

Report

	CFL_ICFL_10
# contigs (>= 0 bp)	14
# contigs (>= 1000 bp)	14
# contigs (>= 5000 bp)	14
# contigs (>= 10000 bp)	14
# contigs (>= 25000 bp)	14
# contigs (>= 50000 bp)	14
Total length (>= 0 bp)	1481615
Total length (>= 1000 bp)	1481615
Total length (>= 5000 bp)	1481615
Total length (>= 10000 bp)	1481615
Total length (>= 25000 bp)	1481615
Total length (>= 50000 bp)	1481615
# contigs	14
Largest contig	155632
Total length	1481615
Reference length	4686137
GC (%)	50.49
Reference GC (%)	50.78
N50	116803
NG50	-
N90	75314
NG90	-
auN	114568.8
auNG	36223.2
L50	6
LG50	-
L90	12
LG90	-
# 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 (%)	29.850
Duplication ratio	1.059
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	155632
Total aligned length	1481615
NA50	116803
NGA50	-
NA90	75314
NGA90	-
auNA	114568.8
auNGA	36223.2
LA50	6
LGA50	-
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

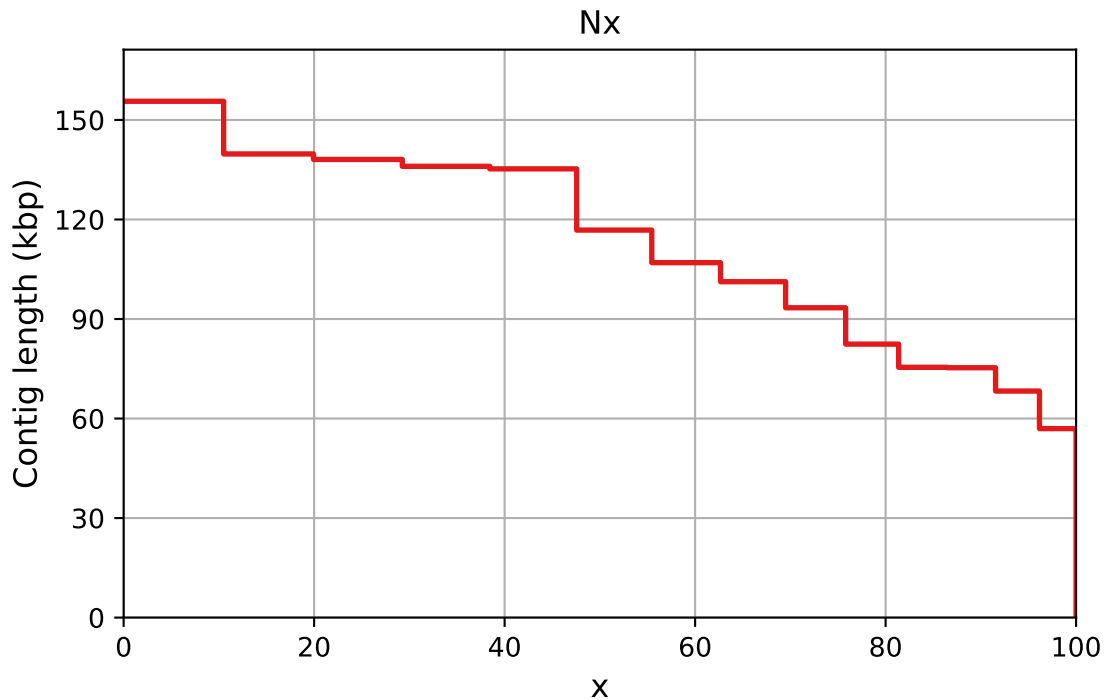
	CFL_ICFL_10
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	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

