

Report

	min5_CFL_ICFL_R_35_50
# 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)	4642541
Total length (>= 1000 bp)	4642541
Total length (>= 5000 bp)	4642541
Total length (>= 10000 bp)	4642541
Total length (>= 25000 bp)	4642541
Total length (>= 50000 bp)	4642541
# contigs	3
Largest contig	3607891
Total length	4642541
Reference length	4686137
GC (%)	50.82
Reference GC (%)	50.78
N50	3607891
NG50	3607891
N90	858552
NG90	858552
auN	2969279.0
auNG	2941655.3
L50	1
LG50	1
L90	2
LG90	2
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	3607891
# 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 (%)	97.485
Duplication ratio	1.016
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	3100255
Total aligned length	4642541
NA50	3100255
NGA50	3100255
NA90	507636
NGA90	507636
auNA	2291287.8
auNGA	2269971.5
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

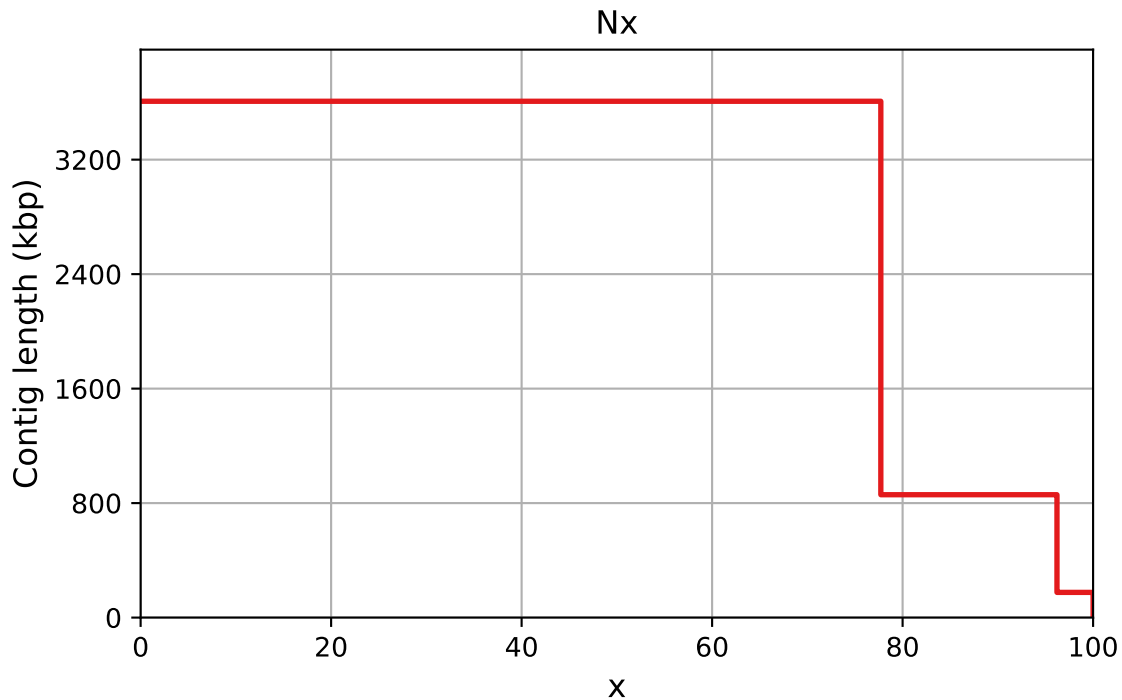
	min5_CFL_ICFL_R_35_50
# misassemblies	1
# contig misassemblies	1
# c. relocations	1
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	3607891
# local misassemblies	0
# scaffold 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  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

