

# Report

|                             | AJ218.CanuH.cr |
|-----------------------------|----------------|
| # contigs (>= 0 bp)         | 2000           |
| # contigs (>= 1000 bp)      | 1984           |
| # contigs (>= 5000 bp)      | 1444           |
| # contigs (>= 10000 bp)     | 916            |
| # contigs (>= 25000 bp)     | 39             |
| # contigs (>= 50000 bp)     | 0              |
| Total length (>= 0 bp)      | 20102430       |
| Total length (>= 1000 bp)   | 20091414       |
| Total length (>= 5000 bp)   | 18587926       |
| Total length (>= 10000 bp)  | 14650618       |
| Total length (>= 25000 bp)  | 1118002        |
| Total length (>= 50000 bp)  | 0              |
| # contigs                   | 1997           |
| Largest contig              | 33906          |
| Total length                | 20101596       |
| Reference length            | 5465981        |
| GC (%)                      | 57.22          |
| Reference GC (%)            | 57.29          |
| N50                         | 14464          |
| NG50                        | 21252          |
| N75                         | 9454           |
| NG75                        | 19392          |
| L50                         | 533            |
| LG50                        | 110            |
| L75                         | 960            |
| LG75                        | 178            |
| # misassemblies             | 7              |
| # misassembled contigs      | 7              |
| Misassembled contigs length | 120658         |
| # local misassemblies       | 28             |
| # unaligned mis. contigs    | 1              |
| # unaligned contigs         | 111 + 60 part  |
| Unaligned length            | 840325         |
| Genome fraction (%)         | 94.825         |
| Duplication ratio           | 3.716          |
| # N's per 100 kbp           | 0.00           |
| # mismatches per 100 kbp    | 36.12          |
| # indels per 100 kbp        | 218.56         |
| Largest alignment           | 33903          |
| Total aligned length        | 19237150       |
| NA50                        | 13970          |
| NGA50                       | 21170          |
| NA75                        | 8727           |
| NGA75                       | 19329          |
| LA50                        | 539            |
| LGA50                       | 111            |
| LA75                        | 991            |
| LGA75                       | 179            |

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

## Misassemblies report

|                             | AJ218.CanuH.cr |
|-----------------------------|----------------|
| # misassemblies             | 7              |
| # relocations               | 6              |
| # translocations            | 0              |
| # inversions                | 1              |
| # misassembled contigs      | 7              |
| Misassembled contigs length | 120658         |
| # local misassemblies       | 28             |
| # unaligned mis. contigs    | 1              |
| # mismatches                | 1872           |
| # indels                    | 11328          |
| # indels ( $\leq 5$ bp)     | 11249          |
| # indels ( $> 5$ bp)        | 79             |
| Indels length               | 14726          |

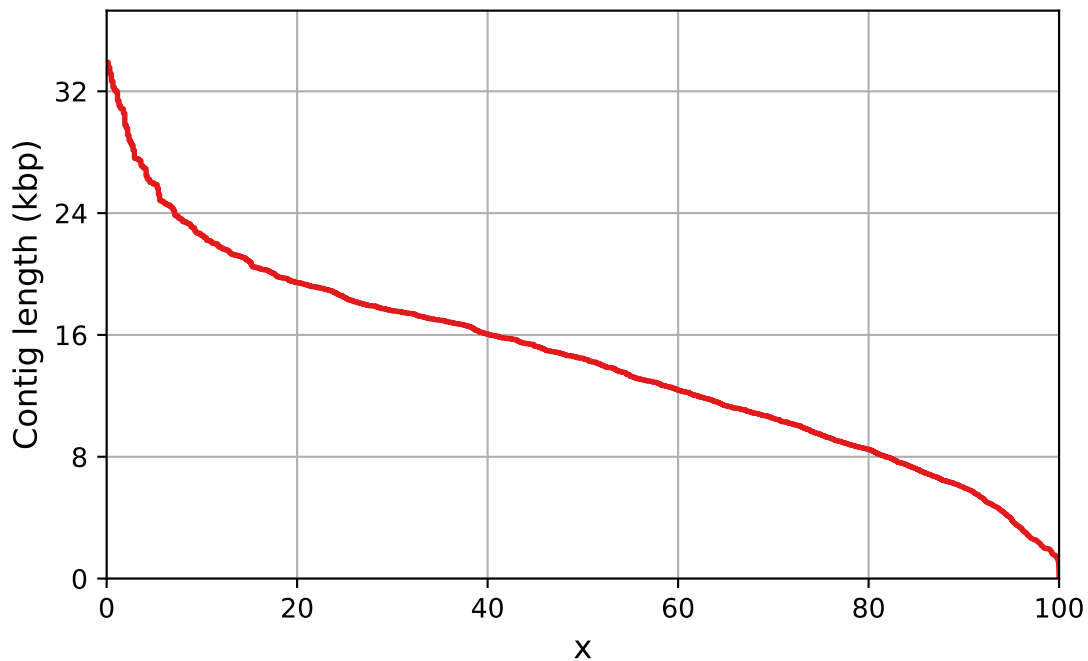
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

