

Report

	CFL_ICFL_R_35_50
# contigs (>= 0 bp)	3
# contigs (>= 1000 bp)	3
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	3
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	4647429
Total length (>= 1000 bp)	4647429
Total length (>= 5000 bp)	4647429
Total length (>= 10000 bp)	4647429
Total length (>= 25000 bp)	4647429
Total length (>= 50000 bp)	4647429
# contigs	3
Largest contig	3981970
Total length	4647429
Reference length	4686137
GC (%)	50.75
Reference GC (%)	50.78
N50	3981970
NG50	3981970
N90	513470
NG90	513470
auN	3473498.4
auNG	3444806.9
L50	1
LG50	1
L90	2
LG90	2
# misassemblies	2
# misassembled contigs	1
Misassembled contigs length	151989
# 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	0.982
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	3981970
Total aligned length	4532966
NA50	3981970
NGA50	3981970
NA90	513470
NGA90	513470
auNA	3474584.9
auNGA	3445884.4
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

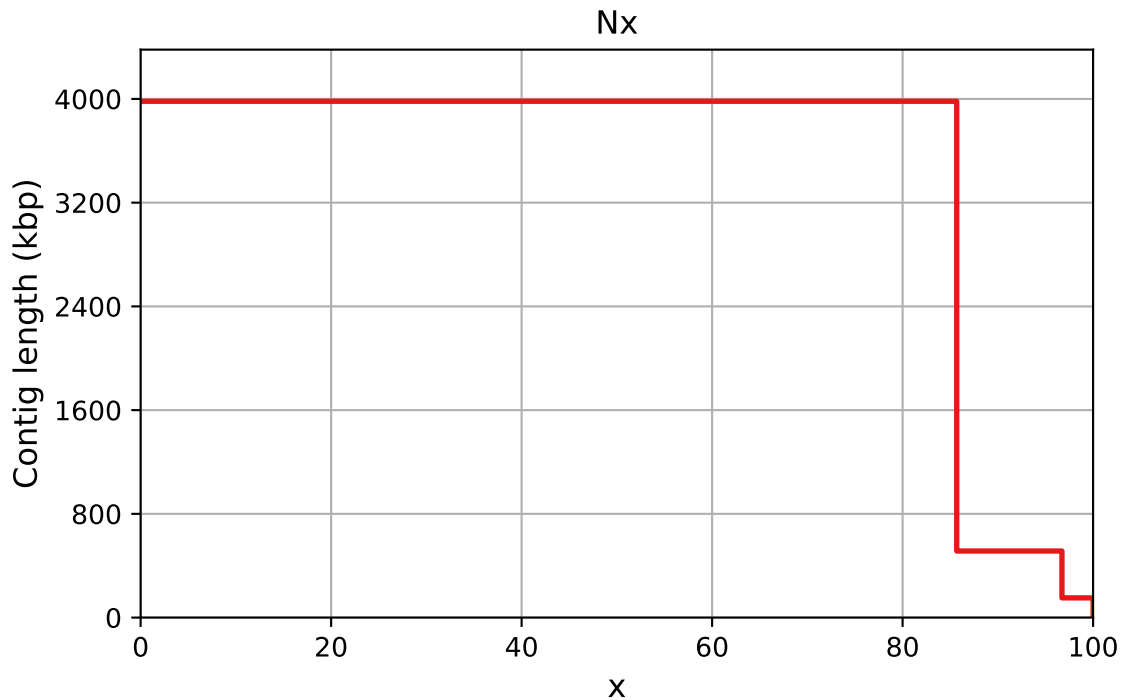
	CFL_ICFL_R_35_50
# misassemblies	2
# contig misassemblies	2
# c. relocations	2
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	151989
# local misassemblies	0
# scaffold gap 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

