

Report

	CFL_ICFL_R_25_25
# contigs (>= 0 bp)	7
# contigs (>= 1000 bp)	7
# contigs (>= 5000 bp)	7
# contigs (>= 10000 bp)	7
# contigs (>= 25000 bp)	7
# contigs (>= 50000 bp)	7
Total length (>= 0 bp)	4733237
Total length (>= 1000 bp)	4733237
Total length (>= 5000 bp)	4733237
Total length (>= 10000 bp)	4733237
Total length (>= 25000 bp)	4733237
Total length (>= 50000 bp)	4733237
# contigs	7
Largest contig	3004181
Total length	4733237
Reference length	4686137
GC (%)	50.76
Reference GC (%)	50.78
N50	3004181
NG50	3004181
N90	366524
NG90	366524
auN	2049016.2
auNG	2069610.7
L50	1
LG50	1
L90	4
LG90	4
# misassemblies	3
# misassembled contigs	2
Misassembled contigs length	586849
# 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 (%)	97.923
Duplication ratio	1.031
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	3004181
Total aligned length	4733237
NA50	3004181
NGA50	3004181
NA90	177260
NGA90	177260
auNA	2026281.8
auNGA	2046647.8
LA50	1
LGA50	1
LA90	5
LGA90	5

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

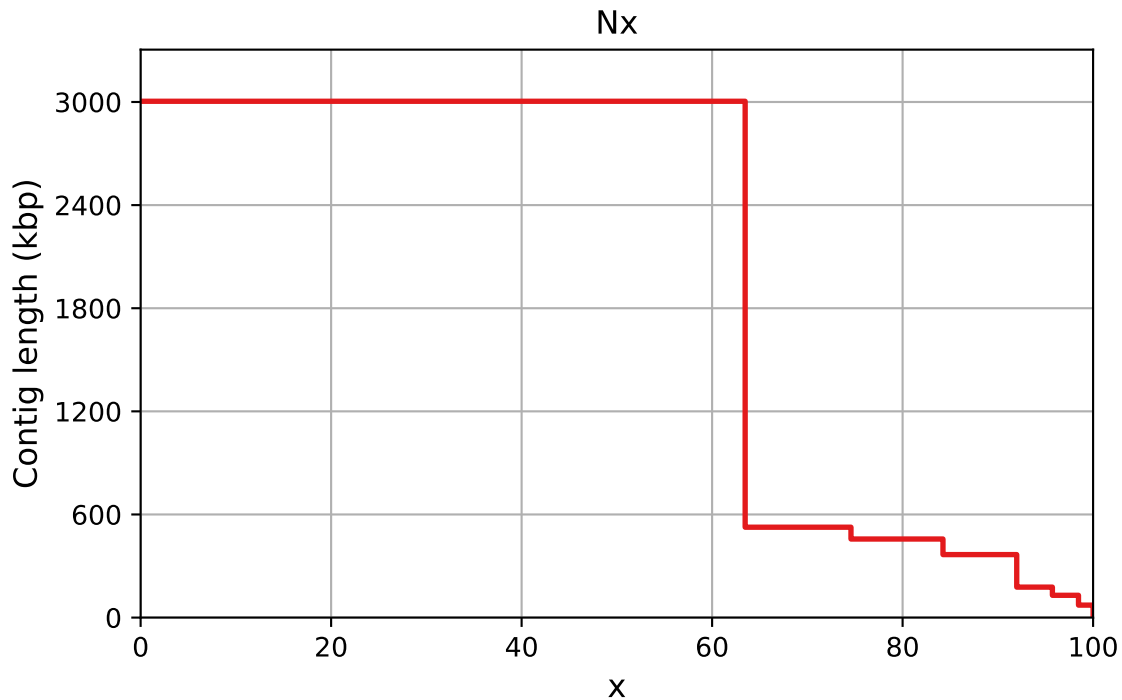
	CFL_ICFL_R_25_25
# misassemblies	3
# contig misassemblies	3
# c. relocations	3
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	2
Misassembled contigs length	586849
# local misassemblies	0
# scaffold gap 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