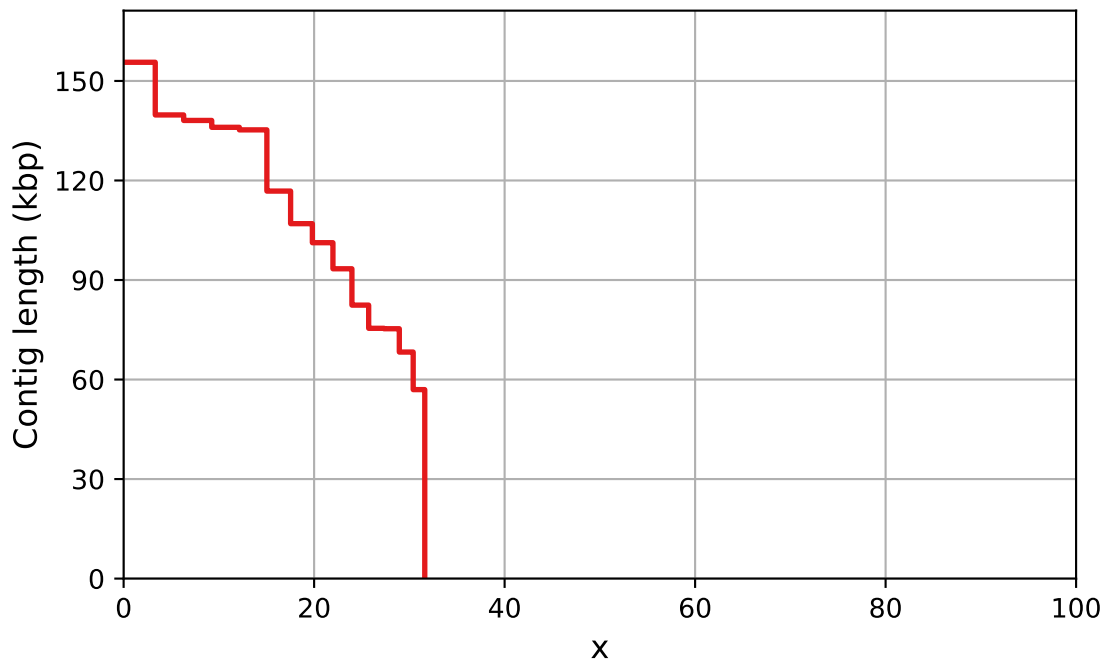
	CFL_ICFL_10
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).

