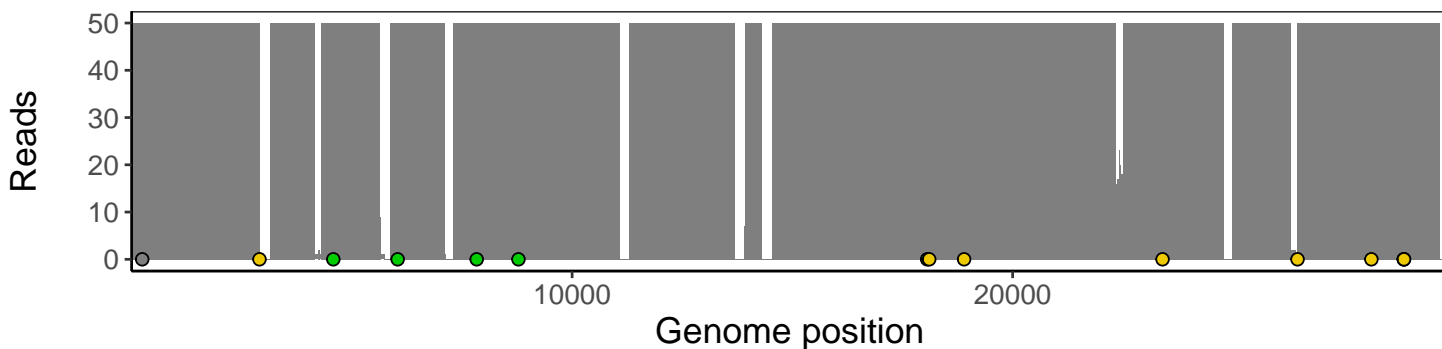
Analyses of individual experiments and composite results.

VSP0079 | 2020-04-24 | NP-OP-HI | 234noh-t | composite result

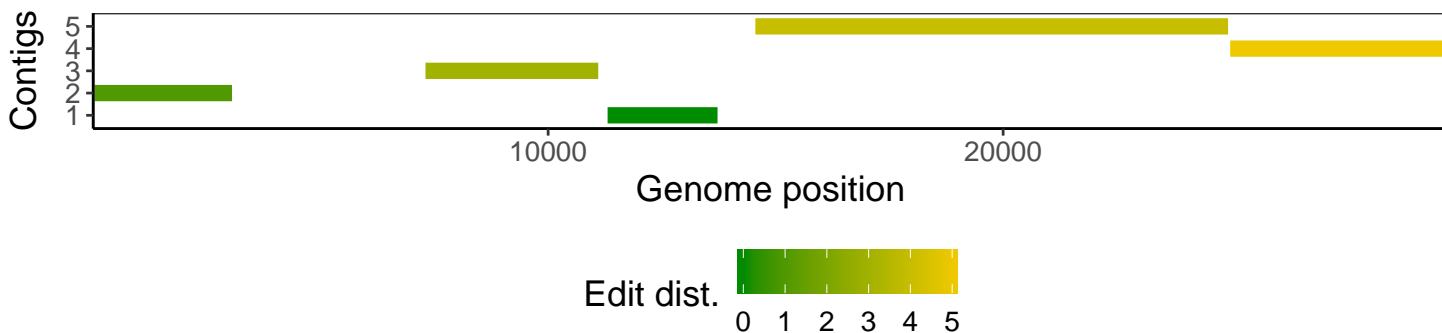
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



