# Report

| | CFL_ICFL_COMB_R_10 |
|---|---|
| # contigs (>= 0 bp) | 15 |
| # contigs (>= 1000 bp) | 15 |
| # contigs (>= 5000 bp) | 15 |
| # contigs (>= 10000 bp) | 15 |
| # contigs (>= 25000 bp) | 15 |
| # contigs (>= 50000 bp) | 15 |
| Total length (>= 0 bp) | 4055481 |
| Total length (>= 1000 bp) | 4055481 |
| Total length (>= 5000 bp) | 4055481 |
| Total length (>= 10000 bp) | 4055481 |
| Total length (>= 25000 bp) | 4055481 |
| Total length (>= 50000 bp) | 4055481 |
| # contigs | 15 |
| Largest contig | 897427 |
| Total length | 4055481 |
| Reference length | 4686137 |
| GC (%) | 50.83 |
| Reference GC (%) | 50.78 |
| N50 | 370503 |
| NG50 | 307734 |
| N90 | 114752 |
| NG90 | - |
| auN | 462684.7 |
| auNG | 400417.0 |
| L50 | 4 |
| LG50 | 5 |
| L90 | 11 |
| LG90 | - |
| # misassemblies | 1 |
| # misassembled contigs | 1 |
| Misassembled contigs length | 641992 |
| # 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 (%) | 85.705 |
| Duplication ratio | 1.010 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 0.00 |
| # indels per 100 kbp | 0.00 |
| Largest alignment | 897427 |
| Total aligned length | 4055481 |
| NA50 | 370503 |
| NGA50 | 307734 |
| NA90 | 114752 |
| NGA90 | - |
| auNA | 414210.1 |
| auNGA | 358466.1 |
| LA50 | 4 |
| LGA50 | 5 |
| LA90 | 12 |
| LGA90 | - |

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).
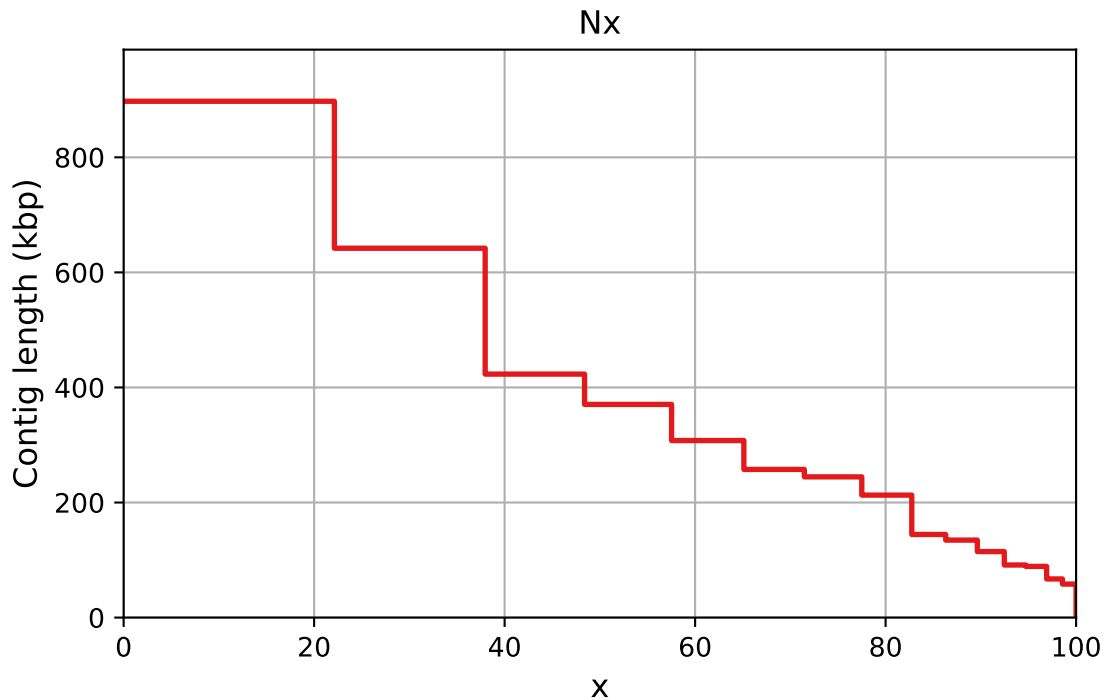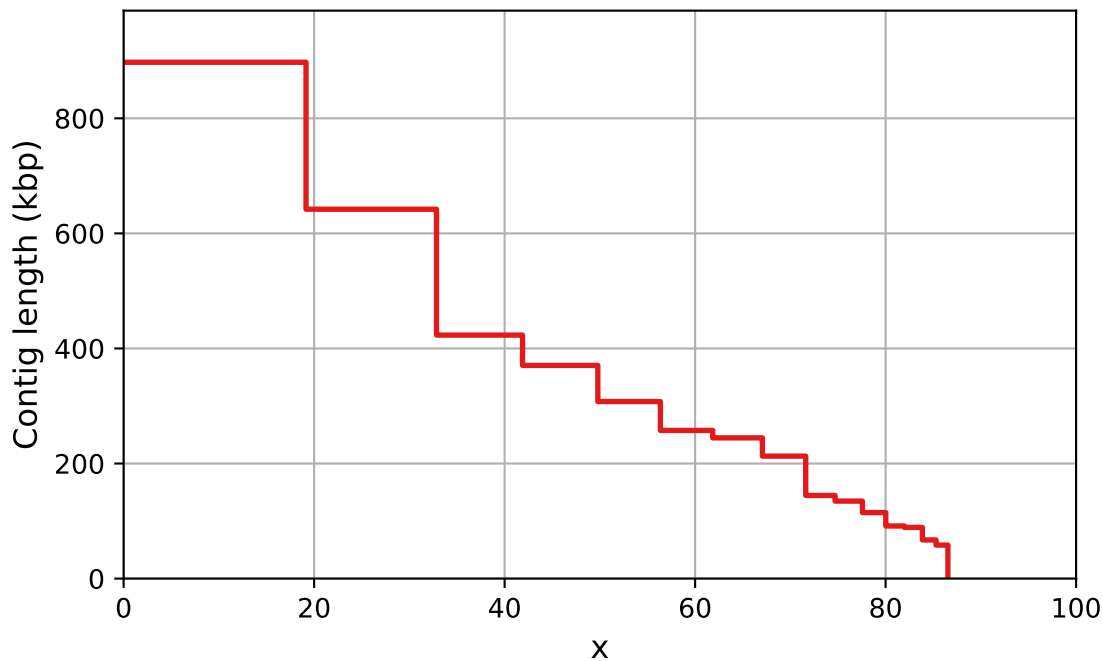
# Misassemblies report

