# Report

| | URI87H |
|---|---|
| # contigs (>= 0 bp) | 66 |
| # contigs (>= 1000 bp) | 24 |
| # contigs (>= 5000 bp) | 19 |
| # contigs (>= 10000 bp) | 19 |
| # contigs (>= 25000 bp) | 18 |
| # contigs (>= 50000 bp) | 2 |
| Total length (>= 0 bp) | 1505755 |
| Total length (>= 1000 bp) | 1491333 |
| Total length (>= 5000 bp) | 1482048 |
| Total length (>= 10000 bp) | 1482048 |
| Total length (>= 25000 bp) | 1460107 |
| Total length (>= 50000 bp) | 964183 |
| # contigs | 34 |
| Largest contig | 910570 |
| Total length | 1498567 |
| Reference length | 1521208 |
| GC (%) | 28.22 |
| Reference GC (%) | 28.18 |
| N50 | 910570 |
| NG50 | 910570 |
| N90 | 29801 |
| NG90 | 28162 |
| auN | 565982.2 |
| auNG | 557558.3 |
| L50 | 1 |
| LG50 | 1 |
| L90 | 14 |
| LG90 | 15 |
| # misassemblies | 12 |
| # misassembled contigs | 9 |
| Misassembled contigs length | 246397 |
| # local misassemblies | 1 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 0 |
| # unaligned contigs | 0 + 4 part |
| Unaligned length | 14744 |
| Genome fraction (%) | 93.766 |
| Duplication ratio | 1.040 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 152.86 |
