

Report

	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)	4665807
Total length (>= 1000 bp)	4665807
Total length (>= 5000 bp)	4665807
Total length (>= 10000 bp)	4665807
Total length (>= 25000 bp)	4665807
Total length (>= 50000 bp)	4665807
# contigs	3
Largest contig	3967812
Total length	4665807
Reference length	4686137
GC (%)	50.81
Reference GC (%)	50.78
N50	3967812
NG50	3967812
N90	387062
NG90	387062
auN	3427066.0
auNG	3412198.2
L50	1
LG50	1
L90	2
LG90	2
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	3967812
# 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 (%)	97.529
Duplication ratio	1.021
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	3456150
Total aligned length	4665807
NA50	3456150
NGA50	3456150
NA90	387062
NGA90	387062
auNA	2669048.9
auNGA	2657469.7
LA50	1
LGA50	1
LA90	3
LGA90	3

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

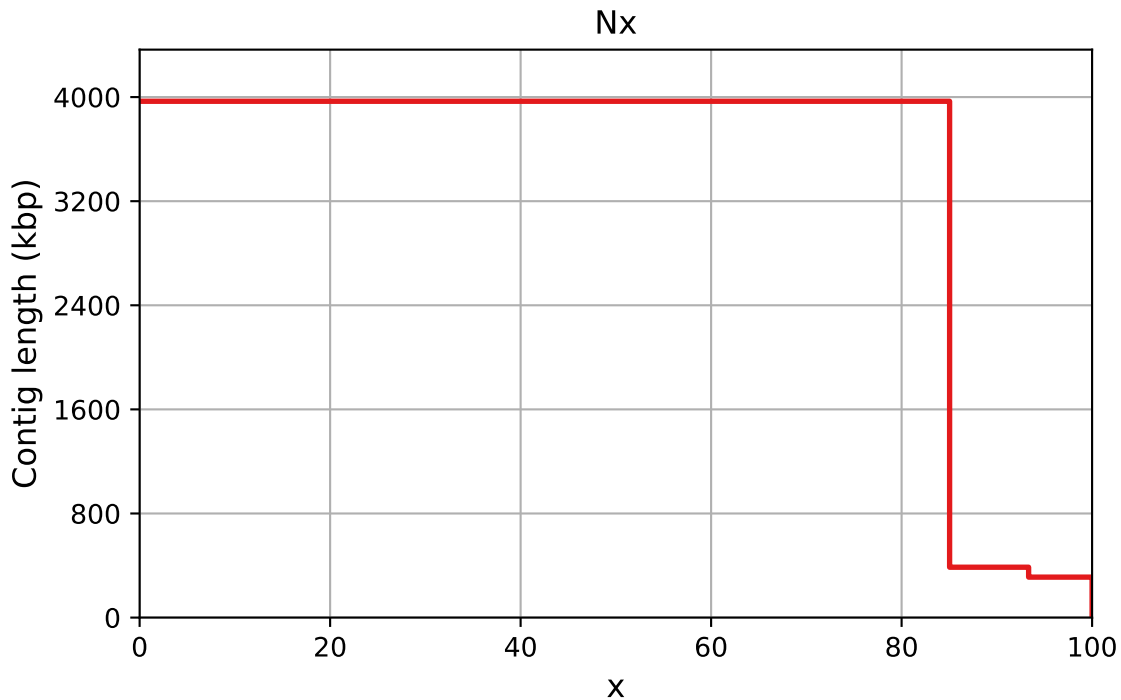
	CFL_ICFL_30_COMB_100
# misassemblies	1
# contig misassemblies	1
# c. relocations	1
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	3967812
# local misassemblies	0
# scaffold 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

