

# Report

|                             | SC2252.consensus |
|-----------------------------|------------------|
| # contigs (>= 0 bp)         | 1                |
| # contigs (>= 1000 bp)      | 1                |
| # contigs (>= 5000 bp)      | 1                |
| # contigs (>= 10000 bp)     | 1                |
| # contigs (>= 25000 bp)     | 1                |
| # contigs (>= 50000 bp)     | 0                |
| Total length (>= 0 bp)      | 29902            |
| Total length (>= 1000 bp)   | 29902            |
| Total length (>= 5000 bp)   | 29902            |
| Total length (>= 10000 bp)  | 29902            |
| Total length (>= 25000 bp)  | 29902            |
| Total length (>= 50000 bp)  | 0                |
| # contigs                   | 1                |
| Largest contig              | 29902            |
| Total length                | 29902            |
| Reference length            | 29903            |
| GC (%)                      | 38.01            |
| Reference GC (%)            | 37.97            |
| N50                         | 29902            |
| NG50                        | 29902            |
| N75                         | 29902            |
| NG75                        | 29902            |
| L50                         | 1                |
| LG50                        | 1                |
| L75                         | 1                |
| LG75                        | 1                |
| # misassemblies             | 0                |
| # misassembled contigs      | 0                |
| Misassembled contigs length | 0                |
| # local misassemblies       | 0                |
| # scaffold gap ext. mis.    | 0                |
| # scaffold gap loc. mis.    | 0                |
| # unaligned mis. contigs    | 0                |
| # unaligned contigs         | 0 + 0 part       |
| Unaligned length            | 0                |
| Genome fraction (%)         | 99.766           |
| Duplication ratio           | 1.002            |
| # N's per 100 kbp           | 234.10           |
| # mismatches per 100 kbp    | 56.98            |
| # indels per 100 kbp        | 3.35             |
| # genomic features          | 21 + 3 part      |
| Largest alignment           | 29832            |
| Total aligned length        | 29832            |
| NA50                        | 29832            |
| NGA50                       | 29832            |
| NA75                        | 29832            |
| NGA75                       | 29832            |
| LA50                        | 1                |
| LGA50                       | 1                |
| LA75                        | 1                |
| LGA75                       | 1                |

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

|                             | SC2252.consensus |
|-----------------------------|------------------|
| # misassemblies             | 0                |
| # contig misassemblies      | 0                |
| # c. relocations            | 0                |
| # c. translocations         | 0                |
| # c. inversions             | 0                |
| # scaffold misassemblies    | 0                |
| # s. relocations            | 0                |
| # s. translocations         | 0                |
| # s. inversions             | 0                |
| # misassembled contigs      | 0                |
| Misassembled contigs length | 0                |
| # local misassemblies       | 0                |
| # scaffold gap ext. mis.    | 0                |
| # scaffold gap loc. mis.    | 0                |
| # unaligned mis. contigs    | 0                |
| # mismatches                | 17               |
| # indels                    | 1                |
| # indels (<= 5 bp)          | 1                |
| # indels (> 5 bp)           | 0                |
| Indels length               | 1                |