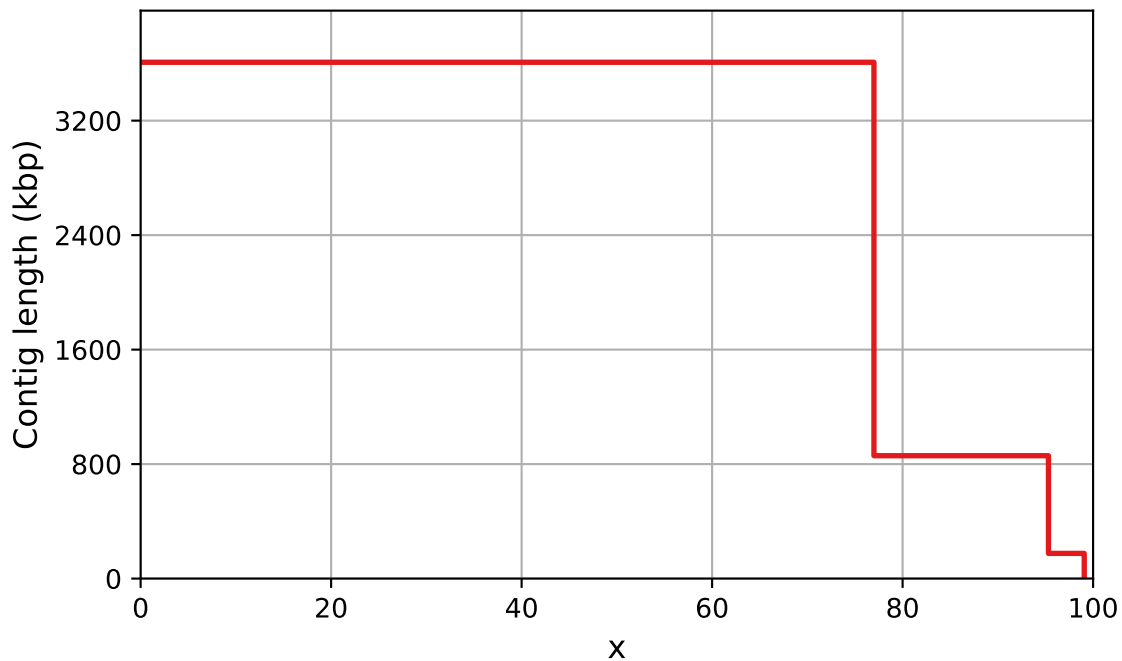
	min5_CFL_ICFL_R_35_50
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

