

# Report

	min5_CFL_ICFL_R_35_100
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	4571054
Total length (>= 1000 bp)	4571054
Total length (>= 5000 bp)	4571054
Total length (>= 10000 bp)	4571054
Total length (>= 25000 bp)	4571054
Total length (>= 50000 bp)	4571054
# contigs	1
Largest contig	4571054
Total length	4571054
Reference length	4686137
GC (%)	50.79
Reference GC (%)	50.78
N50	4571054
NG50	4571054
N90	4571054
NG90	4571054
auN	4571054.0
auNG	4458797.2
L50	1
LG50	1
L90	1
LG90	1
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	4571054
# 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 (%)	97.544
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	4058919
Total aligned length	4571054
NA50	4058919
NGA50	4058919
NA90	512135
NGA90	512135
auNA	3661541.9
auNGA	3571621.1
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

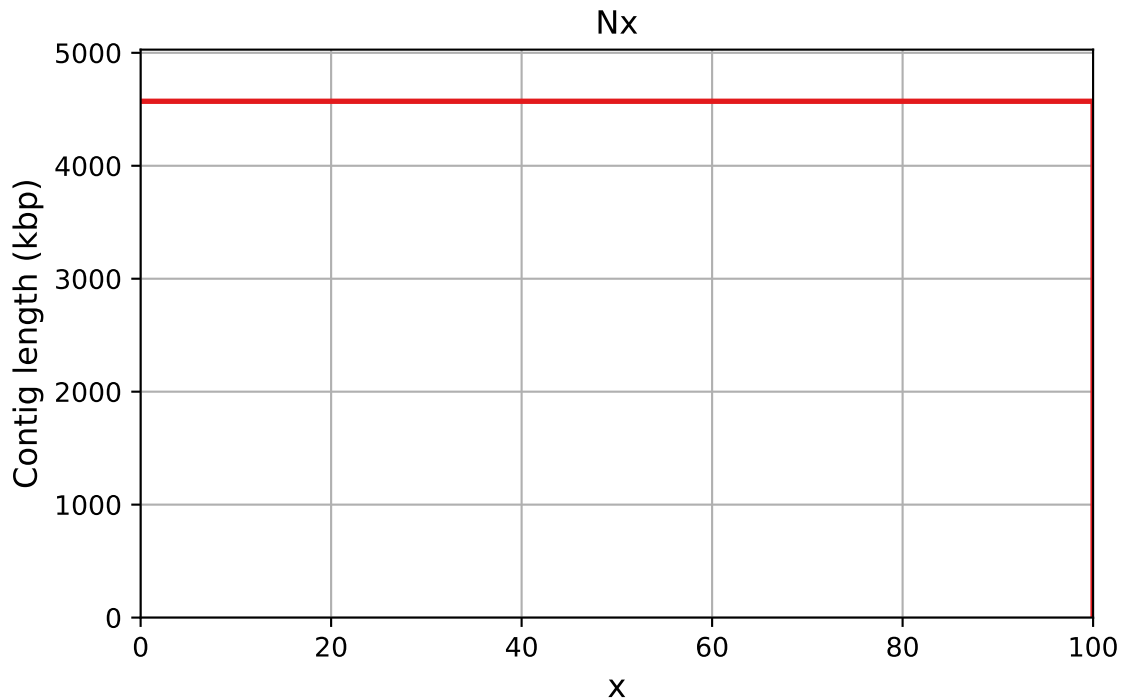
	min5_CFL_ICFL_R_35_100
# misassemblies	1
# contig misassemblies	1
# c. relocations	1
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	4571054
# local misassemblies	0
# scaffold 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

