

Report

	sim5M.MiniCH
# 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)	5029350
Total length (>= 1000 bp)	5029350
Total length (>= 5000 bp)	5029350
Total length (>= 10000 bp)	5029350
Total length (>= 25000 bp)	5029350
Total length (>= 50000 bp)	5029350
# contigs	3
Largest contig	3537045
Total length	5029350
Reference length	5000040
GC (%)	35.86
Reference GC (%)	35.84
N50	3537045
NG50	3537045
N75	1235134
NG75	1235134
L50	1
LG50	1
L75	2
LG75	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.896
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.28
# indels per 100 kbp	165.99
Largest alignment	3537045
Total aligned length	5029349
NA50	3537045
NGA50	3537045
NA75	1235133
NGA75	1235133
LA50	1
LGA50	1
LA75	2
LGA75	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

	sim5M.MiniCH
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	64
# indels	8291
# indels (≤ 5 bp)	8276
# indels (> 5 bp)	15
Indels length	12254

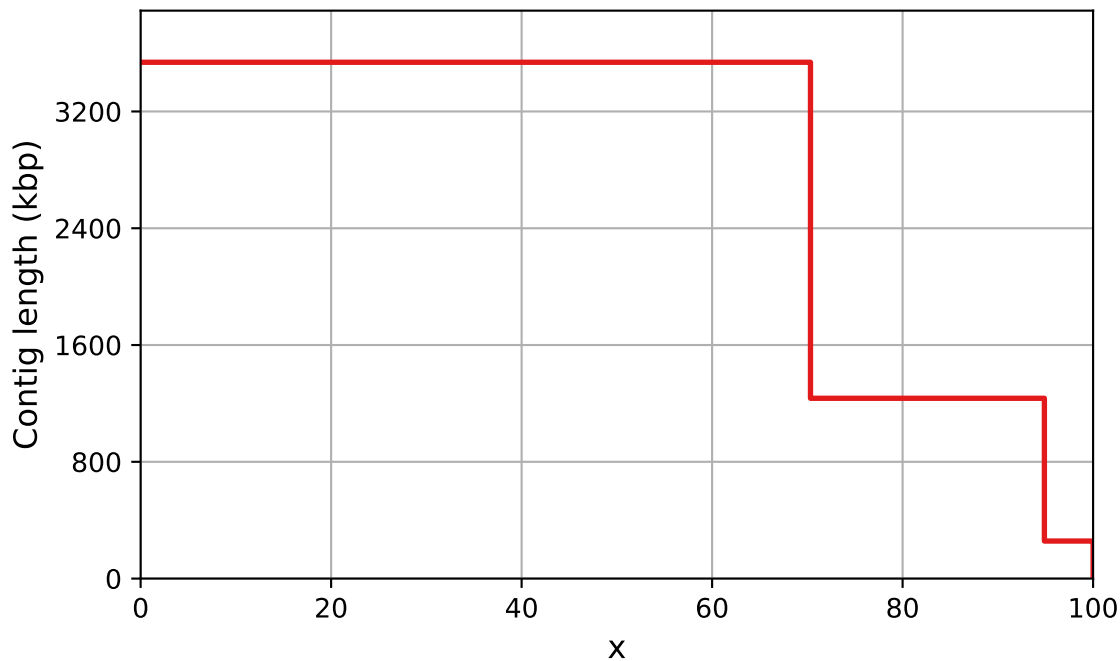
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	sim5M.Minich
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

