Report

	CFL_ICFL_R_35_COMB_50
# contigs (>= 0 bp)	5
# contigs (>= 1000 bp)	5
# contigs (>= 5000 bp)	5
# contigs (>= 10000 bp)	5
# contigs (>= 25000 bp)	5
# contigs (>= 50000 bp)	5
Total length (>= 0 bp)	4735982
Total length (>= 1000 bp)	4735982
Total length (>= 5000 bp)	4735982
Total length (>= 10000 bp)	4735982
Total length (>= 25000 bp)	4735982
Total length (>= 50000 bp)	4735982
# contigs	5
Largest contig	3944785
Total length	4735982
Reference length	4686137
GC (%)	50.75
Reference GC (%)	50.78
N50	3944785
NG50	3944785
N90	513470
NG90	513470
auN	3347216.0
auNG	3382819.3
L50	1
LG50	1
L90	2
LG90	2
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	125872
# 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 (%)	98.492
Duplication ratio	1.026
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	3944785
Total aligned length	4735982
NA50	3944785
NGA50	3944785
NA90	513470
NGA90	513470
auNA	3347054.6
auNGA	3382656.2
LA50	1
LGA50	1
LA90	2
LGA90	2

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).
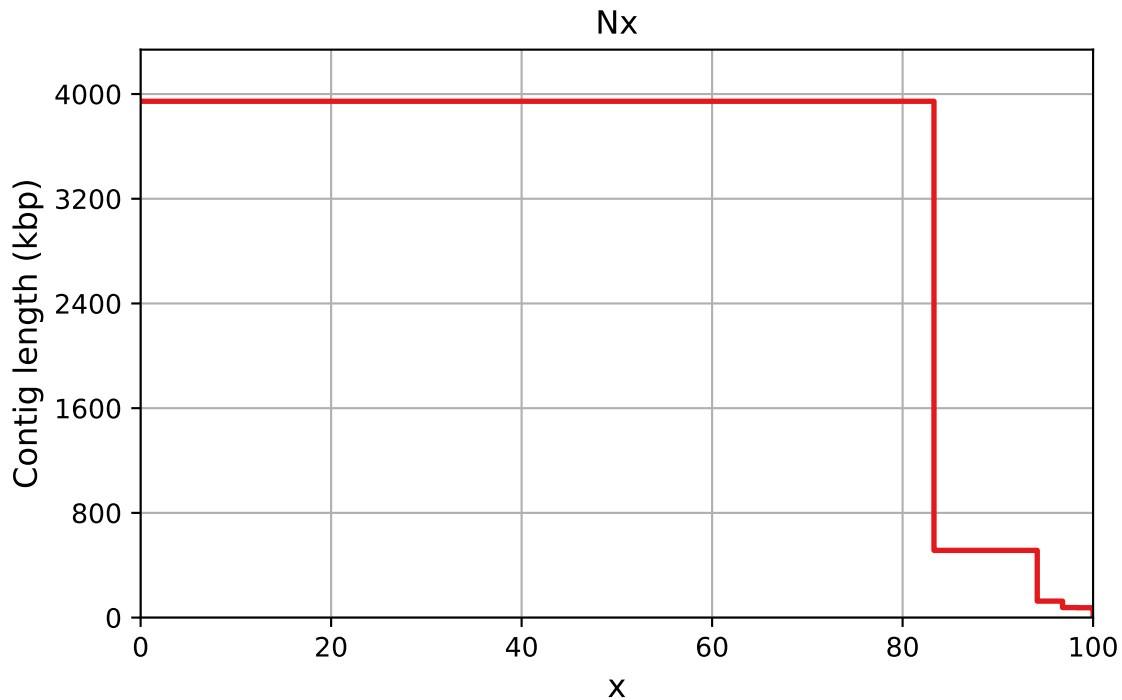
Misassemblies report
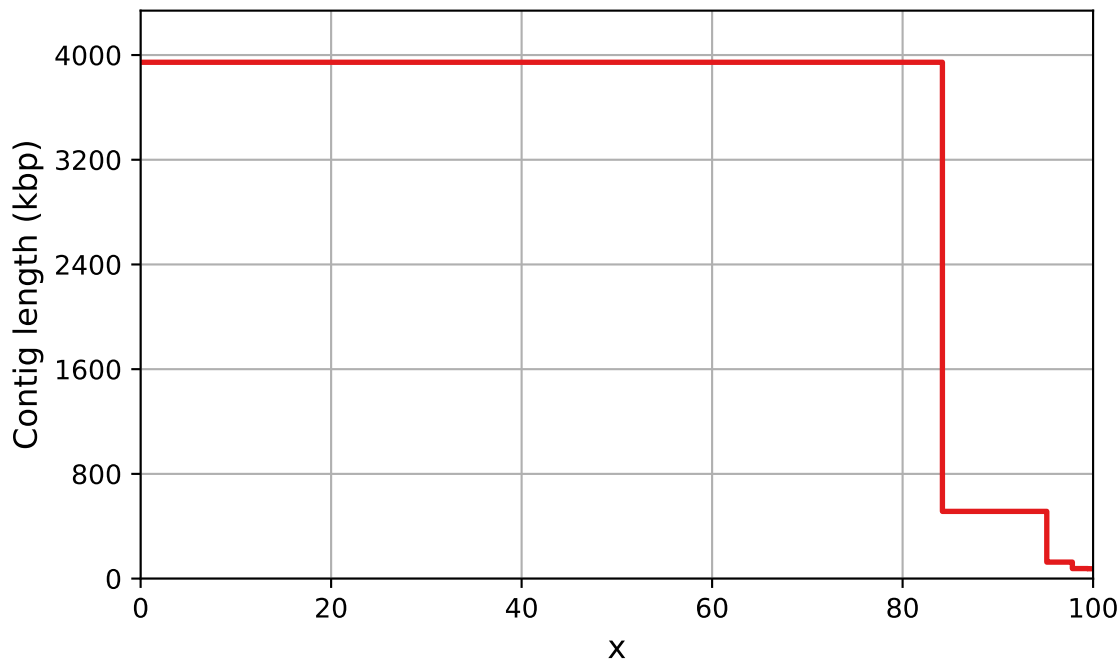
	CFL_ICFL_R_35_COMB_50
# misassemblies	1
# contig misassemblies	1
# c. relocations	1
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	125872
# local misassemblies	0
# scaffold 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).
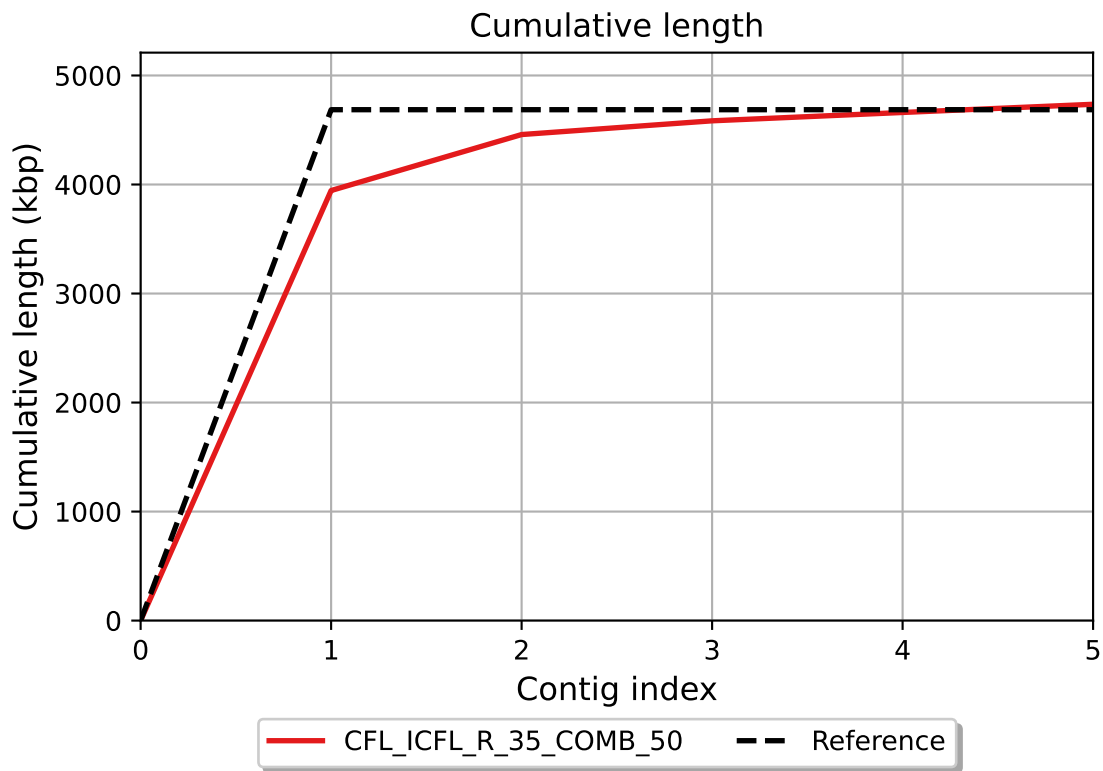
Unaligned report

