

Report

	CFL_ICFL_R_35_100
# contigs (>= 0 bp)	4
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	4
# contigs (>= 50000 bp)	4
Total length (>= 0 bp)	4727843
Total length (>= 1000 bp)	4727843
Total length (>= 5000 bp)	4727843
Total length (>= 10000 bp)	4727843
Total length (>= 25000 bp)	4727843
Total length (>= 50000 bp)	4727843
# contigs	4
Largest contig	3980974
Total length	4727843
Reference length	4686137
GC (%)	50.72
Reference GC (%)	50.78
N50	3980974
NG50	3980974
N90	529247
NG90	529247
auN	3416996.0
auNG	3447406.8
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 (%)	98.742
Duplication ratio	1.022
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.00
# indels per 100 kbp	0.00
Largest alignment	3980974
Total aligned length	4727701
NA50	3980974
NGA50	3980974
NA90	529247
NGA90	529247
auNA	3416987.1
auNGA	3447397.9
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

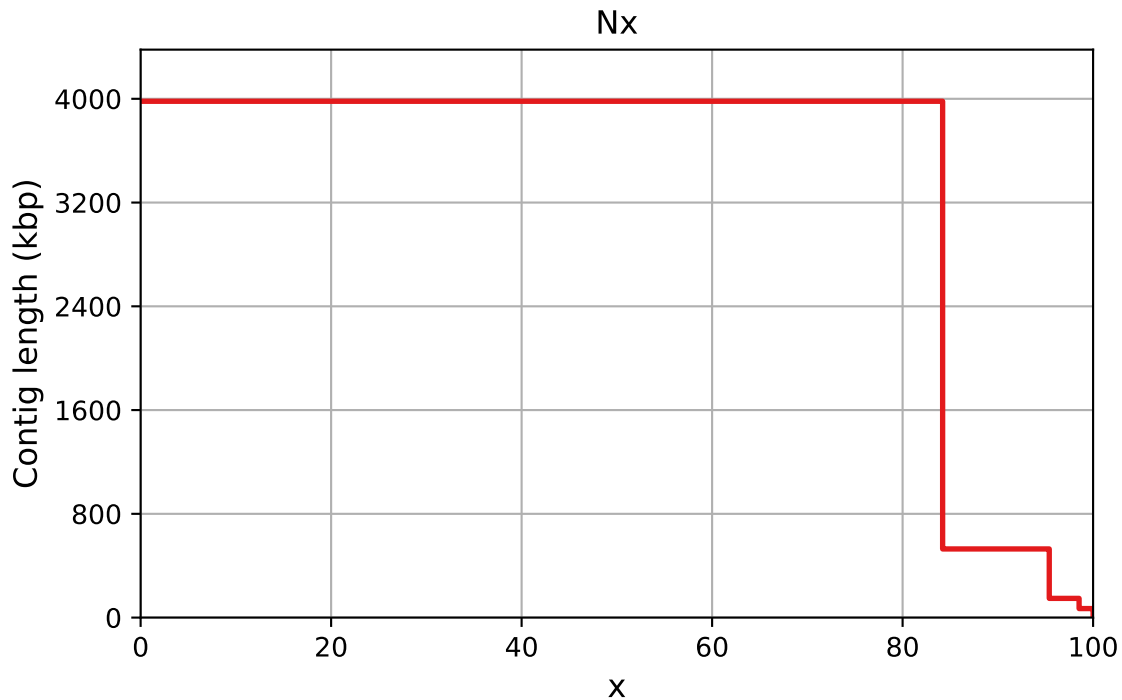
	CFL_ICFL_R_35_100
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	142
# 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

