

Report

|                             | pilon      |
|-----------------------------|------------|
| # contigs (>= 0 bp)         | 11         |
| # contigs (>= 1000 bp)      | 11         |
| # contigs (>= 5000 bp)      | 10         |
| # contigs (>= 10000 bp)     | 10         |
| # contigs (>= 25000 bp)     | 7          |
| # contigs (>= 50000 bp)     | 4          |
| Total length (>= 0 bp)      | 3190116    |
| Total length (>= 1000 bp)   | 3190116    |
| Total length (>= 5000 bp)   | 3186441    |
| Total length (>= 10000 bp)  | 3186441    |
| Total length (>= 25000 bp)  | 3142519    |
| Total length (>= 50000 bp)  | 3044718    |
| # contigs                   | 11         |
| Largest contig              | 1414516    |
| Total length                | 3190116    |
| Reference length            | 2919198    |
| GC (%)                      | 37.71      |
| Reference GC (%)            | 37.88      |
| N50                         | 1362697    |
| NG50                        | 1362697    |
| N75                         | 1362697    |
| NG75                        | 1362697    |
| L50                         | 2          |
| LG50                        | 2          |
| L75                         | 2          |
| LG75                        | 2          |
| # misassemblies             | 190        |
| # misassembled contigs      | 2          |
| Misassembled contigs length | 2777213    |
| # local misassemblies       | 37         |
| # scaffold gap ext. mis.    | 0          |
| # scaffold gap loc. mis.    | 0          |
| # unaligned mis. contigs    | 6          |
| # unaligned contigs         | 2 + 9 part |
| Unaligned length            | 591173     |
| Genome fraction (%)         | 84.952     |
| Duplication ratio           | 1.048      |
| # N's per 100 kbp           | 0.00       |
| # mismatches per 100 kbp    | 398.60     |
| # indels per 100 kbp        | 15.04      |
| Largest alignment           | 137660     |
| Total aligned length        | 2597046    |
| NA50                        | 24276      |
| NGA50                       | 29114      |
| NA75                        | 2923       |
| NGA75                       | 10307      |
| LA50                        | 32         |
| LGA50                       | 27         |
| LA75                        | 97         |
| LGA75                       | 66         |

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

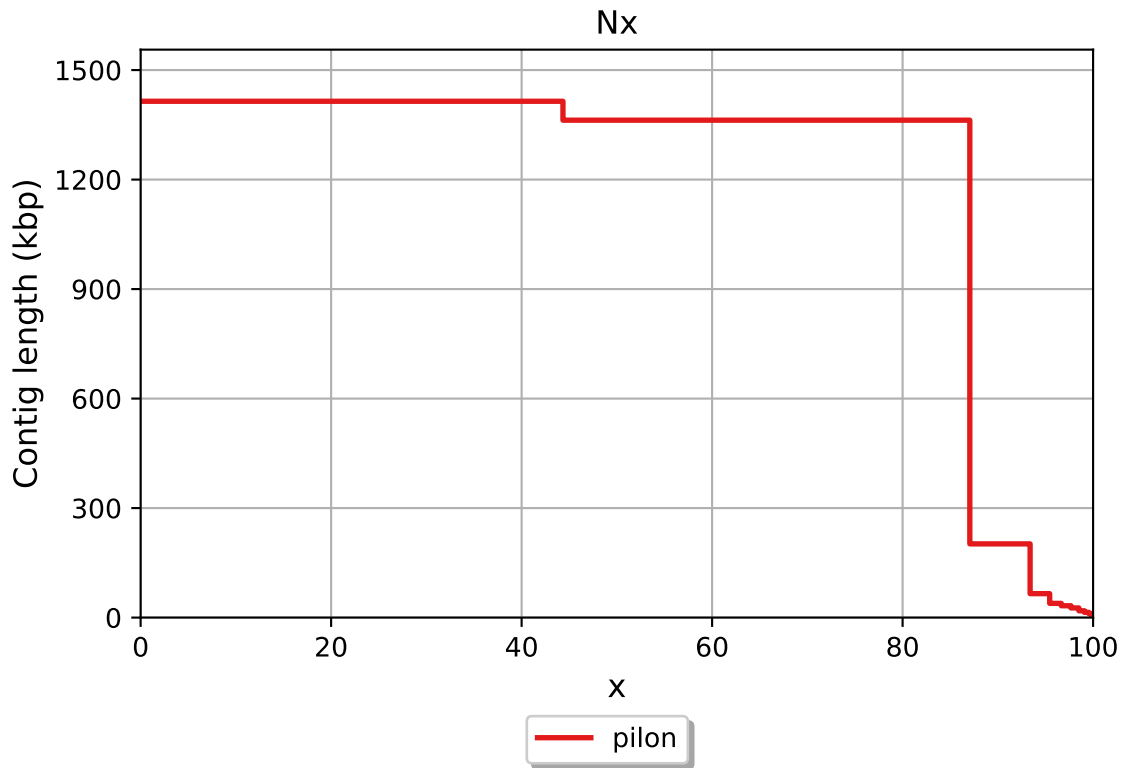
|                             | pilon   |
|-----------------------------|---------|
| # misassemblies             | 190     |
| # contig misassemblies      | 190     |
| # c. relocations            | 173     |
| # c. translocations         | 14      |
| # c. inversions             | 3       |
| # scaffold misassemblies    | 0       |
| # s. relocations            | 0       |
| # s. translocations         | 0       |
| # s. inversions             | 0       |
| # misassembled contigs      | 2       |
| Misassembled contigs length | 2777213 |
| # local misassemblies       | 37      |
| # scaffold gap ext. mis.    | 0       |
| # scaffold gap loc. mis.    | 0       |
| # unaligned mis. contigs    | 6       |
| # mismatches                | 9885    |
| # indels                    | 373     |
| # indels (<= 5 bp)          | 336     |
| # indels (> 5 bp)           | 37      |
| Indels length               | 1463    |