	CFL_ICFL_R_35_COMB_50
# 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).
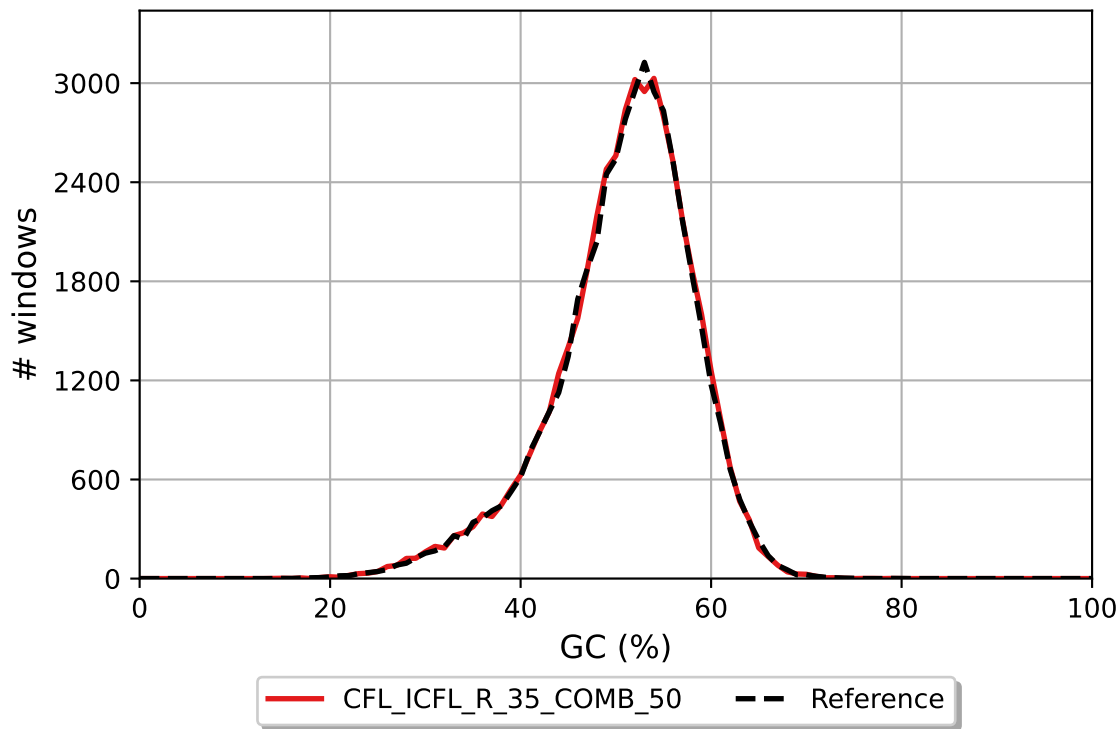