| # indels per 100 kbp | 15.37 |
| # genomic features | 1547 + 38 part |
| Largest alignment | 910570 |
| Total aligned length | 1483054 |
| NA50 | 910570 |
| NGA50 | 910570 |
| NA90 | 16800 |
| NGA90 | 14682 |
| auNA | 563861.9 |
| auNGA | 555469.6 |
| LA50 | 1 |
| LGA50 | 1 |
| LA90 | 16 |
| LGA90 | 17 |

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).
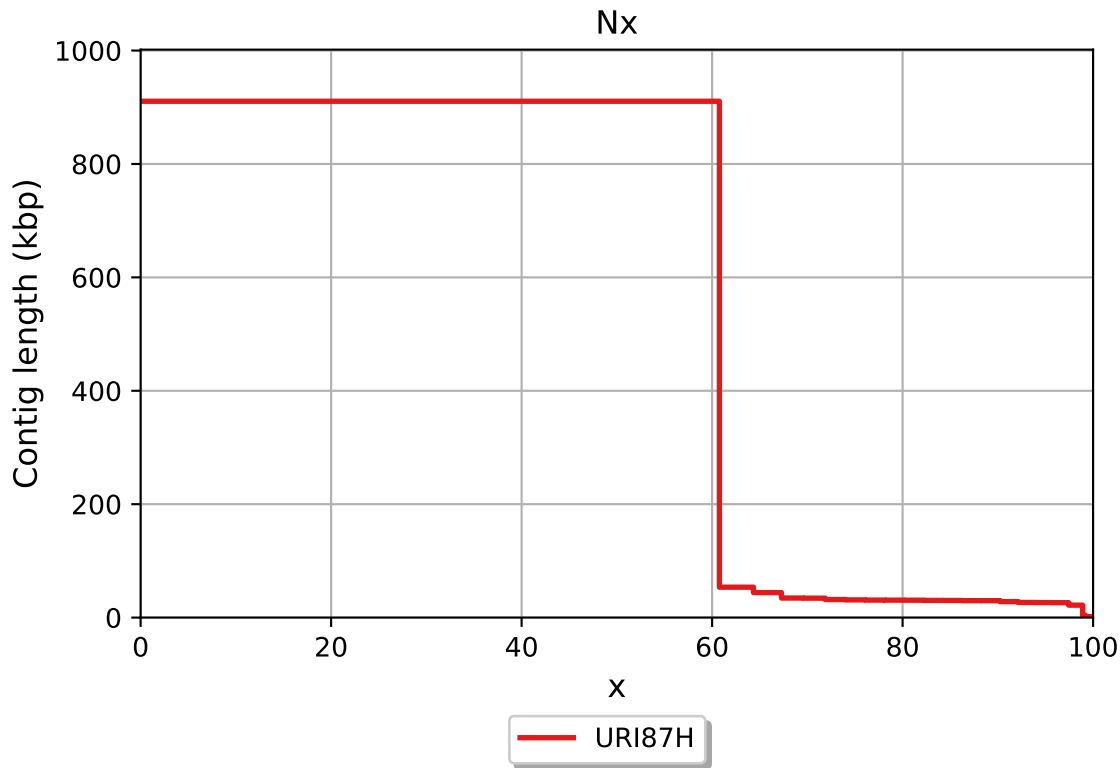
# Misassemblies report
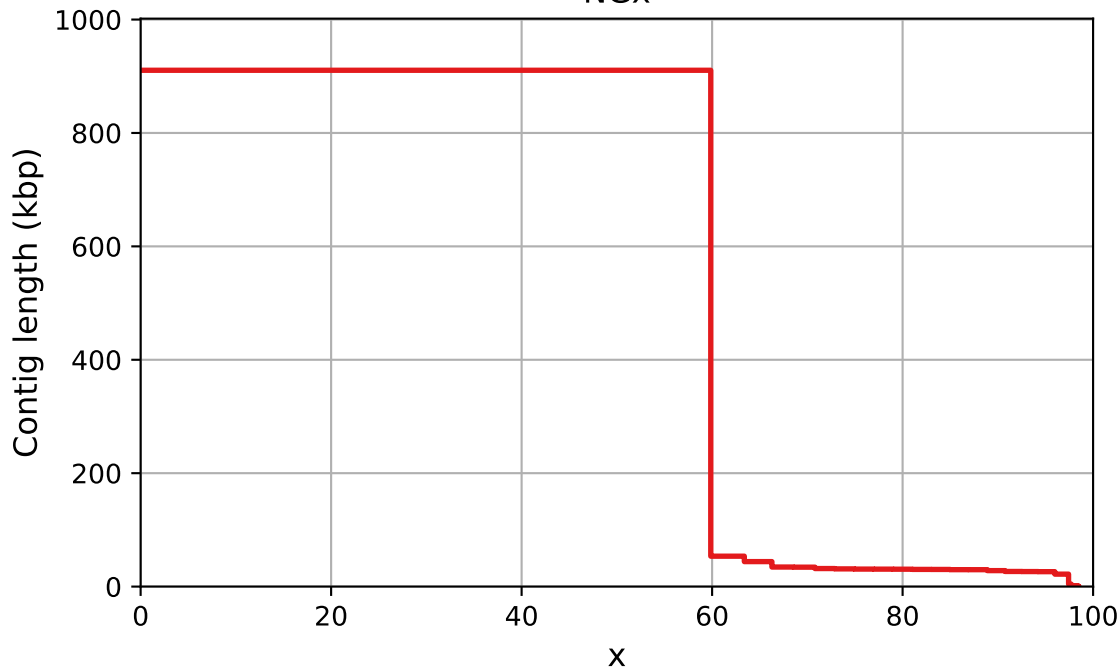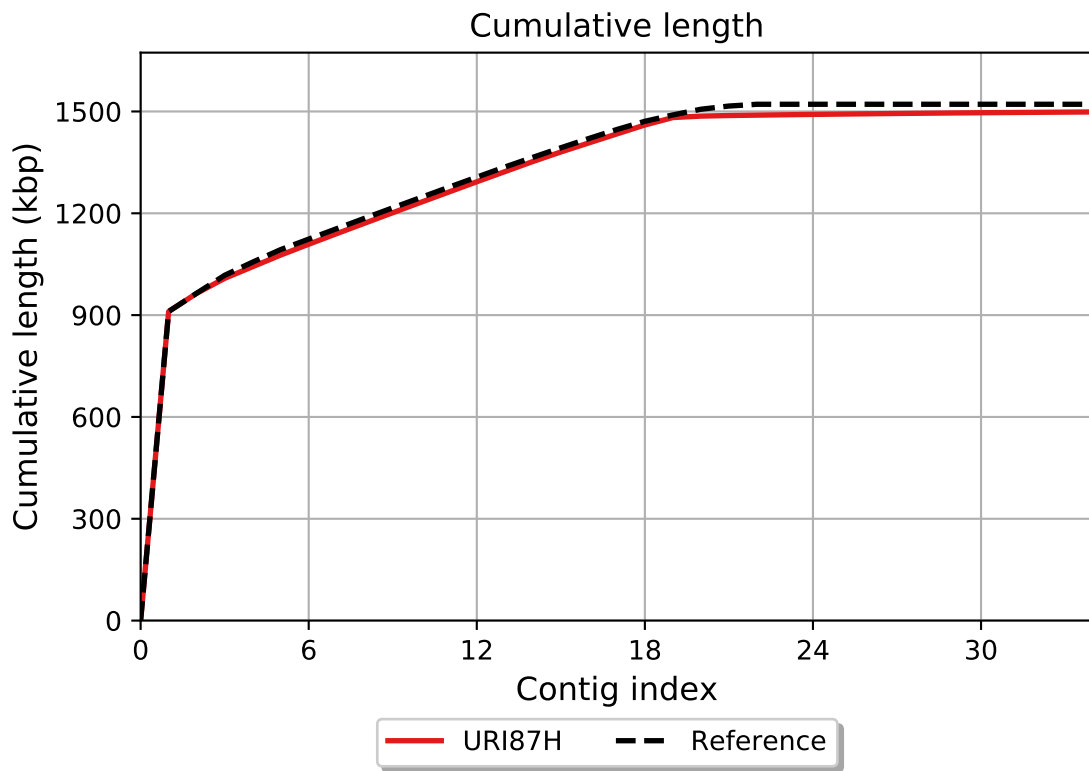
| | URI87H |
|---|---|
| # misassemblies | 12 |
| # contig misassemblies | 12 |
| # c. relocations | 6 |
| # c. translocations | 6 |
| # c. inversions | 0 |
| # scaffold misassemblies | 0 |
| # s. relocations | 0 |
| # s. translocations | 0 |