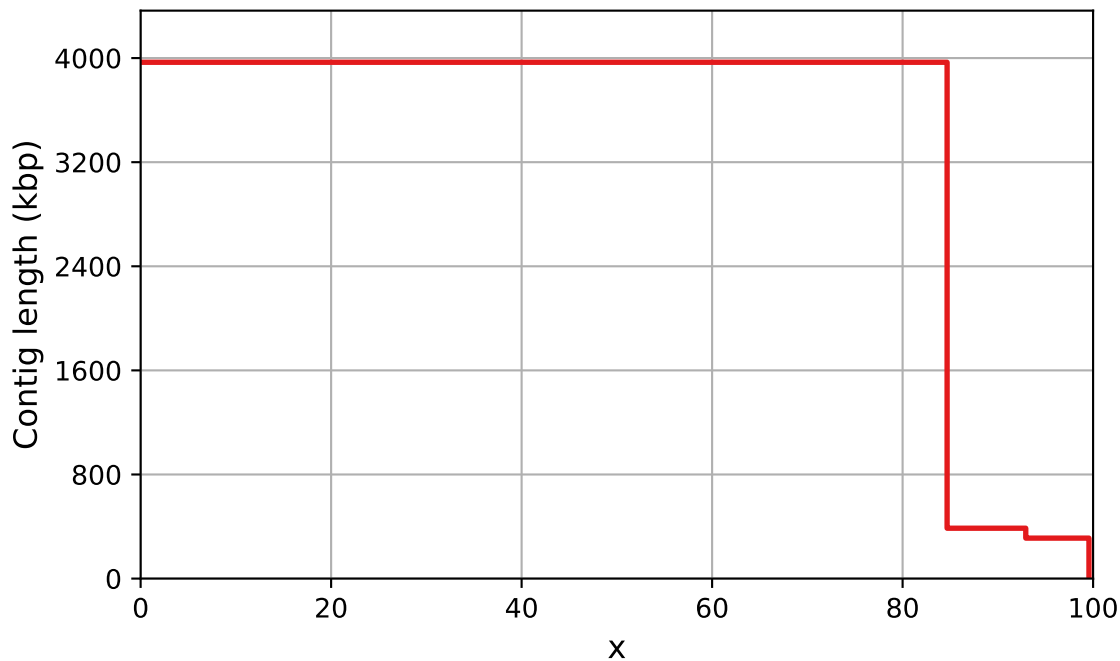
	CFL_ICFL_30_COMB_100
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).