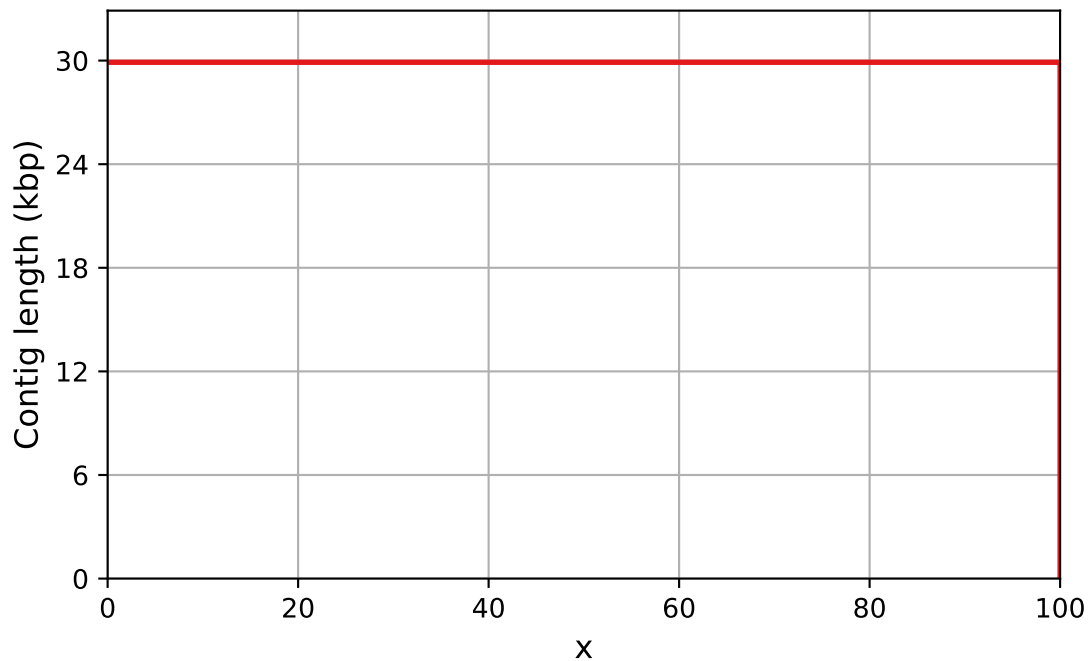
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

|                               | SC2252.consensus |
|-------------------------------|------------------|
| # fully unaligned contigs     | 0                |
| Fully unaligned length        | 0                |
| # partially unaligned contigs | 0                |
| Partially unaligned length    | 0                |
| # N's                         | 70               |

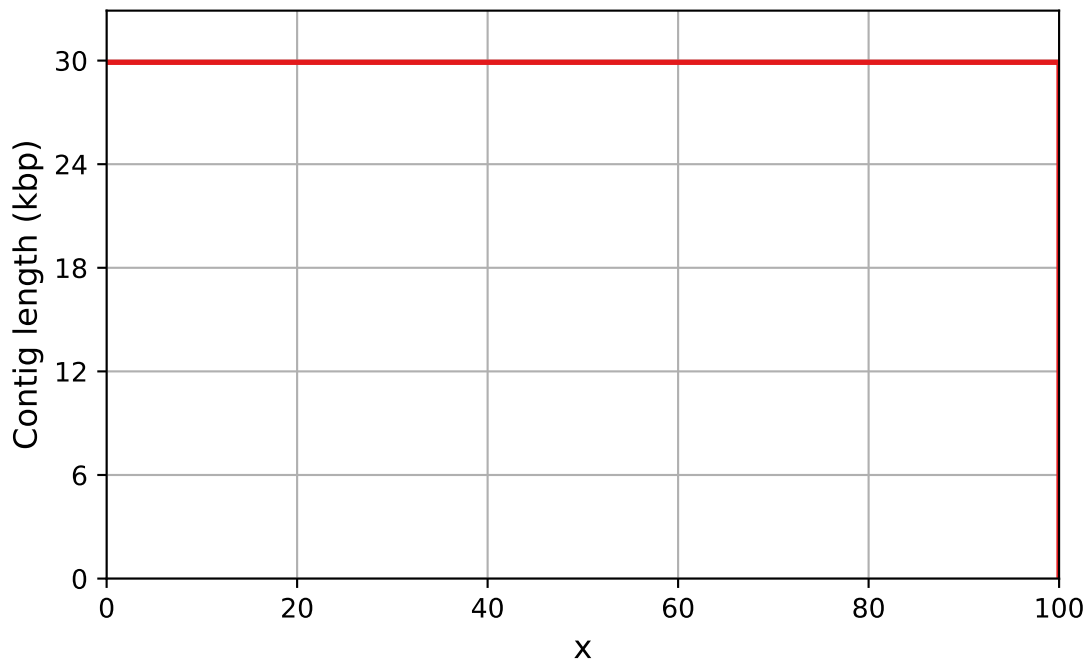
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