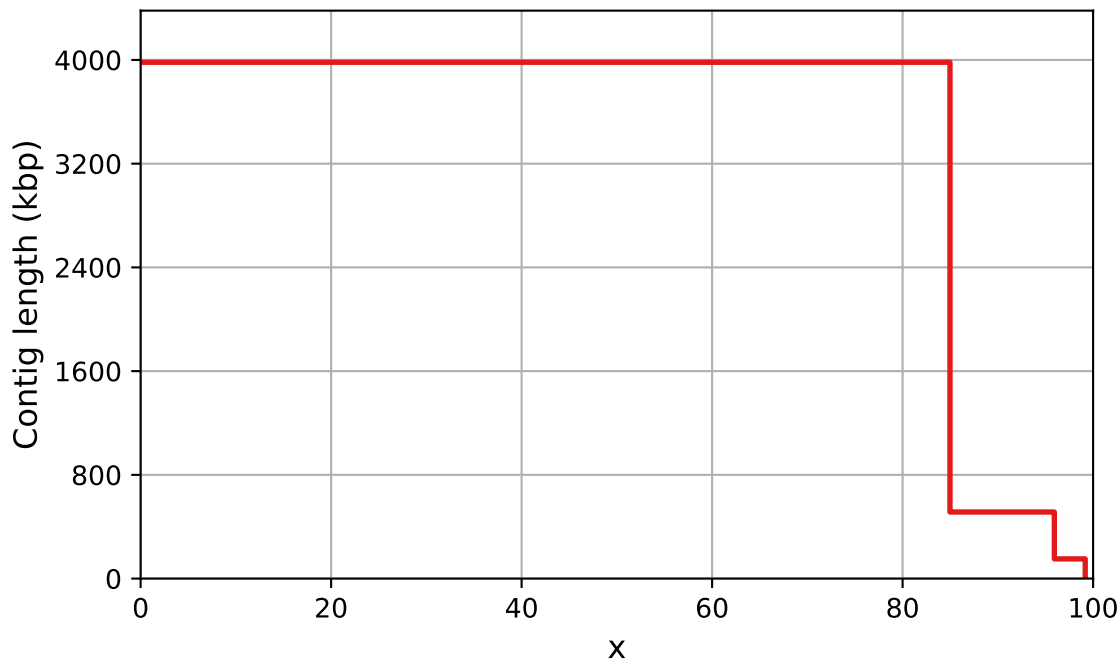
	CFL_ICFL_R_35_50
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).