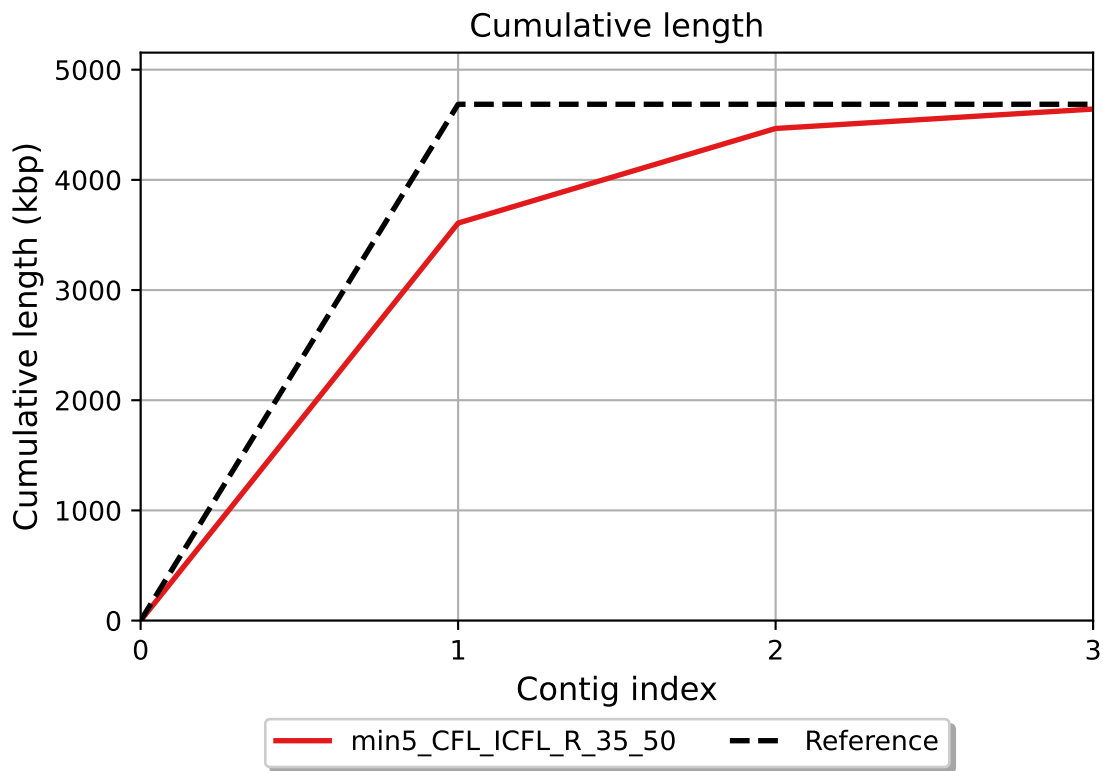


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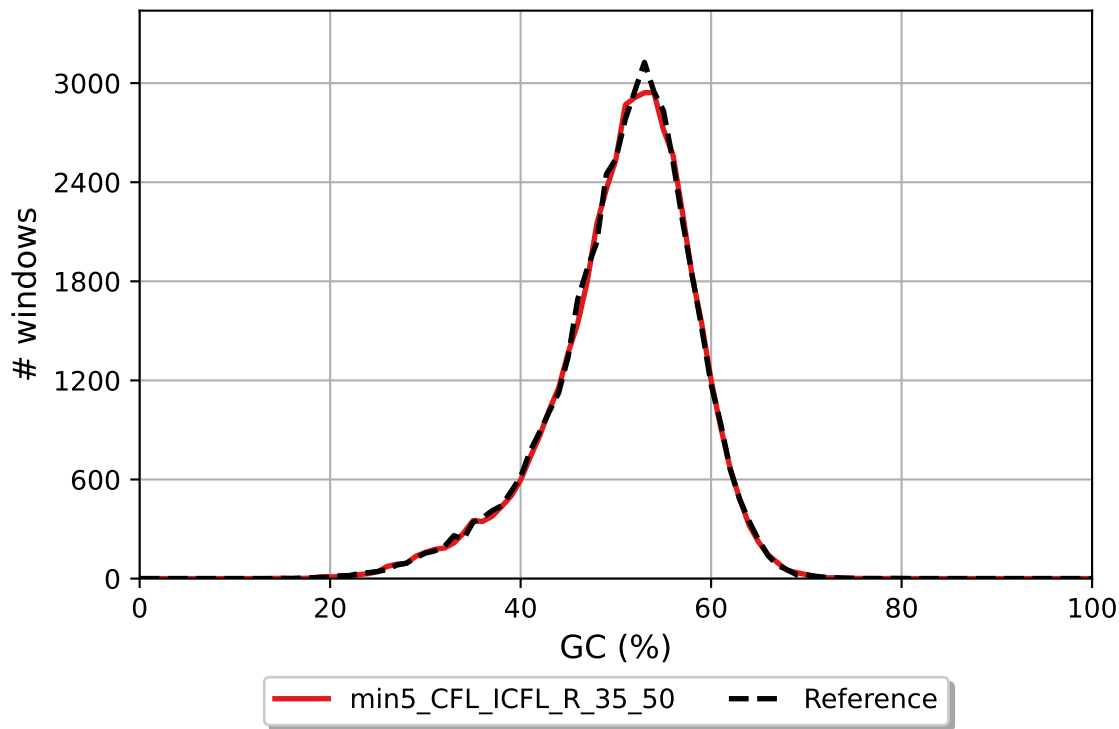
NGx



