

Report

	mini-ava-pb_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)	4701475
Total length (>= 1000 bp)	4701475
Total length (>= 5000 bp)	4701475
Total length (>= 10000 bp)	4701475
Total length (>= 25000 bp)	4701475
Total length (>= 50000 bp)	4701475
# contigs	3
Largest contig	3981954
Total length	4701475
Reference length	4686137
GC (%)	50.77
Reference GC (%)	50.78
N50	3981954
NG50	3981954
N90	556774
NG90	556774
auN	3444119.5
auNG	3455392.3
L50	1
LG50	1
L90	2
LG90	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# 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 (%)	99.344
Duplication ratio	1.010
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.28
Largest alignment	3981954
Total aligned length	4701398
NA50	3981954
NGA50	3981954
NA90	556774
NGA90	556774
auNA	3444114.1
auNGA	3455386.9
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

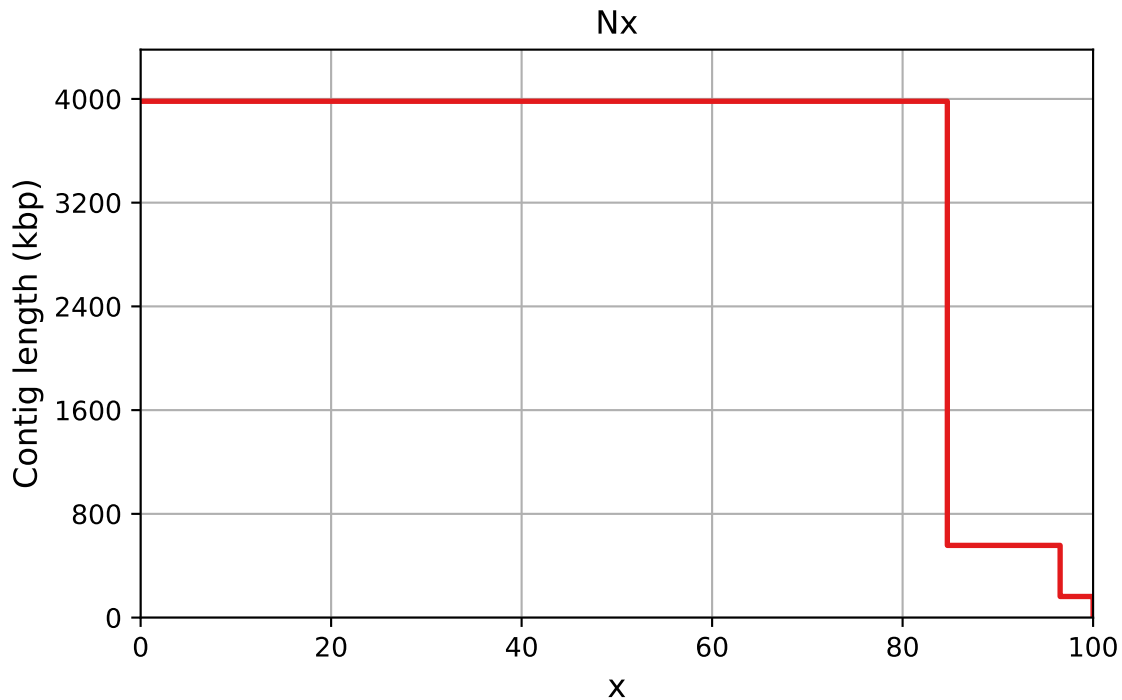
	mini-ava-pb_50
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	0
# indels	13
# indels (<= 5 bp)	13
# indels (> 5 bp)	0
Indels length	16

