

Report

	min5_CFL_ICFL_30_COMB_25
# 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)	4653364
Total length (>= 1000 bp)	4653364
Total length (>= 5000 bp)	4653364
Total length (>= 10000 bp)	4653364
Total length (>= 25000 bp)	4653364
Total length (>= 50000 bp)	4653364
# contigs	3
Largest contig	3978193
Total length	4653364
Reference length	4686137
GC (%)	50.75
Reference GC (%)	50.78
N50	3978193
NG50	3978193
N90	524882
NG90	524882
auN	3465043.2
auNG	3440810.1
L50	1
LG50	1
L90	2
LG90	2
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	150289
# 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 (%)	98.058
Duplication ratio	1.013
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	3978193
Total aligned length	4653364
NA50	3978193
NGA50	3978193
NA90	524882
NGA90	524882
auNA	3463191.4
auNGA	3438971.2
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

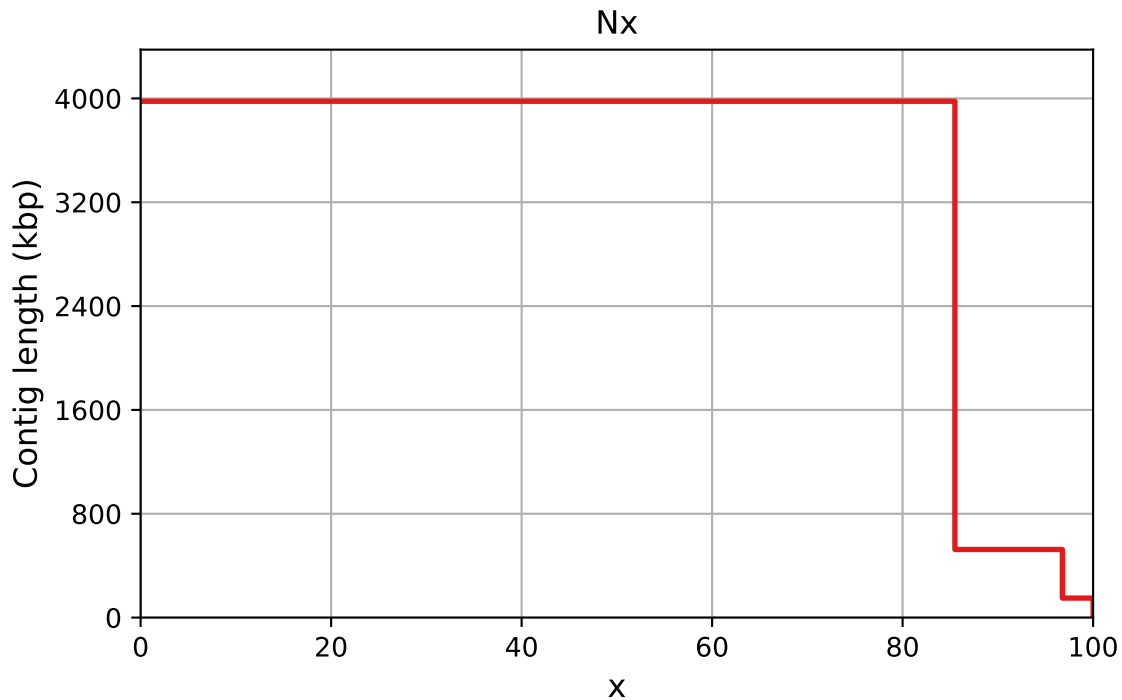
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# misassemblies	1
# contig misassemblies	1
# c. relocations	1
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	150289
# 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