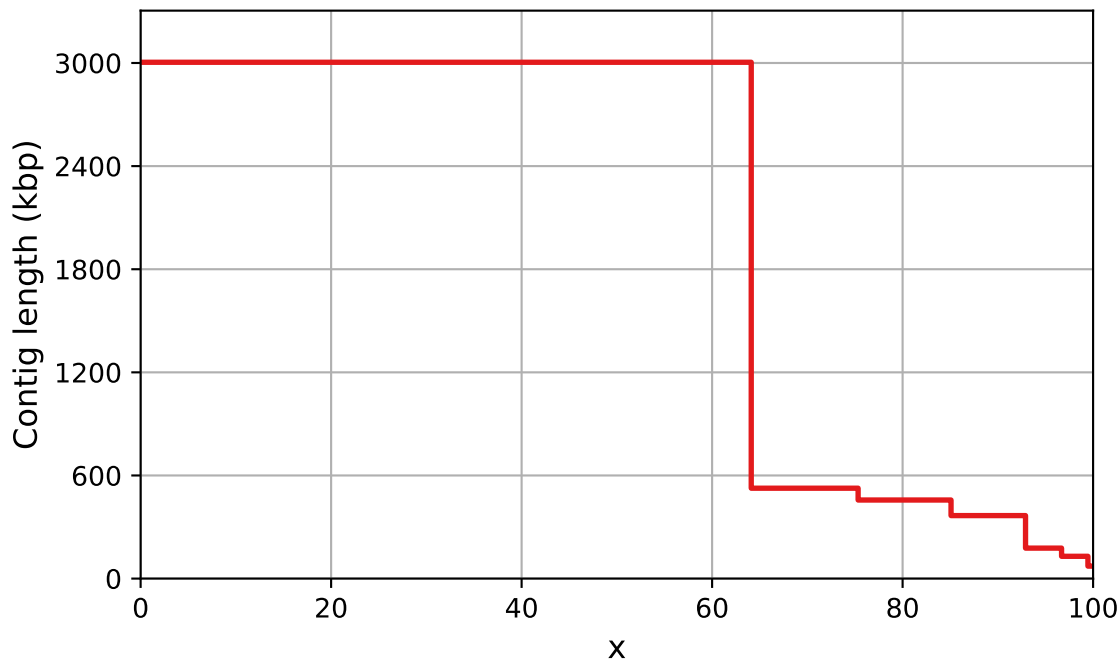
	CFL_ICFL_R_25_25
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).