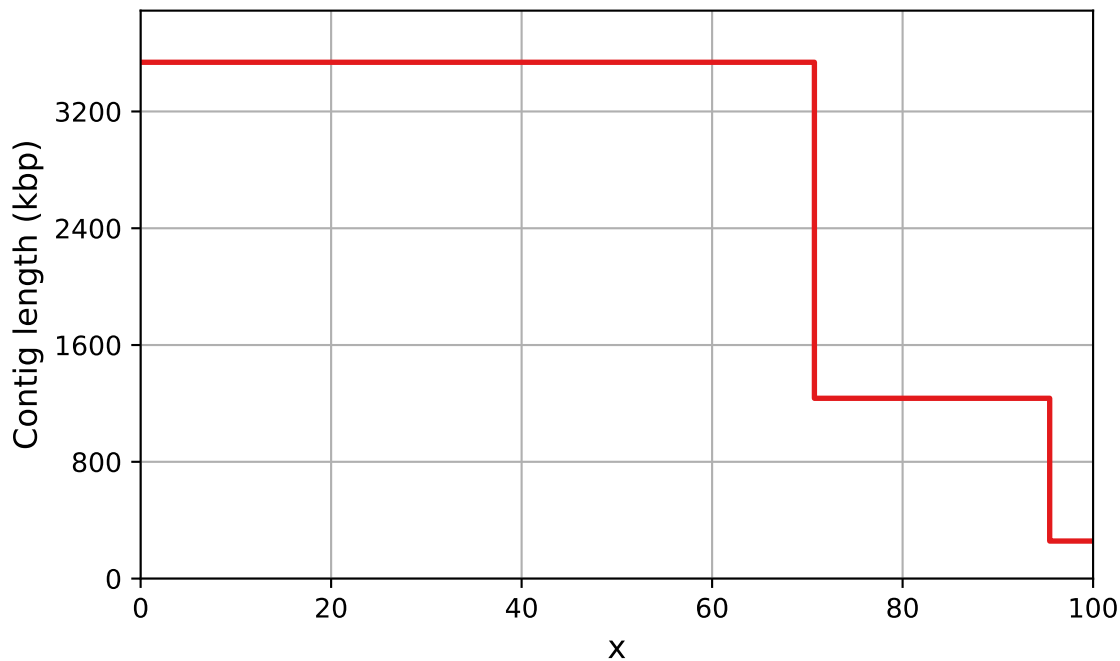
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