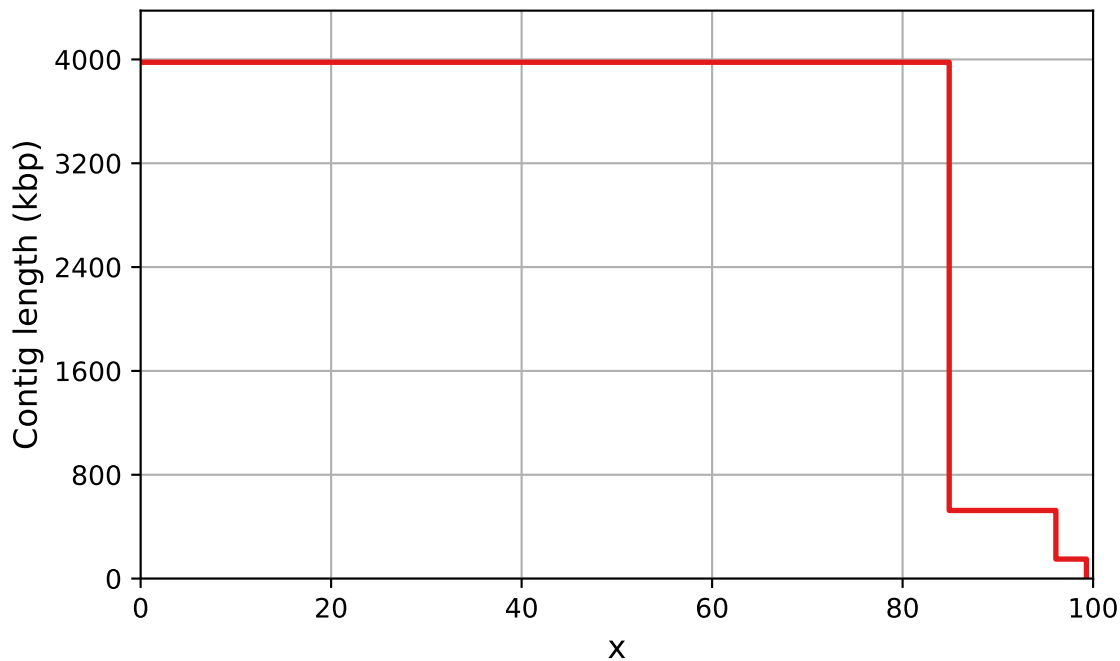
	min5_CFL_ICFL_30_COMB_25
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).