|                               | AJ218.CanuH.cr |
|-------------------------------|----------------|
| # fully unaligned contigs     | 111            |
| Fully unaligned length        | 620906         |
| # partially unaligned contigs | 60             |
| Partially unaligned length    | 219419         |
| # N's                         | 0              |

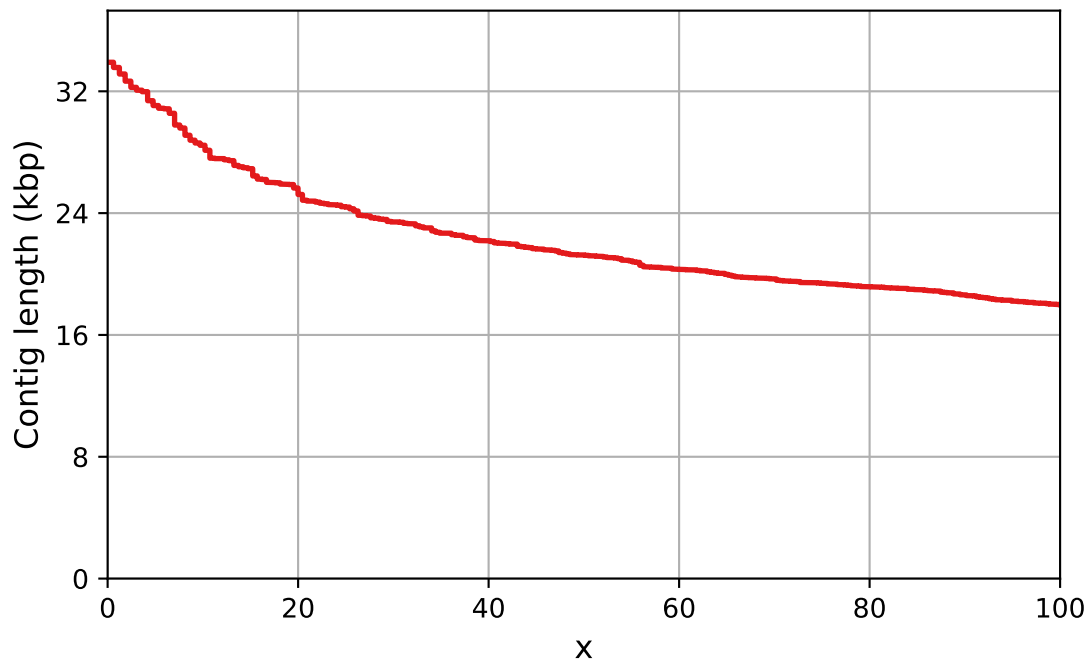
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