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).

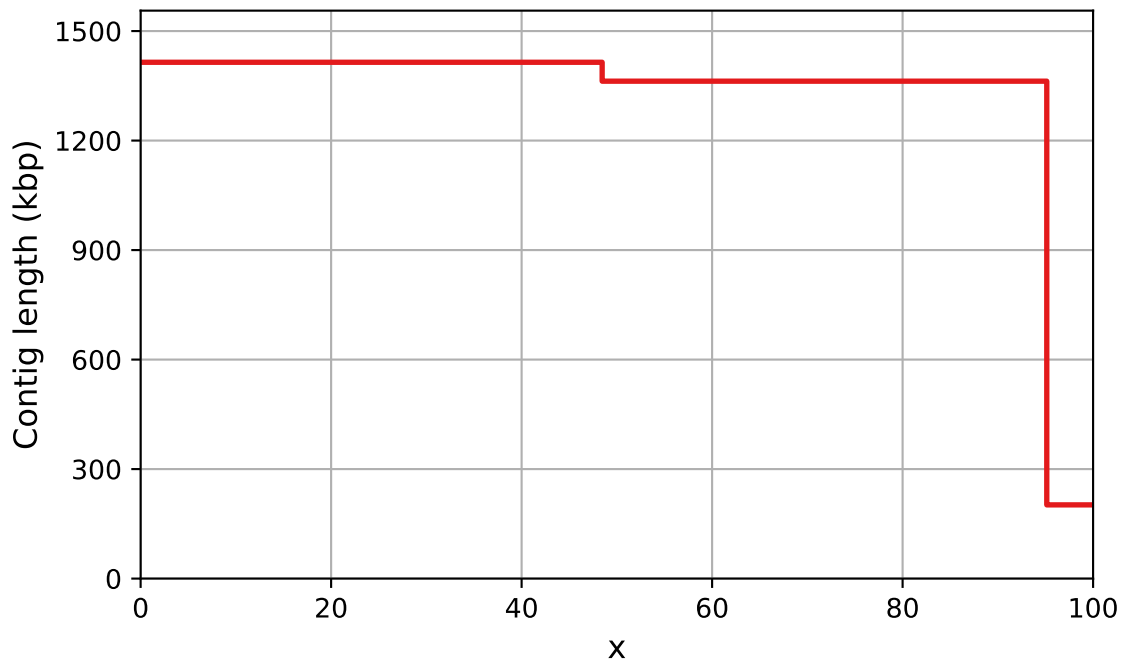
## Unaligned report

|                               | pilon  |
|-------------------------------|--------|
| # fully unaligned contigs     | 2      |
| Fully unaligned length        | 22311  |
| # partially unaligned contigs | 9      |
| Partially unaligned length    | 568862 |
| # 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).