| # s. inversions | 0 |
| # misassembled contigs | 9 |
| Misassembled contigs length | 246397 |
| # local misassemblies | 1 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 0 |
| # mismatches | 2267 |
| # indels | 228 |
| # indels (<= 5 bp) | 203 |
| # indels (> 5 bp) | 25 |
| Indels length | 1331 |

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).
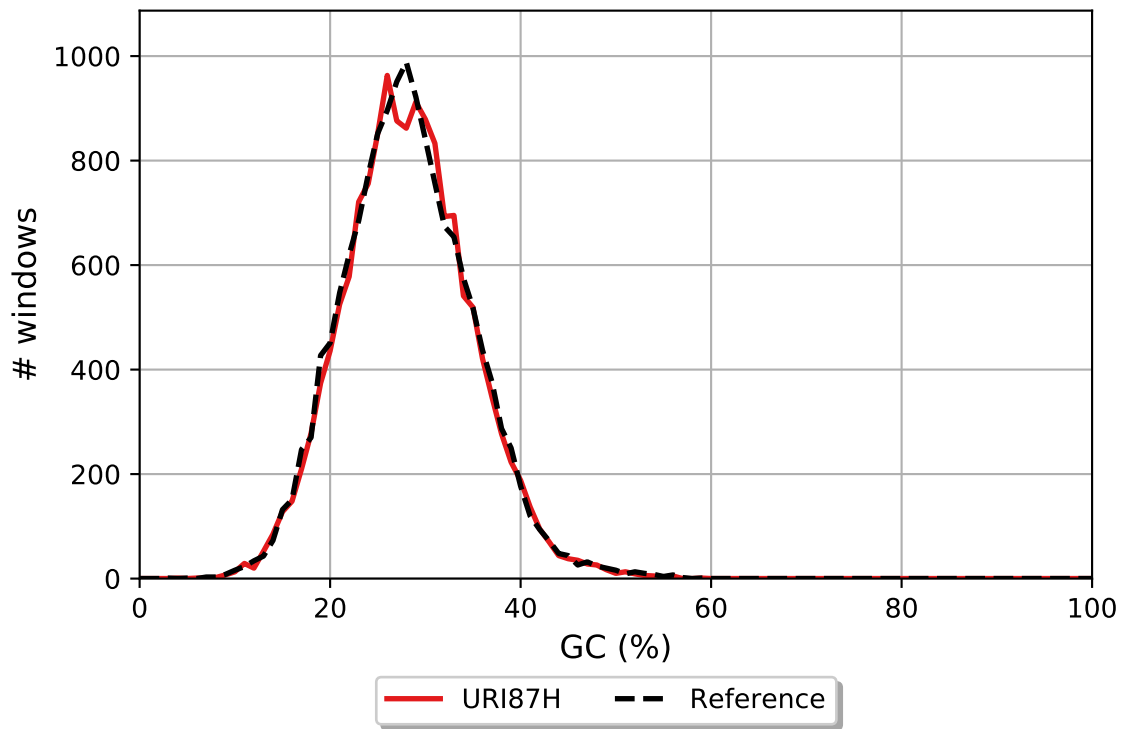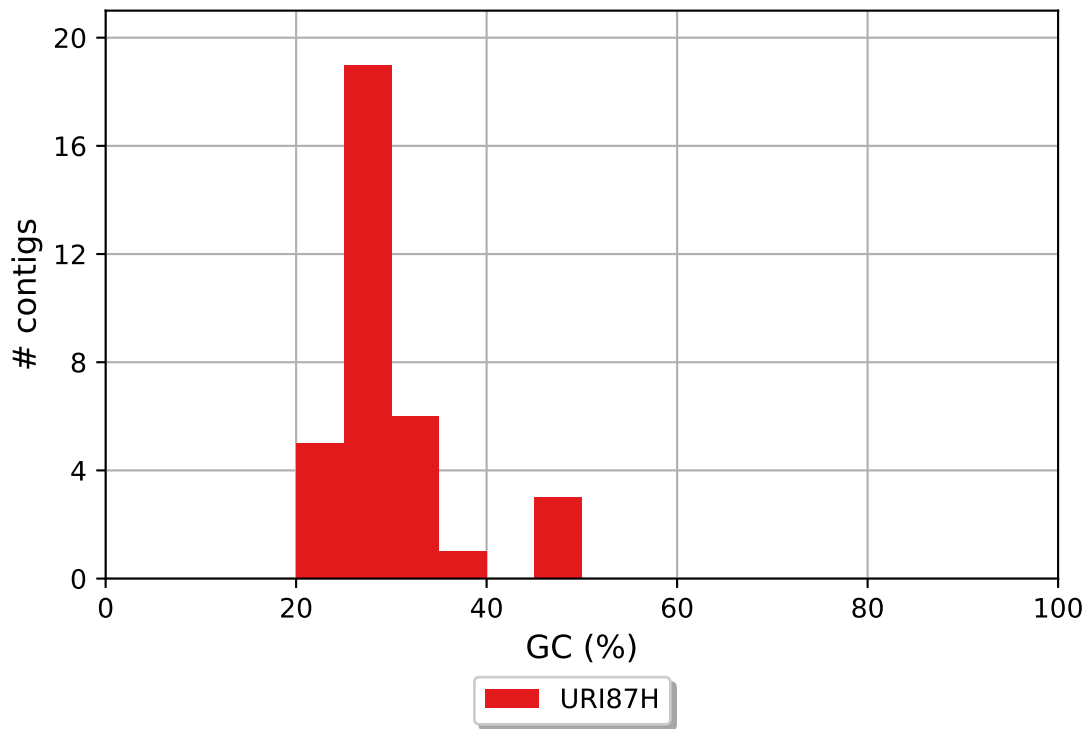
# Unaligned report

| | URI87H |
|---|---|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 4 |
| Partially unaligned length | 14744 |
| # 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
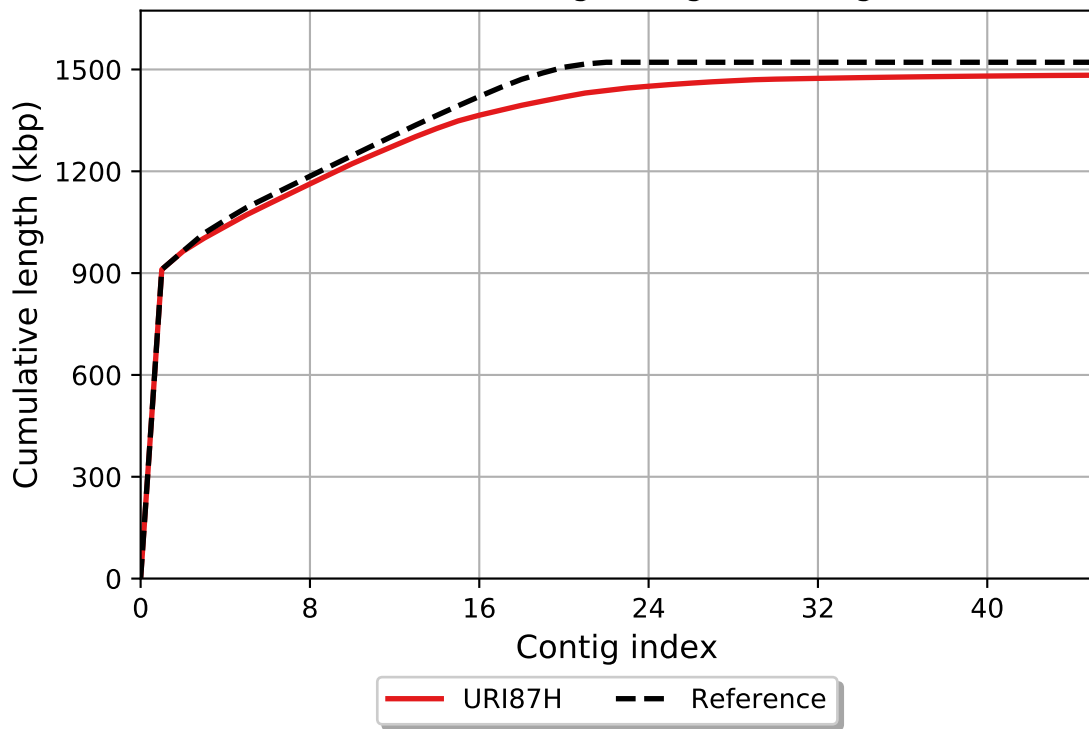
GC content

URI87H GC content

Misassemblies
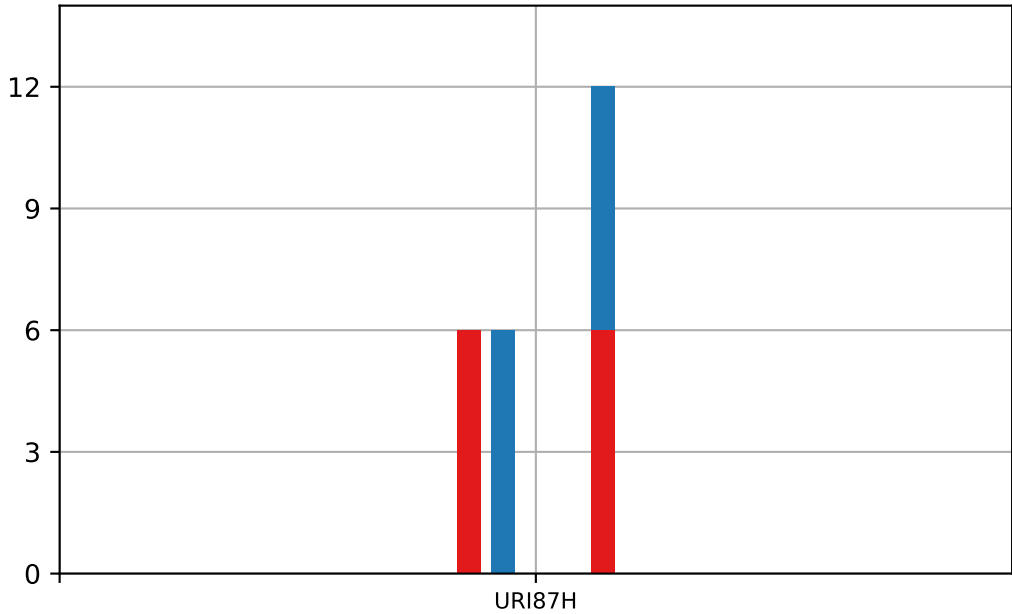
URI87H