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

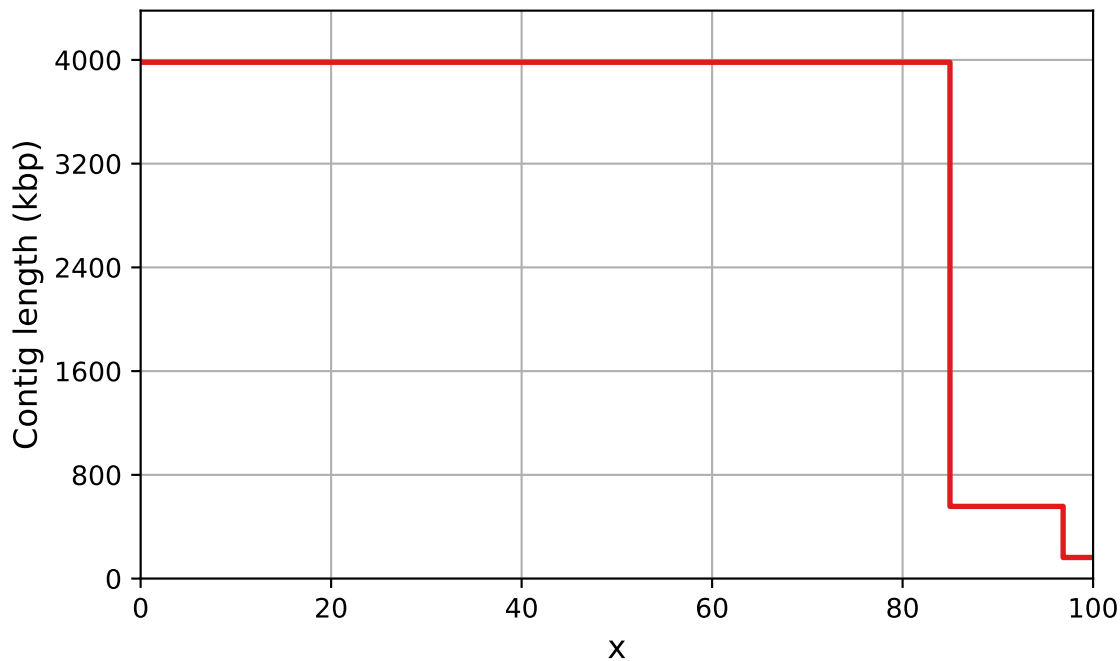
	mini-ava-pb_50
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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