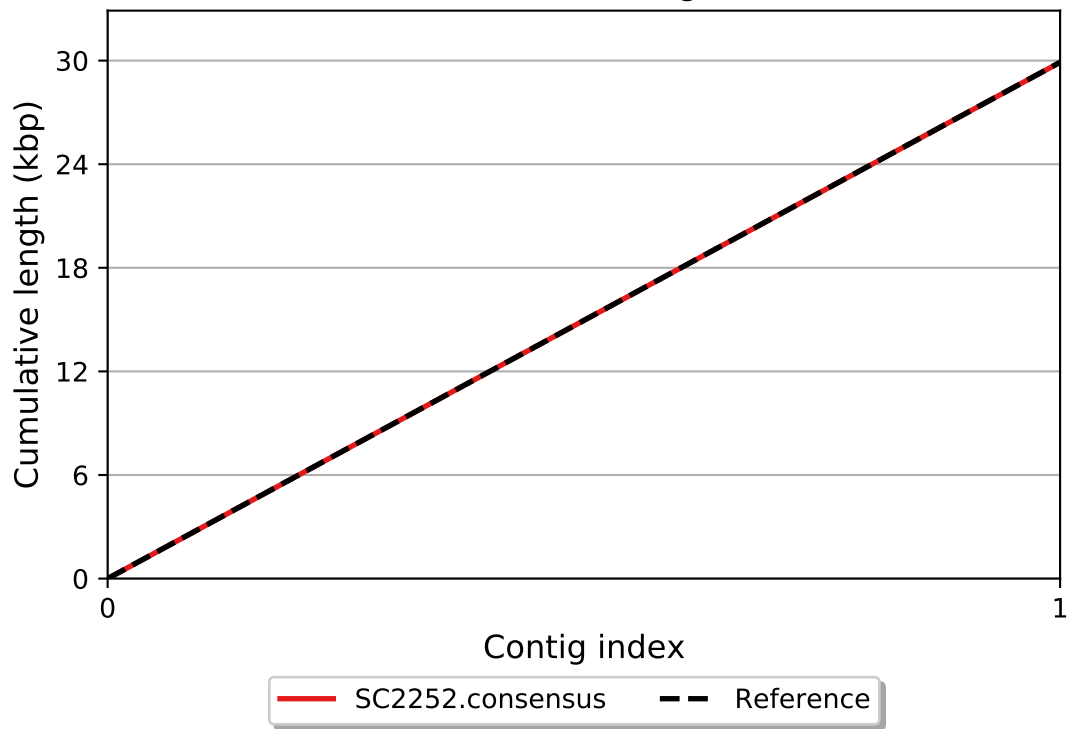
— SC2252.consensus

NGx

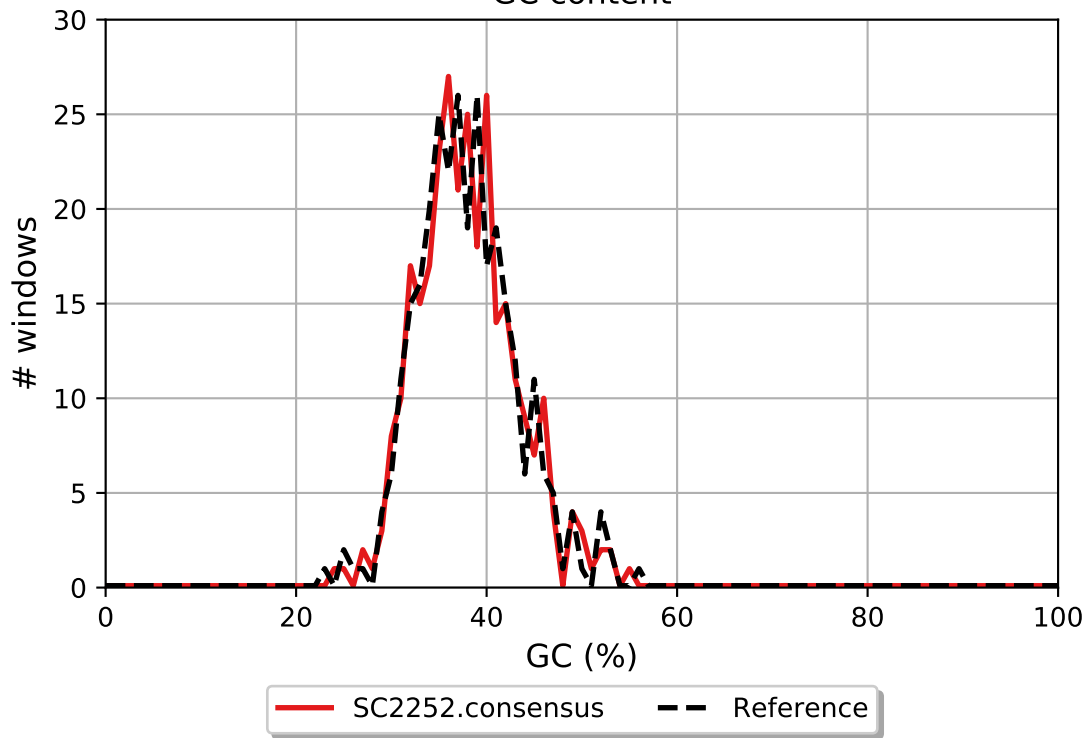