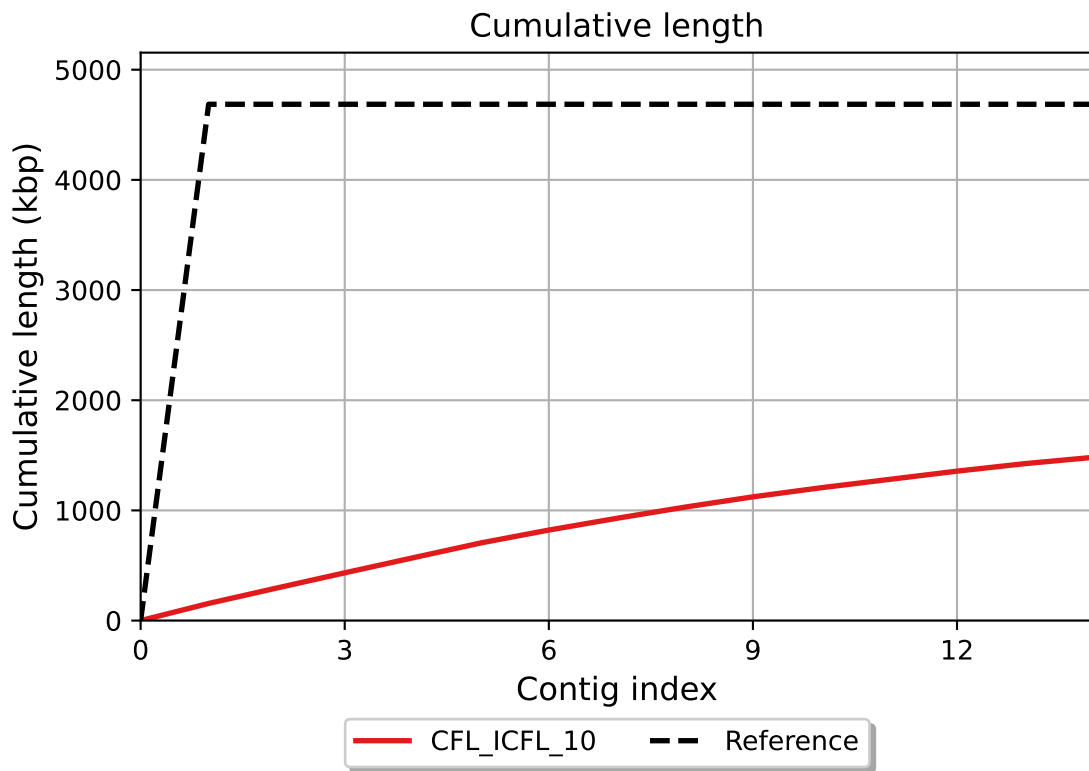


CFL_ICFL_10

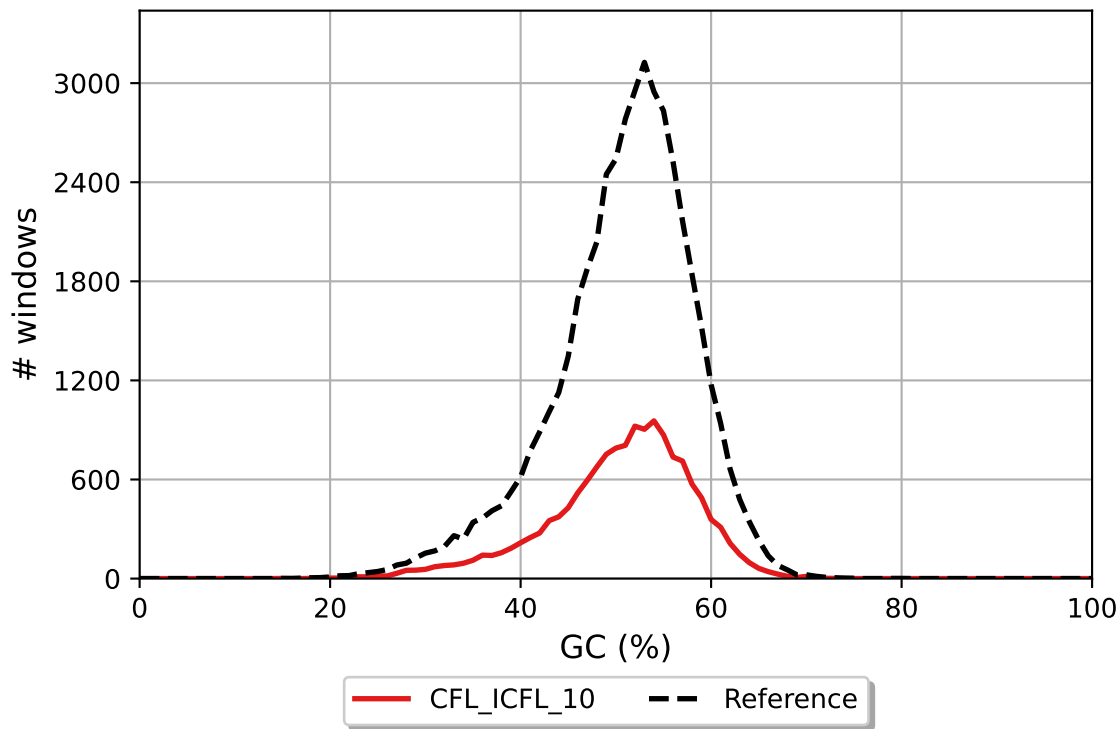
NGx



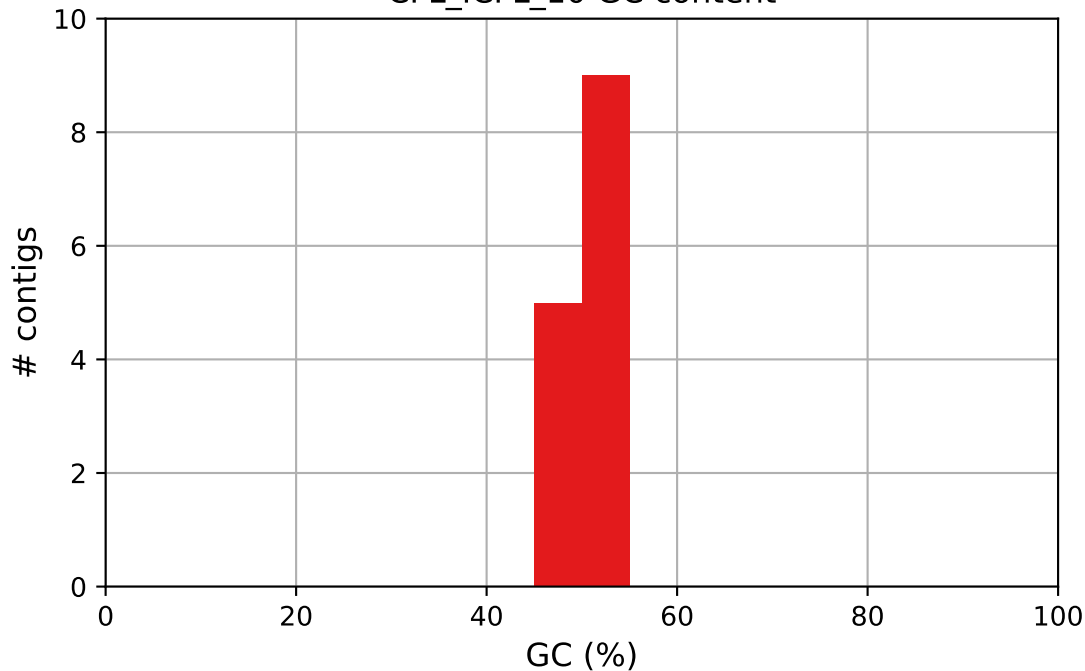