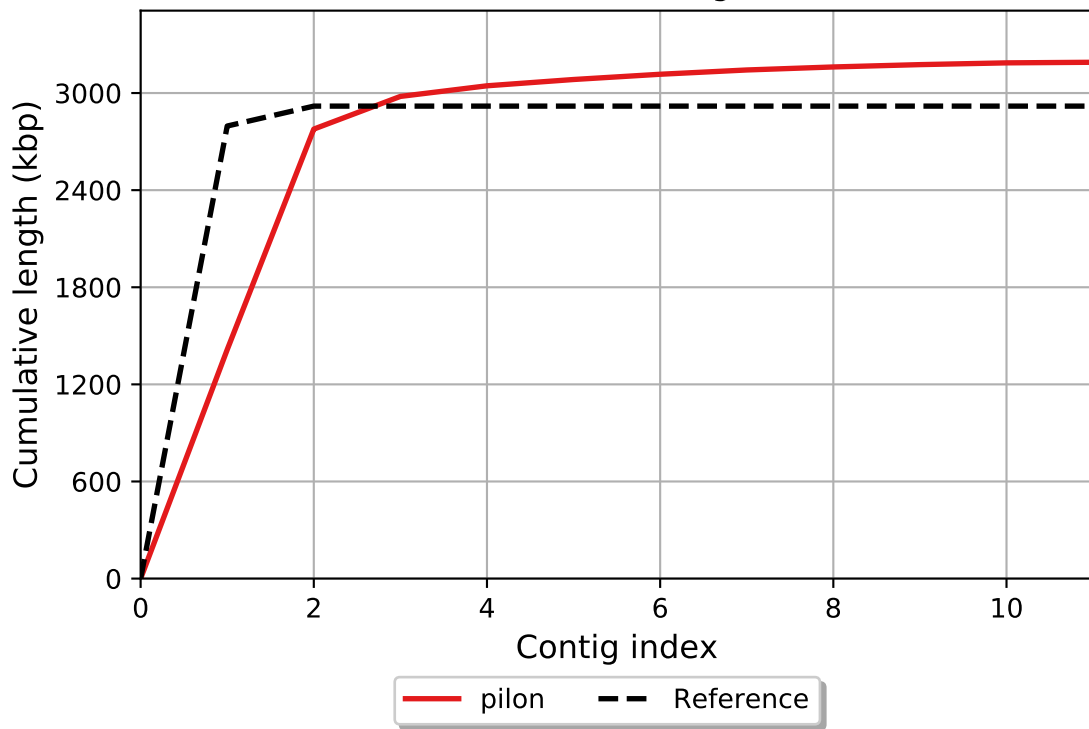


NGx

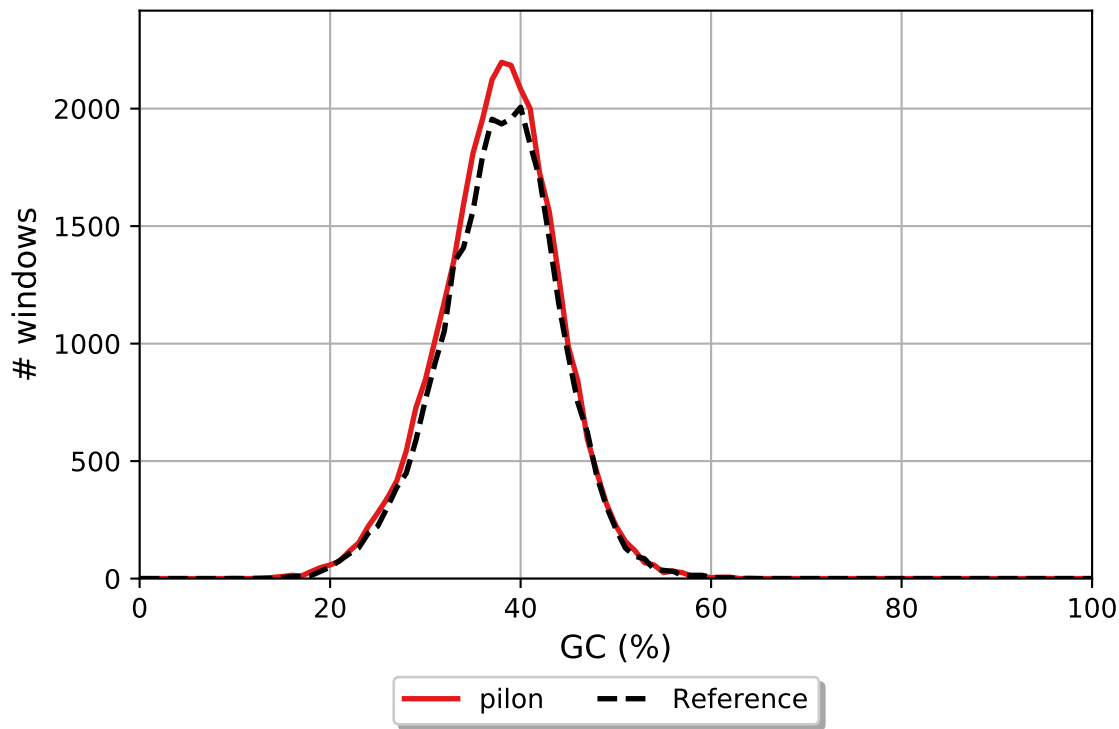


— pilon

