

Report

	min5_CFL_ICFL_R_25_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)	4582416
Total length (>= 1000 bp)	4582416
Total length (>= 5000 bp)	4582416
Total length (>= 10000 bp)	4582416
Total length (>= 25000 bp)	4582416
Total length (>= 50000 bp)	4582416
# contigs	3
Largest contig	3952705
Total length	4582416
Reference length	4686137
GC (%)	50.75
Reference GC (%)	50.78
N50	3952705
NG50	3952705
N90	516451
NG90	516451
auN	3470533.1
auNG	3393717.7
L50	1
LG50	1
L90	2
LG90	2
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	113260
# 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 (%)	97.334
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	3952705
Total aligned length	4582416
NA50	3952705
NGA50	3952705
NA90	516451
NGA90	516451
auNA	3469428.9
auNGA	3392638.0
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

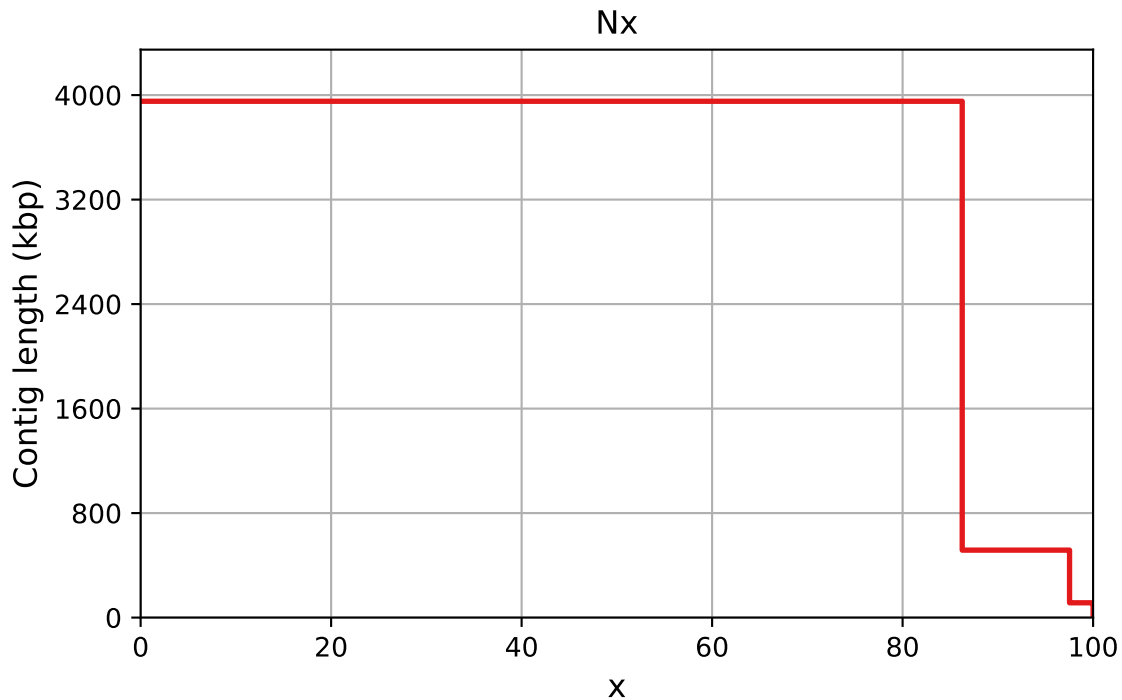
	min5_CFL_ICFL_R_25_25
# misassemblies	1
# contig misassemblies	1
# c. relocations	1
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	113260
# local misassemblies	0
# scaffold 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

