

Report

min5_CFL_ICFL_30_COMB_100	
# 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)	4699144
Total length (>= 1000 bp)	4699144
Total length (>= 5000 bp)	4699144
Total length (>= 10000 bp)	4699144
Total length (>= 25000 bp)	4699144
Total length (>= 50000 bp)	4699144
# contigs	3
Largest contig	3980818
Total length	4699144
Reference length	4686137
GC (%)	50.77
Reference GC (%)	50.78
N50	3980818
NG50	3980818
N90	561605
NG90	561605
auN	3444643.0
auNG	3454204.1
L50	1
LG50	1
L90	2
LG90	2
# 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 (%)	99.215
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	3980818
Total aligned length	4699002
NA50	3980818
NGA50	3980818
NA90	561605
NGA90	561605
auNA	3444633.6
auNGA	3454194.6
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

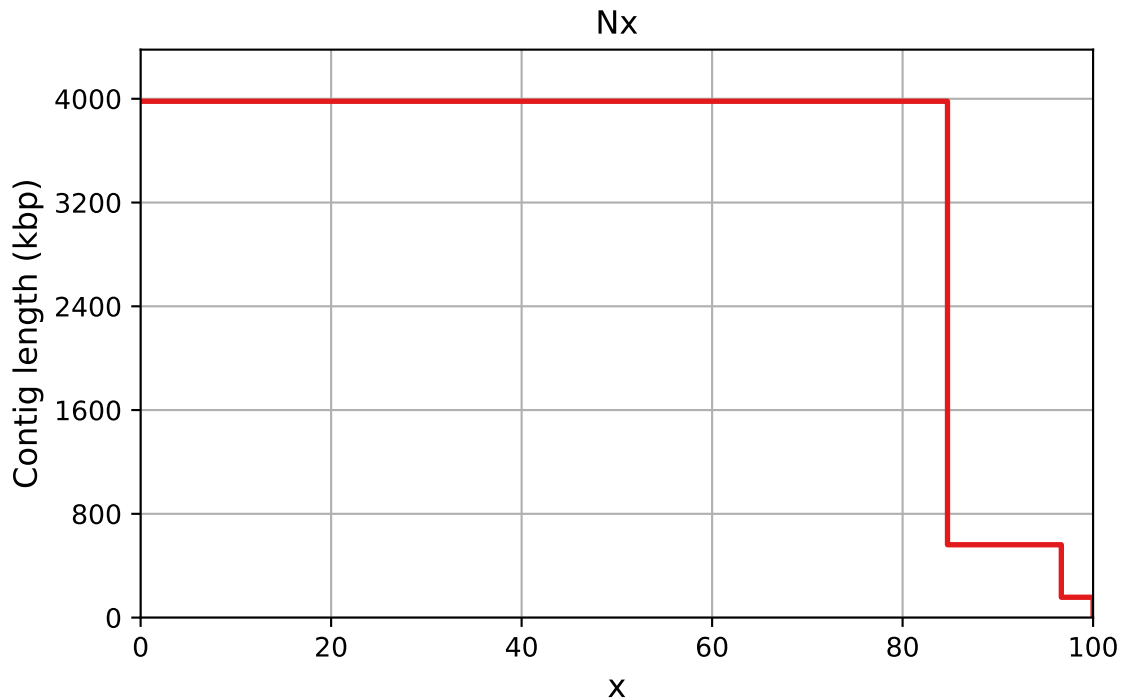
	min5_CFL_ICFL_30_COMB_100
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold 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