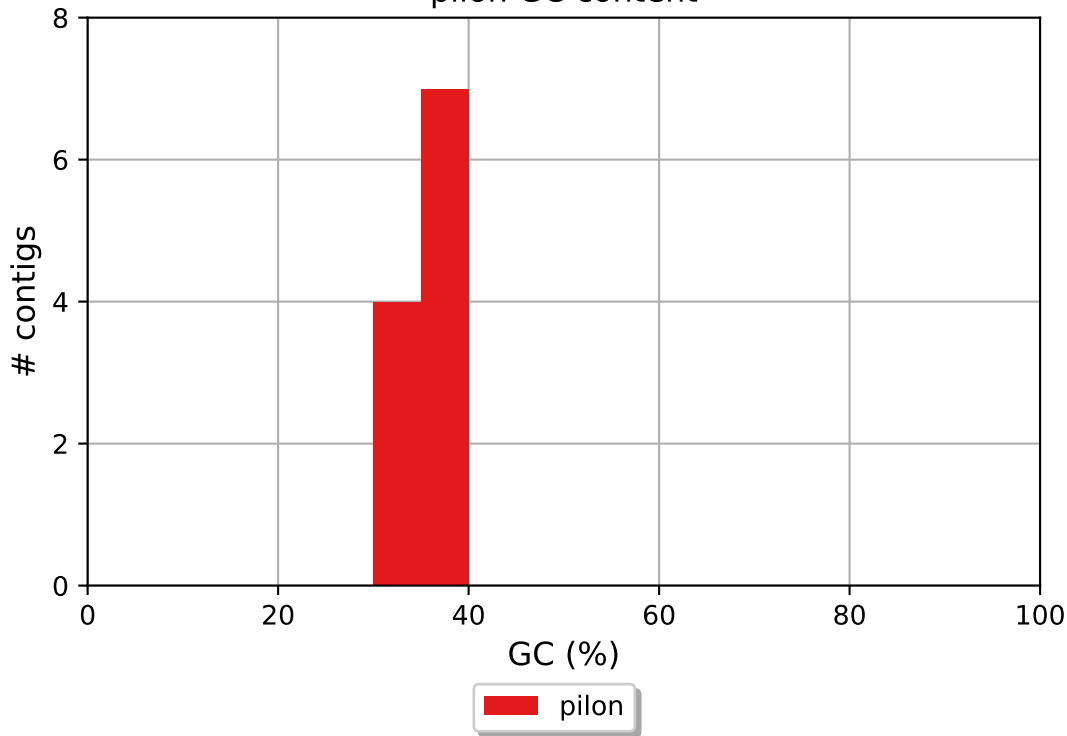
Cumulative length



## GC content

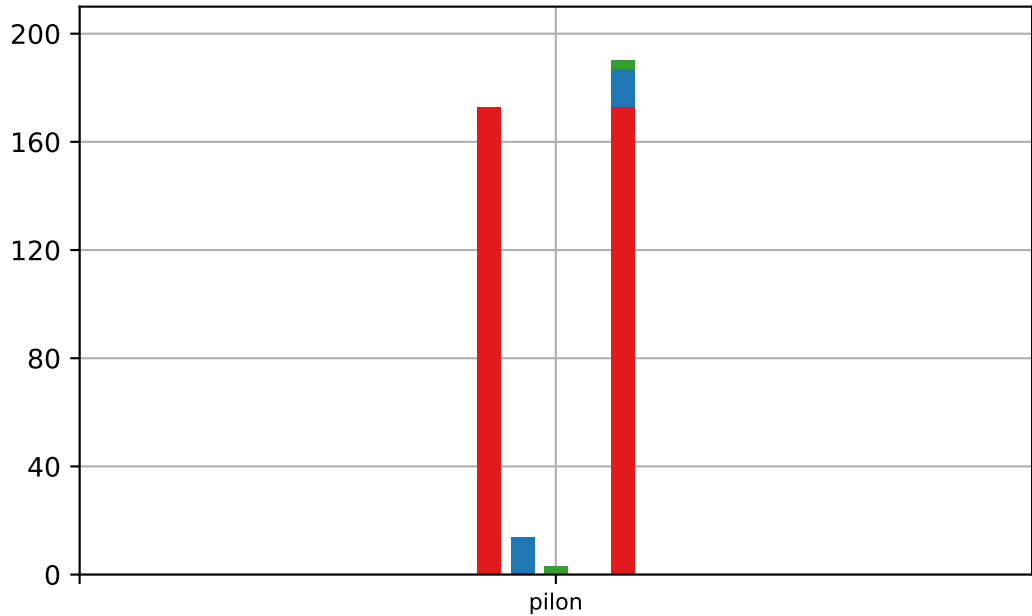