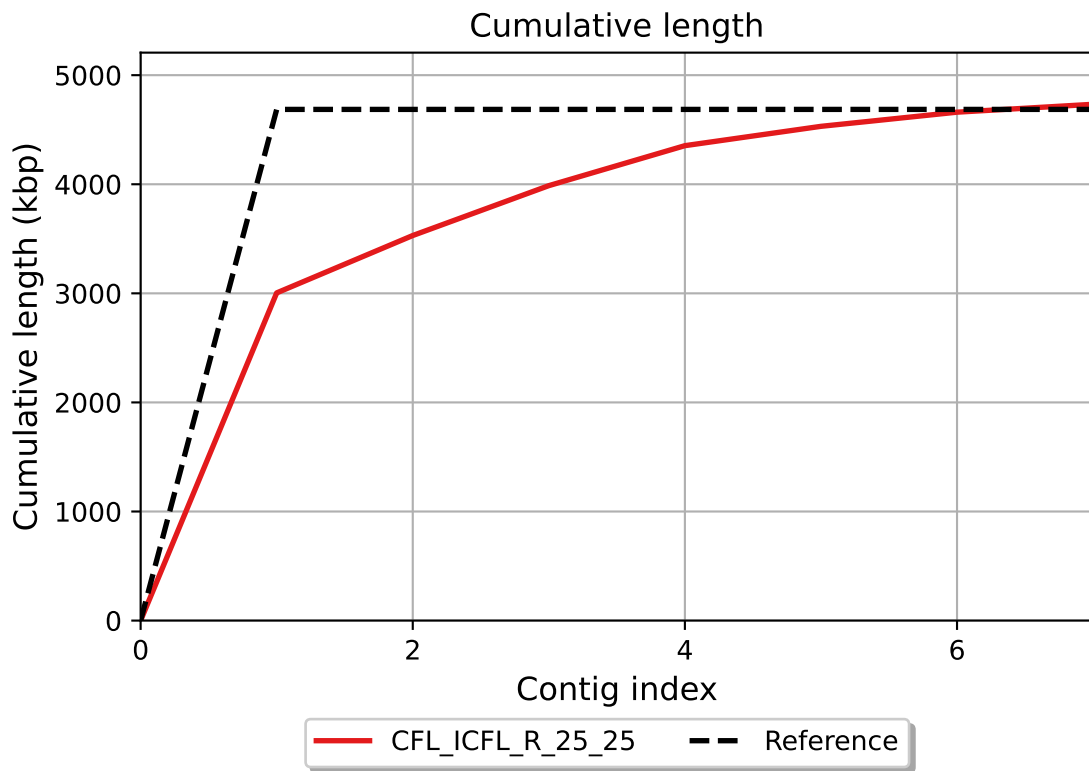


CFL_ICFL_R_25_25

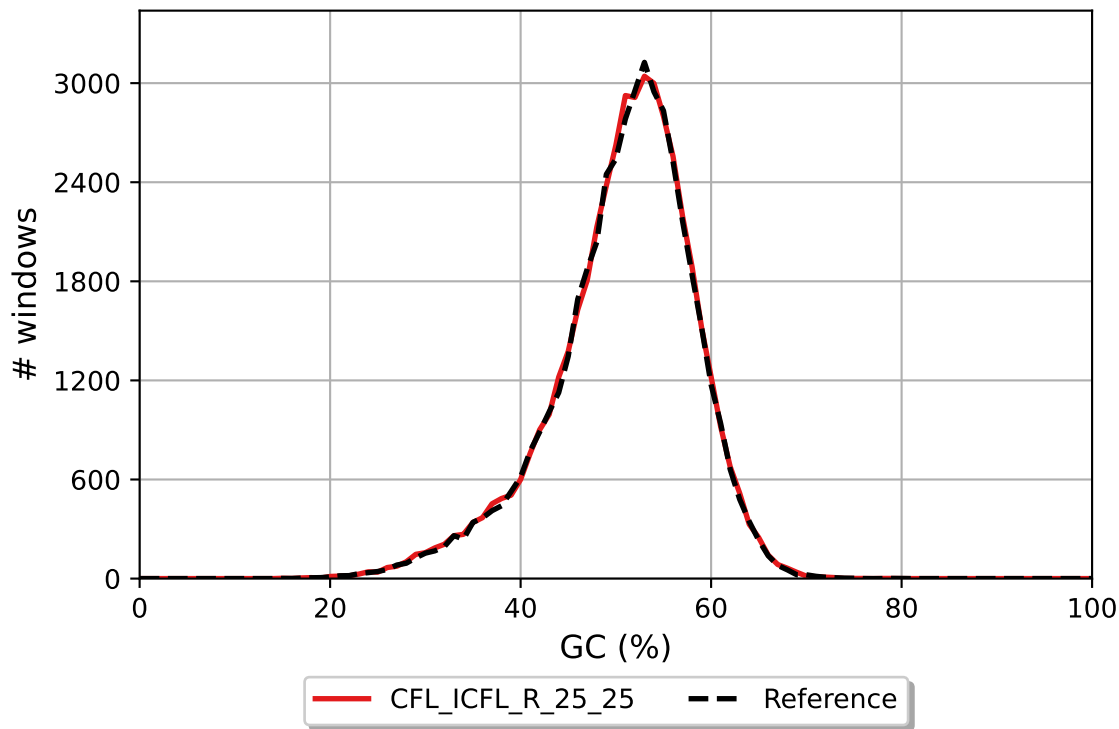
NGx



