

Report

	min5_CFL_ICFL_30_COMB_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)	4692298
Total length (>= 1000 bp)	4692298
Total length (>= 5000 bp)	4692298
Total length (>= 10000 bp)	4692298
Total length (>= 25000 bp)	4692298
Total length (>= 50000 bp)	4692298
# contigs	3
Largest contig	3981651
Total length	4692298
Reference length	4686137
GC (%)	50.74
Reference GC (%)	50.78
N50	3981651
NG50	3981651
N90	555456
NG90	555456
auN	3449516.7
auNG	3454051.9
L50	1
LG50	1
L90	2
LG90	2
# misassemblies	2
# misassembled contigs	1
Misassembled contigs length	155191
# 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 (%)	99.044
Duplication ratio	1.011
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	3981651
Total aligned length	4691095
NA50	3981651
NGA50	3981651
NA90	555456
NGA90	555456
auNA	3449119.2
auNGA	3453653.9
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

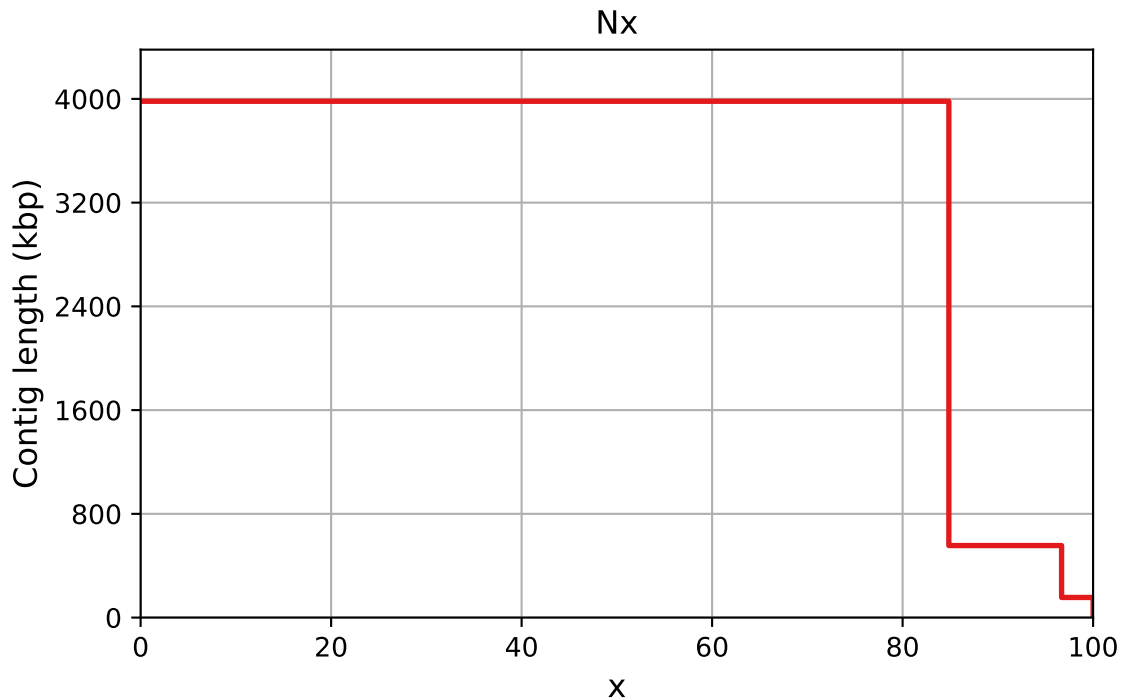
	min5_CFL_ICFL_30_COMB_50
# misassemblies	2
# contig misassemblies	2
# c. relocations	2
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	155191
# local misassemblies	0
# scaffold 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

