

Report

	min5_CFL_ICFL_r_25
# contigs (>= 0 bp)	14
# contigs (>= 1000 bp)	14
# contigs (>= 5000 bp)	14
# contigs (>= 10000 bp)	14
# contigs (>= 25000 bp)	14
# contigs (>= 50000 bp)	14
Total length (>= 0 bp)	3975597
Total length (>= 1000 bp)	3975597
Total length (>= 5000 bp)	3975597
Total length (>= 10000 bp)	3975597
Total length (>= 25000 bp)	3975597
Total length (>= 50000 bp)	3975597
# contigs	14
Largest contig	897427
Total length	3975597
Reference length	4686137
GC (%)	50.78
Reference GC (%)	50.78
N50	605795
NG50	423213
N90	115887
NG90	-
auN	500601.8
auNG	424697.6
L50	3
LG50	4
L90	10
LG90	-
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	619574
# 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 (%)	84.837
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	897427
Total aligned length	3975597
NA50	367458
NGA50	257519
NA90	115887
NGA90	-
auNA	453996.5
auNGA	385158.8
LA50	4
LGA50	5
LA90	11
LGA90	-

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
# 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	619574
# 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

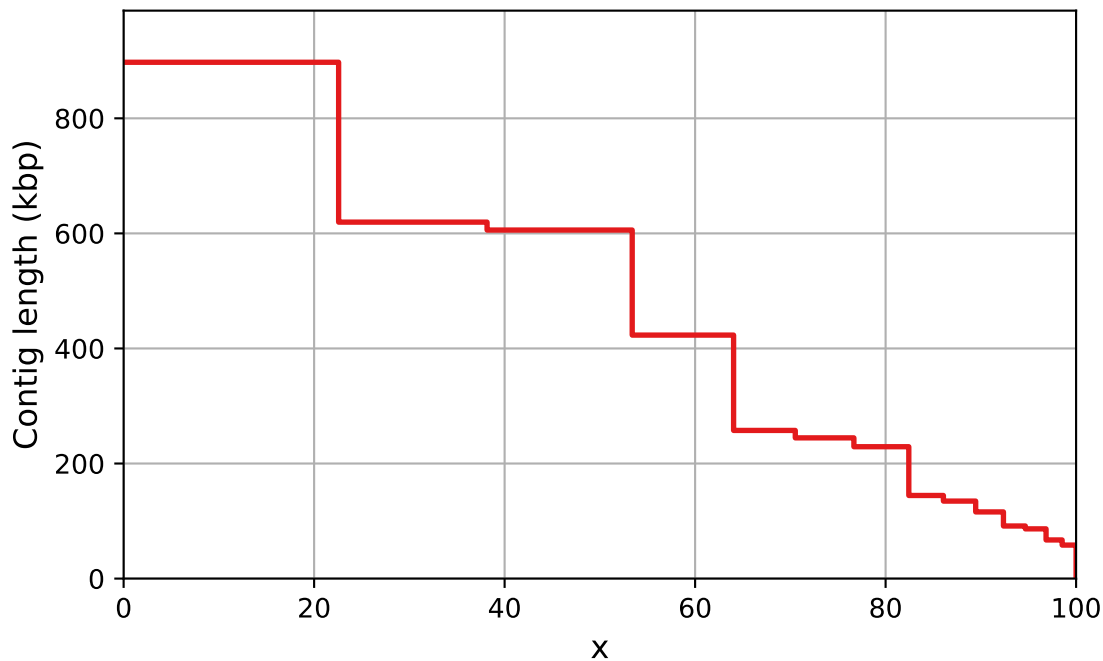
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	min5_CFL_ICFL_r_25
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