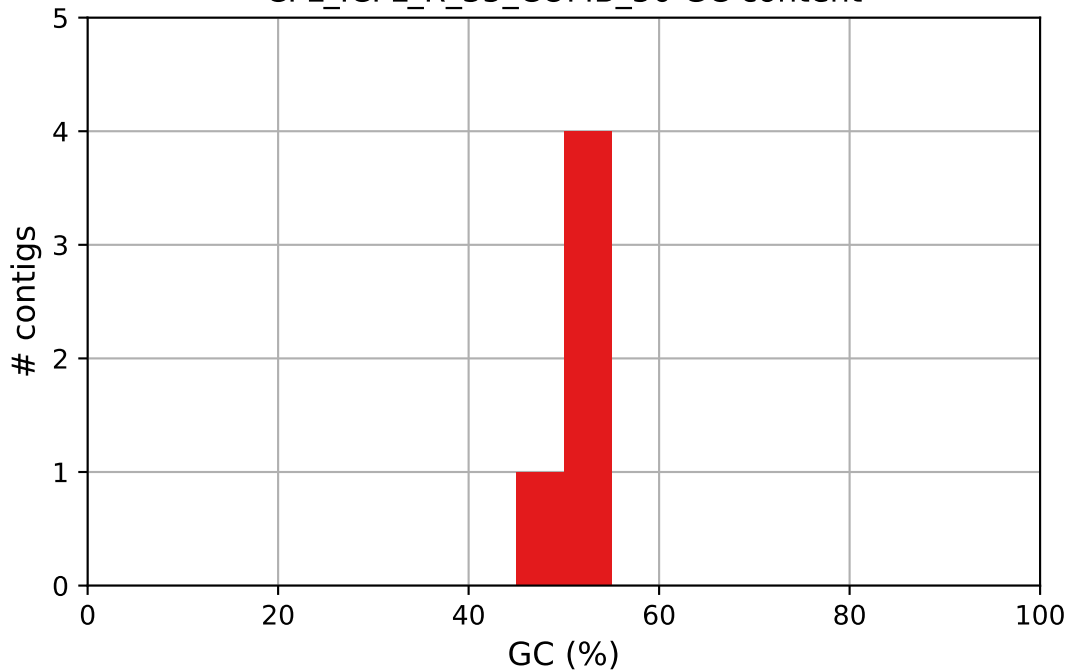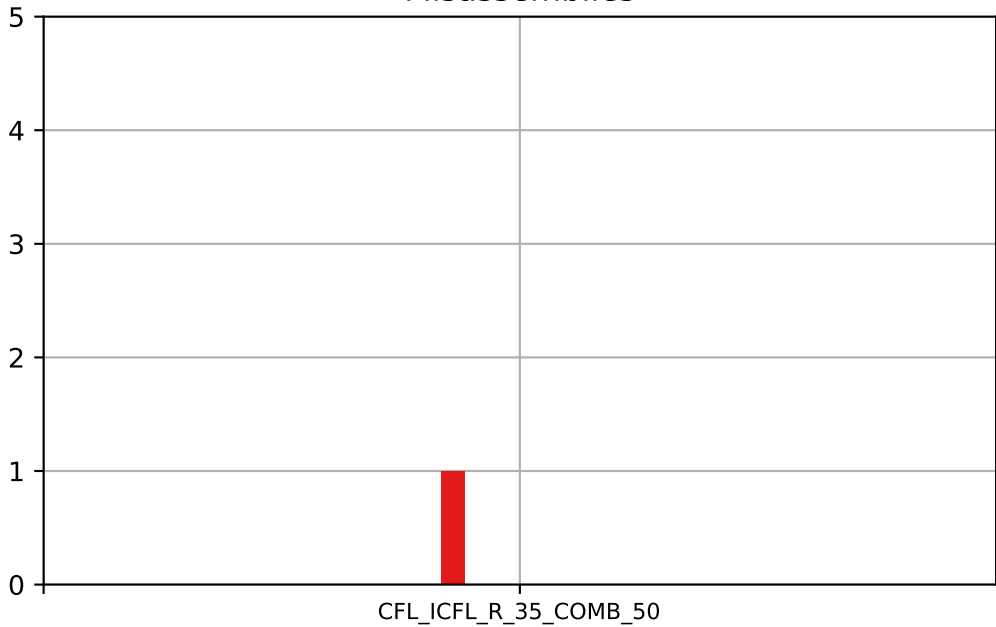
Nx