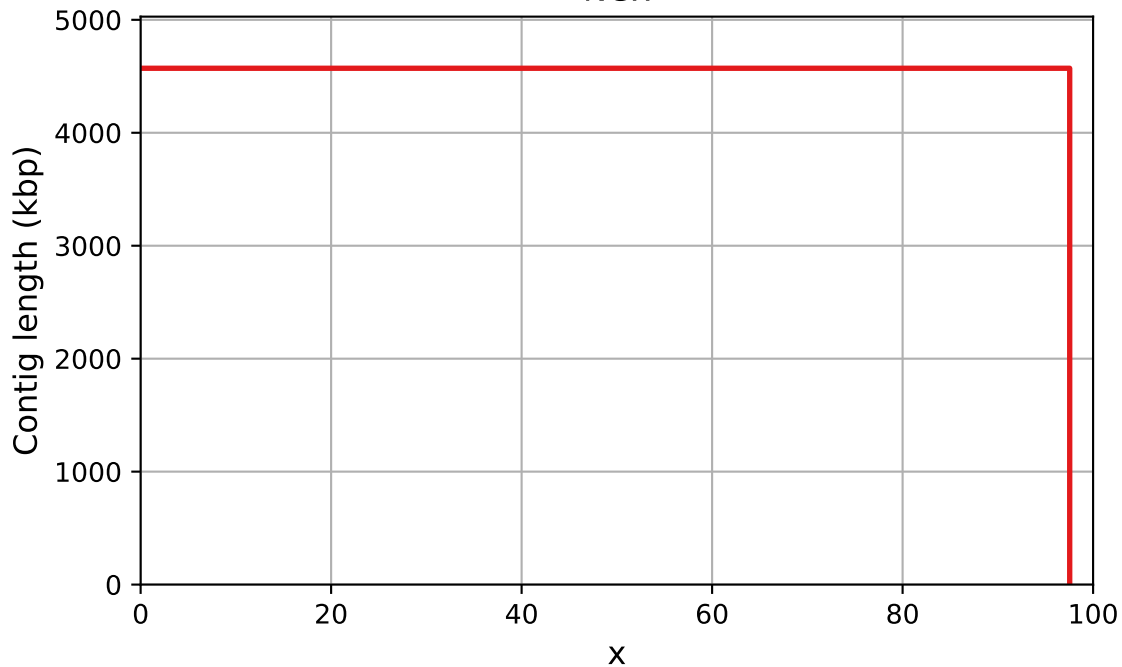
	min5_CFL_ICFL_R_35_100
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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