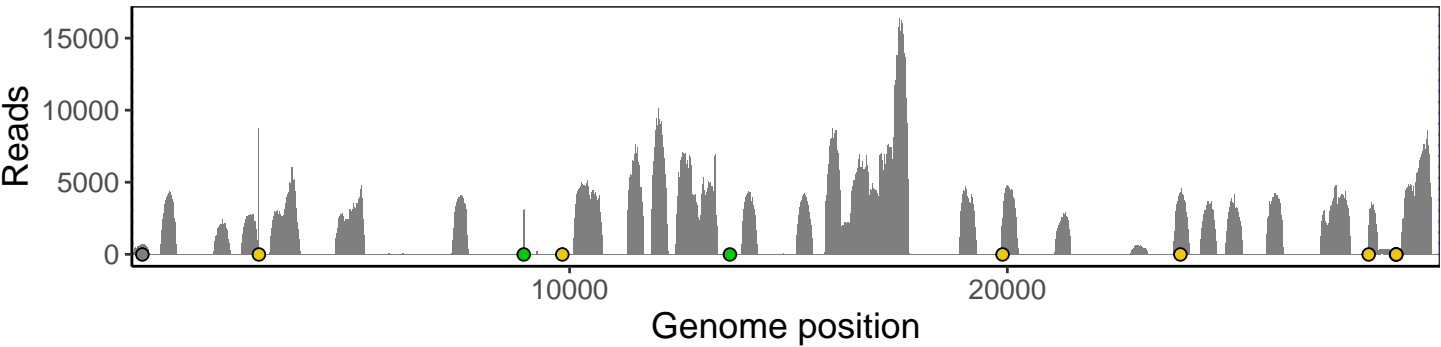
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



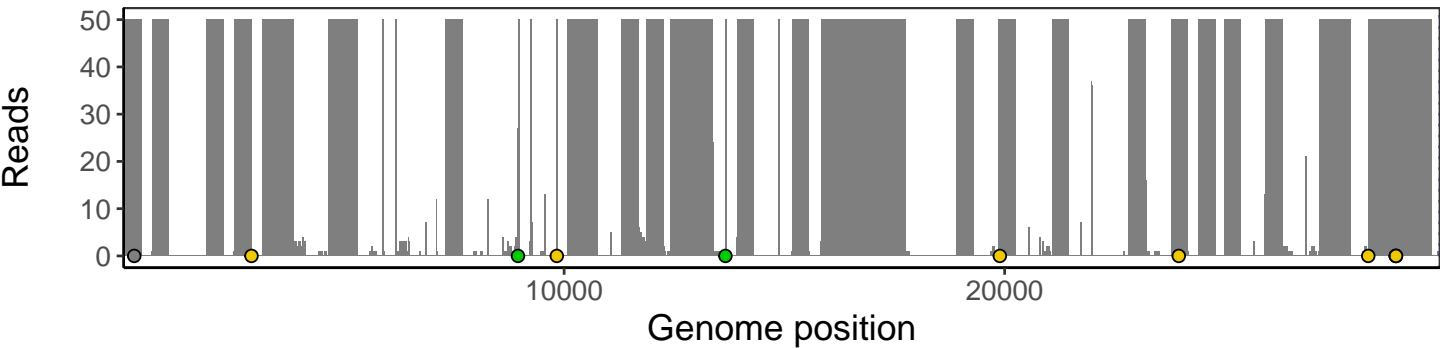
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



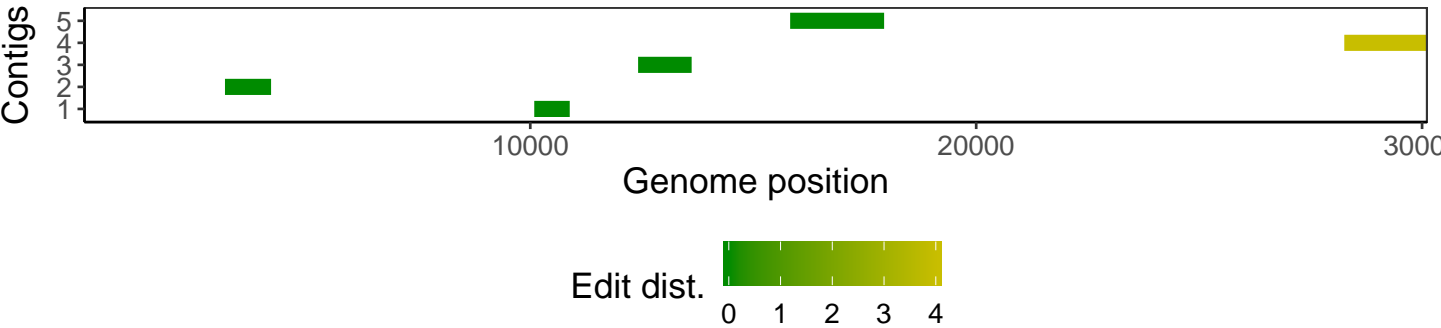