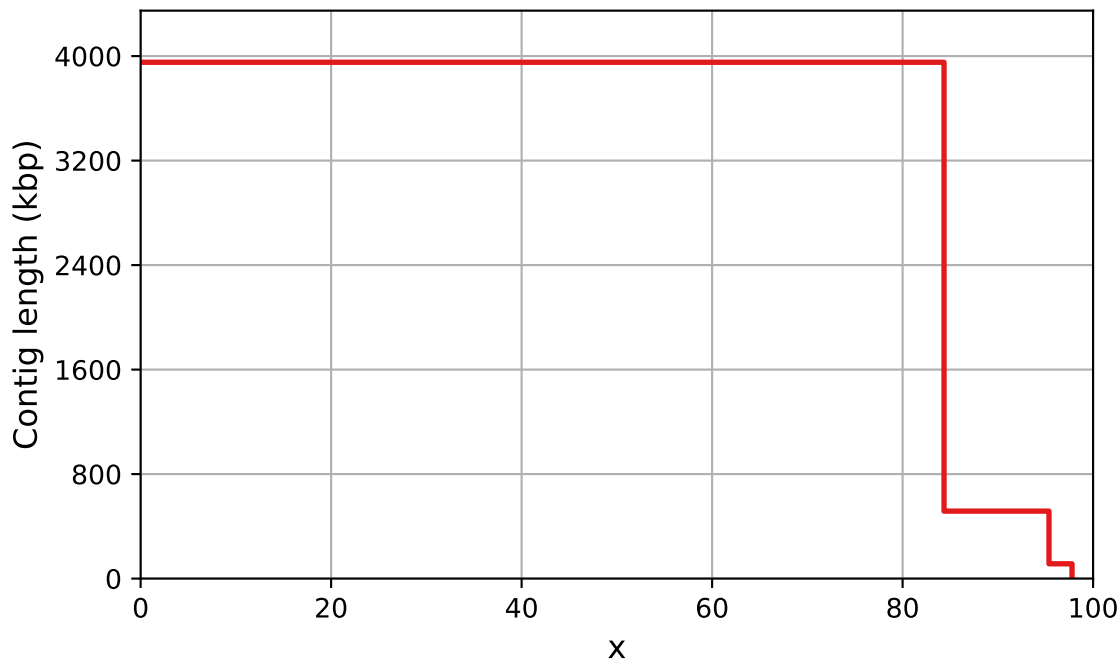
	min5_CFL_ICFL_R_25_25
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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