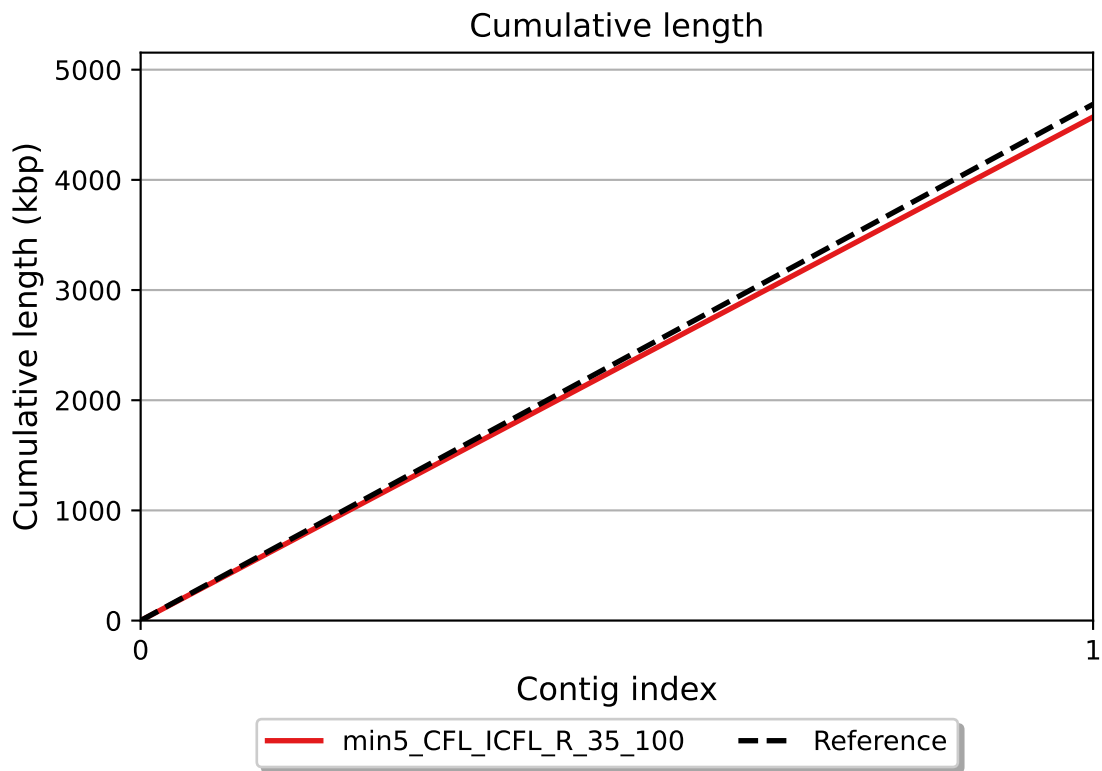


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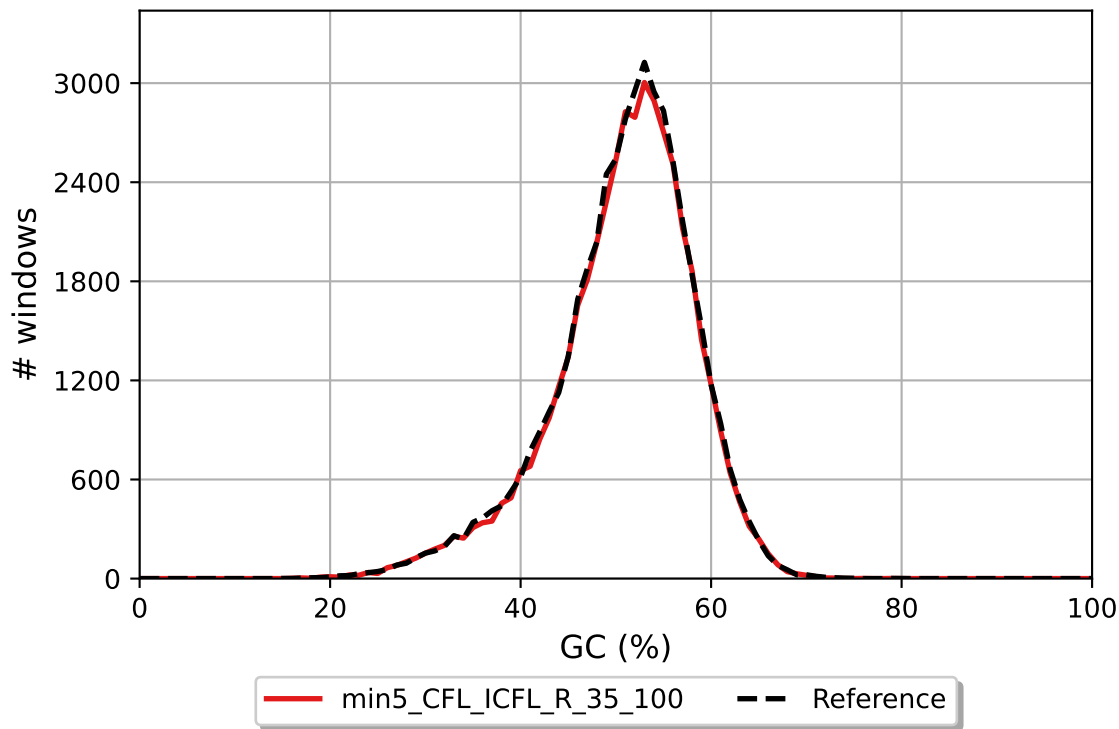
NGx



