

Report

	mini-ava-pb_25
# contigs (>= 0 bp)	4
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	4
# contigs (>= 50000 bp)	4
Total length (>= 0 bp)	4715465
Total length (>= 1000 bp)	4715465
Total length (>= 5000 bp)	4715465
Total length (>= 10000 bp)	4715465
Total length (>= 25000 bp)	4715465
Total length (>= 50000 bp)	4715465
# contigs	4
Largest contig	3978169
Total length	4715465
Reference length	4686137
GC (%)	50.75
Reference GC (%)	50.78
N50	3978169
NG50	3978169
N90	553590
NG90	553590
auN	3424778.2
auNG	3446212.1
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 (%)	98.974
Duplication ratio	1.017
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.30
Largest alignment	3978169
Total aligned length	4715465
NA50	3978169
NGA50	3978169
NA90	553590
NGA90	553590
auNA	3424778.2
auNGA	3446212.1
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

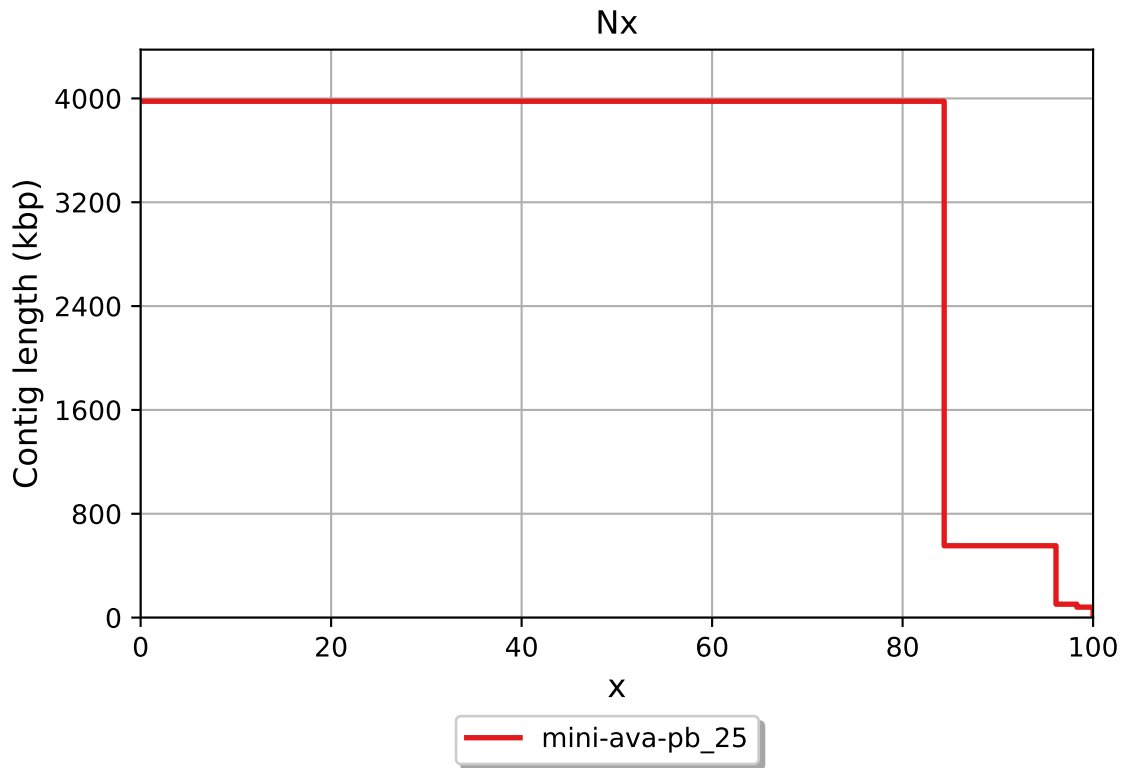
	mini-ava-pb_25
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	0
# indels	14
# indels (<= 5 bp)	14
# indels (> 5 bp)	0
Indels length	21

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).