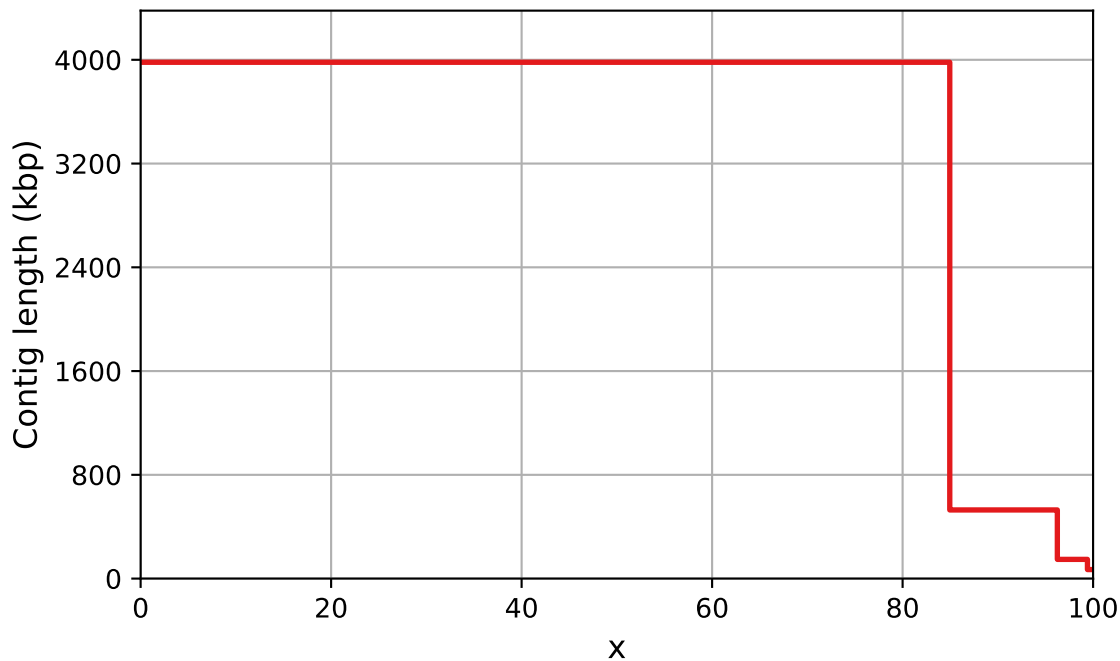
	CFL_ICFL_R_35_100
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).