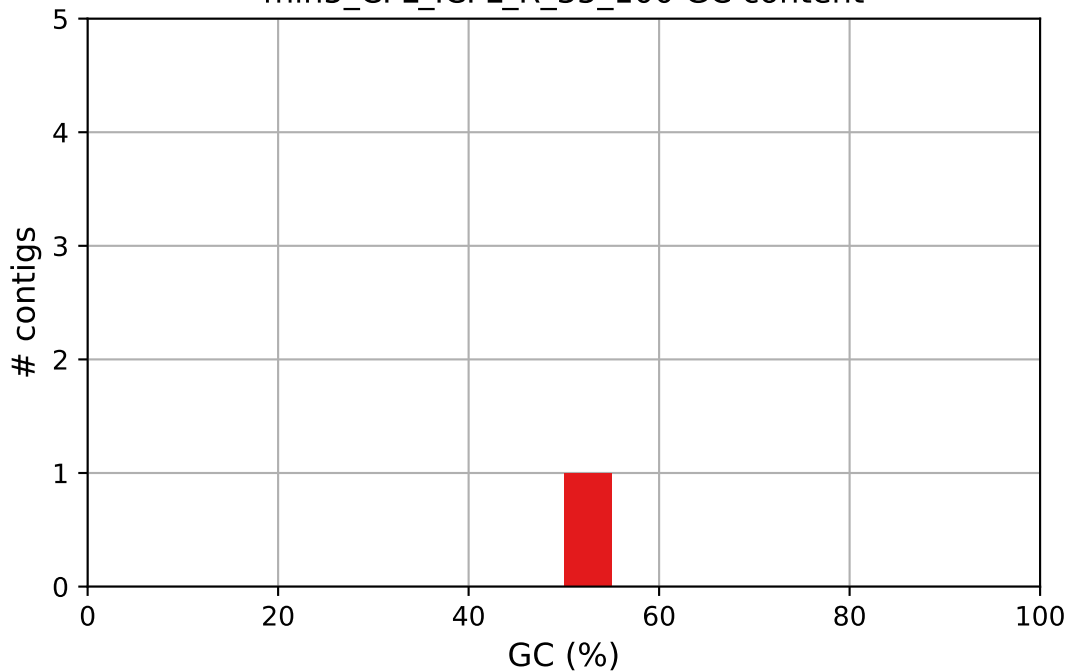
min5\_CFL\_ICFL\_R\_35\_100



## GC content



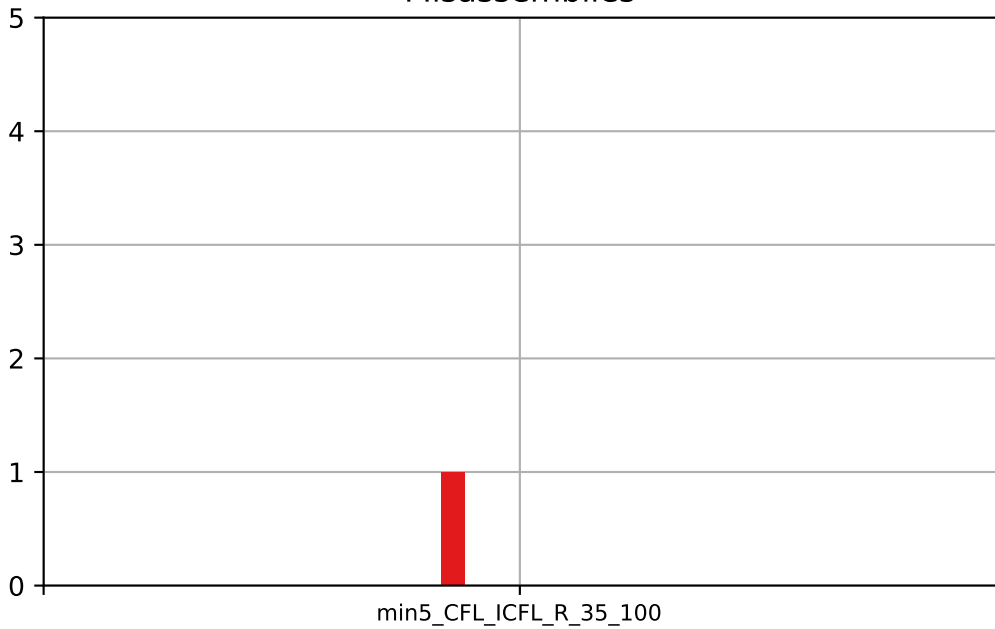
min5\_CFL\_ICFL\_R\_35\_100 GC content



