# Report

| | UCT124H |
|---|---|
| # contigs (>= 0 bp) | 50 |
| # contigs (>= 1000 bp) | 25 |
| # contigs (>= 5000 bp) | 23 |
| # contigs (>= 10000 bp) | 20 |
| # contigs (>= 25000 bp) | 15 |
| # contigs (>= 50000 bp) | 2 |
| Total length (>= 0 bp) | 1510565 |
| Total length (>= 1000 bp) | 1502065 |
| Total length (>= 5000 bp) | 1499582 |
| Total length (>= 10000 bp) | 1471277 |
| Total length (>= 25000 bp) | 1357766 |
| Total length (>= 50000 bp) | 954420 |
| # contigs | 31 |
| Largest contig | 900914 |
| Total length | 1506196 |
| Reference length | 1521208 |
| GC (%) | 28.23 |
| Reference GC (%) | 28.18 |
| N50 | 900914 |
| NG50 | 900914 |
| N90 | 25182 |
| NG90 | 24711 |
| auN | 551160.4 |
| auNG | 545721.3 |
| L50 | 1 |
| LG50 | 1 |
| L90 | 15 |
| LG90 | 16 |
| # misassemblies | 9 |
| # misassembled contigs | 9 |
| Misassembled contigs length | 245290 |
| # local misassemblies | 9 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 1 |
| # unaligned contigs | 3 + 6 part |
| Unaligned length | 41536 |
| Genome fraction (%) | 90.035 |
| Duplication ratio | 1.068 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 405.69 |
| # indels per 100 kbp | 34.88 |
| # genomic features | 1451 + 42 part |
| Largest alignment | 900907 |
| Total aligned length | 1462204 |
| NA50 | 900907 |
| NGA50 | 900907 |
| NA90 | 14024 |
| NGA90 | 12845 |
| auNA | 548604.7 |
| auNGA | 543190.8 |
| LA50 | 1 |
| LGA50 | 1 |
| LA90 | 19 |
| LGA90 | 20 |