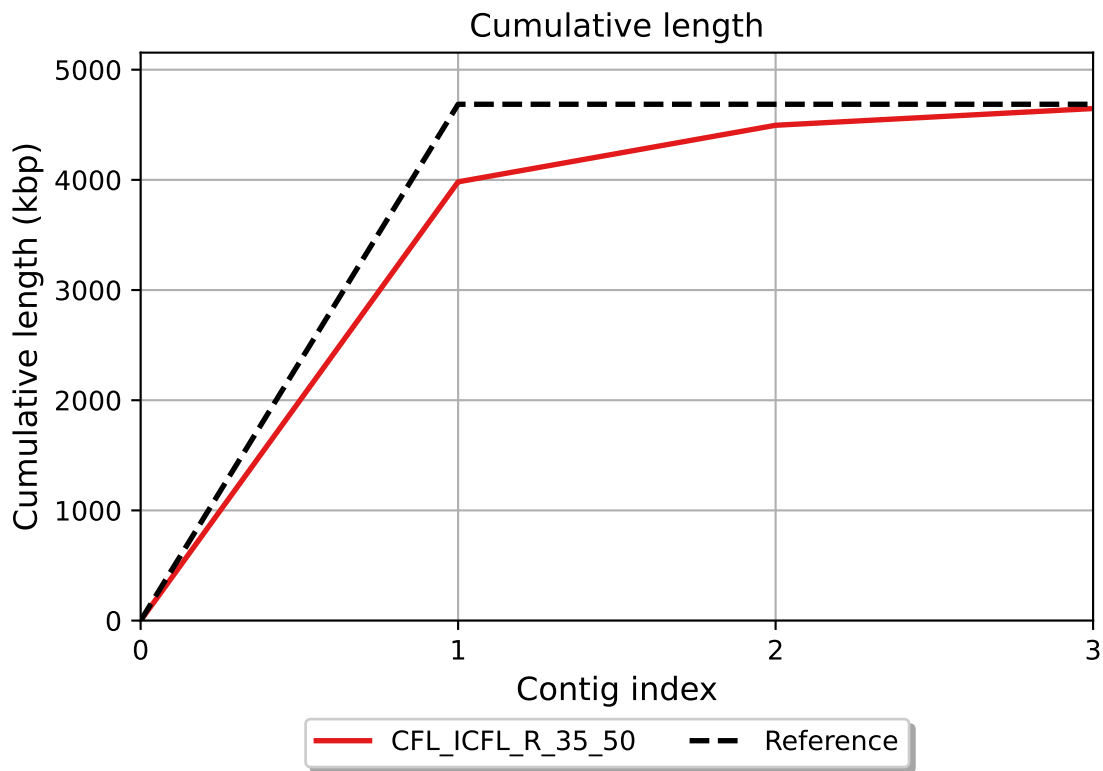


CFL_ICFL_R_35_50

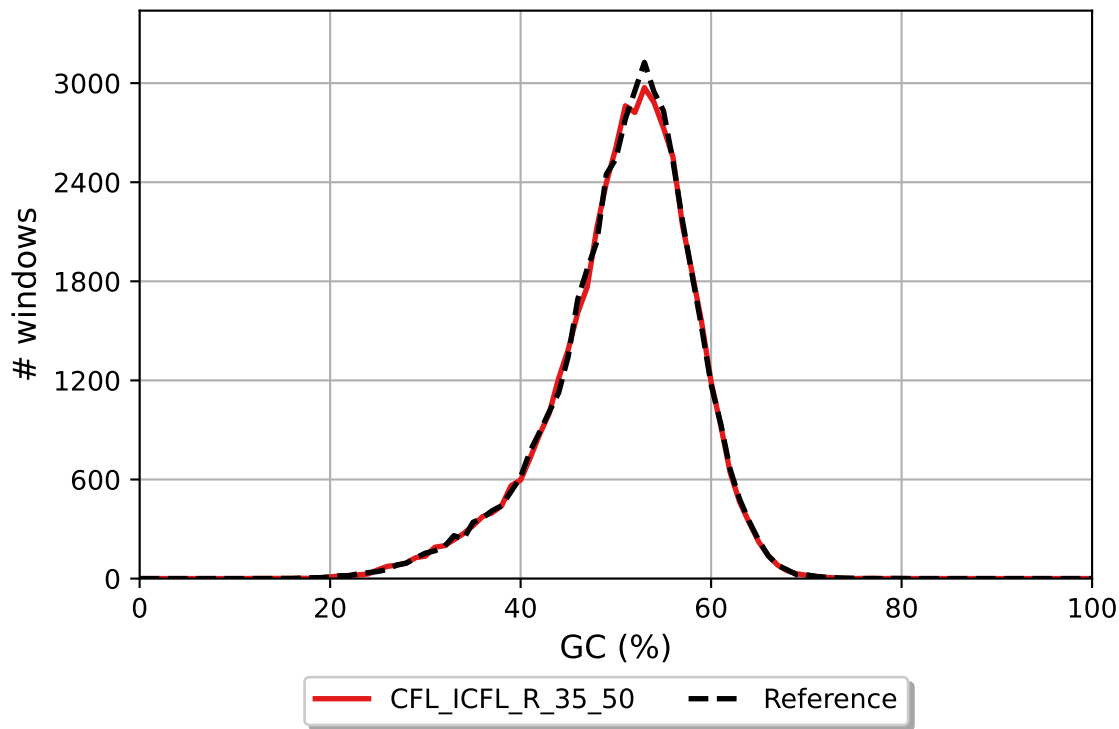
NGx



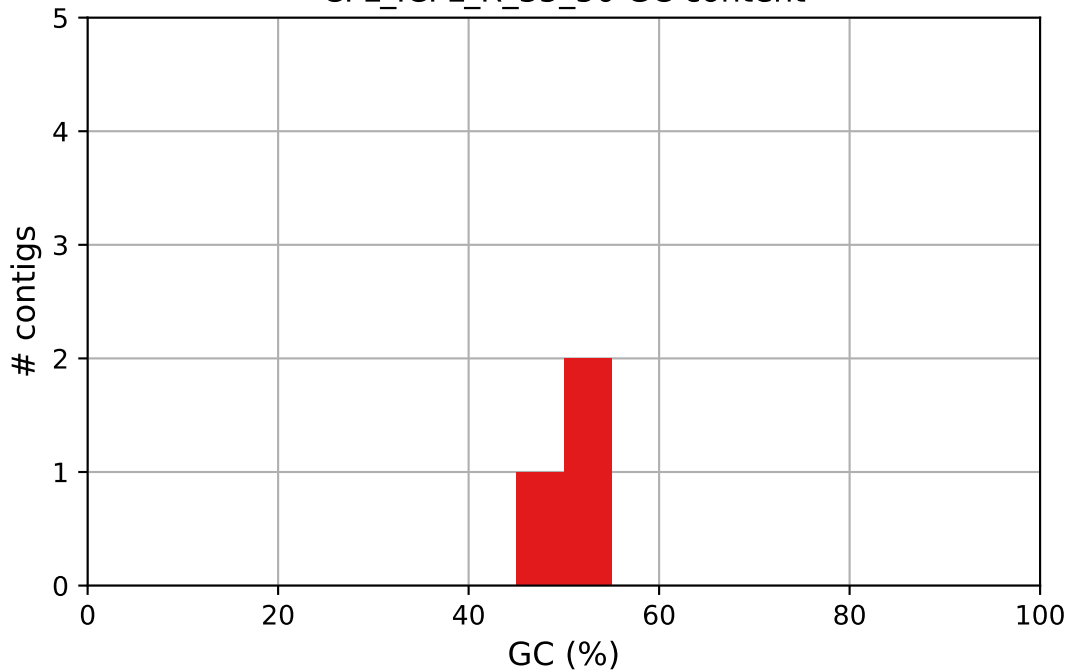