— SC2252.consensus

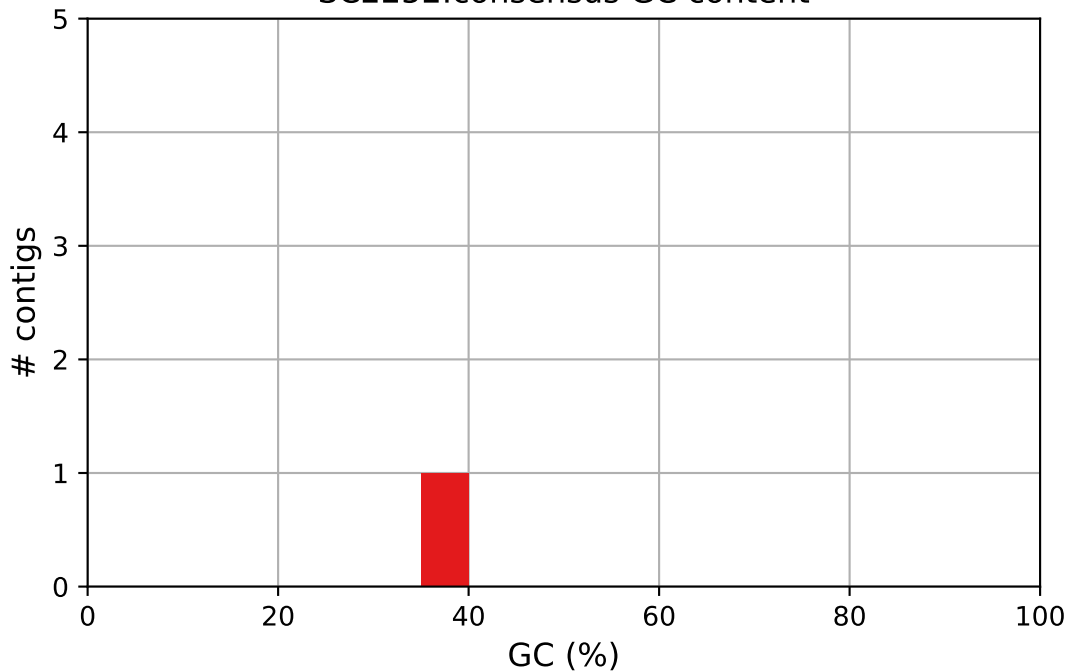
Cumulative length



# GC content



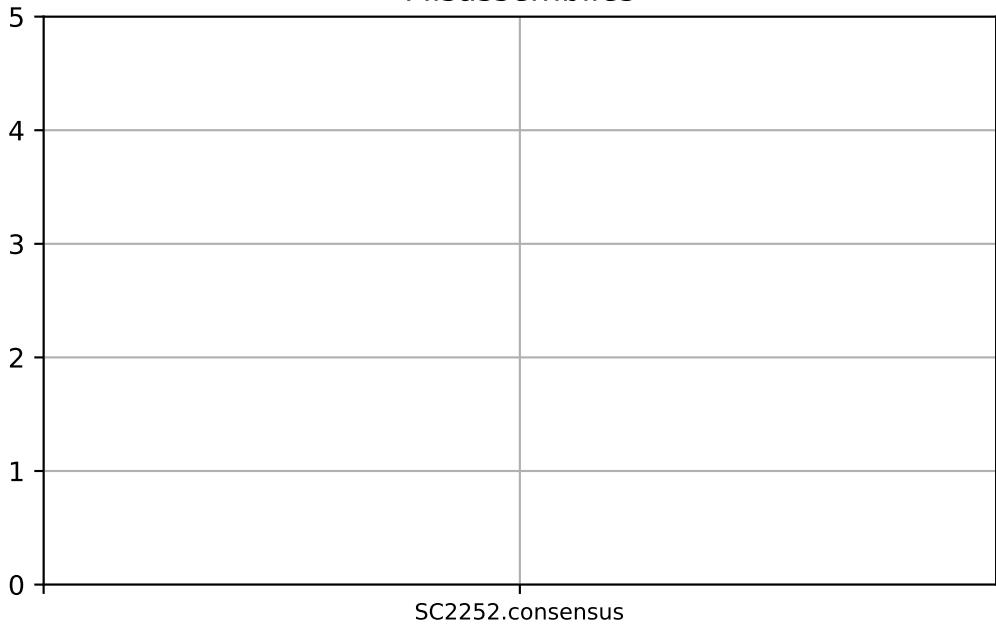