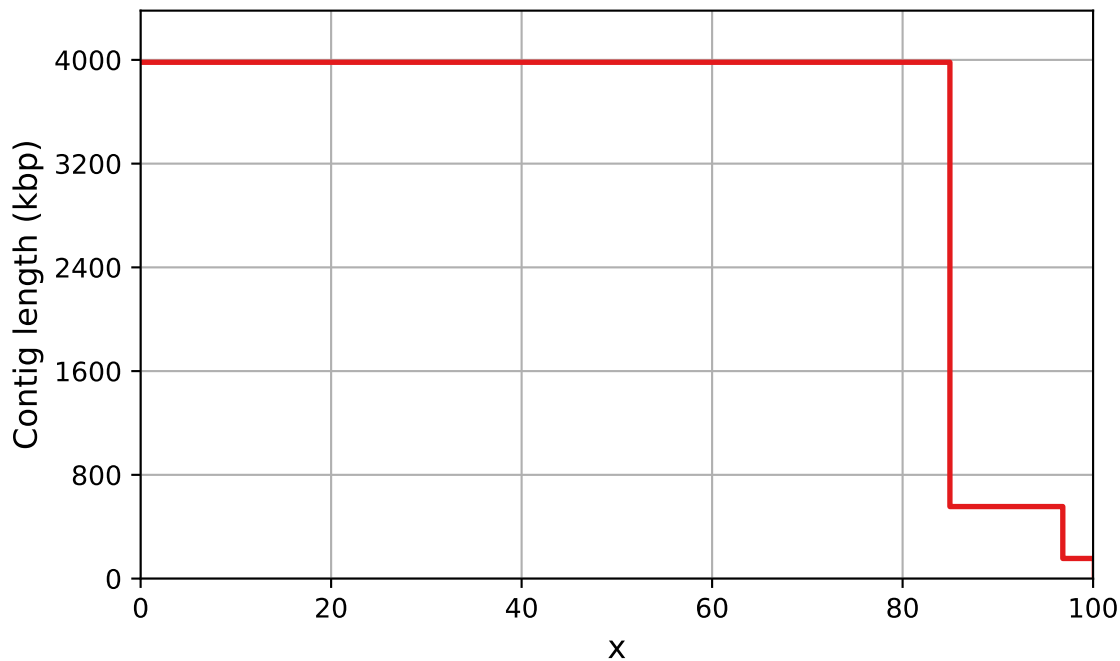
	min5_CFL_ICFL_30_COMB_50
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).