pilon GC content





## Misassemblies



# relocations

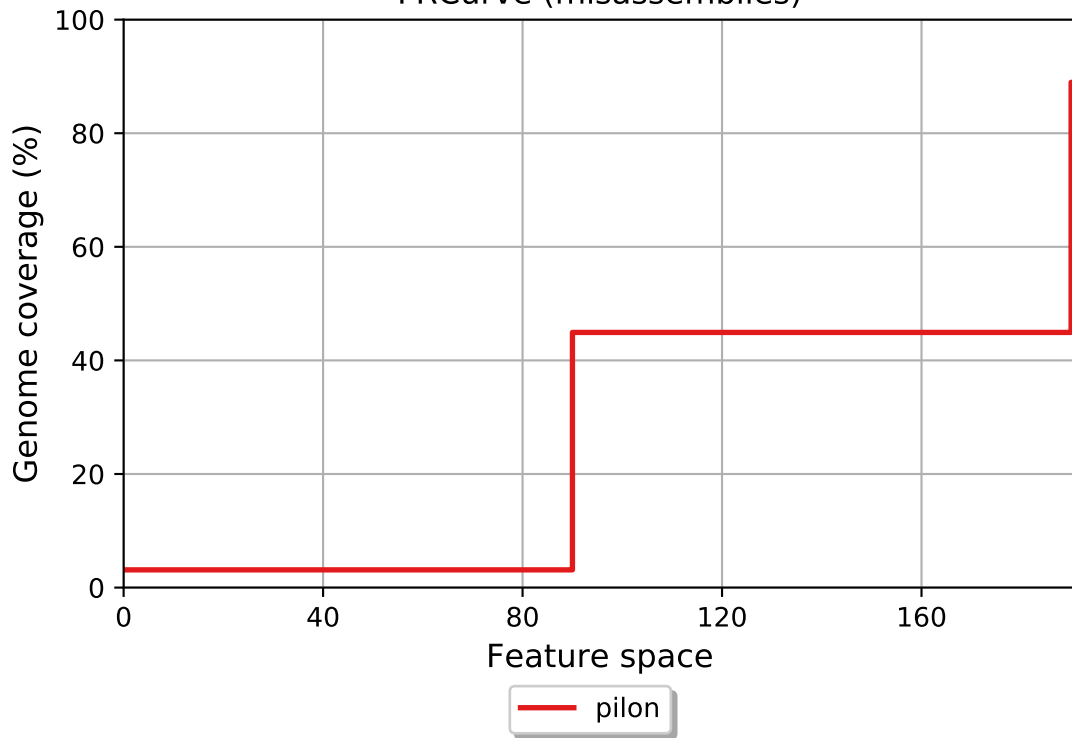


# translocations