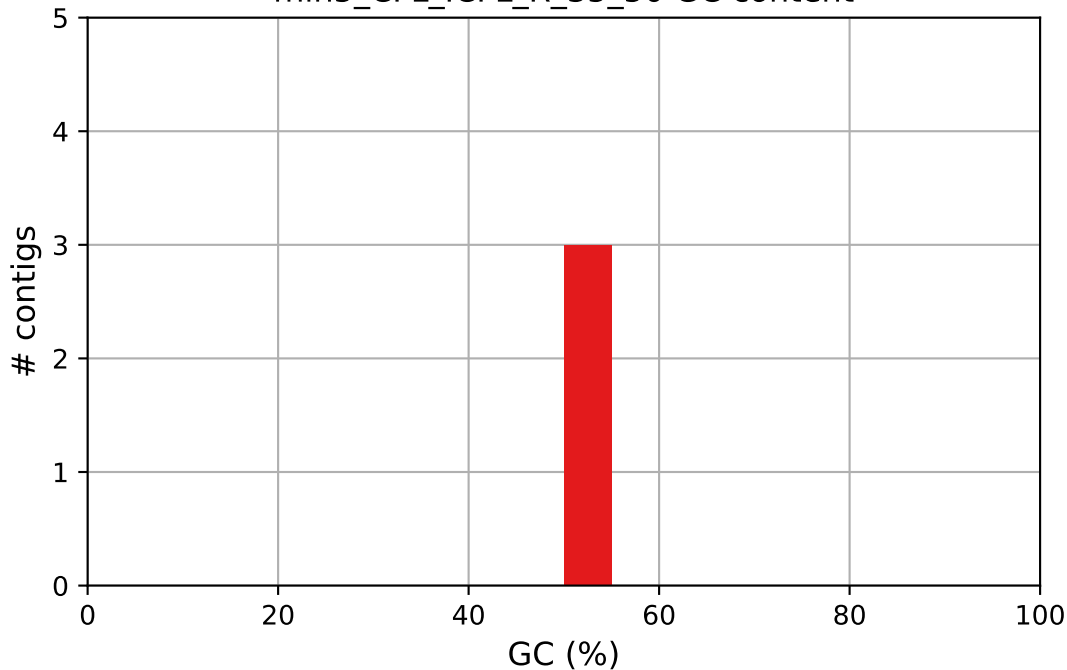
min5\_CFL\_ICFL\_R\_35\_50



## GC content



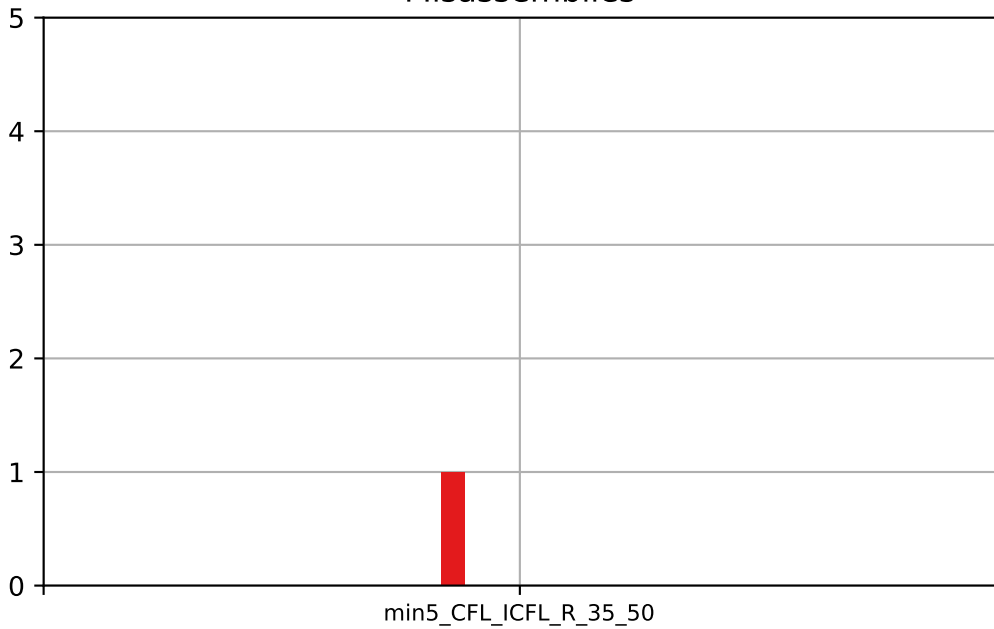
min5\_CFL\_ICFL\_R\_35\_50 GC content