CFL_ICFL_R_35_50



GC content

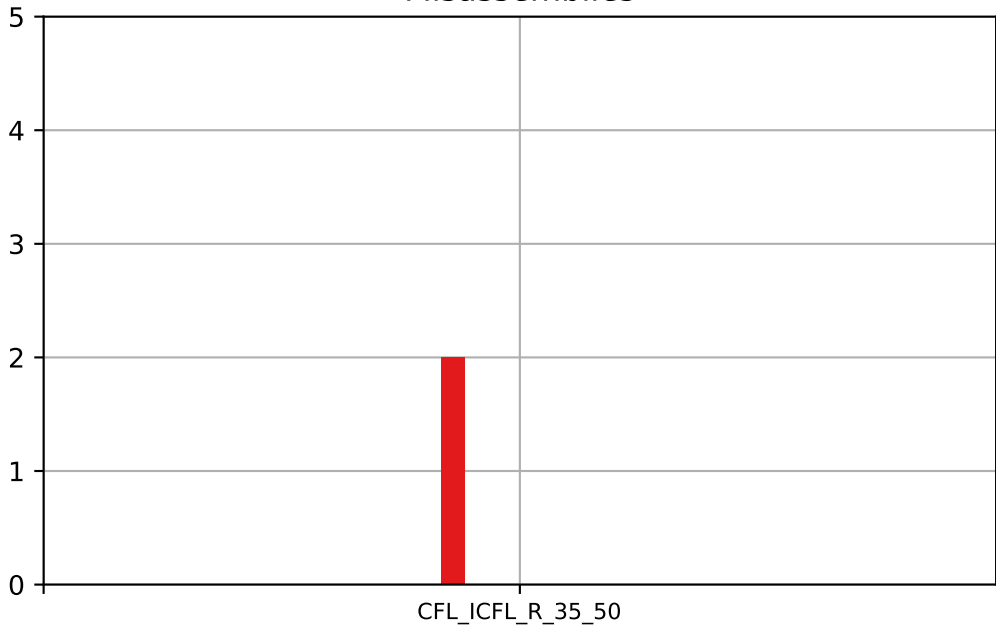


CFL_ICFL_R_35_50 GC content