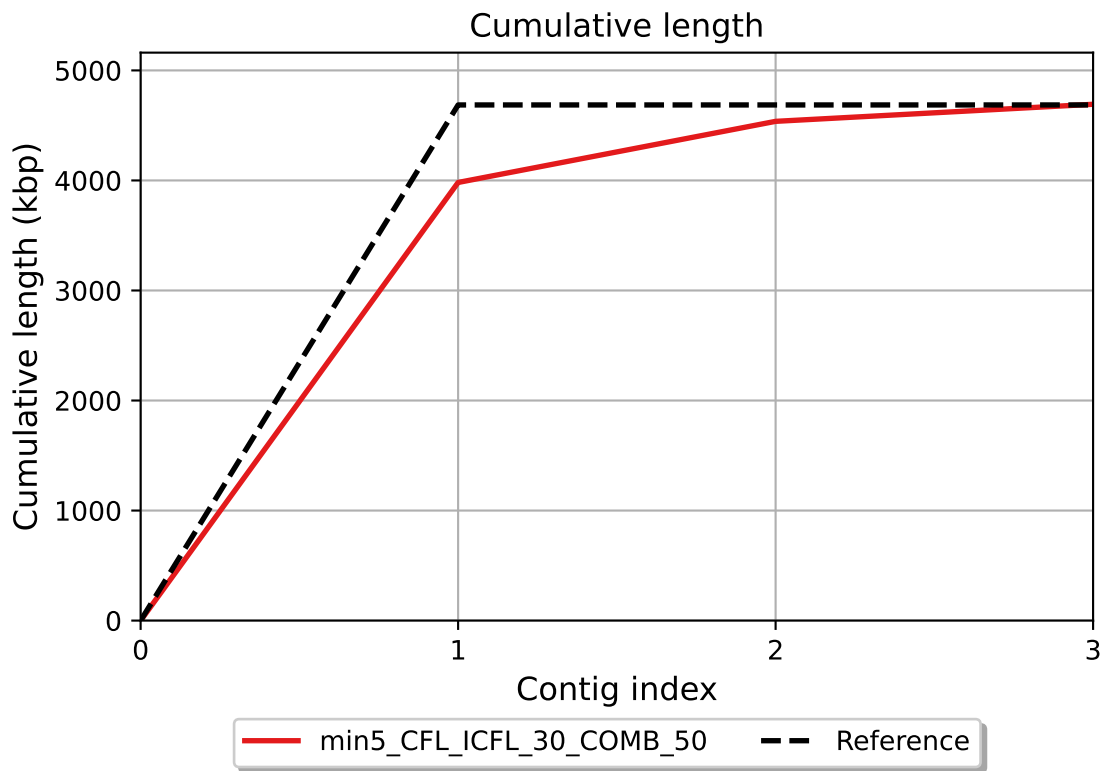


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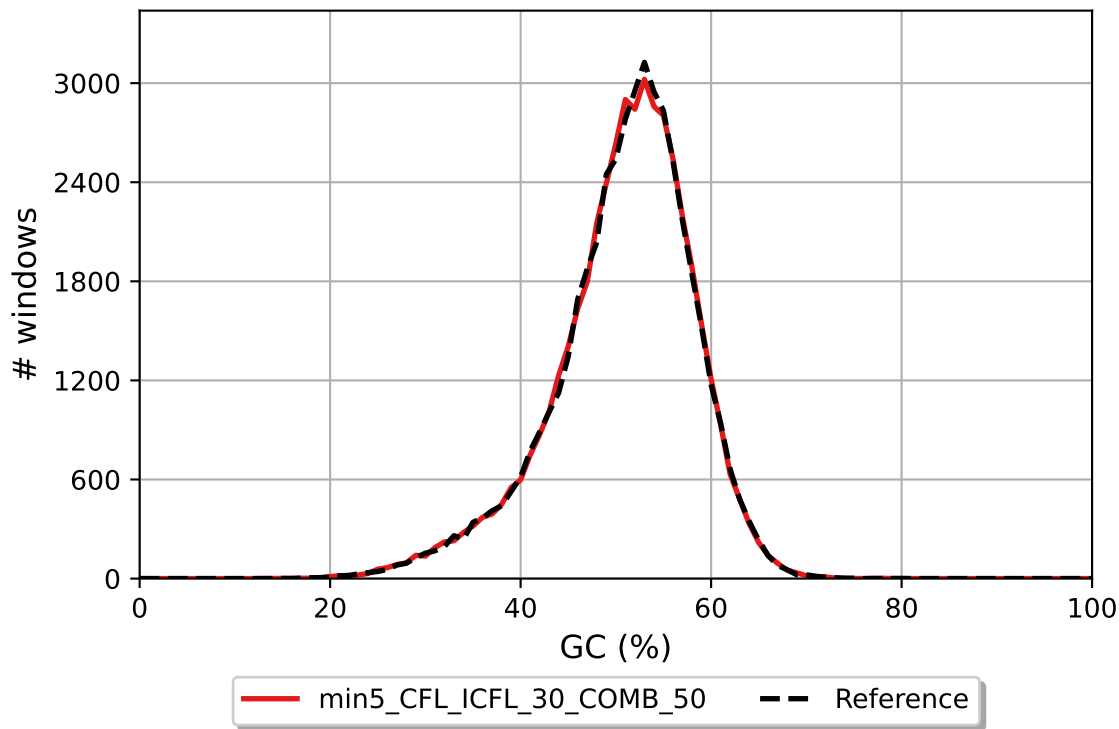
NGx