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).
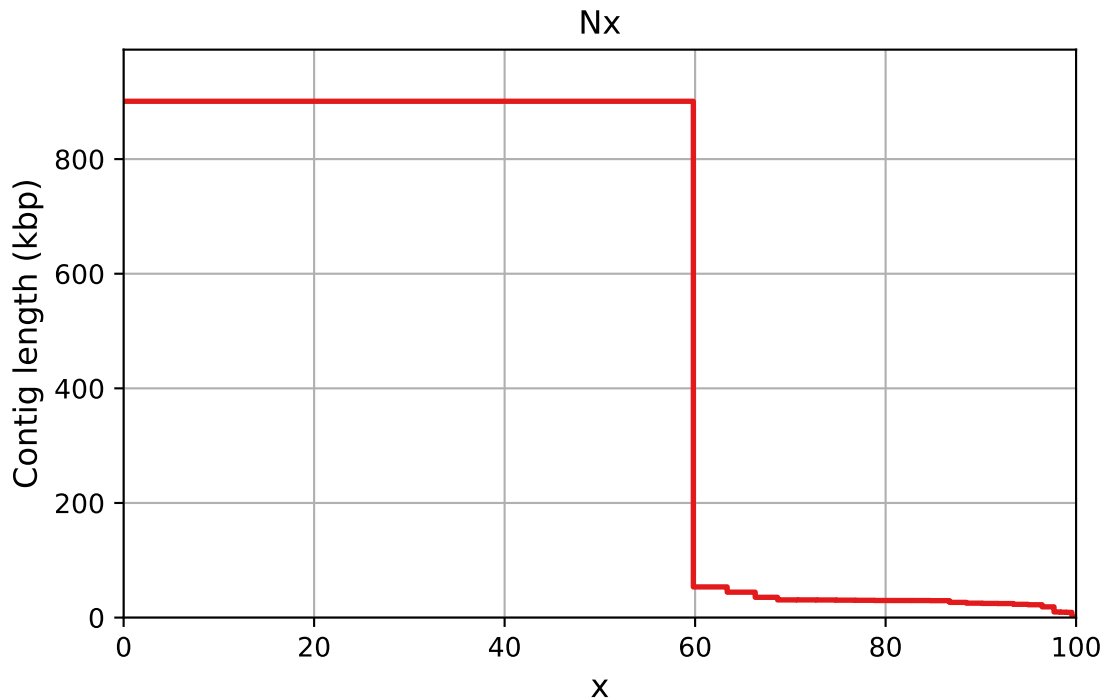
# Misassemblies report
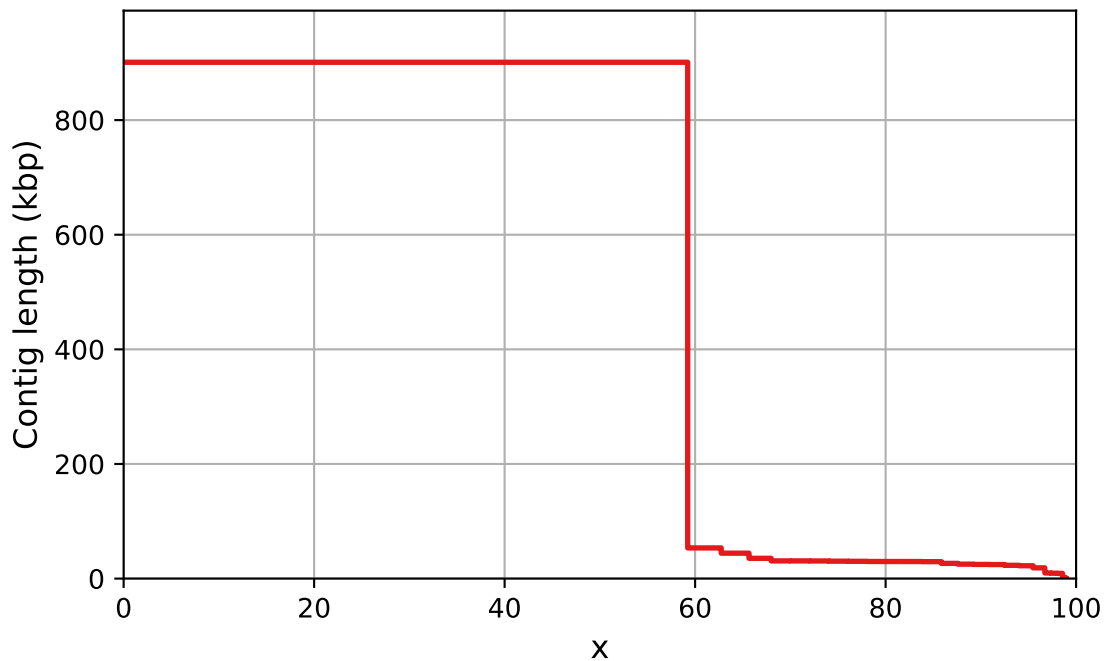
| | UCT124H |
|---|---|
| # misassemblies | 9 |
| # contig misassemblies | 9 |
| # c. relocations | 4 |
| # c. translocations | 4 |
| # c. inversions | 1 |
| # scaffold misassemblies | 0 |
| # s. relocations | 0 |
| # s. translocations | 0 |
| # s. inversions | 0 |
| # misassembled contigs | 9 |
| Misassembled contigs length | 245290 |
| # local misassemblies | 9 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 1 |
| # mismatches | 5932 |
| # indels | 510 |
| # indels (<= 5 bp) | 449 |
| # indels (> 5 bp) | 61 |
| Indels length | 2235 |