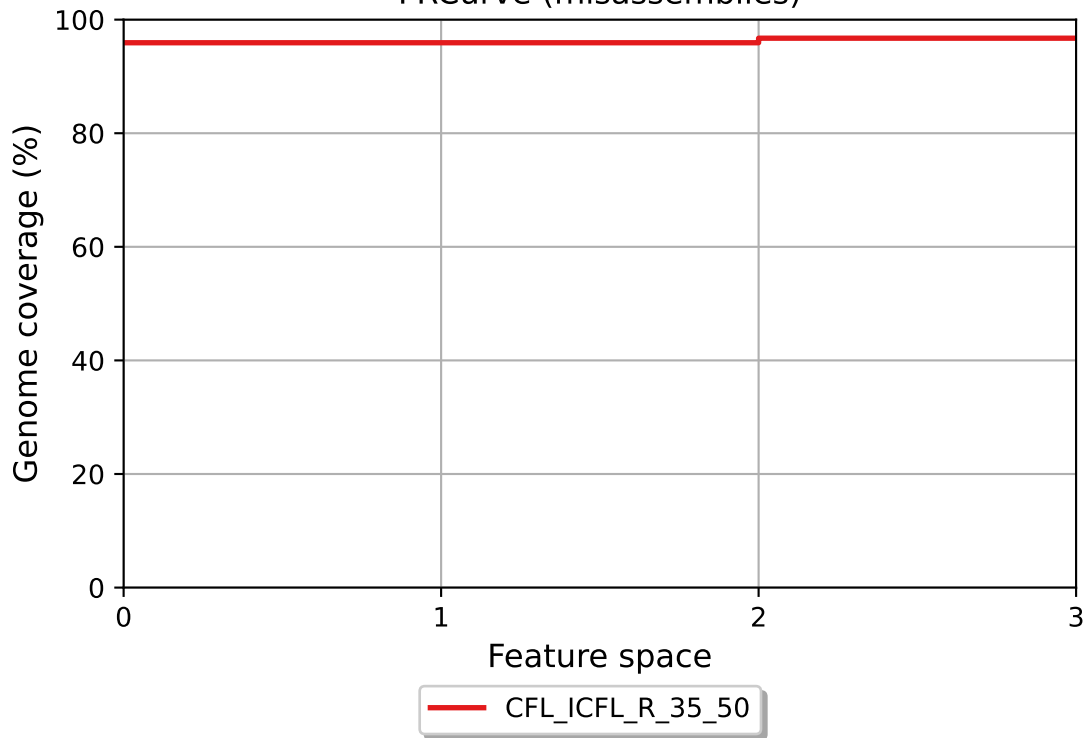


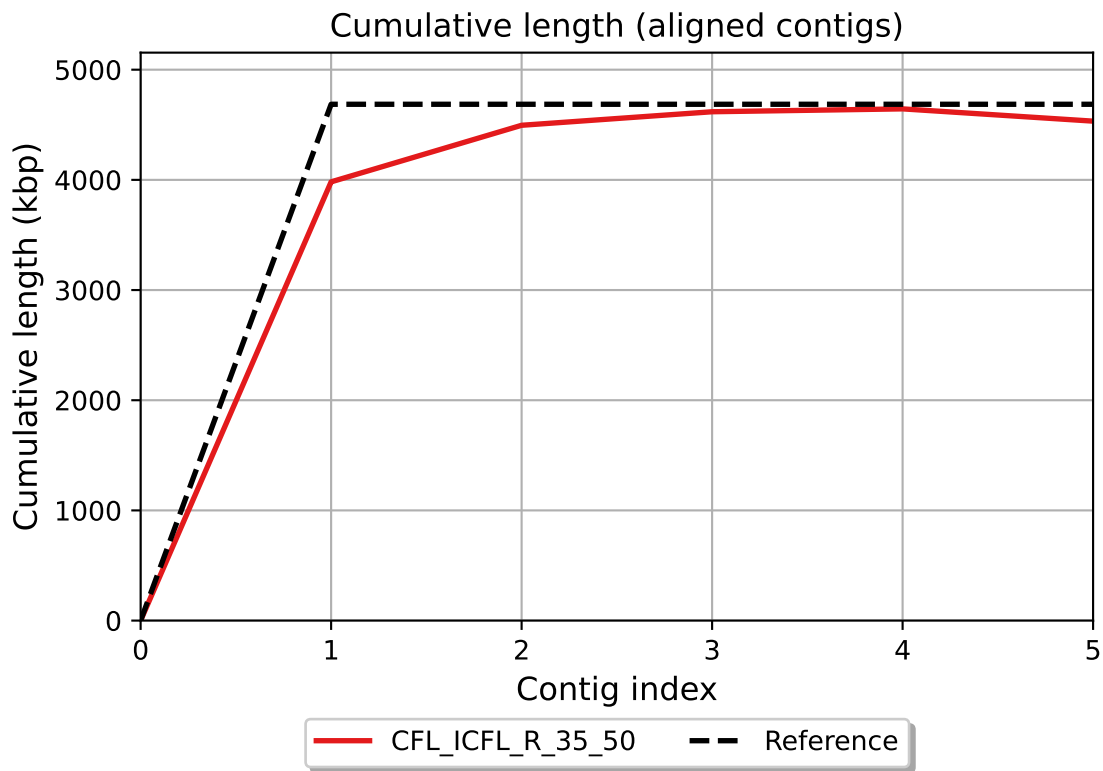
CFL_ICFL_R_35_50

Misassemblies

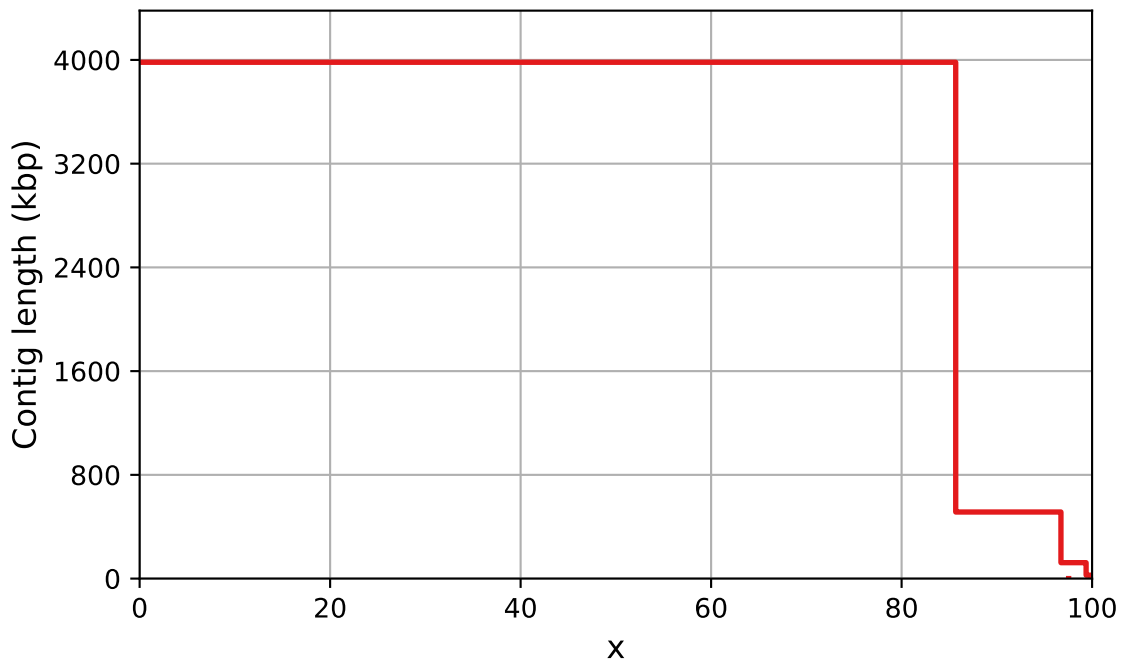