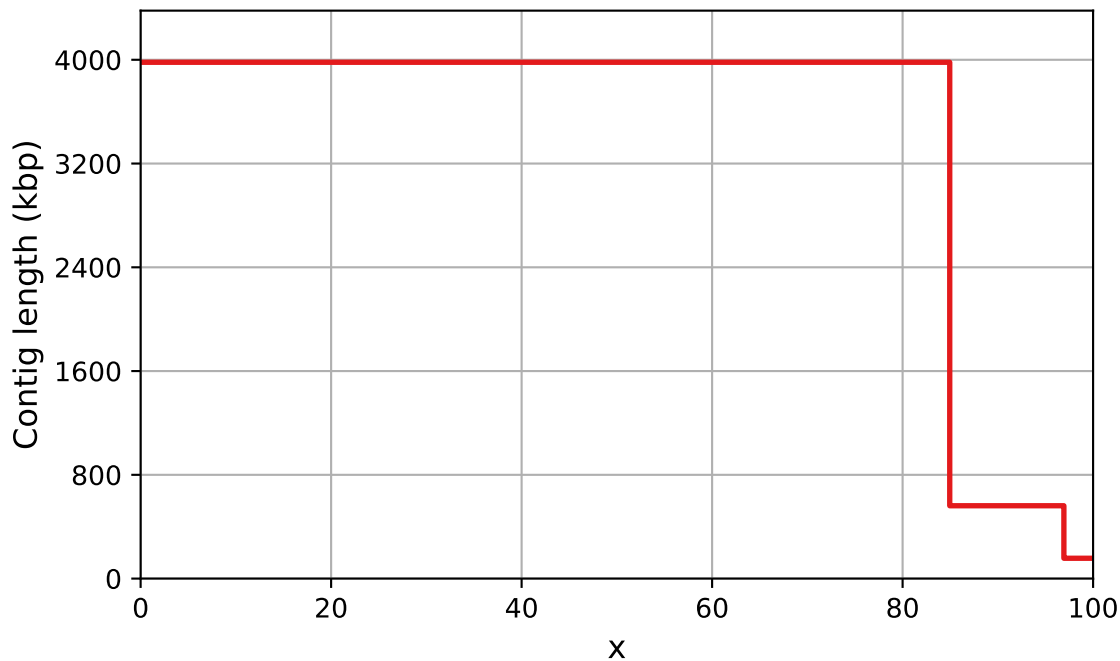
	min5_CFL_ICFL_30_COMB_100
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).