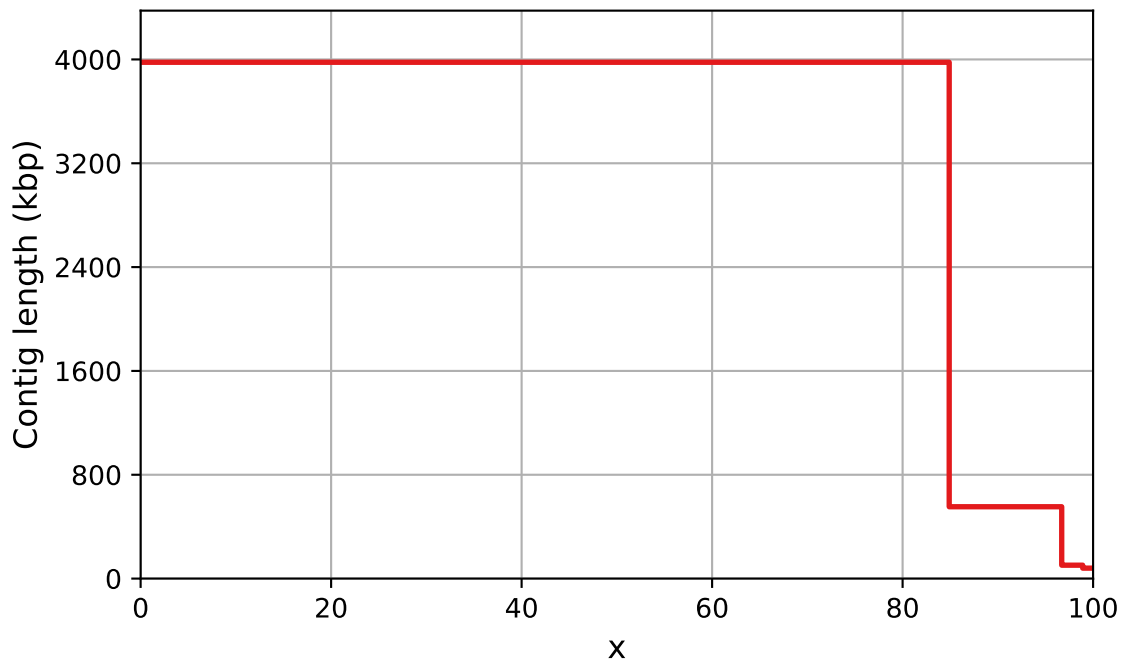
Unaligned report

	mini-ava-pb_25
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

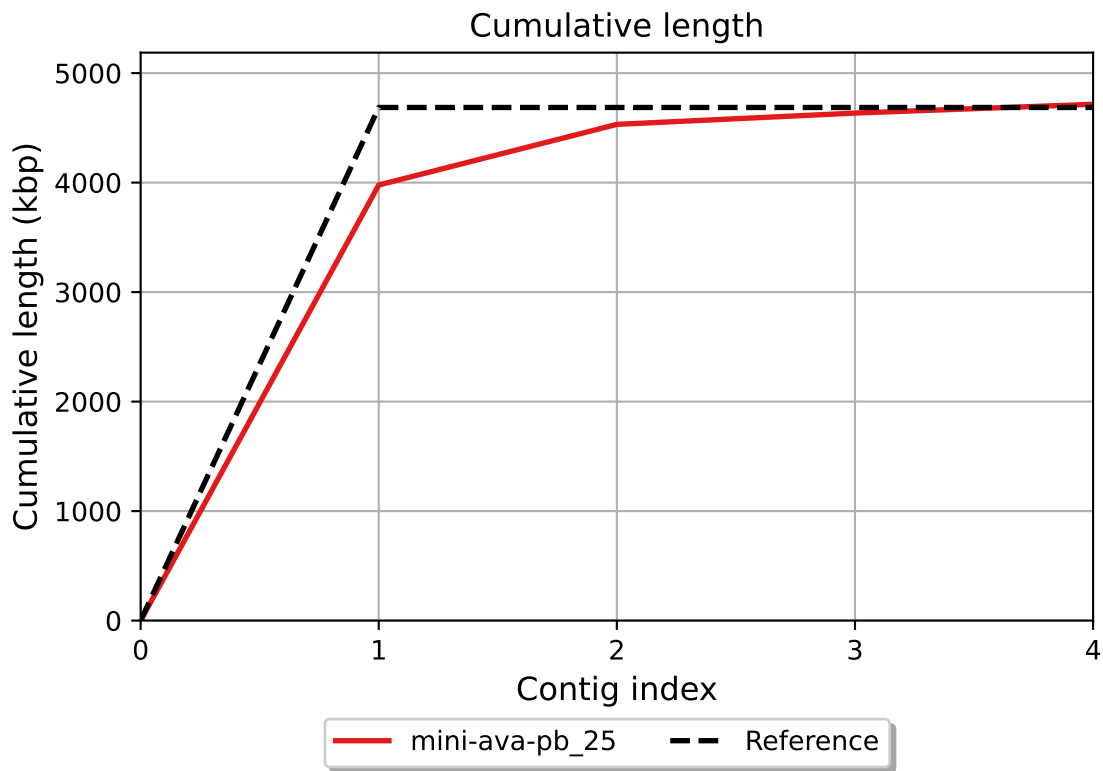
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