SC2252.consensus GC content



SC2252.consensus



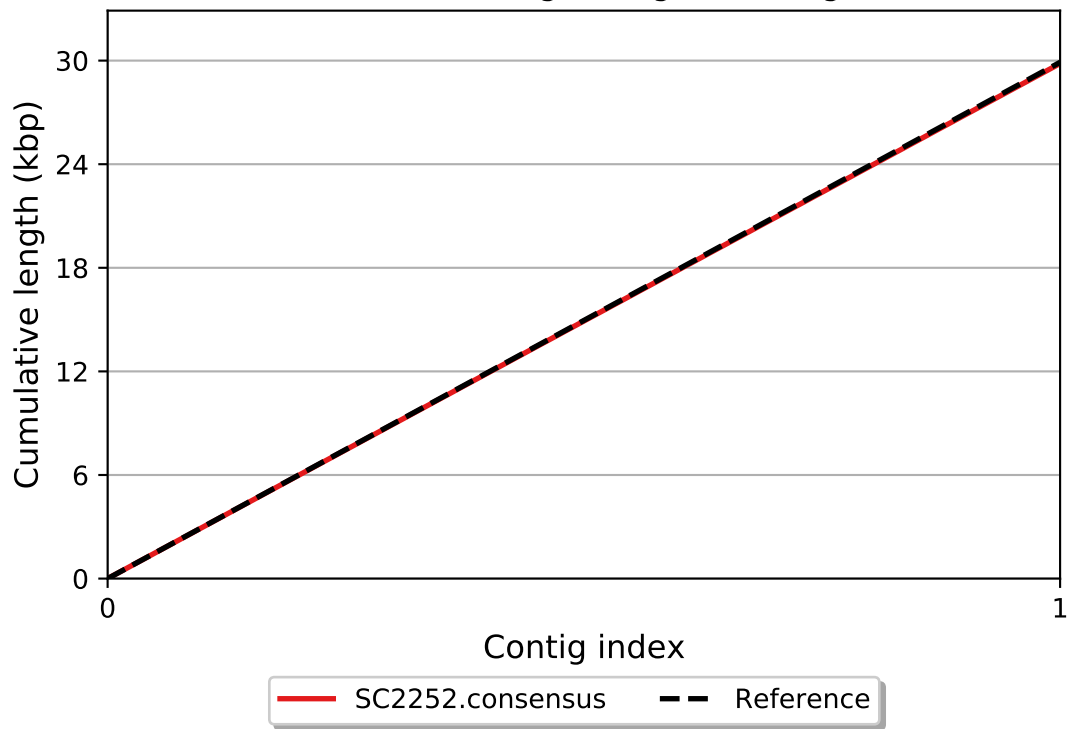