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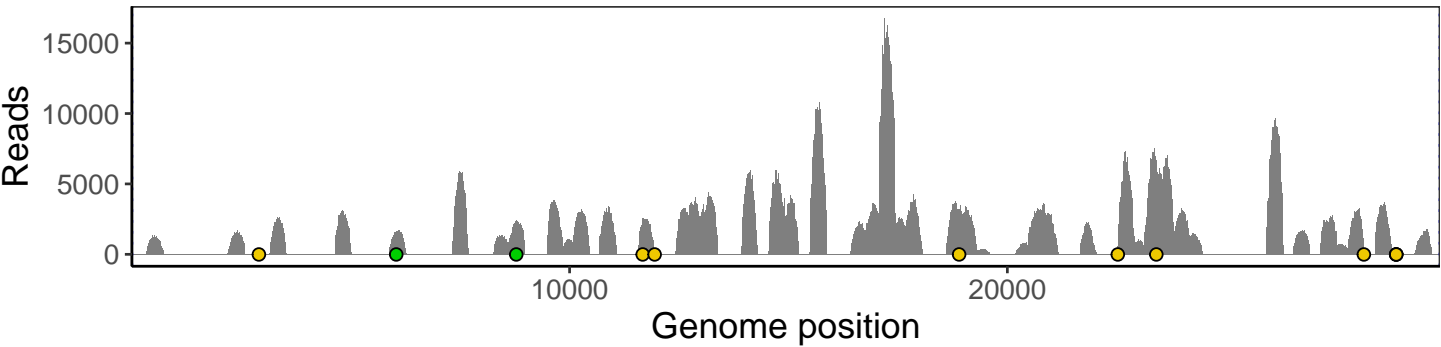
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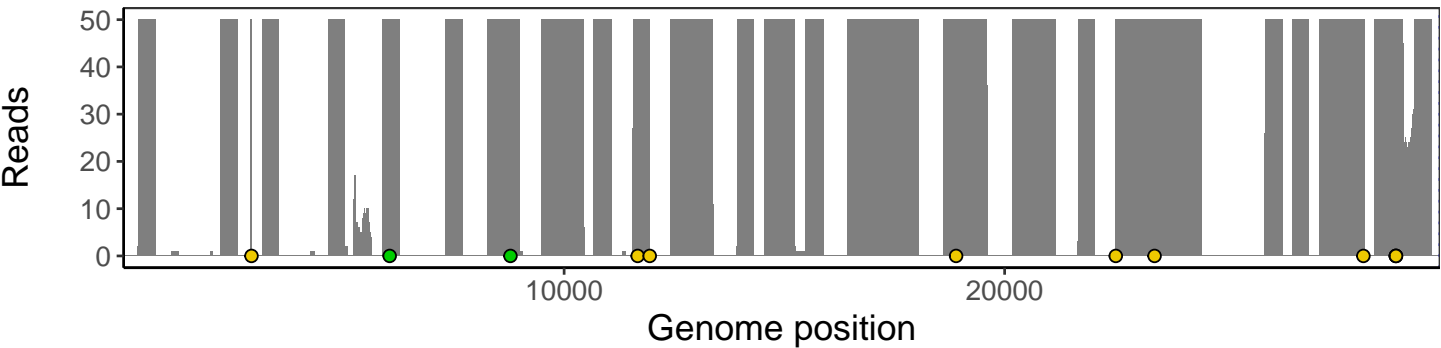
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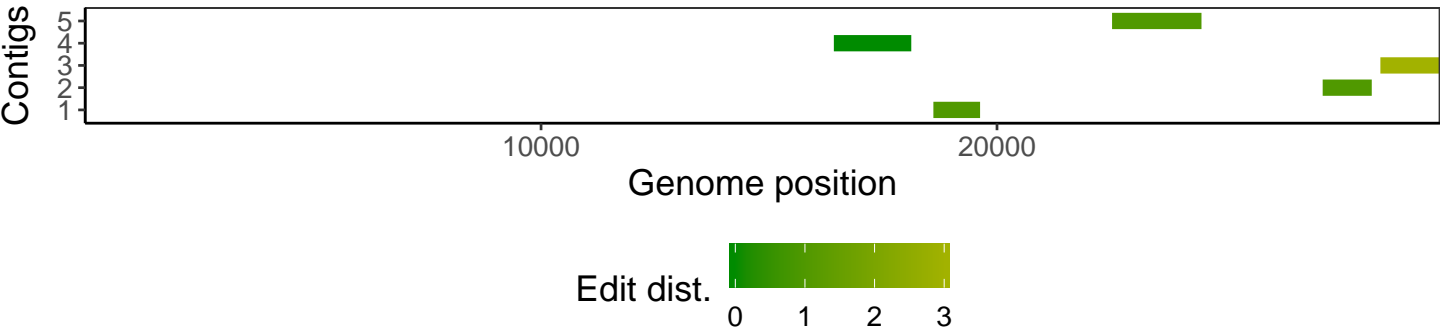