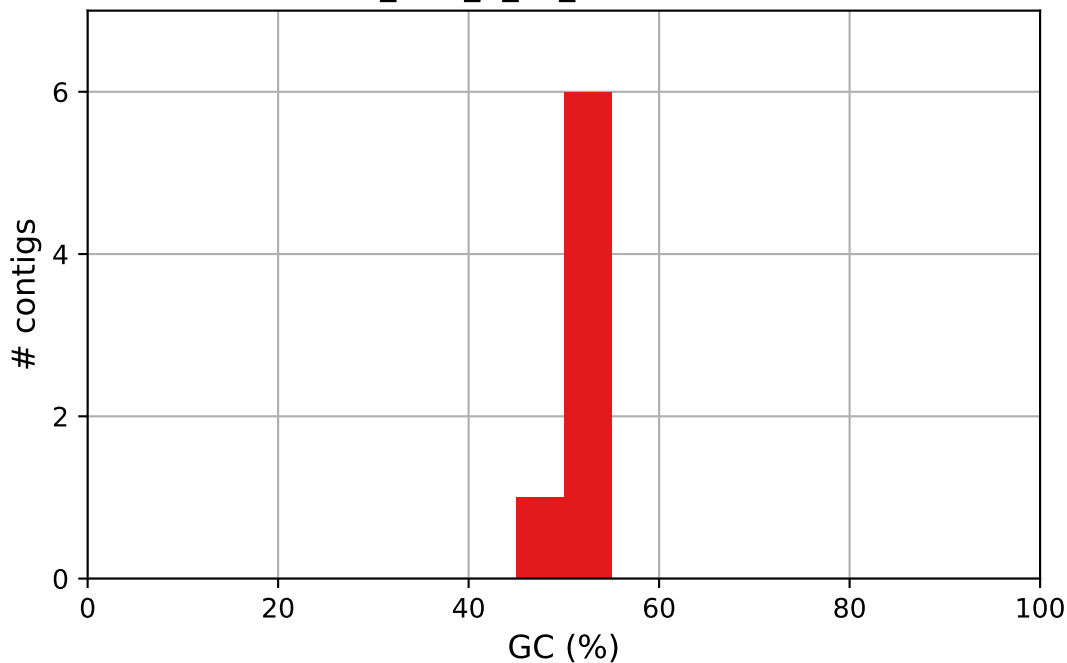
CFL_ICFL_R_25_25



GC content

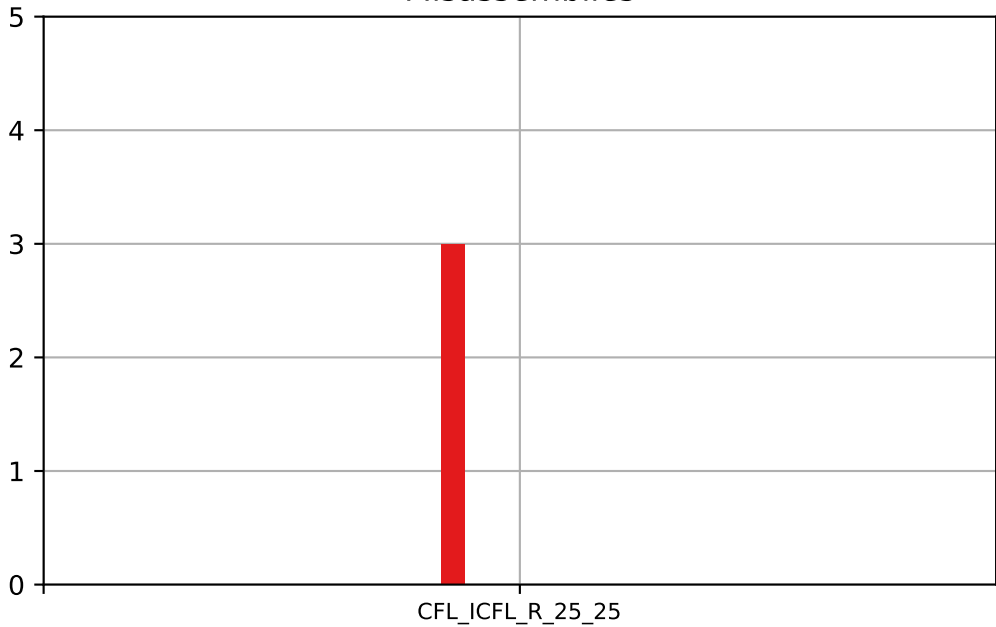


CFL_ICFL_R_25_25 GC content