CFL_ICFL_R_35_COMB_50

NGx

CFL_ICFL_R_35_COMB_50

Cumulative length

GC content

CFL_ICFL_R_35_COMB_50 GC content

Misassemblies

CFL_ICFL_R_35_COMB_50

relocations

FRCurve (misassemblies)

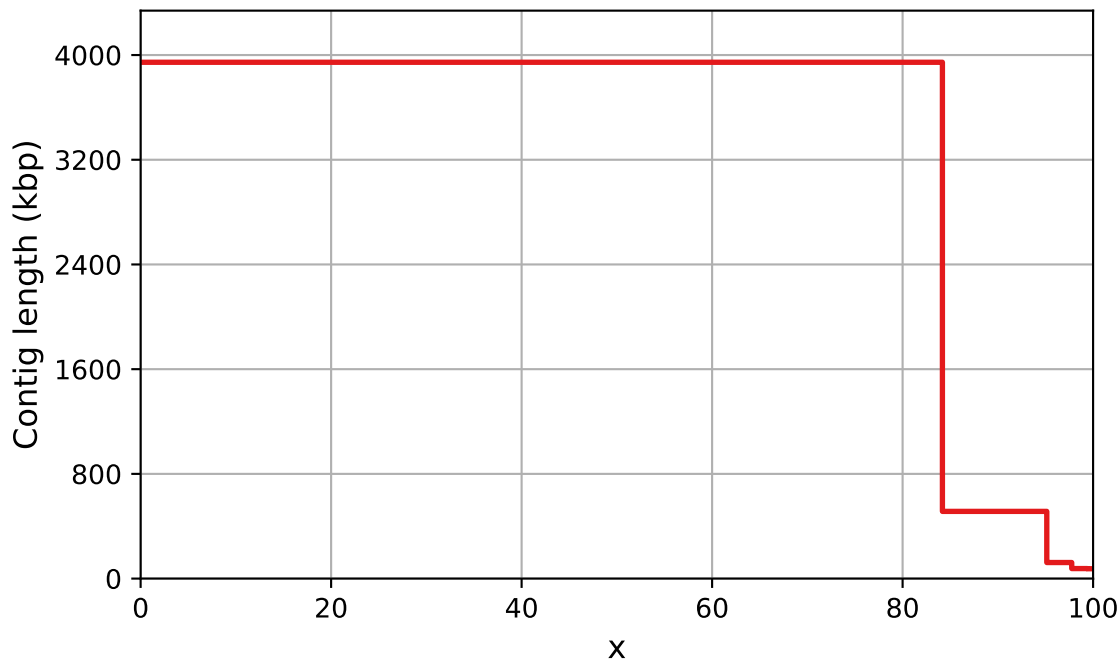CFL_ICFL_R_35_COMB_50

Cumulative length (aligned contigs)