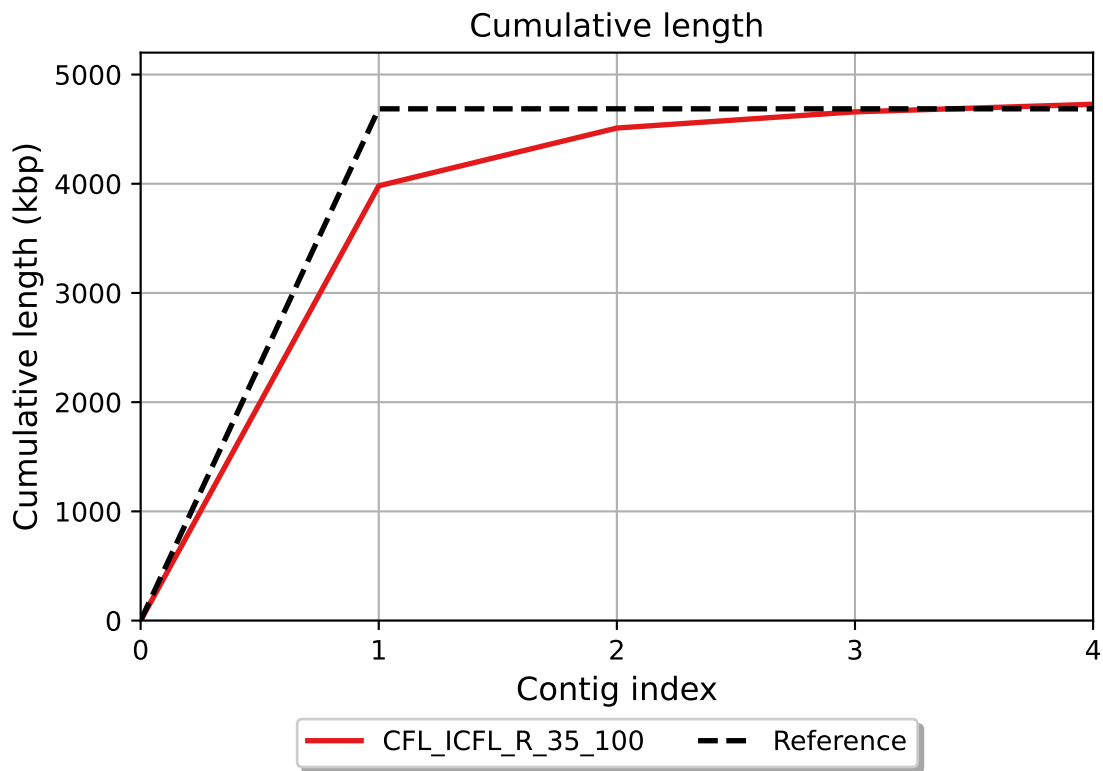


CFL_ICFL_R_35_100

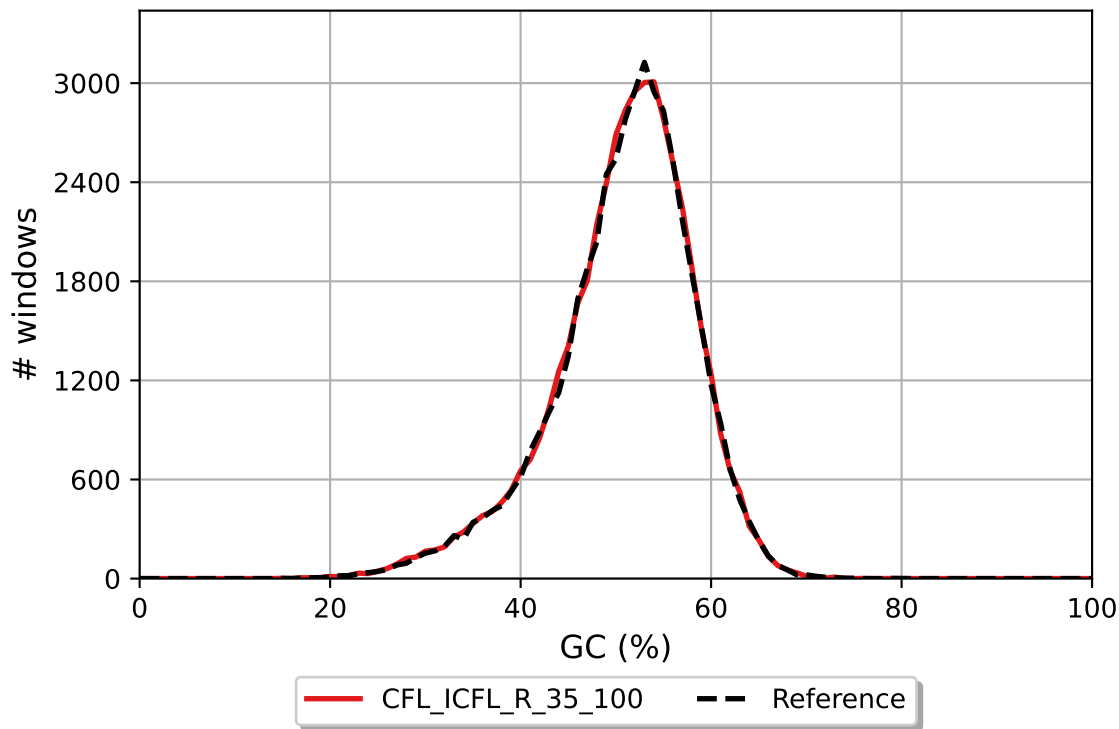
NGx



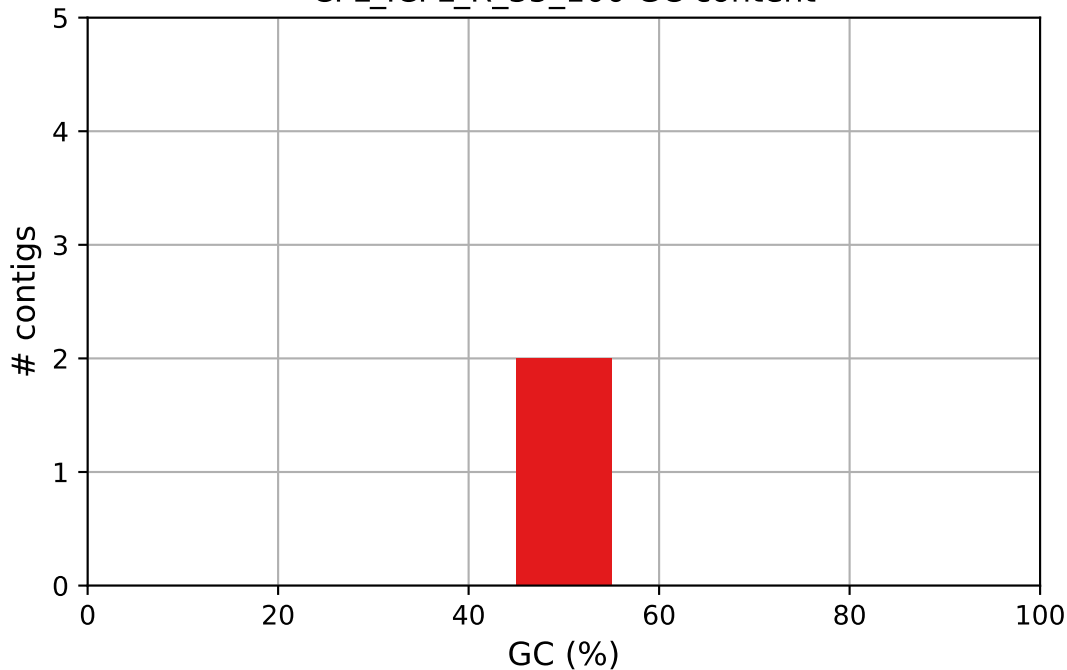