FRCurve (misassemblies)



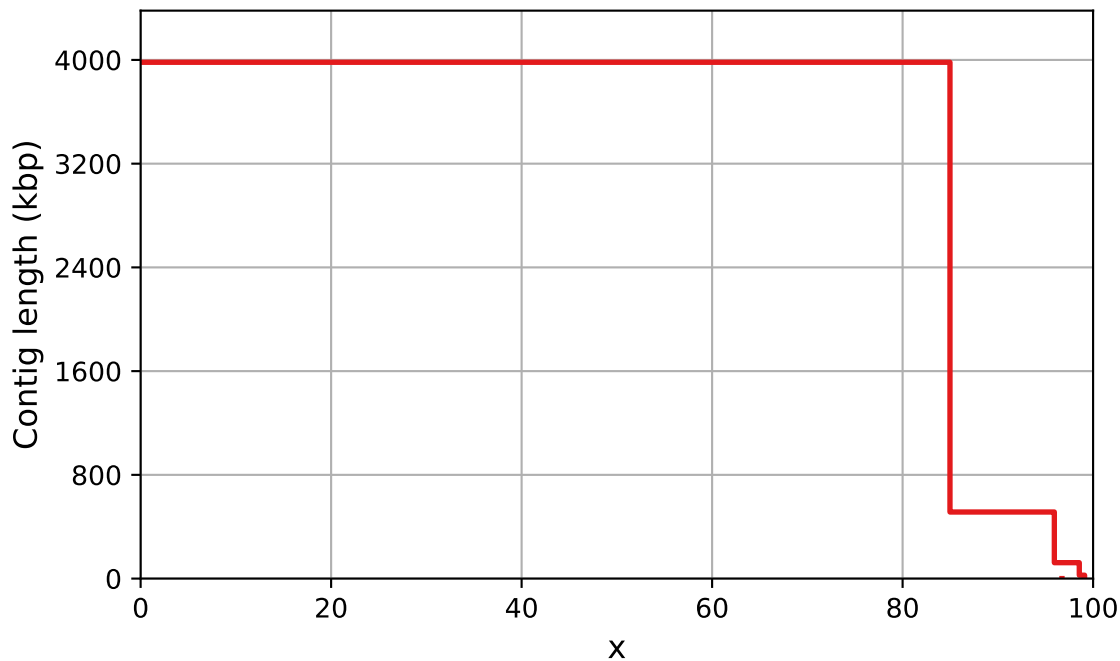


NAx



CFL_ICFL_R_35_50

NGAx



CFL_ICFL_R_35_50