|  | CFL_ICFL_COMB_R_10 |
| --- | --- |
| # misassemblies | 1 |
| # contig misassemblies | 1 |
| # c. relocations | 1 |
| # c. translocations | 0 |
| # c. inversions | 0 |
| # scaffold misassemblies | 0 |
| # s. relocations | 0 |
| # s. translocations | 0 |
| # s. inversions | 0 |
| # misassembled contigs | 1 |
| Misassembled contigs length | 641992 |
| # local misassemblies | 0 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 0 |
| # mismatches | 0 |
| # indels | 0 |
| # indels (<= 5 bp) | 0 |
| # indels (> 5 bp) | 0 |
| Indels length | 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).
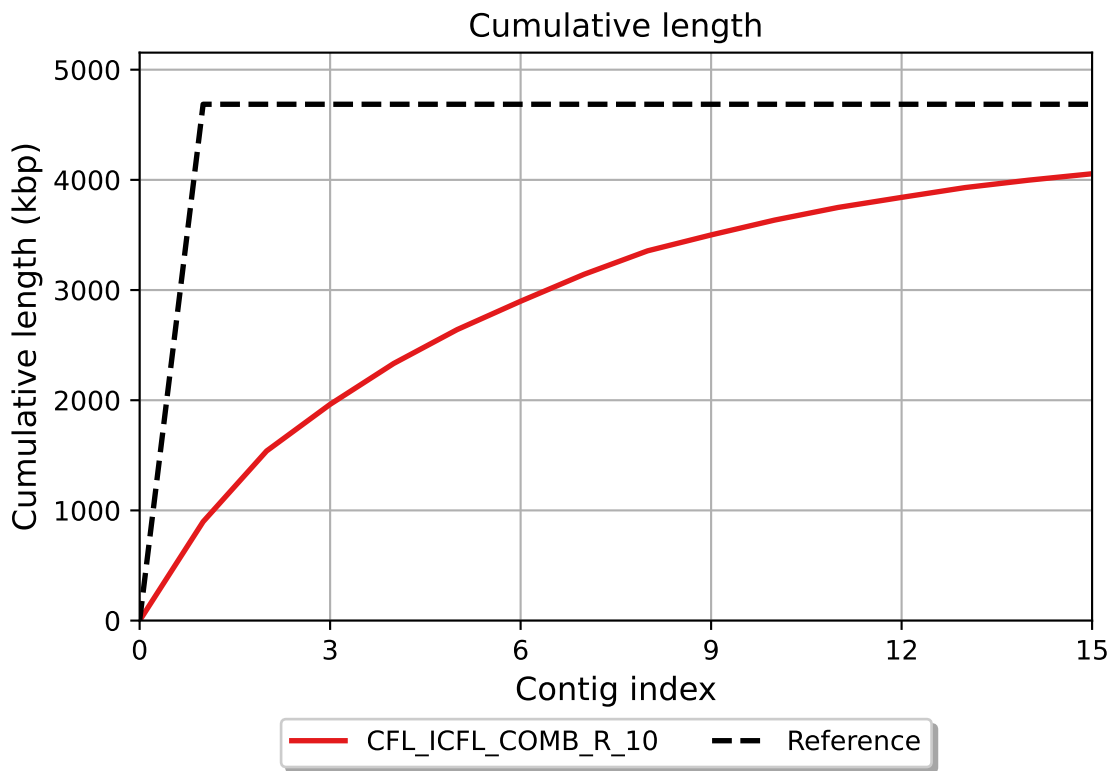
# Unaligned report