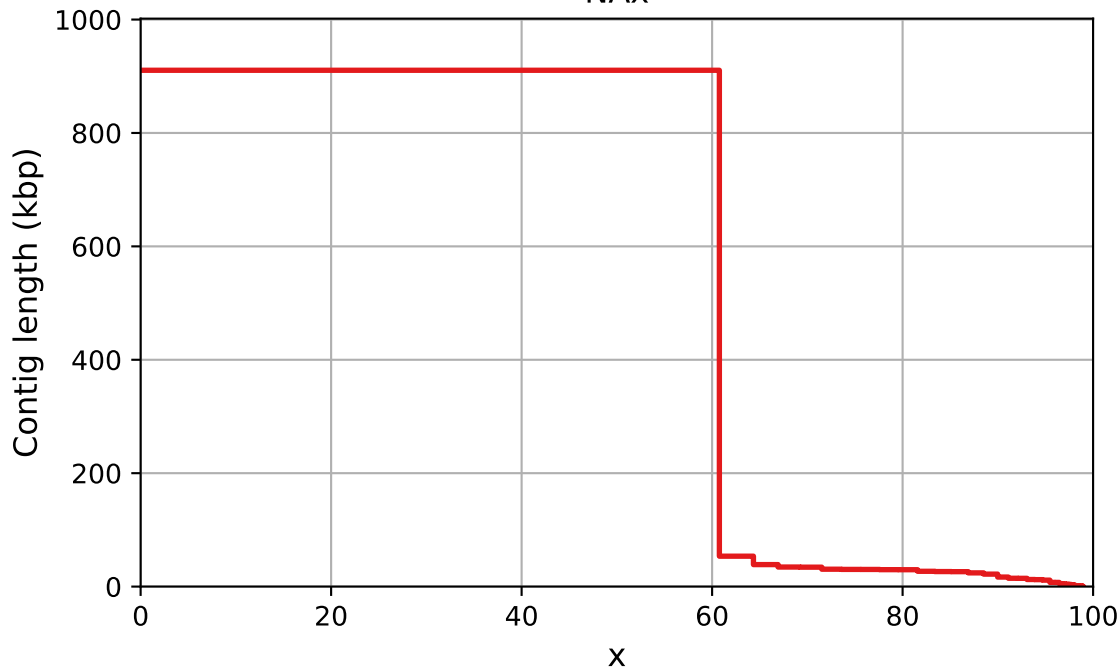# relocations    # translocations

FRCurve (misassemblies)
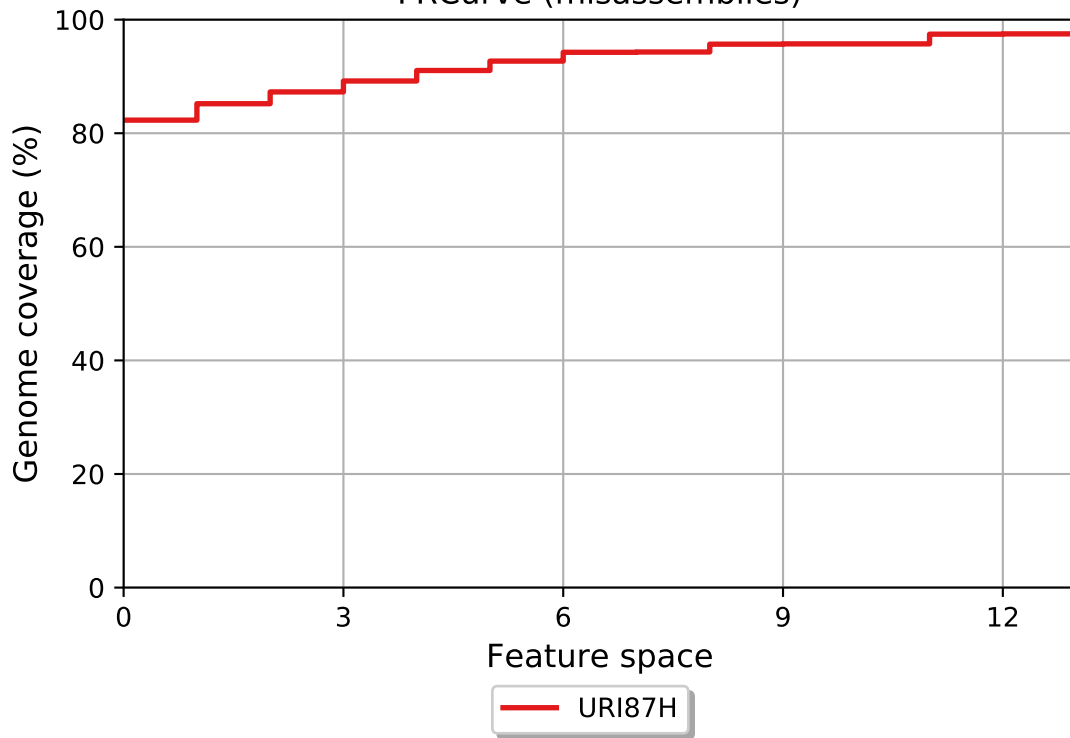
URI87H

Cumulative length (aligned contigs)

NAx

NGAx

Cumulative # complete genomic features
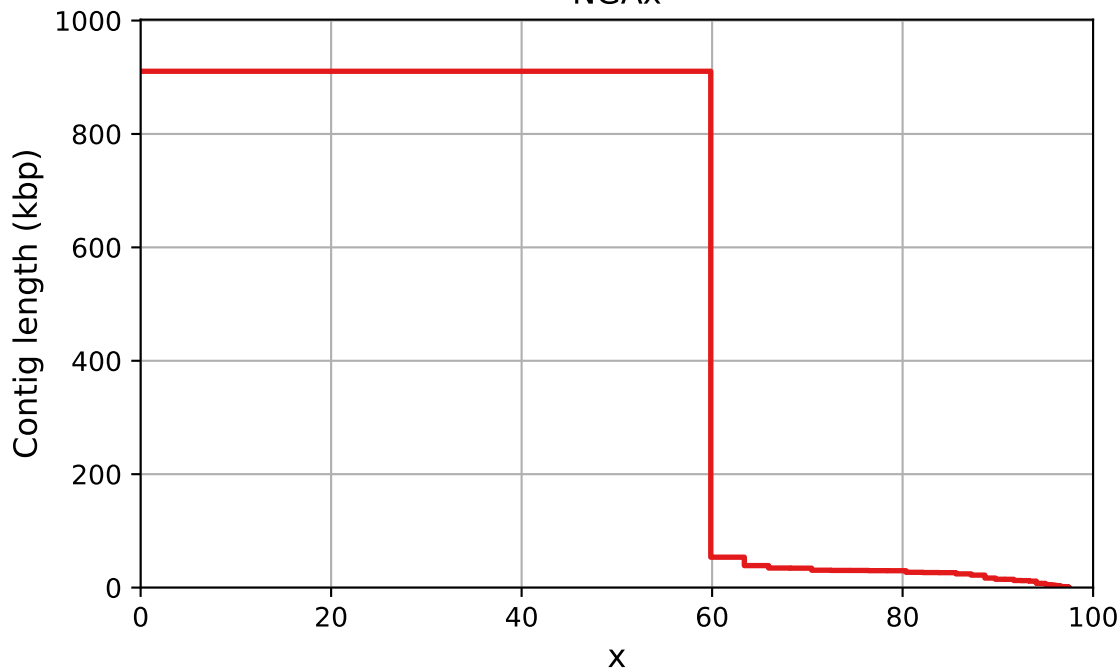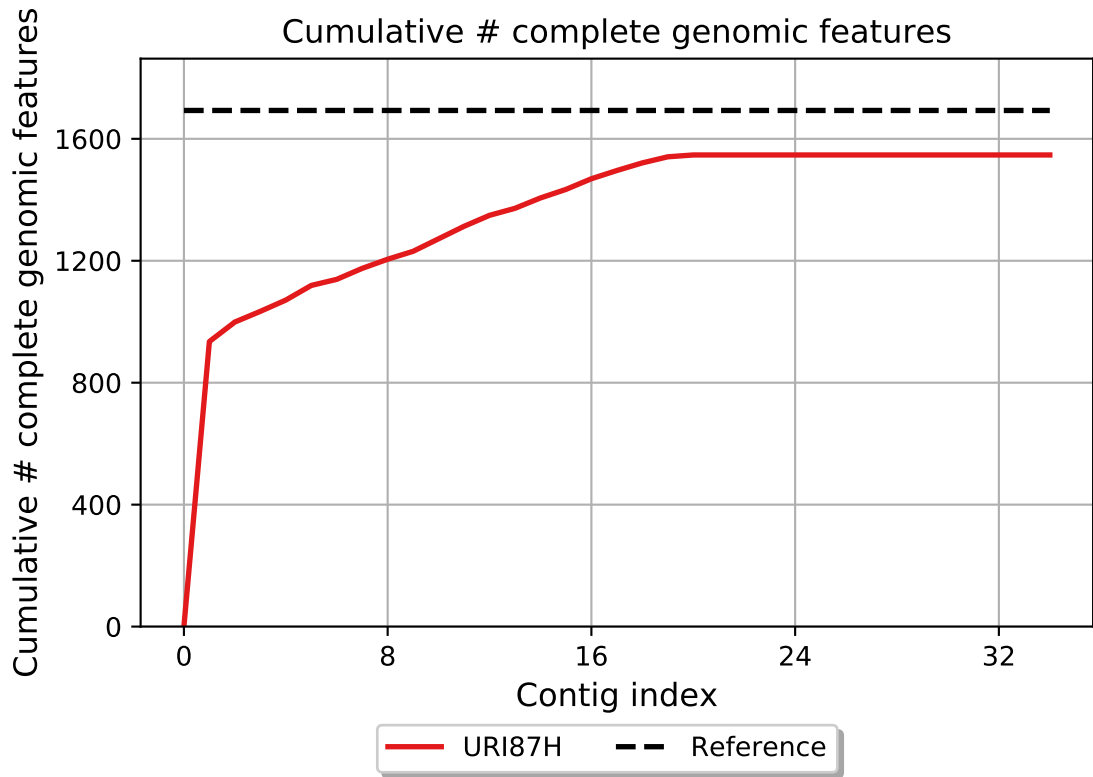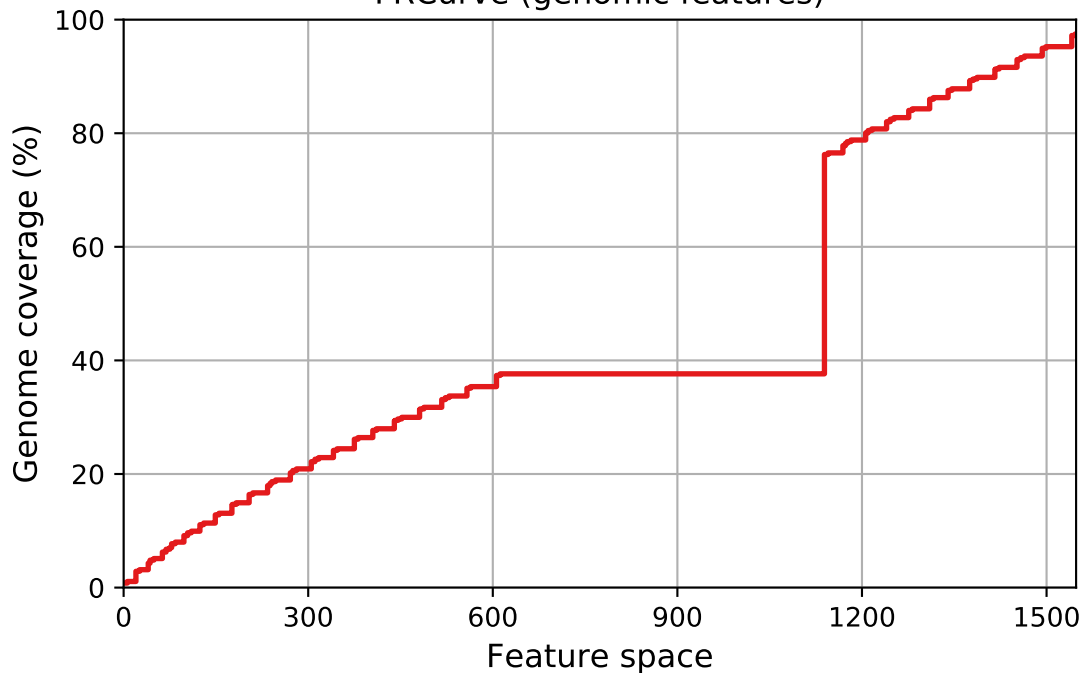
FRCurve (genomic features)