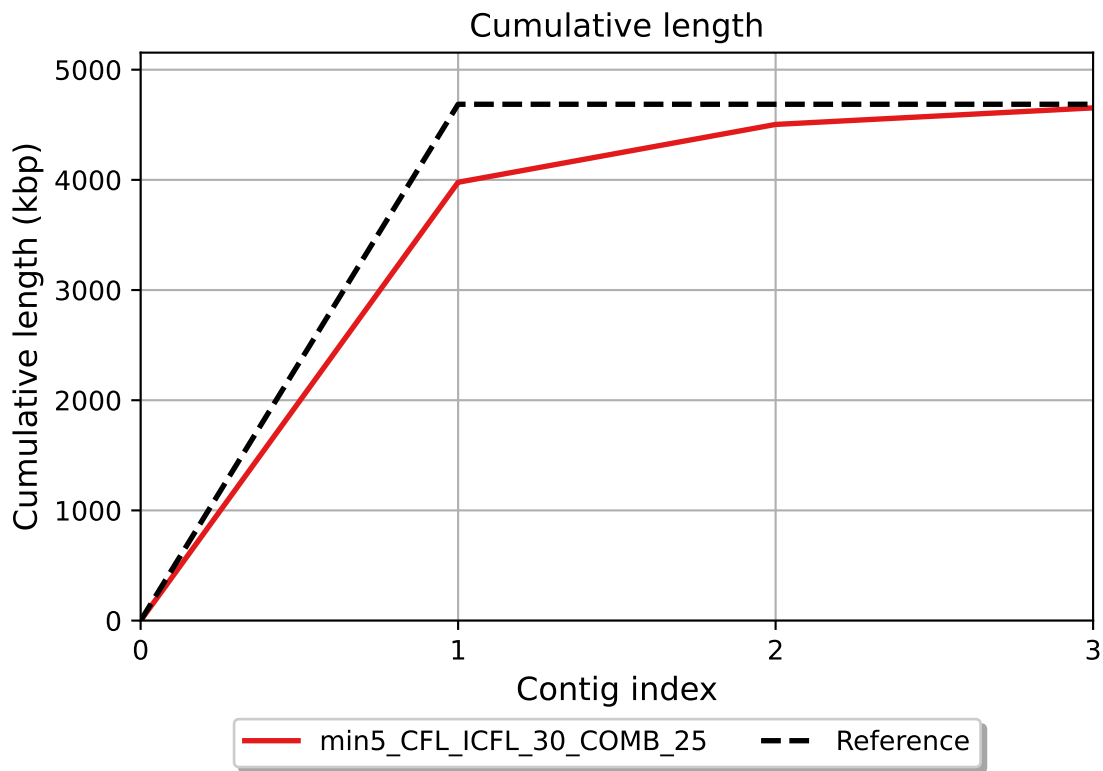


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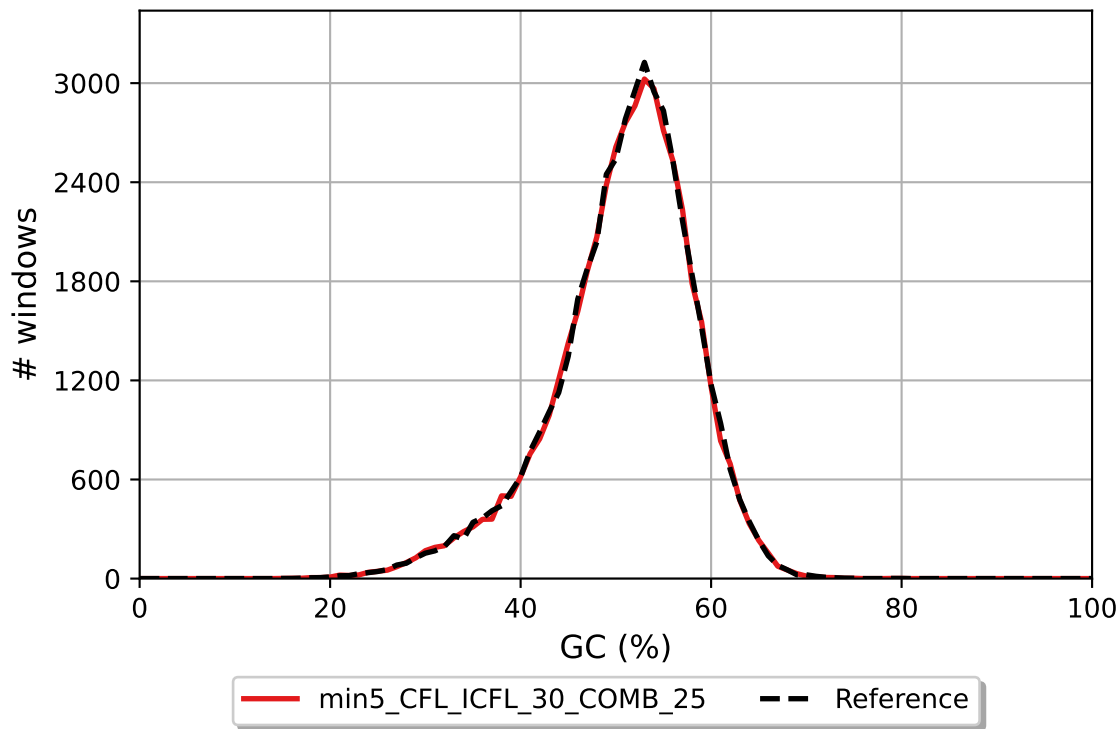