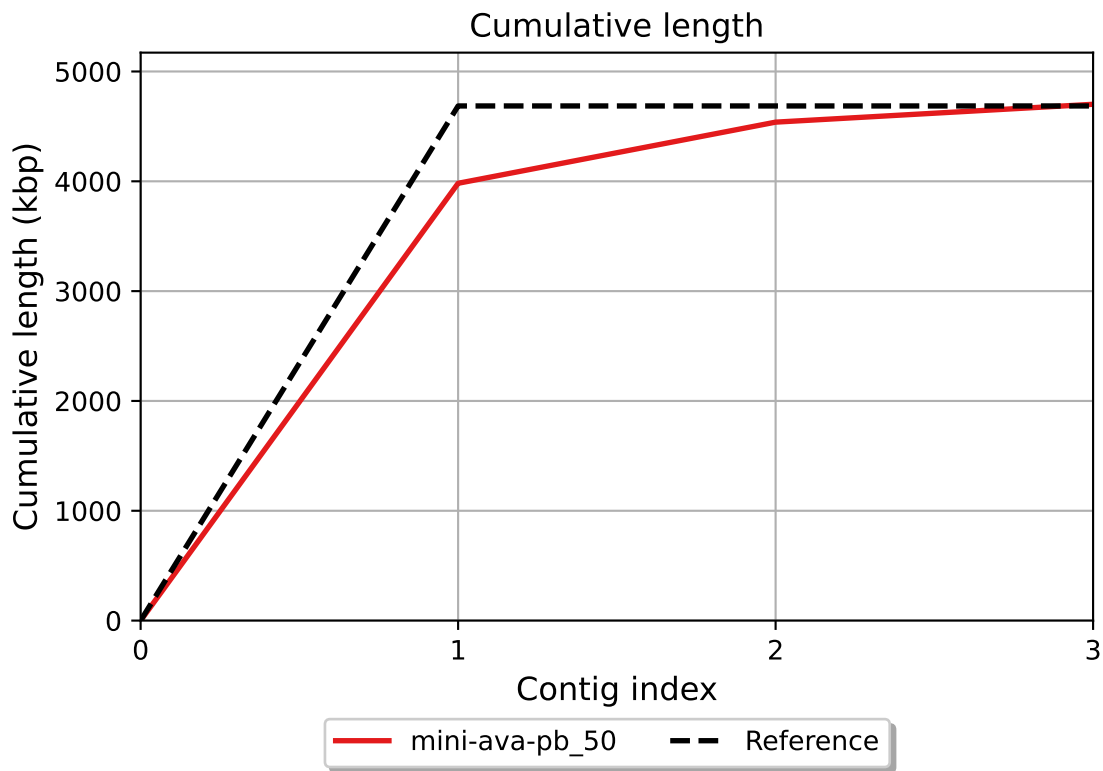


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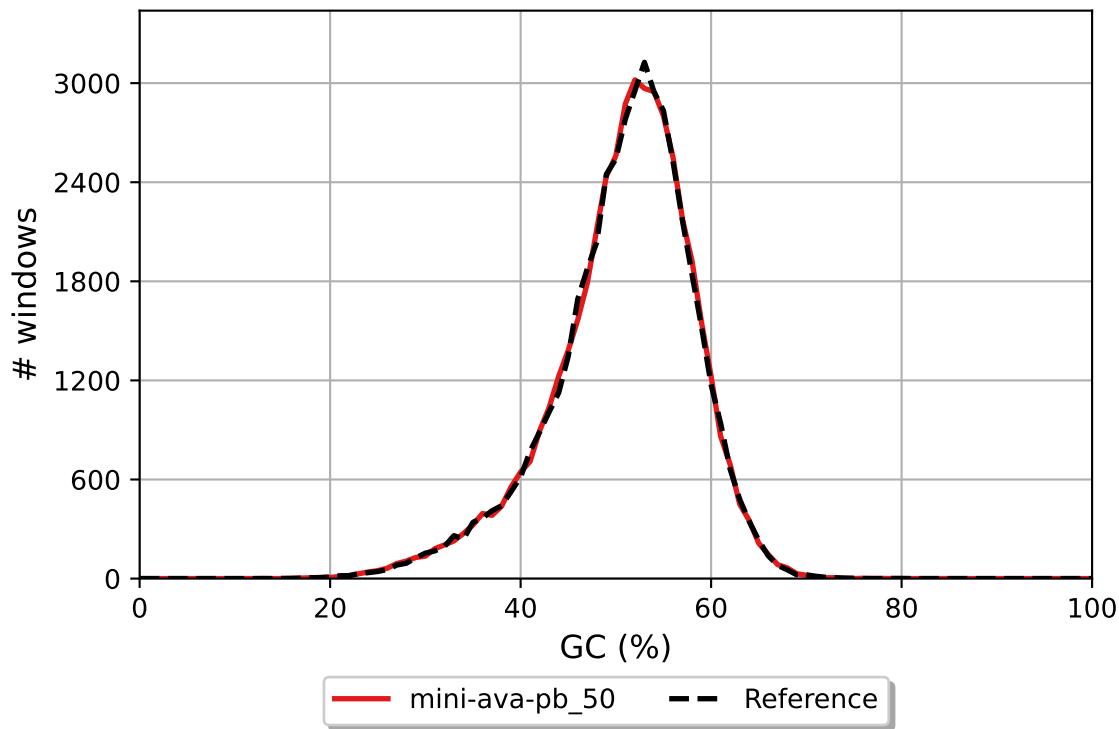
NGx