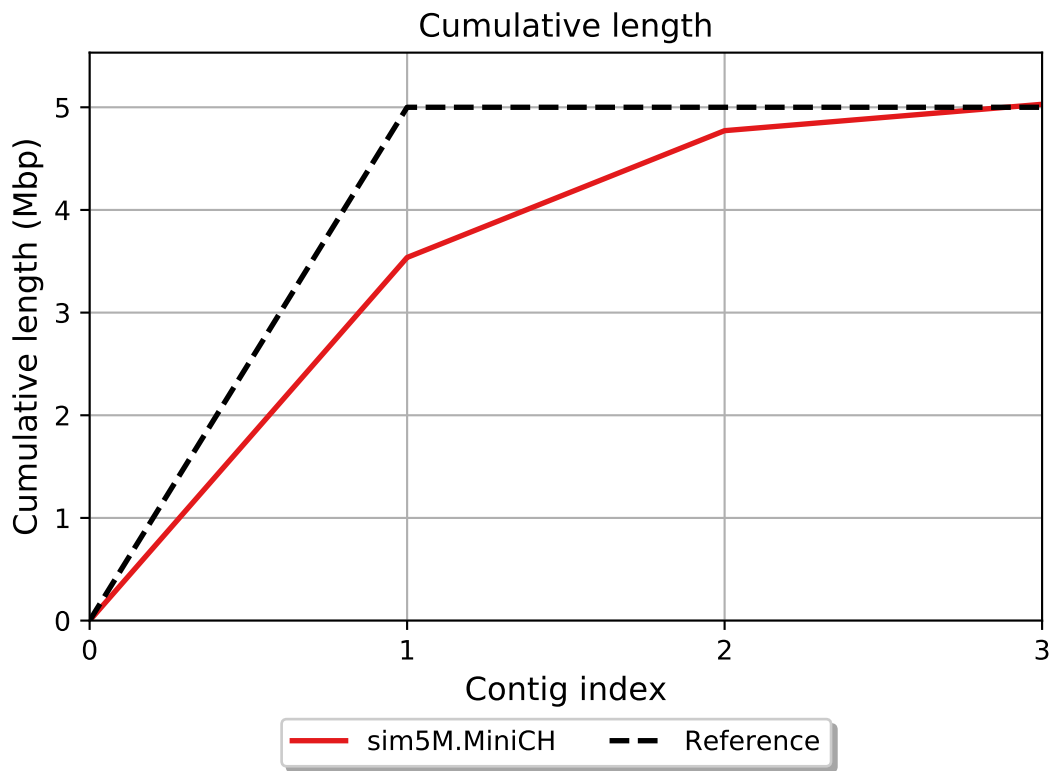


sim5M.MiniCH

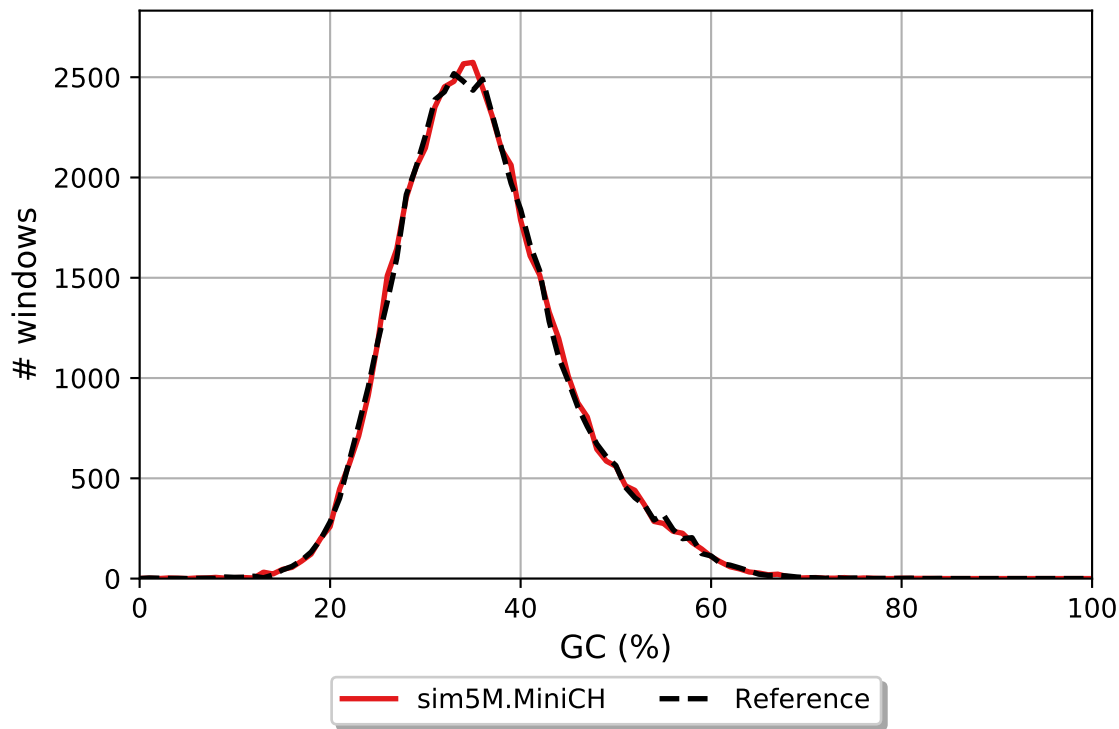
NGx



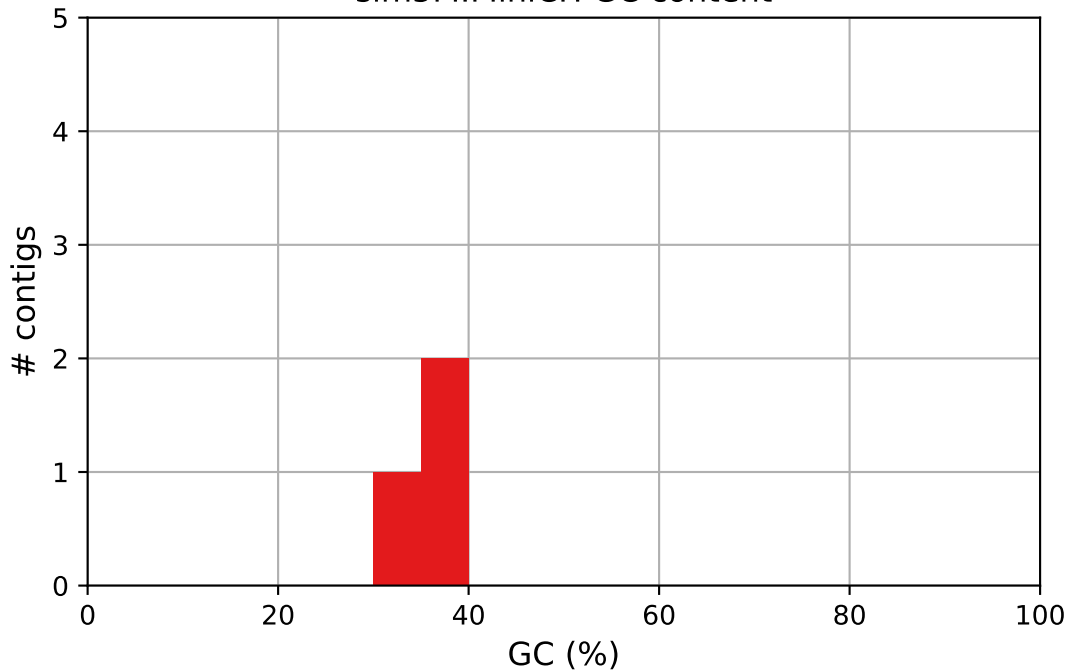
— sim5M.MiniCH