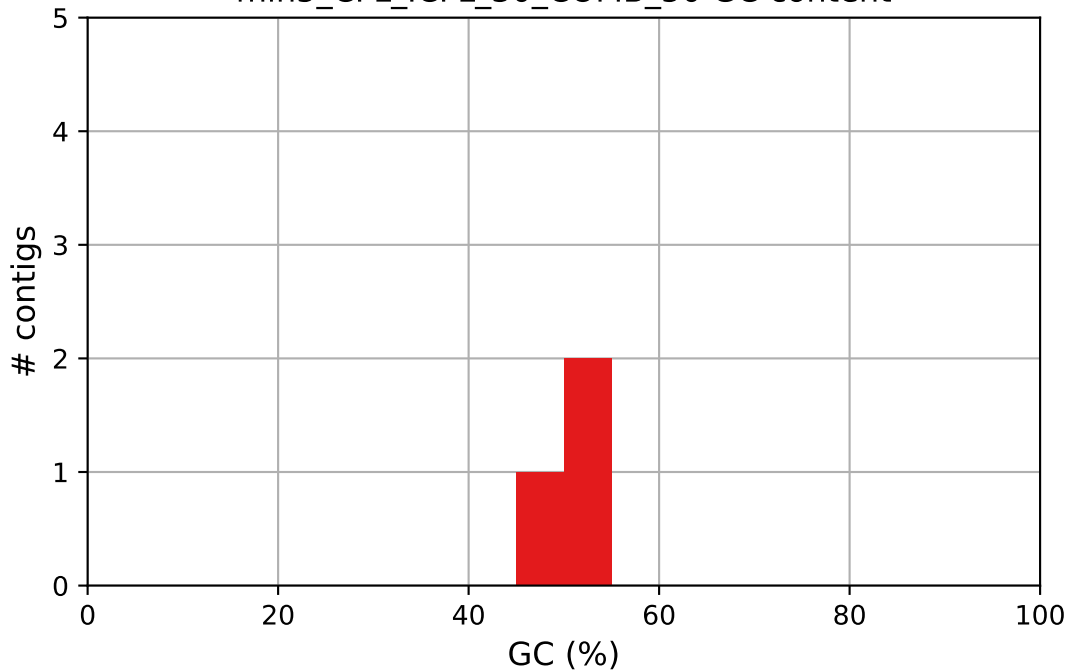
min5_CFL_ICFL_30_COMB_50



GC content

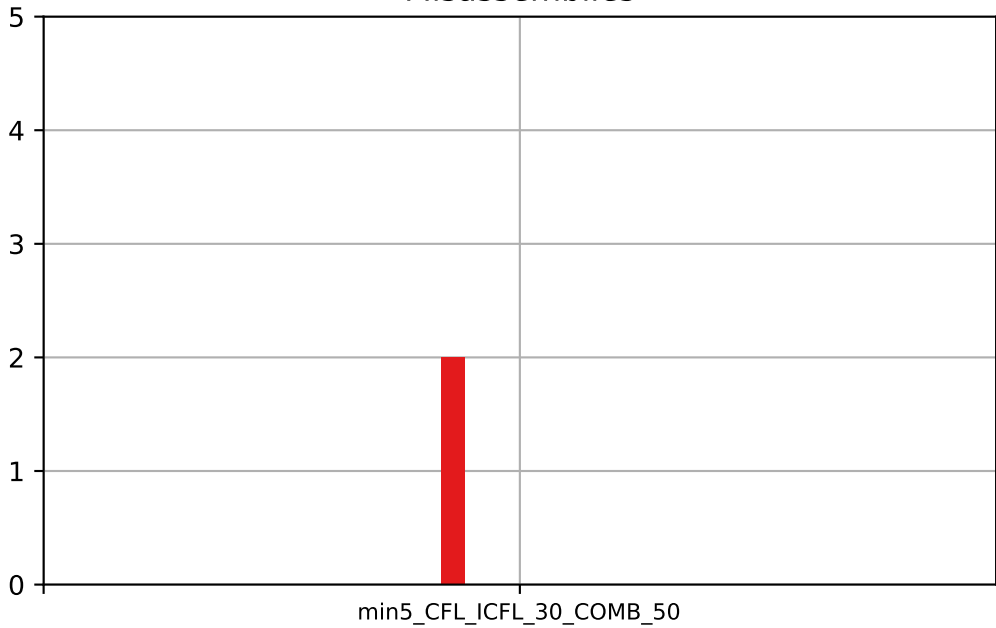


min5_CFL_ICFL_30_COMB_50 GC content