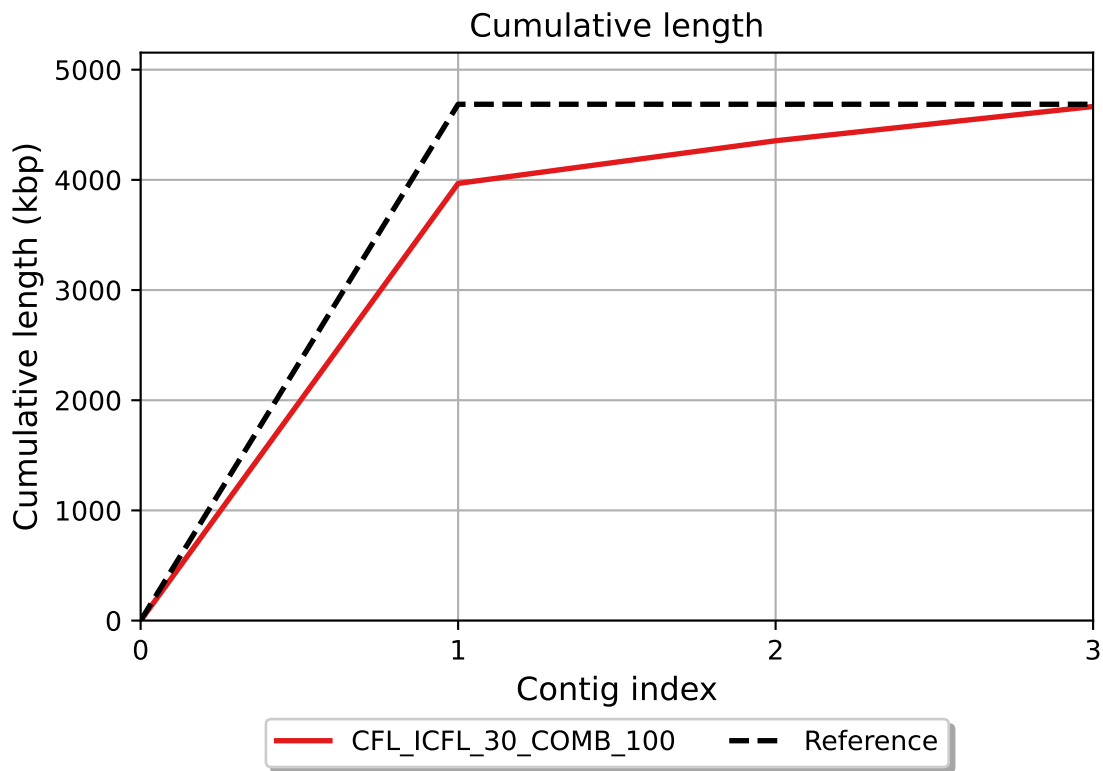


— CFL_ICFL_30_COMB_100

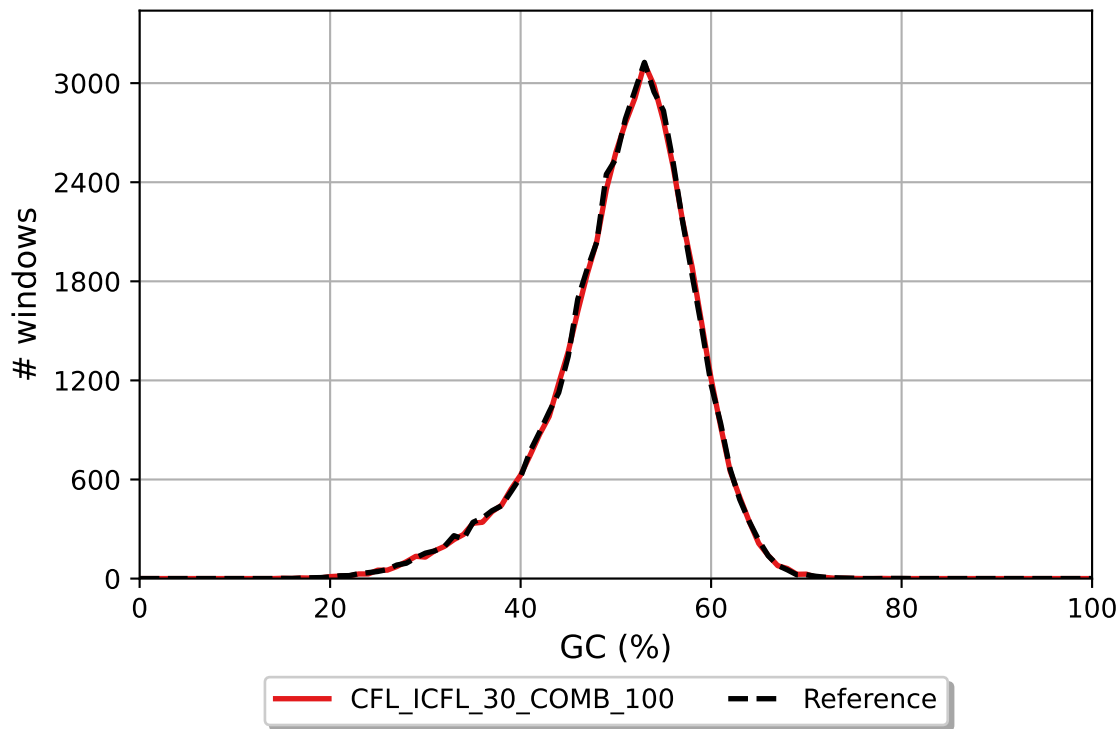
NGx



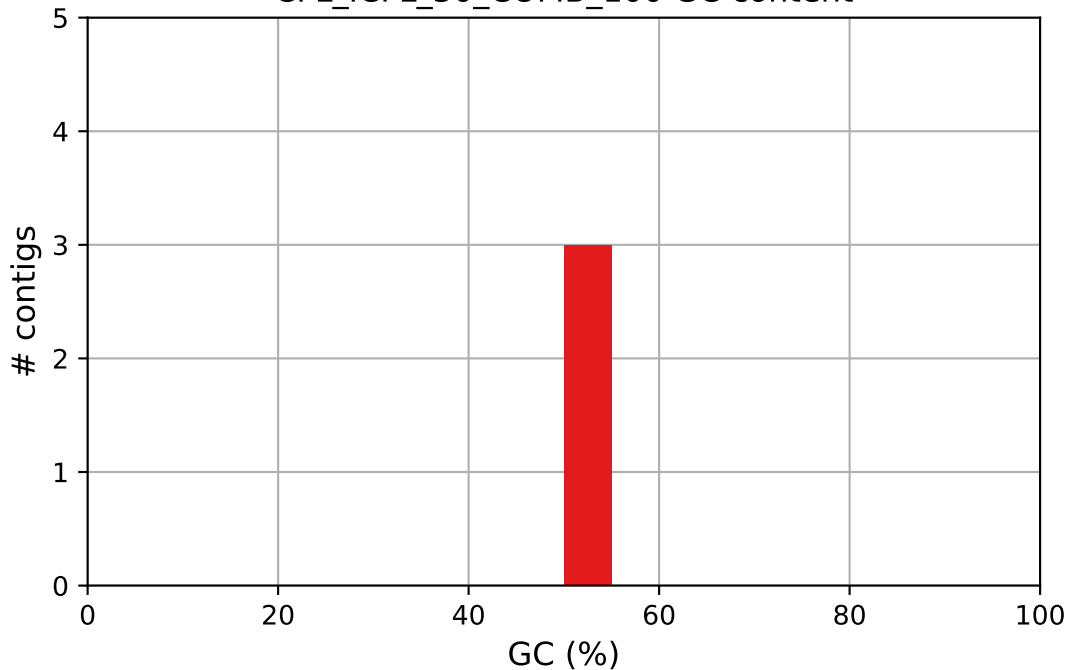