NGx



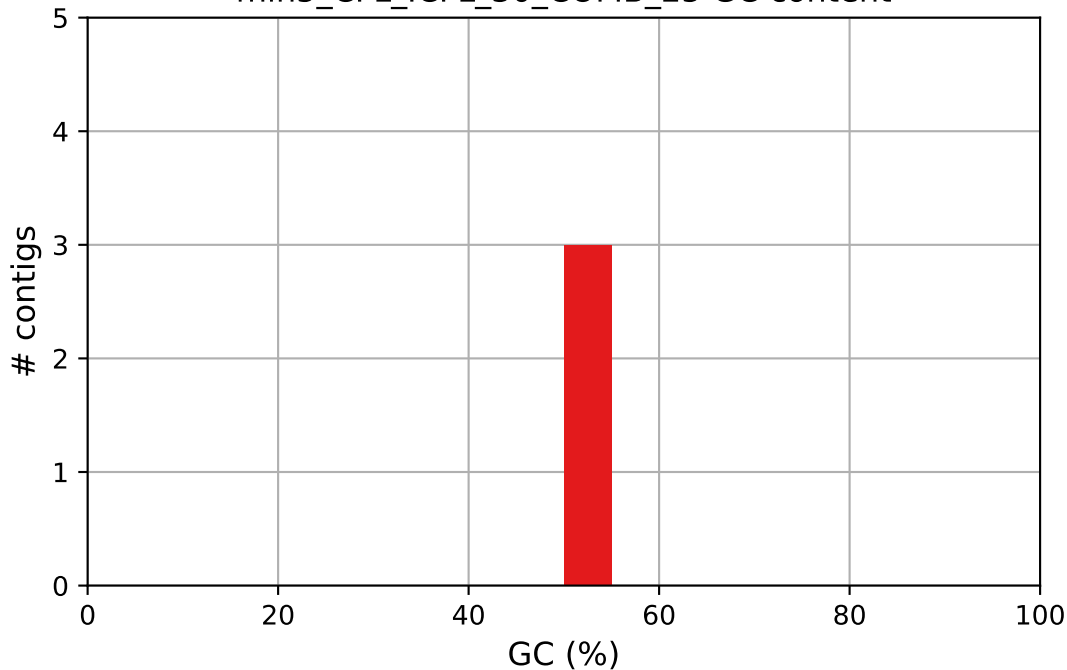
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GC content