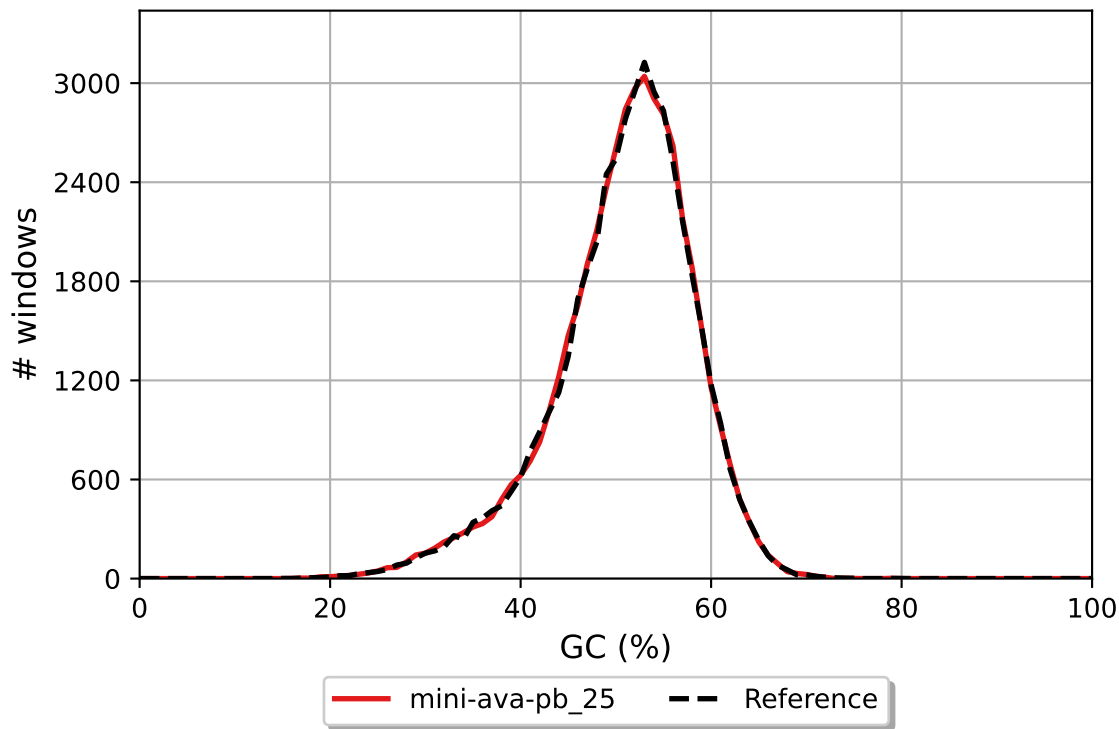
NGx



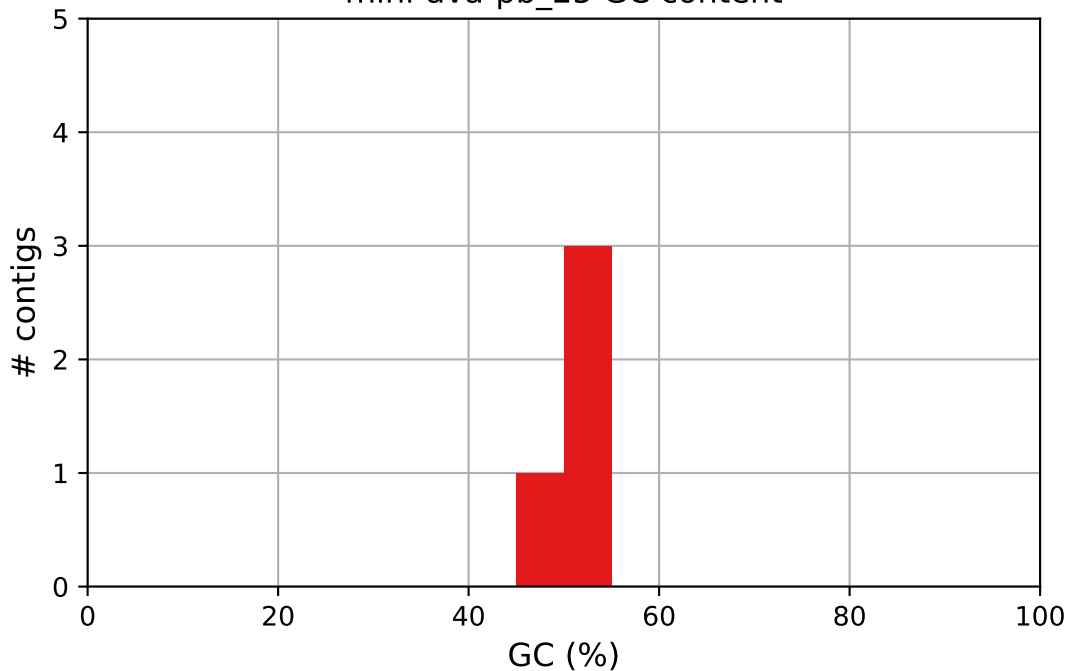
mini-ava-pb_25



GC content