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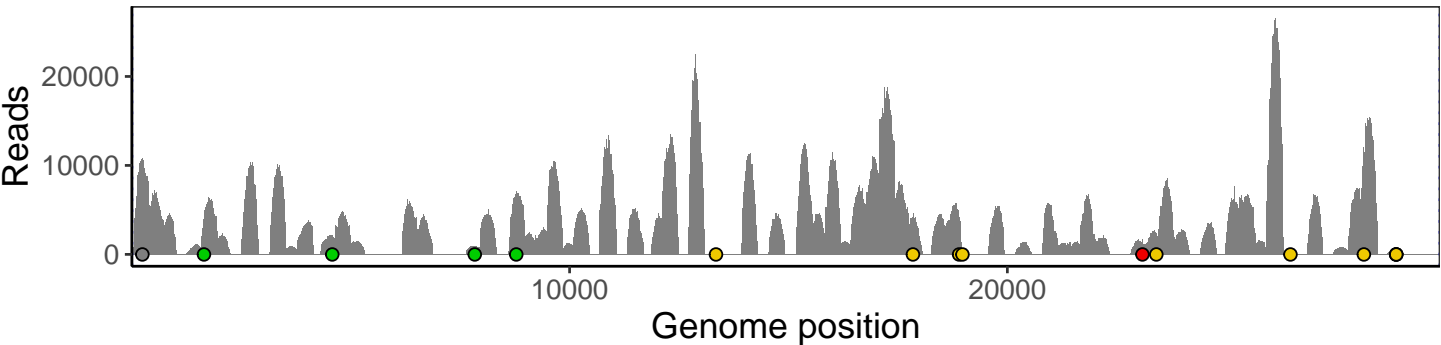
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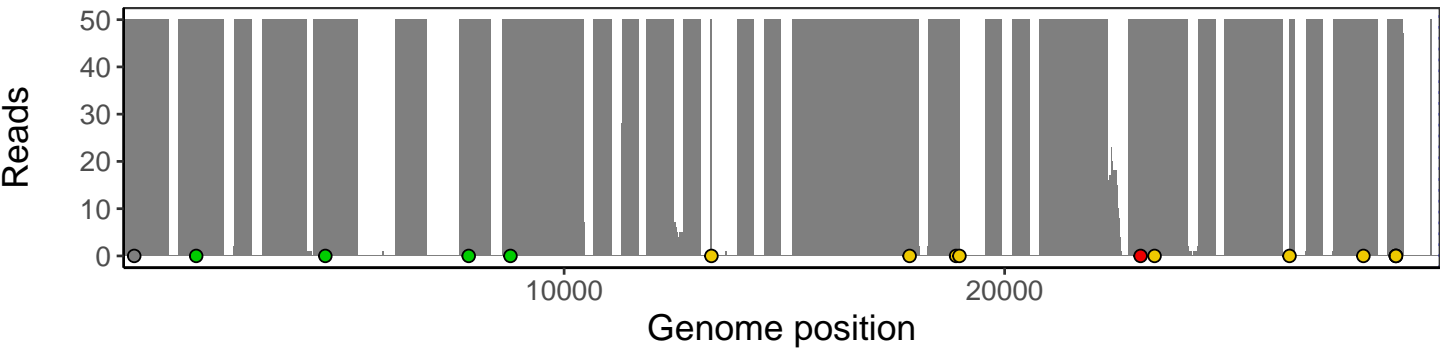
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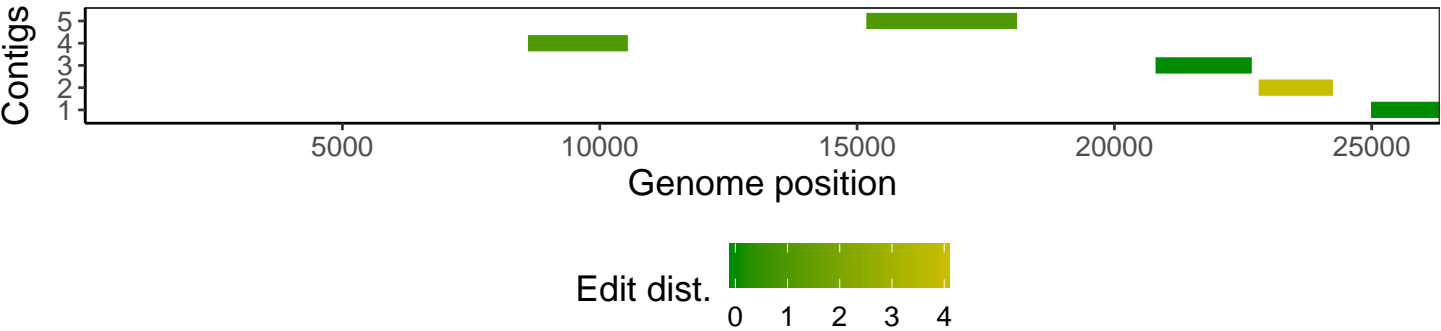