— CFL_ICFL_R_35_100



GC content

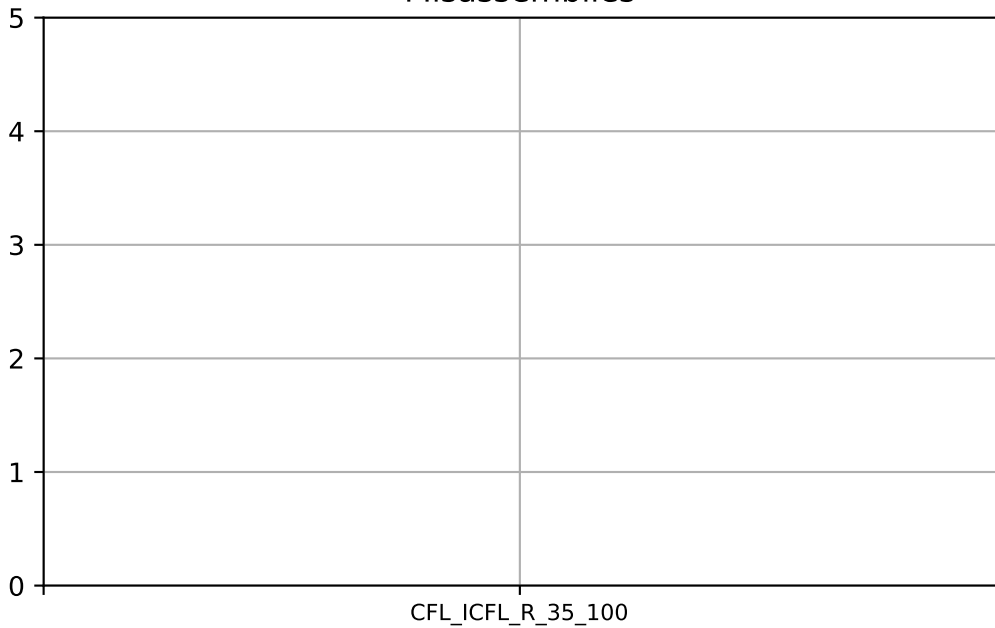


CFL_ICFL_R_35_100 GC content