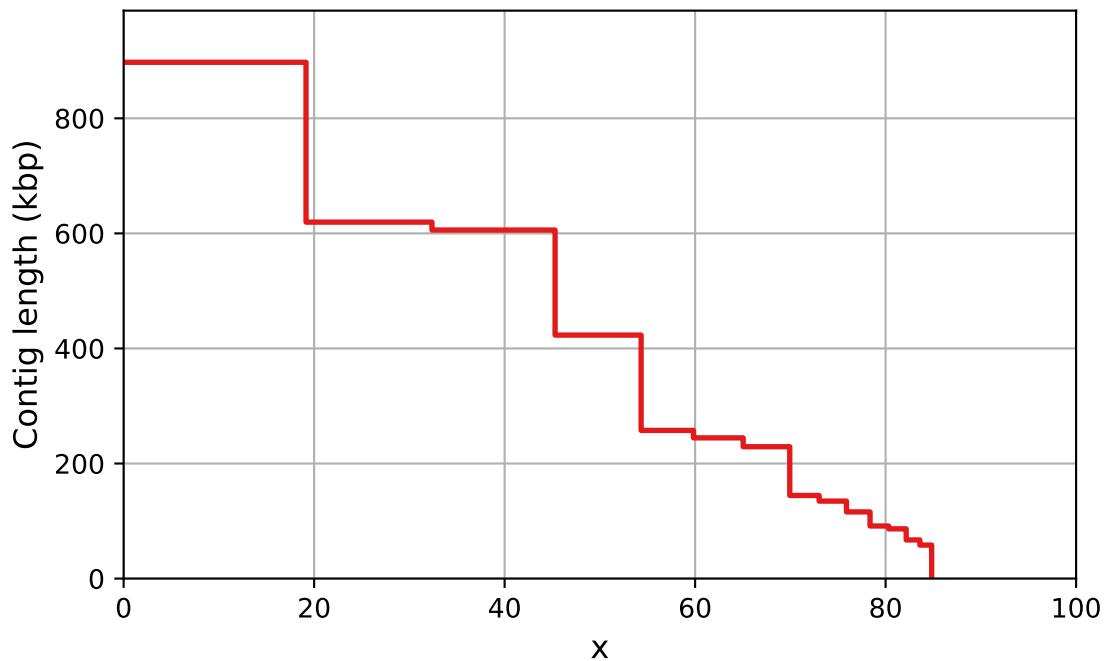
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