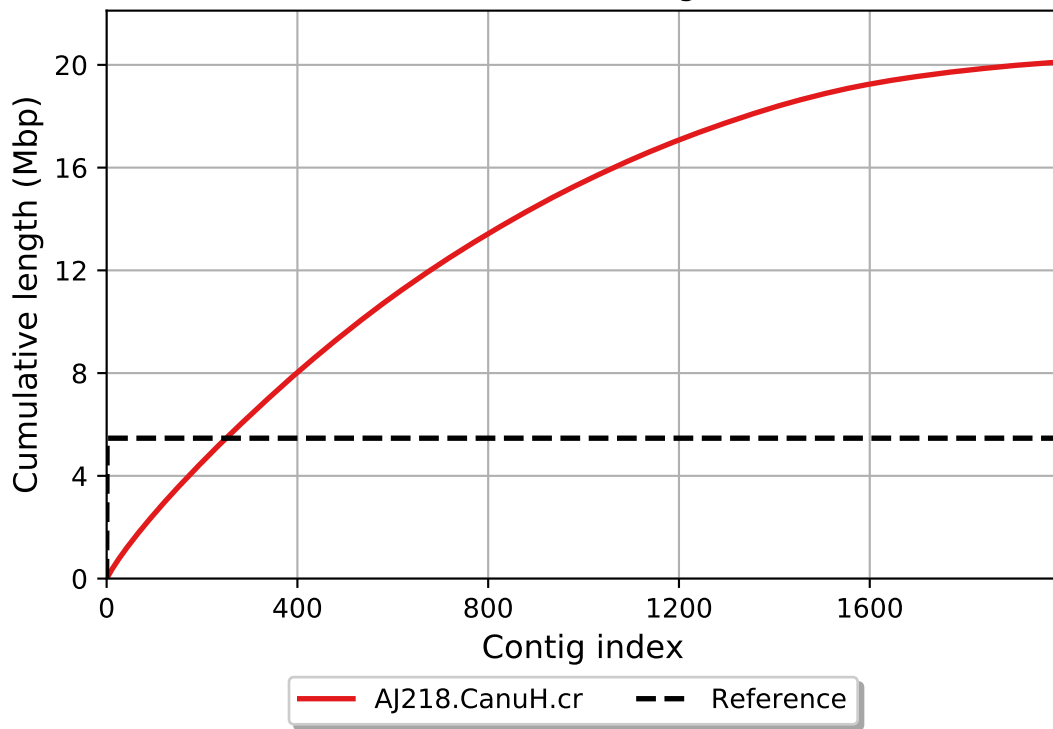
Aj218.CanuH.cr

NGx

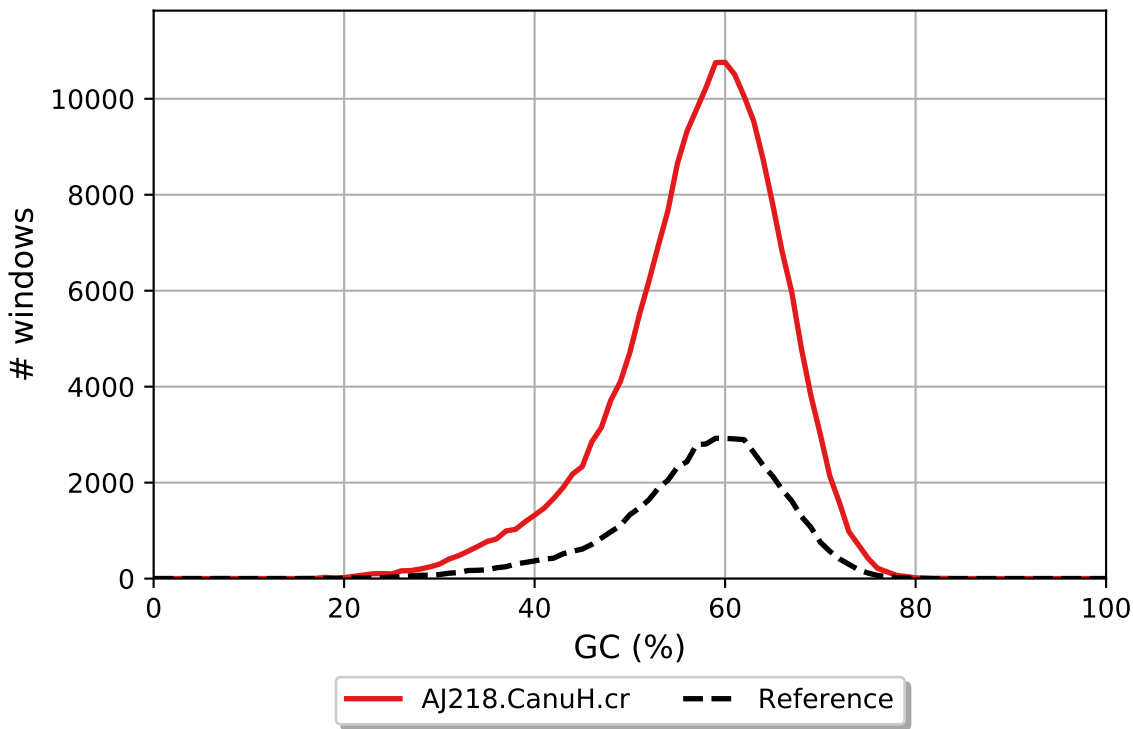


Aj218.CanuH.cr