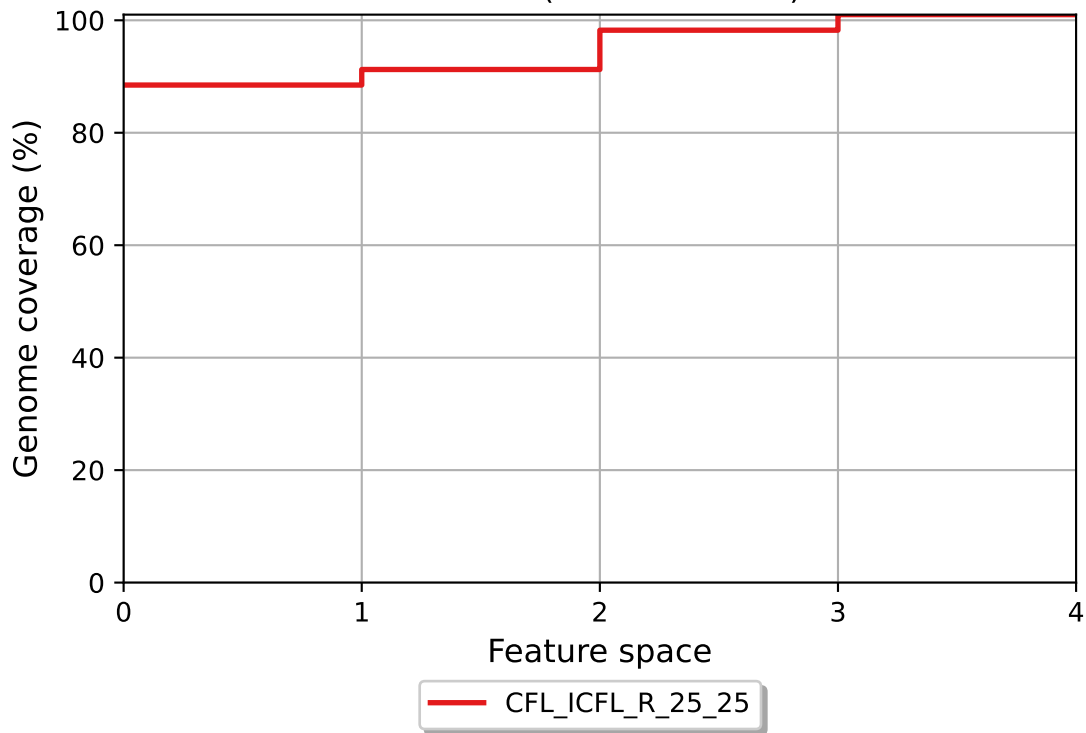


CFL_ICFL_R_25_25

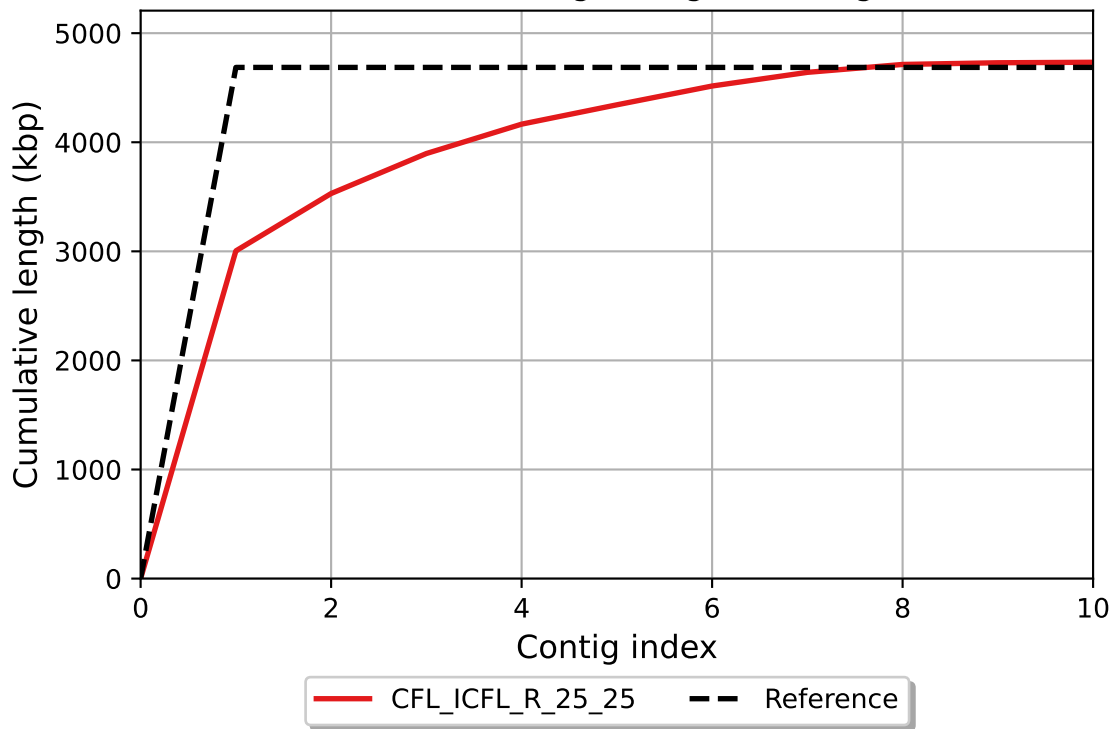