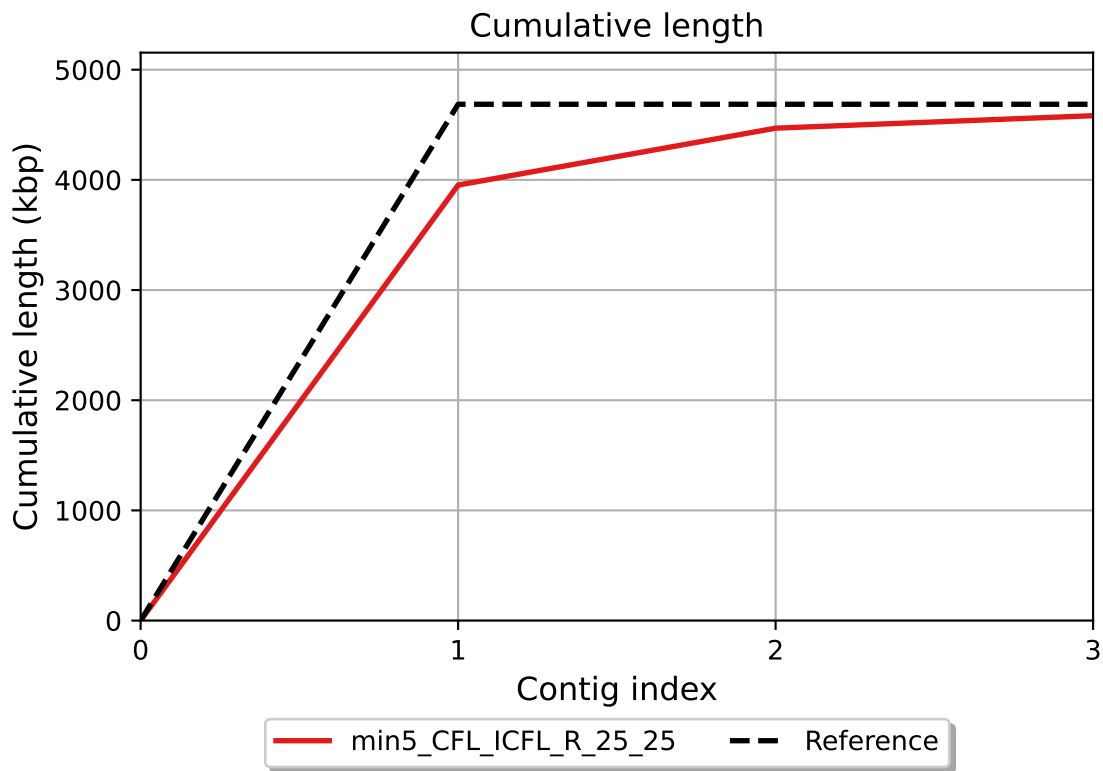


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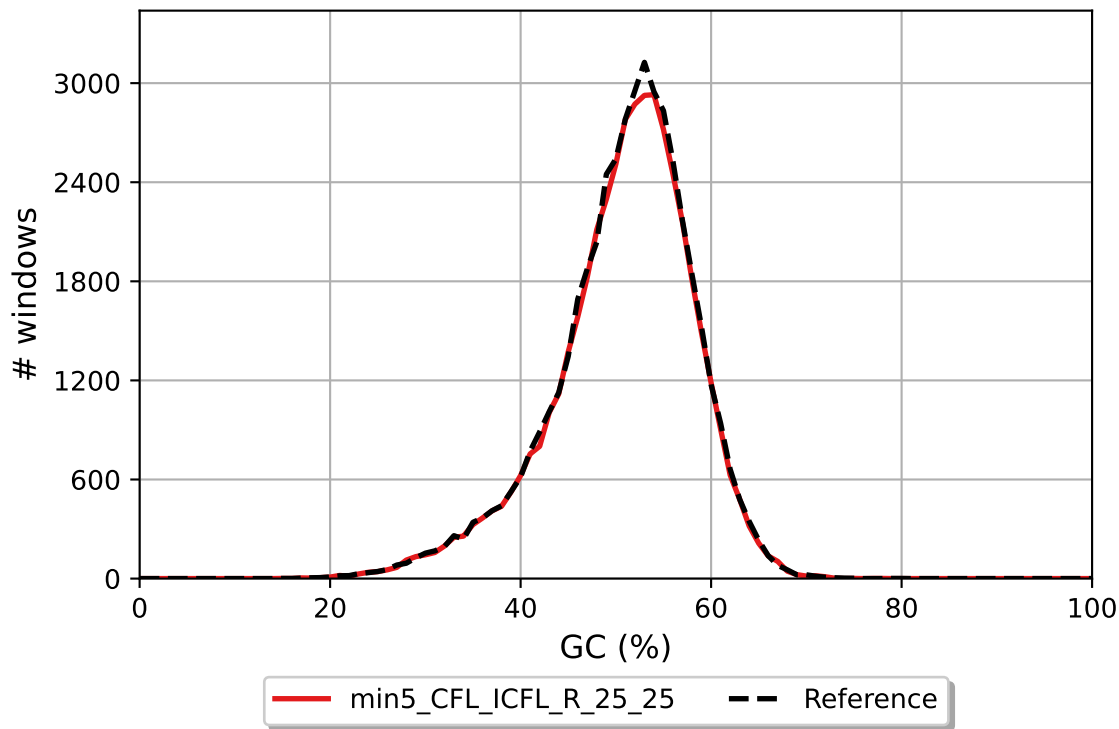
NGx