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).
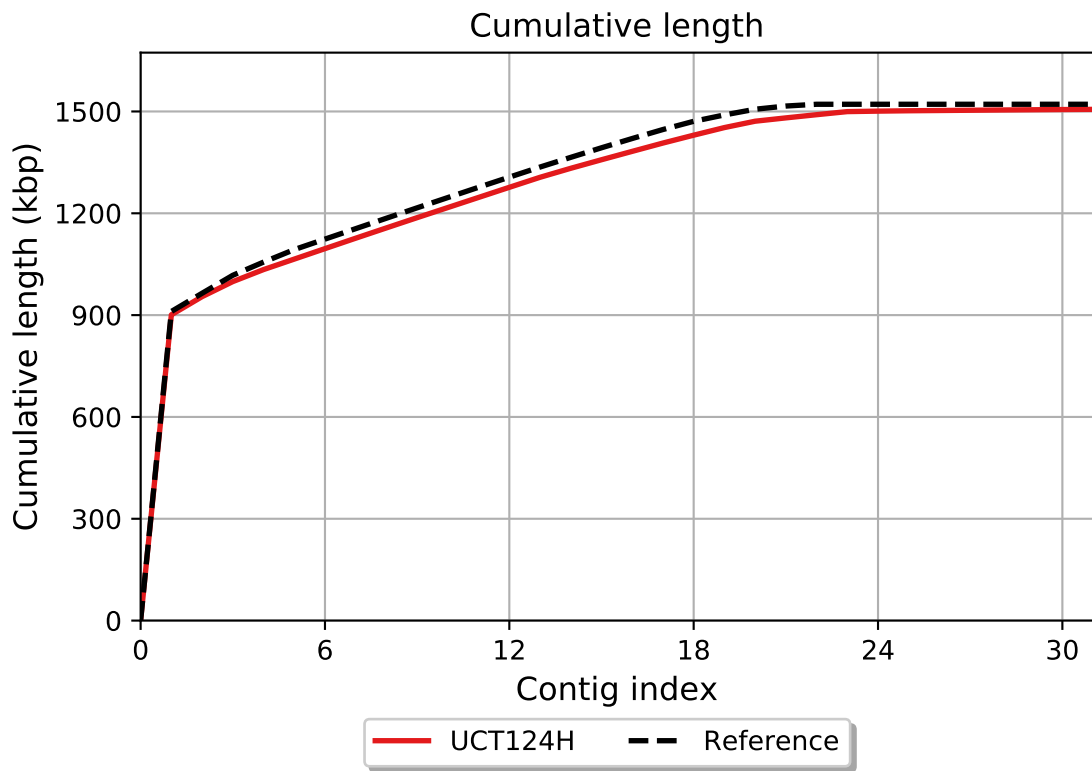