## Misassemblies



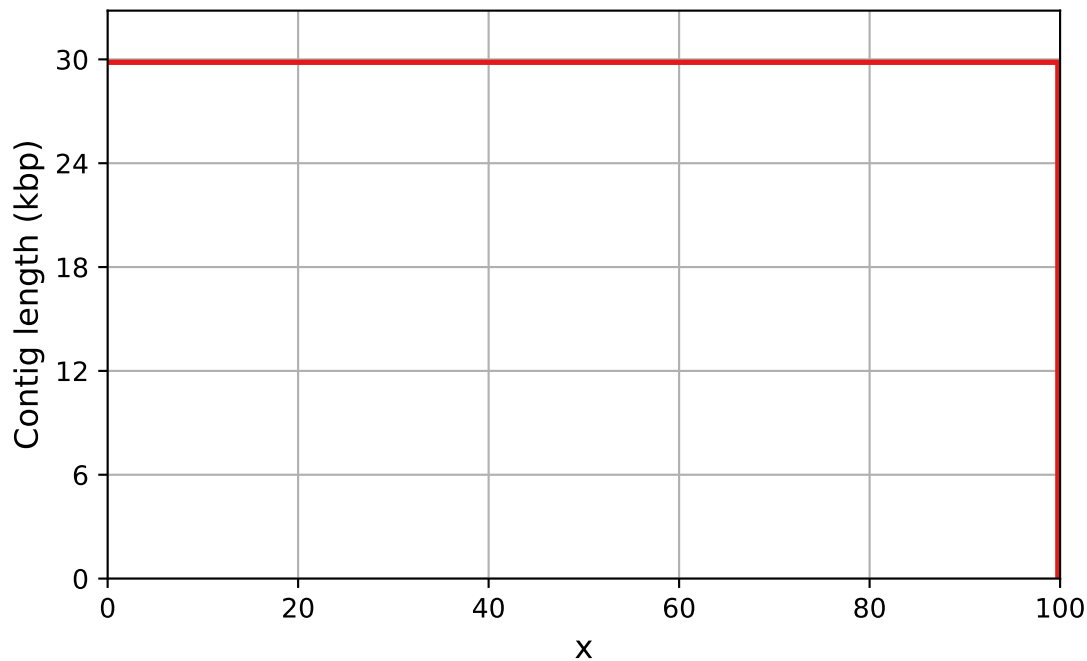
FRCurve (misassemblies)



Cumulative length (aligned contigs)