| | CFL_ICFL_COMB_R_10 |
|---|---|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 0 |
| Partially unaligned length | 0 |
| # 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).
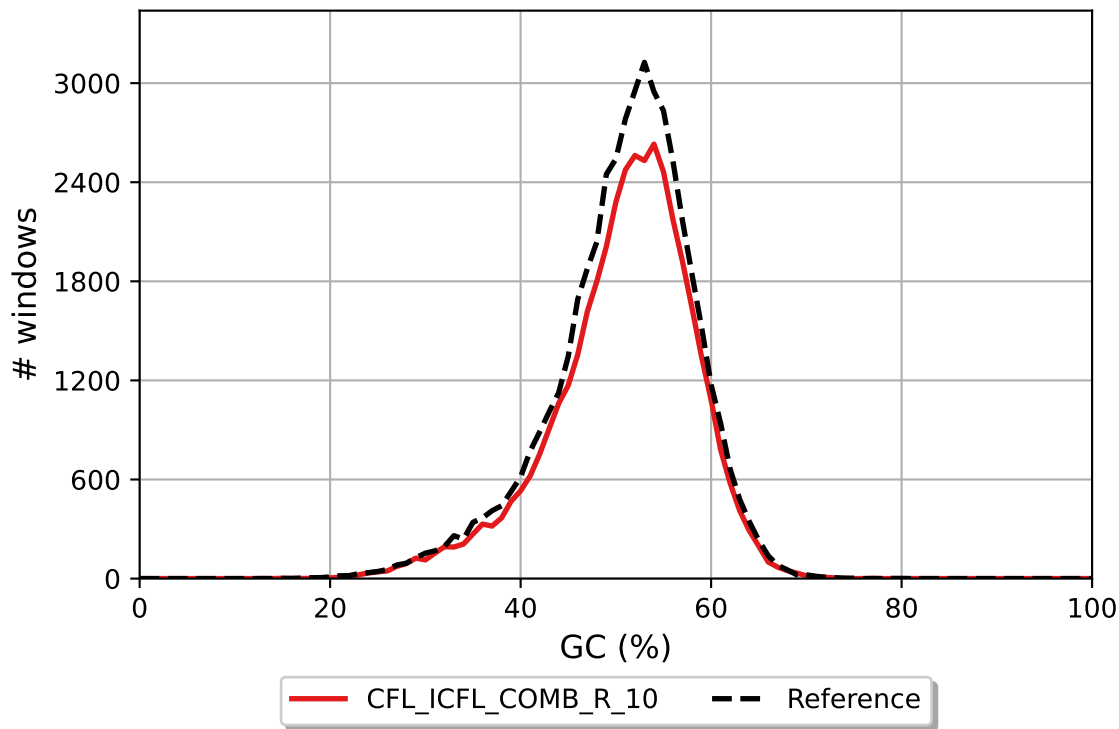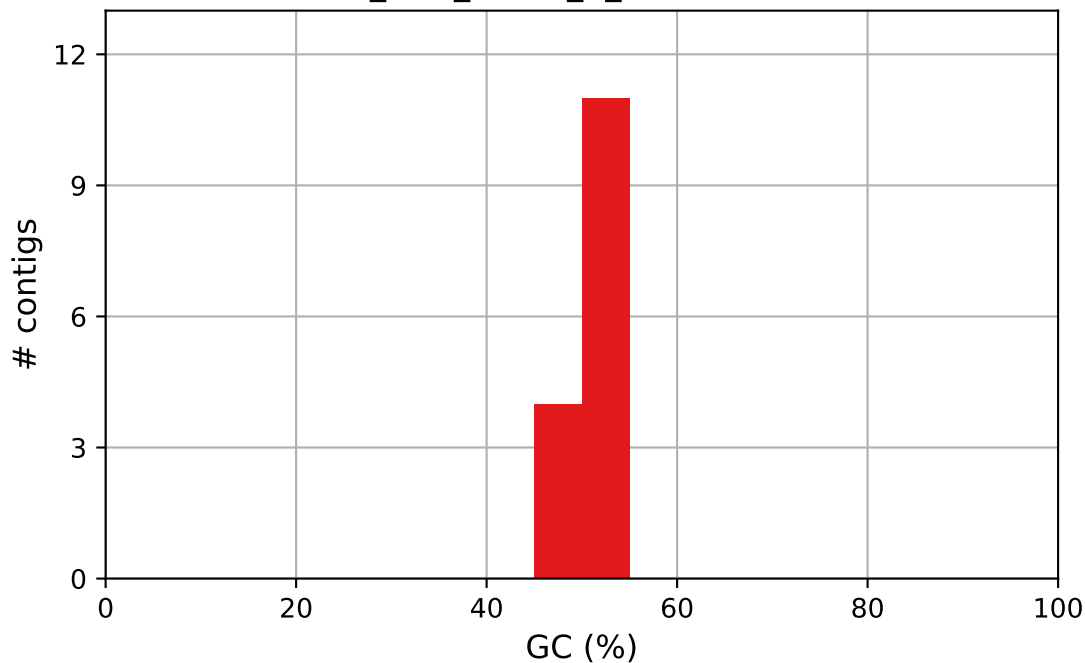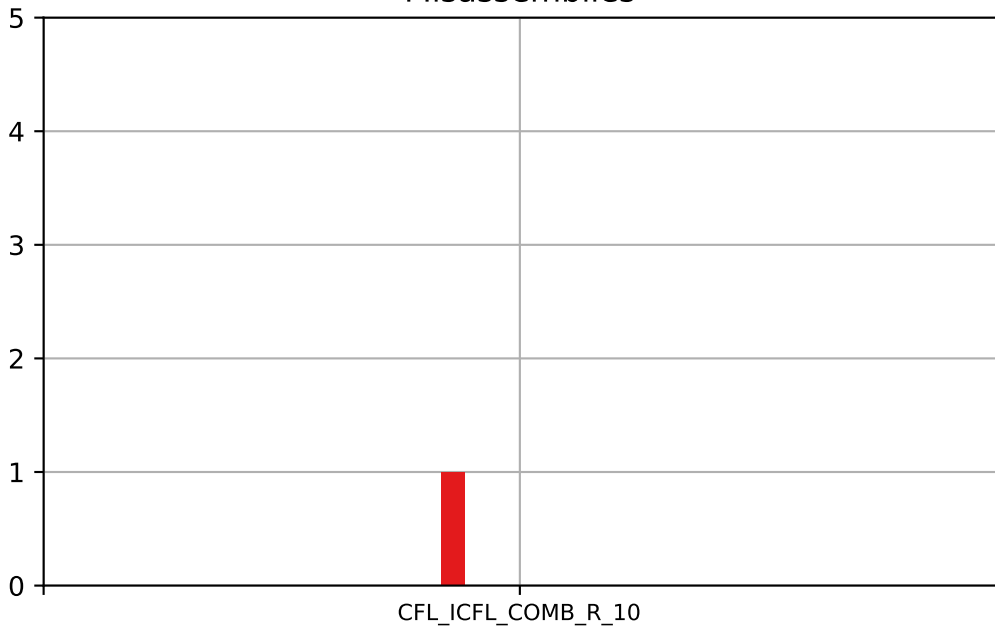
Nx