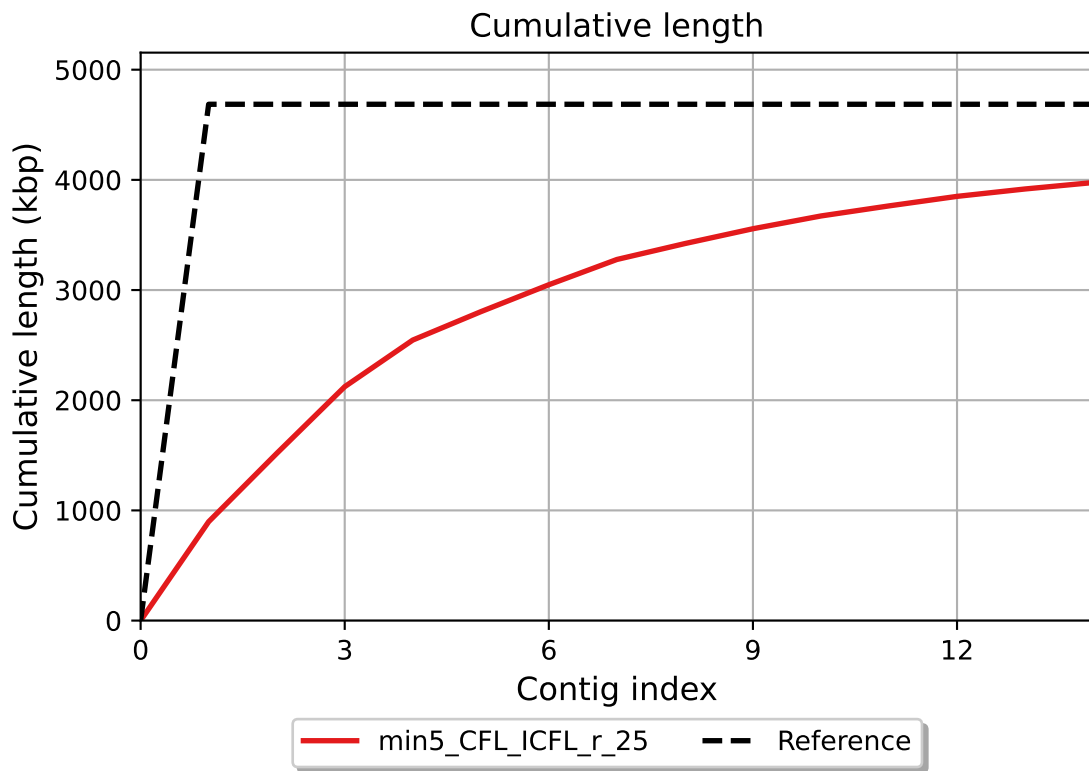


min5\_CFL\_ICFL\_r\_25

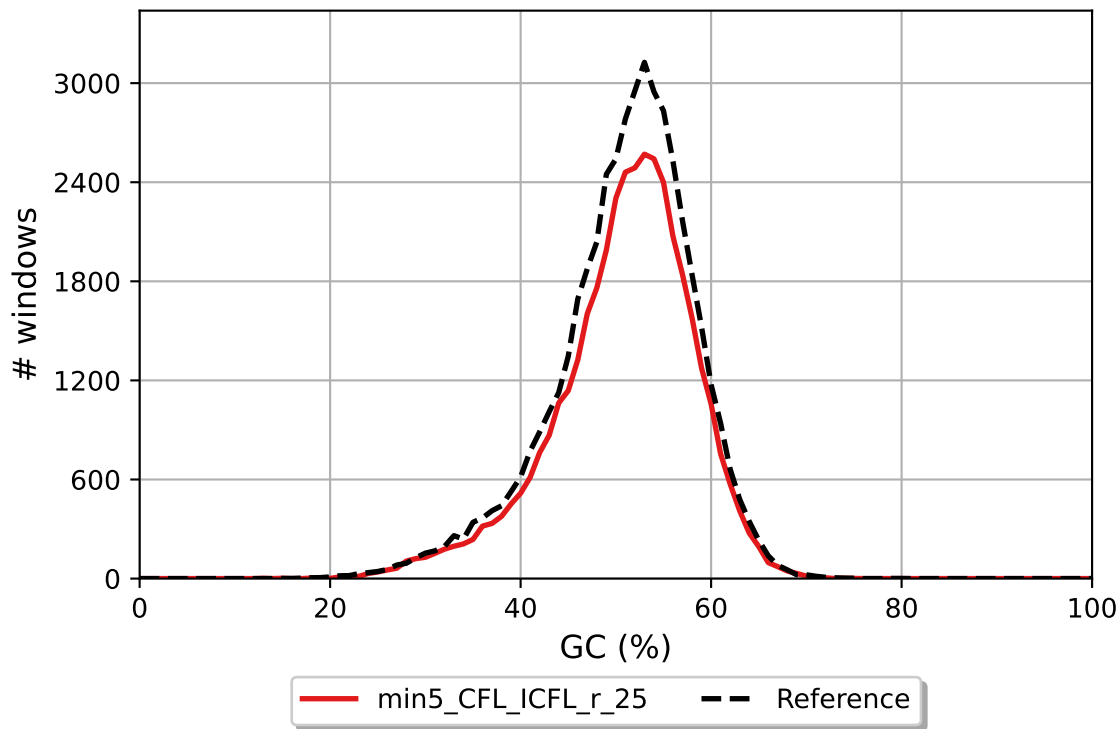
NGx



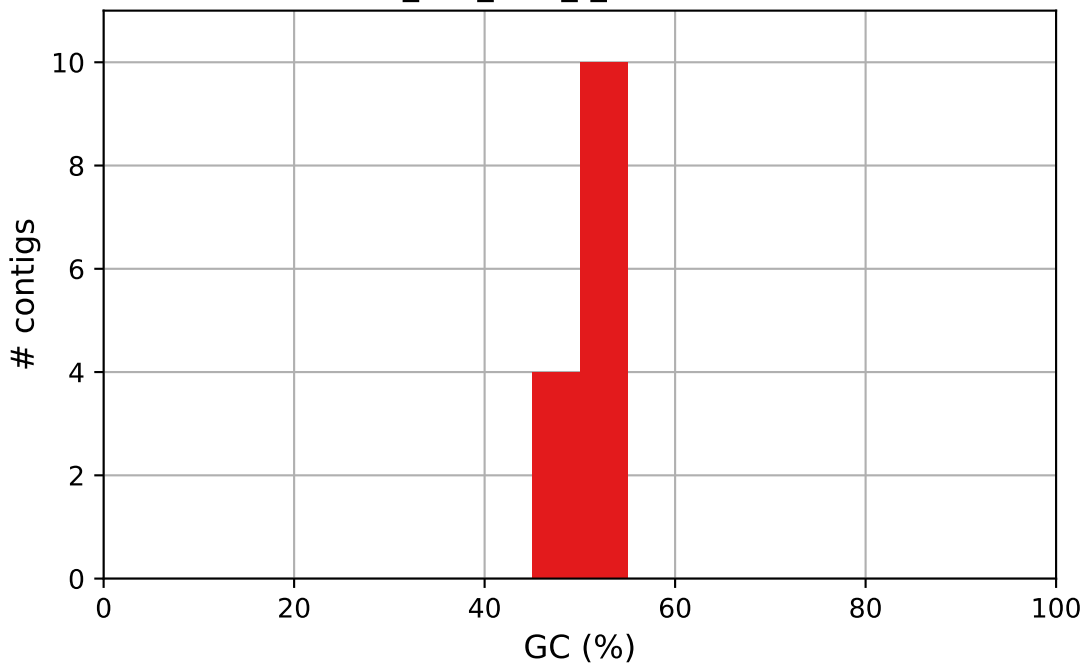