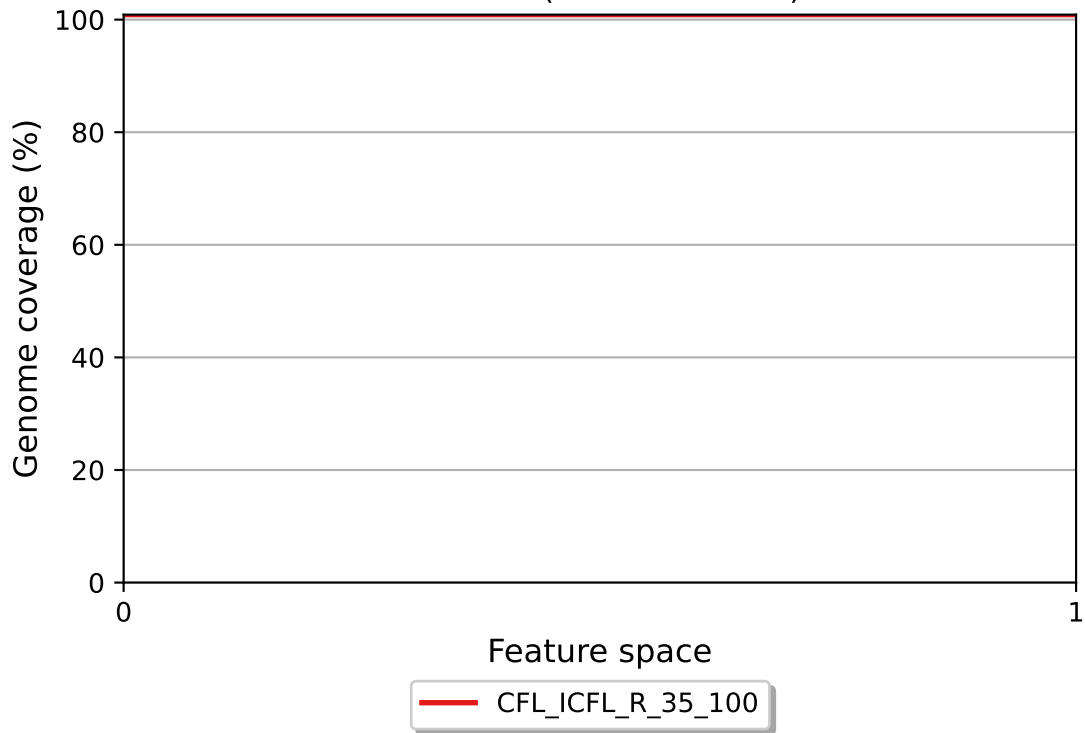


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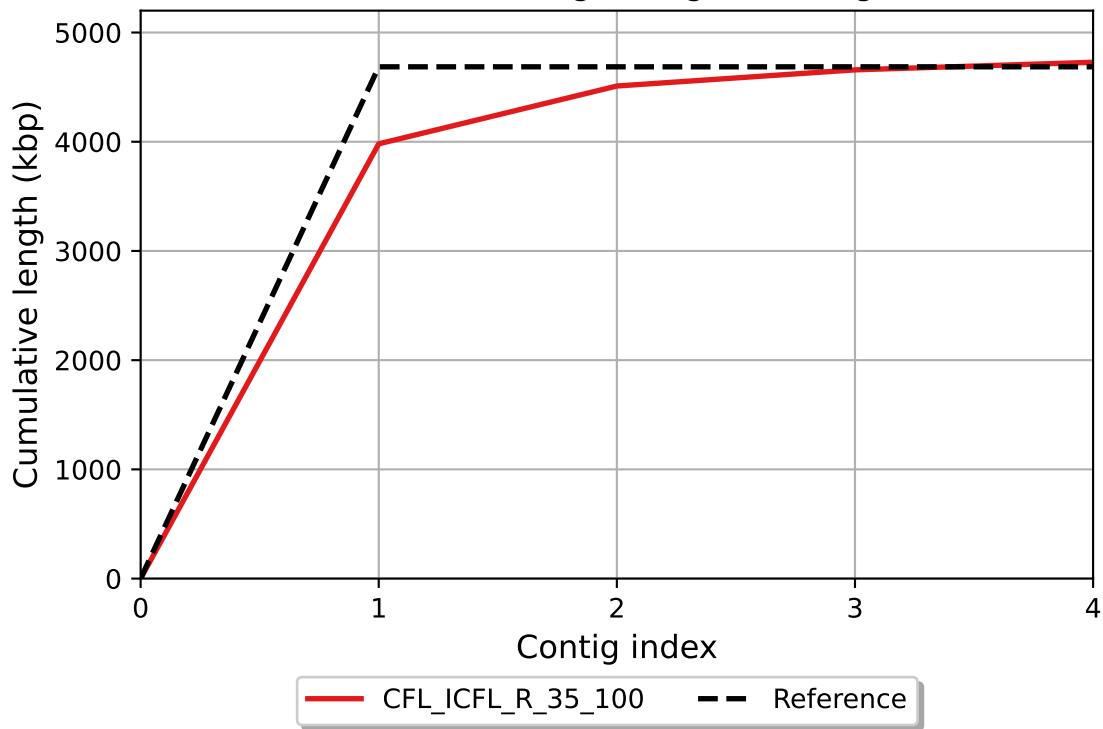
Misassemblies