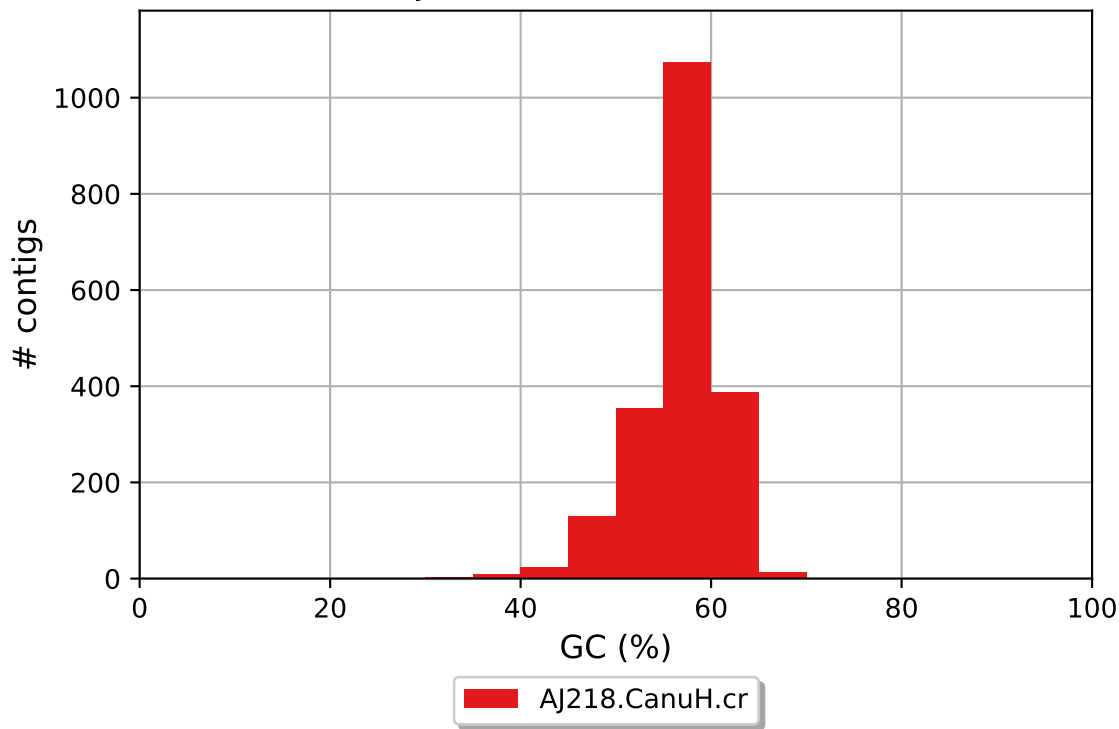
Cumulative length



# GC content

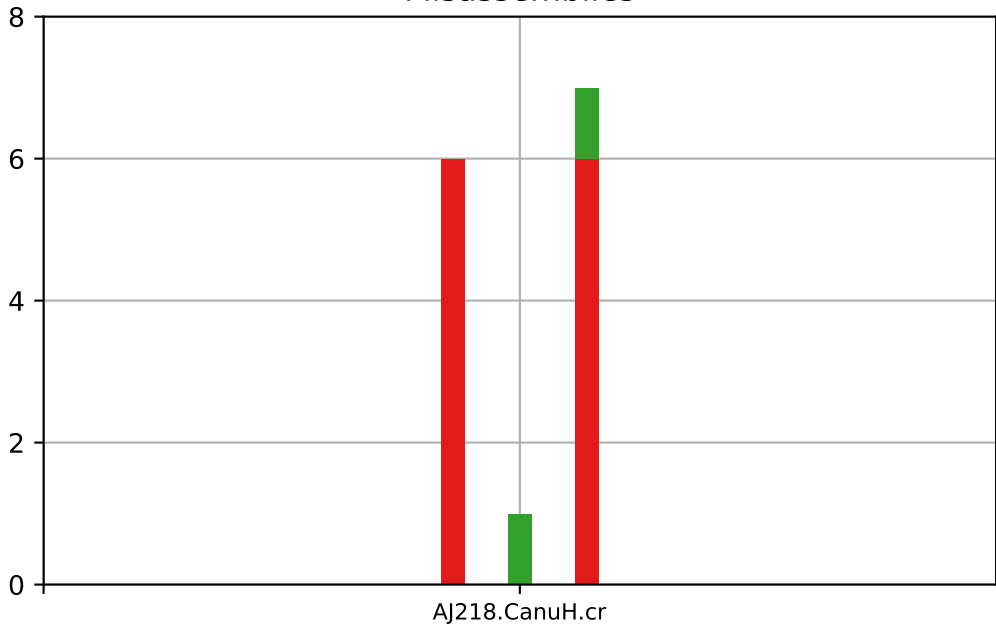