— CFL_ICFL_30_COMB_100



GC content

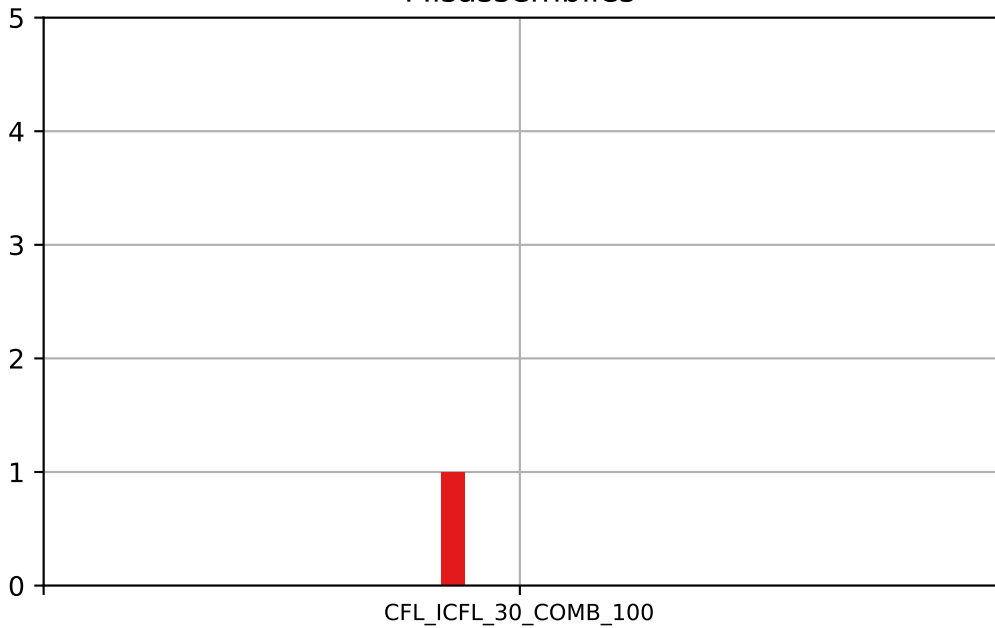


CFL_ICFL_30_COMB_100 GC content

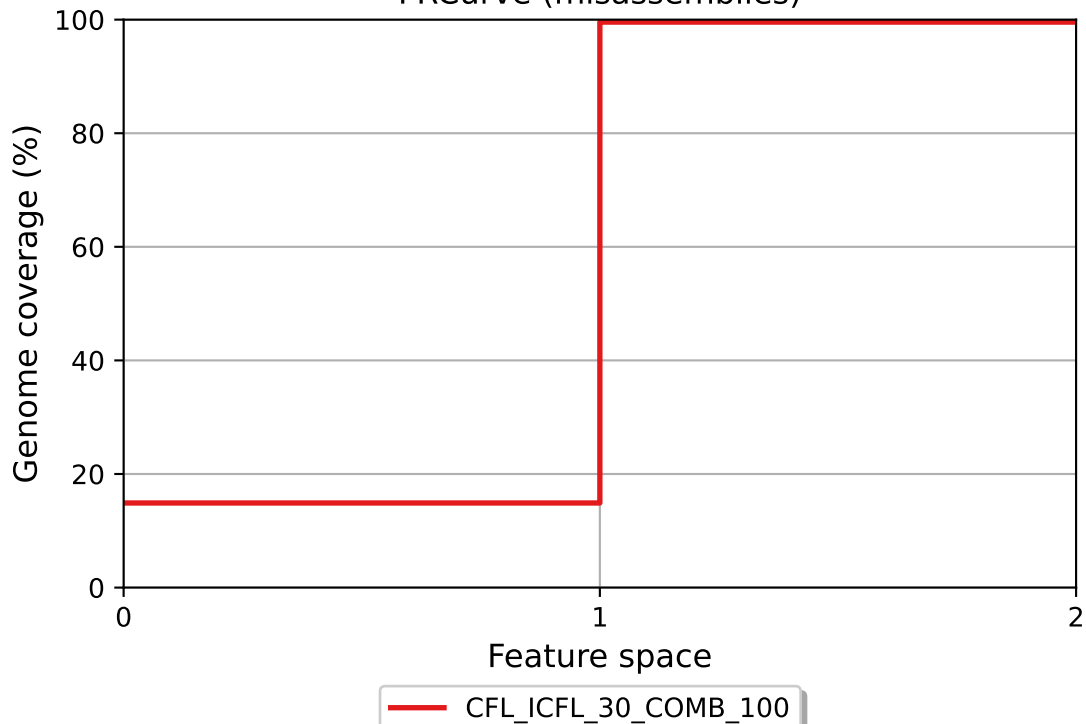