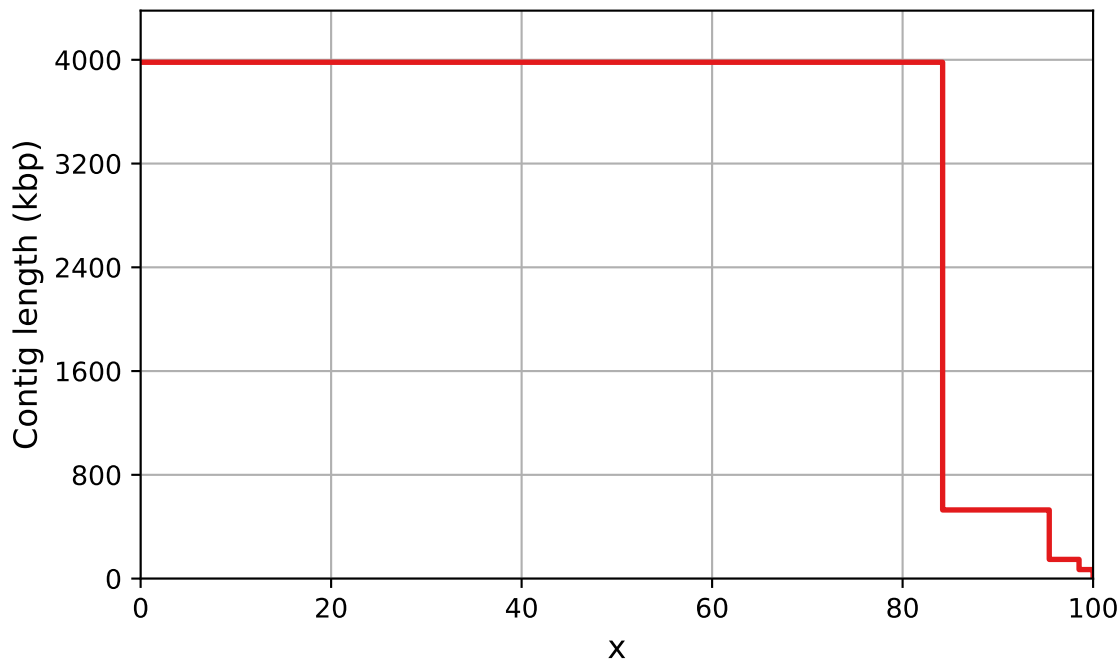
FRCurve (misassemblies)



Cumulative length (aligned contigs)

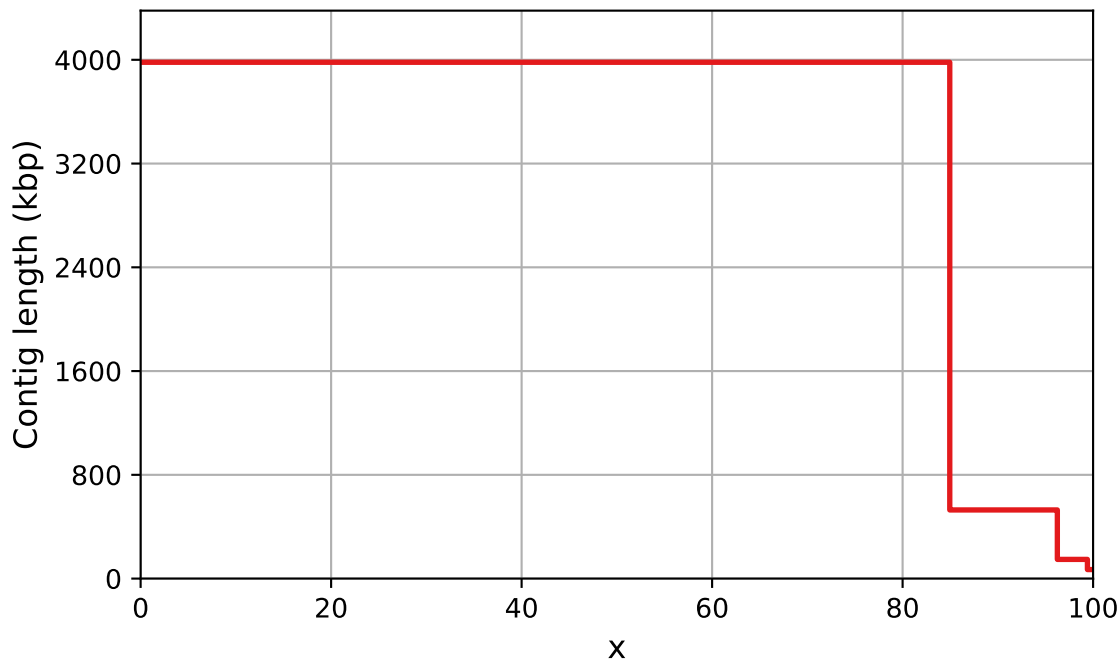


NAx



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NGAx



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