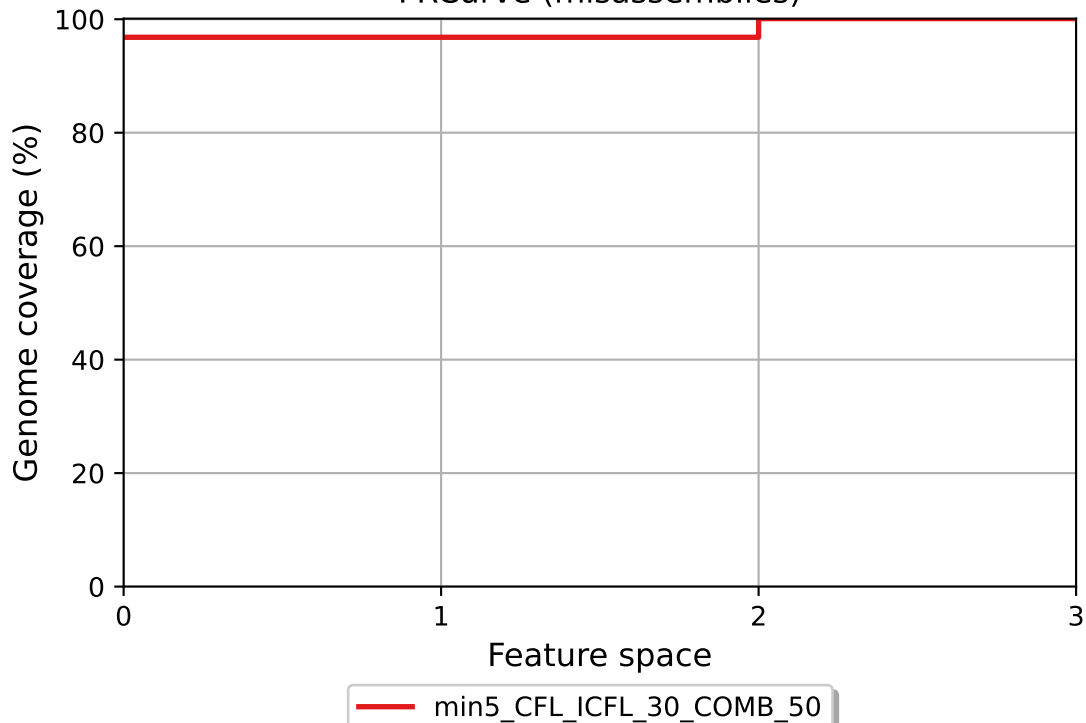
min5_CFL_ICFL_30_COMB_50

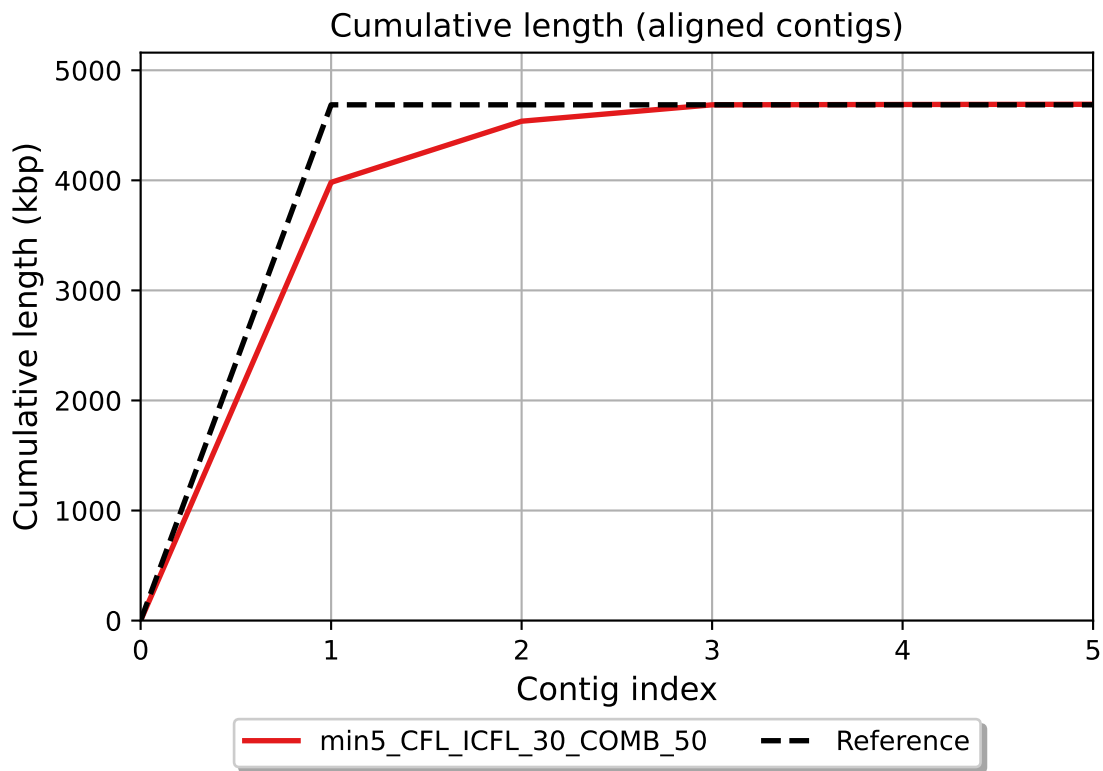
Misassemblies



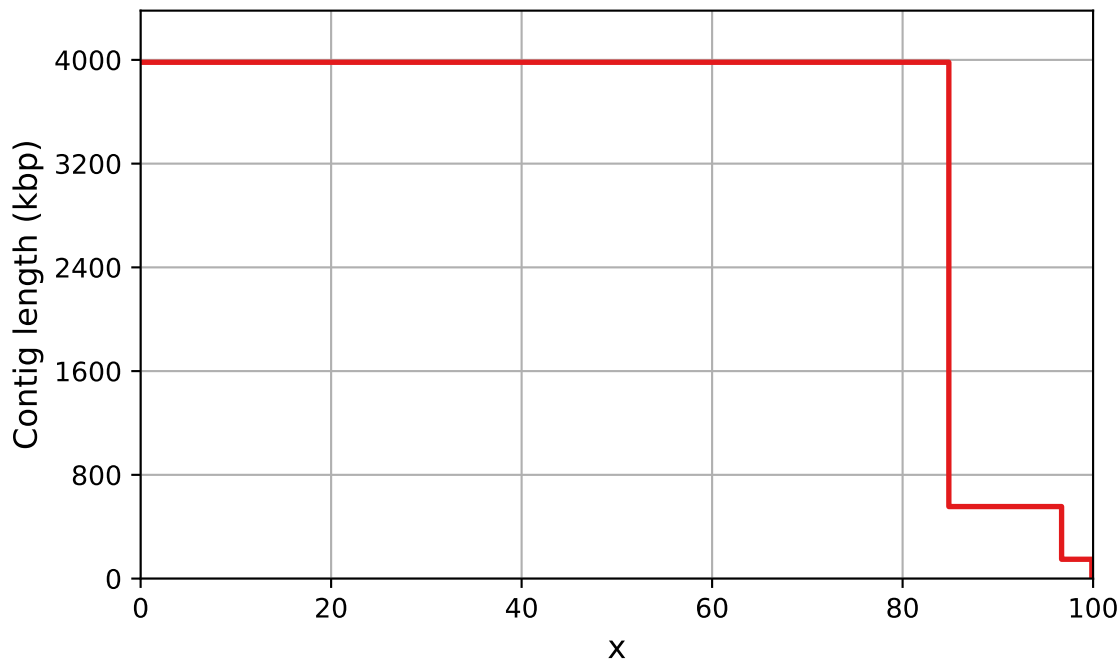