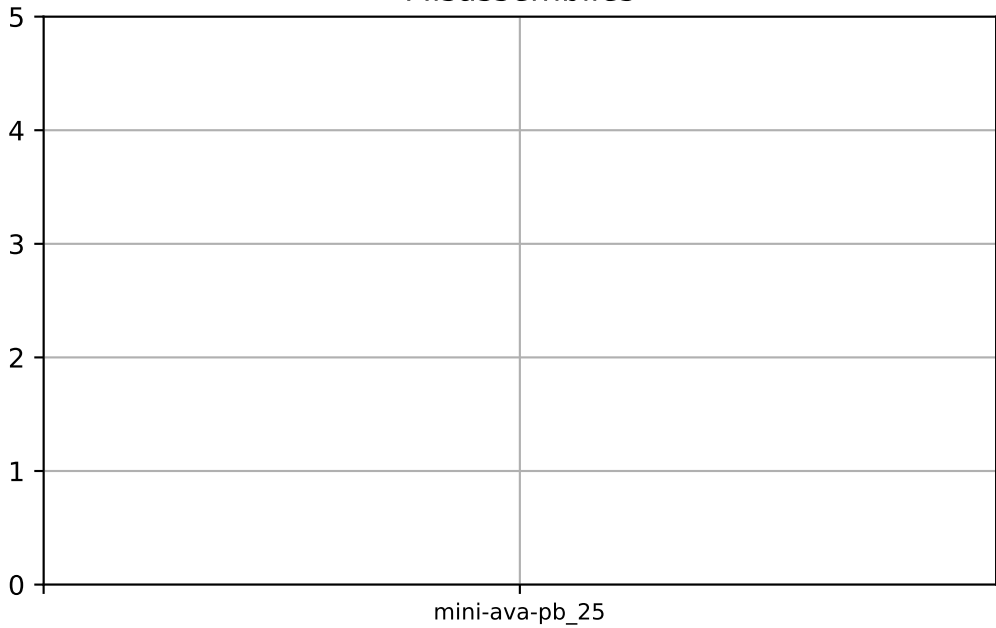


mini-ava-pb_25 GC content

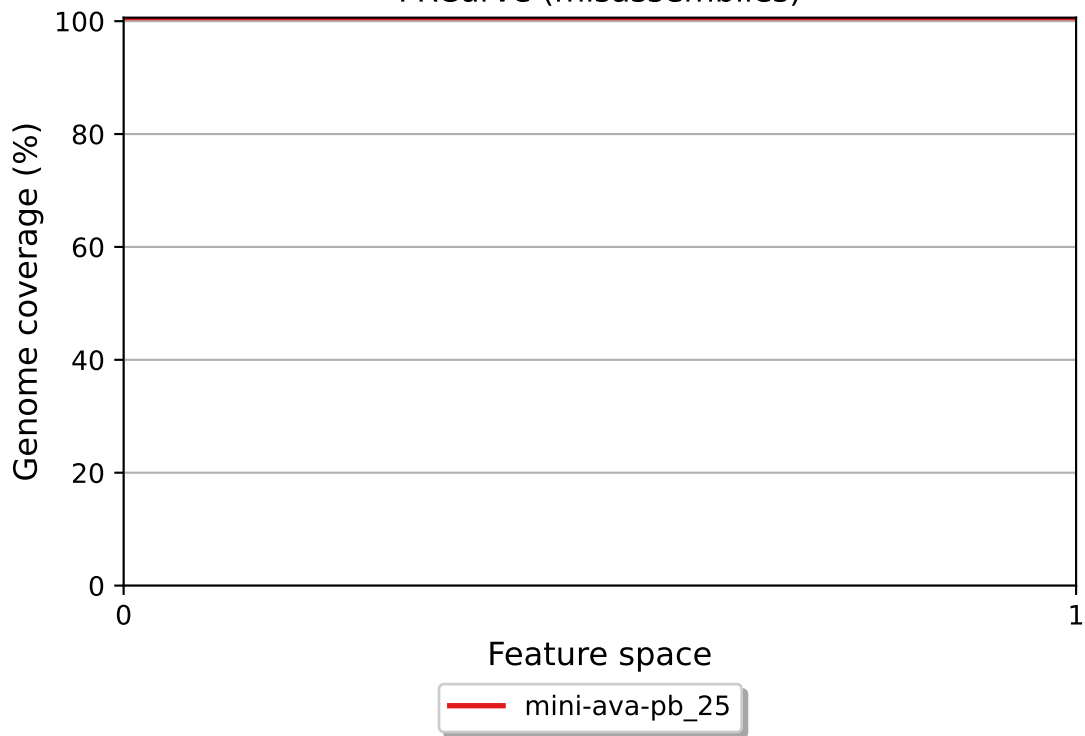