AJ218.CanuH.cr GC content





## Misassemblies

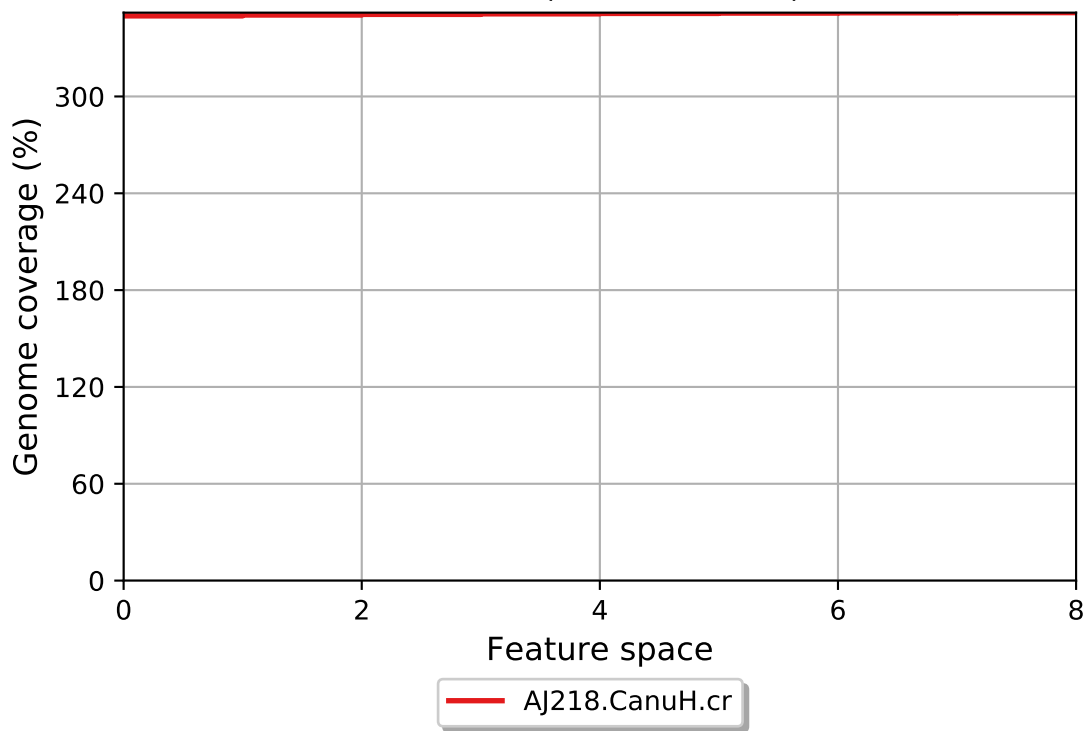


# relocations

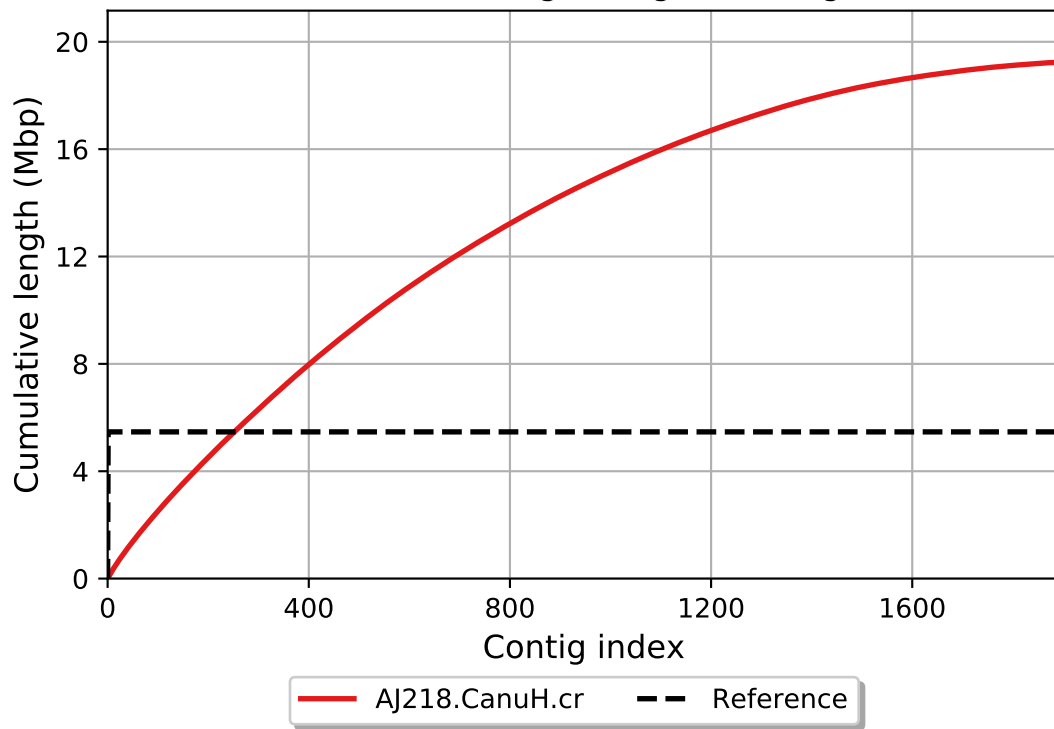