Misassemblies



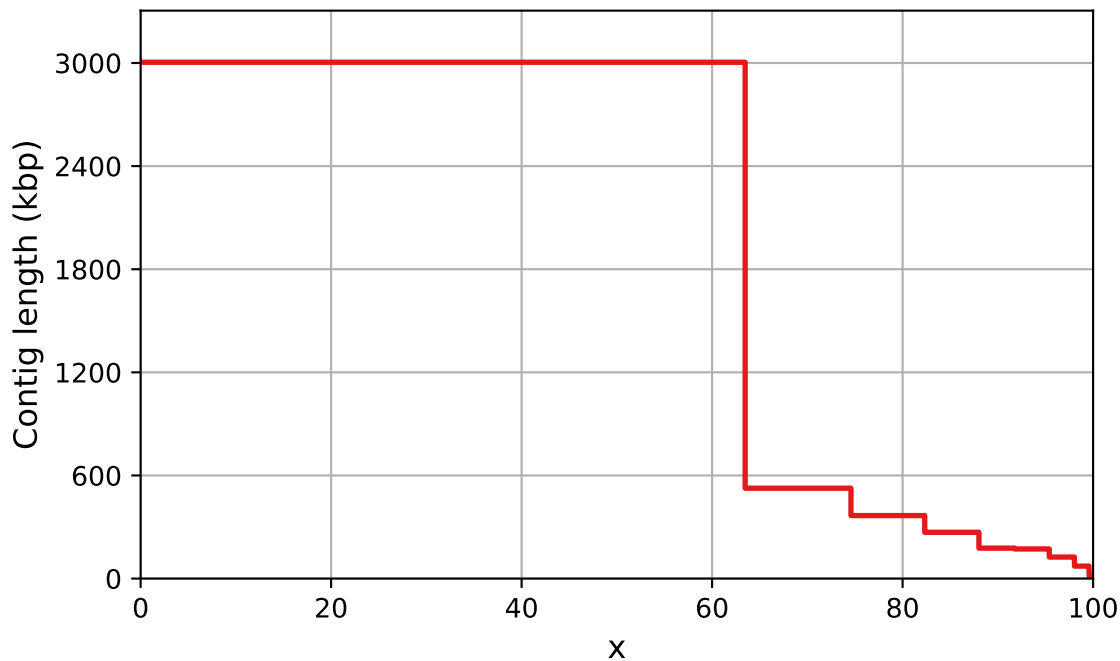
FRCurve (misassemblies)



Cumulative length (aligned contigs)