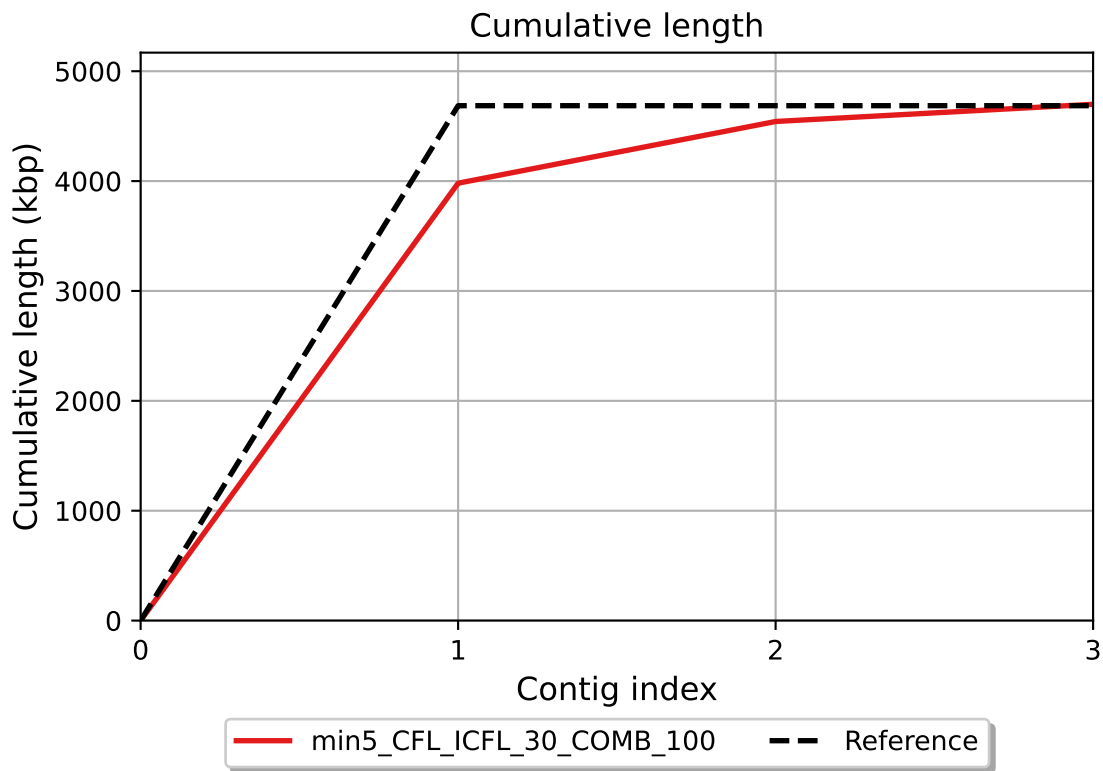


min5_CFL_ICFL_30_COMB_100

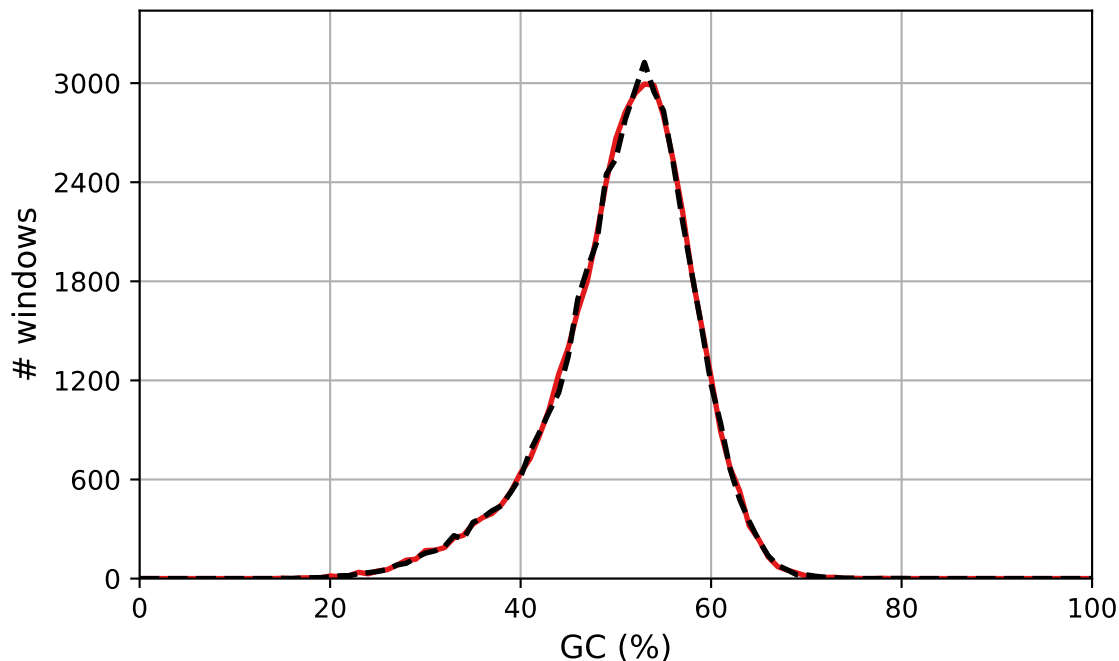
NGx



— min5_CFL_ICFL_30_COMB_100