# inversions

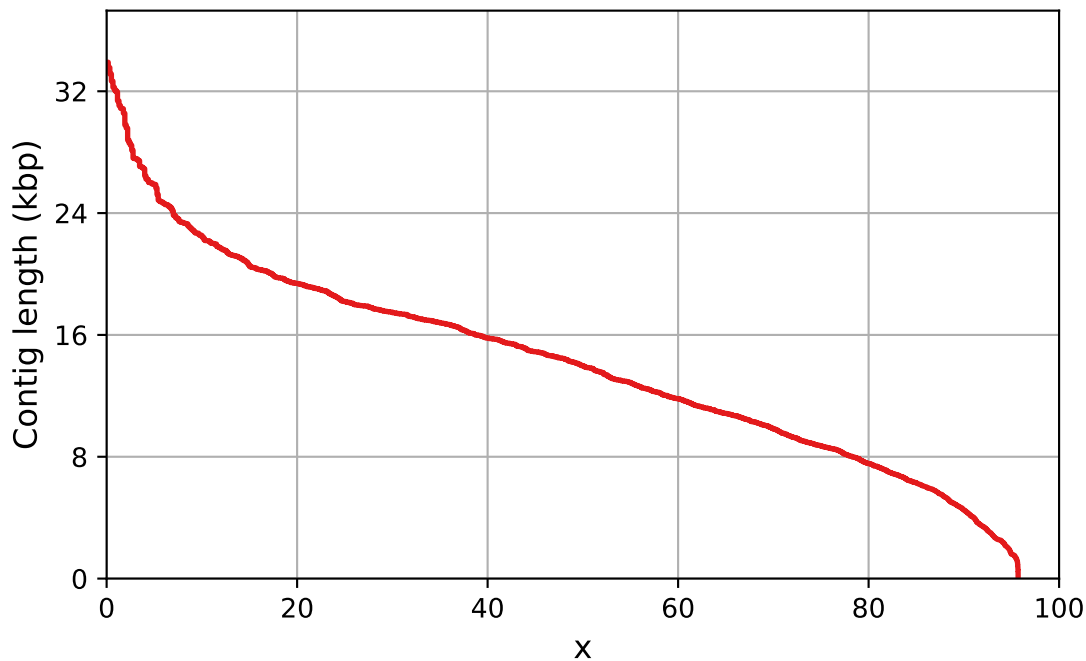
FRCurve (misassemblies)



Cumulative length (aligned contigs)