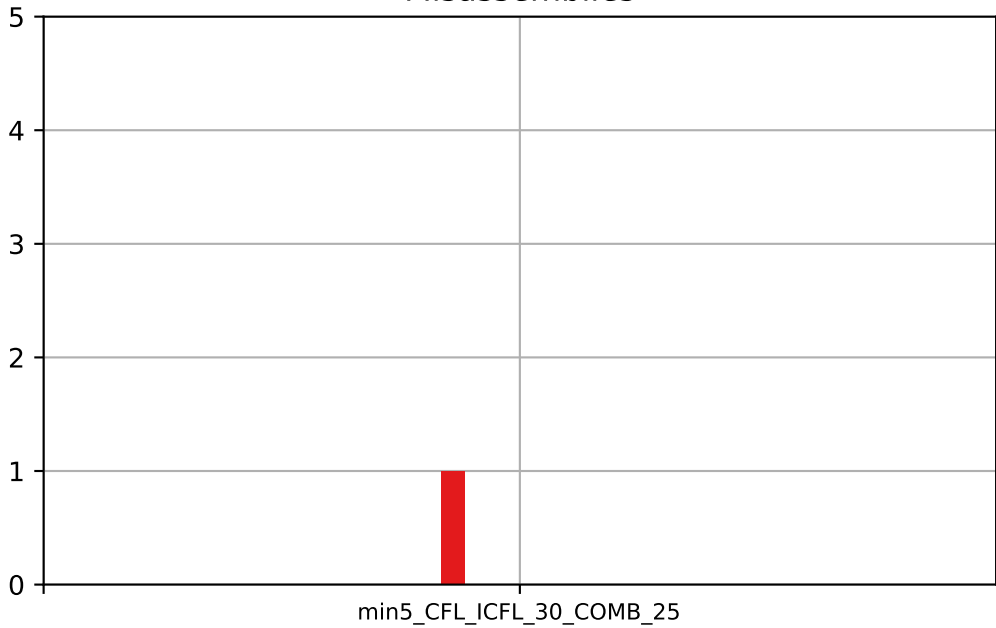


min5_CFL_ICFL_30_COMB_25 GC content



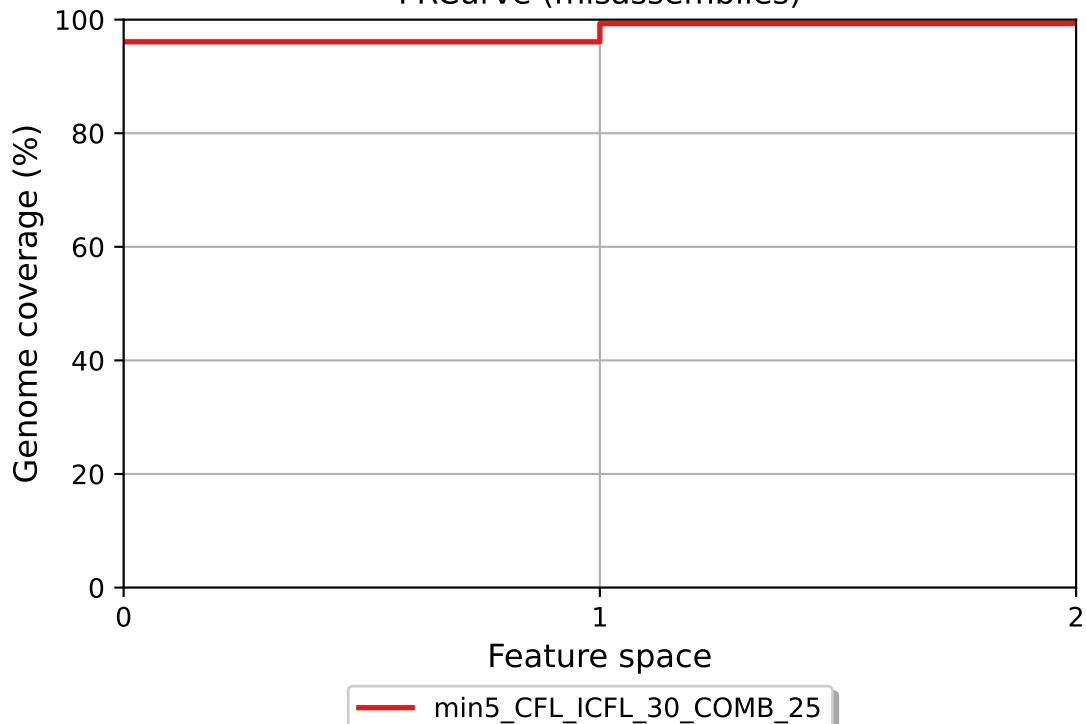
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Misassemblies