— CFL_ICFL_10



GC content

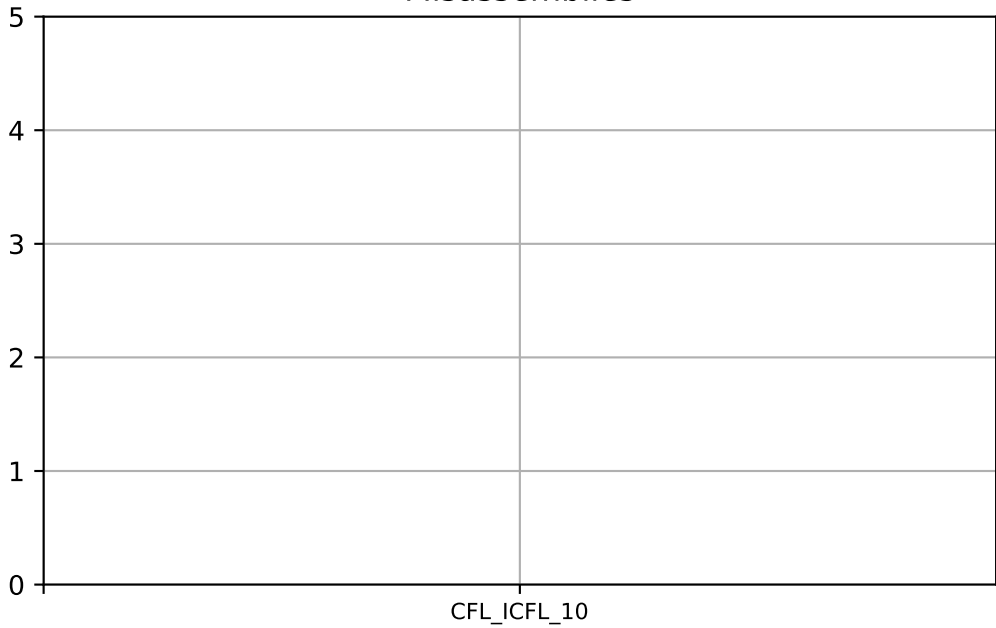


CFL_ICFL_10 GC content

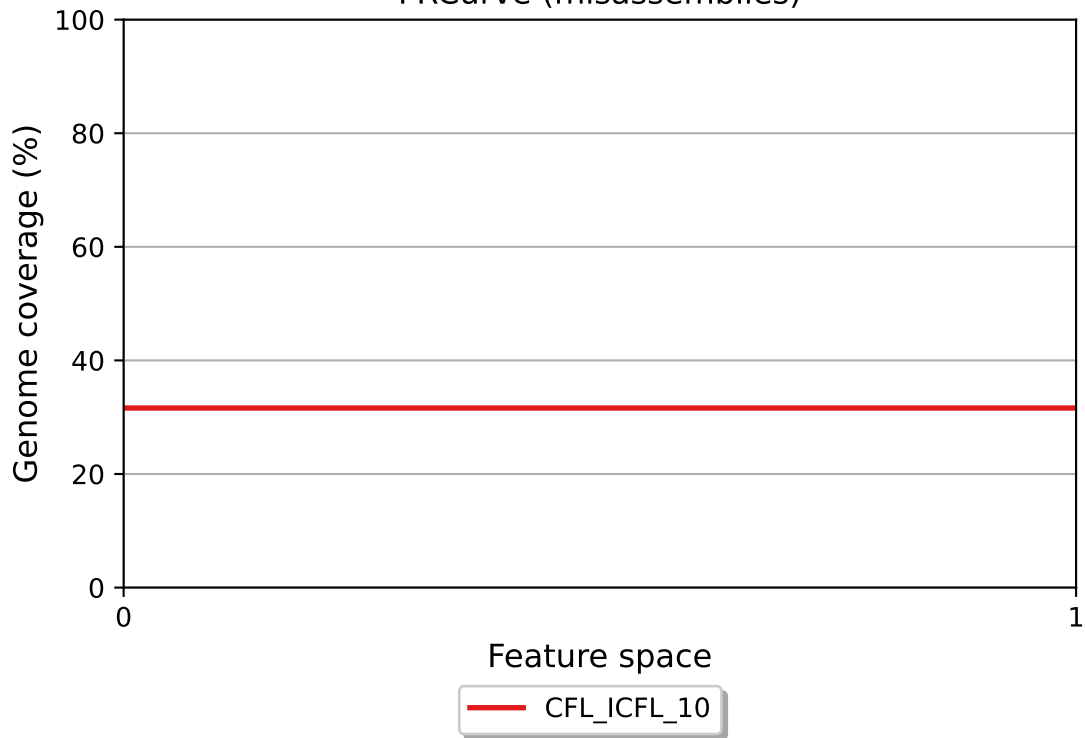