 # relocations

FRCurve (misassemblies)



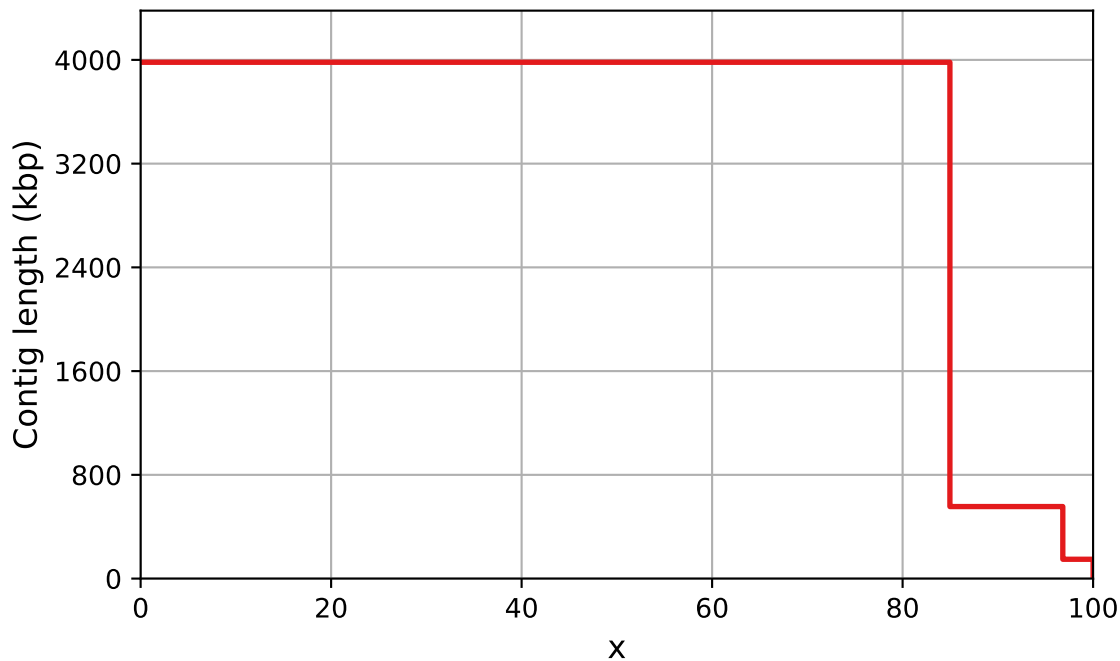


NAx



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NGAx



min5_CFL_ICFL_30_COMB_50