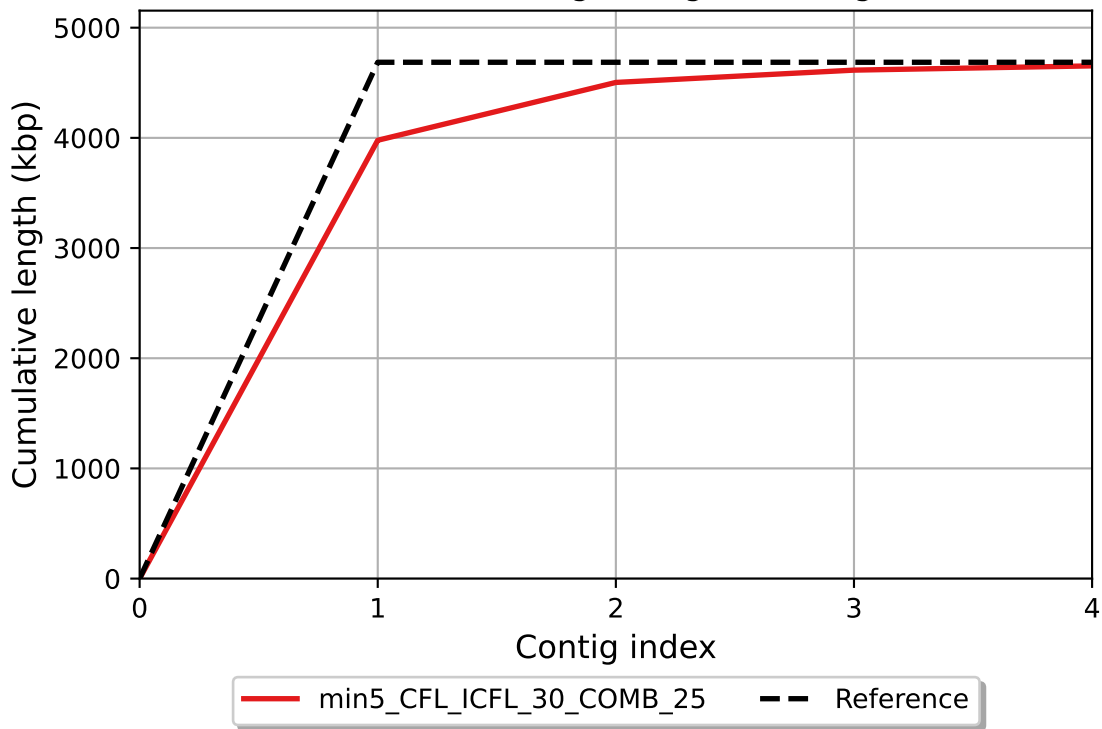


 # relocations

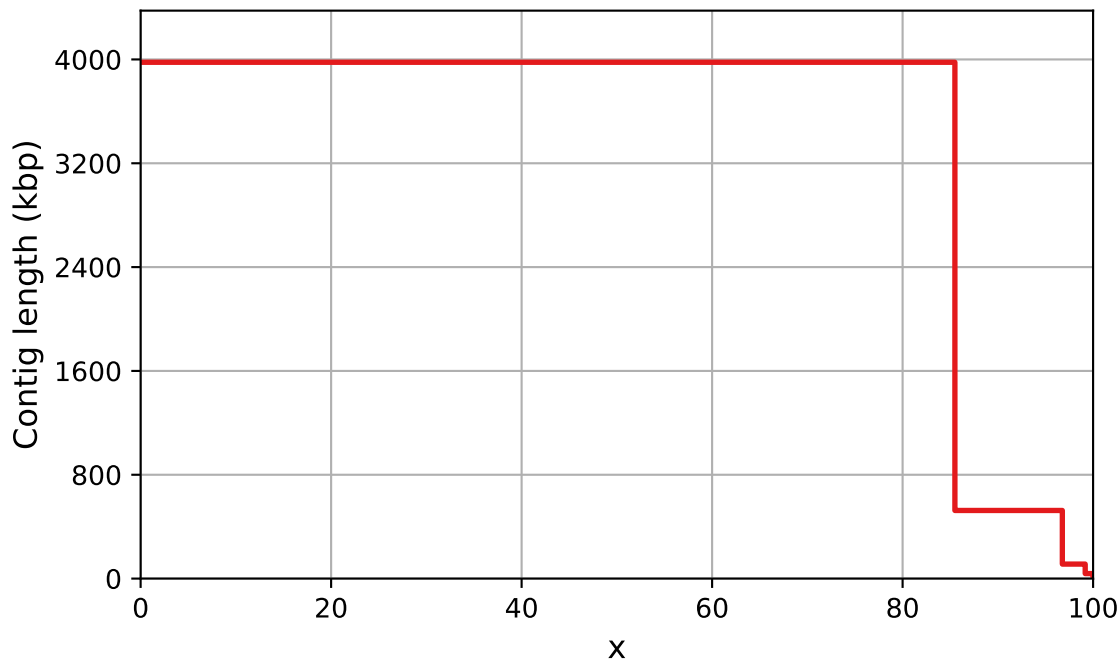
FRCurve (misassemblies)



Cumulative length (aligned contigs)

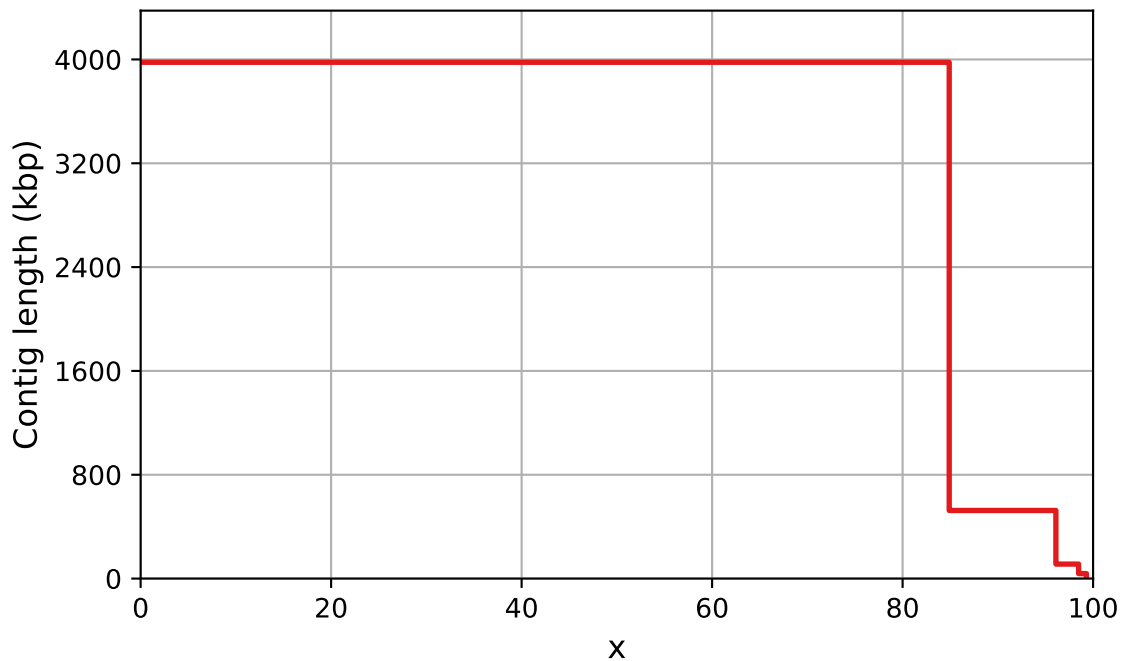


NAx



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NGAx



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