GC content

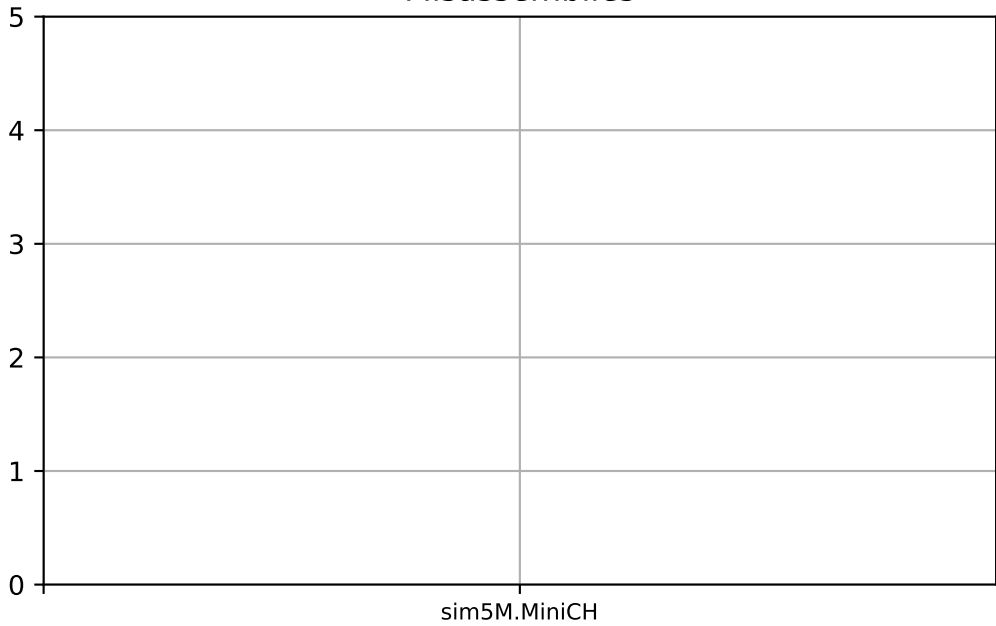


sim5M.Minich GC content

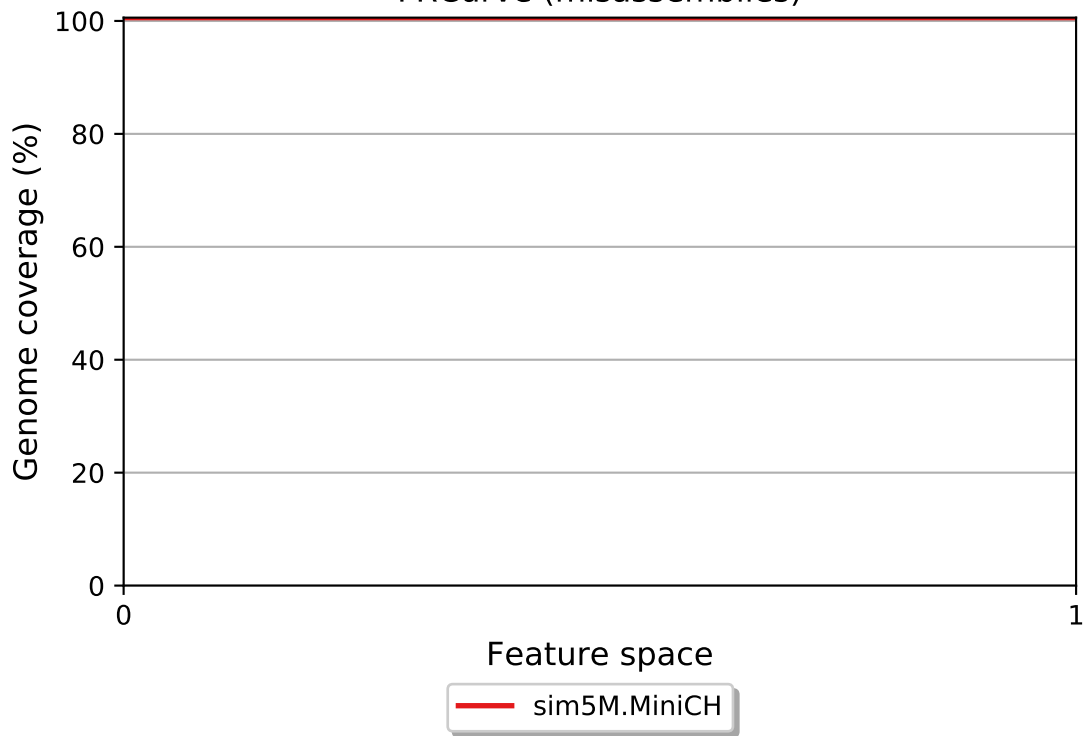


sim5M.Minich