min5\_CFL\_ICFL\_r\_25



GC content



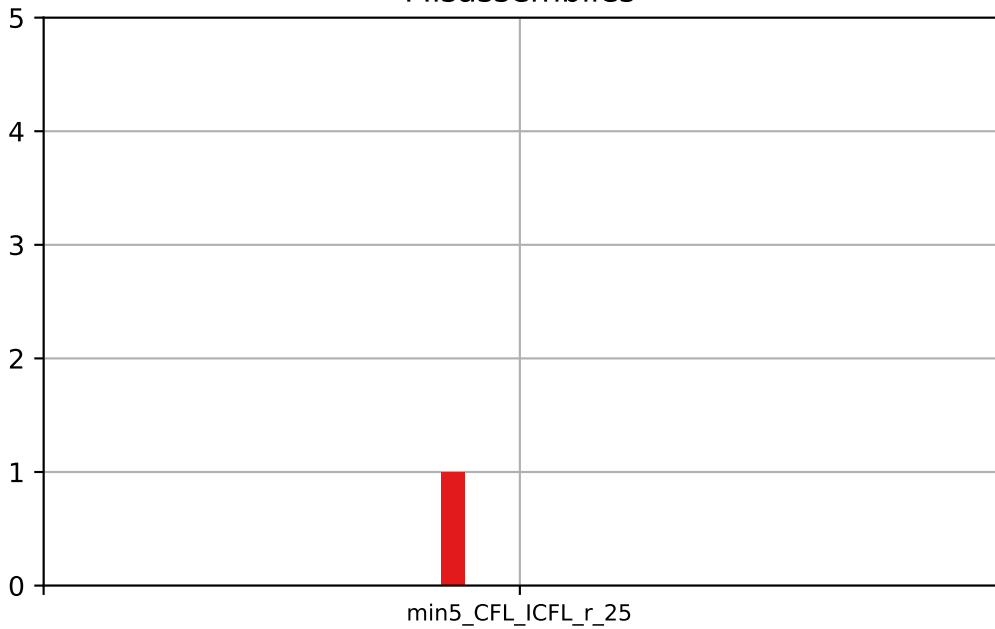
min5\_CFL\_ICFL\_r\_25 GC content



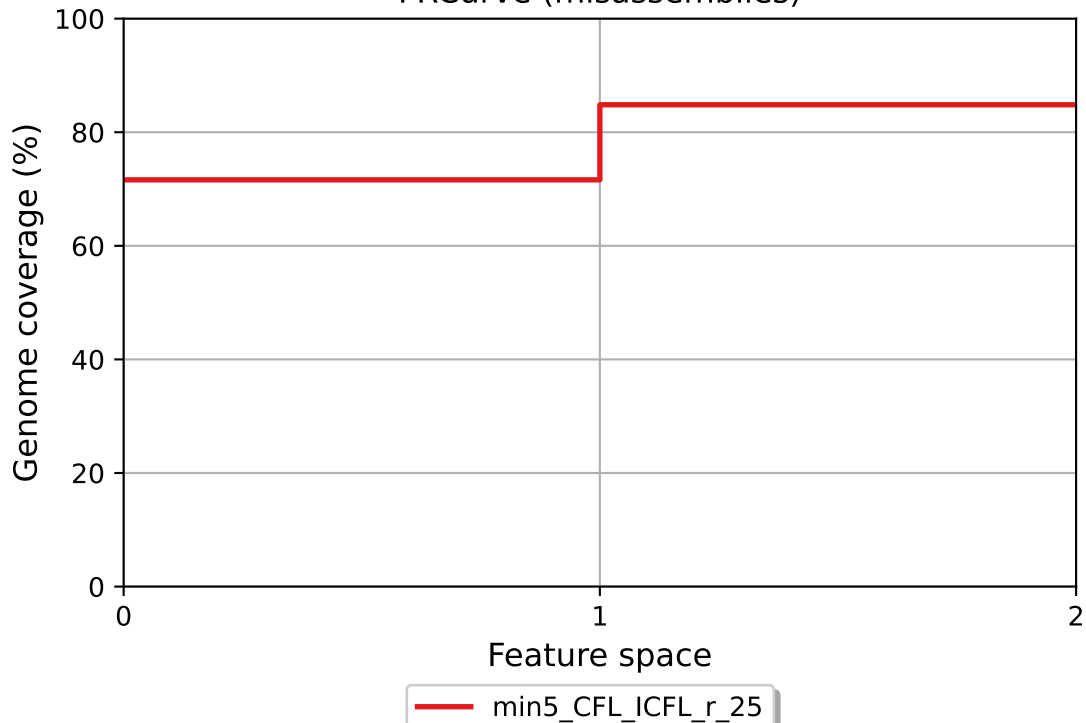
min5\_CFL\_ICFL\_r\_25