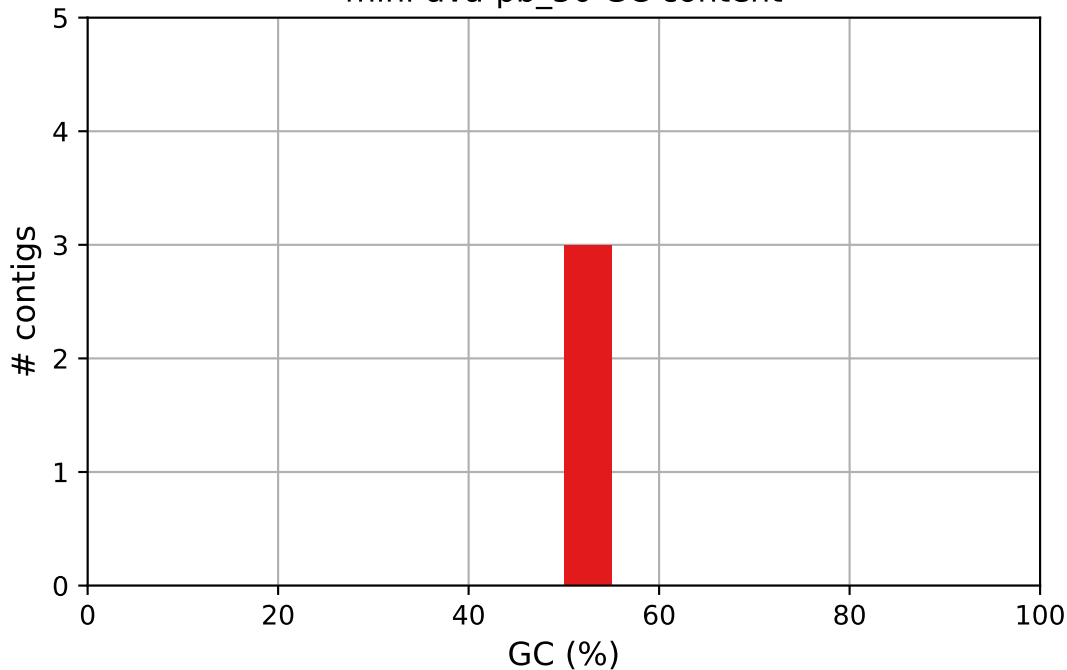
mini-ava-pb_50



GC content

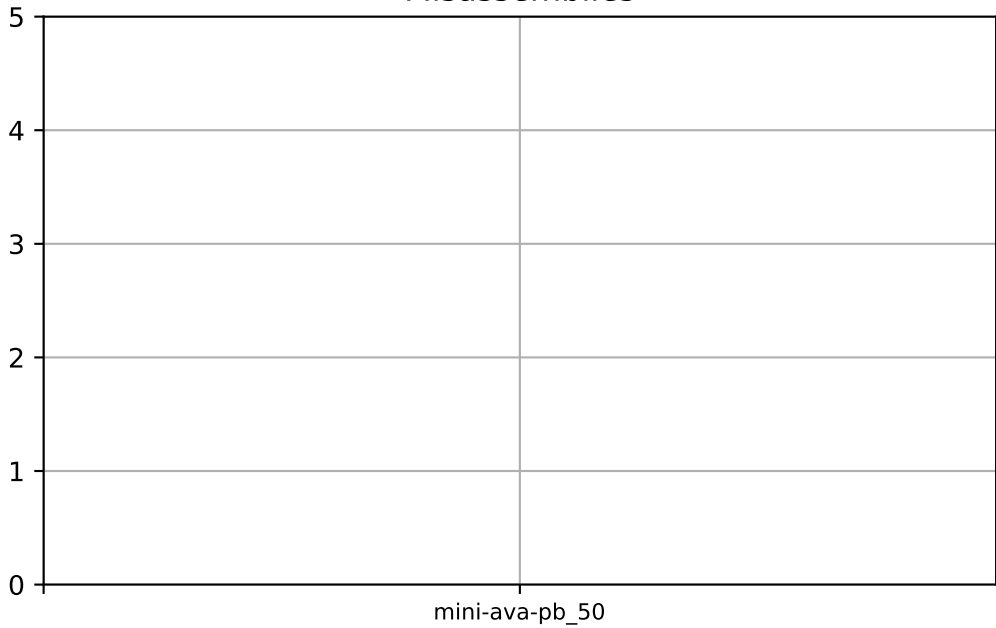


mini-ava-pb_50 GC content

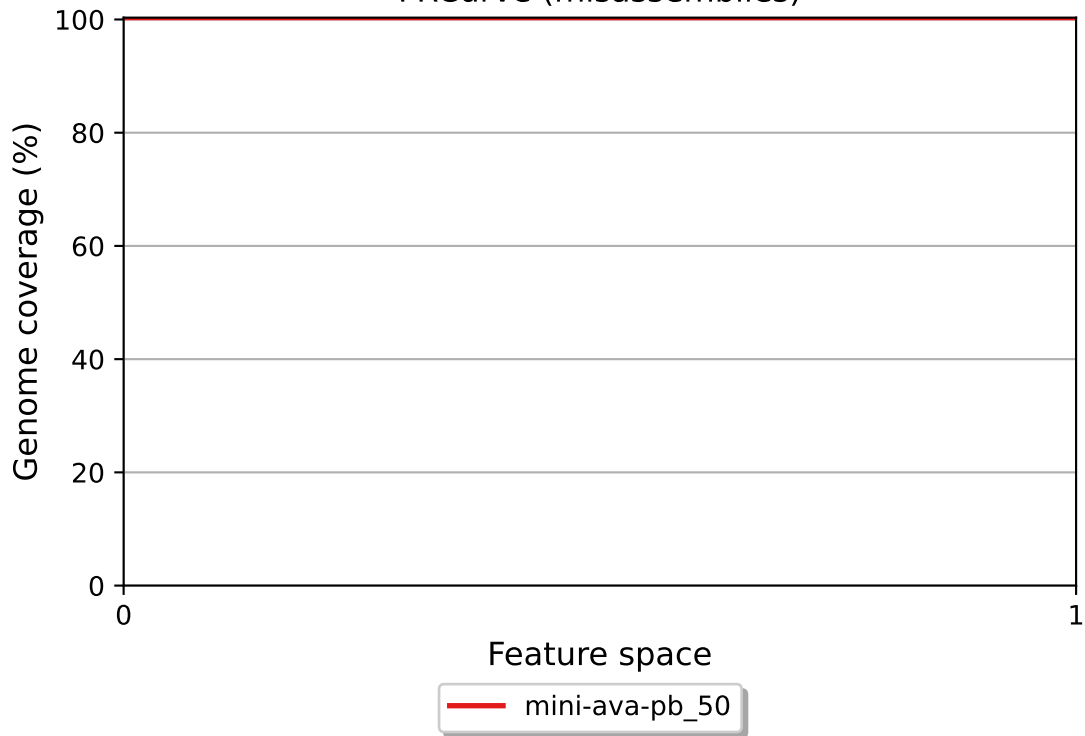