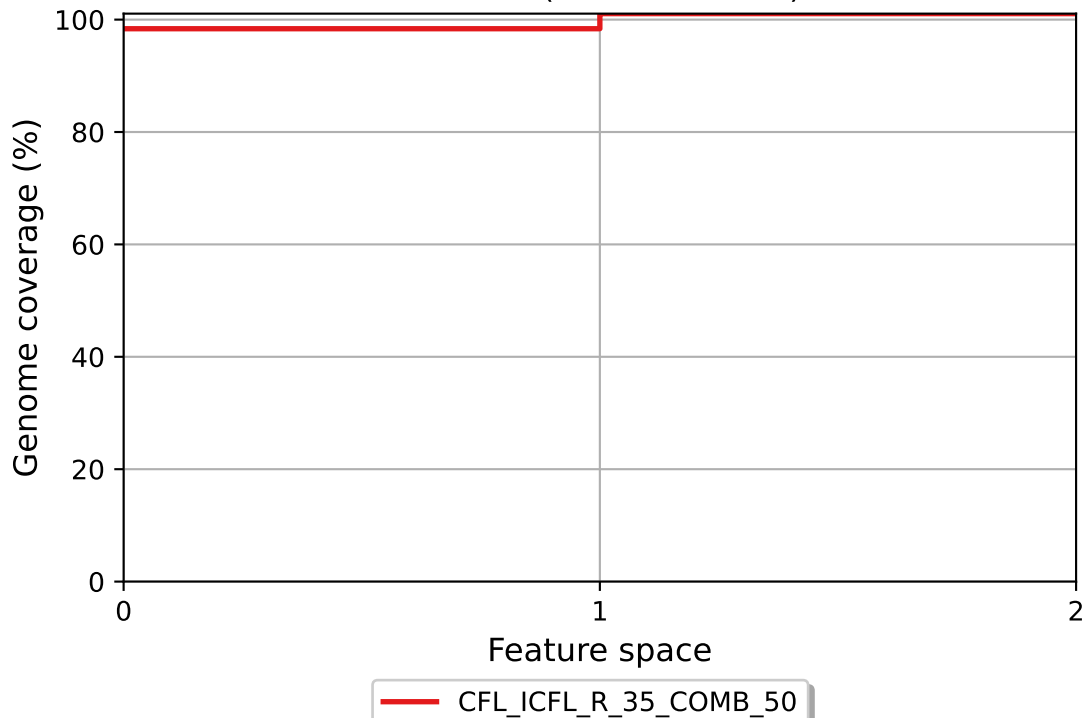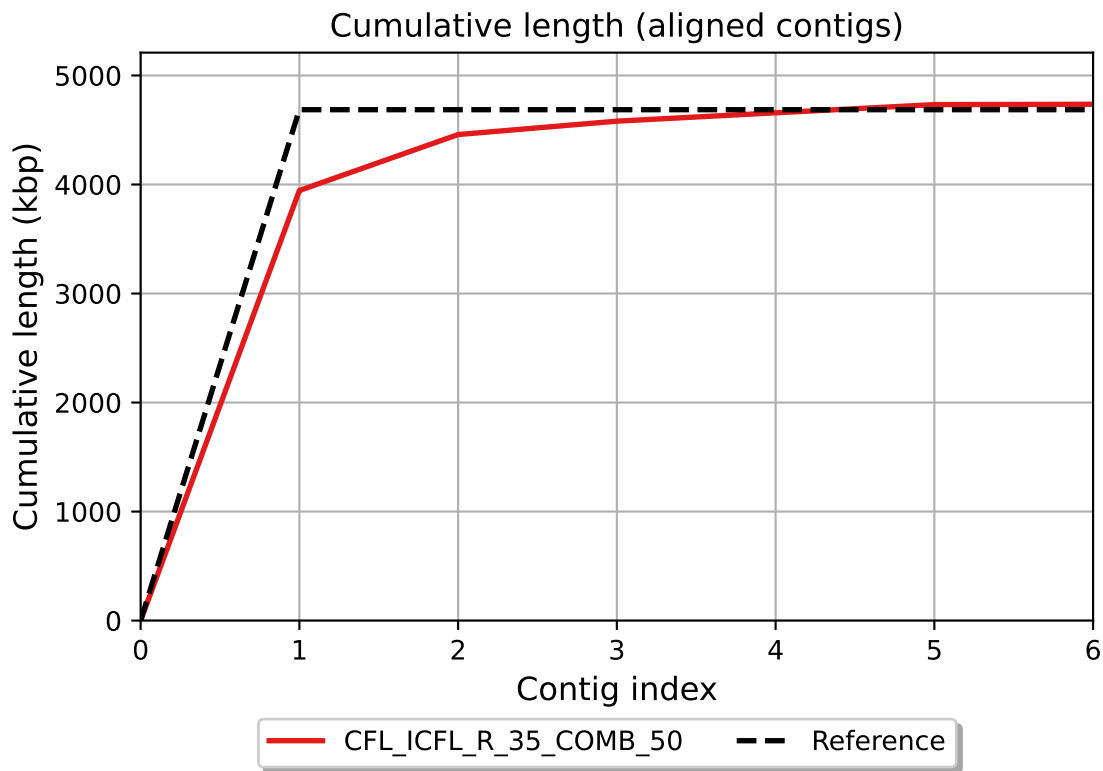
NAx
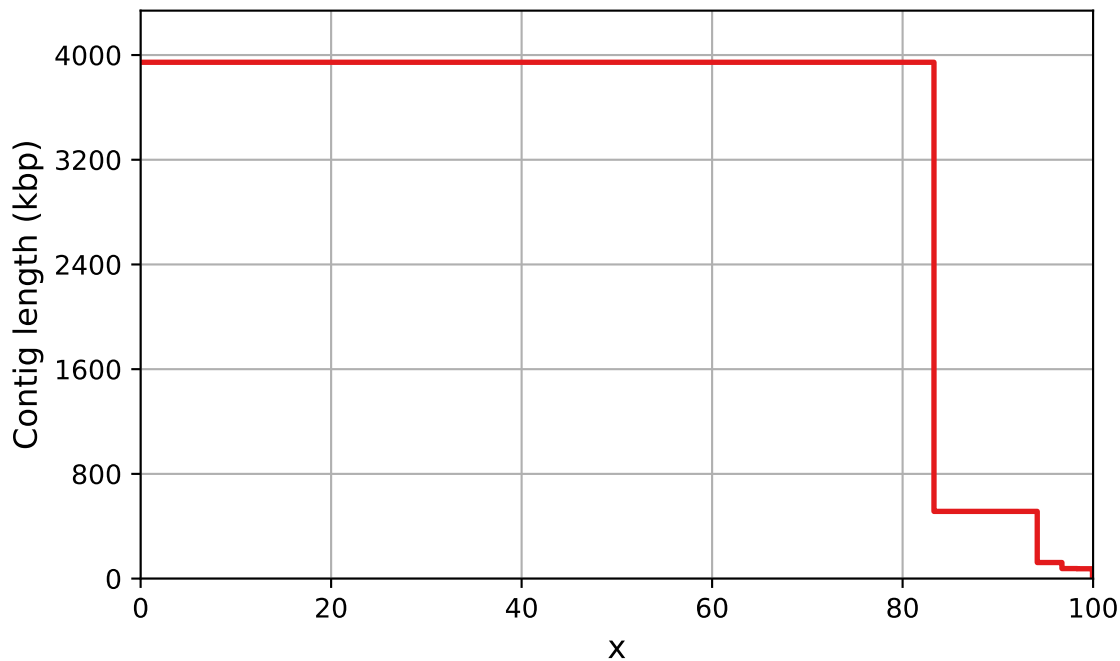
CFL_ICFL_R_35_COMB_50

NGAx

CFL_ICFL_R_35_COMB_50