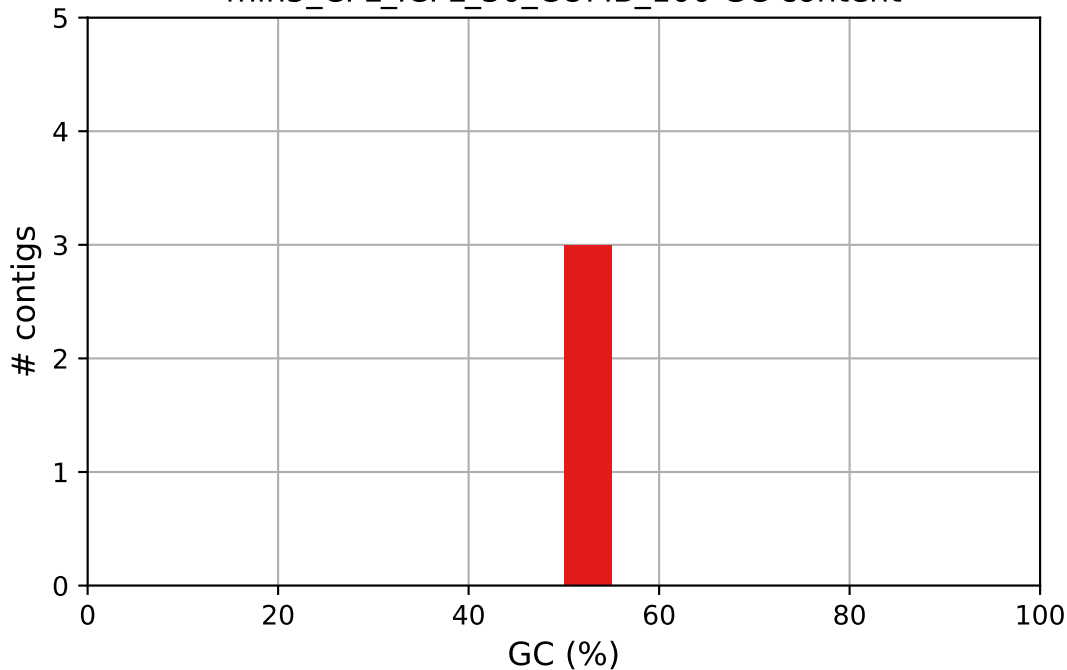


GC content



— min5_CFL_ICFL_30_COMB_100 - - Reference

min5_CFL_ICFL_30_COMB_100 GC content

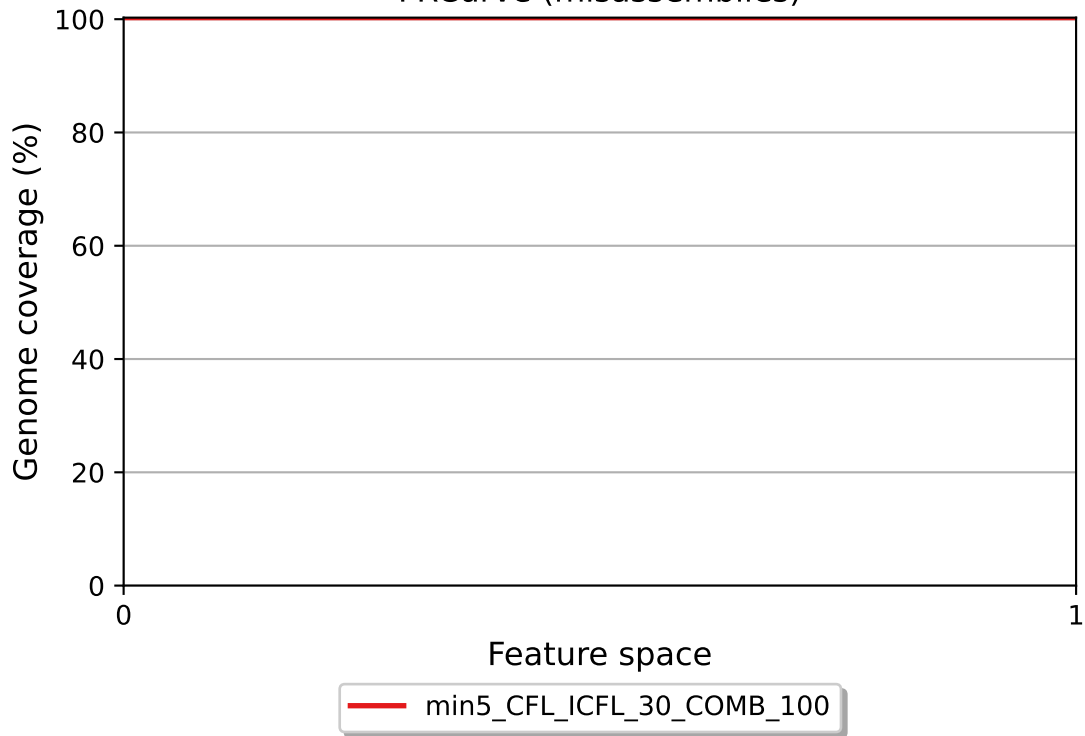