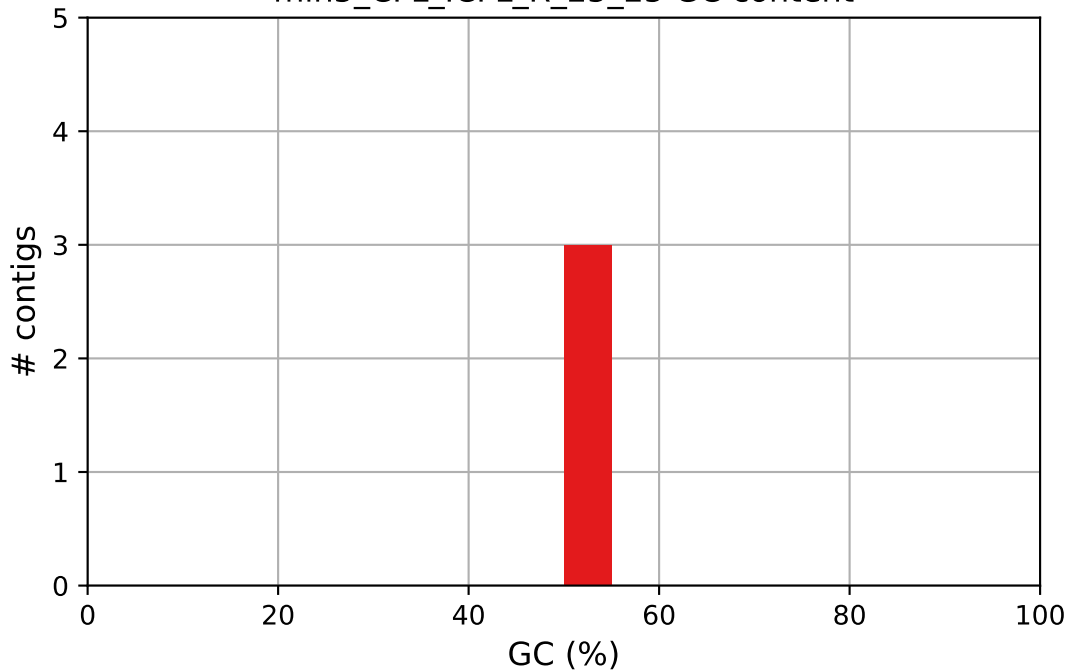
min5\_CFL\_ICFL\_R\_25\_25



## GC content



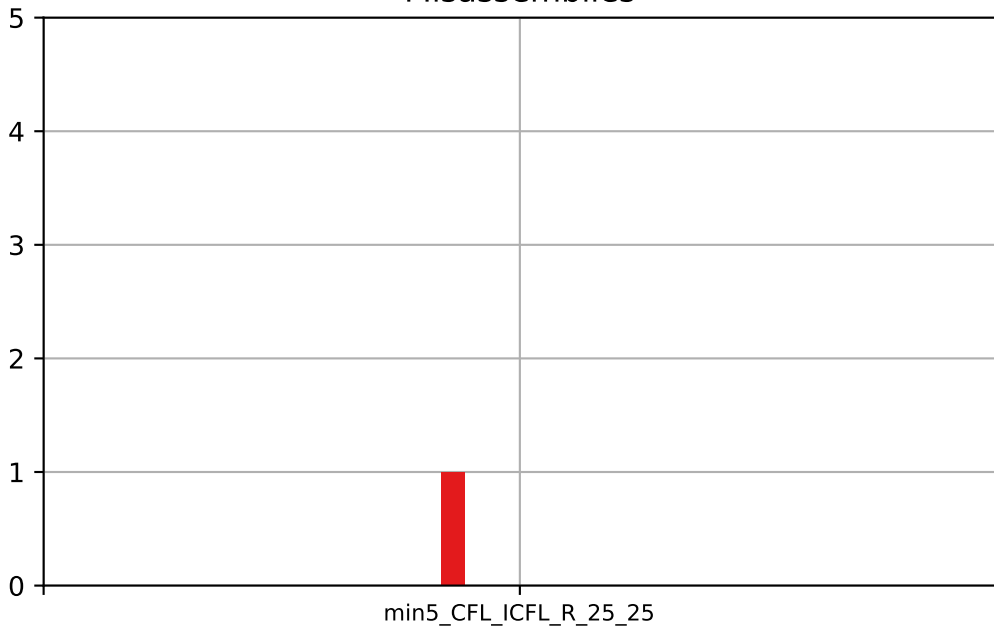
min5\_CFL\_ICFL\_R\_25\_25 GC content



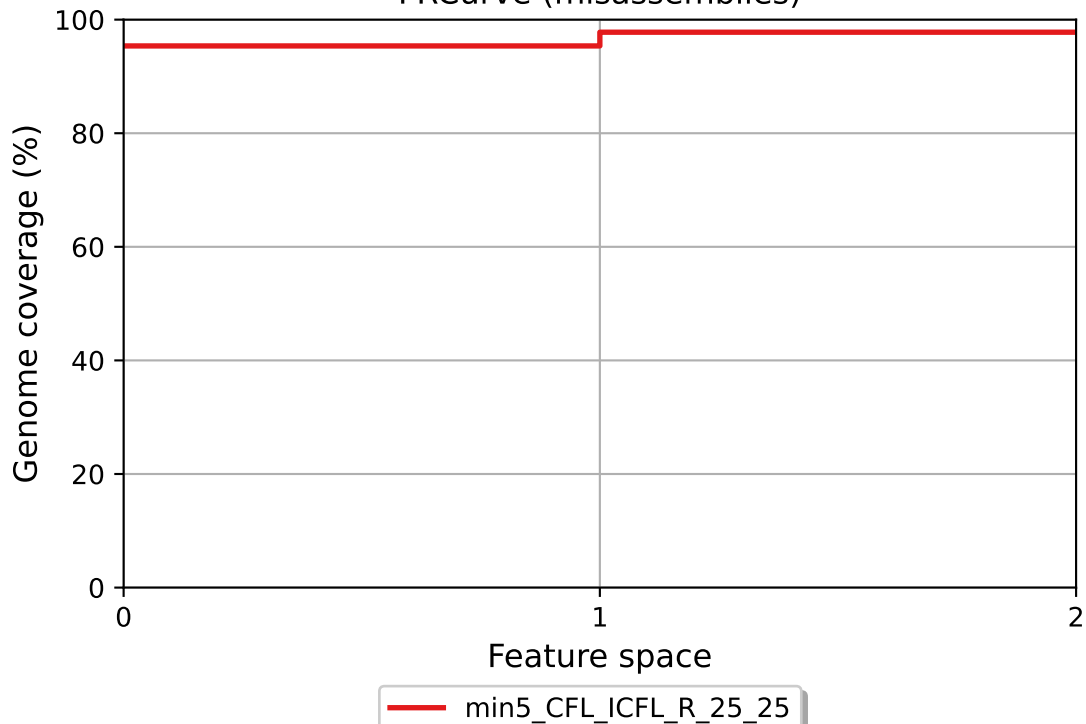