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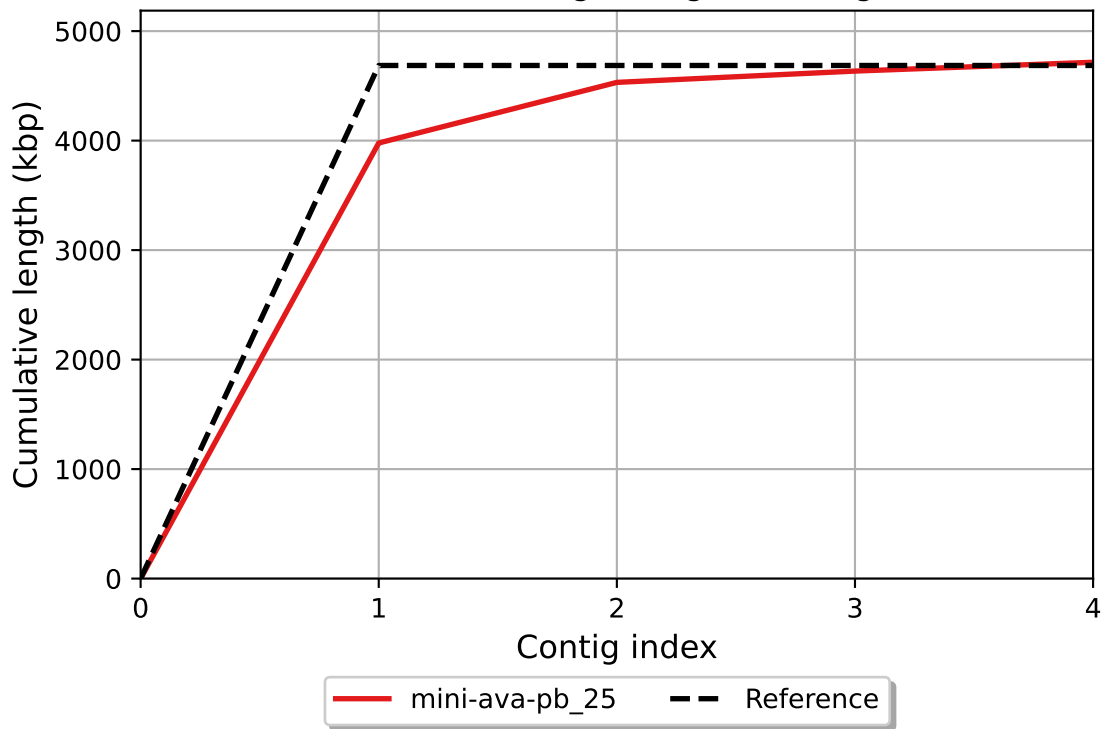
Misassemblies