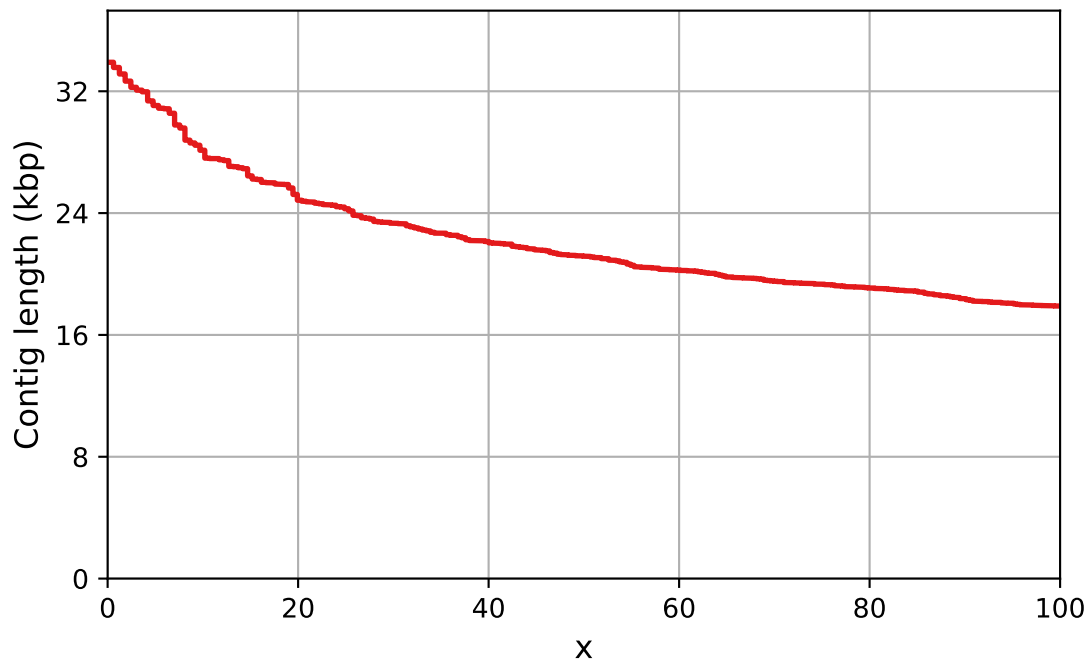


NAx



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# NGAx



— Aj218.CanuH.cr