mini-ava-pb_50

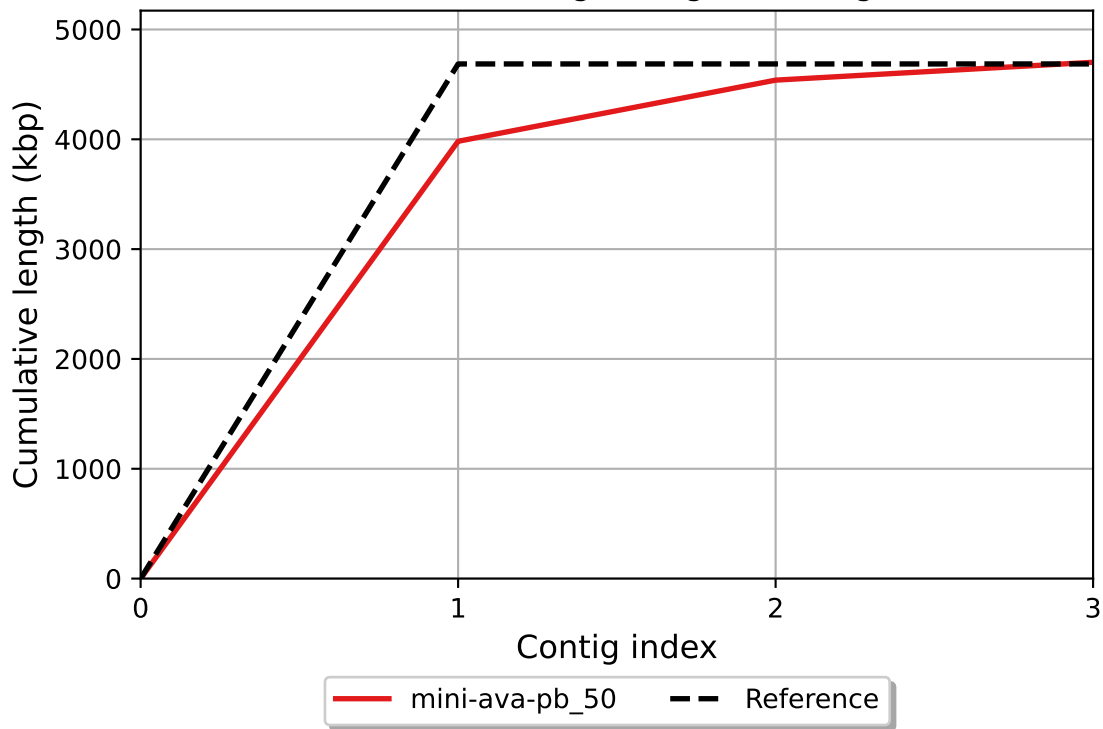
Misassemblies



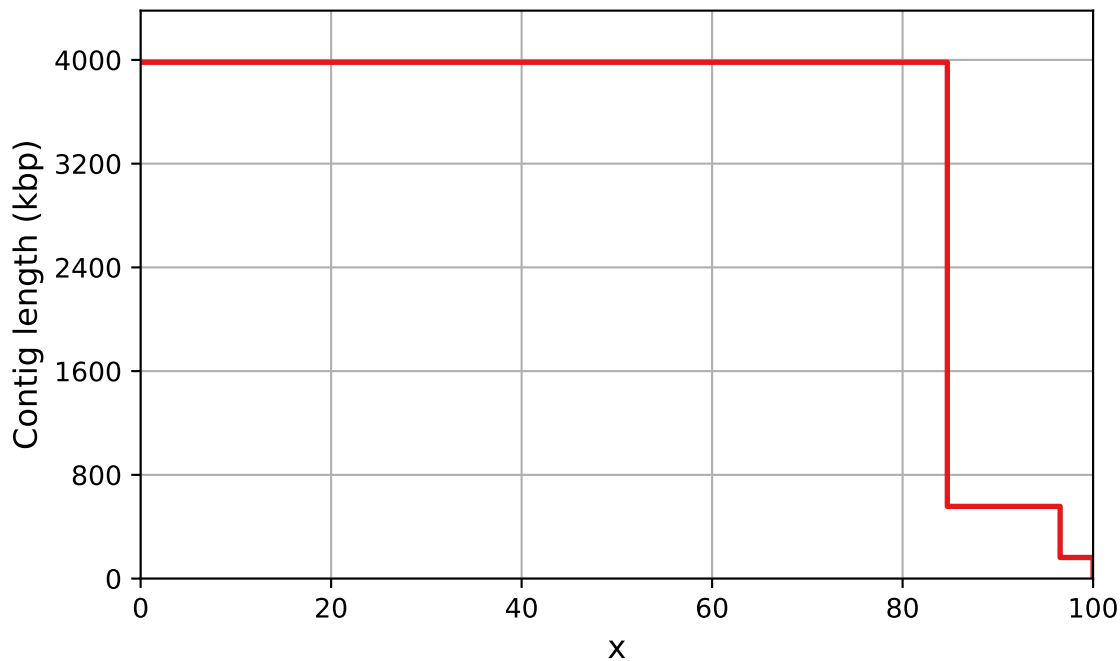
FRCurve (misassemblies)



Cumulative length (aligned contigs)