CFL_ICFL_10

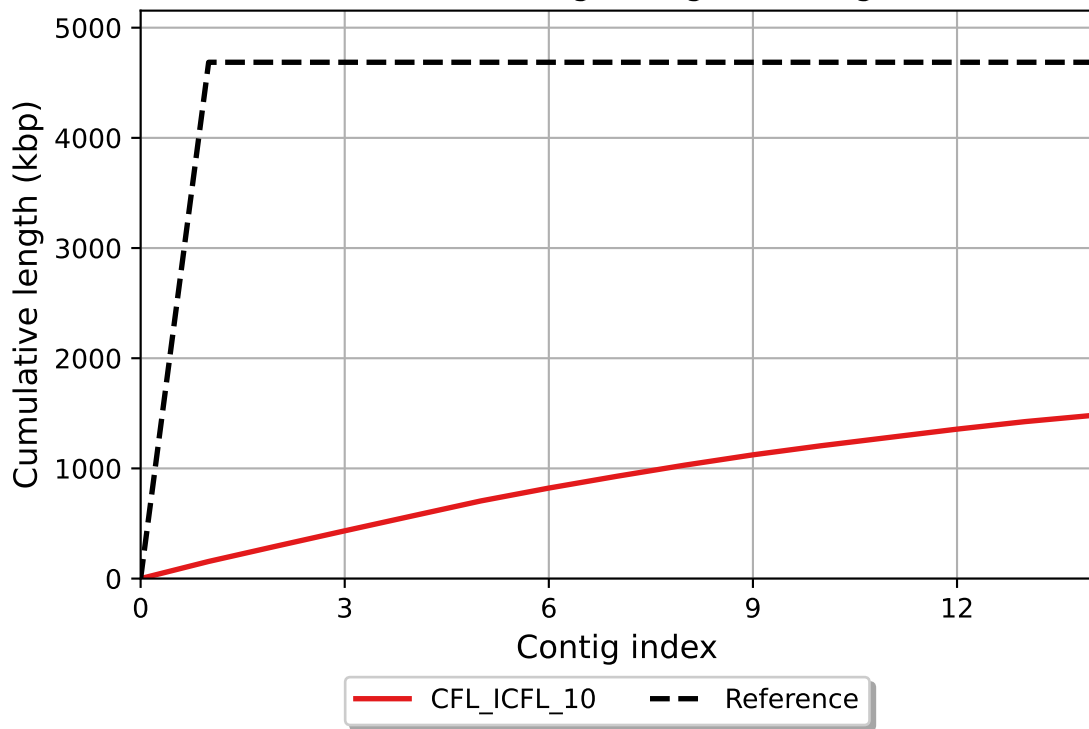
Misassemblies



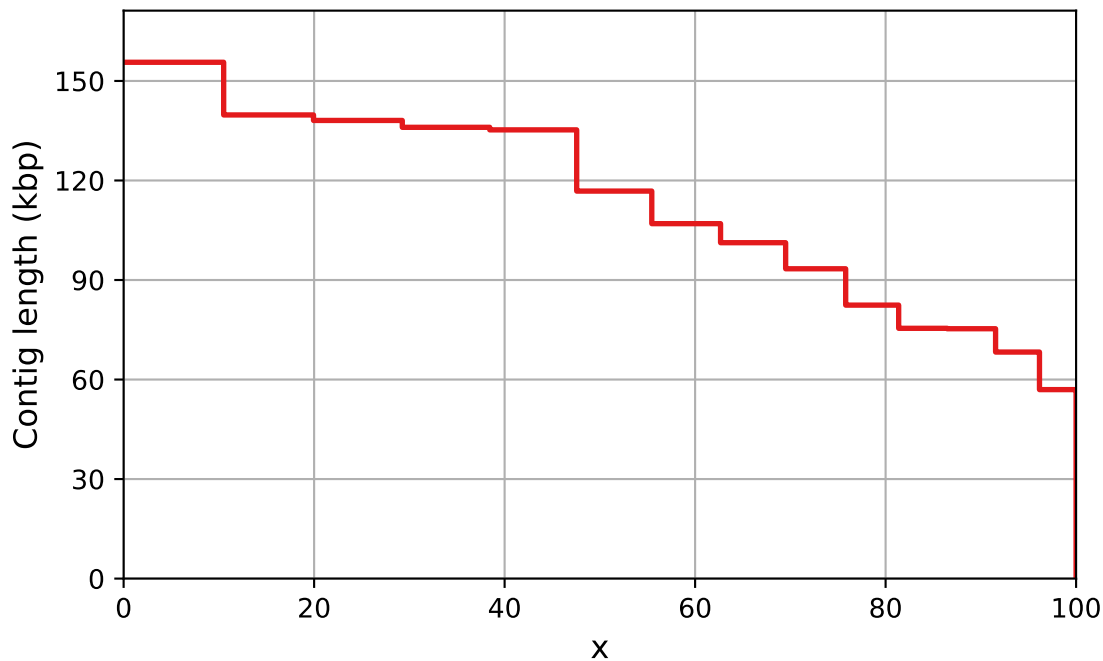