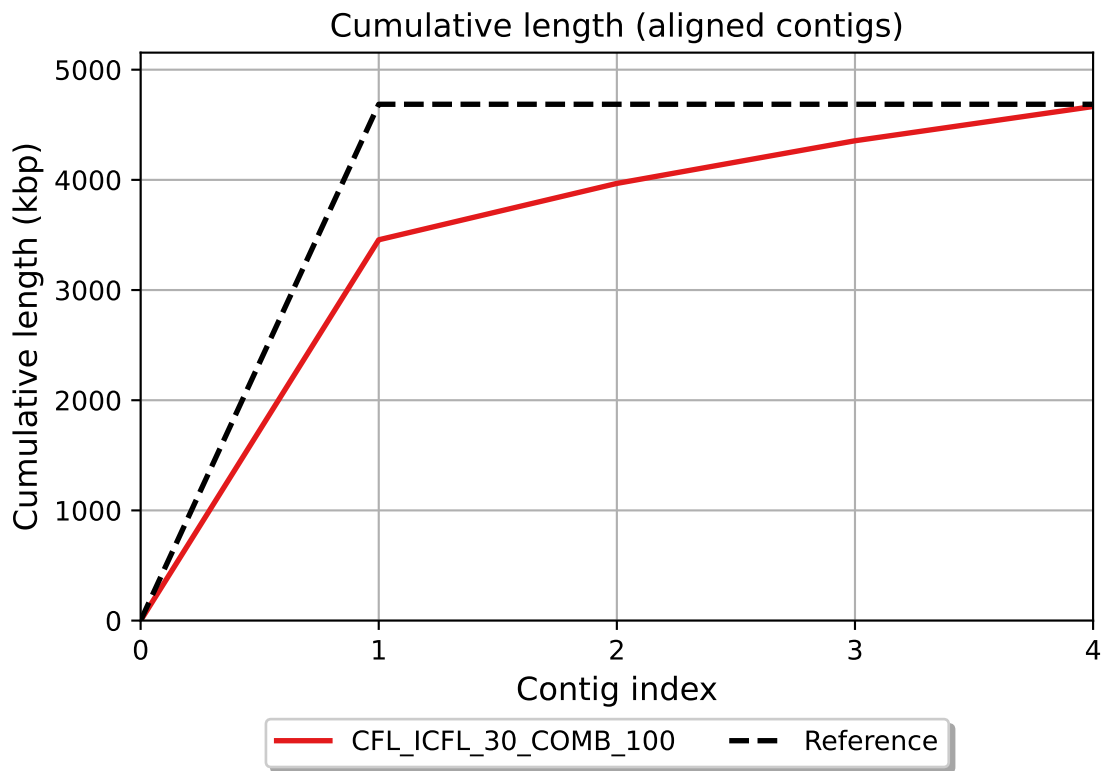
CFL_ICFL_30_COMB_100

Misassemblies

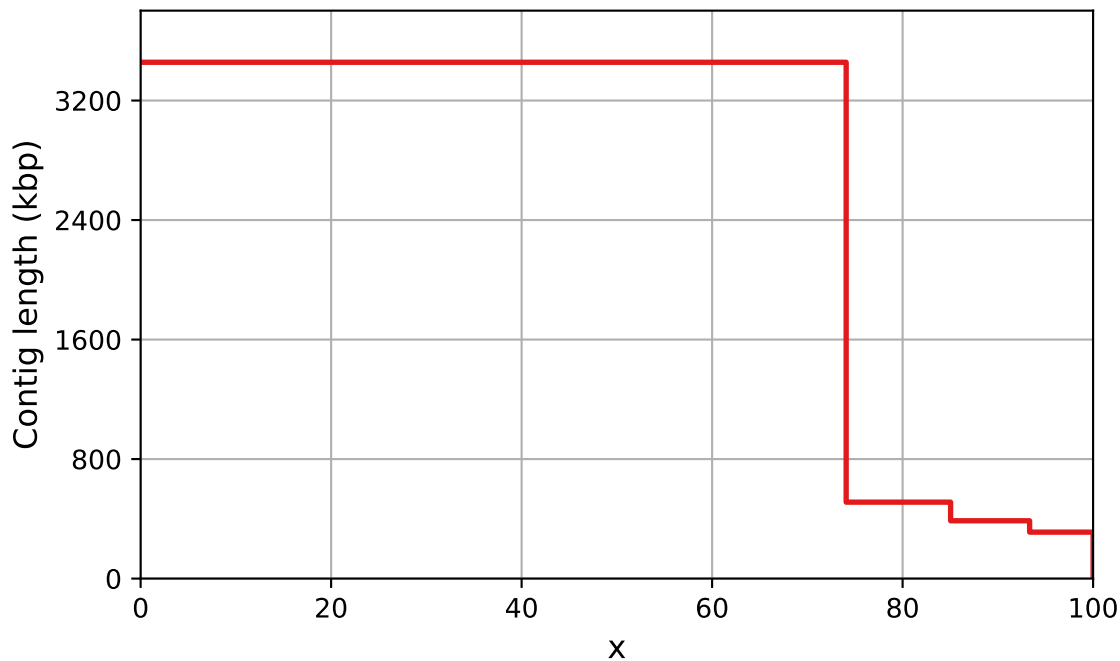


FRCurve (misassemblies)