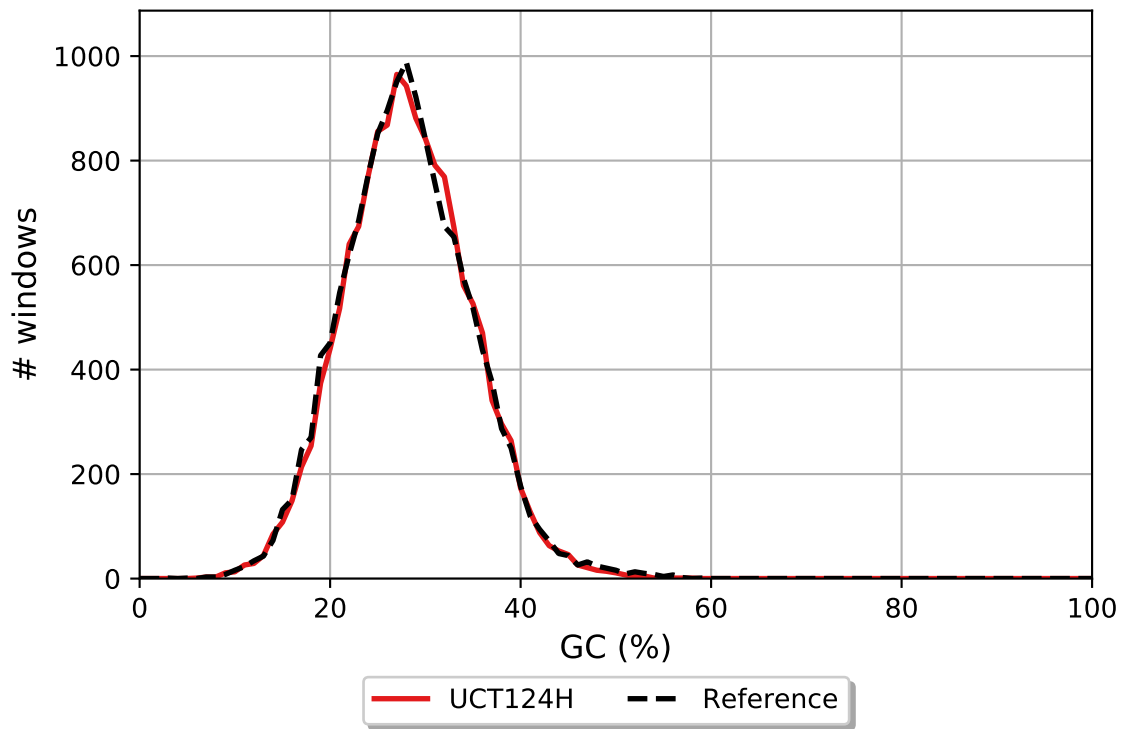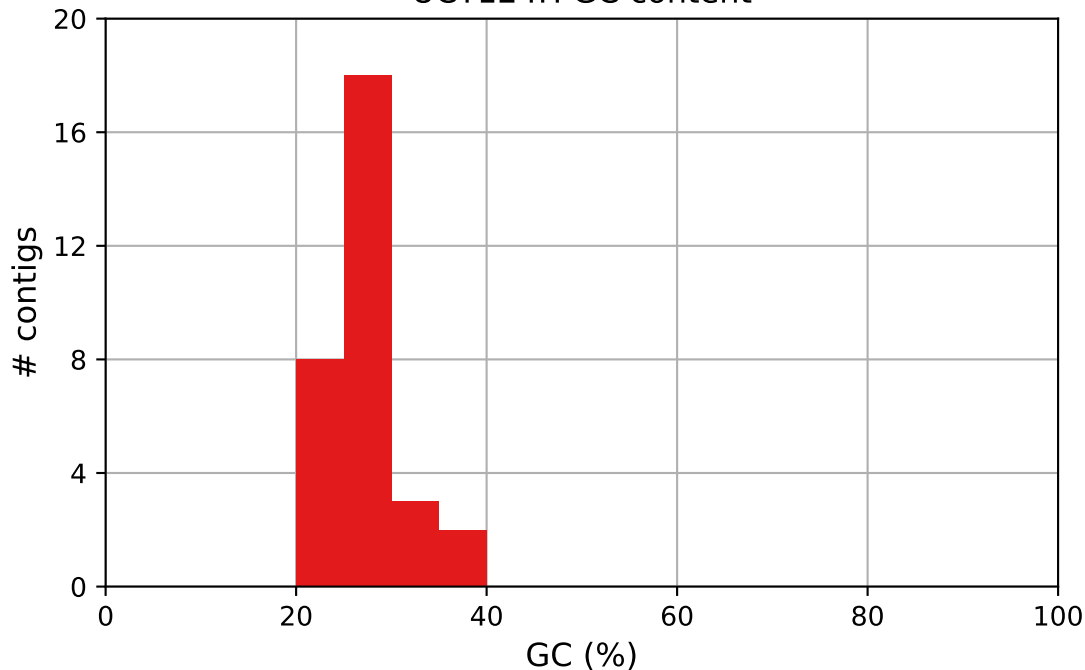
# Unaligned report