min5\_CFL\_ICFL\_R\_35\_50

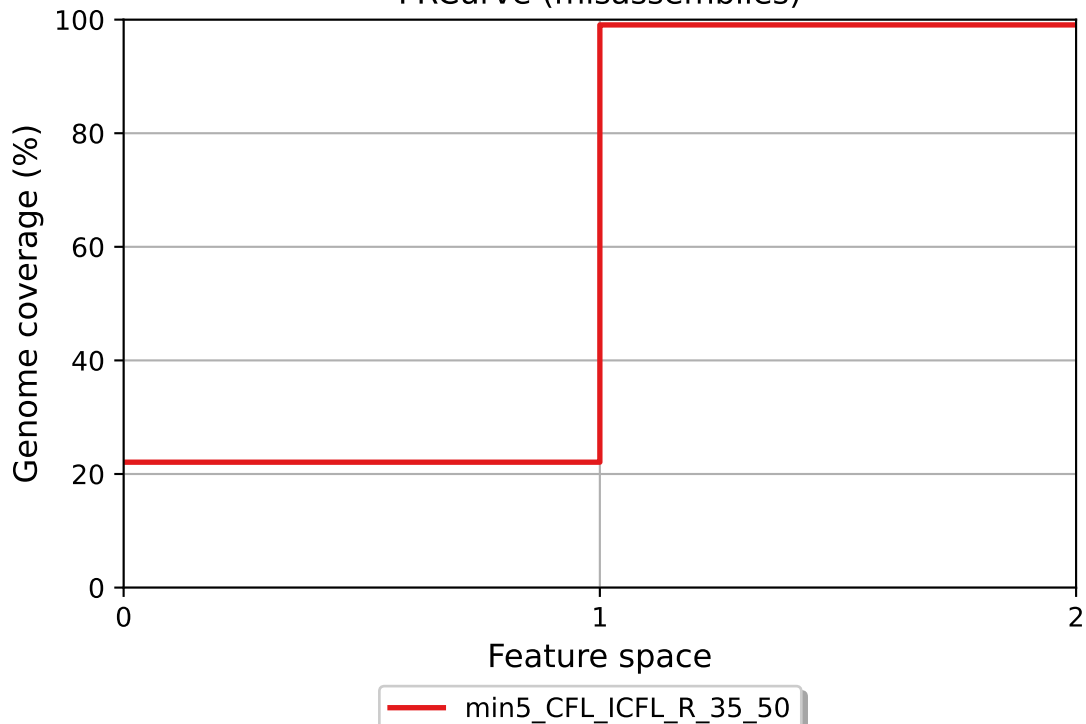


## Misassemblies

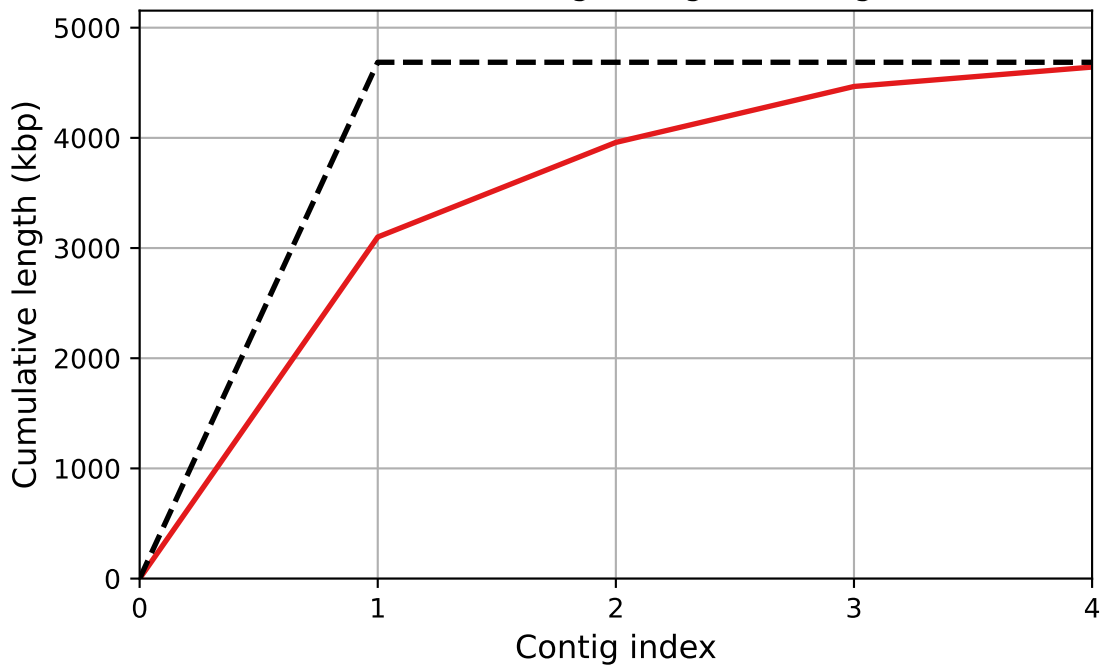


 # relocations

FRCurve (misassemblies)