FRCurve (misassemblies)



Cumulative length (aligned contigs)

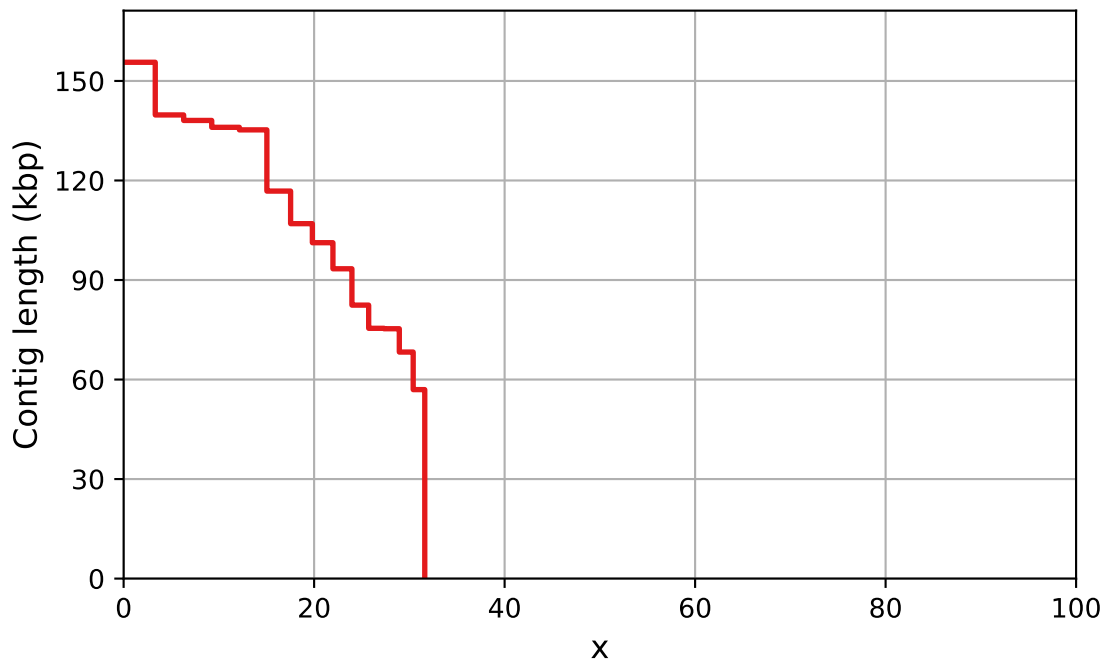


NAx



CFL_ICFL_10

NGAx



— CFL_ICFL_10