|                                | UCT124H |
|--------------------------------|--------:|
| # fully unaligned contigs      |       3 |
| Fully unaligned length         |    2197 |
| # partially unaligned contigs  |       6 |
| Partially unaligned length     |   39339 |
| # N's                          |       0 |

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).

Nx

NGx

Cumulative length

GC content

UCT124H GC content
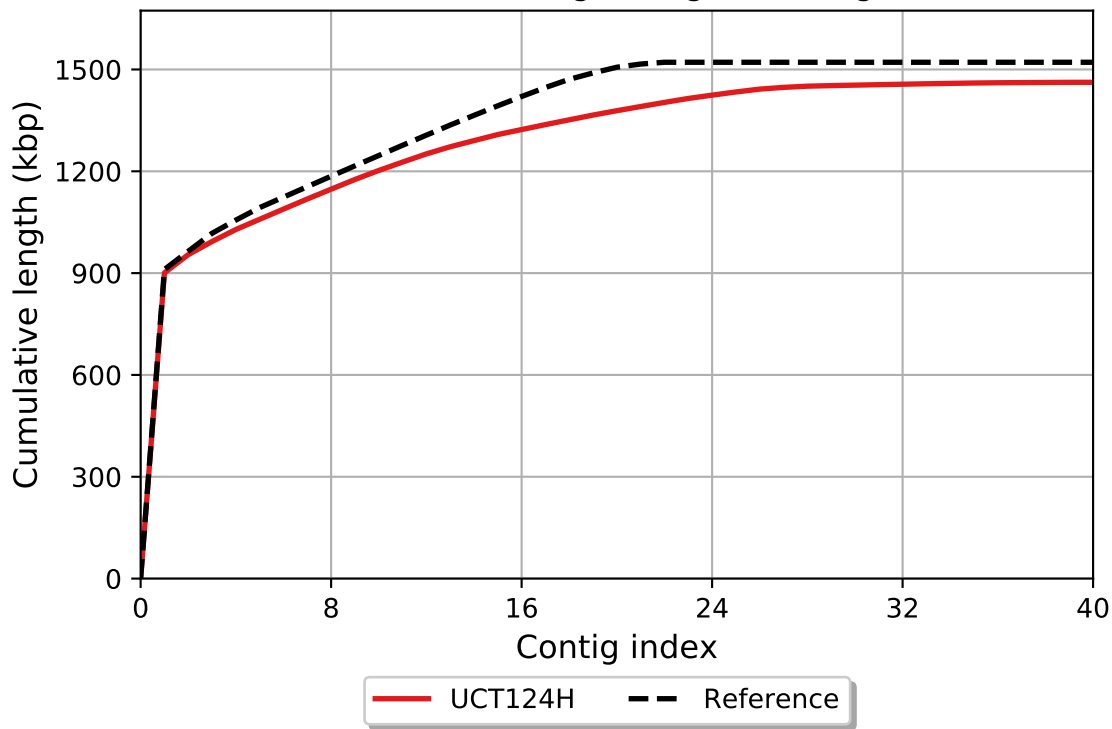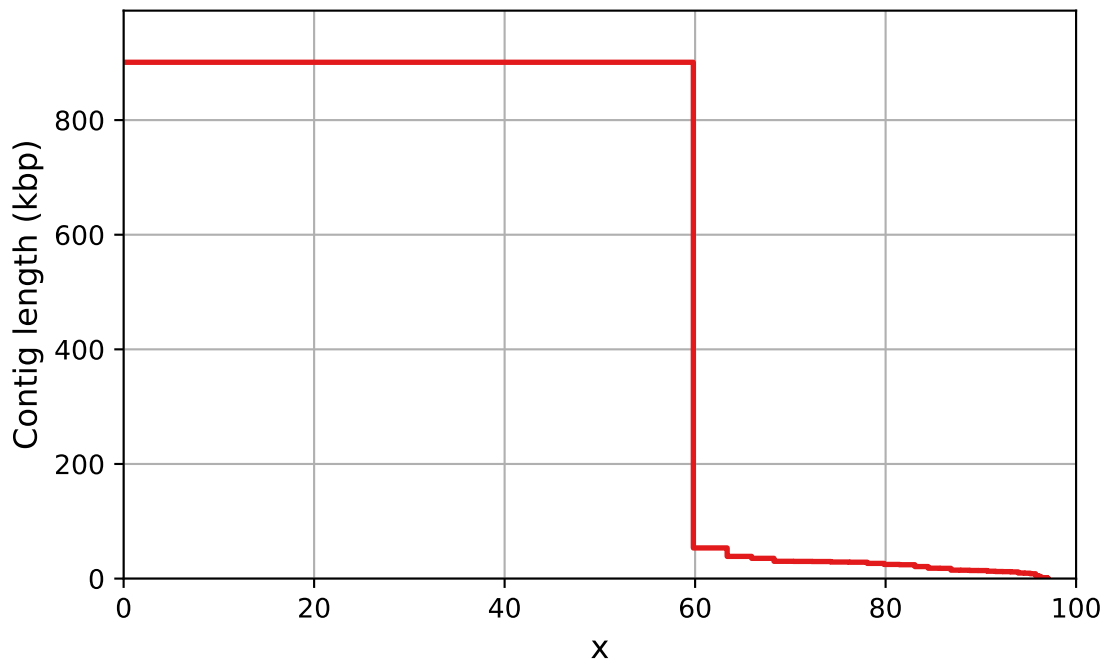
Misassemblies