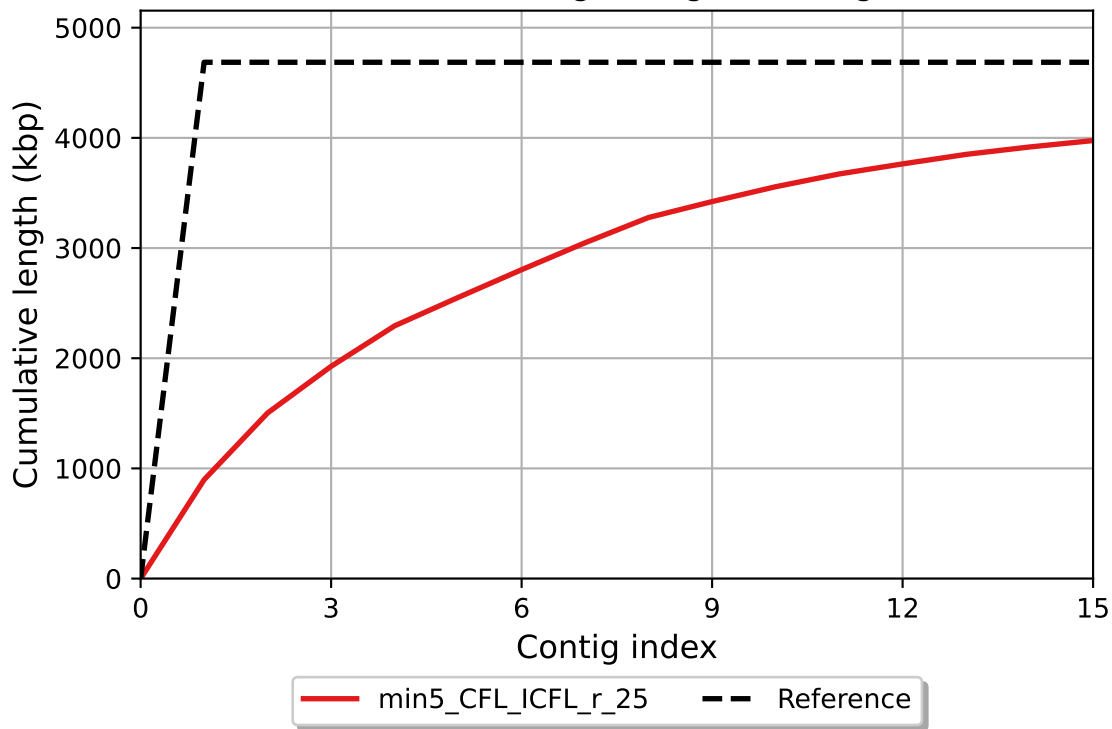
## Misassemblies



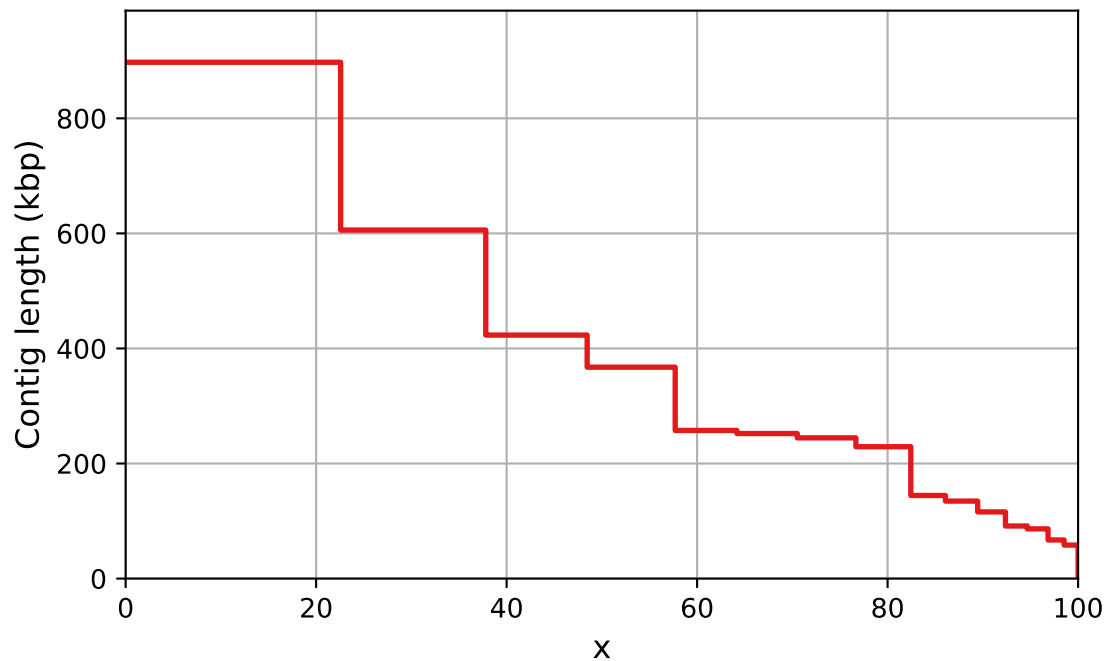
FRCurve (misassemblies)



Cumulative length (aligned contigs)