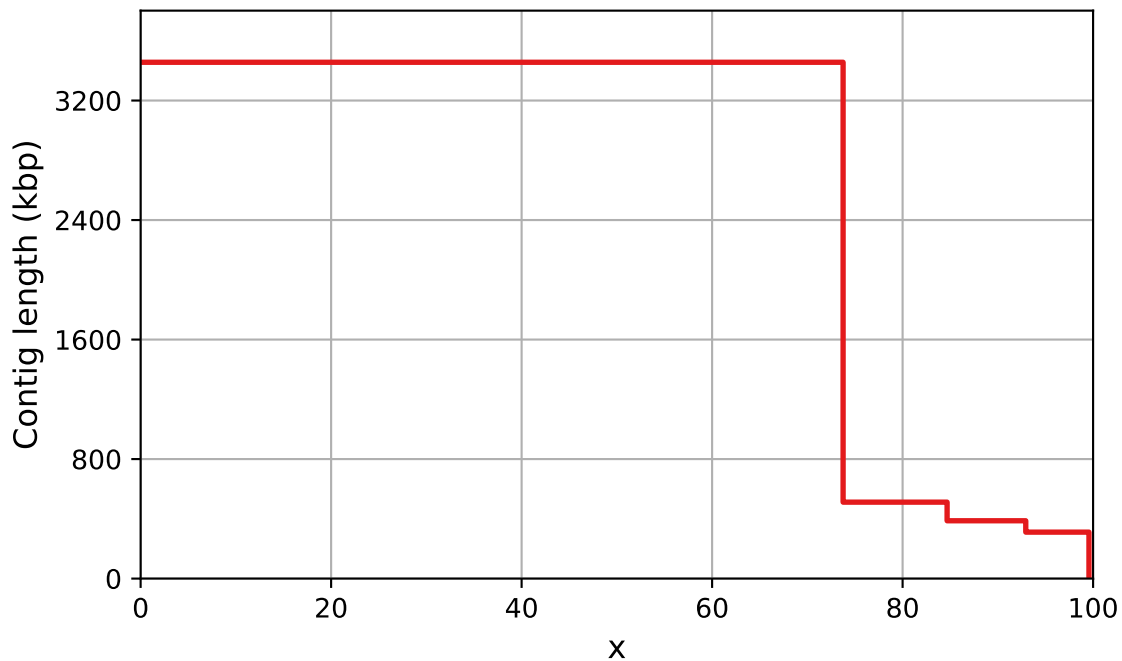


NAx



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NGAx



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