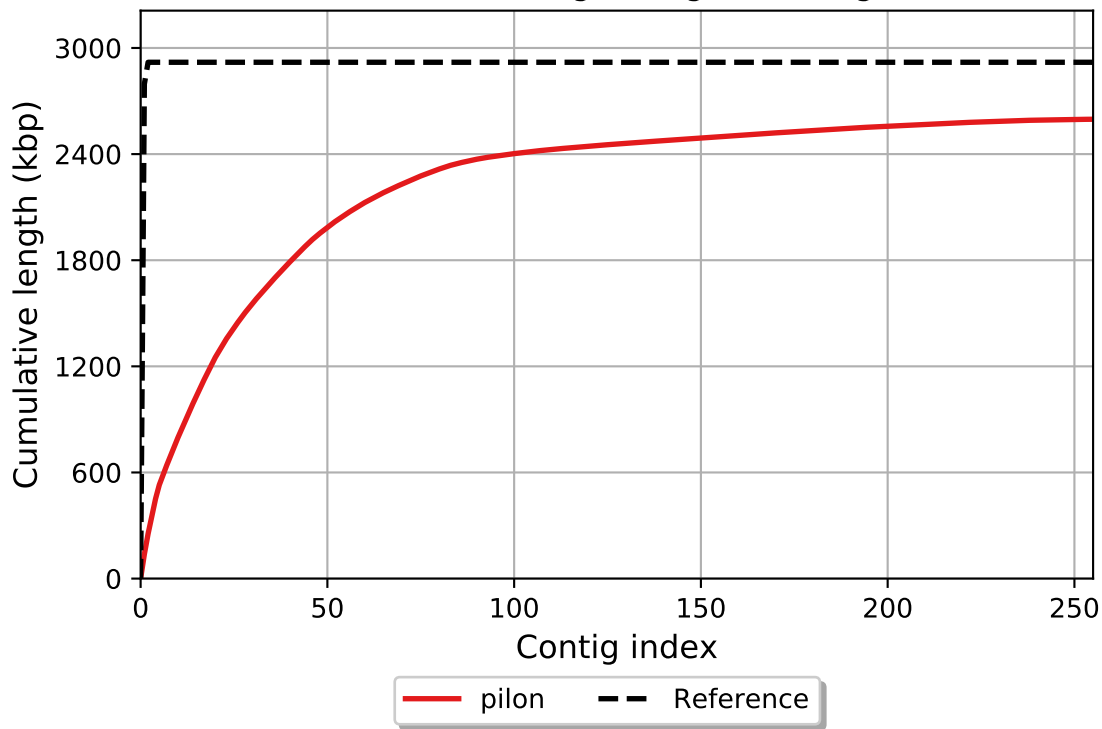


# inversions

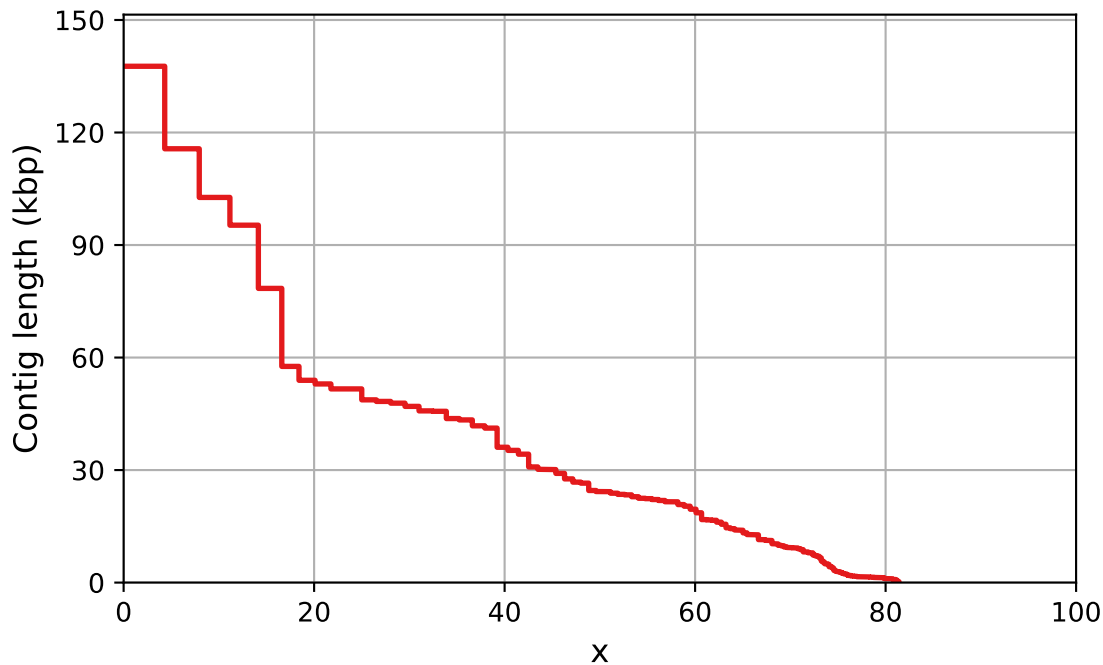
FRCurve (misassemblies)