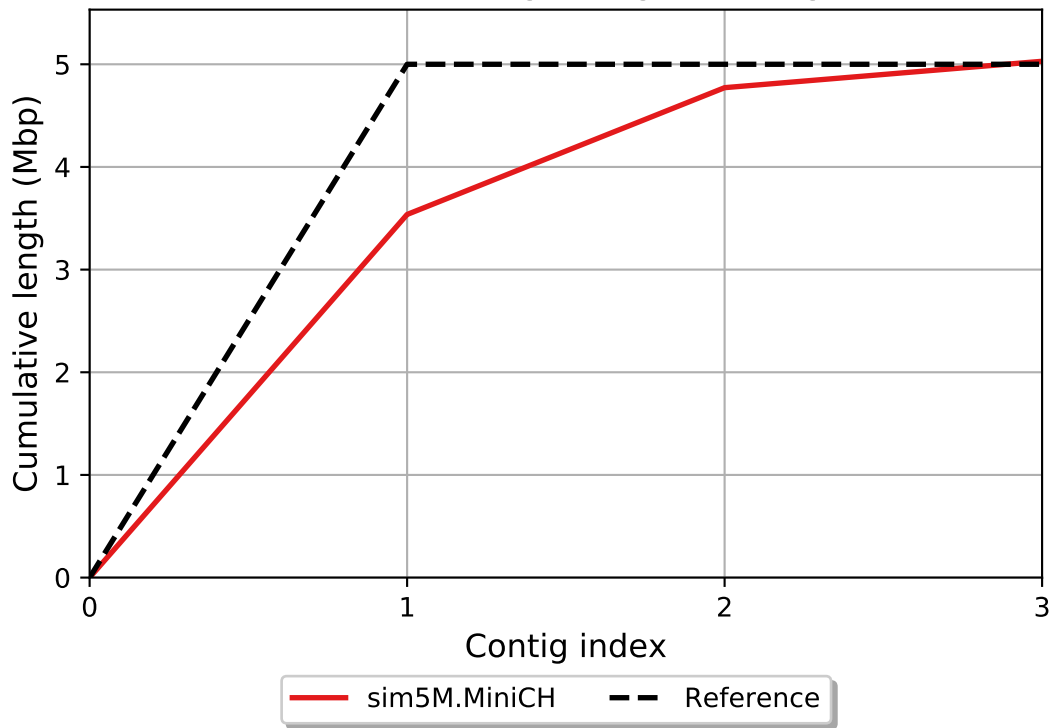
Misassemblies



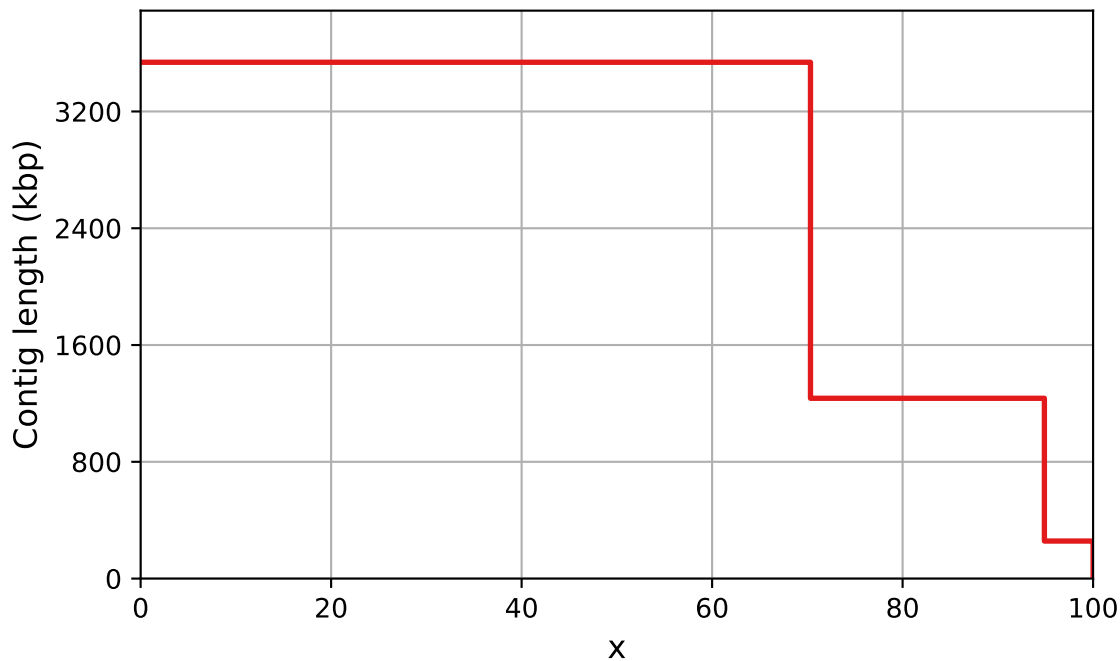
FRCurve (misassemblies)



Cumulative length (aligned contigs)