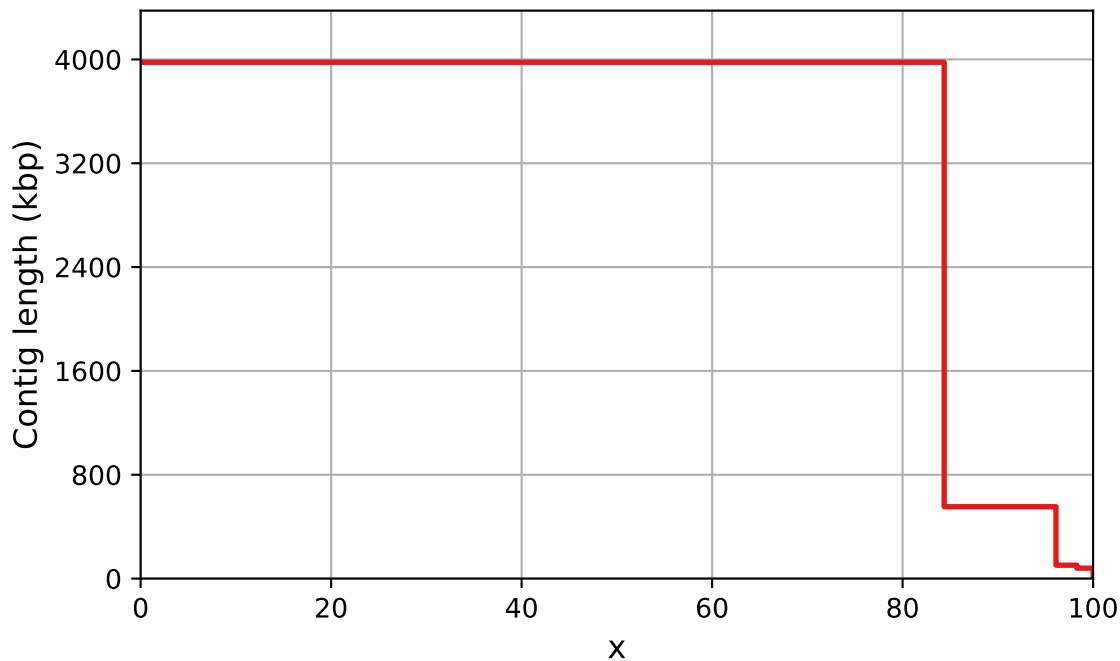
FRCurve (misassemblies)



Cumulative length (aligned contigs)

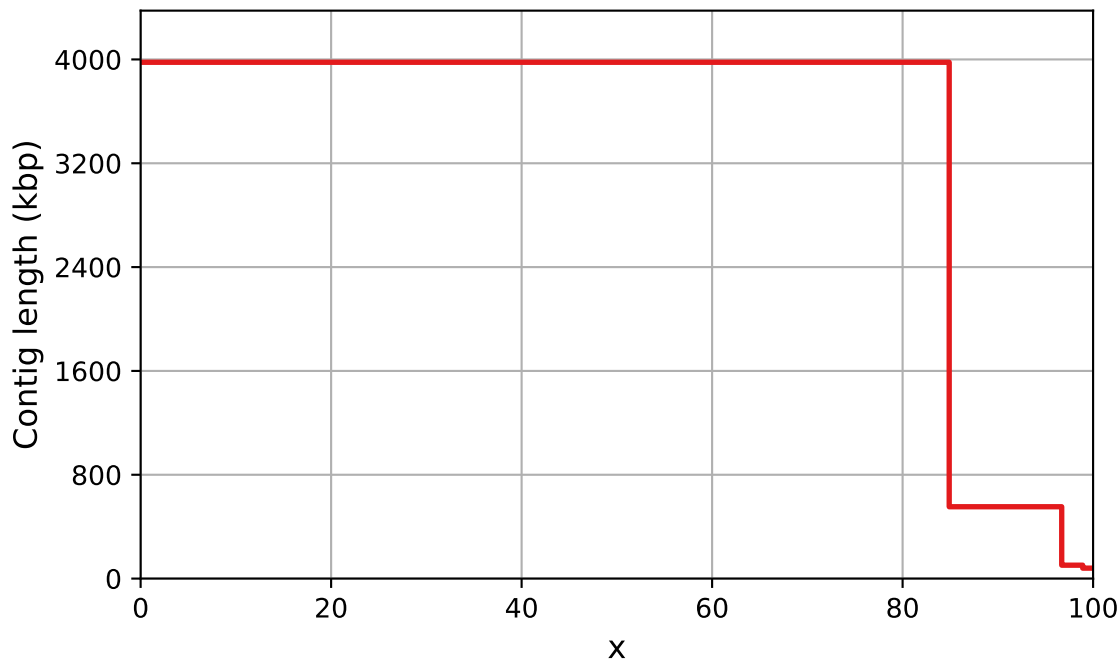


NAx



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NGAx



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