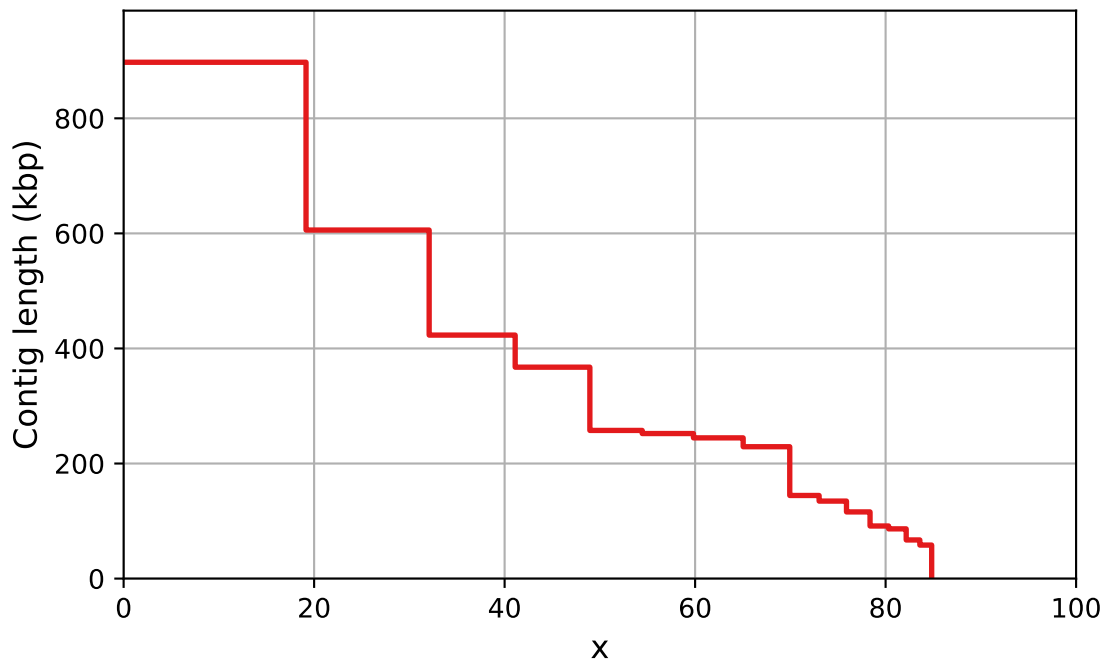


NAx



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# NGAx



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