min5_CFL_ICFL_30_COMB_100

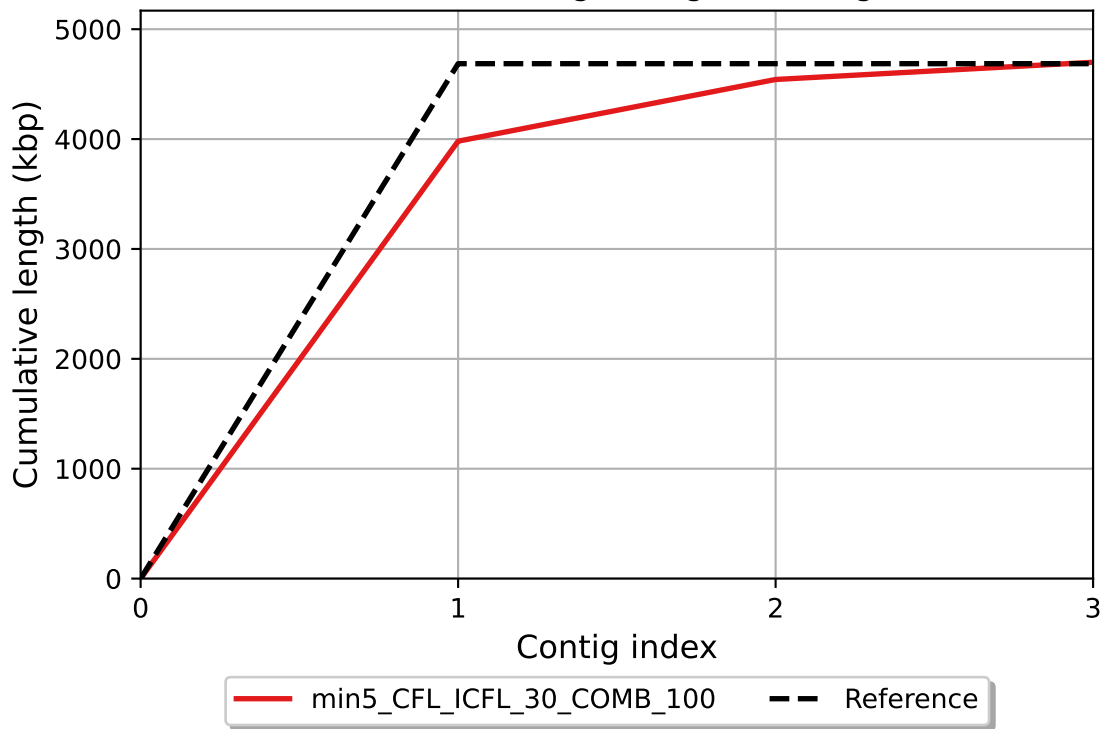
Misassemblies



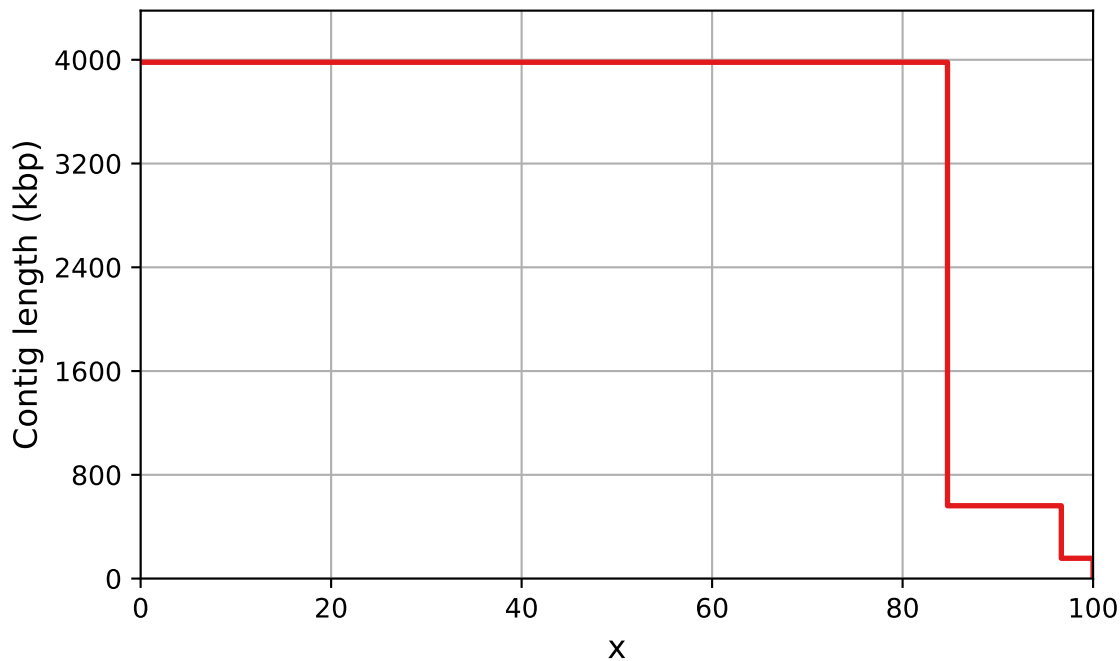
FRCurve (misassemblies)