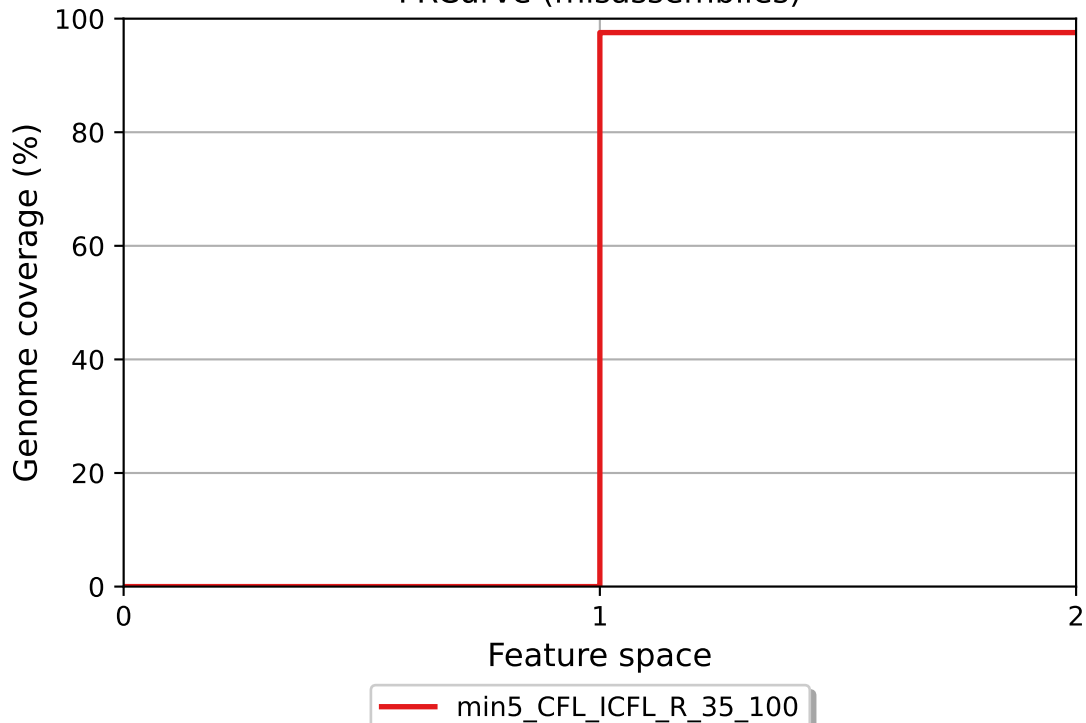
min5\_CFL\_ICFL\_R\_35\_100



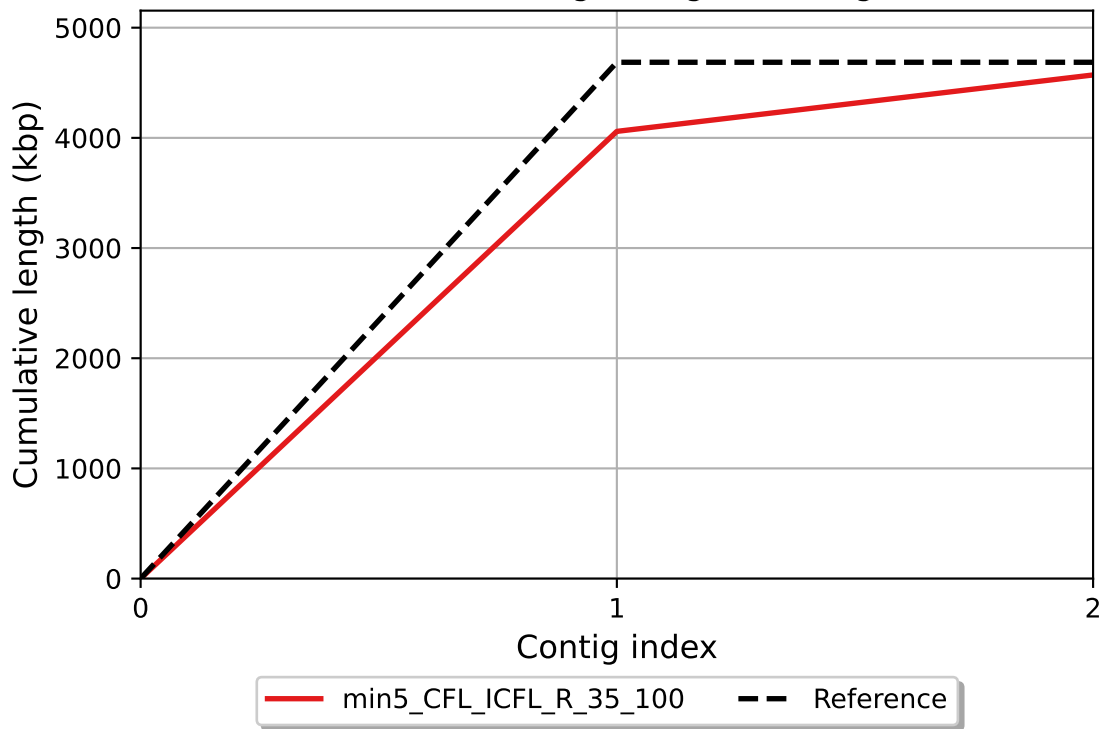
## Misassemblies



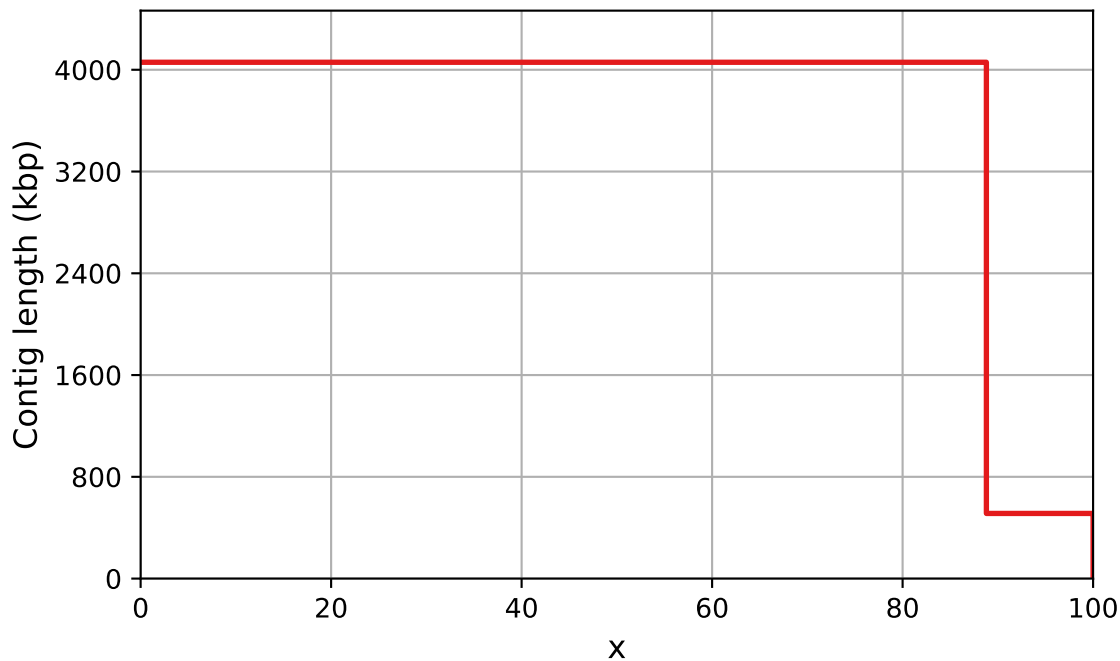
FRCurve (misassemblies)