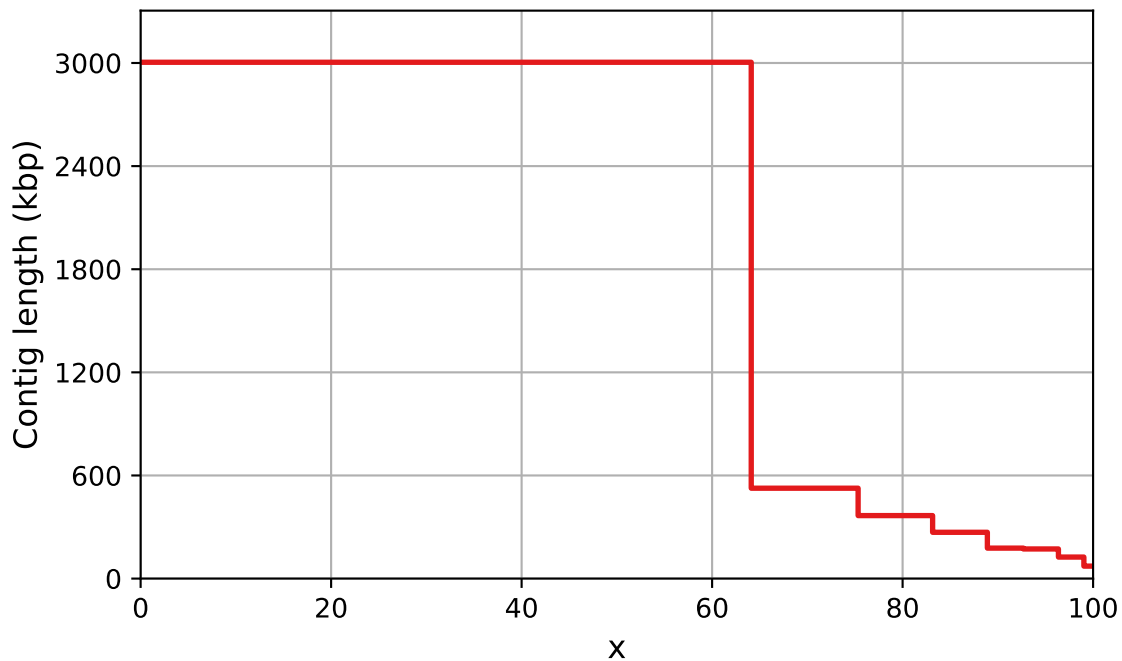


NAx



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NGAx



CFL_ICFL_R_25_25