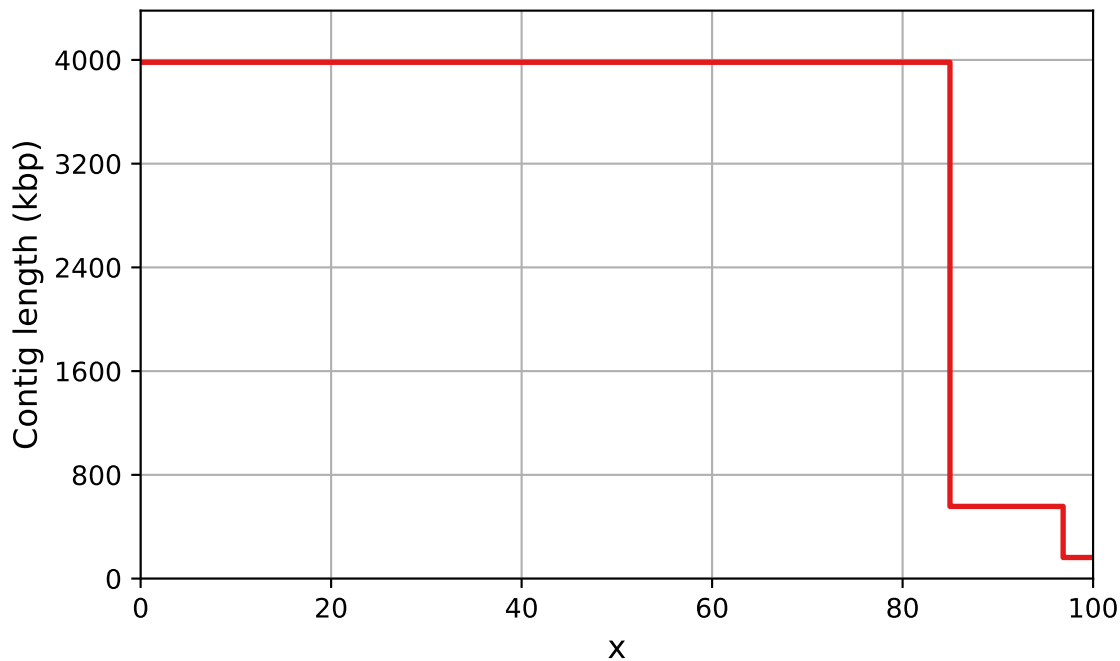


NAx



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NGAx



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