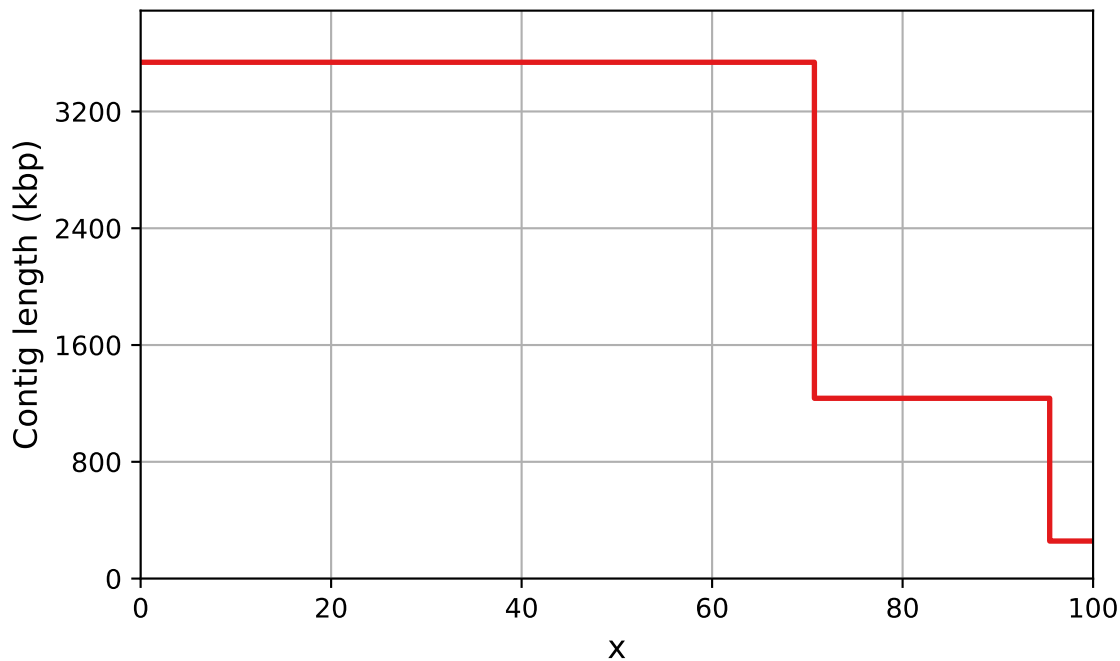


NAx



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NGAx



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