min5\_CFL\_ICFL\_R\_25\_25



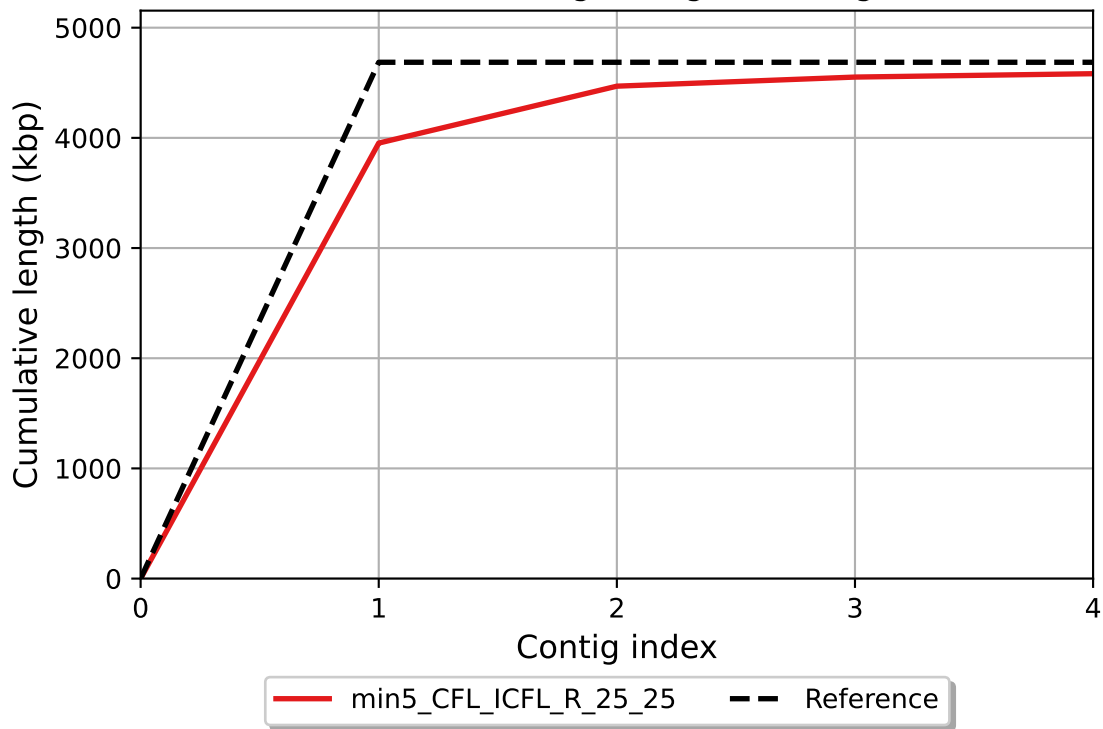
## Misassemblies



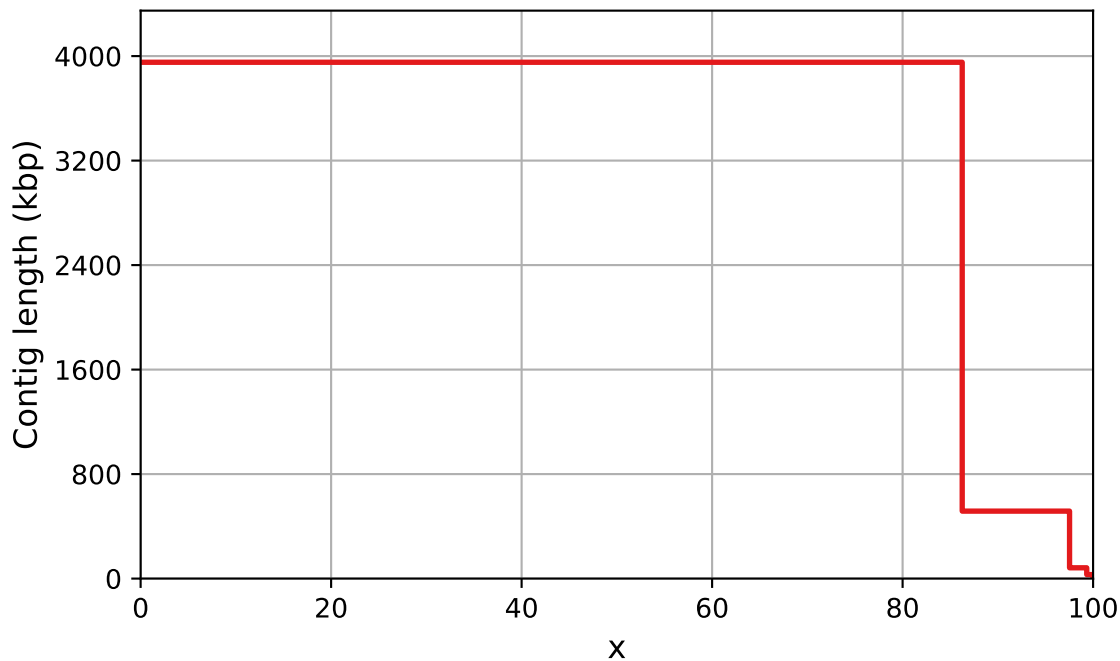
FRCurve (misassemblies)