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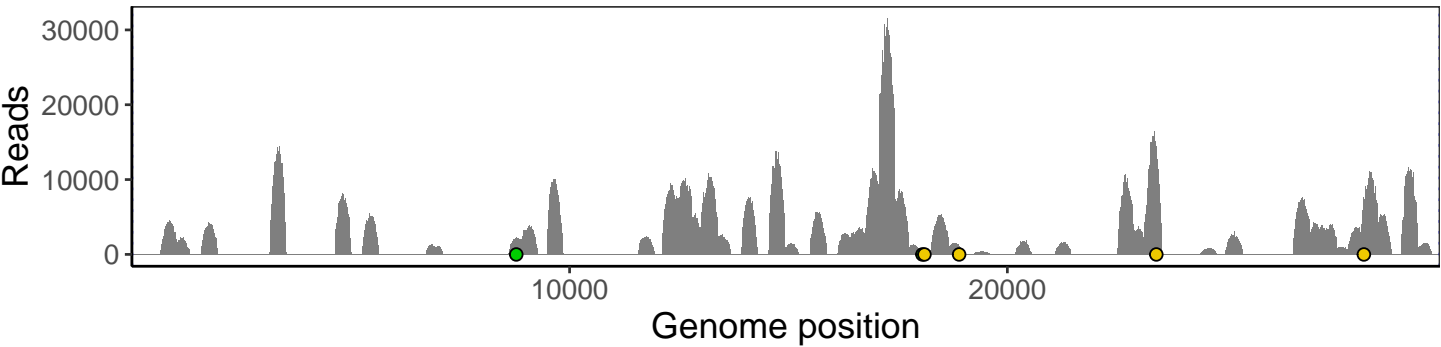
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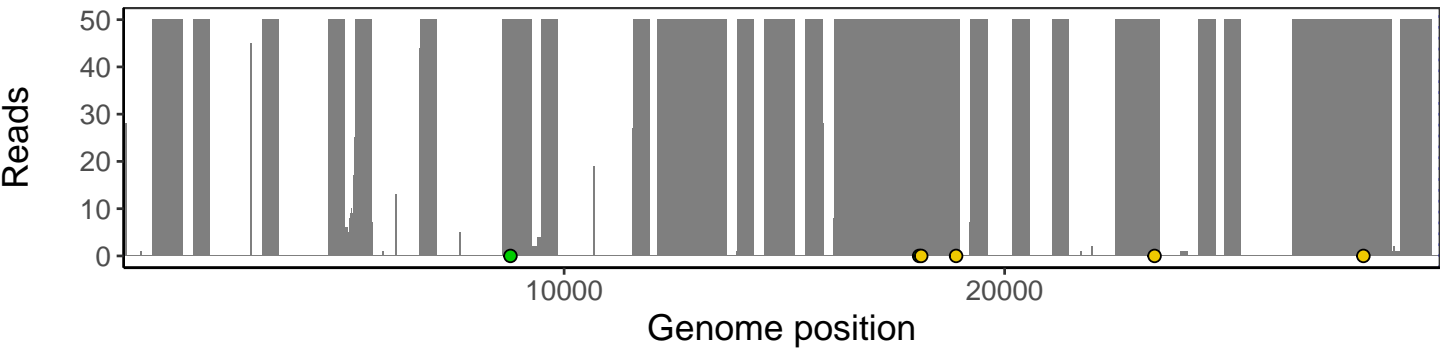
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