- # relocations
- # translocations
- # inversions

FRCurve (misassemblies)
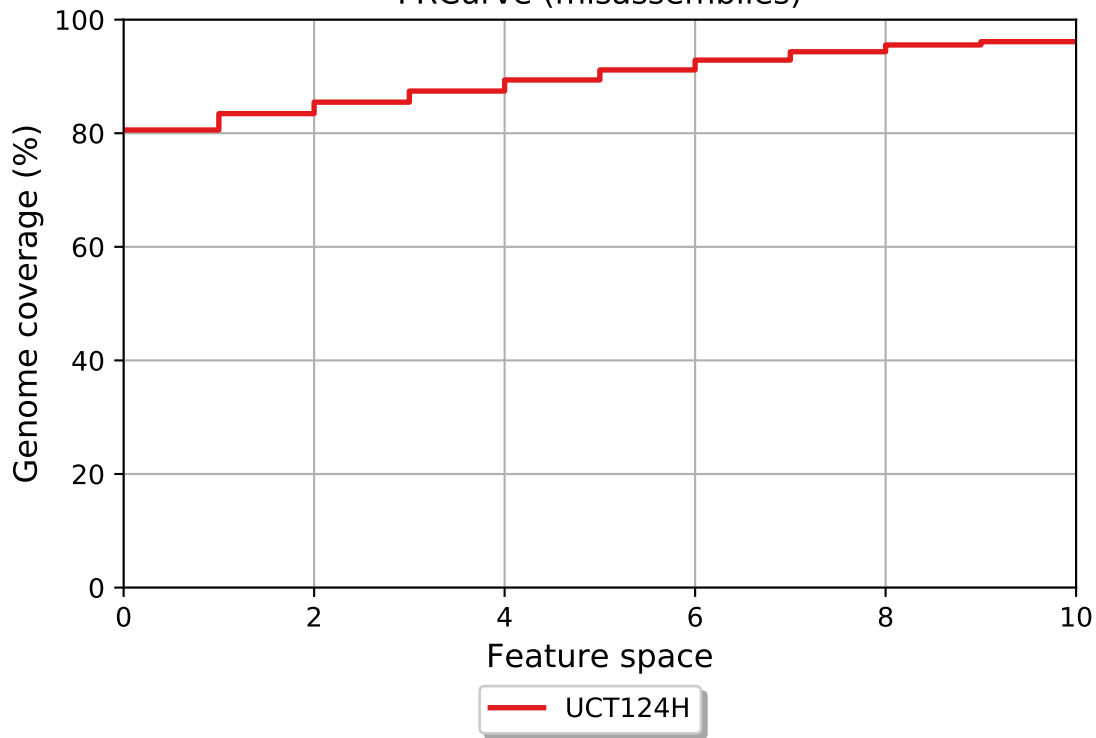
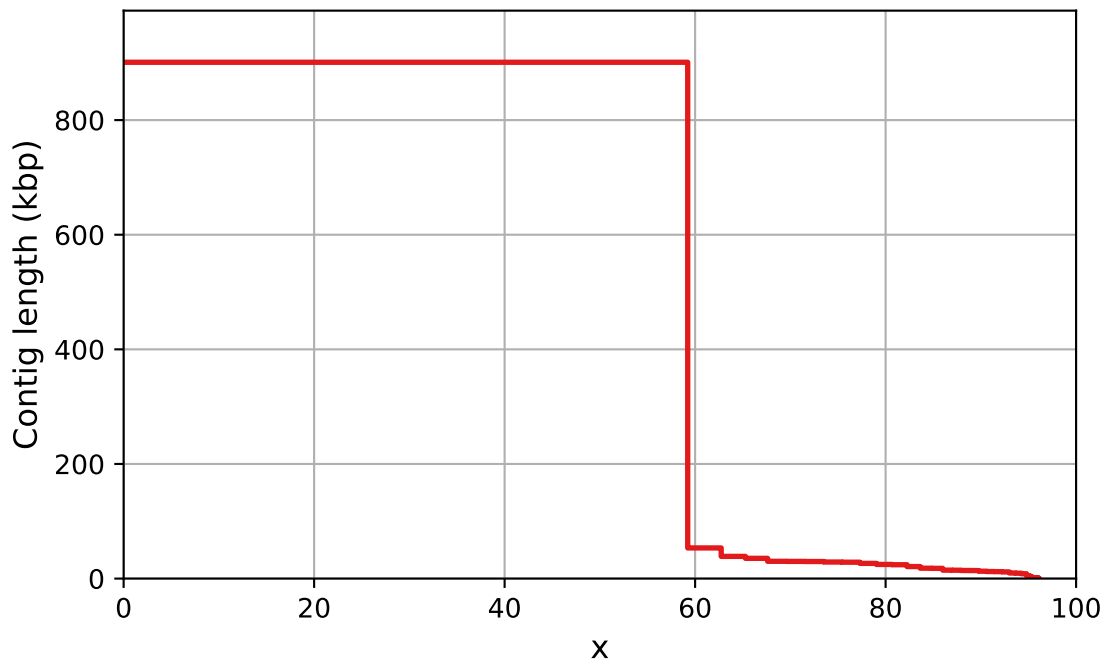