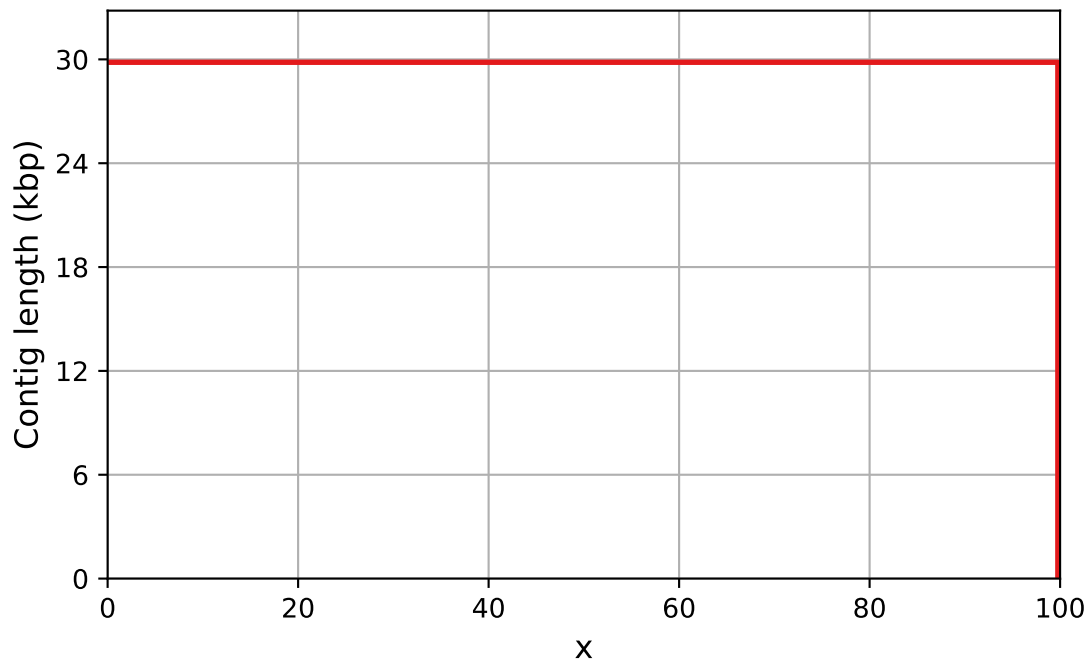


NAx

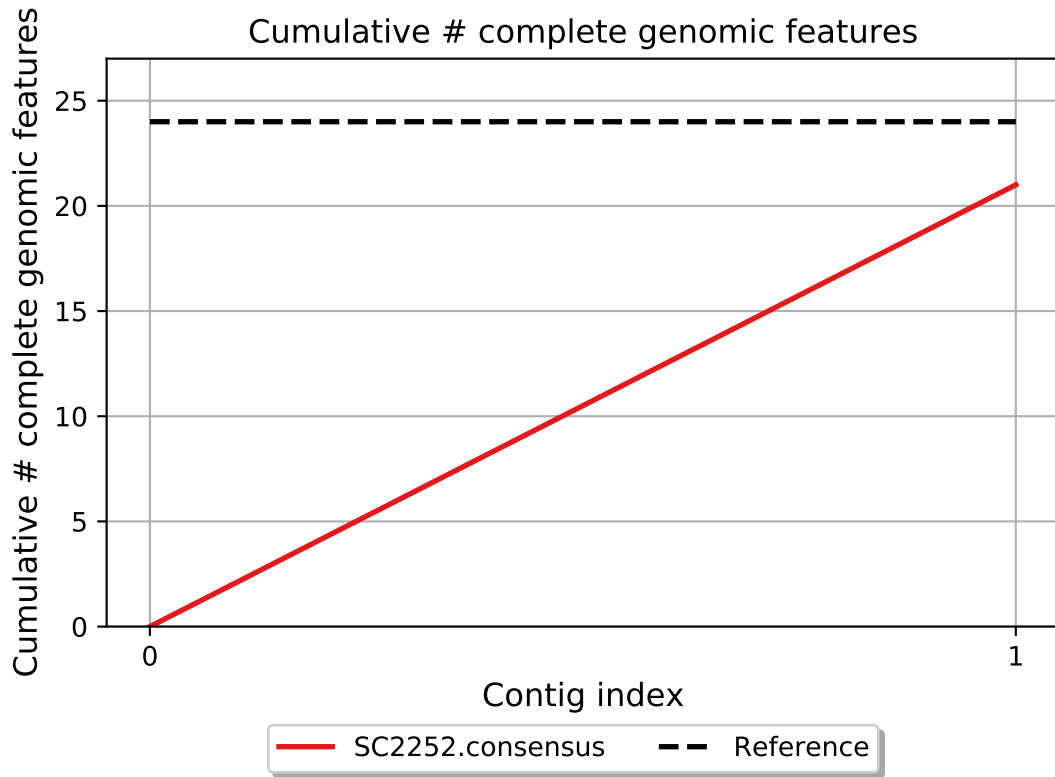


— SC2252.consensus

# NGAx



— SC2252.consensus



FRCurve (genomic features)