Cumulative length (aligned contigs)

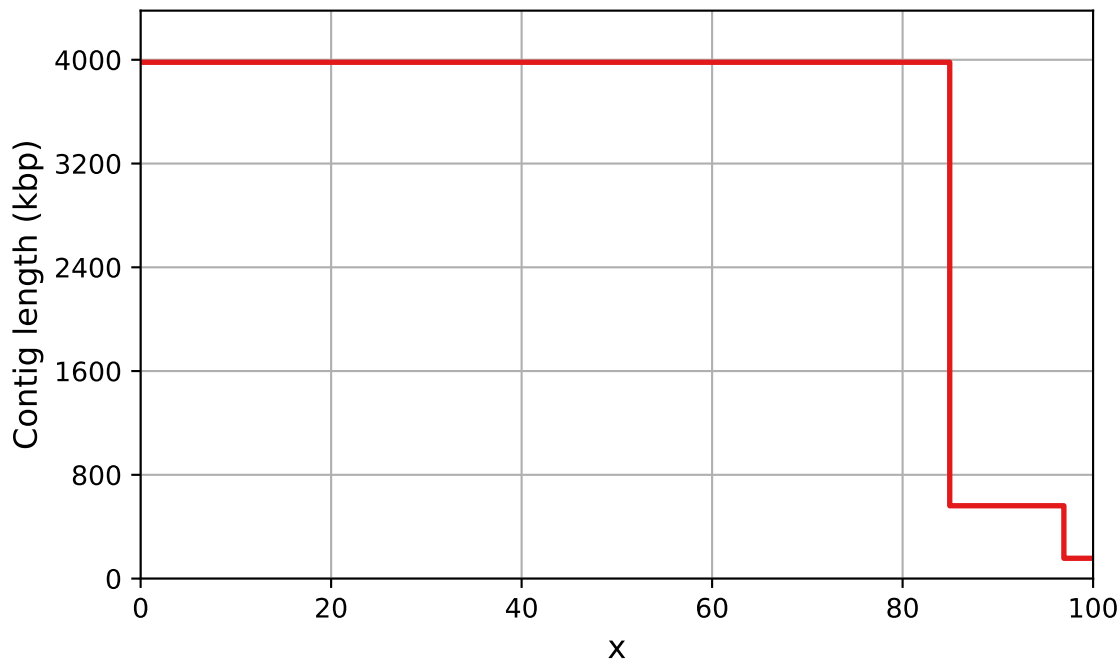


NAx



min5_CFL_ICFL_30_COMB_100

NGAx



— min5_CFL_ICFL_30_COMB_100