Cumulative length (aligned contigs)

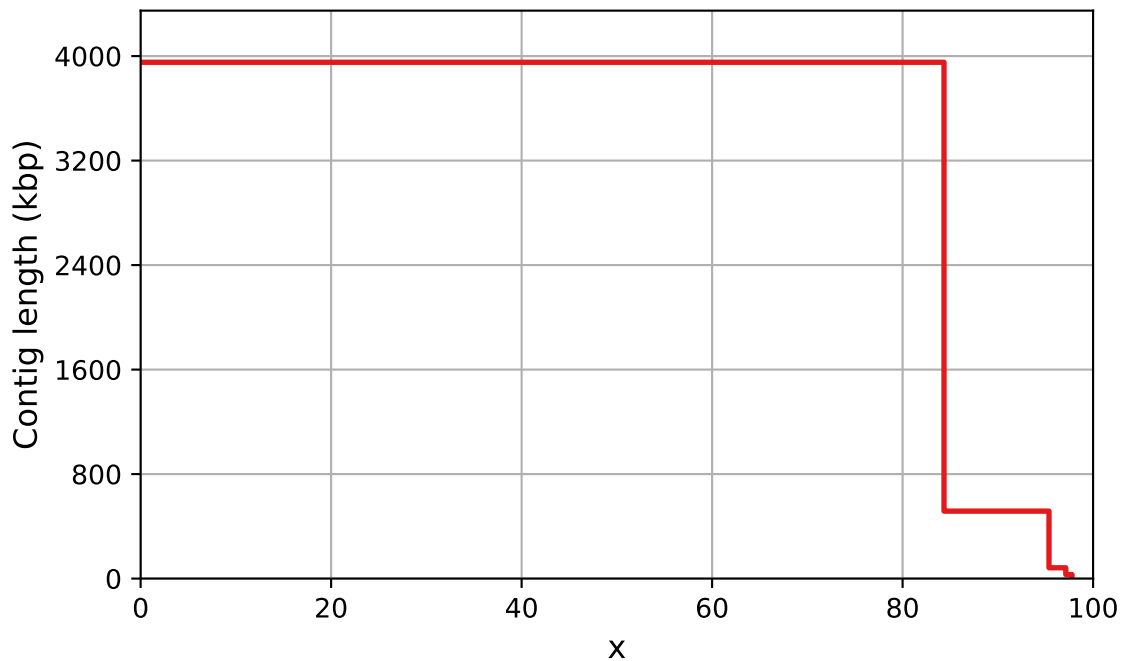


NAx



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# NGAx



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