Cumulative length (aligned contigs)

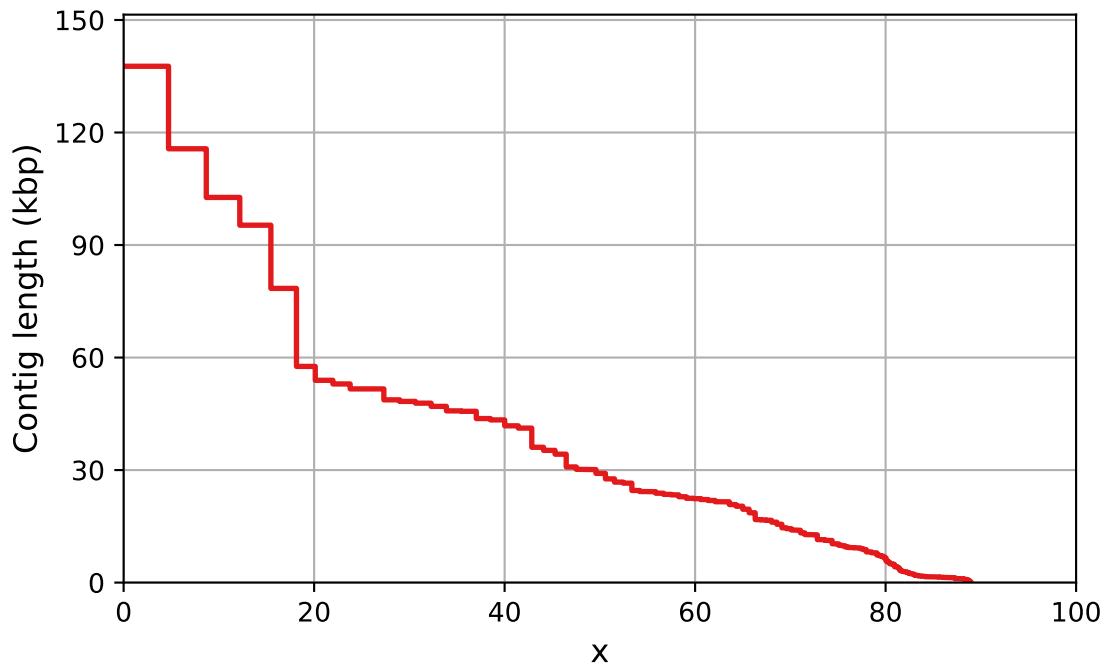


# NAx



pilon

# NGAx



pilon