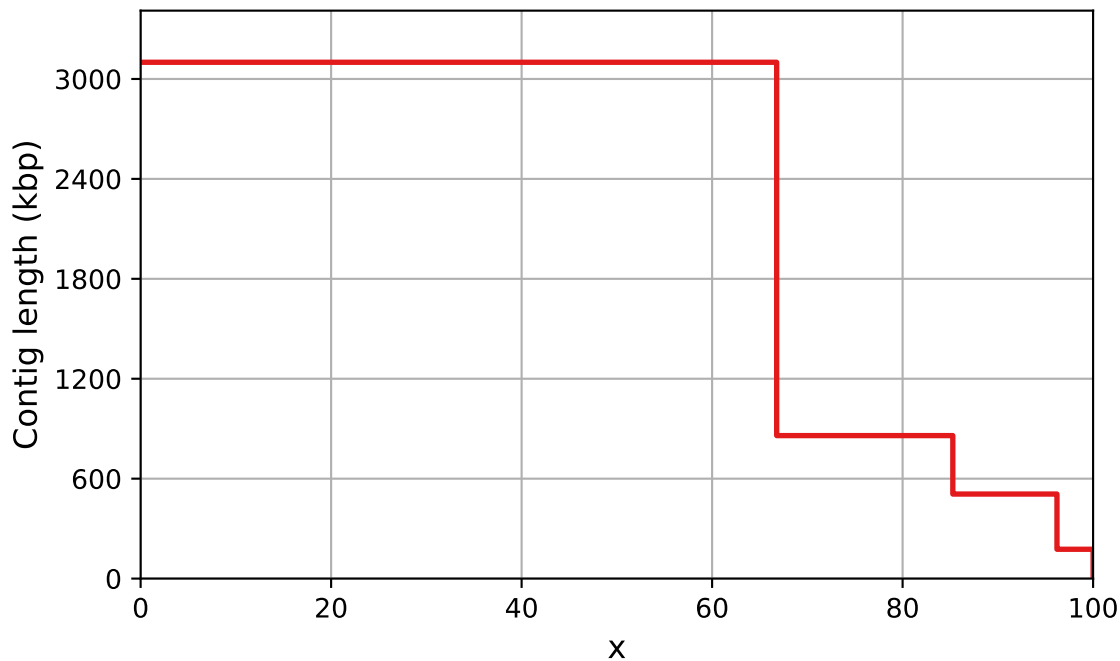


Cumulative length (aligned contigs)



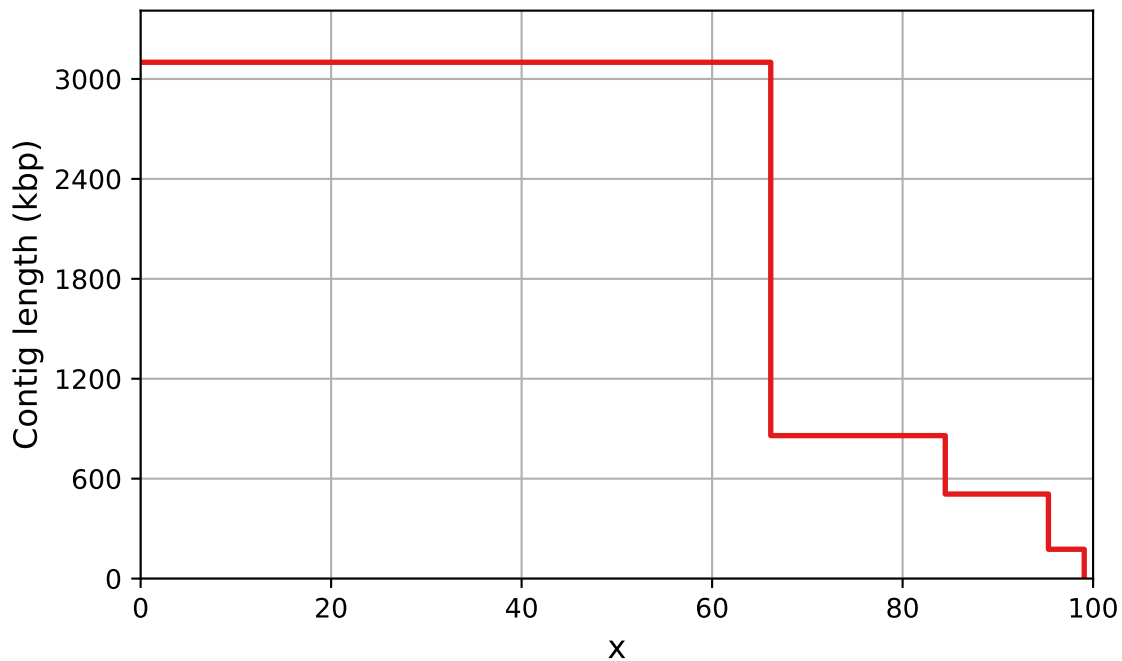
min5\_CFL\_ICFL\_R\_35\_50      Reference

NAx



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# NGAx



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