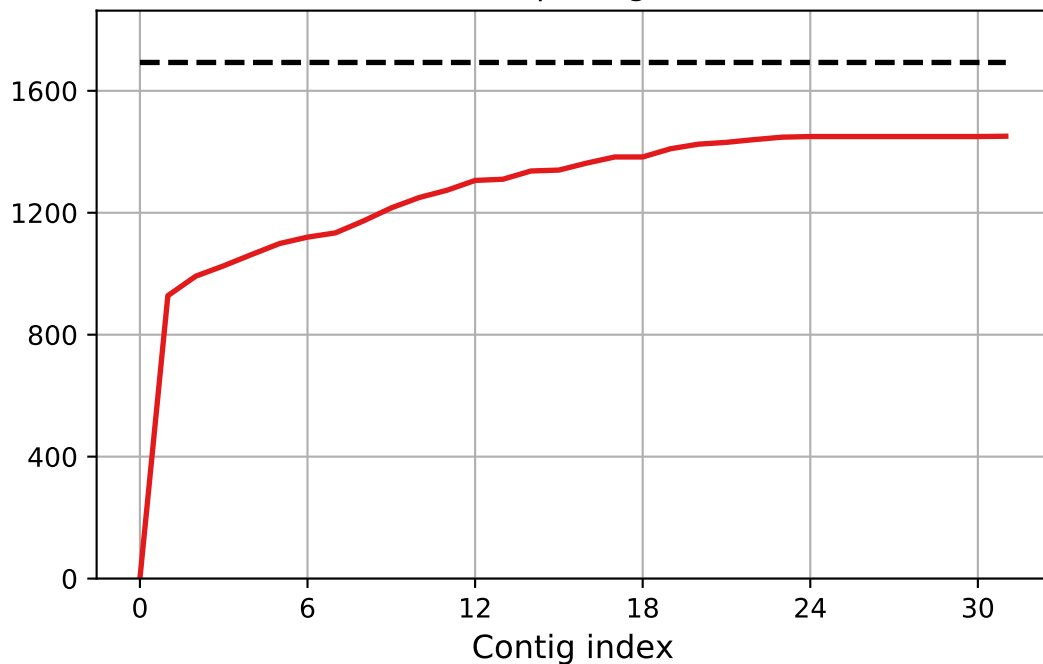**Cumulative length (aligned contigs)**

NAx

NGAx

Cumulative # complete genomic features

FRCurve (genomic features)