CFL_ICFL_COMB_R_10

NGx

Cumulative length

GC content

CFL_ICFL_COMB_R_10 GC content
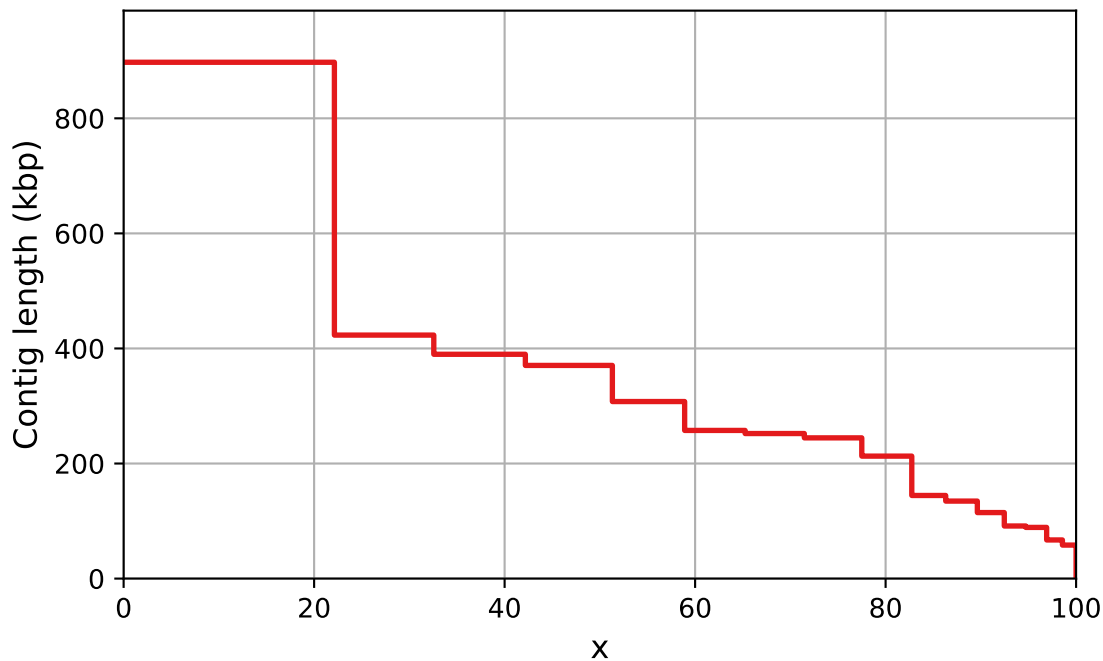
CFL_ICFL_COMB_R_10

Misassemblies

FRCurve (misassemblies)
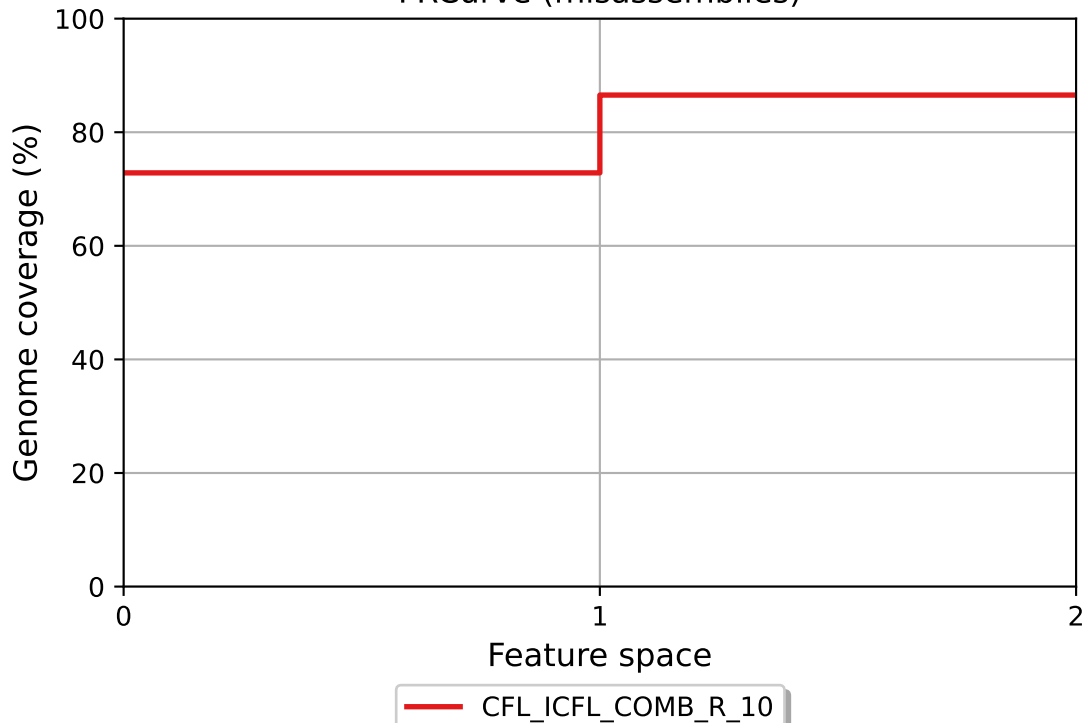
CFL_ICFL_COMB_R_10

Cumulative length (aligned contigs)

NAx

CFL_ICFL_COMB_R_10

NGAx