Cumulative length (aligned contigs)

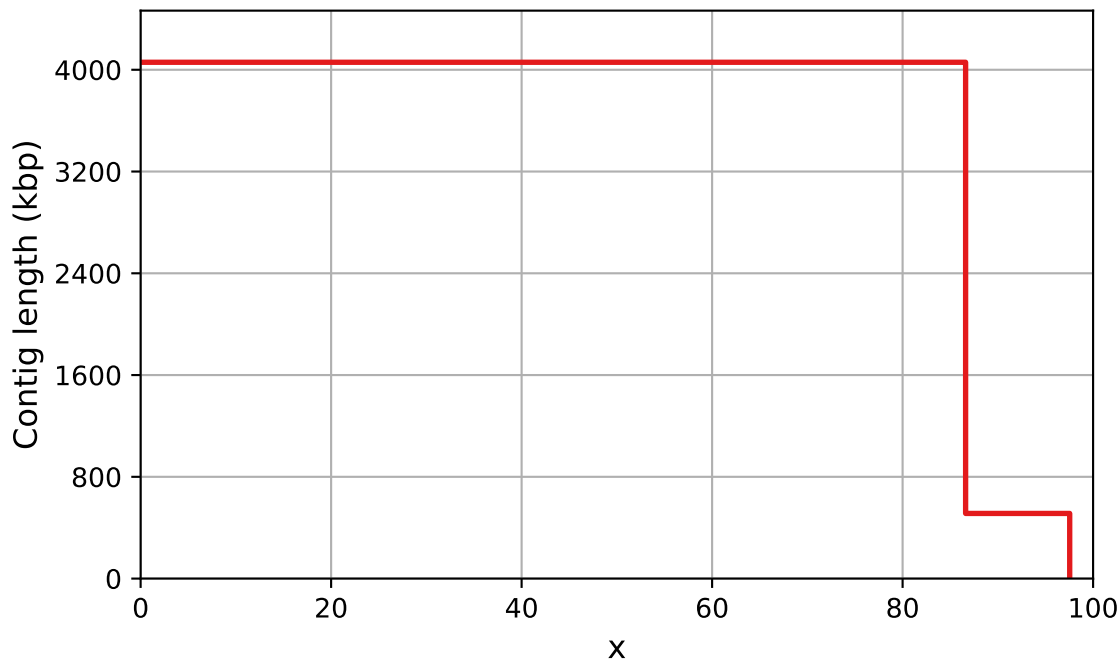


NAx



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# NGAx



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